Title: Reduced CXCL1 expression promotes context-dependent tumour aggressiveness in triple-negative breast cancer

Authors (ORCID ID): Clàudia Martínez Miralles[1], Evangelos Manousakis[1], Cristina Moreta-Moraleda[1], Houda Baccara[2], Luke Mahon[1], Laia Liñán Franquet[1], Montserrat Montañes i Albó[1], Anna Tomás Pujolá[1] , Roberto Ferrari[2] and Roni H. G. Wright[1*]

Affiliations:

1. Department of Biomedical Sciences, Faculty of Medicine and Health Sciences, Universitat Internacional de Catalunya, Barcelona, Spain.
2. Department of Chemistry, Life Sciences and Environmental Sustainability, University of Parma, Parma, Italy.

***Corresponding author:** Roni Wright

Email: rhgwright@uic.es

Supplementary Information

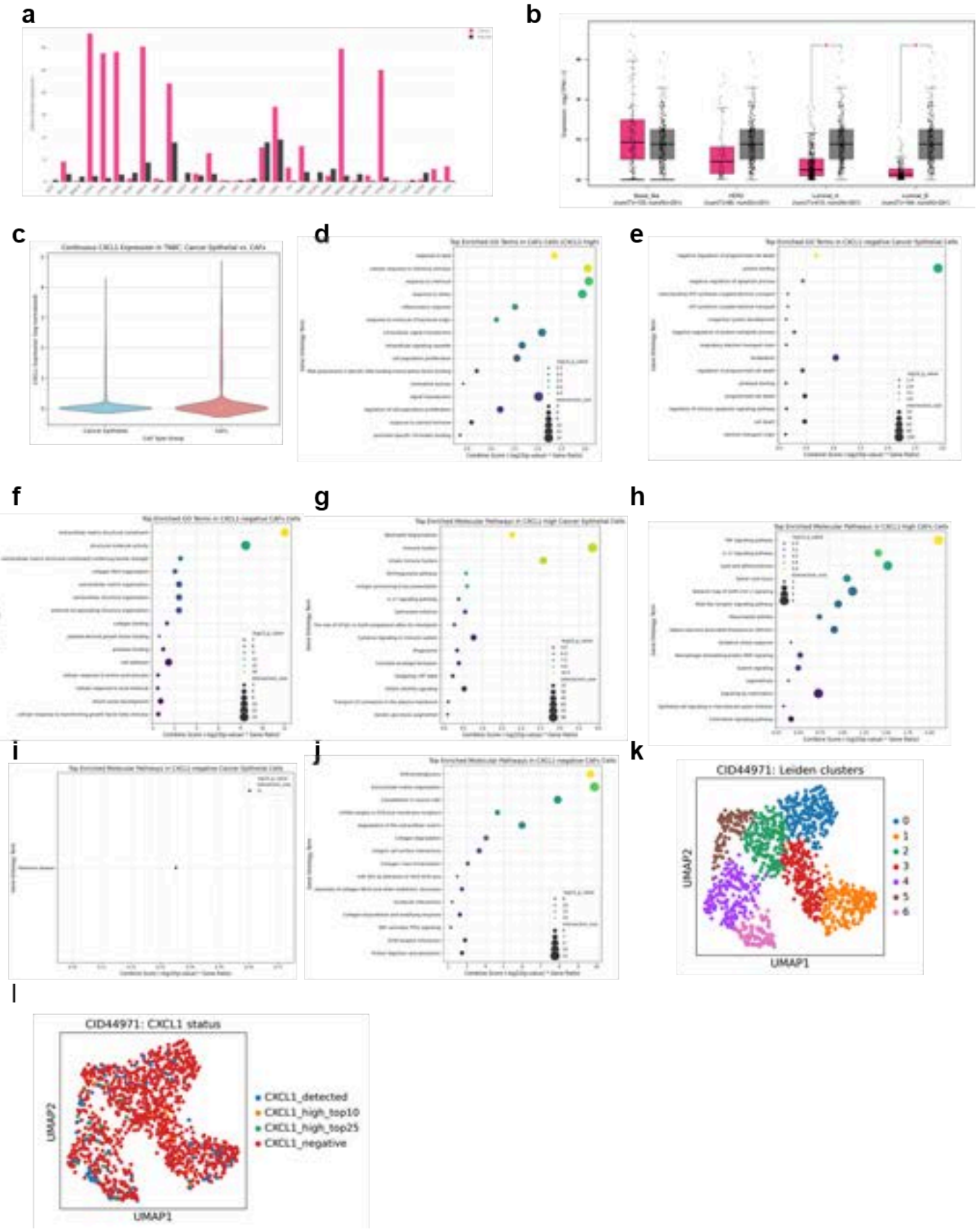
Supplementary Information 1. Supplementary Figures S1-S4

Supplementary Information 2. Supplementary Materials and Methods

Supplementary Information 3. Supplementary Tables S1-S8

Supplementary Information 1. Supplementary Figures

Fig.S1 Complementary data to figure 1 related to CXCL1 median expression in different



cancer types. **(a)** CXCL1 expression in all cancer types analysed in GEPIA2 database.

CXCL1 expression in the tumour tissue is presented in pink-coloured bars and the others relate to the expression in normal tissue. Expression is presented in transcript per million (TPM). **(b)** CXCL1 expression in different breast cancer subtypes retrieved from GEPIA2. Samples from tumour tissue are in colour purple while samples from normal tissue are in grey. **(c)** Distribution of the CXCL1 expression through the cancer epithelial and CAF cell types in single cell analysis. **(d)** Biological process GO analysis for the CXCL1 positive cells in CAFs cell type. The size of the dot represents the percentage of genes in the set. **(e)** Biological process GO analysis for the CXCL1 negative cells in cancer epithelial cell type. The size of the dot represents the percentage of genes in the set. **(f)** Biological process GO analysis for the CXCL1 negative cells in CAFs cell type. The size of the dot represents the percentage of genes in the set. **(g)** Molecular function GO analysis for the CXCL1 positive cells in cancer epithelial cell type. The size of the dot represents the percentage of genes in the set. **(h)** Molecular function GO analysis for the CXCL1 positive cells in CAFs cell type. The size of the dot represents the percentage of genes in the set. **(i)** Molecular function GO analysis for the CXCL1 negative cells in cancer epithelial cell type. The size of the dot represents the percentage of genes in the set. **(j)** Molecular function GO analysis for the CXCL1 negative cells in CAFs cell type. The size of the dot represents the percentage of genes in the set. **(k)** UMAP plot showing the distribution of the different leiden clusters from spatial transcriptomics analysis. **(l)** UMAP plot showing the distribution of CXCL1 levels in the different leiden clusters

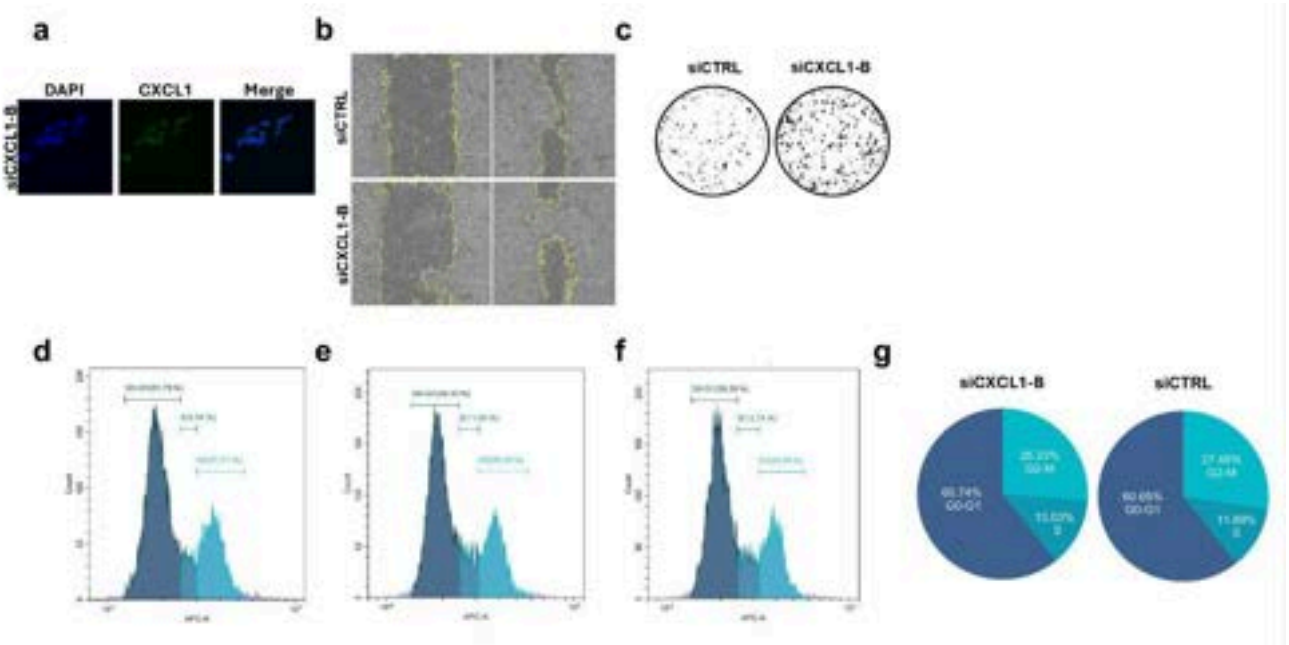


Fig.S2 Complementary siCXCL1-B data to figure 2 phenotypic assays. **(a)** Immunofluorescence images from MDA-MB-231 CXCL1 KD cells quantified in figure 2. **(b,c)** Images of the percentage of closed gap in 48h in an scratch assay and colony formation capacity comparing CXCL1 knock-down with control conditions with siCXCL1-2. **(d-f)** Raw plots retrieved from CytoFlex Software when determining the effect of the silencing in the control and both siRNA conditions. **(g)** Processed data on the effect of the silencing using the siCXCL1-B in the cell cycle

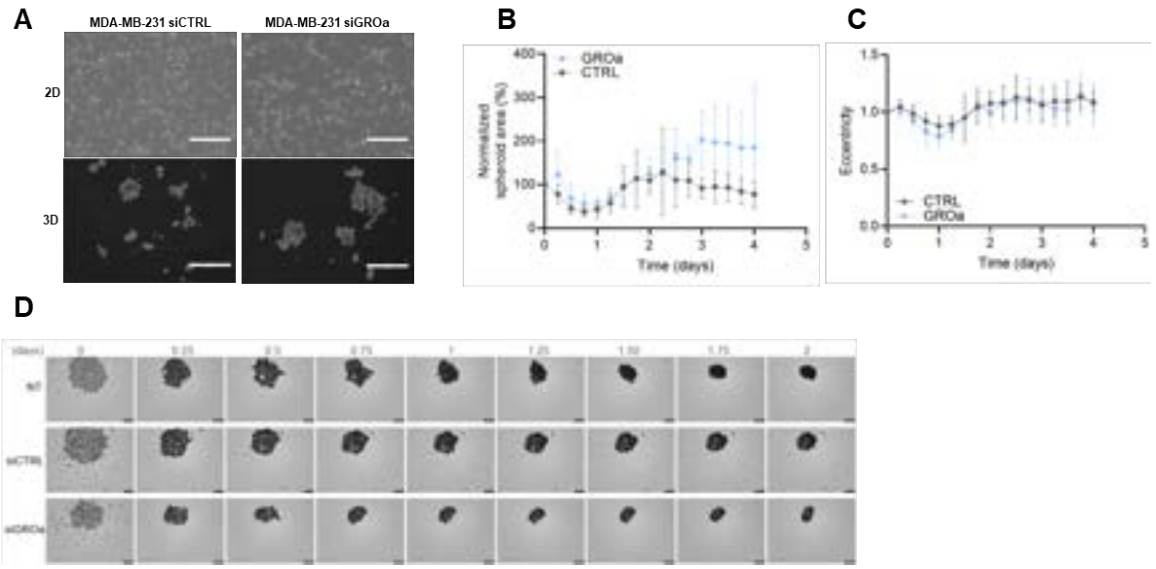


Fig.S3 Complementary data to figure 3 spheroid analysis. **(a)** Representative images showing morphological differences between the 2D and 3D cultures in transfected cells compared to the transfection control. Scale = 300 µm. **(b)** Normalized spheroid area in percentage analysis obtained from Incucyte SX5 (Sartorius). Images were obtained every 6 hours for 4 days. **(c)** Eccentricity measured in spheroids from different transfection conditions obtained from Incucyte SX5 (Sartorius). Images captured every 6 hours for 4 days. **(d)** Brightfield images captured by Incucyte SX5 (Satrorius) from day 0 to day 2 for the different transfection conditions. Scale = 400 µm

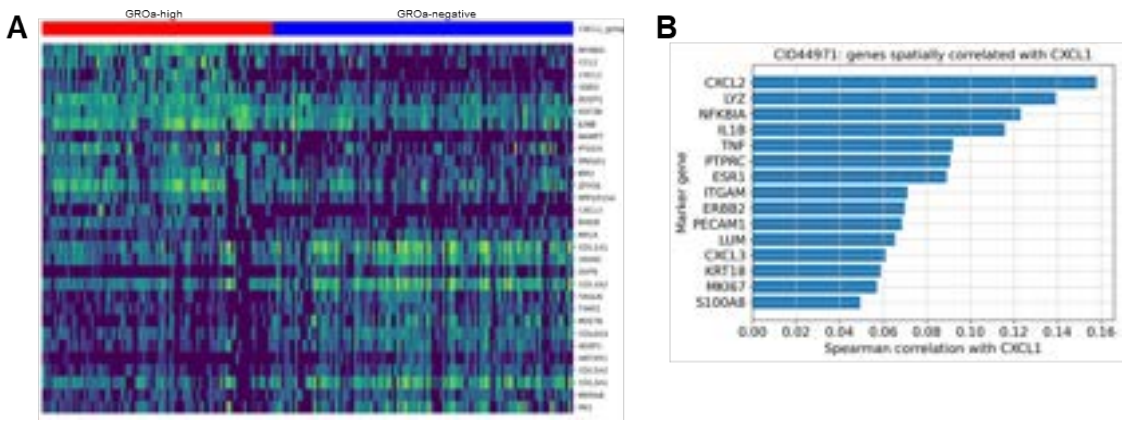


Fig.S4 Complementary data to figure 4 single cell and spatial transcriptomics analysis. **(a)** Heatmap comparing the genetic signature in CXCL1-high or CXCL1-negative cells in CAFs cell type. **(b)** Genes spatially correlated with CXCL1 expression in spatial transcriptomics. Correlation is represented using Spearman correlation considering a weak correlation from 0-0.39, 0.4-0.59 moderate and 0.6-1 strong

Supplementary Information 2. Supplementary Materials and Methods

Suppliers and catalog numbers of the reagents used in Materials and Methods section.

Material	Supplier	Catalog number
DMEM	Merck Group	D5671
FBS	ThermoFisher Scientific	17479633
P/S	Merck Group	P0781
Glutamine	LabClinics	X0551-100
non-adherent hydrogel coated plates	Merck Group	CLS3471-24EA
DMEM/F12	ThermoFisher Scientific	11320-074
B27	ThermoFisher Scientific	17504044
EGF	STEMCELL Technologies	78006.1
6-well plates	Merck Group	CLS3471-24EA
Lipofectamine™ 2000	ThermoFisher Scientific	11668-019
CXCL1 siRNA	ThermoFisher Scientific	4392420 (s6215, s6217)
NZY Total RNA Isolation kit	NZYtech	MB13402

High-Capacity cDNA Reverse Transcription Kit	ThermoFisher Scientific	4368814
SsoAdvanced Universal SYBR® Green Supermix	Bio-Rad Laboratories	1725272
µ-Slide 8-wells high chambers	ibidi GmbH	80806
Paraformaldehyde	Merck Group	F8775
Triton-X100	Merck Group	Cat#X100-1L
BSA	Merck Group	10735086001
CXCL1 antibody	Abcam, Danaher Corporation	ab89318
Alexa Fluor 488 goat α-Rabbit	ThermoFisher Scientific	A11008
Antifade mounting media with DAPI	ThermoFisher Scientific	S36938
Leica Confocal DMi8	Leica Microsystems GmbH	DM6000
Invasion chambers	Merck Group	PTEP24H48
24-well plate	Merck Group	CLS3473-24EA
Crystal violet	Merck Group	V5265-250ML
Methanol	VWR, Avantor	20847.307
EVOS M5000 Imaging System	ThermoFisher Scientific	AMF5000
ImageJ	Developer: Wayne Rasband	
Cytoflex S cytometer	Beckman Coulter, Danaher Corporation	V4-B1-Y4-R3
CytExpert software	Beckman Coulter, Danaher Corporation	
96-wells U-bottom plate	ThermoFisher Scientific	174929
LIVE/DEAD™ Viability/Cytotoxicity Kit, for mammalian cells	ThermoFisher Scientific	L3224
Incucyte SX5	Sartorius AG	4816
21G needle	VWR, Avantor	613-3935
Geltrex	ThermoFisher Scientific	A1569601

PolyFreeze Tissue Freezing Medium	Merck Group	SHH0026-6X120ML
Cryostat	Palex Group	HM525NX
Alexa Fluor 568 α-Mouse	ThermoFisher Scientific	A1101
Hoechst 33258	Merck Group	14530-100MG
KAP1 antibody	Abcam, Danaher Corporation	ab22553
Mounting media	SouthernBiotech	0100-01

Single Cell Analysis

Analysis was performed in Python environment using the packages *Scanpy, AnnData, pandas, NumPy, seaborn,Matplotlib* and *gseapy*. Expression matrix was loaded from Matrix Market format together with the corresponding gene and barcode identifiers. Apart from the ones established on the metadata, there was no new cell-type annotation in this work-flow. Gene symbols were standardised to uppercase to ensure consistent gene matching across the expression matrix and marker sets. Count values were normalised to a total of 10000 counts per cell and log-transformed using log1p. Log-normalised values were used for CXCL1 detection, visualization, correlation-style summaries, differential expression analysis and heatmap generation.

Determination of CXCL1 levels in different breast cancer subtypes and cell type

CXCL1 expression was extracted from the log-normalised expression matrix. Cells were classified as $CXCL1^{+}$ when the log-normalised expression value was greater than zero. Binary metadata was generated to indicate $CXCL1^{+}$ and $CXCL1^{-}$ cells. This threshold was used as a detection criteria and should be interpreted as detectable transcript abundance after normalisation rather than as a biological expression cutoff.

In order to determine patient-level aggregation across breast cancer subtypes, bias caused by unequal number of cells per patient was reduced by performing subtype comparisons at

the patient level. For each patient, $CXCL1^+$ cells were calculated within each major cell type category by averaging the binary $CXCL1^+$ variable across cells grouped by patient identifier, tumor subtype and major cell type. In this analysis, the patient was treated as the unit of comparison for subtype-level summaries. Main cell populations selected for comparison were cancer epithelial cells, cancer-associated fibroblasts and myeloid cells. Patient-level $CXCL1^+$ fractions were visualized using boxplots. Breast cancer subtype was plotted on the x-axis, and the patient-level $CXCL1^+$ fraction was plotted on the y-axis. Major cell types were included as a grouping variable to compare CXCL1 detection across different compartments. Subtypes were consistently named across plots and outliers were optionally suppressed for graphical clarity affecting only visualization and did not alter the patient-level values.

CXCL1$^{\pm}$ distribution and differential expression in TNBC cancer epithelial cells and CAFs

Further analysis was performed in TNBC samples to compare CXCL1 behaviour in CAFs and cancer epithelial cells. Cells were first filtered to only maintain TNBC subtype and then splitted in the two cell populations of interest. Distribution of total CXCL1 or positive expression was inspected using violin plots by cell type. In the TNBC subset, cells were classified according to CXCL1 expression. $CXCL1^-$ cells were defined as cells with zero expression of CXCL1. CXCL1 positive cells were subclassified in CXCL1-high and CXCL1-low. CXCL1-high corresponded to those whose expression levels were above the 90th percentile while CXCL1-low were the rest. Because CXCL1-negative cells were predominant in the sample, for each cell-type specific comparison, the CXCL1-negative group was limited to approximately five times the number of CXCL1-high cells. This was performed in order to reduce group imbalance while retaining broader biological variability.

Differential expression analysis was performed separately for TNBC CAFs and TNBC cancer epithelial cells. In each population, CXCL1-high cells were compared with the $CXCL1^-$ reference group using the Wilcoxon rank-sum test implemented in Scanpy. Genes were considered differentially expressed when adjusted P value was less than 0.05 and the absolute log fold change was greater than 0.25. In order to focus on biologically relevant

genetic signatures, CXCL1 was excluded from the analysis as well as mitochondrial and ribosomal protein genes. Mitochondrial genes were identified by the MT-prefix and ribosomal genes by RPS or RPL prefixes. Differential expression was plotted in a heatmap. The top upregulated and downregulated genes were filtered from the gene list and both top 15 ranked by adjusted P value were used to generate heatmaps comparing CXCL1-high and CXCL1- cells. Heatmaps were generated with seaborn clustermap and cells were annotated by CXCL1 expression groups to facilitate the interpretation of the different groups.

Gene Ontology enrichment analysis was performed using *gseapy* with the Enrichr interface. Enrichment was assessed for the GO Biological Process 2021 and GO Molecular Functions 2021 gene-set libraries. Separate enrichment analyses were performed for genes enriched in CXCL1-high or CXCL1- subsets, checking the CAFs and the cancer epithelial subgroups separately. For each analysis, terms were ranked by adjusted P value, and the top enriched terms were visualized using bubble plots.

Spatial Transcriptomic Analysis

Analysis was performed in Python using *Scanpy, AnnData, Squidpy, pandas, NumPy, SciPy* and *Matplotlib*. Filtered 10x Genomics Matrix Market expression files corresponding to CID44971 were loaded into AnnData object. Spot-level spatial coordinates, tissue-position information, image scale factors and available metadata were matched to the expression matrix using the corresponding barcode identifiers. Quality control metrics were calculated for each Visium spot, including total UMI counts, number of detected genes and percentage of mitochondrial transcripts. Mitochondrial genes were identified by gene symbols labelled as MT-. Since the analysis used filtered count matrices, additional filtering was conservative. Spots were retained if they were located within tissue and satisfied all of the following criteria: at least 500 UMI counts, 200 detected genes and no more than 30% mitochondrial counts. The original UMI count matrix was preserved prior to normalisation. Counts were library-size normalised to 10000 counts per spot and log-transformed using log1p. The full log-normalised expression matrix was stored before highly variable gene selection to allow

posterior extraction of genes that might not be retained among highly variable genes. Highly variable genes were selected using the Seurat method implemented in Scanpy, retaining the top 3000 genes. Expression values for highly variable genes were scaled with a maximum value of 10. Principal component analysis was performed using 30 components. A nearest-neighbor graph was constructed using 15 neighbors and 30 principal components. Uniform manifold approximation and projection was used for visualization of transcriptional similarity between spots. Expression-defined spatial domains were identified using Leiden clustering at a resolution of 0.6.

Determination of the architecture linked to CXCL1 expression

CXCL1 expression was extracted from the full log-normalised expression matrix rather than from the highly variable gene-filtered matrix to ensure that CXCL1 was retained for analysis. For each spot, the log-normalised CXCL1 value was stored as a spot-level metadata variable. Spots with log-normalised CXCL1 expression higher than zero were classified as CXCL1-detected. To identify regions with a stronger CXCL1 signal, thresholds were defined among CXCL1-detected spots. Spots in the upper 25% of CXCL1 expression were labelled as CXCL1-high top 25%, and spots in the upper 10% were classified as CXCL1-high top 10%. The upper 10% group was used as the stringent CXCL1-high category for differential expression analysis. These thresholds were defined within CID44971 and were therefore interpreted as sample-relative categories rather than universal biological cutoffs.

CXCL1 expression was visualized on the corresponding hematoxylin and eosin tissue image using Visium spatial coordinates. Log-normalised CXCL1 expression was plotted to assess the spatial intensity and distribution of CXCL1 across the tissue section. A categorical CXCL1 status map was also generated in order to distinguish between CXCL1-negative, CXCL1-detected, CXCL1-high top 25% and CXCL1-high top 10% spots. Leiden clusters were projected onto the tissue image to compare CXCL1-rich regions with expression-defined spatial domains.

Transcriptional analysis of CXCL1$^{\pm}$ spatial regions

To evaluate transcriptional features associated with CXCL1-positive spatial regions maker expression was assessed in three predefined gene panels. The immune marker panel included CD68, CD163, S100A8, S100A9, CD8A and GZMB. The stemness-associated panel included CD44, ALDH1A, VIM, ITGA6 and KRT14. The epithelial-to-mesenchymal transition marker panel included EPCAM, CDH1, VIM and CXCL1. Prior to visualization, marker lists were filtered to retain only genes detected in spatial transcriptomics dataset. Dot blots were generated comparing CXCL1-negative and CXCL1-high spatial regions, the dot size represents the number of Visium spots while the dot color represents the mean expression level of that marker. Expression values were standard scaled by gene to facilitate the comparison of relative expression patterns across the two CXCL1-defined spatial groups. Marker expression patterns were interpreted as spot-level enrichment profiles rather than single-cell identity assignments.

Supplementary Information 3. Supplementary Tables S1-S8

Title: Reduced CXCL1 expression promotes context-dependent tumour aggressiveness in triple-negative breast cancer

Authors (ORCID ID): Clàudia Martínez Miralles (1), Evangelos Manousakis (1), Cristina Moreta-Moraleda (1), Houda Baccara (2), Luke Mahon (1), Laia Liñán Franquet (1), Montserrat Montañes i Albó (1), Anna Tomás Pujolá (1) , Roberto Ferrari (2) and Roni H. G. Wright (1)*

Affiliations:

(1) Department of Biomedical Sciences, Faculty of Medicine and Health Sciences, Universitat Internacional de Catalunya, Barcelona, Spain.

(2) Department of Chemistry, Life Sciences and Environmental Sustainability, University of Parma, Parma, Italy.

*Corresponding author: Roni Wright

Email: rhgwright@uic.es

Supplementary tables titles and legends.

Supplementary table 1. List of the primers used in gene expression analysis. In the table is presented the name of the target and the sequence of the forward and reverse in 5□3' sense.

Supplementary table 2. Supplementary data regarding the top hits in the figure 1A. Hits were grouped in order to show the results in a comprehensive way. Affections belonging to the different groups are listed above.

Supplementary table 3. Supplementary data complementing figure 1B. Bibliography referencing the different groups of diseases that literature implied CXCL1 to have a role.

Supplementary table 4. Full name of the abbreviations used in figure 1C-D.

Supplementary table 5. MDA-MB-231 RNA sequencing used to identify the different genes used as targets for stemness.

Supplementary table 6. Gene ontology results for single cell analysis.

Supplementary table 7. Log1p expression values used to create the heatmap comparing CXCL1-high vs. CXCL1-negative in single cell analysis.

Supplementary table 8. Expression values used to create the dot blots for different panels comparing CXCL1-high vs. CXCL1-negative in spatial transcriptomics analysis.

Gene and oligonucleotide	**Sequence (5'-->3')**
ACKR1	
Forward	CCCTCAACTGAGAACTCAAGTC
Reverse	AGGTTGGCACCATAGTCTCCA
ALU	
Forward	CGAGGCGGGTGGATCATGAGGT
Reverse	TTTTTTGAGACGGAGTCTCGC
Chicken 16S	
Forward	CTCTAGCCCGACAAACTCGT
Reverse	CTATCGCCTATACTGGGACAAT
CXCR2	
Forward	CCTGTCTTACTTTTCCGAAGGAC
Reverse	TTGCTGTATTGTTGCCCATGT
GAPDH	
Forward	GTCTCCTCTGACTTCAACAGCG
Reverse	ACCACCCTGTTGCTGTAGCCAA
CXCL1	
Forward	GATTGTGCCTAATGTGTT
Reverse	ATCCAGATTGAACTAACTTG
KISS1	
Forward	CTGCTTTTCCTCTGTGCCAC
Reverse	CCAGGGATTCTAGCTGCTGG
MUC5A	
Forward	GCGACTGTCTTCCCATCTCT
Reverse	GTCTTGTAGTGGAAGCTGCC

Group	Affections
Cardiovascular System	Cardiovascular damage
	Cardiovascular reperfusion
Pathological conditions	COPD
	Inflammations
	Shock, Hemmorhagic
Respiratoy tract affections	Pneumonia
	Bronchial Hyperreactivities
Digestive system	Liver neoplasm
	Liver cell carcinoma
	Autoimmune Hepatitides
	Malignant neoplasm of colon

Group	Paper of reference
Cardiovascular System	M. -M. Wu, Y. -C. Yang, Y. -X. Cai, et al., "Anti-CTLA-4 m2a Antibody Exacerbates Cardiac Injury in Experimental Autoimmune Myocarditis Mice By Promoting Ccl5-Neutrophil Infiltration" Advanced Science 11 (2024) 2400486. https://doi.org/10.1002/advs.202400486
Pathological conditions	A. D. Schwab, A. J. Nelson, A. M. Gleason, O. W. Schanze, T. A. Wyatt, D. D. Shinde, et al., "Aconitate decarboxylase 1 mediates the acute airway inflammatory response to environmental exposures" Frontiers Immunology 15 (2024) 1432334. https://doi.org/10.3389/fimmu.2024.1432334
Respiratoy tract affections	S. Gunasekara, M. T. Selvan, C. L. Murphy, S. Shatnawi, S. Cowan, S. More, et al., "Characterization of Neutrophil Functional Responses to SARS-CoV-2 Infection in a Translational Feline Model for COVID-19", International Journal of Molecular Sciences 25 (2024) 1005. https://doi.org/10.3390/ijms251810054
Digestive system	Y. Deng, Z. Zhao, M. Sheldon, Y. Zhao, H. Teng, C. Martinez, et al., "LIFR regulates cholesterol-driven bidirectional hepatocyte–neutrophil cross-talk to promote liver regeneration" Nature Metabolism 6 (2024): 1756-1774. https://doi.org/10.1038/s42255-024-01110-y

TCGA	Detail
ACC	Adrenocortical carcinoma
BRCA	Breast invasive carcinoma
CESC	Cervical squamous cell carcinoma and endocervical carcinoma
CHOL	Cholangio carcinoma
COAD	Colon adenocarcinoma
DLBC	Lymphoid Neoplasm Diffuse Large B-cell Lymphoma
ESCA	Esophaegal carcinoma
HNSC	Head and Neck squamous cell carcinoma
KICH	Kidney Chromophobe
LUSC	Lung squamous cell carcinoma
PCPG	Pheochromocytoma and Paraganglioma
READ	Rectum adenocarcinoma
SARC	Sarcoma
STAD	Stomach adenocarcinoma
THYM	Thymoma

GeneID	padj	-log10(padj)	pvalue	lfcSE	stat	log2FoldChange	baseMean	Symbol	Description
110806276	9,29E-20	1,90E+01	3,11E-20	1	9	10,89532391	216,49	LINC02474	long intergenic non-protein coding RNA 2474
345557	6,43E-15	1,42E+01	2,50E-15	1	8	9,37098947	146,73	PLCXD3	phosphatidylinositol specific phospholipase C X domain containing 3
4973	1,90E-13	1,27E+01	7,74E-14	1	7	8,91476419	54,87	OLR1	oxidized low density lipoprotein receptor 1
84189	6,68E-13	1,22E+01	2,77E-13	1	7	8,72984134	48,22	SLITRK6	SLIT and NTRK like family member 6
374462	7,35E-27	2,61E+01	2,03E-27	1	11	7,90602651	198,26	PTPRQ	protein tyrosine phosphatase receptor type Q
100505817	8,34E-211	2,10E+02	9,41E-213	0	31	7,76398346	1572,53	LINC02582	long intergenic non-protein coding RNA 2582
3932	1,97E-09	8,71E+00	9,31E-10	1	6	7,46259431	20,09	LCK	LCK proto-oncogene, Src family tyrosine kinase
347731	2,53E-09	8,60E+00	1,20E-09	1	6	7,41762348	19,4	LRRTM3	leucine rich repeat transmembrane neuronal 3
105370700	7,72E-09	8,11E+00	3,74E-09	1	6	7,21875187	16,92	LOC1053707	uncharacterized LOC105370700
140801	1,19E-08	7,92E+00	5,83E-09	1	6	7,14460334	16,1	RPL10L	ribosomal protein L10 like
645553	1,27E-08	7,90E+00	6,21E-09	1	6	7,13283762	15,97	IGFL2-AS1	IGFL2 antisense RNA 1
7092	1,36E-08	7,87E+00	6,70E-09	1	6	7,11534187	15,76	TLL1	tolloid like 1
147920	4,42E-08	7,35E+00	2,22E-08	1	6	6,78112051	24,58	IGFL2	IGF like family member 2
283392	1,12E-07	6,95E+00	5,75E-08	1	5	6,74330187	12,2	TRHDE-AS1	TRHDE antisense RNA 1
251	7,13E-08	7,15E+00	3,62E-08	1	6	6,67780433	22,87	ALPG	alkaline phosphatase, germ cell
10225	2,11E-27	2,67E+01	5,74E-28	1	11	6,62119533	122,8	CD96	CD96 molecule
100616396	9,96E-08	7,00E+00	5,09E-08	1	5	6,6122616	21,86	MIR4712	microRNA 4712
101927239	3,05E-07	6,52E+00	1,60E-07	1	5	6,55236411	10,68	LINC01989	long intergenic non-protein coding RNA 1989
105374007	1,52E-07	6,82E+00	7,87E-08	1	5	6,53795474	20,77	LOC1053740	uncharacterized LOC105374007
101927332	3,48E-07	6,46E+00	1,83E-07	1	5	6,52755791	10,48	LINC01582	long intergenic non-protein coding RNA 1582
105370311	1,58E-06	5,80E+00	8,63E-07	1	5	6,25883309	8,73	LOC1053703	uncharacterized LOC105370311
105373331	1,53E-06	5,82E+00	8,34E-07	1	5	6,2513666	8,67	LOC1053733	uncharacterized LOC105373331
793	2,37E-06	5,63E+00	1,30E-06	1	5	6,18052237	8,25	CALB1	calbindin 1
105370356	4,05E-06	5,39E+00	2,26E-06	1	5	6,10109392	7,8	LOC1053703	uncharacterized LOC105370356
105370422	4,56E-06	5,34E+00	2,55E-06	1	5	6,02433608	7,39	LINC02300	long intergenic non-protein coding RNA 2300
250	1,62E-79	7,88E+01	1,35E-80	0	19	5,9647745	300,2	ALPP	alkaline phosphatase, placental
2313	1,51E-11	1,08E+01	6,56E-12	1	7	5,92143573	38,01	FLI1	Fli-1 proto-oncogene, ETS transcription factor
147495	1,14E-05	4,94E+00	6,55E-06	1	5	5,85135369	6,55	APCDD1	APC down-regulated 1
56979	5,10E-06	5,29E+00	2,86E-06	1	5	5,80645136	12,6	PRDM9	PR/SET domain 9
5239	9,33E-93	9,20E+01	6,08E-94	0	21	5,76783967	331,12	PGM5	phosphoglucomutase 5
440107	1,60E-05	4,80E+00	9,22E-06	1	4	5,7655951	6,18	PLEKHG7	pleckstrin homology and RhoGEF domain containing G7
105374491	1,82E-05	4,74E+00	1,05E-05	1	4	5,74331195	6,1	LOC1053744	uncharacterized LOC105374491
101927318	9,35E-06	5,03E+00	5,32E-06	1	5	5,68671486	11,58	AQP5-AS1	AQP5 and AQP2 antisense RNA 2
8581	1,14E-05	4,94E+00	6,55E-06	1	5	5,63959775	11,25	LY6D	lymphocyte antigen 6 family member D
53904	3,61E-05	4,44E+00	2,13E-05	1	4	5,61255485	5,57	MYO3A	myosin IIIA
159963	3,99E-05	4,40E+00	2,36E-05	1	4	5,57681422	5,44	SLC5A12	solute carrier family 5 member 12
282763	4,09E-05	4,39E+00	2,42E-05	1	4	5,56516027	5,38	OR51B5	olfactory receptor family 51 subfamily B member 5
100500802	4,67E-05	4,33E+00	2,77E-05	1	4	5,53529534	5,28	MIR3685	microRNA 3685
650226	5,63E-05	4,25E+00	3,36E-05	1	4	5,49329285	5,12	LOC650226	ankyrin repeat domain containing 26 pseudogene
107985534	8,29E-10	9,08E+00	3,86E-10	1	6	5,37769371	71,42	LOC1079855	uncharacterized LOC107985534
10599	4,15E-05	4,38E+00	2,46E-05	1	4	5,33830684	9,17	SLCO1B1	solute carrier organic anion transporter family member 1B1
29119	2,61E-09	8,58E+00	1,24E-09	1	6	5,33490331	25,49	CTNNA3	catenin alpha 3
107984832	4,41E-05	4,36E+00	2,61E-05	1	4	5,30943381	9	LOC107984832	
85329	1,35E-04	3,87E+00	8,24E-05	1	4	5,29632023	4,47	LGALS12	galectin 12
64284	1,15E-23	2,29E+01	3,46E-24	1	10	5,16922745	68,49	RAB17	RAB17, member RAS oncogene family
100874137	9,01E-05	4,05E+00	5,45E-05	1	4	5,14508817	8,05	LINC00351	long intergenic non-protein coding RNA 351
3814	5,94E-216	2,15E+02	6,26E-218	0	32	5,13744364	708,36	KISS1	KiSS-1 metastasis suppressor
751580	9,26E-05	4,03E+00	5,61E-05	1	4	5,13702269	7,98	LINC00106	long intergenic non-protein coding RNA 106
80177	7,26E-63	6,21E+01	8,64E-64	0	17	5,10503494	189,78	MYCT1	MYC target 1
101926978	7,73E-18	1,71E+01	2,74E-18	1	9	5,0526946	49,28	LINC01111	long intergenic non-protein coding RNA 1111
29091	1,75E-10	9,76E+00	7,92E-11	1	7	4,99954355	27,07	STXBP6	syntaxin binding protein 6
1016	9,85E-44	4,30E+01	1,82E-44	0	14	4,97142006	126,5	CDH18	cadherin 18
84779	1,87E-04	3,73E+00	1,16E-04	1	4	4,95521738	7,08	NAA11	N-alpha-acetyltransferase 11, NatA catalytic subunit
101929750	1,84E-04	3,74E+00	1,14E-04	1	4	4,95412808	7,07	LOC1019297	uncharacterized LOC101929750
112268434	2,76E-10	9,56E+00	1,26E-10	1	6	4,94939244	26,33	LOC112268434	
109616991	2,04E-04	3,69E+00	1,27E-04	1	4	4,93288608	6,97	SNORD19C	small nucleolar RNA, C/D box 19C
105376577	7,88E-08	7,10E+00	4,01E-08	1	5	4,88950269	18,99	LOC1053765	uncharacterized LOC105376577
654835	2,52E-04	3,60E+00	1,58E-04	1	4	4,88631522	6,72	FAM138C	family with sequence similarity 138 member C
100302137	2,54E-04	3,60E+00	1,59E-04	1	4	4,87260349	6,7	MIR1914	microRNA 1914
572558	2,60E-04	3,59E+00	1,63E-04	1	4	4,86751664	6,66	PGM5-AS1	PGM5 antisense RNA 1
3481	1,29E-68	6,79E+01	1,36E-69	0	18	4,80619127	196,82	IGF2	insulin like growth factor 2
723961	2,42E-68	6,76E+01	2,56E-69	0	18	4,79771171	195,7	INS-IGF2	INS-IGF2 readthrough
105377180	2,54E-05	4,60E+00	1,48E-05	1	4	4,78424699	11,67	LINC02008	long intergenic non-protein coding RNA 2008
107985164	1,70E-07	6,77E+00	8,81E-08	1	5	4,78169379	17,6	LOC1079851	uncharacterized LOC107985164
3169	7,25E-30	2,91E+01	1,85E-30	0	11	4,77291095	81,49	FOXA1	forkhead box A1
112268468	2,08E-11	1,07E+01	9,08E-12	1	7	4,75218003	28,67	LOC1122684	uncharacterized LOC112268468
255928	4,07E-04	3,39E+00	2,59E-04	1	4	4,74700866	6,16	SYT14	synaptotagmin 14
9627	2,99E-70	6,95E+01	3,04E-71	0	18	4,72716081	198,19	SNCAIP	synuclein alpha interacting protein
692197	2,89E-05	4,54E+00	1,69E-05	1	4	4,72396466	11,33	SNORD77	small nucleolar RNA, C/D box 77
102465454	4,83E-04	3,32E+00	3,09E-04	1	4	4,70798727	5,98	MIR6758	microRNA 6758
388743	5,35E-04	3,27E+00	3,44E-04	1	4	4,69383646	5,92	CAPN8	calpain 8
105377627	4,28E-11	1,04E+01	1,89E-11	1	7	4,67415708	27,35	LOC1053776	uncharacterized LOC105377627
165679	4,30E-09	8,37E+00	2,06E-09	1	6	4,66835779	21,81	SPTSSB	serine palmitoyltransferase small subunit B
29953	5,94E-11	1,02E+01	2,64E-11	1	7	4,6668232	27,02	TRHDE	thyrotropin releasing hormone degrading enzyme
4908	1,34E-29	2,89E+01	3,43E-30	0	11	4,64205675	80	NTF3	neurotrophin 3
100996511	1,17E-12	1,19E+01	4,90E-13	1	7	4,61774902	31,61	LINC01355	long intergenic non-protein coding RNA 1355
23650	7,69E-33	3,21E+01	1,82E-33	0	12	4,59159096	87,82	TRIM29	tripartite motif containing 29
161635	8,06E-04	3,09E+00	5,25E-04	1	3	4,56507272	5,45	CSNK1A1P1	casein kinase 1 alpha 1 pseudogene 1
26802	6,49E-32	3,12E+01	1,57E-32	0	12	4,54854833	85,17	SNORD47	small nucleolar RNA, C/D box 47
105378419	2,66E-63	6,26E+01	3,14E-64	0	17	4,54040711	174,95	LOC1053784	uncharacterized LOC105378419
693175	9,10E-04	3,04E+00	5,95E-04	1	3	4,52934289	5,32	MIR590	microRNA 590
5046	3,36E-29	2,85E+01	8,68E-30	0	11	4,50564309	78,08	PCSK6	proprotein convertase subtilisin/kexin type 6
90161	1,96E-31	3,07E+01	4,80E-32	0	12	4,50516417	82,95	HS6ST2	heparan sulfate 6-O-sulfotransferase 2
92558	1,36E-06	5,87E+00	7,39E-07	1	5	4,50179336	14,54	BICDL1	BICD family like cargo adaptor 1
102723789	3,59E-10	9,44E+00	1,65E-10	1	6	4,49239893	24,16	LOC1027237	uncharacterized LOC102723789
13	1,72E-06	5,76E+00	9,39E-07	1	5	4,46960153	14,28	AADAC	arylacetamide deacetylase
9502	1,18E-04	3,93E+00	7,19E-05	1	4	4,42591638	9,29	XAGE2	X antigen family member 2
91156	1,27E-04	3,90E+00	7,77E-05	1	4	4,42198364	9,23	IGFN1	immunoglobulin like and fibronectin type III domain containing 1
107985285	1,33E-03	2,88E+00	8,81E-04	1	3	4,41495071	4,94	LOC1079852	uncharacterized LOC107985285
1301	3,43E-06	5,46E+00	1,90E-06	1	5	4,39856437	13,49	COL11A1	collagen type XI alpha 1 chain
64881	6,02E-23	2,22E+01	1,84E-23	0	10	4,39604313	59,08	PCDH20	protocadherin 20
153163	1,38E-04	3,86E+00	8,44E-05	1	4	4,38886497	9,01	MGC32805	uncharacterized LOC153163
407006	5,42E-60	5,93E+01	6,95E-61	0	16	4,38641349	162,72	MIR221	microRNA 221
105370469	1,68E-04	3,77E+00	1,04E-04	1	4	4,35184912	8,84	LRFN5-DT	LRFN5 divergent transcript
57549	1,80E-04	3,74E+00	1,12E-04	1	4	4,34705276	8,8	IGSF9	immunoglobulin superfamily member 9
641648	1,06E-07	6,97E+00	5,43E-08	1	5	4,33669739	17,45	SNORD87	small nucleolar RNA, C/D box 87
677778	1,79E-03	2,75E+00	1,20E-03	1	3	4,33117644	4,65	SCARNA15	small Cajal body-specific RNA 15
200504	1,75E-12	1,18E+01	7,36E-13	1	7	4,31926173	30,18	GKN2	gastrokine 2
692088	5,85E-09	8,23E+00	2,82E-09	1	6	4,28614279	21,05	SNORD50B	small nucleolar RNA, C/D box 50B
692063	8,21E-19	1,81E+01	2,82E-19	0	9	4,27372878	50,07	SNORA32	small nucleolar RNA, H/ACA box 32
693232	1,63E-07	6,79E+00	8,43E-08	1	5	4,26175034	16,64	MIR647	microRNA 647
105378550	1,41E-10	9,85E+00	6,36E-11	1	7	4,25345752	24,71	LOC1053785	uncharacterized LOC105378550
362	1,13E-13	1,29E+01	4,55E-14	1	8	4,25313825	33,09	AQP5	aquaporin 5
407007	2,91E-07	6,54E+00	1,52E-07	1	5	4,22126155	16,19	MIR222	microRNA 222
105369954	8,70E-06	5,06E+00	4,95E-06	1	5	4,20961309	12,02	C12orf75-AS	C12orf75 antisense RNA 1
91975	4,12E-64	6,34E+01	4,78E-65	0	17	4,19979182	171,35	ZNF300	zinc finger protein 300
105369867	2,77E-03	2,56E+00	1,89E-03	1	3	4,19281393	4,26	LOC1053698	uncharacterized LOC105369867
105374433	1,23E-27	2,69E+01	3,33E-28	0	11	4,19012881	71,3	LOC1053744	uncharacterized LOC105374433
105379426	3,06E-07	6,51E+00	1,60E-07	1	5	4,18940302	15,84	LOC1053794	putative ankyrin repeat domain-containing protein 20A2
407975	1,29E-27	2,69E+01	3,49E-28	0	11	4,18768482	71,33	MIR17HG	miR-17-92a-1 cluster host gene
101927921	1,45E-05	4,84E+00	8,35E-06	1	4	4,14890518	11,55	LINC01478	long intergenic non-protein coding RNA 1478
23284	1,53E-08	7,82E+00	7,51E-09	1	6	4,14765227	19,36	ADGRL3	adhesion G protein-coupled receptor L3
101928151	2,42E-14	1,36E+01	9,58E-15	1	8	4,14650333	34,69	LINC01179	long intergenic non-protein coding RNA 1179
148808	4,57E-04	3,34E+00	2,92E-04	1	4	4,12800697	7,63	MFSD4A	major facilitator superfamily domain containing 4A
9721	1,73E-06	5,76E+00	9,46E-07	1	5	4,11748307	30,46	GPRIN2	G protein regulated inducer of neurite outgrowth 2
109617006	4,37E-11	1,04E+01	1,93E-11	1	7	4,08397951	25,86	SNORA63B	small nucleolar RNA, H/ACA box 63B
284415	1,96E-16	1,57E+01	7,25E-17	0	8	4,08122412	40,57	VSTM1	V-set and transmembrane domain containing 1
7033	1,08E-21	2,10E+01	3,41E-22	0	10	4,07164988	54,93	TFF3	trefoil factor 3
11082	1,25E-82	8,19E+01	9,82E-84	0	19	4,0429393	222,65	ESM1	endothelial cell specific molecule 1
56776	6,40E-04	3,19E+00	4,14E-04	1	4	4,02455775	7,14	FMN2	formin 2

5865	1,45E-14	1,38E+01	5,71E-15	1	8	4,00569604	35,11	RAB3B	RAB3B, member RAS oncogene family
169834	1,96E-14	1,37E+01	7,72E-15	1	8	3,99156312	34,81	ZNF883	zinc finger protein 883
119437	1,61E-06	5,79E+00	8,77E-07	1	5	3,98443078	13,93	CTAGE7P	CTAGE family member 7, pseudogene
107986198	1,19E-07	6,92E+00	6,12E-08	1	5	3,9809851	17,12	LOC107986	uncharacterized LOC107986198
10178	3,95E-192	1,91E+02	5,45E-194	0	30	3,95450531	546,23	TENM1	teneurin transmembrane protein 1
105371401	2,92E-10	9,53E+00	1,34E-10	1	6	3,94296771	23,58	LOC105371	uncharacterized LOC105371401
57615	2,34E-28	2,76E+01	6,19E-29	0	11	3,91214575	72,74	ZNF492	zinc finger protein 492
112267951	1,03E-03	2,99E+00	6,77E-04	1	3	3,90322764	6,6	LOC112267	951
646864	6,01E-05	4,22E+00	3,59E-05	1	4	3,88738448	9,81	ZNF723	zinc finger protein 723
28234	5,80E-299	2,98E+02	2,99E-301	0	37	3,86405941	931,32	SLCO1B3	solute carrier organic anion transporter family member 1B3
338821	6,42E-17	1,62E+01	2,34E-17	0	8	3,8601412	41,62	SLCO1B7	solute carrier organic anion transporter family member 1B7 (putative)
9182	3,83E-13	1,24E+01	1,58E-13	1	7	3,84781247	31,63	RASSF9	Ras association domain family member 9
105376944	1,13E-15	1,49E+01	4,27E-16	0	8	3,84366379	37,94	LOC105376	uncharacterized LOC105376944
100422936	8,19E-05	4,09E+00	4,94E-05	1	4	3,84278497	9,54	MIR3153	microRNA 3153
406938	2,95E-14	1,35E+01	1,17E-14	0	8	3,82336194	34,28	MIR146A	microRNA 146a
3786	7,94E-42	4,11E+01	1,53E-42	0	14	3,81827658	108,85	KCNQ3	potassium voltage-gated channel subfamily Q member 3
338588	2,14E-09	8,67E+00	1,01E-09	1	6	3,80238457	21,54	LINC00705	long intergenic non-protein coding RNA 705
649946	3,47E-15	1,45E+01	1,34E-15	0	8	3,80159638	37,01	RPL23AP64	ribosomal protein L23a pseudogene 64
26793	1,35E-19	1,89E+01	4,54E-20	0	9	3,78167717	48,44	SNORD56	small nucleolar RNA, C/D box 56
112268274	6,69E-36	3,52E+01	1,47E-36	0	13	3,78109761	93,92	LOC112268	uncharacterized LOC112268274
7080	1,67E-11	1,08E+01	7,25E-12	1	7	3,76258441	27,03	NKX2-1	NK2 homeobox 1
406929	2,45E-19	1,86E+01	8,31E-20	0	9	3,74565477	50,47	MIR138-1	microRNA 138-1
101928188	1,44E-04	3,84E+00	8,83E-05	1	4	3,73595547	8,86	LOC101928	uncharacterized LOC101928188
135932	3,50E-11	1,05E+01	1,54E-11	1	7	3,71999234	26,33	TMEM139	transmembrane protein 139
100506433	7,22E-08	7,14E+00	3,66E-08	1	6	3,71809935	17,46	LINC00648	long intergenic non-protein coding RNA 648
107986031	4,58E-11	1,03E+01	2,03E-11	1	7	3,70763598	26,02	LOC107986	uncharacterized LOC107986031
5294	6,84E-36	3,52E+01	1,50E-36	0	13	3,69089301	94,15	PIK3CG	phosphatidylinositol-4,5-bisphosphate 3-kinase catalytic subunit gamma
55016	3,40E-61	6,05E+01	4,25E-62	0	17	3,69080175	166,41	MARCHF1	membrane associated ring-CH-type finger 1
595100	1,20E-06	5,92E+00	6,49E-07	1	5	3,68114833	14,21	SNORD18C	small nucleolar RNA, C/D box 18C
105374160	2,02E-08	7,69E+00	1,00E-08	1	6	3,67131992	19,85	LOC105374	160
102723694	1,07E-34	3,40E+01	2,42E-35	0	12	3,66375994	93,1	MIR30DHG	MIR30D and MIR30B host gene
389791	2,30E-04	3,64E+00	1,43E-04	1	4	3,65866686	8,35	PTGES2-AS	PTGES2 antisense RNA 1 (head to head)
115072896	2,24E-239	2,39E+02	1,87E-241	0	33	3,64785761	724,11	SLCO1B3-SI	SLCO1B3-SLCO1B7 readthrough
101930129	2,20E-05	4,66E+00	1,28E-05	1	4	3,62443178	10,96	LOC101930	uncharacterized LOC101930129
729468	2,20E-08	7,66E+00	1,09E-08	1	6	3,60132203	18,89	PGM5P4	phosphoglucomutase 5 pseudogene 4
10003	1,96E-22	2,17E+01	6,08E-23	0	10	3,5912078	59,09	NAALAD2	N-acetylated alpha-linked acidic dipeptidase 2
56163	3,22E-05	4,49E+00	1,89E-05	1	4	3,58755817	10,79	RNF17	ring finger protein 17
105374019	2,71E-16	1,56E+01	1,01E-16	0	8	3,58526328	40,15	LOC105374	replaced by ID 105374020
6000	8,14E-45	4,41E+01	1,47E-45	0	14	3,57114069	122,24	RGS7	regulator of G protein signaling 7
112935960	3,93E-07	6,41E+00	2,07E-07	1	5	3,56784943	15,79	SCAT2	S-phase cancer associated transcript 2
652995	0	#NUM!	0	0	51	3,56707765	2074,23	UCA1	urothelial cancer associated 1
692058	3,88E-03	2,41E+00	2,68E-03	1	3	3,56678804	5,22	SNORD11	small nucleolar RNA, C/D box 11
645520	3,81E-03	2,42E+00	2,63E-03	1	3	3,5536939	5,22	FAM138A	family with sequence similarity 138 member A
1380	5,29E-06	5,28E+00	2,97E-06	1	5	3,54131164	12,92	CR2	complement C3d receptor 2
728755	3,84E-04	3,42E+00	2,44E-04	1	4	3,53285825	7,77	MIR3171HG	MIR3171 host gene
100616387	1,15E-52	5,19E+01	1,73E-53	0	15	3,53178663	147,53	MIR3064	microRNA 3064
677839	1,51E-11	1,08E+01	6,56E-12	1	7	3,51768941	28,32	SNORA71C	small nucleolar RNA, H/ACA box 71C
729447	4,60E-04	3,34E+00	2,94E-04	1	4	3,51492261	7,7	GAGE2A	G antigen 2A
105374436	4,39E-03	2,36E+00	3,04E-03	1	3	3,51375089	5,14	LINC02383	long intergenic non-protein coding RNA 2383
105370941	1,24E-08	7,91E+00	6,09E-09	1	6	3,50598112	20,43	LOC105370	uncharacterized LOC105370941
442898	4,99E-20	1,93E+01	1,66E-20	0	9	3,49796169	50,62	MIR324	microRNA 324
2793	5,79E-04	3,24E+00	3,73E-04	1	4	3,49781533	7,51	GNGT2	G protein subunit gamma transducin 2
105369601	4,53E-17	1,63E+01	1,65E-17	0	9	3,49609693	42,92	LOC105369	uncharacterized LOC105369601
100506060	1,19E-10	9,92E+00	5,33E-11	1	7	3,48324176	25,09	SMG1P7	SMG1 pseudogene 7
26770	9,57E-18	1,70E+01	3,40E-18	0	9	3,48008989	45,05	SNORD79	small nucleolar RNA, C/D box 79
9300	3,63E-12	1,14E+01	1,54E-12	0	7	3,47104959	30,01	SNORD28	small nucleolar RNA, C/D box 28
101928969	7,87E-29	2,81E+01	2,05E-29	0	11	3,47009104	74,61	RHOXF1-AS	RHOXF1 antisense RNA 1
107985293	6,14E-04	3,21E+00	3,96E-04	1	4	3,46217216	7,46	LOC107985	uncharacterized LOC107985293
139628	7,61E-04	3,12E+00	4,95E-04	1	3	3,45695377	7,29	FOXR2	forkhead box R2
57451	2,28E-30	2,96E+01	5,75E-31	0	12	3,43774086	80,24	TENM2	teneurin transmembrane protein 2
692072	6,23E-10	9,21E+00	2,88E-10	1	6	3,43438866	24,21	SNORD5	small nucleolar RNA, C/D box 5
619568	5,21E-18	1,73E+01	1,84E-18	0	9	3,43337584	46,24	SNORA4	small nucleolar RNA, H/ACA box 4
5332	9,95E-95	9,40E+01	6,23E-96	0	21	3,42986748	269	PLCB4	phospholipase C beta 4
107985291	6,98E-04	3,16E+00	4,53E-04	1	4	3,42449523	7,25	LOC107985	uncharacterized LOC107985291
101930307	1,01E-42	4,20E+01	1,91E-43	0	14	3,41865567	120,79	LOC101930	307
26806	6,07E-23	2,22E+01	1,86E-23	0	10	3,409748	59,96	SNORD44	small nucleolar RNA, C/D box 44
100616408	7,11E-133	1,32E+02	2,20E-134	0	25	3,39458844	427,93	MIR5047	microRNA 5047
105377865	1,51E-04	3,82E+00	9,28E-05	1	4	3,38263541	9,28	LOC105377	uncharacterized LOC105377865
100505875	4,72E-67	6,63E+01	5,16E-68	0	17	3,38243631	188,12	LINC01088	long intergenic non-protein coding RNA 1088
105374020	1,94E-22	2,17E+01	6,00E-23	0	10	3,3806727	58,98	LOC105374	uncharacterized LOC105374020
8549	4,21E-35	3,44E+01	9,43E-36	0	12	3,37671399	95,8	LGR5	leucine rich repeat containing G protein-coupled receptor 5
353189	6,77E-14	1,32E+01	2,71E-14	0	8	3,35413994	34,7	SLCO4C1	solute carrier organic anion transporter family member 4C1
283131	0	#NUM!	0	0	58	3,35121554	4379	NEAT1	nuclear paraspeckle assembly transcript 1
222537	1,54E-04	3,81E+00	9,50E-05	1	4	3,34171172	9,12	HS3ST5	heparan sulfate-glucosamine 3-sulfotransferase 5
105372338	3,42E-299	2,98E+02	1,75E-301	0	37	3,33660087	1057,96	LOC105372	uncharacterized LOC105372338
102724852	1,07E-03	2,97E+00	7,06E-04	1	3	3,32926794	6,83	LOC102724	replaced by ID 100033819
692223	2,30E-05	4,64E+00	1,34E-05	1	4	3,32288344	11,33	SNORD97	small nucleolar RNA, C/D box 97
6092	1,05E-20	2,00E+01	3,43E-21	0	9	3,31944205	54,12	ROBO2	roundabout guidance receptor 2
112268254	2,74E-15	1,46E+01	1,05E-15	0	8	3,29948109	40,15	LOC112268254	
105374140	1,31E-03	2,88E+00	8,68E-04	1	3	3,29499557	6,68	LOC105374	uncharacterized LOC105374140
107075116	1,55E-214	2,14E+02	1,67E-216	0	31	3,29258385	668,41	MIR3142HG	MIR3142 host gene
378938	6,72E-97	9,62E+01	4,04E-98	0	21	3,29126546	1331,46	MALAT1	metastasis associated lung adenocarcinoma transcript 1
109136579	8,03E-96	9,51E+01	4,91E-97	0	21	3,28825234	1265,16	TALAM1	TALAM1 transcript, MALAT1 antisense RNA
23553	4,72E-06	5,33E+00	2,64E-06	1	5	3,27973602	13,29	HYAL4	hyaluronidase 4
55512	3,61E-17	1,64E+01	1,31E-17	0	9	3,27706399	44,01	SMPD3	sphingomyelin phosphodiesterase 3
2674	1,66E-22	2,18E+01	5,15E-23	0	10	3,2602218	60,87	GFRA1	GDNF family receptor alpha 1
103695433	1,46E-28	2,78E+01	3,85E-29	0	11	3,2582336	78,41	LINC01322	long intergenic non-protein coding RNA 1322
105372581	2,91E-04	3,54E+00	1,83E-04	1	4	3,25793258	8,64	LOC105372	uncharacterized LOC105372581
23242	1,84E-39	3,87E+01	3,73E-40	0	13	3,23864181	109,54	COBL	cordon-bleu WH2 repeat protein
105379065	2,83E-04	3,55E+00	1,78E-04	1	4	3,23394113	8,56	LOC105379	uncharacterized LOC105379065
401261	2,65E-09	8,58E+00	1,26E-09	1	6	3,22035809	23,5	LOC401261	uncharacterized LOC401261
137868	2,77E-04	3,56E+00	1,74E-04	1	4	3,21971593	8,51	SGCZ	sarcoglycan zeta
1690	4,86E-08	7,31E+00	2,45E-08	1	6	3,21555404	19,04	COCH	cochlin
100861517	7,14E-08	7,15E+00	3,62E-08	1	6	3,20779793	18,86	OCIAD1-AS	OCIAD1 antisense RNA 1
101805492	3,33E-04	3,48E+00	2,11E-04	1	4	3,20694523	8,41	CASC9	cancer susceptibility 9
102466751	5,38E-05	4,27E+00	3,20E-05	1	4	3,20576546	10,54	MIR6859-1	microRNA 6859-1
163702	8,59E-65	6,41E+01	9,80E-66	0	17	3,20048903	184,54	IFNLR1	interferon lambda receptor 1
339829	6,14E-21	2,02E+01	1,99E-21	0	10	3,19457907	56,39	CCDC39	coiled-coil domain containing 39
283981	2,57E-06	5,59E+00	1,41E-06	1	5	3,19029534	14,64	LINC00685	long intergenic non-protein coding RNA 685
100506622	1,98E-03	2,70E+00	1,33E-03	0,9935	3,20992	3,18892736	6,24	LINC00540	long intergenic non-protein coding RNA 540
10100	2,54E-24	2,36E+01	7,51E-25	0,3097	10,293908	3,18779896	66,6	TSPAN2	tetraspanin 2
105374005	7,56E-05	4,12E+00	4,55E-05	0,7801	4,077643	3,1810009	10,35	LOC105374	uncharacterized LOC105374005
105378808	3,68E-04	3,43E+00	2,34E-04	0,862	3,6796346	3,17184308	8,27	LOC105378	uncharacterized LOC105378808
102723872	2,27E-06	5,64E+00	1,25E-06	0,6542	4,8481525	3,17142415	14,41	LOC102723	uncharacterized LOC102723872
79993	7,51E-125	1,24E+02	2,74E-126	0,1325	23,9046285	3,16738874	433,62	ELOVL7	ELOVL fatty acid elongase 7
27178	4,01E-04	3,40E+00	2,55E-04	0,8643	3,6573604	3,16095058	8,19	IL37	interleukin 37
201651	1,87E-74	7,37E+01	1,73E-75	0,1715	18,3849283	3,15244113	219,74	AADACP1	arylacetamide deacetylase pseudogene 1
5733	2,79E-03	2,55E+00	1,90E-03	1,0148	3,1053793	3,15133048	6,04	PTGER3	prostaglandin E receptor 3
64399	1,25E-127	1,27E+02	4,29E-129	0,1302	24,1729198	3,14803774	398,08	HHIP	hedgehog interacting protein
642484	1,52E-05	4,82E+00	8,75E-06	0,707	4,4459075	3,14339635	12,14	LOC642484	uncharacterized LOC642484
725	0	#NUM!	0	0,0637	49,2478006	3,13781024	2270,93	C4BPB	complement component 4 binding protein beta
283120	2,58E-03	2,59E+00	1,75E-03	0,9996	3,1299567	3,12882099	6,02	H19	H19 imprinted maternally expressed transcript
5314	3,07E-10	9,51E+00	1,40E-10	0,4871	6,4154471	3,12497943	25,98	PKHD1	PKHD1 ciliary IPT domain containing fibrocystin/polyductin
149499	1,60E-07	6,80E+00	8,27E-08	0,5814	5,3611508	3,1168791	17,9	LRRC71	leucine rich repeat containing 71
163071	3,81E-224	2,23E+02	3,65E-226	0,0971	32,1058423	3,11657945	738,04	ZNF114	zinc finger protein 114
100500849	8,83E-48	4,71E+01	1,47E-48	0,2123	14,643908	3,10836072	136,67	MIR3916	microRNA 3916
105372235	6,75E-04	3,17E+00	4,37E-04	0,8835	3,5165	3,10671551	7,99	LOC105372	uncharacterized LOC105372235
84570	3,34E-03	2,48E+00	2,29E-03	1,0182	3,0495052	3,10487675	5,84	COL25A1	collagen type XXV alpha 1 chain
677850	5,78E-04	3,24E+00	3,73E-04	0,8689	3,5586381	3,09212688	7,82	SNORD1C	small nucleolar RNA, C/D box 1C
440714	3,06E-03	2,51E+00	2,09E-03	1,0038	3,0768504	3,08865149	5,87	LINC02869	long intergenic non-protein coding RNA 2869

100500873	3,82E-05	4,42E+00	2,26E-05	0,7285	4,2379767	3,08736403	11,66	MIR3934	microRNA 3934
105372290	3,14E-19	1,85E+01	1,07E-19	0,339	9,0818482	3,0783221	52,66	LINC01764	long intergenic non-protein coding RNA 1764
143662	2,71E-21	2,06E+01	8,70E-22	0,3208	9,5912403	3,07668865	58,28	MUC15	mucin 15, cell surface associated
338322	1,09E-12	1,20E+01	4,56E-13	0,4248	7,2378853	3,07451259	32,95	NLRP10	NLR family pyrin domain containing 10
2707	9,21E-20	1,90E+01	3,08E-20	0,3333	9,2161126	3,07187102	54,2	GJB3	gap junction protein beta 3
221400	4,15E-03	2,38E+00	2,87E-03	1,0299	2,9811443	3,07028738	5,71	TDRD6	tudor domain containing 6
107987098	2,89E-05	4,54E+00	1,70E-05	0,7135	4,3016168	3,06914212	11,65	LOC107987098	
84541	5,94E-32	3,12E+01	1,44E-32	0,2582	11,8838608	3,06854182	90,87	KBTBD8	kelch repeat and BTB domain containing 8
105373102	1,47E-04	3,83E+00	9,02E-05	0,7823	3,915523	3,06312393	9,6	LOC105373	uncharacterized LOC105373102
1241	2,49E-170	1,70E+02	4,54E-172	0,1095	27,963289	3,06270579	566,1	LTB4R	leukotriene B4 receptor
102465910	6,70E-04	3,17E+00	4,34E-04	0,8705	3,51843	3,06270405	7,73	MIR6859-3	microRNA 6859-3
9723	6,98E-26	2,52E+01	1,98E-26	0,2875	10,6383028	3,05884255	72,96	SEMA3E	semaphorin 3E
101928601	3,64E-03	2,44E+00	2,50E-03	1,0113	3,0229043	3,05720228	5,77	MEI4	meiotic double-stranded break formation protein 4
1439	3,69E-03	2,43E+00	2,54E-03	1,0124	3,0188558	3,0561429	5,7	CSF2RB	colony stimulating factor 2 receptor subunit beta
107985556	7,71E-04	3,11E+00	5,02E-04	0,8775	3,4797293	3,05363286	7,61	LOC107985556	
56853	9,69E-06	5,01E+00	5,52E-06	0,6711	4,5438817	3,04932479	13,29	CELF4	CUGBP Elav-like family member 4
26805	1,76E-06	5,75E+00	9,62E-07	0,6212	4,8993062	3,04335866	15,32	SNORD45A	small nucleolar RNA, C/D box 45A
26774	1,07E-07	6,97E+00	5,48E-08	0,5581	5,4348415	3,0329688	100,16	SNORD80	small nucleolar RNA, C/D box 80
107985497	8,64E-06	5,06E+00	4,91E-06	0,6635	4,5687728	3,03159081	13,28	LOC107985497	
100132565	1,41E-09	8,85E+00	6,64E-10	0,4907	6,1745147	3,03004718	24,46	GOLGA8F	golgin A8 family member F
9299	4,33E-35	3,44E+01	9,71E-36	0,2424	12,4790984	3,0244677	103,63	SNORD30	small nucleolar RNA, C/D box 30
112806053	4,07E-05	4,39E+00	2,41E-05	0,7158	4,2232345	3,02294683	11,31	TBILA	TGF-beta induced lncRNA
105369618	1,22E-05	4,91E+00	7,01E-06	0,6723	4,4935194	3,02117233	13,04	LOC105369	uncharacterized LOC105369618
57575	7,80E-15	1,41E+01	3,04E-15	0,3823	7,8891063	3,01584798	41,25	PCDH10	protocadherin 10
7070	1,86E-17	1,67E+01	6,67E-18	0,3494	8,6204798	3,01173857	48,72	THY1	Thy-1 cell surface antigen
105377347	1,35E-07	6,87E+00	6,92E-08	0,557	5,3931711	3,00382674	18,51	LOC105377	uncharacterized LOC105377347
203447	3,25E-146	1,45E+02	8,41E-148	0,1159	25,8909977	3,00143469	472,74	NRK	Nik related kinase
3606	0	#NUM!	0	0,0768	39,0211463	2,99745837	1298,2	IL18	interleukin 18
26771	1,08E-03	2,97E+00	7,09E-04	0,8841	3,3860093	2,99357308	7,39	SNORD102	small nucleolar RNA, C/D box 102
144100	0	#NUM!	0	0,0712	42,003691	2,99003259	1567,17	PLEKHA7	pleckstrin homology domain containing A7
26791	2,26E-09	8,65E+00	1,07E-09	0,4895	6,098407	2,9853724	23,92	SNORD58A	small nucleolar RNA, C/D box 58A
107984338	1,95E-89	8,87E+01	1,35E-90	0,1471	20,1841519	2,96908891	296,31	LOC107984338	
105378751	4,64E-171	1,70E+02	8,35E-173	0,1059	28,0237422	2,96864706	596,75	LOC105378	uncharacterized LOC105378751
100506142	5,60E-08	7,25E+00	2,83E-08	0,5336	5,5518374	2,96245722	20,02	RHOQ-AS1	RHOQ antisense RNA 1
53942	7,37E-08	7,13E+00	3,74E-08	0,535	5,5027975	2,94423684	19,64	CNTN5	contactin 5
7223	5,74E-03	2,24E+00	4,02E-03	1,0232	2,8766575	2,94343018	5,32	TRPC4	transient receptor potential cation channel subfamily C member 4
692198	8,83E-06	5,05E+00	5,02E-06	0,6416	4,5638372	2,92828186	14,16	SNORD78	small nucleolar RNA, C/D box 78
105379282	2,30E-08	7,64E+00	1,14E-08	0,5127	5,7088123	2,92682716	21,28	LOC105379282	
70	8,76E-05	4,06E+00	5,29E-05	0,7236	4,0422479	2,92515631	10,6	ACTC1	actin alpha cardiac muscle 1
27284	3,85E-04	3,41E+00	2,45E-04	0,7957	3,6674778	2,91815776	8,89	SULT1B1	sulfotransferase family 1B member 1
9301	2,38E-15	1,46E+01	9,13E-16	0,3624	8,0380277	2,91276655	44,17	SNORD27	small nucleolar RNA, C/D box 27
283358	3,41E-11	1,05E+01	1,50E-11	0,4313	6,747524	2,90989412	29,81	B4GALNT3	beta-1,4-N-acetyl-galactosaminyltransferase 3
105374937	4,32E-22	2,14E+01	1,35E-22	0,2965	9,7814606	2,90001385	66,37	LOC105374	uncharacterized LOC105374937
107984583	1,90E-03	2,72E+00	1,27E-03	0,8983	3,2219572	2,89437537	6,99	LOC107984583	
595099	6,77E-03	2,17E+00	4,78E-03	1,0257	2,8216844	2,89411904	5,22	SNORD18B	small nucleolar RNA, C/D box 18B
253970	3,05E-05	4,52E+00	1,79E-05	0,6745	4,2892845	2,89302931	12,14	SFTA3	surfactant associated 3
26804	1,11E-04	3,95E+00	6,76E-05	0,725	3,9846314	2,88876144	10,37	SNORD45B	small nucleolar RNA, C/D box 45B
57604	4,86E-09	8,31E+00	2,34E-09	0,4831	5,9725428	2,88557001	24,19	TRMT9B	tRNA methyltransferase 9B (putative)
79442	6,22E-21	2,02E+01	2,02E-21	0,303	9,5041167	2,87972373	63,95	LRRC2	leucine rich repeat containing 2
367	1,59E-41	4,08E+01	3,09E-42	0,2111	13,6190162	2,87441624	126,93	AR	androgen receptor
653145	5,26E-183	1,82E+02	8,00E-185	0,0991	28,9932792	2,87251654	646,96	ANXA8	annexin A8
3910	2,17E-179	1,79E+02	3,50E-181	0,0999	28,7029843	2,8661594	726,04	LAMA4	laminin subunit alpha 4
692085	1,61E-07	6,79E+00	8,30E-08	0,5346	5,3604236	2,86543135	20,26	SNORD45C	small nucleolar RNA, C/D box 45C
105372429	9,82E-11	1,00E+01	4,40E-11	0,4347	6,5900169	2,86441712	28,98	ZNF114-AS1	ZNF114 antisense RNA 1
999	4,58E-13	1,23E+01	1,89E-13	0,3891	7,3562829	2,86236402	37,54	CDH1	cadherin 1
116828	1,46E-10	9,84E+00	6,59E-11	0,4379	6,5298073	2,85957427	28,93	N4BP2L2-IT	N4BPL2 intronic transcript 2
730101	3,87E-154	1,53E+02	8,85E-156	0,1074	26,5900562	2,85592129	566,79	LOC730101	uncharacterized LOC730101
285513	1,30E-05	4,89E+00	7,47E-06	0,637	4,4798481	2,85383576	13,62	GPRIN3	GPRIN family member 3
102465909	2,04E-03	2,69E+00	1,37E-03	0,8893	3,2009358	2,84665494	6,76	MIR6859-2	microRNA 6859-2
6512	7,68E-17	1,61E+01	2,81E-17	0,3357	8,454297	2,83814401	48,71	SLC1A7	solute carrier family 1 member 7
101928550	3,90E-11	1,04E+01	1,72E-11	0,4216	6,727732	2,83617108	31,78	SMC2-DT	SMC2 divergent transcript
3216	1,96E-09	8,71E+00	9,30E-10	0,4628	6,1209233	2,8327041	25	HOXB6	homeobox B6
105372704	4,60E-05	4,34E+00	2,73E-05	0,6739	4,1949712	2,82681694	11,68	LOC105372	uncharacterized LOC105372704
284454	5,69E-166	1,65E+02	1,11E-167	0,1023	27,6001803	2,82450945	627,28	MIR23AHG	miR-23a/27a/24-2 cluster host gene
9535	3,14E-16	1,55E+01	1,17E-16	0,3401	8,2862379	2,8179957	47,81	GMFG	glia maturation factor gamma
107987152	4,40E-10	9,36E+00	2,02E-10	0,4431	6,3595862	2,81774053	28,2	LOC107987	152
102723166	6,73E-07	6,17E+00	3,59E-07	0,553	5,0894041	2,81440076	18,02	STAM-DT	STAM divergent transcript
79974	1,32E-106	1,06E+02	6,60E-108	0,1273	22,0667089	2,80826039	355,87	CPED1	cadherin like and PC-esterase domain containing 1
338440	2,87E-05	4,54E+00	1,68E-05	0,6506	4,3030746	2,79970282	13,2	ANO9	anoctamin 9
105375018	2,61E-04	3,58E+00	1,63E-04	0,7425	3,7697166	2,798985	9,76	LOC105375	uncharacterized LOC105375018
105369690	3,37E-03	2,47E+00	2,31E-03	0,9187	3,0465635	2,79876037	6,43	LOC105369	uncharacterized LOC105369690
100129726	7,59E-05	4,12E+00	4,57E-05	0,6856	4,0766157	2,79505665	11,43	LINC01126	long intergenic non-protein coding RNA 1126
105378626	5,61E-10	9,25E+00	2,59E-10	0,4411	6,3212434	2,78806131	27,75	LOC105378	uncharacterized LOC105378626
1591	1,67E-81	8,08E+01	1,34E-82	0,1446	19,252518	2,78299142	287,15	CYP24A1	cytochrome P450 family 24 subfamily A member 1
619499	9,22E-04	3,04E+00	6,03E-04	0,8108	3,4303977	2,78124306	8,06	SNORA27	small nucleolar RNA, H/ACA box 27
107986633	5,49E-08	7,26E+00	2,77E-08	0,5003	5,5553412	2,77942303	21,04	LOC107986	uncharacterized LOC107986633
11096	1,16E-06	5,94E+00	6,30E-07	0,5576	4,9818129	2,77806374	17,82	ADAMTS5	ADAM metallopeptidase with thrombospondin type 1 motif 5
440270	2,27E-259	2,59E+02	1,58E-261	0,0802	34,547003	2,77232473	1005,56	GOLGA8B	golgin A8 family member B
107986986	8,82E-06	5,05E+00	5,01E-06	0,6068	4,5641853	2,7696208	14,41	LOC107986	uncharacterized LOC107986986
55024	4,97E-82	8,13E+01	3,94E-83	0,1432	19,3159558	2,76545739	296,39	BANK1	B cell scaffold protein with ankyrin repeats 1
107985037	2,93E-04	3,53E+00	1,84E-04	0,7385	3,7394596	2,76151606	9,63	LOC107985037	
105372217	1,13E-02	1,95E+00	8,12E-03	1,0383	2,6470885	2,74855245	4,82	LOC105372	uncharacterized LOC105372217
105379171	7,48E-10	9,13E+00	3,47E-10	0,4372	6,2760823	2,74377299	26,92	LOC105379	uncharacterized LOC105379171
105372190	3,07E-06	5,51E+00	1,70E-06	0,5726	4,7867214	2,740858	15,79	LOC105372	uncharacterized LOC105372190
109623452	1,09E-03	2,96E+00	7,16E-04	0,8088	3,3833629	2,73660079	7,93	SNORD159	small nucleolar RNA, C/D box 159
677792	5,22E-06	5,28E+00	2,93E-06	0,5852	4,6760112	2,73634949	15,89	SNORA1	small nucleolar RNA, H/ACA box 1
283768	4,83E-10	9,32E+00	2,22E-10	0,43	6,3450452	2,72861167	28,18	GOLGA8G	golgin A8 family member G
23015	1,72E-143	1,43E+02	4,64E-145	0,1063	25,6463522	2,7270453	512,88	GOLGA8A	golgin A8 family member A
10748	1,16E-06	5,94E+00	6,28E-07	0,5469	4,982488	2,72498019	17,18	KLRA1P	killer cell lectin like receptor A1, pseudogene
105370304	4,26E-03	2,37E+00	2,95E-03	0,9133	2,973008	2,71524042	6,27	LOC105370	uncharacterized LOC105370304
404266	1,20E-03	2,92E+00	7,92E-04	0,8088	3,3556857	2,71422465	7,83	HOXB-AS3	HOXB cluster antisense RNA 3
107986293	1,95E-05	4,71E+00	1,13E-05	0,6165	4,3901207	2,70639707	13,94	LOC107986	uncharacterized LOC107986293
677798	7,00E-08	7,15E+00	3,55E-08	0,4908	5,5120055	2,70519224	21,69	SNORA9	small nucleolar RNA, H/ACA box 9
9369	1,54E-26	2,58E+01	4,30E-27	0,2509	10,7795966	2,70494483	83,53	NRXN3	neurexin 3
103344932	1,52E-14	1,38E+01	5,97E-15	0,346	7,80454	2,70056101	43,38	PGM5P4-AS	PGM5P4 antisense RNA 1
89792	1,44E-04	3,84E+00	8,81E-05	0,6879	3,9211377	2,69752205	10,72	GAL3ST3	galactose-3-O-sulfotransferase 3
109617013	1,71E-05	4,77E+00	9,88E-06	0,6091	4,4197489	2,69188511	13,78	SNORD63B	small nucleolar RNA, C/D box 63B
4846	5,25E-06	5,28E+00	2,95E-06	0,5756	4,6744802	2,69043597	15,36	NOS3	nitric oxide synthase 3
81553	2,17E-54	5,37E+01	3,13E-55	0,1717	15,6537053	2,68726931	183,29	CYRIA	CYFIP related Rac1 interactor A
1131	2,61E-29	2,86E+01	6,74E-30	0,2365	11,3584161	2,68681612	93,44	CHRM3	cholinergic receptor muscarinic 3
441234	6,97E-17	1,62E+01	2,55E-17	0,3173	8,4657419	2,68644006	50,56	ZNF716	zinc finger protein 716
100128653	5,13E-10	9,29E+00	2,37E-10	0,424	6,3353631	2,68609172	28,98	LOC100128	uncharacterized LOC100128653
57035	1,92E-148	1,48E+02	4,82E-150	0,1029	26,0893539	2,6845738	581,6	RSRP1	arginine and serine rich protein 1
105374808	5,68E-05	4,25E+00	3,39E-05	0,6464	4,1458537	2,68005588	12,19	LOC105374	replaced by ID 10505
692196	3,69E-36	3,54E+01	8,06E-37	0,2114	12,6757719	2,67918489	117,63	SNORD76	small nucleolar RNA, C/D box 76
56413	2,05E-19	1,87E+01	6,95E-20	0,2934	9,1284791	2,67869721	59,46	LTB4R2	leukotriene B4 receptor 2
105369151	1,71E-04	3,77E+00	1,06E-04	0,6906	3,8770319	2,67737993	10,64	LOC105369	uncharacterized LOC105369151
144203	4,95E-03	2,31E+00	3,45E-03	0,9143	2,9246119	2,67386448	6,11	OVOS2	alpha-2-macroglobulin like 1 pseudogene
2262	1,08E-06	5,97E+00	5,85E-07	0,535	4,9961825	2,67285677	18,3	GPC5	glypican 5
619567	3,53E-15	1,45E+01	1,36E-15	0,3341	7,9886486	2,66916225	45,43	SNORD2	small nucleolar RNA, C/D box 2
100616194	7,94E-11	1,01E+01	3,55E-11	0,4028	6,6218518	2,66753678	31,75	MIR4477B	microRNA 4477b
728963	1,72E-04	3,76E+00	1,06E-04	0,6882	3,8759604	2,66725899	10,56	RPS15AP10	ribosomal protein S15a pseudogene 10
441666	1,06E-34	3,40E+01	2,40E-35	0,2149	12,4067516	2,66601798	116,46	LOC441666	zinc finger protein 91 pseudogene
222584	2,57E-11	1,06E+01	1,13E-11	0,3923	6,7893146	2,66352805	33,07	FAM83B	family with sequence similarity 83 member B
112267861	4,47E-09	8,35E+00	2,15E-09	0,4447	5,9863282	2,66232902	25,6	LOC112267861	
6539	1,66E-03	2,78E+00	1,11E-03	0,8161	3,2616313	2,66180131	7,55	SLC6A12	solute carrier family 6 member 12
4688	0	#NUM!	0	0,0653	40,7215179	2,65900961	1929,83	NCF2	neutrophil cytosolic factor 2
101928592	1,02E-06	5,99E+00	5,48E-07	0,5306	5,0085503	2,6574873	17,93	LOC101928592	
401097	7,61E-06	5,12E+00	4,31E-06	0,5779	4,5960843	2,65623342	15,07	C3orf80	chromosome 3 open reading frame 80
55784	4,02E-44	4,34E+01	7,36E-45	0,1888	14,0532673	2,65303051	153,05	MCTP2	multiple C2 and transmembrane domain containing 2

658	1,92E-47	4,67E+01	3,23E-48	0,1818	14,5903904	2,65223316	157,37	BMPR1B	bone morphogenetic protein receptor type 1B
152078	6,62E-05	4,18E+00	3,97E-05	0,6449	4,1093072	2,64992833	11,96	SLC66A1L	solute carrier family 66 member 1 like
1427	2,34E-04	3,63E+00	1,46E-04	0,697	3,7978228	2,64704234	10,48	CRYGS	crystallin gamma S
84848	1,37E-33	3,29E+01	3,19E-34	0,2165	12,1980033	2,64102962	111,82	MIR503HG	MIR503 host gene
3993	2,89E-61	6,05E+01	3,60E-62	0,1583	16,639565	2,63333721	224,09	LLGL2	LLGL scribble cell polarity complex component 2
101928650	1,04E-03	2,98E+00	6,84E-04	0,7754	3,3959224	2,63306107	8,88	GORAB-AS1	GORAB antisense RNA 1
105375669	2,17E-03	2,66E+00	1,46E-03	0,8274	3,1821868	2,63290451	7,47	LOC105375(	uncharacterized LOC105375669
105379083	6,87E-11	1,02E+01	3,06E-11	0,3959	6,6437023	2,63011474	32,37	LOC105379(	uncharacterized LOC105379083
2045	2,69E-09	8,57E+00	1,28E-09	0,4327	6,0698189	2,62629923	26,53	EPHA7	EPH receptor A7
112268177	1,39E-05	4,86E+00	7,97E-06	0,5877	4,4660018	2,6245966	14,8	LOC112268177	
107985302	1,37E-23	2,29E+01	4,13E-24	0,2591	10,1285275	2,6238284	78,05	LOC107985302	
692247	3,41E-06	5,47E+00	1,89E-06	0,5507	4,7647485	2,62379404	16,24	LMNTD2-AS	LMNTD2 antisense RNA 1
105379377	7,59E-04	3,12E+00	4,94E-04	0,7508	3,4841846	2,61605995	8,87	LOC105379(	uncharacterized LOC105379377
113835	2,43E-10	9,61E+00	1,11E-10	0,4049	6,4516726	2,61235398	30,73	ZNF257	zinc finger protein 257
2840	1,16E-18	1,79E+01	4,02E-19	0,292	8,936499	2,60953558	61,18	GPR17	G protein-coupled receptor 17
2239	6,80E-07	6,17E+00	3,63E-07	0,5124	5,0874199	2,60692819	18,9	GPC4	glypican 4
84951	3,45E-49	4,85E+01	5,55E-50	0,1752	14,8650903	2,60459588	184,13	TNS4	tensin 4
9037	1,20E-15	1,49E+01	4,57E-16	0,3201	8,1224604	2,59965308	47,97	SEMA5A	semaphorin 5A
57101	3,04E-22	2,15E+01	9,46E-23	0,2641	9,8175286	2,59326777	71,05	ANO2	anoctamin 2
151354	3,81E-07	6,42E+00	2,01E-07	0,4979	5,1985492	2,58849336	20,15	LRATD1	LRAT domain containing 1
4648	5,20E-19	1,83E+01	1,78E-19	0,2865	9,0262104	2,58636531	62,06	MYO7B	myosin VIIB
2888	5,66E-07	6,25E+00	3,01E-07	0,5024	5,1229073	2,57389657	20	GRB14	growth factor receptor bound protein 14
112267941	3,83E-19	1,84E+01	1,31E-19	0,284	9,0597749	2,57268064	61,5	LOC112267941	
100130733	1,06E-03	2,97E+00	6,95E-04	0,7569	3,3916825	2,56715665	8,58	LRRC70	leucine rich repeat containing 70
115265	7,48E-28	2,71E+01	2,01E-28	0,232	11,057918	2,56552531	95,57	DDIT4L	DNA damage inducible transcript 4 like
105369942	1,07E-05	4,97E+00	6,10E-06	0,5663	4,523015	2,56124084	15,76	LINC02456	long intergenic non-protein coding RNA 2456
26281	8,37E-03	2,08E+00	5,96E-03	0,9281	2,7500211	2,55236548	5,68	FGF20	fibroblast growth factor 20
107986637	2,30E-05	4,64E+00	1,34E-05	0,586	4,3540589	2,55149081	14,18	LOC107986(	uncharacterized LOC107986637
85004	4,50E-04	3,35E+00	2,88E-04	0,7033	3,6263032	2,55027901	9,83	RERG	RAS like estrogen regulated growth inhibitor
112267943	9,47E-06	5,02E+00	5,39E-06	0,558	4,5489465	2,5385016	15,38	LOC112267(	replaced by ID 153396
100289097	5,76E-47	4,62E+01	9,81E-48	0,1748	14,514483	2,5375654	163,92	FRG1CP	FSHD region gene 1 family member C, pseudogene
101928020	6,84E-05	4,16E+00	4,10E-05	0,6182	4,1017494	2,5358513	12,69	KANSL1L-AS	KANSL1L antisense RNA 1
54734	5,87E-13	1,22E+01	2,43E-13	0,3461	7,3226475	2,53423609	40,53	RAB39A	RAB39A, member RAS oncogene family
375033	2,21E-221	2,21E+02	2,18E-223	0,0794	31,9062912	2,53409093	1003,03	PEAR1	platelet endothelial aggregation receptor 1
10819	4,88E-09	8,31E+00	2,35E-09	0,4243	5,9716643	2,53368509	27,73	OR7E14P	olfactory receptor family 7 subfamily E member 14 pseudogene
80336	3,52E-222	2,21E+02	3,45E-224	0,0792	31,9640149	2,53228042	984,78	PABPC1L	poly(A) binding protein cytoplasmic 1 like
85439	4,50E-10	9,35E+00	2,07E-10	0,3983	6,3560252	2,53177408	30,81	STON2	stonin 2
728113	2,43E-106	1,06E+02	1,22E-107	0,1147	22,0389149	2,52728665	428,1	ANXA8L1	annexin A8 like 1
5788	2,46E-04	3,61E+00	1,54E-04	0,6676	3,7844418	2,52655192	11,24	PTPRC	protein tyrosine phosphatase receptor type C
7852	3,48E-268	2,67E+02	2,28E-270	0,0718	35,1308362	2,52267204	1205,99	CXCR4	C-X-C motif chemokine receptor 4
102724917	1,70E-07	6,77E+00	8,80E-08	0,471	5,3498394	2,51952196	22,13	LINC02327	long intergenic non-protein coding RNA 2327
85478	2,52E-06	5,60E+00	1,38E-06	0,5217	4,8271696	2,5183742	17,85	CCDC65	coiled-coil domain containing 65
55283	1,96E-55	5,47E+01	2,77E-56	0,1593	15,8072414	2,51756588	200,58	MCOLN3	mucolipin TRP cation channel 3
135398	1,11E-58	5,80E+01	1,46E-59	0,1545	16,2762431	2,51401586	208,74	C6orf141	chromosome 6 open reading frame 141
692057	6,06E-04	3,22E+00	3,91E-04	0,7086	3,5458755	2,51257601	9,73	SNORD12	small nucleolar RNA, C/D box 12
3352	1,14E-21	2,09E+01	3,61E-22	0,2594	9,6815904	2,51093054	71,87	HTR1D	5-hydroxytryptamine receptor 1D
101929703	4,01E-03	2,40E+00	2,77E-03	0,8373	2,9922482	2,50543598	6,93	LOC101929(	uncharacterized LOC101929703
105371055	2,23E-04	3,65E+00	1,39E-04	0,6564	3,81035	2,50094913	11,02	LOC105371(	uncharacterized LOC105371055
112268426	4,03E-27	2,64E+01	1,10E-27	0,2293	10,9039609	2,5007831	91,71	LOC112268426	
6043	1,10E-10	9,96E+00	4,92E-11	0,3793	6,5732622	2,49318865	35,64	SNORA63	small nucleolar RNA, H/ACA box 63
374879	9,91E-233	2,32E+02	8,73E-235	0,0761	32,717761	2,48946065	1184,93	ZNF699	zinc finger protein 699
90527	9,10E-12	1,10E+01	3,92E-12	0,3582	6,9400865	2,48569807	38,29	DUOXA1	dual oxidase maturation factor 1
2824	1,25E-08	7,90E+00	6,12E-09	0,427	5,8134631	2,4823742	27,25	GPM6B	glycoprotein M6B
107984011	5,09E-05	4,29E+00	3,03E-05	0,5949	4,1713683	2,48168984	13,64	LOC107984(	uncharacterized LOC107984011
105378011	1,04E-02	1,98E+00	7,44E-03	0,9258	2,6765979	2,47798923	5,43	LOC105378(	uncharacterized LOC105378011
2796	8,89E-13	1,21E+01	3,70E-13	0,3409	7,2660552	2,47702565	40,64	GNRH1	gonadotropin releasing hormone 1
3698	1,71E-03	2,77E+00	1,14E-03	0,7615	3,2523216	2,47652879	8,16	ITIH2	inter-alpha-trypsin inhibitor heavy chain 2
285973	1,67E-03	2,78E+00	1,12E-03	0,7596	3,2596893	2,4759645	8,17	ATG9B	autophagy related 9B
2875	7,13E-04	3,15E+00	4,63E-04	0,7062	3,501301	2,47272283	9,38	GPT	glutamic--pyruvic transaminase
3299	8,96E-60	5,90E+01	1,15E-60	0,1502	16,4308062	2,46872758	223,26	HSF4	heat shock transcription factor 4
105748977	1,23E-04	3,91E+00	7,51E-05	0,6232	3,9595902	2,46749656	12,15	NTRAS	non-coding transcript regulating alternative splicing
643365	8,12E-30	2,91E+01	2,07E-30	0,2149	11,4610274	2,46248601	105,64	LINC00452	long intergenic non-protein coding RNA 452
107984529	4,10E-04	3,39E+00	2,61E-04	0,673	3,6512425	2,45734228	10,73	LOC107984529	
401337	9,39E-31	3,00E+01	2,34E-31	0,2107	11,648283	2,45396127	116,02	LINC01446	long intergenic non-protein coding RNA 1446
728643	2,99E-15	1,45E+01	1,15E-15	0,3062	8,0096844	2,4527057	50,47	HNRNPA1P3	heterogeneous nuclear ribonucleoprotein A1 pseudogene 33
100873989	2,38E-05	4,62E+00	1,39E-05	0,5636	4,3455599	2,44927426	14,61	GRM5-AS1	GRM5 antisense RNA 1
100508631	4,99E-13	1,23E+01	2,06E-13	0,3331	7,3447342	2,44677699	42,59	LINC02616	long intergenic non-protein coding RNA 2616
102465495	1,35E-04	3,87E+00	8,27E-05	0,6209	3,9363185	2,44411696	11,98	MIR6824	microRNA 6824
101927345	6,06E-05	4,22E+00	3,62E-05	0,5916	4,1302746	2,44330707	13,22	LOC101927(	putative ankyrin repeat domain-containing protein 20A12
59082	1,22E-02	1,91E+00	8,81E-03	0,9321	2,6194495	2,44156922	5,28	CARD18	caspase recruitment domain family member 18
105375731	8,93E-09	8,05E+00	4,34E-09	0,4156	5,87066	2,43988891	27,64	LOC105375(	uncharacterized LOC105375731
26822	4,09E-04	3,39E+00	2,60E-04	0,6662	3,652022	2,43315867	10,63	SNORD14A	small nucleolar RNA, C/D box 14A
57211	0	#NUM!	0	0,0558	43,6162942	2,43310371	2967,66	ADGRG6	adhesion G protein-coupled receptor G6
105375475	5,59E-04	3,25E+00	3,60E-04	0,6809	3,5678688	2,42930538	10,53	LINC02476	long intergenic non-protein coding RNA 2476
101927220	5,63E-04	3,25E+00	3,63E-04	0,6797	3,5659057	2,42371236	10,39	DEPDC1-AS	DEPDC1 antisense RNA 1
374860	3,66E-06	5,44E+00	2,03E-06	0,5097	4,7501398	2,42102082	18,42	ANKRD30B	ankyrin repeat domain 30B
221662	1,13E-173	1,73E+02	1,96E-175	0,0857	28,2387286	2,4191893	802,51	RBM24	RNA binding motif protein 24
284443	3,35E-31	3,05E+01	8,25E-32	0,2061	11,7368427	2,41906753	113,76	ZNF493	zinc finger protein 493
131368	1,21E-04	3,92E+00	7,37E-05	0,6097	3,9640688	2,41700123	12,88	ZPLD1	zona pellucida like domain containing 1
2070	1,08E-54	5,40E+01	1,55E-55	0,1536	15,6982556	2,41105005	210,03	EYA4	EYA transcriptional coactivator and phosphatase 4
109616995	1,95E-04	3,71E+00	1,21E-04	0,6267	3,844498	2,40937018	11,7	SNORD70B	small nucleolar RNA, C/D box 70B
51351	2,51E-07	6,60E+00	1,31E-07	0,4557	5,2775413	2,40512537	22,01	ZNF117	zinc finger protein 117
107986632	7,84E-11	1,01E+01	3,50E-11	0,3629	6,6238078	2,4034821	34,95	LOC107986(	uncharacterized LOC107986632
7275	4,55E-19	1,83E+01	1,55E-19	0,2652	9,0409436	2,39749351	65,83	TUB	TUB bipartite transcription factor
5028	2,47E-04	3,61E+00	1,55E-04	0,6324	3,7837127	2,39283148	11,6	P2RY1	purinergic receptor P2Y1
112267938	1,34E-03	2,87E+00	8,87E-04	0,7192	3,3239757	2,39063373	8,96	LOC112267938	
375316	4,39E-05	4,36E+00	2,60E-05	0,5682	4,2057099	2,38966346	14,11	RBM44	RNA binding motif protein 44
101928096	2,85E-08	7,55E+00	1,42E-08	0,4213	5,6708905	2,38936483	25,74	LOC101928(	replaced by ID 60487
101101776	9,48E-11	1,00E+01	4,24E-11	0,3622	6,5953392	2,38915603	34,69	BMS1P17	BMS1 pseudogene 17
100128537	5,91E-08	7,23E+00	2,98E-08	0,431	5,542346	2,3884871	24,37	MIR29B2CH	MIR29B2 and MIR29C host gene
53832	1,25E-08	7,90E+00	6,13E-09	0,4105	5,8130564	2,38620589	28,01	IL20RA	interleukin 20 receptor subunit alpha
105373105	6,61E-03	2,18E+00	4,66E-03	0,8429	2,8296727	2,3850061	6,43	LINC02968	long intergenic non-protein coding RNA 2968
2044	1,09E-33	3,30E+01	2,54E-34	0,195	12,2164323	2,38219419	132,59	EPHA5	EPH receptor A5
677838	8,49E-15	1,41E+01	3,32E-15	0,3023	7,8783636	2,38180448	49,82	SNORA61	small nucleolar RNA, H/ACA box 61
100216546	1,13E-13	1,29E+01	4,55E-14	0,3154	7,5441395	2,37933003	46,04	LINC01004	long intergenic non-protein coding RNA 1004
9495	2,00E-51	5,07E+01	3,06E-52	0,156	15,2095768	2,37198786	195,45	AKAP5	A-kinase anchoring protein 5
107986119	3,00E-08	7,52E+00	1,49E-08	0,4173	5,6622969	2,3631276	27,68	GSK3B-DT	GSK3B divergent transcript
256764	1,81E-34	3,37E+01	4,11E-35	0,1911	12,3636745	2,36231386	126,27	WDR72	WD repeat domain 72
100124533	1,05E-09	8,98E+00	4,90E-10	0,3796	6,2223422	2,36176586	31,65	SCARNA27	small Cajal body-specific RNA 27
105377188	8,87E-15	1,41E+01	3,47E-15	0,2999	7,8728082	2,36132187	51,91	LOC105377(	uncharacterized LOC105377188
148198	2,60E-07	6,59E+00	1,36E-07	0,4478	5,270972	2,36028217	22,86	ZNF98	zinc finger protein 98
10663	1,51E-03	2,82E+00	1,00E-03	0,7171	3,289402	2,35888847	8,89	CXCR6	C-X-C motif chemokine receptor 6
9302	9,64E-13	1,20E+01	4,02E-13	0,3249	7,2548381	2,35706797	45,72	SNORD26	small nucleolar RNA, C/D box 26
284836	3,37E-03	2,47E+00	2,31E-03	0,7732	3,046743	2,35582131	7,55	LINC00319	long intergenic non-protein coding RNA 319
105378936	7,72E-03	2,11E+00	5,47E-03	0,8479	2,7777764	2,35525726	6,23	LOC105378(	replaced by ID 26227
286097	1,80E-36	3,57E+01	3,88E-37	0,1849	12,7329605	2,35372378	138,42	MICU3	mitochondrial calcium uptake family member 3
26040	1,90E-11	1,07E+01	8,29E-12	0,3443	6,8334209	2,3530596	38,93	SETBP1	SET binding protein 1
5137	1,45E-214	2,14E+02	1,55E-216	0,0748	31,4084965	2,34799944	1040,72	PDE1C	phosphodiesterase 1C
785	1,01E-32	3,20E+01	2,39E-33	0,195	12,0327294	2,34579664	126,4	CACNB4	calcium voltage-gated channel auxiliary subunit beta 4
440081	4,89E-147	1,46E+02	1,24E-148	0,0903	25,9646713	2,34424823	685,78	DDX12P	DEAD/H-box helicase 12, pseudogene
105378724	2,92E-05	4,53E+00	1,72E-05	0,5447	4,2990373	2,34162064	14,99	LOC105378(	uncharacterized LOC105378724
100129434	2,69E-07	6,57E+00	1,41E-07	0,4434	5,2643766	2,33404663	23,52	LOC100129(	uncharacterized LOC100129434
105379365	1,07E-04	3,97E+00	6,50E-05	0,5831	3,9939465	2,32882699	13,55	LOC105379(	uncharacterized LOC105379365
105369468	1,24E-06	5,91E+00	6,74E-07	0,4681	4,9688105	2,32609124	21,14	LOC105369(	uncharacterized LOC105369468
440348	1,62E-19	1,88E+01	5,47E-20	0,2536	9,154266	2,32120782	71,31	NPIPB15	nuclear pore complex interacting protein family member B15
375690	2,60E-31	3,06E+01	6,40E-32	0,1974	11,7583043	2,32051393	117,3	WASH5P	WASP family homolog 5, pseudogene
105371762	2,42E-04	3,62E+00	1,52E-04	0,6125	3,7885187	2,32048265	12,44	LOC105371(	uncharacterized LOC105371762
100506071	1,92E-03	2,72E+00	1,29E-03	0,719	3,2187332	2,31420722	8,58	LOC100506(	uncharacterized LOC100506071
4826	1,80E-16	1,57E+01	6,67E-17	0,277	8,3527625	2,31335857	60,41	NNAT	neuronatin
84830	9,33E-41	4,00E+01	1,83E-41	0,1714	13,4883552	2,31245549	160,48	ADTRP	androgen dependent TFPI regulating protein

653061	8,80E-03	2,06E+00	6,28E-03	0,8461	2,7329012	2,31219662	6,12	GOLGA8S	golgin A8 family member S
105370672	1,01E-05	5,00E+00	5,75E-06	0,5096	4,5351964	2,31101843	17,23	LOC105370(	uncharacterized LOC105370672
102723648	5,67E-05	4,25E+00	3,38E-05	0,5572	4,1462946	2,31023515	14,62	BRPF3-AS1	BRPF3 antisense RNA 1
107986980	4,12E-04	3,39E+00	2,62E-04	0,6312	3,6500139	2,30391584	11	LINC02055	long intergenic non-protein coding RNA 2055
102723436	4,24E-03	2,37E+00	2,93E-03	0,7737	2,974761	2,30149833	7,34	LOC102723(	uncharacterized LOC102723436
105376951	6,11E-07	6,21E+00	3,25E-07	0,4504	5,1081766	2,30054987	21,9	LOC105376(	uncharacterized LOC105376951
101928689	4,40E-03	2,36E+00	3,05E-03	0,7757	2,9624486	2,29793505	7,27	LINC01424	long intergenic non-protein coding RNA 1424
4739	2,43E-128	1,28E+02	8,22E-130	0,0946	24,2410493	2,29432906	586,09	NEDD9	neural precursor cell expressed, developmentally down-regulated 9
51361	3,77E-62	6,14E+01	4,56E-63	0,1369	16,7629269	2,29431239	259,63	HOOK1	hook microtubule tethering protein 1
101929141	2,07E-04	3,68E+00	1,29E-04	0,599	3,8291437	2,29355826	12,17	LOC101929(	coiled-coil domain-containing protein 144A-like
79970	5,39E-69	6,83E+01	5,64E-70	0,1297	17,6833203	2,29292786	295,11	ZNF767P	zinc finger family member 767, pseudogene
58538	2,92E-53	5,25E+01	4,33E-54	0,1481	15,4858057	2,29273246	215,08	MPP4	MAGUK p55 scaffold protein 4
160287	2,29E-04	3,64E+00	1,43E-04	0,6023	3,8032849	2,29076162	12,09	LDHAL6A	lactate dehydrogenase A like 6A
9297	1,20E-36	3,59E+01	2,58E-37	0,1794	12,764609	2,2900597	145,41	SNORD29	small nucleolar RNA, C/D box 29
5742	2,53E-17	1,66E+01	9,09E-18	0,2667	8,584875	2,28961519	63,07	PTGS1	prostaglandin-endoperoxide synthase 1
319089	2,47E-03	2,61E+00	1,67E-03	0,7273	3,1431658	2,28609103	8,4	TTC6	tetratricopeptide repeat domain 6
84699	1,53E-06	5,82E+00	8,35E-07	0,4635	4,9269902	2,2835832	20,46	CREB3L3	cAMP responsive element binding protein 3 like 3
2564	2,20E-67	6,67E+01	2,39E-68	0,1305	17,4708461	2,28033108	285,09	GABRE	gamma-aminobutyric acid type A receptor subunit epsilon
692212	5,53E-08	7,26E+00	2,79E-08	0,4103	5,5541935	2,27876847	26,53	SNORD99	small nucleolar RNA, C/D box 99
284047	2,79E-47	4,66E+01	4,71E-48	0,1564	14,5646472	2,27837352	200,21	CCDC144BF	coiled-coil domain containing 144B, pseudogene
22999	1,64E-29	2,88E+01	4,21E-30	0,1998	11,3993656	2,27764498	111,86	RIMS1	regulating synaptic membrane exocytosis 1
256815	1,63E-06	5,79E+00	8,91E-07	0,4634	4,914244	2,27719542	20,55	C10orf67	chromosome 10 open reading frame 67
642846	2,00E-95	9,47E+01	1,23E-96	0,1091	20,8601826	2,27665591	460,39	LOC642846	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 11-like
414763	1,66E-10	9,78E+00	7,54E-11	0,3487	6,509595	2,26962907	35,98	BMS1P18	BMS1 pseudogene 18
2321	1,68E-17	1,68E+01	6,02E-18	0,2628	8,632129	2,26893136	64,74	FLT1	fms related receptor tyrosine kinase 1
283663	2,42E-05	4,62E+00	1,41E-05	0,5218	4,3420544	2,26565899	18,09	LINC00926	long intergenic non-protein coding RNA 926
109617007	5,77E-03	2,24E+00	4,05E-03	0,7857	2,8744362	2,25843668	7,09	SNORA63E	small nucleolar RNA, H/ACA box 63E
102724355	2,29E-10	9,64E+00	1,04E-10	0,3493	6,4606858	2,25681603	35,7	LOC102724(	uncharacterized LOC102724355
107984754	2,82E-24	2,35E+01	8,35E-25	0,2194	10,2836202	2,25655365	97,38	LOC107984754	
107984685	5,55E-03	2,26E+00	3,88E-03	0,7803	2,8876564	2,25334179	7,16	LOC107984(	uncharacterized LOC107984685
10388	1,46E-10	9,84E+00	6,61E-11	0,345	6,5292615	2,25289467	37,9	SYCP2	synaptonemal complex protein 2
91752	1,45E-183	1,83E+02	2,18E-185	0,0776	29,0379444	2,25278872	896,09	ZNF804A	zinc finger protein 804A
8944	2,48E-06	5,61E+00	1,37E-06	0,4657	4,8300074	2,24949012	20,2	SNORD73A	small nucleolar RNA, C/D box 73A
55282	1,97E-04	3,71E+00	1,22E-04	0,5855	3,8411272	2,24909944	12,9	LRRC36	leucine rich repeat containing 36
677847	2,54E-05	4,60E+00	1,48E-05	0,5179	4,3309983	2,24298123	16,62	SNORA81	small nucleolar RNA, H/ACA box 81
6947	2,28E-11	1,06E+01	1,00E-11	0,3294	6,8064825	2,24238763	41,45	TCN1	transcobalamin 1
105376794	7,50E-121	1,20E+02	2,94E-122	0,0953	23,5139273	2,23974647	558,4	LOC105376794	
283011	6,50E-08	7,19E+00	3,29E-08	0,4053	5,5251997	2,23960093	27,11	FLJ37201	tigger transposable element derived 2 pseudogene
105373796	2,71E-08	7,57E+00	1,35E-08	0,3942	5,6801323	2,23918406	28,39	LOC105373(	uncharacterized LOC105373796
112268259	4,49E-62	6,13E+01	5,45E-63	0,1336	16,7523257	2,23742114	267,93	LOC112268259	
112268235	6,18E-03	2,21E+00	4,34E-03	0,7843	2,8521122	2,23677152	7,08	LOC112268(	uncharacterized LOC112268235
163255	1,79E-04	3,75E+00	1,11E-04	0,5774	3,8648948	2,23176374	12,88	ZNF540	zinc finger protein 540
255738	1,41E-127	1,27E+02	4,83E-129	0,0923	24,1679964	2,23093103	641,39	PCSK9	proprotein convertase subtilisin/kexin type 9
105374421	1,19E-05	4,92E+00	6,83E-06	0,495	4,4987953	2,22703706	17,57	LOC105374(	uncharacterized LOC105374421
105373264	1,03E-03	2,99E+00	6,73E-04	0,6543	3,4004415	2,2248545	10,55	LOC105373264	
4045	4,83E-04	3,32E+00	3,09E-04	0,6153	3,6076105	2,21981712	11,59	LSAMP	limbic system associated membrane protein
221806	2,88E-49	4,85E+01	4,63E-50	0,1488	14,8772146	2,21421588	213,86	VWDE	von Willebrand factor D and EGF domains
102723305	1,60E-03	2,80E+00	1,07E-03	0,6768	3,2714013	2,2140688	9,31	LOC102723(	uncharacterized LOC102723305
2915	4,27E-04	3,37E+00	2,72E-04	0,608	3,640684	2,21365571	11,57	GRM5	glutamate metabotropic receptor 5
114569	1,72E-172	1,72E+02	3,02E-174	0,0785	28,1418185	2,20815167	898,54	MAL2	mal, T cell differentiation protein 2
205860	1,53E-87	8,68E+01	1,10E-88	0,1105	19,9656554	2,20577821	391,52	TRIML2	tripartite motif family like 2
100423020	1,26E-03	2,90E+00	8,32E-04	0,658	3,341839	2,19883984	10,46	MIR4258	microRNA 4258
103504738	5,46E-03	2,26E+00	3,81E-03	0,7596	2,8932519	2,19779665	8,07	MIR6859-4	microRNA 6859-4
107986035	9,29E-04	3,03E+00	6,08E-04	0,6405	3,4280067	2,19556933	10,34	LOC107986(	035
3861	6,52E-04	3,19E+00	4,22E-04	0,6215	3,5260057	2,19125657	11,36	KRT14	keratin 14
93099	2,90E-24	2,35E+01	8,60E-25	0,213	10,2808595	2,19008366	96,35	DMKN	dermokine
100505881	2,81E-38	3,76E+01	5,85E-39	0,1677	13,0563413	2,18983694	172,19	MAGI2-AS3	MAGI2 antisense RNA 3
55632	7,09E-172	1,71E+02	1,25E-173	0,0778	28,0912471	2,18531695	1101,96	G2E3	G2/M-phase specific E3 ubiquitin protein ligase
101927391	6,14E-04	3,21E+00	3,97E-04	0,616	3,5422603	2,18213255	11,45	MIOS-DT	MIOS divergent transcript
105375726	3,31E-23	2,25E+01	1,01E-23	0,2173	10,0410304	2,18195001	93,65	MAL2-AS1	MAL2 antisense RNA 1
105373041	2,93E-06	5,53E+00	1,62E-06	0,4546	4,7960414	2,18050669	20,55	LOC105373(	uncharacterized LOC105373041
5159	5,33E-28	2,73E+01	1,43E-28	0,1966	11,0885299	2,1804166	113,88	PDGFRB	platelet derived growth factor receptor beta
102723564	4,82E-26	2,53E+01	1,36E-26	0,2043	10,6731919	2,17999957	109,35	LOC102723(	E3 ubiquitin-protein ligase HERC2-like
221322	2,51E-23	2,26E+01	7,61E-24	0,2164	10,0685554	2,17922469	99,51	TBC1D32	TBC1 domain family member 32
347051	1,56E-04	3,81E+00	9,60E-05	0,5584	3,9004898	2,17802616	13,66	SLC10A5	solute carrier family 10 member 5
105377845	1,90E-32	3,17E+01	4,53E-33	0,1811	11,9797949	2,17001607	133,35	LOC105377(	uncharacterized LOC105377845
7103	3,48E-29	2,85E+01	8,99E-30	0,1914	11,3331154	2,16912826	120,78	TSPAN8	tetraspanin 8
140828	4,45E-240	2,39E+02	3,70E-242	0,0652	33,2321508	2,16672744	1494,72	LINC00261	long intergenic non-protein coding RNA 261
6925	4,98E-45	4,43E+01	8,91E-46	0,1522	14,2019565	2,16222753	201,63	TCF4	transcription factor 4
7644	1,36E-127	1,27E+02	4,67E-129	0,0894	24,1694305	2,16068141	653,28	ZNF91	zinc finger protein 91
401265	1,09E-04	3,96E+00	6,63E-05	0,5415	3,9891716	2,16002555	14,65	KLHL31	kelch like family member 31
107985031	7,20E-07	6,14E+00	3,85E-07	0,4253	5,0764697	2,15910426	24,85	LOC107985(	uncharacterized LOC107985031
79940	3,95E-166	1,65E+02	7,62E-168	0,0782	27,6137146	2,15861829	915,21	LINC00472	long intergenic non-protein coding RNA 472
100132101	7,49E-04	3,13E+00	4,87E-04	0,6185	3,4878268	2,15716305	11,28	HERC2P7	HERC2 pseudogene 7
104548971	9,00E-03	2,05E+00	6,43E-03	0,7914	2,725214	2,15681917	6,73	SALRNA1	senescence associated long non-coding RNA 1
55349	2,33E-20	1,96E+01	7,68E-21	0,2298	9,3640149	2,15141442	82,76	CHDH	choline dehydrogenase
23769	3,57E-05	4,45E+00	2,10E-05	0,5052	4,2538627	2,14894126	16,84	FLRT1	fibronectin leucine rich transmembrane protein 1
117155	8,24E-06	5,08E+00	4,67E-06	0,4688	4,579009	2,14684339	18,99	CATSPER2	cation channel sperm associated 2
110841583	6,12E-05	4,21E+00	3,66E-05	0,5201	4,1279589	2,14676324	15,73	LAMC1-AS1	LAMC1 antisense RNA 1
105372130	2,21E-12	1,17E+01	9,33E-13	0,3004	7,1400512	2,14453431	49,21	LOC105372(	uncharacterized LOC105372130
400765	1,90E-72	7,17E+01	1,84E-73	0,1182	18,1301748	2,14210909	331,99	MIR137HG	MIR137 host gene
85390	5,58E-08	7,25E+00	2,81E-08	0,3854	5,5526806	2,14022554	29,11	SNORD14D	small nucleolar RNA, C/D box 14D
105370282	5,71E-03	2,24E+00	4,00E-03	0,743	2,8782018	2,13855395	7,75	LOC105370(	uncharacterized LOC105370282
105378980	8,70E-07	6,06E+00	4,67E-07	0,4242	5,0394166	2,13771804	25,46	LOC105378(	uncharacterized LOC105378980
105373802	1,03E-05	4,99E+00	5,90E-06	0,4709	4,529772	2,13328871	18,83	LOC105373802	
645323	2,05E-09	8,69E+00	9,70E-10	0,3482	6,1142743	2,12929167	35,28	LINC00461	long intergenic non-protein coding RNA 461
112268121	2,28E-08	7,64E+00	1,13E-08	0,3727	5,7097441	2,12780319	30,83	LOC112268121	
400655	3,57E-17	1,64E+01	1,29E-17	0,249	8,5445508	2,1273114	72,62	LINC02864	long intergenic non-protein coding RNA 2864
107985393	1,02E-02	1,99E+00	7,29E-03	0,7926	2,6832083	2,12684132	6,68	LOC107985393	
168374	3,99E-46	4,54E+01	6,95E-47	0,1479	14,379628	2,12609473	206,56	ZNF92	zinc finger protein 92
102723780	1,15E-16	1,59E+01	4,24E-17	0,2529	8,406051	2,12591838	66,31	FRG1FP	FSHD region gene 1 family member F, pseudogene
4878	1,71E-03	2,77E+00	1,14E-03	0,6535	3,2524007	2,1255264	9,84	NPPA	natriuretic peptide A
4112	2,30E-09	8,64E+00	1,09E-09	0,3487	6,0951782	2,12533757	36,62	MAGEB1	MAGE family member B1
81706	9,59E-10	9,02E+00	4,47E-10	0,3407	6,2365822	2,12492425	39,87	PPP1R14C	protein phosphatase 1 regulatory inhibitor subunit 14C
24	1,79E-03	2,75E+00	1,20E-03	0,656	3,2386852	2,12470591	10,04	ABCA4	ATP binding cassette subfamily A member 4
105373805	1,58E-03	2,80E+00	1,05E-03	0,6481	3,2766411	2,12346666	9,88	STAT4-AS1	STAT4 antisense RNA 1
26792	1,86E-16	1,57E+01	6,86E-17	0,2542	8,3493774	2,1223535	66,01	SNORD57	small nucleolar RNA, C/D box 57
9481	1,56E-25	2,48E+01	4,46E-26	0,2006	10,5622311	2,11876261	109,1	SLC25A27	solute carrier family 25 member 27
100616403	3,05E-03	2,52E+00	2,08E-03	0,688	3,0784796	2,11810565	8,78	MIR4691	microRNA 4691
105747689	1,24E-06	5,91E+00	6,74E-07	0,4263	4,9687439	2,11802259	23,11	NABP1-OT1	replaced by ID 64859
2560	3,66E-03	2,44E+00	2,52E-03	0,701	3,0215093	2,11801156	8,82	GABRB1	gamma-aminobutyric acid type A receptor subunit beta1
5343	2,93E-03	2,53E+00	2,00E-03	0,6847	3,0907071	2,11613886	8,78	PLGLB1	plasminogen like B1
202559	1,07E-02	1,97E+00	7,67E-03	0,7929	2,666431	2,1140889	6,61	KHDRBS2	KH RNA binding domain containing, signal transduction associated 2
6335	3,36E-35	3,45E+01	7,51E-36	0,1688	12,4995458	2,10989863	176,57	SCN9A	sodium voltage-gated channel alpha subunit 9
107987222	1,17E-16	1,59E+01	4,28E-17	0,2507	8,4049779	2,10739959	66,71	LOC107987222	
10052	8,97E-15	1,40E+01	3,51E-15	0,2677	7,8713803	2,10717794	62,17	GJC1	gap junction protein gamma 1
9509	6,10E-03	2,21E+00	4,29E-03	0,7367	2,8561282	2,10409917	7,61	ADAMTS2	ADAM metallopeptidase with thrombospondin type 1 motif 2
102723534	3,29E-07	6,48E+00	1,73E-07	0,4022	5,2263734	2,10226947	26,26	LOC102723(	HECT and RLD domain containing E3 ubiquitin protein ligase 2 pseudogene
644285	1,21E-02	1,92E+00	8,73E-03	0,7994	2,6226295	2,0966482	6,48	LOC644285	uncharacterized LOC644285
102723624	4,08E-03	2,39E+00	2,81E-03	0,7018	2,9873394	2,09661928	8,6	LOC102723(	uncharacterized LOC102723624
654320	7,67E-20	1,91E+01	2,56E-20	0,2269	9,2361032	2,09603895	84,87	SNORA8	small nucleolar RNA, H/ACA box 8
390595	7,75E-06	5,11E+00	4,39E-06	0,4561	4,5921084	2,09437146	20,58	UBAP1L	ubiquitin associated protein 1 like
253018	1,77E-05	4,75E+00	1,02E-05	0,4734	4,4124025	2,08863986	19,61	HCG27	HLA complex group 27
594839	9,32E-08	7,03E+00	4,76E-08	0,3825	5,4601662	2,08863435	29,14	SNORA33	small nucleolar RNA, H/ACA box 33
100144602	1,16E-09	8,94E+00	5,44E-10	0,3361	6,205788	2,08570895	39,97	EPHA5-AS1	EPHA5 antisense RNA 1
55096	7,37E-05	4,13E+00	4,43E-05	0,5106	4,0838093	2,08528079	16,16	EBLN2	endogenous Bornavirus like nucleoprotein 2
100506215	1,99E-13	1,27E+01	8,09E-14	0,2791	7,4688434	2,08436235	54,03	PAXBP1-AS1	PAXBP1 antisense RNA 1
57191	5,18E-06	5,29E+00	2,90E-06	0,4454	4,6775362	2,08336448	21,55	VN1R1	vomeronasal 1 receptor 1
8997	1,50E-32	3,18E+01	3,58E-33	0,1736	11,9993394	2,08329461	152,4	KALRN	kalirin RhoGEF kinase
55335	3,68E-06	5,43E+00	2,04E-06	0,4386	4,7490254	2,08274718	21,58	NIPSNAP3B	nipsnap homolog 3B

266722	5,95E-33	3,22E+01	1,40E-33	0,1725	12,0767164	2,08274493	145,67	HS6ST3	heparan sulfate 6-O-sulfotransferase 3
5445	2,87E-32	3,15E+01	6,88E-33	0,1743	11,9452169	2,08166094	151,47	PON2	paraoxonase 2
256435	1,62E-06	5,79E+00	8,84E-07	0,4233	4,9158623	2,08069162	23,69	ST6GALNAC	ST6 N-acetylgalactosaminide alpha-2,6-sialyltransferase 3
105377303	2,04E-19	1,87E+01	6,90E-20	0,2278	9,1292137	2,08006342	80,8	PRDM8-AS1	PRDM8 antisense RNA 1
112267868	2,86E-06	5,54E+00	1,58E-06	0,4331	4,8013363	2,07942121	23,67	LOC112267	uncharacterized LOC112267868
100506885	4,48E-05	4,35E+00	2,66E-05	0,495	4,2010539	2,07942068	17,24	LNC-LBCS	lncRNA bladder and prostate cancer suppressor, hnRNPK interacting
692073	4,83E-08	7,32E+00	2,43E-08	0,3726	5,5783672	2,07825013	30,94	SNORA16A	small nucleolar RNA, H/ACA box 16A
101241892	3,86E-06	5,41E+00	2,15E-06	0,4381	4,7390553	2,07606642	21,45	NPTN-IT1	NPTN intronic transcript 1
26800	6,98E-12	1,12E+01	2,99E-12	0,2972	6,9780937	2,07423117	47,31	SNORD49A	small nucleolar RNA, C/D box 49A
105376375	4,08E-11	1,04E+01	1,80E-11	0,3085	6,7212478	2,07380887	44,78	LOC105376	uncharacterized LOC105376375
4060	5,15E-06	5,29E+00	2,89E-06	0,4432	4,6787666	2,07376318	22,63	LUM	lumican
101928106	8,76E-09	8,06E+00	4,26E-09	0,3524	5,8738848	2,06981842	34,1	LINC02522	long intergenic non-protein coding RNA 2522
2982	4,11E-04	3,39E+00	2,61E-04	0,5663	3,6507516	2,06748819	12,87	GUCY1A1	guanylate cyclase 1 soluble subunit alpha 1
729747	3,22E-14	1,35E+01	1,28E-14	0,2682	7,7077156	2,06714248	61,23	ZNF878	zinc finger protein 878
7700	5,80E-90	8,92E+01	3,96E-91	0,102	20,2446258	2,065933	469,99	ZNF141	zinc finger protein 141
283970	2,15E-85	8,47E+01	1,60E-86	0,1046	19,7152283	2,06254855	425,07	PDXDC2P-N	PDXDC2P-NPIPB14P readthrough
9028	2,90E-09	8,54E+00	1,38E-09	0,34	6,0575821	2,05969817	38,3	RHBDL1	rhomboid like 1
105370676	8,43E-03	2,07E+00	6,00E-03	0,7494	2,747673	2,0591077	7,4	LINC02320	long intergenic non-protein coding RNA 2320
107986197	1,06E-02	1,97E+00	7,65E-03	0,7705	2,666965	2,05486186	7,51	LOC107986	uncharacterized LOC107986197
126353	4,21E-66	6,54E+01	4,68E-67	0,1187	17,300333	2,05381152	321,33	MISP	mitotic spindle positioning
55432	3,36E-151	1,50E+02	8,19E-153	0,078	26,3323054	2,0530669	1241,4	YOD1	YOD1 deubiquitinase
85444	2,10E-135	1,35E+02	6,27E-137	0,0824	24,9068427	2,05300085	804,92	LRRCC1	leucine rich repeat and coiled-coil centrosomal protein 1
102724273	1,43E-02	1,84E+00	1,04E-02	0,801	2,5629159	2,05287396	6,31	LOC102724	uncharacterized LOC102724273
4886	5,99E-11	1,02E+01	2,66E-11	0,3079	6,6641522	2,05182282	43,54	NPY1R	neuropeptide Y receptor Y1
1734	1,70E-13	1,28E+01	6,88E-14	0,2739	7,4900987	2,05141961	57,38	DIO2	iodothyronine deiodinase 2
107987118	1,83E-03	2,74E+00	1,23E-03	0,6344	3,2326395	2,05094073	10,67	LOC107987	replaced by ID 401548
124093	3,18E-19	1,85E+01	1,08E-19	0,2258	9,0804438	2,05063043	83,66	CCDC78	coiled-coil domain containing 78
80055	4,90E-71	7,03E+01	4,91E-72	0,1142	17,948694	2,04936258	352,89	PGAP1	post-GPI attachment to proteins inositol deacylase 1
57512	2,12E-29	2,87E+01	5,47E-30	0,1796	11,3765936	2,04296835	131,79	GPR158	G protein-coupled receptor 158
102724434	7,65E-42	4,11E+01	1,47E-42	0,1494	13,6729927	2,04225903	230,42	LOC102724	uncharacterized LOC102724434
6347	6,72E-62	6,12E+01	8,21E-63	0,1219	16,7278986	2,03955677	327,23	CCL2	C-C motif chemokine ligand 2
151126	5,81E-16	1,52E+01	2,18E-16	0,248	8,2117008	2,03620702	67,27	ZNF385B	zinc finger protein 385B
105376042	2,69E-10	9,57E+00	1,23E-10	0,316	6,4360239	2,03404029	43,93	LOC105376	uncharacterized LOC105376042
105375384	3,09E-03	2,51E+00	2,11E-03	0,6613	3,0739821	2,03283234	9,35	LOC105375	uncharacterized LOC105375384
64921	4,05E-66	6,54E+01	4,50E-67	0,1171	17,3026108	2,02598286	327,47	CASD1	CAS1 domain containing 1
107986566	2,57E-05	4,59E+00	1,50E-05	0,4674	4,3286176	2,02340284	18,78	LOC107986	566
9720	2,88E-09	8,54E+00	1,37E-09	0,3335	6,058442	2,02040833	36,45	CCDC144A	coiled-coil domain containing 144A
107984285	1,94E-05	4,71E+00	1,13E-05	0,46	4,3909667	2,02002222	20,63	LOC107984	replaced by ID 23185
158056	6,17E-23	2,22E+01	1,89E-23	0,2022	9,9787352	2,01774128	113,69	MAMDC4	MAM domain containing 4
100142659	1,69E-02	1,77E+00	1,24E-02	0,8063	2,5014131	2,01677542	6,24	CTAGE8	CTAGE family member 8
57864	1,01E-02	2,00E+00	7,25E-03	0,751	2,6850282	2,01640938	7,2	SLC46A2	solute carrier family 46 member 2
54463	2,81E-06	5,55E+00	1,55E-06	0,4194	4,8047904	2,01532284	24,03	RETREG1	reticulophagy regulator 1
58487	2,31E-128	1,28E+02	7,77E-130	0,0831	24,2433338	2,01512413	1038,77	CREBZF	CREB/ATF bZIP transcription factor
3294	2,69E-07	6,57E+00	1,40E-07	0,3825	5,2647937	2,0139027	28,87	HSD17B2	hydroxysteroid 17-beta dehydrogenase 2
4093	6,02E-16	1,52E+01	2,26E-16	0,245	8,2073663	2,01082813	68,25	SMAD9	SMAD family member 9
503569	1,78E-52	5,17E+01	2,67E-53	0,1308	15,368403	2,01035684	251,59	RGMB-AS1	RGMB antisense RNA 1
9304	1,14E-17	1,69E+01	4,08E-18	0,2317	8,6764796	2,01019569	83,52	SNORD22	small nucleolar RNA, C/D box 22
340390	1,51E-08	7,82E+00	7,42E-09	0,3474	5,7811463	2,00864986	34,18	WDR97	WD repeat domain 97
100885778	8,80E-05	4,06E+00	5,32E-05	0,497	4,0411435	2,00849456	16,58	NALCN-AS1	NALCN antisense RNA 1
27237	1,63E-11	1,08E+01	7,08E-12	0,2929	6,8560366	2,00817078	47,49	ARHGEF16	Rho guanine nucleotide exchange factor 16
124989	1,98E-11	1,07E+01	8,65E-12	0,2941	6,8273516	2,00779682	47,71	EFCAB13	EF-hand calcium binding domain 13
100616184	1,14E-03	2,94E+00	7,53E-04	0,5958	3,3694603	2,00746059	11,44	MIR4477A	microRNA 4477a
112268030	4,37E-03	2,36E+00	3,02E-03	0,6769	2,9653332	2,00711681	9,42	LOC112268	uncharacterized LOC112268030
7049	8,63E-180	1,79E+02	1,38E-181	0,0696	28,73536	2,00052532	1197,23	TGFBR3	transforming growth factor beta receptor 3
10655	9,82E-09	8,01E+00	4,78E-09	0,3416	5,8546706	1,99999319	34,96	DMRT2	doublesex and mab-3 related transcription factor 2
158257	5,71E-09	8,24E+00	2,76E-09	0,3363	5,9453913	1,99952743	38,2	LINC02603	long intergenic non-protein coding RNA 2603
51334	2,85E-109	1,09E+02	1,36E-110	0,0895	22,344822	1,99897546	621,26	PRR16	proline rich 16
105369313	1,14E-05	4,94E+00	6,51E-06	0,4433	4,509125	1,9988475	20,52	LOC105369	uncharacterized LOC105369313
753	6,76E-03	2,17E+00	4,77E-03	0,7077	2,8224265	1,99737955	8,16	LDLRAD4	low density lipoprotein receptor class A domain containing 4
26772	6,12E-03	2,21E+00	4,30E-03	0,6992	2,8552493	1,99632069	8,19	SNORD4B	small nucleolar RNA, C/D box 4B
57569	6,33E-17	1,62E+01	2,31E-17	0,2353	8,4771614	1,99429072	75,74	ARHGAP20	Rho GTPase activating protein 20
137209	4,62E-06	5,34E+00	2,58E-06	0,4238	4,7017679	1,99251832	22,67	ZNF572	zinc finger protein 572
107986556	4,29E-04	3,37E+00	2,74E-04	0,5474	3,6390898	1,9919354	13,3	LOC107986	uncharacterized LOC107986556
102238594	1,93E-05	4,71E+00	1,12E-05	0,453	4,3926119	1,98980914	20,46	SPACA6-AS	SPACA6 antisense RNA 1
56920	8,81E-11	1,01E+01	3,94E-11	0,3008	6,6063265	1,98733928	44,92	SEMA3G	semaphorin 3G
406882	3,47E-02	1,46E+00	2,63E-02	0,8942	2,2215174	1,98646612	5,05	MIRLET7A2	microRNA let-7a-2
7767	2,13E-80	7,97E+01	1,74E-81	0,1038	19,1193302	1,98530012	432,66	ZNF224	zinc finger protein 224
105376041	8,39E-12	1,11E+01	3,61E-12	0,2855	6,9517855	1,98456517	51,2	LOC105376	uncharacterized LOC105376041
80031	7,75E-09	8,11E+00	3,76E-09	0,3362	5,8944577	1,98194117	37,95	SEMA6D	semaphorin 6D
105378526	9,36E-09	8,03E+00	4,55E-09	0,3378	5,8627489	1,98029752	37,7	LOC105378	526
106614088	1,52E-12	1,18E+01	6,40E-13	0,2749	7,1916799	1,9771351	53,67	MIR34AHG	MIR34A host gene
64388	1,99E-02	1,70E+00	1,47E-02	0,8092	2,4395245	1,97413174	6,05	GREM2	gremlin 2, DAN family BMP antagonist
58496	6,17E-92	9,12E+01	4,08E-93	0,0964	20,4688705	1,974096	497,12	LY6G5B	lymphocyte antigen 6 family member G5B
112268037	4,05E-05	4,39E+00	2,39E-05	0,4671	4,2246007	1,97318859	18,26	LOC112268	037
135	5,58E-14	1,33E+01	2,24E-14	0,2583	7,6362891	1,97248	61,64	ADORA2A	adenosine A2a receptor
348654	1,01E-161	1,61E+02	2,09E-163	0,0723	27,2416525	1,97052478	1202,43	GEN1	GEN1 Holliday junction 5' flap endonuclease
399959	8,35E-172	1,71E+02	1,48E-173	0,0701	28,085308	1,96914069	1230,94	MIR100HG	mir-100-let-7a-2-mir-125b-1 cluster host gene
259232	4,73E-51	5,03E+01	7,32E-52	0,1299	15,1522486	1,96900604	267,72	NALCN	sodium leak channel, non-selective
153579	1,40E-02	1,85E+00	1,01E-02	0,7657	2,5709831	1,9686252	7,14	BTNL9	butyrophilin like 9
145957	2,36E-35	3,46E+01	5,25E-36	0,1571	12,5279424	1,96807965	170,72	NRG4	neuregulin 4
100302143	9,96E-04	3,00E+00	6,53E-04	0,5771	3,4085933	1,96705692	12,21	MIR1248	microRNA 1248
102724711	1,37E-04	3,86E+00	8,37E-05	0,4999	3,9335908	1,96643593	16,13	LOC102724	uncharacterized LOC102724711
100616487	7,19E-03	2,14E+00	5,08E-03	0,7014	2,8015998	1,96509242	8,09	MIR4517	microRNA 4517
112268214	1,23E-02	1,91E+00	8,86E-03	0,7503	2,617541	1,96381163	7,06	LOC112268	214
1612	8,16E-167	1,66E+02	1,56E-168	0,0709	27,6710993	1,96144721	1135,1	DAPK1	death associated protein kinase 1
79986	1,88E-104	1,04E+02	9,81E-106	0,0898	21,8393575	1,96143501	633,14	ZNF702P	zinc finger protein 702, pseudogene
5139	1,41E-03	2,85E+00	9,37E-04	0,5927	3,3088654	1,96111497	12	PDE3A	phosphodiesterase 3A
9099	1,15E-03	2,94E+00	7,62E-04	0,5816	3,366268	1,95775042	11,93	USP2	ubiquitin specific peptidase 2
152110	1,54E-08	7,81E+00	7,56E-09	0,3388	5,7779973	1,95731097	36,3	NEK10	NIMA related kinase 10
104472717	2,86E-125	1,25E+02	1,03E-126	0,0817	23,945386	1,95703525	750,3	LINC01224	long intergenic non-protein coding RNA 1224
117608	1,31E-48	4,79E+01	2,14E-49	0,1324	14,7744704	1,95666822	258,17	ZNF354B	zinc finger protein 354B
91351	7,13E-208	2,07E+02	8,35E-210	0,0633	30,9115553	1,95636404	1445,82	DDX60L	DExD/H-box 60 like
7562	2,83E-31	3,05E+01	6,96E-32	0,1664	11,751184	1,95568037	164,4	ZNF708	zinc finger protein 708
100287329	2,68E-02	1,57E+00	2,01E-02	0,8396	2,3246042	1,95162516	5,89	LOC100287	uncharacterized LOC100287329
55084	5,75E-13	1,22E+01	2,38E-13	0,2664	7,3253777	1,95129394	61,19	SOBP	sine oculis binding protein homolog
257019	1,17E-116	1,16E+02	4,93E-118	0,0844	23,0972667	1,94982796	751,49	FRMD3	FERM domain containing 3
53637	1,49E-23	2,28E+01	4,51E-24	0,1926	10,1199069	1,9491675	113,21	S1PR5	sphingosine-1-phosphate receptor 5
115677	6,19E-24	2,32E+01	1,85E-24	0,1909	10,2067576	1,94837085	116,3	NOSTRIN	nitric oxide synthase trafficking
107985354	1,42E-02	1,85E+00	1,03E-02	0,7598	2,5640339	1,94810852	6,94	LOC107985	uncharacterized LOC107985354
100652865	2,27E-02	1,64E+00	1,68E-02	0,8144	2,3906358	1,9469501	5,97	LINC00539	long intergenic non-protein coding RNA 539
107984275	1,91E-03	2,72E+00	1,28E-03	0,6045	3,2197674	1,94640433	10,97	LOC107984	uncharacterized LOC107984275
2273	3,07E-112	1,12E+02	1,39E-113	0,0858	22,6503045	1,9445282	650,32	FHL1	four and a half LIM domains 1
130940	7,36E-08	7,13E+00	3,73E-08	0,3531	5,5030508	1,94321476	34,17	CCDC148	coiled-coil domain containing 148
653073	2,41E-04	3,62E+00	1,51E-04	0,5126	3,7897131	1,9425871	14,92	GOLGA8J	golgin A8 family member J
57650	0	#NUM!	0	0,0462	41,965878	1,93955155	4770,34	CIP2A	cellular inhibitor of PP2A
100113381	3,40E-06	5,47E+00	1,88E-06	0,407	4,7654533	1,93932274	25,92	SNORD19B	small nucleolar RNA, C/D box 19B
220416	1,38E-02	1,86E+00	1,01E-02	0,7532	2,5739139	1,93854354	6,93	LRRC63	leucine rich repeat containing 63
401024	3,80E-42	4,14E+01	7,27E-43	0,1412	13,7242672	1,9378962	215,79	FSIP2	fibrous sheath interacting protein 2
101929356	2,15E-04	3,67E+00	1,34E-04	0,5068	3,8191199	1,93566595	15,93	LOC101929	356
4820	0	#NUM!	0	0,0484	40,0029314	1,93474539	3785,08	NKTR	natural killer cell triggering receptor
57684	2,73E-72	7,16E+01	2,66E-73	0,1068	18,1099686	1,93392436	389,23	ZBTB26	zinc finger and BTB domain containing 26
6657	8,17E-06	5,09E+00	4,63E-06	0,4221	4,5807254	1,93362282	26,16	SOX2	SRY-box transcription factor 2
407043	1,54E-03	2,81E+00	1,03E-03	0,5887	3,28232	1,93237989	12	MIR7-1	microRNA 7-1
1462	2,30E-09	8,64E+00	1,09E-09	0,3168	6,095163	1,93120672	41,5	VCAN	versican
390535	2,48E-02	1,61E+00	1,85E-02	0,8199	2,355045	1,9308809	5,99	GOLGA8EP	golgin A8 family member E, pseudogene
157807	2,80E-36	3,56E+01	6,09E-37	0,1519	12,6977091	1,92911863	207,25	CLVS1	clavesin 1
340895	5,72E-03	2,24E+00	4,01E-03	0,6702	2,8776561	1,92872676	8,83	MALRD1	MAM and LDL receptor class A domain containing 1
134429	1,27E-124	1,24E+02	4,65E-126	0,0806	23,8825591	1,925068	980,97	STARD4	StAR related lipid transfer domain containing 4
107986785	8,18E-03	2,09E+00	5,82E-03	0,6977	2,7579894	1,92431861	8,93	LOC107986	uncharacterized LOC107986785
7134	2,62E-03	2,58E+00	1,78E-03	0,6152	3,125009	1,92239973	10,89	TNNC1	troponin C1, slow skeletal and cardiac type

57088	2,30E-60	5,96E+01	2,93E-61	0,1164	16,5136668	1,92181615	348,22	PLSCR4	phospholipid scramblase 4
107987160	1,52E-04	3,82E+00	9,37E-05	0,4916	3,9064321	1,92025461	17,8	LOC107987	uncharacterized LOC107987160
783	2,48E-09	8,61E+00	1,18E-09	0,3156	6,0827474	1,91999128	41,36	CACNB2	calcium voltage-gated channel auxiliary subunit beta 2
112268263	1,87E-42	4,17E+01	3,55E-43	0,1393	13,7761538	1,9193212	225,52	LOC112268	uncharacterized LOC112268263
100874188	1,76E-02	1,75E+00	1,29E-02	0,7717	2,4859585	1,91840136	6,97	LINC00571	long intergenic non-protein coding RNA 571
107986291	3,30E-04	3,48E+00	2,08E-04	0,5172	3,7085852	1,91812256	14,74	LOC107986291	
101929575	1,35E-03	2,87E+00	8,98E-04	0,5769	3,3208095	1,91585753	11,82	CFAP61-AS1	CFAP61 antisense RNA 1
1577	7,07E-11	1,02E+01	3,15E-11	0,2885	6,6392508	1,91529862	48,84	CYP3A5	cytochrome P450 family 3 subfamily A member 5
165055	2,05E-99	9,87E+01	1,18E-100	0,0899	21,2983811	1,91483745	598,2	CCDC138	coiled-coil domain containing 138
619569	4,25E-03	2,37E+00	2,94E-03	0,6437	2,973927	1,91441541	9,88	SNORA41	small nucleolar RNA, H/ACA box 41
170958	1,29E-30	2,99E+01	3,23E-31	0,1647	11,6207576	1,91347974	157,22	ZNF525	zinc finger protein 525
112268458	5,65E-05	4,25E+00	3,37E-05	0,4612	4,1471242	1,91285546	18,69	LOC112268	keratinocyte proline-rich protein-like
101929819	1,04E-12	1,20E+01	4,35E-13	0,2638	7,2441288	1,91091756	57,95	LOC101929	putative uncharacterized protein FLJ44672
126068	5,40E-53	5,23E+01	8,05E-54	0,1237	15,4458454	1,91064253	314,45	ZNF441	zinc finger protein 441
283537	1,67E-74	7,38E+01	1,54E-75	0,1038	18,3912277	1,9089434	534,33	SLC46A3	solute carrier family 46 member 3
2570	2,93E-17	1,65E+01	1,06E-17	0,2227	8,5675636	1,90772939	82,45	GABRR2	gamma-aminobutyric acid type A receptor subunit rho2
27145	5,54E-06	5,26E+00	3,11E-06	0,4086	4,6636113	1,90534842	24,31	FILIP1	filamin A interacting protein 1
5649	1,72E-55	5,48E+01	2,43E-56	0,1205	15,8156018	1,90522541	315,95	RELN	reelin
132430	4,32E-33	3,24E+01	1,02E-33	0,1573	12,1030875	1,90420209	174,34	PABPC4L	poly(A) binding protein cytoplasmic 4 like
102723846	8,57E-05	4,07E+00	5,18E-05	0,4705	4,0474635	1,90419844	17,58	LOC102723	uncharacterized LOC102723846
102724830	1,39E-04	3,86E+00	8,52E-05	0,4844	3,9294115	1,90332156	17,62	LOC102724	uncharacterized LOC102724830
79915	1,35E-173	1,73E+02	2,34E-175	0,0674	28,2324716	1,90327666	1316,66	ATAD5	ATPase family AAA domain containing 5
101927552	8,90E-21	2,01E+01	2,90E-21	0,201	9,4662888	1,90267111	99,42	LOC101927	uncharacterized LOC101927552
144486	2,62E-08	7,58E+00	1,30E-08	0,3345	5,6854238	1,90198748	35,15	CEP83-DT	CEP83 divergent transcript
105369477	3,48E-14	1,35E+01	1,38E-14	0,2468	7,697809	1,89989982	67,17	LOC105369	uncharacterized LOC105369477
221476	3,82E-11	1,04E+01	1,68E-11	0,2822	6,7310322	1,89966753	49,71	PI16	peptidase inhibitor 16
7025	2,53E-124	1,24E+02	9,36E-126	0,0796	23,853314	1,89885955	834,41	NR2F1	nuclear receptor subfamily 2 group F member 1
4254	4,37E-48	4,74E+01	7,26E-49	0,1291	14,6919801	1,89741698	264,79	KITLG	KIT ligand
64220	9,23E-07	6,03E+00	4,96E-07	0,3771	5,0277018	1,8961725	28,21	STRA6	signaling receptor and transporter of retinol STRA6
100506124	1,63E-04	3,79E+00	1,00E-04	0,4874	3,8898945	1,89604793	17,4	LOC100506	uncharacterized LOC100506124
85015	7,14E-77	7,61E+01	6,34E-78	0,1014	18,6867661	1,89558513	488,47	USP45	ubiquitin specific peptidase 45
80039	3,18E-03	2,50E+00	2,18E-03	0,6181	3,0647934	1,89439542	10,56	FAM106A	family with sequence similarity 106 member A
107985007	4,71E-03	2,33E+00	3,28E-03	0,644	2,9405768	1,89373219	9,7	LOC107985	007
9340	2,65E-03	2,58E+00	1,80E-03	0,6058	3,1210125	1,89057952	10,61	GLP2R	glucagon like peptide 2 receptor
653720	6,67E-03	2,18E+00	4,70E-03	0,6672	2,8266776	1,88604247	8,7	GOLGA8M	golgin A8 family member M
102723465	5,02E-04	3,30E+00	3,22E-04	0,5242	3,5967485	1,88544709	14,57	ELF3-AS1	ELF3 antisense RNA 1
55576	8,01E-04	3,10E+00	5,22E-04	0,5432	3,469348	1,88457104	13,47	STAB2	stabilin 2
222663	5,70E-44	4,32E+01	1,05E-44	0,1342	14,0281764	1,88325371	241,32	SCUBE3	signal peptide, CUB domain and EGF like domain containing 3
100616452	1,76E-19	1,88E+01	5,94E-20	0,2055	9,1453641	1,87935511	103,82	MIR2682	microRNA 2682
112543491	8,06E-04	3,09E+00	5,25E-04	0,5395	3,4675471	1,87087592	13,34	LOC112543	linc-UFC1
223117	6,90E-24	2,32E+01	2,06E-24	0,1835	10,196229	1,87067208	121,75	SEMA3D	semaphorin 3D
25956	1,13E-43	4,29E+01	2,08E-44	0,1338	13,9793114	1,87051454	250,89	SEC31B	SEC31 homolog B, COPII coat complex component
64770	1,82E-246	2,46E+02	1,41E-248	0,0555	33,6735612	1,87009724	2242,73	CCDC14	coiled-coil domain containing 14
107984684	1,10E-18	1,80E+01	3,81E-19	0,2091	8,9423897	1,86957269	90,03	LOC107984	uncharacterized LOC107984684
112268256	9,34E-12	1,10E+01	4,02E-12	0,2694	6,9363163	1,86841212	57,57	LOC112268	256
692225	3,35E-03	2,47E+00	2,29E-03	0,6123	3,0491593	1,86706205	10,44	SNORD94	small nucleolar RNA, C/D box 94
1282	6,17E-256	2,55E+02	4,47E-258	0,0544	34,3164031	1,86623126	2439,5	COL4A1	collagen type IV alpha 1 chain
23231	2,92E-60	5,95E+01	3,72E-61	0,1131	16,4991377	1,86535038	341,83	SEL1L3	SEL1L family member 3
2151	1,94E-40	3,97E+01	3,84E-41	0,1388	13,4335846	1,86411048	219,36	F2RL2	coagulation factor II thrombin receptor like 2
114798	9,36E-55	5,40E+01	1,35E-55	0,1186	15,7073681	1,86284792	305,26	SLITRK1	SLIT and NTRK like family member 1
5140	2,67E-55	5,46E+01	3,79E-56	0,1179	15,7876079	1,86127809	324,68	PDE3B	phosphodiesterase 3B
102724398	2,38E-05	4,62E+00	1,38E-05	0,4282	4,3462389	1,8610205	20,96	CH507-42P1	uncharacterized CH507-42P11.6
22873	7,55E-41	4,01E+01	1,48E-41	0,1378	13,5041124	1,86073809	227,13	DZIP1	DAZ interacting zinc finger protein 1
26797	3,73E-05	4,43E+00	2,20E-05	0,4383	4,2433012	1,86001669	20,99	SNORD52	small nucleolar RNA, C/D box 52
105375721	4,70E-04	3,33E+00	3,01E-04	0,514	3,6146536	1,85806657	15,2	LOC105375	uncharacterized LOC105375721
105376781	6,37E-11	1,02E+01	2,84E-11	0,2792	6,6548838	1,8579483	50,34	LOC105376	uncharacterized LOC105376781
149478	5,54E-03	2,26E+00	3,88E-03	0,6424	2,8879377	1,85518475	10,29	BTBD19	BTB domain containing 19
101929680	2,47E-04	3,61E+00	1,55E-04	0,4903	3,7832822	1,85509687	16,1	SCN1A-AS1	SCN1A and SCN9A antisense RNA 1
8809	3,76E-07	6,42E+00	1,98E-07	0,3558	5,2011143	1,85037428	31,4	IL18R1	interleukin 18 receptor 1
440519	9,14E-60	5,90E+01	1,18E-60	0,1126	16,4295351	1,84956204	357,9	ZNF724	zinc finger protein 724
220594	1,06E-34	3,40E+01	2,39E-35	0,1489	12,4071186	1,84782984	203,45	USP32P2	ubiquitin specific peptidase 32 pseudogene 2
105379057	5,29E-29	2,83E+01	1,37E-29	0,1635	11,295978	1,84649028	166,93	EDIL3-DT	EDIL3 divergent transcript
64699	2,43E-04	3,61E+00	1,52E-04	0,4875	3,787688	1,846476	16,95	TMPRSS3	transmembrane serine protease 3
595135	1,02E-39	3,90E+01	2,06E-40	0,1387	13,308751	1,84643128	221,88	PGM5P2	phosphoglucomutase 5 pseudogene 2
100129203	4,85E-05	4,31E+00	2,88E-05	0,4408	4,1825345	1,84363242	19,77	LOC100129	uncharacterized LOC100129203
374887	3,73E-26	2,54E+01	1,05E-26	0,1722	10,6972029	1,84223917	136	YJEFN3	YjeF N-terminal domain containing 3
100505635	4,40E-03	2,36E+00	3,05E-03	0,621	2,9623903	1,83975634	10,33	DAAM2-AS1	DAAM2 antisense RNA 1
440918	3,20E-03	2,49E+00	2,19E-03	0,6005	3,0628325	1,83909898	11,26	FLJ46875	uncharacterized LOC440918
105372978	6,32E-03	2,20E+00	4,44E-03	0,6464	2,844746	1,83887193	9,53	LINC01638	long intergenic non-protein coding RNA 1638
80063	1,23E-11	1,09E+01	5,32E-12	0,2666	6,8968288	1,83859494	56,43	ATF7IP2	activating transcription factor 7 interacting protein 2
65981	1,87E-299	2,99E+02	9,47E-302	0,0494	37,1292923	1,83596057	2922,01	CAPRIN2	caprin family member 2
83690	4,94E-39	3,83E+01	1,01E-39	0,139	13,1892526	1,83367144	216,71	CRISPLD1	cysteine rich secretory protein LCCL domain containing 1
148534	8,61E-68	6,71E+01	9,24E-69	0,1046	17,5249866	1,83303036	411,1	TLCD4	TLC domain containing 4
26353	3,65E-45	4,44E+01	6,51E-46	0,1288	14,2238856	1,8324623	251,6	HSPB8	heat shock protein family B (small) member 8
1136	2,69E-08	7,57E+00	1,34E-08	0,3224	5,6813606	1,8318824	37,46	CHRNA3	cholinergic receptor nicotinic alpha 3 subunit
105374264	4,22E-02	1,37E+00	3,24E-02	0,8552	2,1392747	1,82961139	5,51	LOC105374	uncharacterized LOC105374264
105375001	9,30E-08	7,03E+00	4,75E-08	0,3342	5,4605128	1,82469311	35,38	LOC105375	uncharacterized LOC105375001
374897	3,15E-04	3,50E+00	1,99E-04	0,4903	3,7207459	1,82438609	15,94	SBSN	suprabasin
9298	4,03E-10	9,39E+00	1,85E-10	0,2862	6,3731823	1,82379645	58,03	SNORD31	small nucleolar RNA, C/D box 31
2022	1,81E-12	1,17E+01	7,64E-13	0,2544	7,1674875	1,82336053	64,41	ENG	endoglin
105376387	6,90E-22	2,12E+01	2,17E-22	0,187	9,7334277	1,81973468	111,84	LOC105376	uncharacterized LOC105376387
5268	4,52E-04	3,34E+00	2,88E-04	0,5018	3,6254532	1,81918616	15,84	SERPINB5	serpin family B member 5
105375783	9,26E-03	2,03E+00	6,62E-03	0,6695	2,7154001	1,81798614	9,44	LOC105375	uncharacterized LOC105375783
4286	5,19E-208	2,07E+02	6,06E-210	0,0588	30,9219403	1,81773115	1965,6	MITF	melanocyte inducing transcription factor
51747	4,35E-170	1,69E+02	7,98E-172	0,065	27,9431732	1,81735976	6701,95	LUC7L3	LUC7 like 3 pre-mRNA splicing factor
100190986	7,21E-14	1,31E+01	2,90E-14	0,2384	7,6028078	1,81220605	68,75	LOC100190	uncharacterized LOC100190986
389432	3,90E-43	4,24E+01	7,28E-44	0,1303	13,890073	1,80956211	270,22	SAMD5	sterile alpha motif domain containing 5
3764	1,81E-07	6,74E+00	9,40E-08	0,339	5,3379483	1,80954009	34,26	KCNJ8	potassium inwardly rectifying channel subfamily J member 8
3902	1,33E-02	1,88E+00	9,67E-03	0,699	2,5873043	1,80847713	8,31	LAG3	lymphocyte activating 3
7166	4,21E-10	9,38E+00	1,94E-10	0,2839	6,3662528	1,80748863	48,05	TPH1	tryptophan hydroxylase 1
11146	3,15E-111	1,11E+02	1,45E-112	0,0801	22,5467485	1,80627333	936,81	GLMN	glomulin, FKBP associated protein
8715	1,35E-03	2,87E+00	8,95E-04	0,5436	3,3215153	1,80565745	12,93	NOL4	nucleolar protein 4
574029	3,05E-10	9,52E+00	1,39E-10	0,2814	6,4164811	1,80561138	50,06	DUSP5P1	dual specificity phosphatase 5 pseudogene 1
692204	1,05E-03	2,98E+00	6,93E-04	0,5315	3,3923808	1,80314336	13,83	SNORD88C	small nucleolar RNA, C/D box 88C
112268163	1,08E-03	2,97E+00	7,07E-04	0,5322	3,3866653	1,80242538	13,78	LOC112268	163
105374968	1,76E-02	1,75E+00	1,29E-02	0,7249	2,4862025	1,80224455	7,45	LOC105374	uncharacterized LOC105374968
7169	1,33E-74	7,39E+01	1,23E-75	0,0979	18,4036563	1,80219498	459,07	TPM2	tropomyosin 2
102465502	2,52E-04	3,60E+00	1,58E-04	0,4768	3,7788231	1,80180812	16,63	MIR6835	microRNA 6835
101929127	3,03E-22	2,15E+01	9,42E-23	0,1835	9,8179922	1,80172825	121,64	PGM5P3-AS	PGM5P3 antisense RNA 1
256979	1,77E-16	1,58E+01	6,54E-17	0,2156	8,3550104	1,80127702	92,86	SUN3	Sad1 and UNC84 domain containing 3
653075	3,01E-08	7,52E+00	1,50E-08	0,318	5,6617401	1,80015659	37,79	GOLGA8T	golgin A8 family member T
107984849	1,94E-04	3,71E+00	1,20E-04	0,4679	3,845275	1,79922487	17,52	LOC107984	replaced by ID 100288069
3070	9,48E-230	2,29E+02	8,67E-232	0,0553	32,5063577	1,79684566	2140,63	HELLS	helicase, lymphoid specific
283652	2,72E-15	1,46E+01	1,05E-15	0,224	8,0212279	1,79647636	79,32	SLC24A5	solute carrier family 24 member 5
100034743	1,45E-03	2,84E+00	9,64E-04	0,543	3,3009248	1,79245421	12,81	PDZK1P1	PDZ domain containing 1 pseudogene 1
26769	2,60E-05	4,59E+00	1,52E-05	0,414	4,3262326	1,79124478	22,06	SNORD81	small nucleolar RNA, C/D box 81
155060	3,10E-14	1,35E+01	1,23E-14	0,2322	7,7126828	1,79102567	71,58	LOC155060	AI894139 pseudogene
1000	6,91E-09	8,16E+00	3,34E-09	0,3028	5,9137252	1,79077613	42,15	CDH2	cadherin 2
100874016	1,88E-02	1,73E+00	1,38E-02	0,7272	2,4617185	1,79005678	7,25	SYNPR-AS1	SYNPR antisense RNA 1
286151	2,30E-69	6,86E+01	2,38E-70	0,1009	17,731753	1,78833425	453,58	FBXO43	F-box protein 43
107986849	5,12E-03	2,29E+00	3,57E-03	0,6132	2,9137814	1,7867304	10,12	LOC107986	uncharacterized LOC107986849
26049	1,63E-72	7,18E+01	1,57E-73	0,0985	18,1389785	1,7860678	489,47	FAM169A	family with sequence similarity 169 member A
105375034	1,74E-02	1,76E+00	1,28E-02	0,7168	2,4905018	1,78530298	7,32	LOC105375	uncharacterized LOC105375034
105370528	1,36E-02	1,87E+00	9,89E-03	0,6918	2,5797485	1,7847367	8,12	LOC105370	uncharacterized LOC105370528
107986108	8,68E-11	1,01E+01	3,88E-11	0,2698	6,608622	1,78331118	53,7	LOC107986	uncharacterized LOC107986108
55582	2,28E-104	1,04E+02	1,20E-105	0,0817	21,830338	1,78323882	733,34	KIF27	kinesin family member 27
1744	1,74E-04	3,76E+00	1,08E-04	0,4602	3,8730062	1,78241144	18,33	DLSTP1	dihydrolipoamide S-succinyltransferase pseudogene 1
3592	2,70E-16	1,56E+01	1,00E-16	0,2143	8,3044686	1,77987566	83,95	IL12A	interleukin 12A
100287898	9,65E-03	2,02E+00	6,92E-03	0,6579	2,7008264	1,77686271	9,02	TTC34	tetratricopeptide repeat domain 34
85477	1,57E-04	3,80E+00	9,67E-05	0,4555	3,898777	1,77593583	18,23	SCIN	scinderin

284739	1,25E-04	3,90E+00	7,64E-05	0,4489	3,9553999	1,77557598	19,99	C20orf204	chromosome 20 open reading frame 204
375444	3,46E-81	8,05E+01	2,79E-82	0,0924	19,2145827	1,77548626	566,72	C5orf34	chromosome 5 open reading frame 34
196264	1,25E-18	1,79E+01	4,34E-19	0,1989	8,9279933	1,7754244	99,31	MPZL3	myelin protein zero like 3
107984387	8,53E-04	3,07E+00	5,57E-04	0,5142	3,4517447	1,77490464	14,49	LOC107984387	
9771	6,97E-21	2,02E+01	2,26E-21	0,187	9,4921333	1,77465879	111,91	RAPGEF5	Rap guanine nucleotide exchange factor 5
392636	9,10E-04	3,04E+00	5,95E-04	0,5166	3,4338818	1,77398392	14,67	AGMO	alkylglycerol monooxygenase
100132249	5,05E-04	3,30E+00	3,24E-04	0,4933	3,5952942	1,77365018	15,5	LOC100132249	uncharacterized LOC100132249
26330	3,25E-15	1,45E+01	1,25E-15	0,2217	7,9990502	1,77324188	84,46	GAPDHS	glyceraldehyde-3-phosphate dehydrogenase, spermatogenic
54495	7,44E-204	2,03E+02	9,30E-206	0,0579	30,6089618	1,77129305	2584,98	TMX3	thioredoxin related transmembrane protein 3
100130967	2,62E-02	1,58E+00	1,96E-02	0,7585	2,3345122	1,77074927	7,37	LINC02901	long intergenic non-protein coding RNA 2901
374650	9,67E-10	9,01E+00	4,51E-10	0,2838	6,2351565	1,76979723	48,15	GOLGA6L5P	golgin A6 family like 5, pseudogene
6263	1,44E-07	6,84E+00	7,42E-08	0,3289	5,3806912	1,76953539	35,51	RYR3	ryanodine receptor 3
340481	6,75E-51	5,02E+01	1,05E-51	0,1169	15,128686	1,76920708	339,58	ZDHHC21	zinc finger DHHC-type palmitoyltransferase 21
151613	1,41E-108	1,08E+02	6,79E-110	0,0794	22,2727478	1,76884114	827,86	TTC14	tetratricopeptide repeat domain 14
107985923	8,73E-06	5,06E+00	4,96E-06	0,3871	4,5664891	1,7676889	26,11	LOC107985923	uncharacterized LOC107985923
5803	1,95E-04	3,71E+00	1,21E-04	0,4592	3,8441291	1,76541428	18,01	PTPRZ1	protein tyrosine phosphatase receptor type Z1
107985915	1,31E-02	1,88E+00	9,47E-03	0,68	2,5945277	1,76434471	8,18	LOC107985915	MAGE-like protein 2
57381	2,12E-95	9,47E+01	1,31E-96	0,0846	20,8574074	1,76434243	645,6	RHOJ	ras homolog family member J
5919	2,76E-07	6,56E+00	1,44E-07	0,3354	5,2595989	1,76416333	34,53	RARRES2	retinoic acid receptor responder 2
168448	1,35E-04	3,87E+00	8,26E-05	0,4478	3,9366265	1,76273047	20,08	CDC14C	cell division cycle 14C
133418	8,22E-154	1,53E+02	1,90E-155	0,0664	26,561427	1,76238283	1699,71	EMB	embigin
3174	1,77E-16	1,58E+01	6,55E-17	0,2109	8,3548108	1,76177963	96,89	HNF4G	hepatocyte nuclear factor 4 gamma
81629	5,90E-27	2,62E+01	1,62E-27	0,162	10,8687785	1,76020616	170,44	TSSK3	testis specific serine kinase 3
64582	1,38E-34	3,39E+01	3,12E-35	0,142	12,3857347	1,75822372	227,78	GPR135	G protein-coupled receptor 135
100174949	1,85E-73	7,27E+01	1,75E-74	0,0963	18,2590862	1,75747809	567,69	TRIM59-IFT8	TRIM59-IFT80 protein
26829	6,72E-03	2,17E+00	4,73E-03	0,6222	2,8245405	1,75732571	10	RNU5E-1	RNA, U5E small nuclear 1
107985054	3,24E-14	1,35E+01	1,29E-14	0,228	7,7072737	1,7568821	74,73	LOC107985054	
120071	3,30E-04	3,48E+00	2,09E-04	0,4736	3,7080694	1,75606477	17,25	LARGE2	LARGE xylosyl- and glucuronyltransferase 2
83715	2,14E-10	9,67E+00	9,71E-11	0,2712	6,4713249	1,75493847	52,21	ESPN	espin
127495	1,26E-11	1,09E+01	5,44E-12	0,2546	6,8936593	1,75480752	59,25	LRRC39	leucine rich repeat containing 39
105375668	2,96E-02	1,53E+00	2,23E-02	0,7679	2,2850398	1,75460791	6,28	LOC105375668	
6695	1,12E-73	7,30E+01	1,05E-74	0,0959	18,2868873	1,75404452	475,67	SPOCK1	SPARC (osteonectin), cwcv and kazal like domains proteoglycan 1
54465	3,61E-108	1,07E+02	1,75E-109	0,0789	22,2303571	1,75329635	825,82	ETAA1	ETAA1 activator of ATR kinase
5205	7,67E-185	1,84E+02	1,14E-186	0,0601	29,1393519	1,75141081	1518,54	ATP8B1	ATPase phospholipid transporting 8B1
100129482	1,43E-84	8,38E+01	1,08E-85	0,0893	19,6184086	1,75104664	559,43	ZNF37BP	zinc finger protein 37B, pseudogene
84898	3,49E-32	3,15E+01	8,38E-33	0,1467	11,9287369	1,75012271	210,25	PLXDC2	plexin domain containing 2
102724517	3,24E-06	5,49E+00	1,79E-06	0,3665	4,775697	1,75012126	29,73	LOC102724517	uncharacterized LOC102724517
100506473	2,80E-18	1,76E+01	9,80E-19	0,198	8,8373822	1,74991252	98,68	C2orf49-DT	C2orf49 divergent transcript
389336	2,39E-29	2,86E+01	6,15E-30	0,1537	11,3663802	1,74749107	205,12	C5orf46	chromosome 5 open reading frame 46
767846	3,88E-03	2,41E+00	2,68E-03	0,5818	3,0025224	1,74688988	11,69	PFN1P2	profilin 1 pseudogene 2
22835	3,53E-81	8,05E+01	2,85E-82	0,0909	19,2135859	1,74686382	574,32	ZFP30	ZFP30 zinc finger protein
107985781	1,41E-02	1,85E+00	1,03E-02	0,6798	2,5661866	1,74456322	8,02	FSIP2-AS1	FSIP2 antisense RNA 1
157570	5,12E-118	1,17E+02	2,11E-119	0,075	23,2330718	1,74290767	1127,69	ESCO2	establishment of sister chromatid cohesion N-acetyltransferase 2
164045	1,70E-04	3,77E+00	1,05E-04	0,4492	3,8787868	1,74248488	18,86	HFM1	helicase for meiosis 1
2187	1,35E-54	5,39E+01	1,95E-55	0,1111	15,6837836	1,74234549	349,86	FANCB	FA complementation group B
27334	8,24E-04	3,08E+00	5,37E-04	0,5033	3,4614203	1,74199854	16,25	P2RY10	P2Y receptor family member 10
151246	7,00E-177	1,76E+02	1,17E-178	0,0611	28,5001625	1,74176109	2700,41	SGO2	shugoshin 2
27198	1,36E-31	3,09E+01	3,33E-32	0,1469	11,8134496	1,73564259	195,76	HCAR1	hydroxycarboxylic acid receptor 1
107987366	5,60E-04	3,25E+00	3,60E-04	0,4863	3,5676681	1,73504699	15,95	LOC107987366	uncharacterized LOC107987366
57188	2,16E-08	7,67E+00	1,07E-08	0,3033	5,7191684	1,73447889	45,12	ADAMTSL3	ADAMTS like 3
57574	8,17E-94	9,31E+01	5,21E-95	0,0838	20,6803282	1,73390247	680,5	MARCHF4	membrane associated ring-CH-type finger 4
865	4,31E-192	1,91E+02	5,97E-194	0,0583	29,708473	1,73222222	2654,44	CBFB	core-binding factor subunit beta
6991	2,21E-12	1,17E+01	9,35E-13	0,2424	7,1397743	1,7304148	69,47	DYNLT2	dynein light chain Tctex-type 2
388165	3,46E-06	5,46E+00	1,92E-06	0,3633	4,7618518	1,73005814	28,35	UBE2Q2P1	UBE2Q2 pseudogene 1
100147744	5,68E-05	4,25E+00	3,39E-05	0,4173	4,1455908	1,72989568	22,2	RNU7-1	RNA, U7 small nuclear 1
259266	1,04E-55	5,50E+01	1,46E-56	0,1091	15,8476586	1,72873742	7486,01	ASPM	assembly factor for spindle microtubules
102724093	2,53E-04	3,60E+00	1,58E-04	0,4571	3,777614	1,72664979	17,74	LOC102724093	golgin subfamily A member 6-like protein 4
2331	1,04E-10	9,98E+00	4,68E-11	0,2622	6,5806952	1,72573474	55,01	FMOD	fibromodulin
27330	9,31E-07	6,03E+00	5,01E-07	0,3431	5,0259129	1,72459986	33,57	RPS6KA6	ribosomal protein S6 kinase A6
103171574	1,43E-03	2,84E+00	9,50E-04	0,5213	3,3049492	1,72300043	15,19	LOC103171574	uncharacterized LOC103171574
56651	1,89E-04	3,72E+00	1,18E-04	0,4472	3,851257	1,72245911	18,54	LINC00470	long intergenic non-protein coding RNA 470
105373976	1,44E-02	1,84E+00	1,05E-02	0,6732	2,5586691	1,72241929	9,01	LOC105373976	
10344	9,71E-06	5,01E+00	5,54E-06	0,3789	4,5433493	1,72155535	26,55	CCL26	C-C motif chemokine ligand 26
2250	2,21E-169	1,69E+02	4,09E-171	0,0617	27,8846884	1,72043061	2034,48	FGF5	fibroblast growth factor 5
5083	2,15E-08	7,67E+00	1,06E-08	0,3008	5,7203114	1,72040164	41,51	PAX9	paired box 9
148203	1,56E-41	4,08E+01	3,02E-42	0,1263	13,6205577	1,72013934	259,06	ZNF738	zinc finger protein 738
408186	1,64E-10	9,79E+00	7,41E-11	0,2641	6,5121851	1,71959369	56,65	LOC408186	alpha-2-macroglobulin like 1 pseudogene
10205	1,73E-31	3,08E+01	4,23E-32	0,1458	11,7933164	1,7189779	193,08	MPZL2	myelin protein zero like 2
3175	2,00E-06	5,70E+00	1,09E-06	0,3526	4,8737818	1,71848589	34,05	ONECUT1	one cut homeobox 1
9852	6,67E-133	1,32E+02	2,06E-134	0,0696	24,6735384	1,71800353	1227,41	EPM2AIP1	EPM2A interacting protein 1
389136	9,78E-46	4,50E+01	1,72E-46	0,1198	14,3166212	1,71561036	280,33	VGLL3	vestigial like family member 3
6307	1,26E-114	1,14E+02	5,52E-116	0,0749	22,892469	1,71377059	1268,27	MSMO1	methylsterol monooxygenase 1
339761	1,85E-04	3,73E+00	1,15E-04	0,444	3,8575462	1,7126997	19,22	CYP27C1	cytochrome P450 family 27 subfamily C member 1
27302	2,59E-03	2,59E+00	1,76E-03	0,5473	3,1284581	1,71214162	12,32	BMP10	bone morphogenetic protein 10
83758	8,20E-07	6,09E+00	4,39E-07	0,3389	5,0511559	1,71191374	32,58	RBP5	retinol binding protein 5
105374748	4,02E-02	1,40E+00	3,08E-02	0,7921	2,1596772	1,71059722	6,21	LOC105374748	uncharacterized LOC105374748
641364	1,54E-17	1,68E+01	5,51E-18	0,1978	8,6423849	1,70920592	99,08	SLC7A11-AS1	SLC7A11 antisense RNA 1
106479023	2,74E-23	2,26E+01	8,31E-24	0,1699	10,0598844	1,70882844	138,12	H3P4	H3 histone pseudogene 4
22986	8,65E-05	4,06E+00	5,23E-05	0,4224	4,0450919	1,70857868	21,92	SORCS3	sortilin related VPS10 domain containing receptor 3
101928556	3,52E-02	1,45E+00	2,68E-02	0,7713	2,2151313	1,70842713	6,17	LOC101928556	
104797538	2,75E-04	3,56E+00	1,73E-04	0,4546	3,7561956	1,7075568	19,21	KCNMB2-AS1	KCNMB2 antisense RNA 1
55057	7,64E-04	3,12E+00	4,97E-04	0,4902	3,4823383	1,70701788	15,8	CRYBG2	crystallin beta-gamma domain containing 2
57722	1,32E-77	7,69E+01	1,15E-78	0,0908	18,7774595	1,70553438	546,99	IGDCC4	immunoglobulin superfamily DCC subclass member 4
152573	7,06E-15	1,42E+01	2,75E-15	0,2158	7,9018384	1,70528996	81,5	SHISA3	shisa family member 3
400812	3,23E-06	5,49E+00	1,79E-06	0,3568	4,7763424	1,70420607	29,85	FLJ39095	uncharacterized LOC400812
114819	1,06E-10	9,97E+00	4,77E-11	0,2591	6,5777927	1,70404441	56,97	CROCCP3	CROCC pseudogene 3
6854	1,20E-03	2,92E+00	7,94E-04	0,5079	3,3547745	1,70373701	14,87	SYN2	synapsin II
109504726	4,77E-05	4,32E+00	2,83E-05	0,4066	4,1868368	1,70242172	23,7	ERV3-1-ZNF11	ERV3-1-ZNF117 readthrough
100289274	1,34E-06	5,87E+00	7,26E-07	0,3436	4,9541582	1,70229495	31,46	DNAJC3-DT	DNAJC3 divergent transcript
140609	1,63E-275	2,75E+02	1,01E-277	0,0478	35,6093184	1,70216823	3616,55	NEK7	NIMA related kinase 7
10721	3,00E-86	8,55E+01	2,20E-87	0,0858	19,8153152	1,70104326	705,53	POLQ	DNA polymerase theta
147650	1,37E-30	2,99E+01	3,42E-31	0,1464	11,6159175	1,70047514	195,33	SPACA6	sperm acrosome associated 6
677809	4,56E-03	2,34E+00	3,17E-03	0,5752	2,9508105	1,69740706	11,38	SNORA24	small nucleolar RNA, H/ACA box 24
64105	2,79E-162	1,62E+02	5,69E-164	0,0622	27,2892686	1,69629409	1820,05	CENPK	centromere protein K
51776	1,43E-215	2,15E+02	1,51E-217	0,0539	31,4824264	1,69593748	4287,16	MAP3K20	mitogen-activated protein kinase kinase kinase 20
151230	1,31E-62	6,19E+01	1,58E-63	0,1008	16,8259317	1,69536697	428,68	KLHL23	kelch like family member 23
56131	2,61E-03	2,58E+00	1,77E-03	0,5423	3,1257027	1,6950726	13,11	PCDHB4	protocadherin beta 4
10780	1,47E-53	5,28E+01	2,16E-54	0,109	15,5303774	1,6933746	375,65	ZNF234	zinc finger protein 234
91614	4,32E-11	1,04E+01	1,91E-11	0,252	6,712653	1,6914786	64,67	DEPDC7	DEP domain containing 7
4113	8,66E-06	5,06E+00	4,92E-06	0,3702	4,5681359	1,69124196	28,99	MAGEB2	MAGE family member B2
91624	1,16E-191	1,91E+02	1,61E-193	0,057	29,6750145	1,69123875	2316,63	NEXN	nexilin F-actin binding protein
57560	2,66E-61	6,06E+01	3,31E-62	0,1016	16,644615	1,69112091	465,11	IFT80	intraflagellar transport 80
677825	1,41E-04	3,85E+00	8,65E-05	0,4306	3,9255346	1,69040749	20	SNORA44	small nucleolar RNA, H/ACA box 44
56241	2,87E-05	4,54E+00	1,68E-05	0,3923	4,3035674	1,68822502	24,38	SUSD2	sushi domain containing 2
9699	6,32E-14	1,32E+01	2,54E-14	0,2213	7,6200885	1,68662175	79,04	RIMS2	regulating synaptic membrane exocytosis 2
162681	2,25E-111	1,11E+02	1,03E-112	0,0747	22,5617727	1,68556027	957,46	C18orf54	chromosome 18 open reading frame 54
7832	7,71E-04	3,11E+00	5,02E-04	0,4844	3,479573	1,68554	16,43	BTG2	BTG anti-proliferation factor 2
26508	4,51E-10	9,35E+00	2,08E-10	0,265	6,3556809	1,68420428	56,22	HEYL	hes related family bHLH transcription factor with YRPW motif like
2744	2,09E-168	1,68E+02	3,92E-170	0,0605	27,8036372	1,68118749	2324,88	GLS	glutaminase
57823	3,62E-124	1,23E+02	1,34E-125	0,0705	23,8381932	1,68038668	1001,96	SLAMF7	SLAM family member 7
26013	2,42E-23	2,26E+01	7,32E-24	0,1668	10,0723658	1,68026923	140,19	L3MBTL1	L3MBTL histone methyl-lysine binding protein 1
6693	4,34E-04	3,36E+00	2,76E-04	0,462	3,6364117	1,68010928	17,29	SPN	sialophorin
10149	2,89E-16	1,55E+01	1,08E-16	0,2025	8,2961864	1,67965812	94,28	ADGRG2	adhesion G protein-coupled receptor G2
84101	1,89E-52	5,17E+01	2,85E-53	0,1092	15,3640957	1,67736686	366,36	USP44	ubiquitin specific peptidase 44
692086	2,83E-20	1,95E+01	9,34E-21	0,1795	9,3432989	1,67718758	141,74	SNORD17	small nucleolar RNA, C/D box 17
100526832	1,56E-64	6,38E+01	1,80E-65	0,0981	17,0887376	1,67710099	445,15	PHOSPHO2-K	PHOSPHO2-KLHL23 readthrough
2797	2,36E-04	3,63E+00	1,47E-04	0,4418	3,7953621	1,67688304	19,01	GNRH2	gonadotropin releasing hormone 2
162632	4,03E-03	2,39E+00	2,78E-03	0,5596	2,9906921	1,67349797	12	USP32P1	ubiquitin specific peptidase 32 pseudogene 1
1999	5,51E-30	2,93E+01	1,40E-30	0,1456	11,4949194	1,67325393	185,12	ELF3	E74 like ETS transcription factor 3
105376199	1,72E-04	3,76E+00	1,06E-04	0,4315	3,8761161	1,6726175	19,88	FKTN-AS1	FKTN antisense RNA 1

100379345	1,13E-04	3,95E+00	6,86E-05	0,4199	3,9810868	1,67161458	21,37	MIR181A2H(	MIR181A2 host gene
120114	1,23E-152	1,52E+02	2,91E-154	0,0632	26,4585633	1,67113666	1344,07	FAT3	FAT atypical cadherin 3
101927780	1,15E-27	2,69E+01	3,10E-28	0,1515	11,018922	1,66966448	171,17	LINC01303	long intergenic non-protein coding RNA 1303
101928370	2,06E-02	1,69E+00	1,52E-02	0,6871	2,427823	1,66808414	7,78	S1PR1-DT	S1PR1 divergent transcript
84920	2,22E-32	3,17E+01	5,30E-33	0,1394	11,9667949	1,66796262	237,43	ALG10	ALG10 alpha-1,2-glucosyltransferase
225689	8,57E-03	2,07E+00	6,10E-03	0,6076	2,7422442	1,66627403	10,33	MAPK15	mitogen-activated protein kinase 15
101927415	1,37E-03	2,86E+00	9,11E-04	0,5021	3,3165392	1,66533706	15,28	TMED2-DT	TMED2 divergent transcript
55635	4,00E-179	1,78E+02	6,51E-181	0,058	28,6814233	1,66391714	4715,93	DEPDC1	DEP domain containing 1
643201	4,55E-89	8,83E+01	3,16E-90	0,0826	20,1420093	1,6635999	683,53	LOC643201	centrosomal protein 192kDa pseudogene
2784	7,94E-10	9,10E+00	3,69E-10	0,2654	6,2664948	1,66335019	54,07	GNB3	G protein subunit beta 3
171392	2,04E-58	5,77E+01	2,70E-59	0,1024	16,2384409	1,66272457	415,4	ZNF675	zinc finger protein 675
692109	7,67E-04	3,12E+00	4,99E-04	0,4773	3,4812709	1,66154393	16,21	SNORD69	small nucleolar RNA, C/D box 69
102723757	9,45E-04	3,02E+00	6,19E-04	0,4852	3,423334	1,66111234	15,43	SLC38A2-AS	SLC38A2 antisense RNA 1
407014	8,33E-05	4,08E+00	5,03E-05	0,4096	4,0543283	1,66053643	22,3	MIR25	microRNA 25
767	5,61E-13	1,23E+01	2,32E-13	0,2264	7,3288865	1,65954643	74,59	CA8	carbonic anhydrase 8
107984421	2,59E-07	6,59E+00	1,35E-07	0,3148	5,2719744	1,65940314	38,53	LOC107984	uncharacterized LOC107984421
6843	2,58E-24	2,36E+01	7,63E-25	0,1611	10,2923136	1,65835714	151,24	VAMP1	vesicle associated membrane protein 1
79037	9,84E-05	4,01E+00	5,96E-05	0,4127	4,0141919	1,65675098	22,17	PVRIG	PVR related immunoglobulin domain containing
952	4,18E-03	2,38E+00	2,89E-03	0,5561	2,9789644	1,6565548	11,95	CD38	CD38 molecule
107987172	1,52E-03	2,82E+00	1,01E-03	0,504	3,2864361	1,65635544	14,6	LOC107987	172
57337	2,17E-83	8,27E+01	1,68E-84	0,085	19,4782422	1,65620546	675,44	SENP7	SUMO specific peptidase 7
57181	9,19E-170	1,69E+02	1,70E-171	0,0593	27,9162019	1,65470083	1786,67	SLC39A10	solute carrier family 39 member 10
7516	3,68E-153	1,52E+02	8,61E-155	0,0623	26,5044538	1,65118772	1350,94	XRCC2	X-ray repair cross complementing 2
100133220	7,97E-03	2,10E+00	5,66E-03	0,5964	2,7669459	1,65031219	11,06	GOLGA6L3F	golgin A6 family like 3, pseudogene
339926	8,62E-04	3,06E+00	5,63E-04	0,4782	3,4488587	1,64917168	16,11	EHHADH-AS	EHHADH antisense RNA 1
101927888	6,08E-04	3,22E+00	3,92E-04	0,4651	3,5453229	1,64906942	18,77	LOC101927	uncharacterized LOC101927888
102723828	1,93E-15	1,47E+01	7,38E-16	0,2044	8,0641251	1,64830327	94,67	LINC02506	long intergenic non-protein coding RNA 2506
107986871	1,63E-02	1,79E+00	1,20E-02	0,6554	2,5135963	1,6473955	8,56	LOC107986	871
64078	3,49E-07	6,46E+00	1,83E-07	0,3158	5,2154843	1,64691379	37,5	SLC28A3	solute carrier family 28 member 3
340547	7,58E-12	1,11E+01	3,26E-12	0,2363	6,9662287	1,64598008	68,72	VSIG1	V-set and immunoglobulin domain containing 1
83394	9,55E-81	8,00E+01	7,79E-82	0,0859	19,1613092	1,64592834	600,56	PITPNM3	PITPNM family member 3
100132341	1,15E-10	9,94E+00	5,14E-11	0,2505	6,5666795	1,6450508	59,38	CLUHP3	clustered mitochondria homolog pseudogene 3
340252	3,17E-30	2,95E+01	8,01E-31	0,1425	11,542943	1,64487999	196,93	ZNF680	zinc finger protein 680
107987264	1,31E-08	7,88E+00	6,40E-09	0,2831	5,8058758	1,64353304	47,74	LOC107987	putative zinc finger protein 137
644135	3,15E-07	6,50E+00	1,65E-07	0,3139	5,2345428	1,6433001	37,45	PDE7B-AS1	PDE7B antisense RNA 1
9882	8,74E-181	1,80E+02	1,38E-182	0,057	28,8152368	1,64321957	2091,99	TBC1D4	TBC1 domain family member 4
107985305	1,14E-07	6,94E+00	5,86E-08	0,303	5,4231642	1,64311026	43,34	CEACAM16-	CEACAM16, CEACAM19 and PVR antisense RNA 1
8473	5,10E-270	2,69E+02	3,26E-272	0,0465	35,2514492	1,6400939	6633,63	OGT	O-linked N-acetylglucosamine (GlcNAc) transferase
27085	7,85E-148	1,47E+02	1,98E-149	0,063	26,0351542	1,63939304	1754,2	MTBP	MDM2 binding protein
103021295	1,36E-14	1,39E+01	5,36E-15	0,2096	7,8182027	1,63874807	99,54	LOC103021	uncharacterized LOC103021295
100507062	2,07E-07	6,68E+00	1,08E-07	0,3082	5,3134941	1,6375397	45,41	PSMD6-AS2	PSMD6 antisense RNA 2
102724117	3,80E-06	5,42E+00	2,11E-06	0,3452	4,7421547	1,63678006	31,26	LOC102724	golgin subfamily A member 6-like protein 4
8710	2,52E-07	6,60E+00	1,31E-07	0,31	5,2773601	1,63596548	44,14	SERPINB7	serpin family B member 7
2918	4,11E-03	2,39E+00	2,84E-03	0,5478	2,9848584	1,63497456	12,55	GRM8	glutamate metabotropic receptor 8
57711	1,07E-47	4,70E+01	1,79E-48	0,1117	14,6305422	1,63401976	360,1	ZNF529	zinc finger protein 529
254887	1,82E-35	3,47E+01	4,05E-36	0,1301	12,5484785	1,63221729	244	ZDHHC23	zinc finger DHHC-type palmitoyltransferase 23
286826	1,04E-107	1,07E+02	5,08E-109	0,0736	22,1823633	1,63211031	1053,25	LIN9	lin-9 DREAM MuvB core complex component
390927	3,60E-02	1,44E+00	2,74E-02	0,7396	2,2057062	1,63142018	6,83	ZNF793	zinc finger protein 793
55592	6,93E-20	1,92E+01	2,31E-20	0,1764	9,2469002	1,63107208	127,14	GOLGA2P5	GOLGA2 pseudogene 5
4602	4,80E-18	1,73E+01	1,69E-18	0,1858	8,7763221	1,63044891	111,52	MYB	MYB proto-oncogene, transcription factor
379025	5,42E-94	9,33E+01	3,44E-95	0,0787	20,7003095	1,62921866	969,02	PSMA3-AS1	PSMA3 antisense RNA 1
647121	1,85E-14	1,37E+01	7,31E-15	0,2094	7,7790518	1,62897556	89,48	EMBP1	embigin pseudogene 1
84250	3,94E-115	1,14E+02	1,71E-116	0,071	22,9434899	1,62853976	966,79	SLF1	SMC5-SMC6 complex localization factor 1
618	1,28E-11	1,09E+01	5,53E-12	0,2362	6,8911819	1,62780695	105,55	BCYRN1	brain cytoplasmic RNA 1
266747	4,34E-20	1,94E+01	1,44E-20	0,175	9,2972968	1,62688982	134,26	RGL4	ral guanine nucleotide dissociation stimulator like 4
55783	6,10E-107	1,06E+02	3,03E-108	0,0736	22,1018576	1,62602033	1026,03	CMTR2	cap methyltransferase 2
54033	8,17E-03	2,09E+00	5,81E-03	0,5894	2,7585626	1,6258395	10,9	RBM11	RNA binding motif protein 11
9388	2,00E-37	3,67E+01	4,25E-38	0,126	12,9045051	1,62545353	260,04	LIPG	lipase G, endothelial type
339512	2,39E-66	6,56E+01	2,63E-67	0,0937	17,3333705	1,62489256	478,63	CCDC190	coiled-coil domain containing 190
105369848	1,40E-44	4,39E+01	2,54E-45	0,115	14,1282569	1,62424818	371,63	LNCOG	lncRNA osteogenesis associated
151295	3,55E-03	2,45E+00	2,44E-03	0,535	3,0307884	1,62143468	13,28	SLC23A3	solute carrier family 23 member 3
105372698	5,51E-04	3,26E+00	3,54E-04	0,4535	3,5719672	1,61978842	20,15	LOC105372	uncharacterized LOC105372698
57464	2,98E-110	1,10E+02	1,40E-111	0,072	22,4460445	1,61659761	922,94	STRIP2	striatin interacting protein 2
3557	9,97E-03	2,00E+00	7,15E-03	0,6007	2,6896136	1,61571852	10,05	IL1RN	interleukin 1 receptor antagonist
90592	3,02E-99	9,85E+01	1,73E-100	0,0759	21,2801796	1,61482951	787,51	ZNF700	zinc finger protein 700
105379283	1,05E-03	2,98E+00	6,92E-04	0,4759	3,3927579	1,61471617	16,62	LOC105379	uncharacterized LOC105379283
105372860	3,14E-18	1,75E+01	1,10E-18	0,1828	8,8242205	1,61269017	114,88	UFD1-AS1	UFD1 antisense RNA 1
55075	7,30E-237	2,36E+02	6,26E-239	0,0488	33,0078663	1,61114543	6536,21	UACA	uveal autoantigen with coiled-coil domains and ankyrin repeats
101929823	1,32E-04	3,88E+00	8,11E-05	0,4085	3,9412342	1,61017896	21,66	LOC101929	uncharacterized LOC101929823
8883	2,73E-35	3,46E+01	6,09E-36	0,1285	12,5161559	1,60831151	3112,19	NAE1	NEDD8 activating enzyme E1 subunit 1
684959	1,66E-03	2,78E+00	1,11E-03	0,4931	3,2615206	1,60829782	15,1	SNORA25	small nucleolar RNA, H/ACA box 25
100506606	4,33E-05	4,36E+00	2,56E-05	0,3821	4,2091706	1,60817903	25,81	LOC100506	uncharacterized LOC100506606
728498	1,12E-09	8,95E+00	5,25E-10	0,2589	6,2113681	1,60801885	55,61	GOLGA8H	golgin A8 family member H
9510	2,15E-284	2,84E+02	1,20E-286	0,0444	36,1811845	1,60776696	4668,98	ADAMTS1	ADAM metallopeptidase with thrombospondin type 1 motif 1
100288615	5,81E-19	1,82E+01	1,99E-19	0,1783	9,0137403	1,60704551	124,01	WHAMMP1	WHAMM pseudogene 1
105378797	2,89E-02	1,54E+00	2,17E-02	0,6998	2,2955166	1,60648142	7,53	LOC105378	uncharacterized LOC105378797
400221	4,32E-61	6,04E+01	5,41E-62	0,0967	16,6151725	1,60618698	448,78	LINC03033	long intergenic non-protein coding RNA 3033
28982	3,65E-58	5,74E+01	4,85E-59	0,0991	16,2024398	1,60558257	434,59	FLVCR1	FLVCR heme transporter 1
26776	1,71E-02	1,77E+00	1,25E-02	0,643	2,4963259	1,60502284	9,14	SNORA71B	small nucleolar RNA, H/ACA box 71B
100131564	1,20E-19	1,89E+01	4,03E-20	0,1747	9,1871919	1,60486622	124,12	CCDC18-AS	CCDC18 antisense RNA 1
9765	5,57E-200	1,99E+02	7,18E-202	0,0529	30,3154197	1,60436804	3361,76	ZFYVE16	zinc finger FYVE-type containing 16
105372553	7,79E-05	4,11E+00	4,69E-05	0,3941	4,07037	1,60427111	23,32	LOC105372	553
134637	4,04E-62	6,14E+01	4,89E-63	0,0957	16,7586843	1,60362333	468	ADAT2	adenosine deaminase tRNA specific 2
64386	2,36E-03	2,63E+00	1,60E-03	0,5077	3,1566507	1,60276927	14,2	MMP25	matrix metallopeptidase 25
493911	2,22E-11	1,07E+01	9,69E-12	0,2351	6,8109692	1,6012915	68,79	PHOSPHO2	phosphatase, orphan 2
57730	3,67E-50	4,94E+01	5,79E-51	0,1064	15,0157279	1,59765851	363,28	ANKRD36B	ankyrin repeat domain 36B
53405	3,52E-13	1,25E+01	1,45E-13	0,2158	7,391921	1,59515677	79,36	CLIC5	chloride intracellular channel 5
163786	1,91E-128	1,28E+02	6,38E-130	0,0657	24,2514438	1,59280036	1401,95	SASS6	SAS-6 centriolar assembly protein
284992	9,18E-41	4,00E+01	1,80E-41	0,118	13,4895964	1,59151122	285,67	CCDC150	coiled-coil domain containing 150
101927673	1,73E-10	9,76E+00	7,86E-11	0,2445	6,5032955	1,59001536	68,01	LOC101927	673
105379040	6,91E-03	2,16E+00	4,88E-03	0,5643	2,814674	1,58841665	11,53	LOC105379	uncharacterized LOC105379040
619498	6,54E-05	4,18E+00	3,92E-05	0,3863	4,1123211	1,58839187	24,8	SNORD74	small nucleolar RNA, C/D box 74
6660	8,77E-05	4,06E+00	5,30E-05	0,3929	4,041995	1,58814783	24,68	SOX5	SRY-box transcription factor 5
152225	4,41E-70	6,94E+01	4,51E-71	0,0891	17,8251069	1,5873965	647,03	RDUR	RIG-I dependent antiviral response regulator RNA
105377940	9,31E-04	3,03E+00	6,09E-04	0,4631	3,4274661	1,58714162	17,42	LOC105377	uncharacterized LOC105377940
8796	2,54E-05	4,60E+00	1,48E-05	0,3662	4,331182	1,58608472	27,17	SCEL	sciellin
642826	3,86E-18	1,74E+01	1,36E-18	0,18	8,8009319	1,58427328	116,72	BMS1P2	BMS1 pseudogene 2
148206	5,52E-78	7,73E+01	4,77E-79	0,0842	18,8243709	1,5840863	633,88	ZNF714	zinc finger protein 714
123722	7,41E-08	7,13E+00	3,76E-08	0,2878	5,5016991	1,58336037	43,6	FSD2	fibronectin type III and SPRY domain containing 2
155400	8,75E-35	3,41E+01	1,97E-35	0,1273	12,4224427	1,5815558	261,2	NSUN5P1	NSUN5 pseudogene 1
100289230	1,26E-05	4,90E+00	7,21E-06	0,3523	4,4874595	1,58098728	30,48	LOC100289	uncharacterized LOC100289230
84553	7,74E-16	1,51E+01	2,92E-16	0,1933	8,1765757	1,58081975	103,42	FAXC	failed axon connections homolog, metaxin like GST domain containing
55320	8,25E-273	2,72E+02	5,18E-275	0,0446	35,4336399	1,58014001	5311,93	MIS18BP1	MIS18 binding protein 1
729987	7,45E-10	9,13E+00	3,46E-10	0,2515	6,2766074	1,57840498	60,76	LINC01776	long intergenic non-protein coding RNA 1776
57157	4,11E-166	1,65E+02	7,96E-168	0,0572	27,6121375	1,57823433	2065,06	PHTF2	putative homeodomain transcription factor 2
54602	1,79E-133	1,33E+02	5,50E-135	0,0638	24,7268511	1,57676012	1727,93	NDFIP2	Nedd4 family interacting protein 2
55345	1,34E-82	8,19E+01	1,05E-83	0,0813	19,3841592	1,57656812	760,88	ZGRF1	zinc finger GRF-type containing 1
54482	2,84E-58	5,75E+01	3,76E-59	0,0972	16,218057	1,57652158	493,26	TRMT13	tRNA methyltransferase 13 homolog
107987113	1,94E-11	1,07E+01	8,48E-12	0,2308	6,8302269	1,5764535	70,37	LOC107987	113
100422955	3,17E-02	1,50E+00	2,40E-02	0,6976	2,2577099	1,57490809	7,33	MIR4273	microRNA 4273
10308	7,14E-65	6,41E+01	8,13E-66	0,0919	17,1350609	1,57433022	627,32	ZNF267	zinc finger protein 267
275	3,73E-13	1,24E+01	1,53E-13	0,2131	7,3841317	1,57335784	81,97	AMT	aminomethyltransferase
55631	2,28E-113	1,13E+02	1,01E-114	0,0691	22,7654183	1,57306258	1350,88	LRRC40	leucine rich repeat containing 40
7306	7,67E-03	2,12E+00	5,44E-03	0,5657	2,7796989	1,57255624	11,51	TYRP1	tyrosinase related protein 1
10085	4,01E-165	1,64E+02	7,93E-167	0,0571	27,5288698	1,57233286	4722,6	EDIL3	EGF like repeats and discoidin domains 3
55900	1,75E-115	1,15E+02	7,55E-117	0,0684	22,9790347	1,57228622	1056,97	ZNF302	zinc finger protein 302
85391	5,22E-03	2,28E+00	3,64E-03	0,5405	2,9076887	1,5715386	12,28	SNORD14E	small nucleolar RNA, C/D box 14E
646576	1,31E-29	2,89E+01	3,37E-30	0,1375	11,4187333	1,5700596	209,35	HHIP-AS1	HHIP antisense RNA 1
729176	4,99E-04	3,30E+00	3,20E-04	0,4363	3,5985824	1,56990457	19,54	KATNBL1P6	katanin regulatory subunit B1 like 1 pseudogene 6
375248	2,95E-47	4,65E+01	4,98E-48	0,1078	14,5608545	1,56974873	417,44	ANKRD36	ankyrin repeat domain 36

84680	2,23E-22	2,17E+01	6,93E-23	0,1593	9,8488869	1,56853239	150,37	ACCS	1-aminocyclopropane-1-carboxylate synthase homolog (inactive)
58486	4,41E-98	9,74E+01	2,60E-99	0,0741	21,1528321	1,56783594	1500,3	ZBED5	zinc finger BED-type containing 5
400322	9,25E-167	1,66E+02	1,77E-168	0,0567	27,6664488	1,56762137	1877,75	HERC2P2	HERC2 pseudogene 2
55769	1,20E-88	8,79E+01	8,37E-90	0,078	20,0937358	1,56644461	885,67	ZNF83	zinc finger protein 83
100423037	4,48E-02	1,35E+00	3,45E-02	0,7406	2,1142391	1,56580541	6,53	MIR3176	microRNA 3176
147686	6,19E-28	2,72E+01	1,66E-28	0,1411	11,0749779	1,56302648	203,77	ZNF418	zinc finger protein 418
3344	1,68E-91	9,08E+01	1,12E-92	0,0765	20,4196525	1,56294848	1108,49	FOXN2	forkhead box N2
144363	1,71E-25	2,48E+01	4,88E-26	0,1481	10,5536763	1,56263004	184,98	ETFRF1	electron transfer flavoprotein regulatory factor 1
345895	4,10E-03	2,39E+00	2,83E-03	0,523	2,9854195	1,561496	13,97	RSPH4A	radial spoke head component 4A
9966	1,65E-181	1,81E+02	2,56E-183	0,0541	28,8735753	1,56114653	2518,64	TNFSF15	TNF superfamily member 15
81931	2,66E-50	4,96E+01	4,18E-51	0,1038	15,0373132	1,56093715	385,5	ZNF93	zinc finger protein 93
57662	3,75E-07	6,43E+00	1,97E-07	0,2998	5,2019298	1,55932143	41,42	CAMSAP3	calmodulin regulated spectrin associated protein family member 3
54407	4,92E-38	3,73E+01	1,03E-38	0,1198	13,0132267	1,55887892	12699,42	SLC38A2	solute carrier family 38 member 2
23461	6,90E-40	3,92E+01	1,38E-40	0,1168	13,3383664	1,5585522	331,41	ABCA5	ATP binding cassette subfamily A member 5
167691	9,99E-22	2,10E+01	3,16E-22	0,1605	9,695288	1,55657551	150,21	LCA5	lebercilin LCA5
101927380	4,47E-10	9,35E+00	2,06E-10	0,2446	6,357074	1,55489542	67,61	CARNMT1-A	CARNMT1 antisense RNA 1
729359	2,53E-02	1,60E+00	1,89E-02	0,6624	2,3472088	1,55485224	8,07	PLIN4	perilipin 4
5454	1,07E-10	9,97E+00	4,78E-11	0,2363	6,5776875	1,55462071	64,89	POU3F2	POU class 3 homeobox 2
105373836	2,80E-02	1,55E+00	2,10E-02	0,6734	2,3084969	1,55450309	8,14	LOC105373	uncharacterized LOC105373836
1122	3,47E-211	2,10E+02	3,88E-213	0,0499	31,1586211	1,55424176	4561,56	CHML	CHM like Rab escort protein
80975	3,25E-04	3,49E+00	2,05E-04	0,4186	3,7126203	1,55422954	22,58	TMPRSS5	transmembrane serine protease 5
9411	0	#NUM!	0	0,0389	39,9223813	1,55389477	14670,11	ARHGAP29	Rho GTPase activating protein 29
23266	3,83E-168	1,67E+02	7,23E-170	0,0559	27,7816352	1,55372148	1997,05	ADGRL2	adhesion G protein-coupled receptor L2
374393	2,17E-141	1,41E+02	5,97E-143	0,061	25,456608	1,55366634	3310,15	FAM111B	FAM111 trypsin like peptidase B
728927	2,34E-38	3,76E+01	4,86E-39	0,1189	13,0704002	1,55351767	278,9	ZNF736	zinc finger protein 736
100113407	1,49E-42	4,18E+01	2,81E-43	0,1126	13,7929454	1,55345724	342	TMEM170B	transmembrane protein 170B
360023	1,36E-81	8,09E+01	1,09E-82	0,0806	19,2631576	1,55322063	777,52	ZBTB41	zinc finger and BTB domain containing 41
149069	3,28E-03	2,48E+00	2,25E-03	0,5081	3,0557081	1,55259184	13,73	DCDC2B	doublecortin domain containing 2B
286827	7,51E-43	4,21E+01	1,41E-43	0,1122	13,8425041	1,55249374	327,2	TRIM59	tripartite motif containing 59
107986206	1,93E-02	1,71E+00	1,42E-02	0,6327	2,452773	1,5518991	8,87	LRP2BP-AS	LRP2BP antisense RNA 1
9076	3,23E-104	1,03E+02	1,70E-105	0,0711	21,8142848	1,55147272	966,45	CLDN1	claudin 1
577	1,95E-03	2,71E+00	1,31E-03	0,4823	3,2144455	1,55039668	15,39	ADGRB3	adhesion G protein-coupled receptor B3
441273	4,07E-09	8,39E+00	1,95E-09	0,2583	6,0019618	1,5503682	55,02	SPDYE2	speedy/RINGO cell cycle regulator family member E2
6319	1,99E-293	2,93E+02	1,06E-295	0,0422	36,7525293	1,55032673	8510,59	SCD	stearoyl-CoA desaturase
28984	1,12E-12	1,20E+01	4,68E-13	0,2143	7,2342958	1,55027059	82,69	RGCC	regulator of cell cycle
100652770	6,54E-45	4,42E+01	1,17E-45	0,1092	14,1825877	1,54825623	353,54	DSG2-AS1	DSG2 antisense RNA 1
79830	4,08E-100	9,94E+01	2,31E-101	0,0724	21,374453	1,54788682	1265,18	ZMYM1	zinc finger MYM-type containing 1
27314	1,18E-97	9,69E+01	6,99E-99	0,0733	21,1061261	1,54669281	1009,6	RAB30	RAB30, member RAS oncogene family
107984459	6,27E-09	8,20E+00	3,03E-09	0,2605	5,9300192	1,54499645	58,26	LOC107984	459
55779	3,45E-36	3,55E+01	7,51E-37	0,1218	12,6812658	1,54432709	261,71	CFAP44	cilia and flagella associated protein 44
101928433	5,16E-17	1,63E+01	1,88E-17	0,1816	8,5011981	1,54379848	124,83	ATXN1-AS1	ATXN1 antisense RNA 1
107983998	3,03E-09	8,52E+00	1,44E-09	0,2551	6,0505314	1,54362743	55,48	LOC107983	uncharacterized LOC107983998
3973	3,94E-02	1,40E+00	3,01E-02	0,7116	2,1681554	1,54295113	7,17	LHCGR	luteinizing hormone/choriogonadotropin receptor
345643	6,34E-22	2,12E+01	1,99E-22	0,1583	9,7421769	1,54262566	163,32	MCIDAS	multiciliate differentiation and DNA synthesis associated cell cycle protein
55466	6,74E-03	2,17E+00	4,75E-03	0,5461	2,823407	1,54186428	12,07	DNAJA4	DnaJ heat shock protein family (Hsp40) member A4
400242	3,18E-03	2,50E+00	2,18E-03	0,5029	3,0648638	1,54121722	14,55	DICER1-AS1	DICER1 antisense RNA 1
57691	2,54E-69	6,86E+01	2,64E-70	0,0869	17,7259316	1,54105347	687,85	KIAA1586	KIAA1586
101927952	5,10E-06	5,29E+00	2,85E-06	0,3292	4,6810158	1,54097587	34,68	LOC101927	952
10772	5,95E-230	2,29E+02	5,41E-232	0,0474	32,5208544	1,54047622	9634,97	SRSF10	serine and arginine rich splicing factor 10
151050	1,88E-39	3,87E+01	3,82E-40	0,1162	13,2624613	1,5404714	299,23	KANSL1L	KAT8 regulatory NSL complex subunit 1 like
105371083	1,69E-02	1,77E+00	1,24E-02	0,6158	2,5012089	1,54018529	9,69	LOC105371	uncharacterized LOC105371083
27146	1,18E-11	1,09E+01	5,11E-12	0,2231	6,9025683	1,54002365	74,69	FAM184B	family with sequence similarity 184 member B
122553	2,79E-146	1,46E+02	7,21E-148	0,0595	25,8969278	1,53958158	1974,22	TRAPPC6B	trafficking protein particle complex subunit 6B
83473	6,23E-04	3,21E+00	4,03E-04	0,4351	3,5382881	1,53951541	19,37	KATNAL2	katanin catalytic subunit A1 like 2
79612	1,85E-82	8,17E+01	1,46E-83	0,0795	19,3672046	1,53907568	734,88	NAA16	N-alpha-acetyltransferase 16, NatA auxiliary subunit
388759	4,09E-03	2,39E+00	2,83E-03	0,5154	2,9857684	1,5389392	13,67	LINC02897	long intergenic non-protein coding RNA 2897
3161	8,56E-78	7,71E+01	7,44E-79	0,0818	18,8007654	1,53851712	773,81	HMMR	hyaluronan mediated motility receptor
1953	3,45E-34	3,35E+01	7,89E-35	0,1249	12,3111125	1,53822752	259,62	MEGF6	multiple EGF like domains 6
163131	1,32E-47	4,69E+01	2,22E-48	0,1052	14,6160702	1,53766036	375,11	ZNF780B	zinc finger protein 780B
5021	7,70E-13	1,21E+01	3,20E-13	0,2111	7,2857283	1,53765962	96,77	OXTR	oxytocin receptor
148213	9,62E-23	2,20E+01	2,96E-23	0,1548	9,9339956	1,537631	158,61	ZNF681	zinc finger protein 681
646658	8,73E-05	4,06E+00	5,28E-05	0,38	4,0430365	1,53621422	25,81	SYNDIG1L	synapse differentiation inducing 1 like
730087	4,43E-13	1,24E+01	1,83E-13	0,2086	7,3608861	1,53548489	84,37	ZNF726	zinc finger protein 726
130162	7,69E-32	3,11E+01	1,86E-32	0,1293	11,8620636	1,53419039	232,74	CLHC1	clathrin heavy chain linker domain containing 1
440686	3,54E-32	3,15E+01	8,52E-33	0,1286	11,9274095	1,53327084	237,14	H3-7	H3.7 histone (putative)
85388	3,43E-05	4,46E+00	2,02E-05	0,3596	4,2628368	1,5328186	32,3	SNORD14B	small nucleolar RNA, C/D box 14B
4776	1,56E-07	6,81E+00	8,06E-08	0,2854	5,3658331	1,53166947	47,12	NFATC4	nuclear factor of activated T cells 4
2697	9,35E-73	7,20E+01	8,98E-74	0,0843	18,1696024	1,53133445	749,44	GJA1	gap junction protein alpha 1
7412	1,79E-02	1,75E+00	1,31E-02	0,6172	2,4801839	1,53079978	9,62	VCAM1	vascular cell adhesion molecule 1
5203	1,07E-17	1,70E+01	3,82E-18	0,1762	8,6841579	1,5303708	3144,31	PFDN4	prefoldin subunit 4
79632	9,83E-18	1,70E+01	3,50E-18	0,176	8,6939524	1,53036594	131,37	FAM184A	family with sequence similarity 184 member A
83857	1,76E-08	7,75E+00	8,69E-09	0,2659	5,7544046	1,53032391	51,22	TMTC1	transmembrane O-mannosyltransferase targeting cadherins 1
56164	2,40E-03	2,62E+00	1,62E-03	0,4855	3,1516478	1,53008542	15,13	STK31	serine/threonine kinase 31
64859	8,82E-113	1,12E+02	3,94E-114	0,0674	22,705619	1,52997692	2552,76	NABP1	nucleic acid binding protein 1
645367	2,49E-03	2,60E+00	1,69E-03	0,4871	3,1404957	1,52965264	15,2	GGT8P	gamma-glutamyltransferase 8 pseudogene
101927300	1,07E-08	7,97E+00	5,20E-09	0,2617	5,8407059	1,52831488	55,23	GOT1-DT	GOT1 divergent transcript
348254	1,29E-03	2,89E+00	8,53E-04	0,4582	3,3350104	1,52814336	17,53	CCDC144CP	coiled-coil domain containing 144C, pseudogene
57579	2,25E-72	7,16E+01	2,18E-73	0,0843	18,1208122	1,5277307	809,18	FAM135A	family with sequence similarity 135 member A
814	2,47E-71	7,06E+01	2,45E-72	0,0849	17,9873025	1,52764969	698,56	CAMK4	calcium/calmodulin dependent protein kinase IV
5468	4,72E-152	1,51E+02	1,13E-153	0,0578	26,4072772	1,52720023	1733,1	PPARG	peroxisome proliferator activated receptor gamma
8552	1,27E-02	1,90E+00	9,15E-03	0,5858	2,6063683	1,52679904	10,33	INE1	inactivation escape 1
107986326	2,76E-07	6,56E+00	1,44E-07	0,29	5,259932	1,52550415	42,29	LOC107986	uncharacterized LOC107986326
349152	6,96E-28	2,72E+01	1,87E-28	0,1377	11,0644717	1,5235227	199,93	DPY19L2P2	DPY19L2 pseudogene 2
100288069	5,88E-11	1,02E+01	2,61E-11	0,2285	6,6669398	1,52347293	71,45	LOC100288	uncharacterized LOC100288069
51439	9,00E-84	8,30E+01	6,92E-85	0,078	19,5235873	1,52340127	810,02	FAM8A1	family with sequence similarity 8 member A1
23443	1,62E-102	1,02E+02	8,82E-104	0,0704	21,6328452	1,52197677	1065,91	SLC35A3	solute carrier family 35 member A3
51301	7,38E-06	5,13E+00	4,17E-06	0,3306	4,6026442	1,52183962	33,43	GCNT4	glucosaminyl (N-acetyl) transferase 4
122809	5,46E-127	1,26E+02	1,90E-128	0,0631	24,1114519	1,5215091	1827,91	SOCS4	suppressor of cytokine signaling 4
643253	2,15E-19	1,87E+01	7,27E-20	0,1667	9,1235622	1,52079004	138,22	CCT6P1	chaperonin containing TCP1 subunit 6 pseudogene 1
79738	6,46E-82	8,12E+01	5,16E-83	0,0788	19,3021076	1,52049966	747,3	BBS10	Bardet-Biedl syndrome 10
114792	1,17E-16	1,59E+01	4,30E-17	0,1809	8,4044868	1,5200013	116,75	KLHL32	kelch like family member 32
57544	2,73E-60	5,96E+01	3,48E-61	0,0921	16,503198	1,51950913	574,8	TXNDC16	thioredoxin domain containing 16
85389	1,73E-05	4,76E+00	1,00E-05	0,3437	4,4166753	1,51819766	30,86	SNORD14C	small nucleolar RNA, C/D box 14C
441459	2,58E-05	4,59E+00	1,51E-05	0,3507	4,3275424	1,51765497	31,06	ANKRD18B	ankyrin repeat domain 18B
114800	1,07E-04	3,97E+00	6,52E-05	0,3797	3,9931617	1,5160893	25,45	CCDC85A	coiled-coil domain containing 85A
54751	2,09E-46	4,57E+01	3,61E-47	0,1051	14,4249113	1,51600505	397,74	FBLIM1	filamin binding LIM protein 1
64318	1,65E-133	1,33E+02	5,06E-135	0,0613	24,7302276	1,51596033	2141,78	NOC3L	NOC3 like DNA replication regulator
105369617	1,57E-12	1,18E+01	6,58E-13	0,2109	7,1878146	1,51572249	84,07	LOC105369	uncharacterized LOC105369617
55422	1,72E-78	7,78E+01	1,46E-79	0,0802	18,8868605	1,51485035	696,23	ZNF331	zinc finger protein 331
116984	6,27E-82	8,12E+01	5,00E-83	0,0784	19,3037252	1,51405468	736	ARAP2	ArfGAP with RhoGAP domain, ankyrin repeat and PH domain 2
162655	1,21E-21	2,09E+01	3,84E-22	0,1565	9,6752914	1,51388647	150,85	ZNF519	zinc finger protein 519
221079	6,75E-93	9,22E+01	4,39E-94	0,0735	20,5772101	1,51294913	1401,84	ARL5B	ADP ribosylation factor like GTPase 5B
51026	1,08E-114	1,14E+02	4,74E-116	0,066	22,8991331	1,51172322	1628,95	GOLT1B	golgi transport 1B
339751	7,37E-50	4,91E+01	1,17E-50	0,101	14,9689178	1,51159551	396,47	MAP3K20-A	MAP3K20 antisense RNA 1
2798	1,77E-02	1,75E+00	1,30E-02	0,608	2,4843164	1,51047424	10,2	GNRHR	gonadotropin releasing hormone receptor
9015	2,21E-84	8,37E+01	1,67E-85	0,0771	19,5960734	1,50993036	928,13	TAF1A	TATA-box binding protein associated factor, RNA polymerase I subunit A
359845	2,15E-04	3,67E+00	1,34E-04	0,3951	3,8195036	1,50909993	22,93	RFLNB	refilin B
387119	2,95E-54	5,35E+01	4,29E-55	0,0965	15,6337439	1,50894674	483,29	CEP85L	centrosomal protein 85 like
54801	9,44E-138	1,37E+02	2,75E-139	0,06	25,1235974	1,50813993	2574,07	HAUS6	HAUS augmin like complex subunit 6
80323	2,22E-79	7,87E+01	1,86E-80	0,0794	18,9954453	1,50804291	815,86	CCDC68	coiled-coil domain containing 68
254439	1,99E-02	1,70E+00	1,47E-02	0,6177	2,4400209	1,50710083	9,46	C11orf86	chromosome 11 open reading frame 86
146206	4,26E-03	2,37E+00	2,95E-03	0,5067	2,9731387	1,50657419	14,34	CARMIL2	capping protein regulator and myosin 1 linker 2
57697	1,67E-85	8,48E+01	1,24E-86	0,0763	19,7280559	1,5056664	886,92	FANCM	FA complementation group M
151242	1,44E-05	4,84E+00	8,28E-06	0,3377	4,4578207	1,50552192	32,36	PPP1R1C	protein phosphatase 1 regulatory inhibitor subunit 1C
94104	6,29E-126	1,25E+02	2,24E-127	0,0627	24,0090344	1,50514957	1445,68	PAXBP1	PAX3 and PAX7 binding protein 1
196441	2,65E-188	1,88E+02	3,79E-190	0,0511	29,4125548	1,50423484	3164,98	ZFC3H1	zinc finger C3H1-type containing
23483	1,71E-71	7,08E+01	1,68E-72	0,0835	18,0080698	1,50421208	678,02	TGDS	TDP-glucose 4,6-dehydratase
7745	1,87E-213	2,13E+02	2,04E-215	0,048	31,326396	1,5036382	3035,81	ZKSCAN8	zinc finger with KRAB and SCAN domains 8
388591	4,79E-41	4,03E+01	9,37E-42	0,111	13,5376958	1,50272386	320,67	RNF207	ring finger protein 207
107986822	5,63E-03	2,25E+00	3,94E-03	0,5211	2,8826513	1,50228849	13,36	LOC107986	uncharacterized LOC107986822

6617	1,04E-266	2,66E+02	6,92E-269	0,0429	35,0336433	1,50190628	6322,32	SNAPC1	small nuclear RNA activating complex polypeptide 1
3872	1,68E-22	2,18E+01	5,19E-23	0,152	9,877956	1,50157346	176,53	KRT17	keratin 17
201799	1,15E-93	9,29E+01	7,37E-95	0,0726	20,6635481	1,50055389	947,67	TMEM154	transmembrane protein 154
5540	3,39E-06	5,47E+00	1,88E-06	0,3147	4,7657849	1,49975494	36,83	NPY4R	neuropeptide Y receptor Y4
347902	1,25E-33	3,29E+01	2,92E-34	0,1229	12,2052032	1,49962475	3163,52	AMIGO2	adhesion molecule with Ig like domain 2
134266	1,32E-100	9,99E+01	7,42E-102	0,07	21,4273808	1,4994308	1025,03	GRPEL2	GrpE like 2, mitochondrial
27035	2,78E-02	1,56E+00	2,08E-02	0,6484	2,3112188	1,4985533	8,71	NOX1	NADPH oxidase 1
284611	2,32E-161	1,61E+02	4,86E-163	0,0551	27,210629	1,49828929	2264,33	EEIG2	EEIG family member 2
644192	1,15E-07	6,94E+00	5,90E-08	0,2763	5,4218098	1,49817516	47,21	NR2F2-AS1	NR2F2 antisense RNA 1
23507	8,84E-63	6,21E+01	1,06E-63	0,0888	16,8496416	1,49705245	535,25	LRRC8B	leucine rich repeat containing 8 VRAC subunit B
105372773	3,15E-03	2,50E+00	2,15E-03	0,4878	3,0682557	1,49663004	15	LOC105372	uncharacterized LOC105372773
9134	2,44E-101	1,01E+02	1,35E-102	0,0696	21,5065336	1,4965266	1001,21	CCNE2	cyclin E2
100287171	3,67E-81	8,04E+01	2,97E-82	0,0779	19,2113606	1,4961694	792,7	WASHC1	WASH complex subunit 1
124923	9,66E-21	2,00E+01	3,15E-21	0,1581	9,4576865	1,49529442	157,43	RSKR	ribosomal protein S6 kinase related
105370504	3,18E-03	2,50E+00	2,18E-03	0,4878	3,0650086	1,49514363	14,94	LOC105370	uncharacterized LOC105370504
100128054	1,84E-05	4,74E+00	1,06E-05	0,3395	4,4035505	1,49512827	31,41	PLCE1-AS1	PLCE1 antisense RNA 1
107986823	2,45E-02	1,61E+00	1,83E-02	0,6333	2,3603506	1,49472226	9,3	LOC107986	uncharacterized LOC107986823
51704	1,51E-59	5,88E+01	1,95E-60	0,0911	16,3989087	1,49448219	537,19	GPRC5B	G protein-coupled receptor class C group 5 member B
79441	1,29E-110	1,10E+02	6,02E-112	0,0664	22,4835201	1,49329428	1125,94	HAUS3	HAUS augmin like complex subunit 3
80000	3,49E-42	4,15E+01	6,66E-43	0,1088	13,7306173	1,49320623	336,22	GREB1L	GREB1 like retinoic acid receptor coactivator
595097	7,63E-07	6,12E+00	4,08E-07	0,2947	5,0651088	1,49283222	42,6	SNORD16	small nucleolar RNA, C/D box 16
2099	4,60E-02	1,34E+00	3,55E-02	0,7098	2,1031605	1,49280972	7,11	ESR1	estrogen receptor 1
64064	4,70E-02	1,33E+00	3,63E-02	0,7131	2,0931893	1,49271799	7,09	OXCT2	3-oxoacid CoA-transferase 2
105375061	1,21E-06	5,92E+00	6,56E-07	0,3001	4,9739568	1,49265103	39,23	LOC105375	uncharacterized LOC105375061
26801	2,09E-03	2,68E+00	1,41E-03	0,4674	3,1933647	1,49252987	16,38	SNORD48	small nucleolar RNA, C/D box 48
101927770	8,00E-03	2,10E+00	5,68E-03	0,5392	2,7656589	1,49125166	12,62	LOC101927	uncharacterized LOC101927770
57528	3,66E-04	3,44E+00	2,32E-04	0,4042	3,6815311	1,48819361	22,68	KCTD16	potassium channel tetramerization domain containing 16
26813	3,64E-03	2,44E+00	2,50E-03	0,4922	3,0232567	1,48801014	14,88	SNORD36C	small nucleolar RNA, C/D box 36C
60487	1,65E-98	9,78E+01	9,65E-100	0,0702	21,1994957	1,48729098	1043,15	TRMT11	tRNA methyltransferase 11 homolog
100379224	8,18E-34	3,31E+01	1,89E-34	0,1215	12,2403371	1,48694927	269,7	ZNF225-AS1	ZNF225 and ZNF224 antisense RNA 1
375743	2,35E-127	1,27E+02	8,13E-129	0,0616	24,1464822	1,4864016	1565,31	PTAR1	protein prenyltransferase alpha subunit repeat containing 1
121441	1,08E-140	1,40E+02	3,01E-142	0,0585	25,3929833	1,48619354	2477,7	NEDD1	NEDD1 gamma-tubulin ring complex targeting factor
84281	1,55E-06	5,81E+00	8,44E-07	0,3017	4,9249947	1,48610667	39,16	C2orf88	chromosome 2 open reading frame 88
10157	6,54E-135	1,34E+02	1,97E-136	0,0598	24,8610218	1,485832	1748,14	AASS	aminoadipate-semialdehyde synthase
107984817	1,38E-03	2,86E+00	9,16E-04	0,4481	3,3152755	1,48542863	18,07	LOC107984	817
2242	4,15E-03	2,38E+00	2,87E-03	0,4981	2,9817153	1,48530575	14,79	FES	FES proto-oncogene, tyrosine kinase
5396	8,43E-10	9,07E+00	3,92E-10	0,2374	6,2570971	1,48525072	64,07	PRRX1	paired related homeobox 1
619505	2,33E-02	1,63E+00	1,73E-02	0,6236	2,3795673	1,48383944	9,34	SNORA21	small nucleolar RNA, H/ACA box 21
5806	2,09E-258	2,58E+02	1,48E-260	0,043	34,482319	1,48320004	8360,54	PTX3	pentraxin 3
103611157	1,83E-27	2,67E+01	4,98E-28	0,1351	10,9761181	1,48262013	278,69	TGFB2-OT1	TGFB2 overlapping transcript 1
7913	0	#NUM!	0	0,0366	40,4202491	1,48132819	24023,64	DEK	DEK proto-oncogene
5174	1,28E-05	4,89E+00	7,34E-06	0,3303	4,4835033	1,48086558	32,62	PDZK1	PDZ domain containing 1
93474	8,49E-36	3,51E+01	1,87E-36	0,1174	12,6094373	1,48085241	303,28	ZNF670	zinc finger protein 670
105371131	1,37E-03	2,86E+00	9,11E-04	0,4464	3,3166003	1,48060734	17,99	LOC105371	uncharacterized LOC105371131
6405	1,88E-52	5,17E+01	2,83E-53	0,0963	15,3645493	1,48017454	480,98	SEMA3F	semaphorin 3F
3355	1,45E-07	6,84E+00	7,50E-08	0,2751	5,3787262	1,47968303	47,6	HTR1F	5-hydroxytryptamine receptor 1F
151648	5,72E-130	1,29E+02	1,88E-131	0,0606	24,3962336	1,47875968	1411,5	SGO1	shugoshin 1
105379263	3,43E-03	2,46E+00	2,35E-03	0,4861	3,0416578	1,47855099	14,88	LOC105379	uncharacterized LOC105379263
100132403	1,20E-08	7,92E+00	5,84E-09	0,2539	5,8212273	1,47772134	55,32	FAM157B	family with sequence similarity 157 member B
79805	2,24E-11	1,06E+01	9,81E-12	0,217	6,809308	1,47751006	85,97	VASH2	vasohibin 2
727758	3,28E-13	1,25E+01	1,35E-13	0,1996	7,4015829	1,47723395	95,34	ROCK1P1	Rho associated coiled-coil containing protein kinase 1 pseudogene 1
8436	2,61E-119	1,19E+02	1,05E-120	0,0632	23,3615575	1,47691755	1985,36	CAVIN2	caveolae associated protein 2
677834	2,28E-02	1,64E+00	1,69E-02	0,6181	2,3881555	1,4760321	10,24	SNORA55	small nucleolar RNA, H/ACA box 55
7639	4,12E-39	3,84E+01	8,41E-40	0,1118	13,2031776	1,47568785	332,24	ZNF85	zinc finger protein 85
23500	9,34E-26	2,50E+01	2,65E-26	0,139	10,6107897	1,47472404	203,35	DAAM2	dishevelled associated activator of morphogenesis 2
166968	3,79E-106	1,05E+02	1,91E-107	0,067	22,0186323	1,47455551	1411,39	MIER3	MIER family member 3
2764	5,70E-116	1,15E+02	2,43E-117	0,064	23,0281916	1,47368558	5026,29	GMFB	glia maturation factor beta
340351	1,92E-10	9,72E+00	8,73E-11	0,2271	6,4875216	1,47315943	70,11	AGBL3	AGBL carboxypeptidase 3
9358	6,40E-09	8,19E+00	3,10E-09	0,2485	5,9263852	1,47246487	58,17	ITGBL1	integrin subunit beta like 1
905	2,90E-102	1,02E+02	1,59E-103	0,0681	21,605532	1,47072959	1023,6	CCNT2	cyclin T2
83448	1,37E-119	1,19E+02	5,45E-121	0,0628	23,3896279	1,46855466	1472,49	PUS7L	pseudouridine synthase 7 like
79608	1,00E-08	8,00E+00	4,89E-09	0,2509	5,8510068	1,46828703	56,67	RIC3	RIC3 acetylcholine receptor chaperone
634	2,64E-03	2,58E+00	1,79E-03	0,4701	3,1229711	1,46808333	16,39	CEACAM1	CEA cell adhesion molecule 1
9936	6,01E-41	4,02E+01	1,18E-41	0,1086	13,5210224	1,46797017	355,9	CD302	CD302 molecule
3717	3,21E-42	4,15E+01	6,12E-43	0,1068	13,7366996	1,46702919	344,86	JAK2	Janus kinase 2
107984841	5,38E-08	7,27E+00	2,71E-08	0,2639	5,5591247	1,46702714	55,01	LOC107984	replaced by ID 100288069
170959	2,58E-57	5,66E+01	3,49E-58	0,0912	16,0805352	1,46592925	498,24	ZNF431	zinc finger protein 431
107984847	9,37E-14	1,30E+01	3,78E-14	0,1937	7,568489	1,46568027	96,08	LOC107984	replaced by ID 100288069
64062	8,65E-180	1,79E+02	1,39E-181	0,051	28,7351562	1,46486603	2699,54	RBM26	RNA binding motif protein 26
101928451	1,76E-36	3,58E+01	3,80E-37	0,115	12,7344595	1,46411318	313,02	LOC101928	451
101927521	1,33E-02	1,88E+00	9,64E-03	0,5655	2,5883577	1,46377004	10,82	LOC101927	uncharacterized LOC101927521
79846	1,73E-04	3,76E+00	1,07E-04	0,3776	3,873896	1,4627502	26,14	CFAP69	cilia and flagella associated protein 69
105373780	3,10E-03	2,51E+00	2,11E-03	0,4759	3,0736326	1,46273655	15,47	LOC105373	proline-rich protein 18-like
101060351	2,88E-07	6,54E+00	1,50E-07	0,2785	5,252003	1,46251383	45,61	TBC1D3K	TBC1 domain family member 3K
105374298	1,27E-06	5,90E+00	6,88E-07	0,2944	4,9646947	1,46149526	44,63	LOC105374	keratinocyte proline-rich protein-like
90246	2,06E-02	1,69E+00	1,52E-02	0,6021	2,4269372	1,46123406	10,03	LOC90246	uncharacterized LOC90246
105370503	7,24E-08	7,14E+00	3,67E-08	0,2652	5,5060129	1,46003076	52,93	LINC02331	long intergenic non-protein coding RNA 2331
130271	1,28E-30	2,99E+01	3,20E-31	0,1256	11,6215882	1,45964125	280,24	PLEKHH2	pleckstrin homology, MyTH4 and FERM domain containing H2
904	7,16E-129	1,28E+02	2,39E-130	0,06	24,2919416	1,45872891	1545,79	CCNT1	cyclin T1
727896	9,35E-06	5,03E+00	5,32E-06	0,3205	4,551765	1,45868136	36,17	CHORDC1P	CHORDC1 pseudogene 4
5378	6,46E-89	8,82E+01	4,50E-90	0,0725	20,1245248	1,45860792	950,66	PMS1	PMS1 homolog 1, mismatch repair system component
100507308	3,62E-04	3,44E+00	2,29E-04	0,3956	3,6843777	1,45758318	23,67	TARID	TCF21 antisense RNA inducing promoter demethylation
144245	1,92E-21	2,07E+01	6,14E-22	0,1513	9,6271801	1,4568088	174,17	ALG10B	ALG10 alpha-1,2-glucosyltransferase B
282996	3,90E-02	1,41E+00	2,98E-02	0,6696	2,1727785	1,45484496	7,71	RBM20	RNA binding motif protein 20
100507506	3,46E-04	3,46E+00	2,19E-04	0,3935	3,6961	1,45450701	23,83	ECI2-DT	ECI2 divergent transcript
650794	2,10E-15	1,47E+01	8,04E-16	0,1805	8,0536135	1,45369547	129,39	MIPEPP3	mitochondrial intermediate peptidase pseudogene 3
100147773	7,72E-03	2,11E+00	5,47E-03	0,5233	2,7777761	1,4536134	13,05	TMCO1-AS1	TMCO1 antisense RNA 1
677805	7,76E-17	1,61E+01	2,83E-17	0,172	8,4531813	1,45352944	125,56	SNORA18	small nucleolar RNA, H/ACA box 18
7594	3,48E-52	5,15E+01	5,26E-53	0,0948	15,3243391	1,45313636	471,44	ZNF43	zinc finger protein 43
5924	3,93E-02	1,41E+00	3,01E-02	0,6699	2,1690594	1,45312248	7,71	RASGRF2	Ras protein specific guanine nucleotide releasing factor 2
79694	2,09E-53	5,27E+01	3,09E-54	0,0937	15,5075217	1,45287825	543,64	MANEA	mannosidase endo-alpha
83540	7,19E-175	1,74E+02	1,23E-176	0,0513	28,3365358	1,45247126	4329,24	NUF2	NUF2 component of NDC80 kinetochore complex
646719	1,49E-30	2,98E+01	3,73E-31	0,1251	11,6086142	1,45195433	243,53	NIPBL-DT	NIPBL divergent transcript
9928	9,37E-144	1,43E+02	2,52E-145	0,0566	25,6701553	1,45189973	4247,38	KIF14	kinesin family member 14
167681	2,74E-03	2,56E+00	1,87E-03	0,4661	3,1107831	1,44986475	16,22	PRSS35	serine protease 35
8899	2,66E-166	1,66E+02	5,12E-168	0,0525	27,628091	1,44985791	7672,32	PRPF4B	pre-mRNA processing factor 4B
54626	2,30E-14	1,36E+01	9,11E-15	0,1869	7,7510416	1,44896915	104,85	HES2	hes family bHLH transcription factor 2
27063	0	#NUM!	0	0,0382	37,8911819	1,44883982	17230,84	ANKRD1	ankyrin repeat domain 1
7771	2,02E-28	2,77E+01	5,33E-29	0,1296	11,176179	1,44855044	222,34	ZNF112	zinc finger protein 112
163227	4,43E-49	4,84E+01	7,18E-50	0,0975	14,847843	1,44833721	478,4	ZNF100	zinc finger protein 100
51232	0	#NUM!	0	0,0375	38,6097671	1,4482481	20974,36	CRIM1	cysteine rich transmembrane BMP regulator 1
54953	8,26E-120	1,19E+02	3,27E-121	0,0619	23,41146	1,44821574	1322	ODR4	odr-4 GPCR localization factor homolog
652966	5,31E-04	3,27E+00	3,41E-04	0,404	3,5818062	1,44692215	21,57	SNORD10	small nucleolar RNA, C/D box 10
105372883	1,40E-03	2,85E+00	9,26E-04	0,4368	3,312096	1,44655916	18,43	LINC02767	long intergenic non-protein coding RNA 2767
158158	2,26E-51	5,06E+01	3,46E-52	0,0951	15,2015057	1,44599906	449,93	RASEF	RAS and EF-hand domain containing
1062	1,86E-219	2,19E+02	1,90E-221	0,0455	31,7662147	1,44580075	7994,22	CENPE	centromere protein E
253769	1,57E-35	3,48E+01	3,49E-36	0,115	12,5603114	1,44505634	323,43	WDR27	WD repeat domain 27
1138	1,03E-36	3,60E+01	2,21E-37	0,113	12,7769339	1,44395377	361,33	CHRNA5	cholinergic receptor nicotinic alpha 5 subunit
65012	1,22E-04	3,91E+00	7,42E-05	0,3644	3,9622997	1,44369868	26,88	SLC26A10P	solute carrier family 26 member 10, pseudogene
105376224	3,12E-03	2,51E+00	2,13E-03	0,4699	3,0717619	1,44345817	16,07	LOC105376	uncharacterized LOC105376224
257415	8,79E-52	5,11E+01	1,34E-52	0,0945	15,2635519	1,44277712	472,35	FAM133B	family with sequence similarity 133 member B
375513	2,37E-14	1,36E+01	9,39E-15	0,1862	7,7472311	1,44258814	103,21	GUSBP4	GUSB pseudogene 4
101927957	8,33E-05	4,08E+00	5,03E-05	0,3558	4,0543945	1,44254656	28,16	LINC01572	long intergenic non-protein coding RNA 1572
100128966	2,11E-02	1,68E+00	1,56E-02	0,5964	2,4185001	1,44245949	9,91	LOC100128	uncharacterized LOC100128966
124491	5,59E-81	8,03E+01	4,54E-82	0,0752	19,189356	1,44212731	817,44	TMEM170A	transmembrane protein 170A
90594	1,89E-48	4,77E+01	3,12E-49	0,0978	14,7490891	1,44183392	474,57	ZNF439	zinc finger protein 439
6374	4,70E-02	1,33E+00	3,63E-02	0,6886	2,093932	1,44179976	7,56	CXCL5	C-X-C motif chemokine ligand 5
105369957	9,80E-07	6,01E+00	5,28E-07	0,2874	5,0158158	1,44167413	46,42	LOC105369	uncharacterized LOC105369957
2550	1,61E-46	4,58E+01	2,77E-47	0,0998	14,44313	1,44153	405,55	GABBR1	gamma-aminobutyric acid type B receptor subunit 1
253714	2,26E-95	9,46E+01	1,40E-96	0,0691	20,8542004	1,44067578	1078,18	MMS22L	MMS22 like, DNA repair protein

10536	3,74E-07	6,43E+00	1,97E-07	0,2765	5,2023506	1,43853115	48,17	P3H3	prolyl 3-hydroxylase 3
26050	1,77E-12	1,18E+01	7,47E-13	0,2005	7,170563	1,43757542	98,05	SLITRK5	SLIT and NTRK like family member 5
101929285	2,21E-05	4,66E+00	1,29E-05	0,3294	4,3625884	1,43718654	32,71	LOC1019292	uncharacterized LOC101929285
100506127	4,15E-22	2,14E+01	1,30E-22	0,1468	9,7856688	1,43643389	178,62	GVQW3	GVQW motif containing 3
3981	8,49E-82	8,11E+01	6,78E-83	0,0744	19,2879661	1,4357504	1061,76	LIG4	DNA ligase 4
51277	3,92E-34	3,34E+01	8,98E-35	0,1167	12,3006743	1,43565457	285,02	DNAJC27	DnaJ heat shock protein family (Hsp40) member C27
590	4,00E-04	3,40E+00	2,54E-04	0,3922	3,6578336	1,43473871	23,71	BCHE	butyrylcholinesterase
105376050	8,44E-06	5,07E+00	4,79E-06	0,3136	4,5738612	1,43416007	35,77	LOC105376(	uncharacterized LOC105376050
107984988	3,60E-02	1,44E+00	2,74E-02	0,65	2,2054951	1,43366341	8,31	LOC107984(	uncharacterized LOC107984988
100874028	1,74E-51	5,08E+01	2,67E-52	0,0941	15,2184942	1,43273419	449,84	SGO1-AS1	SGO1 antisense RNA 1
965	1,07E-17	1,70E+01	3,82E-18	0,1648	8,684095	1,43078067	1439,03	CD58	CD58 molecule
101752399	4,28E-55	5,44E+01	6,11E-56	0,0908	15,7574172	1,4303375	513,2	STAG3L5P-F	STAG3L5P-PVRIG2P-PILRB readthrough
100996539	2,44E-02	1,61E+00	1,82E-02	0,6054	2,3621878	1,43003113	9,89	ITPR1-DT	ITPR1 divergent transcript
7220	2,59E-36	3,56E+01	5,61E-37	0,1126	12,7040983	1,4298774	303,68	TRPC1	transient receptor potential cation channel subfamily C member 1
107985492	1,27E-02	1,90E+00	9,15E-03	0,5484	2,6063414	1,42927569	12,83	LOC107985(	uncharacterized LOC107985492
6894	5,00E-87	8,63E+01	3,62E-88	0,0718	19,9058696	1,42844261	969,34	TARBP1	TAR (HIV-1) RNA binding protein 1
100289061	6,99E-05	4,16E+00	4,19E-05	0,3487	4,0964736	1,4282433	28,85	ADAMTSL4-A	ADAMTSL4 antisense RNA 2
27040	1,66E-02	1,78E+00	1,22E-02	0,5692	2,5074328	1,42727428	11,32	LAT	linker for activation of T cells
9057	7,70E-205	2,04E+02	9,46E-207	0,0465	30,6834739	1,42718958	3458,81	SLC7A6	solute carrier family 7 member 6
2196	3,82E-02	1,42E+00	2,92E-02	0,6543	2,1810733	1,42712301	8,39	FAT2	FAT atypical cadherin 2
23421	7,10E-56	5,51E+01	9,94E-57	0,0899	15,8717866	1,42695498	725,09	ITGB3BP	integrin subunit beta 3 binding protein
105374997	8,00E-09	8,10E+00	3,88E-09	0,2422	5,8892949	1,42665018	64,75	LOC105374(	replaced by ID 222696
100316904	3,71E-04	3,43E+00	2,36E-04	0,3879	3,677424	1,42645691	24,43	SAP25	Sin3A associated protein 25
100506365	2,30E-72	7,16E+01	2,23E-73	0,0787	18,1196271	1,42634133	989,47	OTUD6B-AS	OTUD6B antisense RNA 1 (head to head)
6775	2,27E-04	3,64E+00	1,41E-04	0,3746	3,8057384	1,42564009	27,77	STAT4	signal transducer and activator of transcription 4
342909	5,83E-34	3,32E+01	1,34E-34	0,1162	12,2680595	1,4253661	317,68	ZNF284	zinc finger protein 284
92255	1,96E-72	7,17E+01	1,90E-73	0,0786	18,1285153	1,42527653	715,95	LMBRD2	LMBR1 domain containing 2
7072	5,63E-131	1,30E+02	1,81E-132	0,0582	24,4917919	1,42516823	1725,45	TIA1	TIA1 cytotoxic granule associated RNA binding protein
283788	8,86E-12	1,11E+01	3,81E-12	0,2051	6,9439927	1,42426739	98,06	LOC283788	FSHD region gene 1 pseudogene
105378421	3,61E-02	1,44E+00	2,75E-02	0,6462	2,2040568	1,42425025	8,29	PANK1-AS1	PANK1 antisense RNA 1
127602	2,29E-47	4,66E+01	3,86E-48	0,0977	14,5782418	1,42410891	426,19	DNAH14	dynein axonemal heavy chain 14
7561	2,70E-28	2,76E+01	7,17E-29	0,1277	11,1498286	1,42391097	228,8	ZNF14	zinc finger protein 14
105377006	1,08E-02	1,97E+00	7,80E-03	0,5351	2,660781	1,42384322	12,75	LINC02084	long intergenic non-protein coding RNA 2084
3248	1,86E-04	3,73E+00	1,15E-04	0,3693	3,8556023	1,42374565	25,76	HPGD	15-hydroxyprostaglandin dehydrogenase
79677	2,03E-175	1,75E+02	3,44E-177	0,0501	28,3813321	1,42320734	4175,65	SMC6	structural maintenance of chromosomes 6
643707	3,52E-04	3,45E+00	2,23E-04	0,3854	3,6915677	1,4228528	23,52	GOLGA6L4	golgin A6 family like 4
414060	9,12E-10	9,04E+00	4,25E-10	0,2278	6,2444594	1,42274954	69,72	TBC1D3C	TBC1 domain family member 3C
285349	9,08E-07	6,04E+00	4,88E-07	0,2828	5,0309603	1,42256066	43,87	ZNF660	zinc finger protein 660
11209	7,60E-03	2,12E+00	5,39E-03	0,5111	2,7828217	1,42216248	14,59	MST1P2	macrophage stimulating 1 pseudogene 2
57542	6,08E-80	7,92E+01	5,04E-81	0,0746	19,0639108	1,42202641	818,14	KLHL42	kelch like family member 42
7514	1,77E-116	1,16E+02	7,50E-118	0,0616	23,0791724	1,42182142	17220,44	XPO1	exportin 1
114799	6,13E-95	9,42E+01	3,82E-96	0,0683	20,8059367	1,42144168	1987,45	ESCO1	establishment of sister chromatid cohesion N-acetyltransferase 1
55015	2,07E-122	1,22E+02	7,91E-124	0,06	23,6668795	1,42051565	1843,99	PRPF39	pre-mRNA processing factor 39
85465	1,02E-120	1,20E+02	4,01E-122	0,0604	23,5006812	1,41851961	3403,31	SELENOI	selenoprotein I
105377291	1,09E-07	6,96E+00	5,57E-08	0,2611	5,4319991	1,41834229	57,07	LOC105377(	uncharacterized LOC105377291
105379493	8,02E-03	2,10E+00	5,69E-03	0,5128	2,7649838	1,41783319	13,59	CH507-145C	uncharacterized CH507-145C22.1
102723451	4,65E-02	1,33E+00	3,59E-02	0,6751	2,0984922	1,41672498	7,56	LOC102723(	family with sequence similarity 243 member B
54510	1,52E-05	4,82E+00	8,76E-06	0,3186	4,4457787	1,41655581	34,75	PCDH18	protocadherin 18
400798	4,66E-06	5,33E+00	2,61E-06	0,3013	4,6996118	1,4158252	43,56	C1orf220	chromosome 1 putative open reading frame 220
101927603	4,72E-02	1,33E+00	3,65E-02	0,6767	2,0917511	1,4155494	7,56	LOC101927(	uncharacterized LOC101927603
55972	3,03E-59	5,85E+01	3,94E-60	0,0865	16,3560375	1,41506619	544,26	SLC25A40	solute carrier family 25 member 40
100310812	2,81E-09	8,55E+00	1,34E-09	0,2333	6,0628033	1,41447821	69,39	SPDYE2B	speedy/RINGO cell cycle regulator family member E2B
107986178	1,20E-03	2,92E+00	7,90E-04	0,4213	3,3562381	1,4140611	20,2	LOC107986(	uncharacterized LOC107986178
26039	2,49E-83	8,26E+01	1,92E-84	0,0726	19,4712778	1,41361308	896,71	SS18L1	SS18L1 subunit of BAF chromatin remodeling complex
5411	8,15E-166	1,65E+02	1,60E-167	0,0512	27,5869487	1,41320174	9768,75	PNN	pinin, desmosome associated protein
220441	3,20E-32	3,15E+01	7,67E-33	0,1183	11,9360901	1,41160808	275,31	RNF152	ring finger protein 152
121512	1,02E-07	6,99E+00	5,22E-08	0,2593	5,4437986	1,4114108	54,82	FGD4	FYVE, RhoGEF and PH domain containing 4
80117	1,82E-04	3,74E+00	1,13E-04	0,3656	3,8607055	1,41134748	28,79	ARL14	ADP ribosylation factor like GTPase 14
643180	5,80E-10	9,24E+00	2,68E-10	0,2234	6,3160632	1,41093829	72,22	CCT6P3	chaperonin containing TCP1 subunit 6 pseudogene 3
84218	8,98E-05	4,05E+00	5,43E-05	0,3494	4,0361094	1,4102706	28,63	TBC1D3F	TBC1 domain family member 3F
283554	7,73E-30	2,91E+01	1,97E-30	0,1229	11,4653269	1,40911334	284,72	GPR137C	G protein-coupled receptor 137C
57822	2,77E-02	1,56E+00	2,07E-02	0,609	2,3127326	1,40838301	9,75	GRHL3	grainyhead like transcription factor 3
135293	1,88E-153	1,53E+02	4,35E-155	0,0531	26,5301347	1,4081778	2593,76	PM20D2	peptidase M20 domain containing 2
105379326	5,88E-03	2,23E+00	4,13E-03	0,4909	2,8682203	1,40803177	14,27	LOC105379326	
100288413	8,96E-17	1,60E+01	3,28E-17	0,1668	8,4362666	1,40709008	133,18	ERVMER34-	endogenous retrovirus group MER34 member 1, envelope
594837	1,56E-02	1,81E+00	1,14E-02	0,5559	2,5309572	1,40699994	11,32	SNORD101	small nucleolar RNA, C/D box 101
8089	9,77E-106	1,05E+02	4,97E-107	0,064	21,9751972	1,40669705	1634,14	YEATS4	YEATS domain containing 4
105378077	2,70E-02	1,57E+00	2,02E-02	0,6055	2,3224544	1,40629674	9,7	LOC105378077	
494513	4,63E-05	4,33E+00	2,75E-05	0,3353	4,1934801	1,40617446	30,83	PJVK	pejvakin
51473	2,38E-03	2,62E+00	1,61E-03	0,4457	3,1547182	1,40615467	17,91	DCDC2	doublecortin domain containing 2
677802	5,19E-02	1,28E+00	4,03E-02	0,6856	2,0504112	1,40583387	7,47	SNORA14B	small nucleolar RNA, H/ACA box 14B
26779	NA	#VALUE!	NA	2,0179	0,6963485	1,40513705	86,85	SNORA69	small nucleolar RNA, H/ACA box 69
653567	1,93E-02	1,71E+00	1,42E-02	0,5728	2,4514989	1,40431767	11,84	TMEM236	transmembrane protein 236
286103	7,80E-05	4,11E+00	4,70E-05	0,345	4,0699986	1,40407398	29,31	ZNF252P-AS	ZNF252P antisense RNA 1
55599	1,37E-51	5,09E+01	2,08E-52	0,092	15,2345738	1,40155962	513,77	RNPC3	RNA binding region (RNP1, RRM) containing 3
11107	1,50E-67	6,68E+01	1,63E-68	0,0801	17,4928137	1,40117471	665,61	PRDM5	PR/SET domain 5
9963	3,38E-02	1,47E+00	2,56E-02	0,6269	2,2317891	1,39914697	10,36	SLC23A1	solute carrier family 23 member 1
138199	1,24E-70	6,99E+01	1,26E-71	0,0782	17,8965248	1,39878682	909,81	CARNMT1	carnosine N-methyltransferase 1
11080	5,99E-62	6,12E+01	7,32E-63	0,0836	16,7347595	1,39826221	671,68	DNAJB4	DnaJ heat shock protein family (Hsp40) member B4
10150	2,37E-136	1,36E+02	7,04E-138	0,0559	24,9943907	1,39744238	1745,5	MBNL2	muscleblind like splicing regulator 2
140890	1,06E-94	9,40E+01	6,62E-96	0,0672	20,7796058	1,39672394	4129,95	SREK1	splicing regulatory glutamic acid and lysine rich protein 1
9988	1,07E-131	1,31E+02	3,36E-133	0,0568	24,5603198	1,39592742	1739,1	DMTF1	cyclin D binding myb like transcription factor 1
100124516	9,38E-03	2,03E+00	6,71E-03	0,5149	2,7109188	1,39581438	13,41	SNORD58C	small nucleolar RNA, C/D box 58C
100506422	2,00E-07	6,70E+00	1,04E-07	0,2623	5,3199542	1,39530381	54,25	LOC100506(	putative deoxyuridine 5'-triphosphate nucleotidohydrolase-like protein FLJ16323
220042	9,67E-112	1,11E+02	4,39E-113	0,0617	22,5994516	1,39507679	1394,09	DDIAS	DNA damage induced apoptosis suppressor
80862	1,10E-09	8,96E+00	5,15E-10	0,2245	6,2146034	1,39490563	71,75	POLR1HASF	POLR1H antisense, pseudogene
105372310	1,93E-31	3,07E+01	4,74E-32	0,1183	11,7836431	1,39423788	267,81	LOC105372(	uncharacterized LOC105372310
100128553	6,67E-02	1,18E+00	5,26E-02	0,719	1,9384444	1,39368879	6,73	CTAGE4	CTAGE family member 4
56956	1,34E-05	4,87E+00	7,73E-06	0,3116	4,4725856	1,39367894	37,3	LHX9	LIM homeobox 9
10773	4,03E-47	4,64E+01	6,83E-48	0,0958	14,5393301	1,39249722	554,15	ZBTB6	zinc finger and BTB domain containing 6
221302	5,38E-59	5,83E+01	7,04E-60	0,0853	16,3206206	1,39191258	579,52	ZUP1	zinc finger containing ubiquitin peptidase 1
134553	1,64E-112	1,12E+02	7,36E-114	0,0614	22,6781617	1,3918875	2279,52	C5orf24	chromosome 5 open reading frame 24
1763	1,42E-93	9,28E+01	9,07E-95	0,0674	20,6535513	1,3914628	1153,07	DNA2	DNA replication helicase/nuclease 2
283422	1,13E-09	8,95E+00	5,31E-10	0,224	6,2096098	1,39120791	75,64	LINC01559	long intergenic non-protein coding RNA 1559
101752334	2,69E-14	1,36E+01	1,06E-14	0,1799	7,7312509	1,39068324	110,4	PVRIG2P	PVR related immunoglobulin domain containing 2, pseudogene
400954	9,62E-29	2,80E+01	2,52E-29	0,1233	11,2426056	1,38645418	3321,7	EML6	EMAP like 6
2152	8,59E-234	2,33E+02	7,51E-236	0,0423	32,7925734	1,38639151	15222,93	F3	coagulation factor III, tissue factor
26973	2,87E-132	1,32E+02	8,94E-134	0,0563	24,614032	1,38603951	2728,17	CHORDC1	cysteine and histidine rich domain containing 1
101927528	3,51E-11	1,05E+01	1,55E-11	0,2055	6,7434347	1,38600844	84,65	LINC01204	long intergenic non-protein coding RNA 1204
84612	2,85E-24	2,35E+01	8,43E-25	0,1347	10,282731	1,38551768	216,89	PARD6B	par-6 family cell polarity regulator beta
644656	1,62E-06	5,79E+00	8,84E-07	0,2818	4,9157758	1,38536727	46,28	LOC644656	uncharacterized LOC644656
101735302	1,05E-09	8,98E+00	4,92E-10	0,2226	6,2217659	1,38526433	71,94	STAG3L5P	stromal antigen 3-like 5 pseudogene
55872	4,09E-178	1,77E+02	6,70E-180	0,0484	28,6000875	1,38516593	4797,86	PBK	PDZ binding kinase
105373786	1,95E-02	1,71E+00	1,44E-02	0,5656	2,4475725	1,38429511	11,2	CALCRL-AS	CALCRL and TFPI antisense RNA 1
2246	8,53E-26	2,51E+01	2,42E-26	0,1303	10,6194359	1,38324642	233,72	FGF1	fibroblast growth factor 1
112476	1,74E-07	6,76E+00	8,99E-08	0,2587	5,3459822	1,38317288	56,33	PRRT2	proline rich transmembrane protein 2
253639	3,91E-33	3,24E+01	9,18E-34	0,1142	12,1114942	1,38301558	293	ZNF620	zinc finger protein 620
6940	8,54E-72	7,11E+01	8,37E-73	0,0766	18,0467026	1,38299377	913,42	ZNF354A	zinc finger protein 354A
8526	3,97E-13	1,24E+01	1,64E-13	0,1874	7,375673	1,38252597	106,27	DGKE	diacylglycerol kinase epsilon
101927400	7,04E-10	9,15E+00	3,27E-10	0,2199	6,2855926	1,38214163	75,68	LINC02966	long intergenic non-protein coding RNA 2966
105374947	1,23E-02	1,91E+00	8,90E-03	0,5282	2,6157692	1,38166442	12,67	LOC105374(	uncharacterized LOC105374947
107986468	1,51E-02	1,82E+00	1,10E-02	0,5432	2,5418658	1,38068665	11,9	LOC107986(	uncharacterized LOC107986468
22866	4,69E-17	1,63E+01	1,70E-17	0,1621	8,512412	1,38018334	148,02	CNKSR2	connector enhancer of kinase suppressor of Ras 2
126669	6,32E-03	2,20E+00	4,44E-03	0,4851	2,8447599	1,3799237	14,8	SHE	Src homology 2 domain containing E
3400	5,32E-14	1,33E+01	2,13E-14	0,1805	7,6426986	1,37988799	134,98	ID4	inhibitor of DNA binding 4
388610	4,47E-25	2,43E+01	1,29E-25	0,1318	10,4617334	1,37912079	211,89	TRNP1	TMF1 regulated nuclear protein 1
160897	4,28E-80	7,94E+01	3,53E-81	0,0723	19,0825209	1,3788863	919,85	GPR180	G protein-coupled receptor 180
105376361	5,68E-03	2,25E+00	3,98E-03	0,4784	2,8800305	1,3776815	15,56	LOC105376(	uncharacterized LOC105376361
105378443	3,75E-04	3,43E+00	2,38E-04	0,3749	3,674877	1,37755251	24,51	LOC105378(	uncharacterized LOC105378443
163050	2,58E-43	4,26E+01	4,80E-44	0,0989	13,9198038	1,37645428	432,51	ZNF564	zinc finger protein 564

54918	6,86E-129	1,28E+02	2,28E-130	0,0567	24,293735	1,37641126	5662,67	CMTM6	CKLF like MARVEL transmembrane domain containing 6
27120	4,09E-02	1,39E+00	3,13E-02	0,6388	2,1529458	1,37526248	8,91	DKKL1	dickkopf like acrosomal protein 1
100505806	6,41E-05	4,19E+00	3,84E-05	0,334	4,1169826	1,37494458	31,06	SNHG18	small nucleolar RNA host gene 18
388559	1,81E-45	4,47E+01	3,20E-46	0,0963	14,2734705	1,37489984	450,19	ZNF888	zinc finger protein 888
167227	2,20E-109	1,09E+02	1,04E-110	0,0615	22,3565157	1,37425865	2004,42	DCP2	decapping mRNA 2
18	1,34E-03	2,87E+00	8,87E-04	0,4132	3,3242631	1,37346214	21,41	ABAT	4-aminobutyrate aminotransferase
283518	1,41E-05	4,85E+00	8,13E-06	0,3076	4,4616576	1,37233393	42,52	KCNRG	potassium channel regulator
2643	3,47E-42	4,15E+01	6,62E-43	0,0999	13,7310679	1,37214424	441,72	GCH1	GTP cyclohydrolase 1
163051	7,70E-23	2,21E+01	2,36E-23	0,1376	9,9564816	1,37039592	225,57	ZNF709	zinc finger protein 709
105372117	3,83E-07	6,42E+00	2,02E-07	0,2634	5,1976704	1,36911127	51,67	LOC105372	replaced by ID 107985152
6857	3,57E-22	2,14E+01	1,11E-22	0,1397	9,8010434	1,36901598	190,05	SYT1	synaptotagmin 1
7164	1,35E-17	1,69E+01	4,83E-18	0,1581	8,6572626	1,36900678	148,87	TPD52L1	TPD52 like 1
10747	4,90E-05	4,31E+00	2,91E-05	0,3275	4,1802991	1,36891941	32,52	MASP2	MBL associated serine protease 2
51134	2,52E-64	6,36E+01	2,92E-65	0,0802	17,0605559	1,36762316	735,69	CEP83	centrosomal protein 83
57405	3,08E-88	8,75E+01	2,18E-89	0,0682	20,0461711	1,36729851	1054,69	SPC25	SPC25 component of NDC80 kinetochore complex
102724862	2,20E-09	8,66E+00	1,04E-09	0,2239	6,1024467	1,36610327	69,19	TBC1D3I	TBC1 domain family member 3I
642778	6,74E-14	1,32E+01	2,70E-14	0,1795	7,6117625	1,3660273	109,68	NPIPA3	nuclear pore complex interacting protein family member A3
9994	3,50E-117	1,16E+02	1,46E-118	0,059	23,1498026	1,36519523	1577,73	CASP8AP2	caspase 8 associated protein 2
5787	1,42E-15	1,48E+01	5,41E-16	0,1685	8,101871	1,3649147	130,08	PTPRB	protein tyrosine phosphatase receptor type B
101928344	6,46E-08	7,19E+00	3,27E-08	0,2469	5,5264186	1,36466273	60,4	LOC101928	uncharacterized LOC101928344
399761	2,62E-18	1,76E+01	9,18E-19	0,1542	8,8446872	1,36375979	159,11	BMS1P1	BMS1 pseudogene 1
55706	2,37E-191	1,91E+02	3,32E-193	0,046	29,6507247	1,36371472	8303,8	NDC1	NDC1 transmembrane nucleoporin
100128893	6,66E-04	3,18E+00	4,31E-04	0,3874	3,5204198	1,3636621	22,78	GATA6-AS1	GATA6 antisense RNA 1 (head to head)
1564	5,96E-02	1,22E+00	4,67E-02	0,6855	1,9893644	1,36363395	7,35	CYP2D7	cytochrome P450 family 2 subfamily D member 7 (gene/pseudogene)
132200	3,10E-02	1,51E+00	2,34E-02	0,6013	2,2663148	1,36266591	9,58	C3orf49	chromosome 3 open reading frame 49
158401	1,01E-02	2,00E+00	7,23E-03	0,5072	2,6860042	1,36237057	14,03	SHOC1	shortage in chiasmata 1
6526	2,64E-168	1,68E+02	4,98E-170	0,049	27,7950615	1,36208449	4608,11	SLC5A3	solute carrier family 5 member 3
8317	5,09E-149	1,48E+02	1,27E-150	0,0521	26,1404031	1,36196483	2401,66	CDC7	cell division cycle 7
105374845	2,30E-02	1,64E+00	1,71E-02	0,5705	2,3852156	1,3607416	11,05	CHMP3-AS1	CHMP3 and RNF103 antisense RNA 1
54989	1,30E-120	1,20E+02	5,09E-122	0,0579	23,490555	1,36055633	1834,41	ZNF770	zinc finger protein 770
102723798	2,36E-03	2,63E+00	1,59E-03	0,4309	3,1573937	1,360444	18,35	LOC102723	uncharacterized LOC102723798
55876	3,58E-03	2,45E+00	2,46E-03	0,4493	3,0281517	1,36044058	17,6	GSDMB	gasdermin B
100128398	6,97E-11	1,02E+01	3,11E-11	0,2048	6,6414323	1,36039503	85,08	LOC100128	uncharacterized LOC100128398
27152	9,08E-35	3,40E+01	2,05E-35	0,1095	12,419391	1,3599897	366,89	INTU	inturned planar cell polarity protein
2995	2,45E-08	7,61E+00	1,22E-08	0,2387	5,6975946	1,35990938	65,3	GYPC	glycophorin C (Gerbich blood group)
10635	2,15E-126	1,26E+02	7,55E-128	0,0565	24,0541842	1,35976667	1689,99	RAD51AP1	RAD51 associated protein 1
147991	2,96E-72	7,15E+01	2,89E-73	0,0751	18,105475	1,35897838	1067,52	DPY19L3	dpy-19 like C-mannosyltransferase 3
677777	1,41E-05	4,85E+00	8,09E-06	0,3043	4,4626883	1,35808594	38,11	SCARNA12	small Cajal body-specific RNA 12
161514	3,72E-04	3,43E+00	2,36E-04	0,3693	3,6767774	1,35799197	25,55	TBC1D21	TBC1 domain family member 21
653319	1,09E-46	4,60E+01	1,86E-47	0,0938	14,4704629	1,3572313	465,64	MATCAP1	microtubule associated tyrosine carboxypeptidase 1
1285	2,70E-02	1,57E+00	2,02E-02	0,5843	2,3229598	1,35721274	10,25	COL4A3	collagen type IV alpha 3 chain
100507053	4,31E-10	9,37E+00	1,98E-10	0,2133	6,3626331	1,35698265	81,94	LOC100507	uncharacterized LOC100507053
204962	5,22E-24	2,33E+01	1,56E-24	0,1327	10,223527	1,35690283	209,21	SLC44A5	solute carrier family 44 member 5
55970	1,29E-200	2,00E+02	1,65E-202	0,0446	30,3638371	1,35564564	12962,56	GNG12	G protein subunit gamma 12
9194	6,38E-70	6,92E+01	6,55E-71	0,0761	17,8042619	1,35414522	969,25	SLC16A7	solute carrier family 16 member 7
255403	1,63E-57	5,68E+01	2,19E-58	0,084	16,1093656	1,35339829	606,45	ZNF718	zinc finger protein 718
196541	3,63E-05	4,44E+00	2,14E-05	0,3183	4,2498943	1,35256593	36,05	METTL21C	methyltransferase 21C, AARS1 lysine
255231	3,27E-42	4,15E+01	6,24E-43	0,0984	13,7353217	1,35205292	403,64	MCOLN2	mucolipin TRP cation channel 2
130	3,18E-03	2,50E+00	2,18E-03	0,4412	3,0648095	1,35204397	18,26	ADH6	alcohol dehydrogenase 6 (class V)
56986	3,01E-57	5,65E+01	4,08E-58	0,0841	16,0709455	1,35156789	694,42	DTWD1	DTW domain containing 1
101927233	1,60E-02	1,80E+00	1,17E-02	0,536	2,5217699	1,35155974	12,49	SEMA6A-AS	SEMA6A antisense RNA 1
7675	7,85E-108	1,07E+02	3,84E-109	0,0609	22,1949597	1,35064089	1496,97	ZNF121	zinc finger protein 121
101927204	6,96E-11	1,02E+01	3,10E-11	0,2031	6,6416023	1,34873836	86,31	FAM111A-DT	FAM111A divergent transcript
105376033	6,36E-02	1,20E+00	5,00E-02	0,6879	1,960363	1,34852542	7,27	LOC105376	uncharacterized LOC105376033
146822	5,05E-02	1,30E+00	3,92E-02	0,6537	2,0624152	1,34821403	8,09	CDRT15	CMT1A duplicated region transcript 15
9303	6,10E-04	3,21E+00	3,94E-04	0,3802	3,5443818	1,34750611	24,95	SNORD25	small nucleolar RNA, C/D box 25
728833	6,77E-76	7,52E+01	6,12E-77	0,0726	18,5654435	1,34736846	959,29	FAM72D	family with sequence similarity 72 member D
100506827	2,90E-08	7,54E+00	1,44E-08	0,2377	5,6680172	1,34716539	65,24	LINC02475	long intergenic non-protein coding RNA 2475
1604	4,62E-238	2,37E+02	3,94E-240	0,0407	33,0915206	1,34706939	12099,69	CD55	CD55 molecule (Cromer blood group)
101928147	5,04E-02	1,30E+00	3,91E-02	0,653	2,0627924	1,3470116	8,04	C21orf140	chromosome 21 open reading frame 140
105377023	2,00E-55	5,47E+01	2,83E-56	0,0852	15,8059993	1,34687837	572,87	PDCD6IP-DT	PDCD6IP divergent transcript
23512	9,84E-198	1,97E+02	1,29E-199	0,0447	30,1439888	1,34681694	5229,3	SUZ12	SUZ12 polycomb repressive complex 2 subunit
728066	7,59E-11	1,01E+01	3,39E-11	0,2031	6,6285818	1,34653583	95,36	FAM133DP	family with sequence similarity 133, member A pseudogene
195828	1,96E-75	7,47E+01	1,79E-76	0,0727	18,5078365	1,34607678	1269,87	ZNF367	zinc finger protein 367
79596	2,68E-78	7,76E+01	2,30E-79	0,0714	18,8629929	1,34592914	867,68	OBI1	ORC ubiquitin ligase 1
146212	2,32E-03	2,63E+00	1,57E-03	0,4255	3,1618981	1,3455289	19,56	KCTD19	potassium channel tetramerization domain containing 19
3841	8,63E-29	2,81E+01	2,26E-29	0,1195	11,2522594	1,34510574	267,45	KPNA5	karyopherin subunit alpha 5
153733	1,44E-55	5,48E+01	2,03E-56	0,085	15,8268786	1,34497703	663,63	CCDC112	coiled-coil domain containing 112
10224	3,07E-33	3,25E+01	7,20E-34	0,1109	12,1314003	1,34476993	309,85	ZNF443	zinc finger protein 443
5218	8,79E-63	6,21E+01	1,05E-63	0,0797	16,8500234	1,34359064	682,38	CDK14	cyclin dependent kinase 14
9406	2,25E-128	1,28E+02	7,56E-130	0,0554	24,2444955	1,34357886	2907,36	ZRANB2	zinc finger RANBP2-type containing 2
1633	3,28E-138	1,37E+02	9,47E-140	0,0534	25,1658876	1,34302425	2574,85	DCK	deoxycytidine kinase
729873	3,14E-06	5,50E+00	1,73E-06	0,2804	4,7821273	1,34082748	45,12	TBC1D3	TBC1 domain family member 3
644961	7,38E-07	6,13E+00	3,95E-07	0,2644	5,0714609	1,34081959	49,5	ACTG1P20	actin gamma 1 pseudogene 20
107984138	2,49E-07	6,60E+00	1,30E-07	0,254	5,279451	1,34073108	56,82	LOC107984	replaced by ID 100506060
55089	3,36E-36	3,55E+01	7,31E-37	0,1057	12,683355	1,34024003	353,3	SLC38A4	solute carrier family 38 member 4
51435	5,77E-94	9,32E+01	3,67E-95	0,0647	20,6971999	1,33981215	1379,12	SCARA3	scavenger receptor class A member 3
79657	3,56E-147	1,46E+02	9,01E-149	0,0516	25,9769938	1,33914956	2507,22	RPAP3	RNA polymerase II associated protein 3
5983	5,75E-152	1,51E+02	1,39E-153	0,0507	26,3995346	1,3387308	2597,73	RFC3	replication factor C subunit 3
90459	3,21E-110	1,09E+02	1,51E-111	0,0596	22,4427323	1,33867707	1568,67	ERI1	exoribonuclease 1
23390	5,26E-85	8,43E+01	3,94E-86	0,068	19,6694948	1,33844533	1442,43	ZDHHC17	zinc finger DHHC-type palmitoyltransferase 17
100130742	2,27E-03	2,64E+00	1,53E-03	0,4221	3,169023	1,33776199	19,5	LRRC69	leucine rich repeat containing 69
55552	4,34E-51	5,04E+01	6,71E-52	0,0882	15,1579515	1,33740403	535,54	ZNF823	zinc finger protein 823
116461	1,48E-97	9,68E+01	8,80E-99	0,0634	21,0952301	1,33717279	3003,49	TSEN15	tRNA splicing endonuclease subunit 15
101928079	1,88E-02	1,73E+00	1,38E-02	0,5432	2,4614782	1,33711874	12,42	SLC44A3-AS	SLC44A3 antisense RNA 1
23086	2,03E-28	2,77E+01	5,37E-29	0,1196	11,1755178	1,33708125	293,34	EXPH5	exophilin 5
107986063	1,85E-02	1,73E+00	1,36E-02	0,5419	2,4670398	1,33686306	11,62	XPC-AS1	XPC antisense RNA 1
646903	3,89E-03	2,41E+00	2,68E-03	0,4453	3,0022798	1,33685547	18,14	LOC646903	uncharacterized LOC646903
56256	1,79E-61	6,07E+01	2,22E-62	0,0802	16,6685535	1,33683503	756,9	SERTAD4	SERTA domain containing 4
647042	2,56E-05	4,59E+00	1,50E-05	0,3088	4,32911	1,33667364	36,99	GOLGA6L10	golgin A6 family like 10
677822	1,79E-34	3,37E+01	4,07E-35	0,108	12,3644578	1,335764	434,79	SNORA40	small nucleolar RNA, H/ACA box 40
25850	3,46E-13	1,25E+01	1,42E-13	0,1806	7,3943838	1,33546817	111,08	ZNF345	zinc finger protein 345
5101	2,88E-12	1,15E+01	1,22E-12	0,188	7,1027143	1,33504407	117,39	PCDH9	protocadherin 9
110599590	5,66E-02	1,25E+00	4,42E-02	0,6631	2,0118742	1,33401821	7,9	C5-OT1	C5 3' UTR overlapping transcript 1
153396	7,52E-90	8,91E+01	5,15E-91	0,0659	20,2317001	1,33360282	1369,87	TMEM161B	transmembrane protein 161B
100506851	2,80E-02	1,55E+00	2,10E-02	0,5773	2,3078739	1,33228568	11,57	LOC100506	uncharacterized LOC100506851
105374749	4,33E-02	1,36E+00	3,33E-02	0,6258	2,1288722	1,3321762	8,71	C5orf34-AS1	C5orf34 antisense RNA 1
79692	1,62E-87	8,68E+01	1,16E-88	0,0667	19,9626994	1,33173372	1178,3	ZNF322	zinc finger protein 322
889	6,16E-78	7,72E+01	5,34E-79	0,0708	18,8183544	1,33169154	1168,83	KRIT1	KRIT1 ankyrin repeat containing
9735	5,98E-177	1,76E+02	9,93E-179	0,0467	28,5057975	1,33113935	5057,65	KNTC1	kinetochore associated 1
11051	9,15E-158	1,57E+02	2,01E-159	0,0495	26,9032711	1,33039875	7814,81	NUDT21	nudix hydrolase 21
7559	6,00E-59	5,82E+01	7,86E-60	0,0815	16,3139022	1,32925494	639,69	ZNF12	zinc finger protein 12
105369228	9,61E-05	4,02E+00	5,82E-05	0,3305	4,0198468	1,32846543	31,07	LOC105369	uncharacterized LOC105369228
729877	2,72E-05	4,57E+00	1,59E-05	0,3078	4,3158829	1,32836044	36,11	TBC1D3H	TBC1 domain family member 3H
107985532	4,29E-04	3,37E+00	2,73E-04	0,3647	3,639214	1,32707268	26,03	LOC107985	uncharacterized LOC107985532
22837	6,53E-25	2,42E+01	1,90E-25	0,1273	10,4254911	1,32685718	232,83	COBLL1	cordon-bleu WH2 repeat protein like 1
101060389	1,47E-07	6,83E+00	7,58E-08	0,2467	5,376948	1,32656391	57,82	TBC1D3D	TBC1 domain family member 3D
7762	2,46E-45	4,46E+01	4,36E-46	0,0931	14,2518707	1,32644469	475,64	ZNF215	zinc finger protein 215
283624	3,30E-20	1,95E+01	1,09E-20	0,1422	9,3269288	1,32599767	178,94	LINC00641	long intergenic non-protein coding RNA 641
117247	4,68E-06	5,33E+00	2,62E-06	0,2822	4,6987024	1,32578853	43,3	SLC16A10	solute carrier family 16 member 10
22878	5,78E-24	2,32E+01	1,73E-24	0,1298	10,2134838	1,32578813	2820,92	TRAPPC8	trafficking protein particle complex subunit 8
107984921	2,04E-03	2,69E+00	1,37E-03	0,4141	3,2000133	1,32521256	21,51	LINC01772	long intergenic non-protein coding RNA 1772
4603	5,69E-139	1,38E+02	1,63E-140	0,0525	25,2356798	1,32517319	2624,86	MYBL1	MYB proto-oncogene like 1
100861412	2,04E-10	9,69E+00	9,28E-11	0,2045	6,4782603	1,32473669	84,2	FSBP	fibrinogen silencer binding protein
105378580	2,49E-03	2,60E+00	1,69E-03	0,4218	3,1400381	1,32453478	19,47	LINC01409	long intergenic non-protein coding RNA 1409
57633	1,17E-17	1,69E+01	4,16E-18	0,1527	8,6744036	1,32451851	184	LRRN1	leucine rich repeat neuronal 1
11005	1,23E-03	2,91E+00	8,10E-04	0,3954	3,3492089	1,32424097	23,94	SPINK5	serine peptidase inhibitor Kazal type 5
105373774	4,42E-02	1,35E+00	3,40E-02	0,6248	2,1195132	1,3242237	8,65	LOC105373774	
7473	1,31E-27	2,69E+01	3,54E-28	0,1203	11,0069969	1,32379622	294,28	WNT3	Wnt family member 3
9829	7,27E-75	7,41E+01	6,69E-76	0,0718	18,4365681	1,32299811	853,69	DNAJC6	DnaJ heat shock protein family (Hsp40) member C6

1894	5,17E-245	2,44E+02	4,06E-247	0,0394	33,5737341	1,3224564	11188,59	ECT2	epithelial cell transforming 2
100128338	2,25E-02	1,65E+00	1,67E-02	0,5523	2,3943023	1,32234911	12,28	FAM83H-AS	replaced by ID 642574
168507	1,63E-10	9,79E+00	7,37E-11	0,203	6,5128552	1,32233343	90,21	PKD1L1	polycystin 1 like 1, transient receptor potential channel interacting
89838	1,18E-05	4,93E+00	6,75E-06	0,2936	4,5014824	1,32152674	39,58	ULK4P1	ULK4 pseudogene 1
259173	1,50E-61	6,08E+01	1,85E-62	0,0792	16,6795462	1,32128527	696,53	ALS2CL	ALS2 C-terminal like
127933	1,50E-126	1,26E+02	5,25E-128	0,0549	24,0692094	1,32118485	5740,02	UHMK1	U2AF homology motif kinase 1
414224	5,61E-08	7,25E+00	2,83E-08	0,2379	5,5514358	1,32053467	61,95	AGAP12P	ArfGAP with GTPase domain, ankyrin repeat and PH domain 12, pseudogene
342372	6,82E-02	1,17E+00	5,38E-02	0,6846	1,9286088	1,32026516	7,19	PKD1L3	polycystin 1 like 3, transient receptor potential channel interacting
8820	4,11E-04	3,39E+00	2,62E-04	0,3616	3,6503846	1,31987973	27,44	HESX1	HESX homeobox 1
145282	1,36E-40	3,99E+01	2,67E-41	0,098	13,4604584	1,31946884	421,6	MIPOL1	mirror-image polydactyly 1
55183	1,26E-161	1,61E+02	2,61E-163	0,0484	27,2333898	1,31902491	4300,3	RIF1	replication timing regulatory factor 1
105375700	9,13E-02	1,04E+00	7,33E-02	0,7363	1,791	1,31874909	6,42	OXR1-AS1	OXR1 antisense RNA 1
100505648	2,37E-05	4,63E+00	1,38E-05	0,3033	4,3471716	1,31858968	38,2	RAD51-AS1	RAD51 antisense RNA 1
10147	4,65E-215	2,14E+02	4,96E-217	0,0419	31,4446996	1,31852732	5567,63	SUGP2	SURP and G-patch domain containing 2
5734	1,41E-31	3,09E+01	3,44E-32	0,1116	11,810577	1,31839371	307,96	PTGER4	prostaglandin E receptor 4
100507321	4,32E-20	1,94E+01	1,43E-20	0,1417	9,2978529	1,31776996	196,16	ERVK13-1	endogenous retrovirus group K13 member 1
55166	4,35E-103	1,02E+02	2,33E-104	0,0607	21,6941603	1,31761467	1531,7	CENPQ	centromere protein Q
105374852	1,36E-02	1,87E+00	9,88E-03	0,5107	2,5798676	1,31761199	13,74	LOC105374	uncharacterized LOC105374852
6322	2,29E-95	9,46E+01	1,41E-96	0,0632	20,8536393	1,31728993	1495,85	SCML1	Scm polycomb group protein like 1
10008	9,47E-03	2,02E+00	6,78E-03	0,4863	2,7074623	1,31667156	14,42	KCNE3	potassium voltage-gated channel subfamily E regulatory subunit 3
101954271	1,35E-05	4,87E+00	7,74E-06	0,2941	4,472326	1,31549485	41,89	RNU6-9	RNA, U6 small nuclear 9
9108	1,53E-12	1,18E+01	6,43E-13	0,1829	7,1910169	1,31535648	104,62	MTMR7	myotubularin related protein 7
64478	7,04E-03	2,15E+00	4,98E-03	0,4682	2,8086025	1,31500176	15,73	CSMD1	CUB and Sushi multiple domains 1
7179	3,15E-03	2,50E+00	2,15E-03	0,4284	3,0684373	1,31467009	18,7	TPTE	transmembrane phosphatase with tensin homology
677831	1,04E-03	2,98E+00	6,84E-04	0,3871	3,3958137	1,31449095	23,51	SNORA51	small nucleolar RNA, H/ACA box 51
554282	2,46E-76	7,56E+01	2,20E-77	0,0706	18,6203528	1,31445048	1000,3	FAM72C	family with sequence similarity 72 member C
29929	4,47E-16	1,53E+01	1,67E-16	0,1594	8,2433949	1,31403691	844,34	ALG6	ALG6 alpha-1,3-glucosyltransferase
7678	8,05E-29	2,81E+01	2,10E-29	0,1167	11,2585308	1,31379602	279,73	ZNF124	zinc finger protein 124
100270804	3,61E-03	2,44E+00	2,48E-03	0,4342	3,0257777	1,31375276	18,67	LCDR	lysosome cell death regulator
105371586	5,95E-02	1,23E+00	4,66E-02	0,6601	1,9902672	1,31370899	7,91	FAM78B-AS	FAM78B antisense RNA 1
54947	1,88E-43	4,27E+01	3,49E-44	0,0942	13,9426447	1,3129228	501,74	LPCAT2	lysophosphatidylcholine acyltransferase 2
84146	1,39E-141	1,41E+02	3,83E-143	0,0515	25,4740147	1,3126491	2879,9	ZNF644	zinc finger protein 644
205327	2,40E-60	5,96E+01	3,05E-61	0,0794	16,5110797	1,31147144	710,74	C2orf69	chromosome 2 open reading frame 69
203523	1,47E-26	2,58E+01	4,09E-27	0,1216	10,78412	1,31143135	288,16	ZNF449	zinc finger protein 449
105369689	1,04E-09	8,98E+00	4,86E-10	0,2107	6,2236703	1,31131708	82,75	LOC105369	uncharacterized LOC105369689
406975	1,76E-42	4,18E+01	3,34E-43	0,0952	13,7804146	1,31123084	473,44	MIR198	microRNA 198
10926	2,06E-119	1,19E+02	8,27E-121	0,0561	23,3718234	1,31082773	2199,71	DBF4	DBF4 zinc finger
23576	6,40E-146	1,45E+02	1,67E-147	0,0507	25,8645407	1,31039385	3683,65	DDAH1	dimethylarginine dimethylaminohydrolase 1
4772	1,39E-07	6,86E+00	7,14E-08	0,2432	5,3875762	1,31017074	62,12	NFATC1	nuclear factor of activated T cells 1
64092	2,05E-04	3,69E+00	1,27E-04	0,3419	3,8317999	1,3100754	31	SAMSN1	SAM domain, SH3 domain and nuclear localization signals 1
1236	3,52E-04	3,45E+00	2,23E-04	0,3548	3,691818	1,30997771	29,27	CCR7	C-C motif chemokine receptor 7
28629	7,00E-02	1,15E+00	5,53E-02	0,6834	1,916387	1,30974068	7,18	TRBJ2-1	T cell receptor beta joining 2-1
64081	1,43E-07	6,84E+00	7,38E-08	0,2434	5,3815788	1,30973437	59,98	PBLD	phenazine biosynthesis like protein domain containing
3685	1,28E-141	1,41E+02	3,51E-143	0,0514	25,4773752	1,30929477	4231,73	ITGAV	integrin subunit alpha V
388849	2,41E-03	2,62E+00	1,63E-03	0,4155	3,1502957	1,30901726	20,1	CCDC188	coiled-coil domain containing 188
5586	2,85E-125	1,25E+02	1,03E-126	0,0547	23,9456067	1,30900451	3654,8	PKN2	protein kinase N2
107987261	1,30E-06	5,89E+00	7,06E-07	0,2639	4,9597479	1,30877394	52,87	LOC107987	261
284349	2,81E-22	2,16E+01	8,75E-23	0,1331	9,8254318	1,30765757	225,33	ZNF283	zinc finger protein 283
79056	1,28E-21	2,09E+01	4,07E-22	0,1352	9,6693915	1,30691811	202,73	PRRG4	proline rich and Gla domain 4
653125	4,22E-03	2,37E+00	2,92E-03	0,4389	2,9758961	1,30607584	17,79	GOLGA8K	golgin A8 family member K
284697	1,02E-03	2,99E+00	6,70E-04	0,3839	3,4017091	1,30595809	26,3	BTBD8	BTB domain containing 8
1159	3,77E-04	3,42E+00	2,40E-04	0,3552	3,6732004	1,30486725	27,85	CKMT1B	creatine kinase, mitochondrial 1B
10936	1,69E-09	8,77E+00	7,97E-10	0,2122	6,1454344	1,30432553	84,29	GPR75	G protein-coupled receptor 75
142679	5,69E-03	2,24E+00	3,98E-03	0,453	2,8794037	1,30429657	19,5	DUSP19	dual specificity phosphatase 19
63920	6,49E-21	2,02E+01	2,11E-21	0,1373	9,4996677	1,3041637	229,15	FAM200C	family with sequence similarity 200 member C
6507	1,06E-16	1,60E+01	3,87E-17	0,1549	8,4166469	1,30376237	162,3	SLC1A3	solute carrier family 1 member 3
151827	6,57E-16	1,52E+01	2,47E-16	0,159	8,1966544	1,30337664	139,75	LRRC34	leucine rich repeat containing 34
55500	4,69E-42	4,13E+01	8,98E-43	0,0951	13,708925	1,30306482	715,05	ETNK1	ethanolamine kinase 1
79802	1,25E-04	3,90E+00	7,63E-05	0,3294	3,955642	1,302912	32,59	HHIPL2	HHIP like 2
8828	4,00E-93	9,24E+01	2,59E-94	0,0632	20,602803	1,3028688	1366,24	NRP2	neuropilin 2
117178	4,44E-116	1,15E+02	1,89E-117	0,0565	23,0391041	1,30256455	1909,66	SSX2IP	SSX family member 2 interacting protein
10560	3,21E-55	5,45E+01	4,57E-56	0,0826	15,7757213	1,30237601	698,64	SLC19A2	solute carrier family 19 member 2
2822	1,25E-34	3,39E+01	2,83E-35	0,105	12,3936711	1,30130173	371,35	GPLD1	glycosylphosphatidylinositol specific phospholipase D1
162239	1,93E-51	5,07E+01	2,95E-52	0,0855	15,2119775	1,30080956	555,42	ZFP1	ZFP1 zinc finger protein
8481	1,54E-75	7,48E+01	1,40E-76	0,0702	18,5207541	1,30075374	973,94	OFD1	OFD1 centriole and centriolar satellite protein
107984546	3,18E-02	1,50E+00	2,40E-02	0,5762	2,2568394	1,30032392	10,76	LOC107984	546
100507127	1,50E-35	3,48E+01	3,32E-36	0,1035	12,564356	1,29991593	349,8	LINC00707	long intergenic non-protein coding RNA 707
255488	2,26E-95	9,46E+01	1,39E-96	0,0623	20,8542891	1,29948309	1313,99	RNF144B	ring finger protein 144B
1375	2,65E-20	1,96E+01	8,71E-21	0,139	9,3506105	1,29942964	196,75	CPT1B	carnitine palmitoyltransferase 1B
10051	1,33E-253	2,53E+02	9,78E-256	0,038	34,1591628	1,2992689	13867,01	SMC4	structural maintenance of chromosomes 4
149420	6,41E-50	4,92E+01	1,02E-50	0,0867	14,9783115	1,29887192	629,12	PDIK1L	PDLIM1 interacting kinase 1 like
26953	7,29E-70	6,91E+01	7,50E-71	0,073	17,7966809	1,29884308	992,51	RANBP6	RAN binding protein 6
10464	1,32E-60	5,99E+01	1,67E-61	0,0785	16,5474518	1,298741	879,04	PIBF1	progesterone immunomodulatory binding factor 1
403313	5,18E-16	1,53E+01	1,94E-16	0,1578	8,2254879	1,29813082	141,03	PLPP6	phospholipid phosphatase 6
9758	6,86E-04	3,16E+00	4,45E-04	0,3696	3,5118593	1,29806461	25,62	FRMPD4	FERM and PDZ domain containing 4
107984036	1,49E-04	3,83E+00	9,13E-05	0,3317	3,9124895	1,29771431	32,16	RAB33B-AS	RAB33B antisense RNA 1
105372064	1,36E-13	1,29E+01	5,50E-14	0,1726	7,5195445	1,29751828	124,1	LOC105372	uncharacterized LOC105372064
619383	9,07E-02	1,04E+00	7,27E-02	0,7231	1,7944714	1,29750485	6,44	SCARNA9	small Cajal body-specific RNA 9
56242	5,32E-24	2,33E+01	1,59E-24	0,1268	10,2216237	1,29655096	237,99	ZNF253	zinc finger protein 253
117854	3,56E-60	5,94E+01	4,55E-61	0,0786	16,4870065	1,29641835	688,16	TRIM6	tripartite motif containing 6
7273	1,72E-25	2,48E+01	4,92E-26	0,1227	10,5530554	1,2947545	248,94	TTN	titin
64417	1,39E-43	4,29E+01	2,58E-44	0,0927	13,9640315	1,29468679	510,72	TMEM267	transmembrane protein 267
105372782	9,46E-02	1,02E+00	7,61E-02	0,7295	1,7736548	1,29387736	6,47	LOC105372	782
160418	3,17E-94	9,35E+01	2,01E-95	0,0624	20,7262704	1,29382862	1883,73	TMTC3	transmembrane O-mannosyltransferase targeting cadherins 3
91355	8,10E-12	1,11E+01	3,48E-12	0,186	6,956842	1,29373701	102,54	LRP5L	LDL receptor related protein 5 like (pseudogene)
130399	1,12E-03	2,95E+00	7,39E-04	0,3833	3,3746885	1,29357885	24,05	ACVR1C	activin A receptor type 1C
105371414	4,17E-04	3,38E+00	2,65E-04	0,3543	3,646933	1,29195492	28,55	LOC105371	uncharacterized LOC105371414
161779	1,28E-16	1,59E+01	4,72E-17	0,1538	8,3935664	1,29133942	151,93	PGBD4	piggyBac transposable element derived 4
10733	2,28E-140	1,40E+02	6,38E-142	0,0509	25,3634712	1,29093544	3083,1	PLK4	polo like kinase 4
115209	2,50E-35	3,46E+01	5,57E-36	0,1031	12,5233014	1,29093182	505,68	OMA1	OMA1 zinc metallopeptidase
79780	1,51E-145	1,45E+02	3,96E-147	0,05	25,8312211	1,29031963	3221,64	CCDC82	coiled-coil domain containing 82
152559	1,48E-107	1,07E+02	7,29E-109	0,0582	22,1661321	1,29030741	2204,84	PAQR3	progestin and adipoQ receptor family member 3
7272	1,16E-131	1,31E+02	3,67E-133	0,0525	24,5566286	1,29022536	3434,36	TTK	TTK protein kinase
79075	4,24E-66	6,54E+01	4,72E-67	0,0746	17,2998587	1,28978543	1052,54	DSCC1	DNA replication and sister chromatid cohesion 1
102723546	4,08E-15	1,44E+01	1,58E-15	0,1618	7,9707578	1,28959485	150,51	LOC102723	uncharacterized LOC102723546
150946	1,63E-03	2,79E+00	1,09E-03	0,3946	3,2669483	1,28911467	23,56	GAREM2	GRB2 associated regulator of MAPK1 subtype 2
9585	1,12E-131	1,31E+02	3,52E-133	0,0525	24,5583235	1,28859613	5211,79	KIF20B	kinesin family member 20B
100506985	4,04E-13	1,24E+01	1,66E-13	0,1748	7,3733663	1,28854787	113,34	NCMAP-DT	NCMAP divergent transcript
10468	1,94E-98	9,77E+01	1,14E-99	0,0608	21,191849	1,28832907	1487,76	FST	follistatin
642517	8,56E-18	1,71E+01	3,03E-18	0,1477	8,7101729	1,28675295	165,15	AGAP9	ArfGAP with GTPase domain, ankyrin repeat and PH domain 9
5342	8,23E-04	3,08E+00	5,37E-04	0,3715	3,4615801	1,28595176	24,68	PLGLB2	plasminogen like B2
51762	6,49E-117	1,16E+02	2,72E-118	0,0556	23,1230295	1,28525867	3061,36	RAB8B	RAB8B, member RAS oncogene family
105377826	8,89E-05	4,05E+00	5,38E-05	0,3182	4,0385522	1,28504917	33,27	LINC02887	long intergenic non-protein coding RNA 2887
84775	1,32E-36	3,59E+01	2,85E-37	0,1007	12,7570845	1,28488181	394,49	ZNF607	zinc finger protein 607
105376065	2,94E-02	1,53E+00	2,21E-02	0,5614	2,2884438	1,28462349	10,65	LOC105376	uncharacterized LOC105376065
11074	4,02E-02	1,40E+00	3,08E-02	0,5947	2,1598287	1,28452523	10	TRIM31	tripartite motif containing 31
162966	4,38E-38	3,74E+01	9,14E-39	0,0986	13,0222938	1,28406174	466,51	ZNF600	zinc finger protein 600
5074	6,90E-138	1,37E+02	2,00E-139	0,0511	25,1362084	1,28379719	3823,72	PAWR	pro-apoptotic WT1 regulator
692199	2,48E-07	6,61E+00	1,29E-07	0,2431	5,2802284	1,2834787	62,06	SNORD84	small nucleolar RNA, C/D box 84
8515	9,20E-24	2,30E+01	2,76E-24	0,1262	10,1679686	1,28294616	241,21	ITGA10	integrin subunit alpha 10
105371952	7,86E-03	2,10E+00	5,58E-03	0,4623	2,771732	1,28123655	16,19	LOC105371	uncharacterized LOC105371952
387804	7,92E-05	4,10E+00	4,77E-05	0,3149	4,0665488	1,28069978	39,63	VSTM5	V-set and transmembrane domain containing 5
57082	2,92E-174	1,74E+02	5,03E-176	0,0453	28,286729	1,28059673	3909,74	KNL1	kinetochore scaffold 1
9295	6,27E-93	9,22E+01	4,07E-94	0,0622	20,5808999	1,2801712	7050,48	SRSF11	serine and arginine rich splicing factor 11
105377771	4,71E-06	5,33E+00	2,63E-06	0,2722	4,6976661	1,27884741	51,63	LOC105377771	
9738	7,78E-110	1,09E+02	3,67E-111	0,0571	22,4031379	1,27873411	1643,52	CCP110	centriolar coiled-coil protein 110
81669	1,16E-124	1,24E+02	4,25E-126	0,0535	23,8863011	1,27842647	2350,7	CCNL2	cyclin L2
100874222	3,41E-33	3,25E+01	8,00E-34	0,1055	12,1227479	1,27841474	334,82	OBI1-AS1	OBI1 antisense RNA 1
345778	3,52E-108	1,07E+02	1,70E-109	0,0575	22,2315854	1,27829571	2137,75	MTX3	metaxin 3
126070	2,99E-62	6,15E+01	3,62E-63	0,0762	16,7766701	1,27825736	712,72	ZNF440	zinc finger protein 440

100302240	2,38E-04	3,62E+00	1,49E-04	0,337	3,7927979	1,27818794	33,43	MIR1304	microRNA 1304
57494	6,63E-70	6,92E+01	6,82E-71	0,0718	17,8020286	1,27813443	1060,29	RIMKLB	ribosomal modification protein rimK like family member B
105376544	2,69E-07	6,57E+00	1,40E-07	0,2427	5,2647634	1,27787506	58,52	ADM-DT	ADM divergent transcript
130367	1,73E-05	4,76E+00	1,00E-05	0,2891	4,4169392	1,27696877	44,98	SGPP2	sphingosine-1-phosphate phosphatase 2
64395	3,88E-87	8,64E+01	2,80E-88	0,0641	19,9187419	1,27645198	1334,04	GMCL1	germ cell-less 1, spermatogenesis associated
692106	9,87E-04	3,01E+00	6,47E-04	0,374	3,4112392	1,27595198	25,39	SNORD65	small nucleolar RNA, C/D box 65
54809	4,14E-89	8,84E+01	2,87E-90	0,0633	20,1467327	1,27591361	2454,01	SAMD9	sterile alpha motif domain containing 9
54826	9,33E-27	2,60E+01	2,58E-27	0,1178	10,8264576	1,27547382	276,75	GIN1	gypsy retrotransposon integrase 1
100288203	3,44E-14	1,35E+01	1,37E-14	0,1655	7,6992704	1,27457057	131,91	WHAMMP4	WHAMM pseudogene 4
143279	9,38E-35	3,40E+01	2,12E-35	0,1026	12,416808	1,27403051	379,94	HECTD2	HECT domain E3 ubiquitin protein ligase 2
100874058	2,15E-19	1,87E+01	7,27E-20	0,1396	9,1235572	1,27344534	185,38	COX10-DT	COX10 divergent transcript
284323	5,12E-49	4,83E+01	8,31E-50	0,0857	14,8380961	1,27236598	555,21	ZNF780A	zinc finger protein 780A
84230	5,12E-106	1,05E+02	2,59E-107	0,0578	22,004868	1,27231283	1830,38	LRRC8C	leucine rich repeat containing 8 VRAC subunit C
7051	1,40E-07	6,85E+00	7,23E-08	0,2362	5,3854772	1,27226245	65,49	TGM1	transglutaminase 1
221711	1,53E-14	1,38E+01	6,03E-15	0,1629	7,8033601	1,27155701	131,3	SYCP2L	synaptonemal complex protein 2 like
55973	1,23E-61	6,09E+01	1,52E-62	0,0762	16,6913516	1,27116583	1149,34	BCAP29	B cell receptor associated protein 29
339324	2,26E-74	7,36E+01	2,10E-75	0,0692	18,3746751	1,2707056	1037,61	ZNF260	zinc finger protein 260
8814	2,17E-82	8,17E+01	1,71E-83	0,0656	19,3589824	1,27061343	1058,95	CDKL1	cyclin dependent kinase like 1
5593	1,40E-07	6,85E+00	7,23E-08	0,2359	5,3852568	1,27053346	62,4	PRKG2	protein kinase cGMP-dependent 2
57624	2,56E-05	4,59E+00	1,50E-05	0,2934	4,3291949	1,27032378	41,43	NYAP2	neuronal tyrosine-phosphorylated phosphoinositide-3-kinase adaptor 2
79982	3,11E-73	7,25E+01	2,96E-74	0,0697	18,2304856	1,27030174	1253,99	DNAJB14	DnaJ heat shock protein family (Hsp40) member B14
23225	2,19E-122	1,22E+02	8,38E-124	0,0537	23,6644476	1,2696432	2336,52	NUP210	nucleoporin 210
113939912	2,61E-24	2,36E+01	7,72E-25	0,1233	10,2912161	1,26895207	248,51	BMS1P2-AG	BMS1P2-AGAP9 readthrough
91694	3,32E-25	2,45E+01	9,58E-26	0,121	10,4902059	1,26883743	262,35	LONRF1	LON peptidase N-terminal domain and ring finger 1
8817	8,30E-02	1,08E+00	6,62E-02	0,6901	1,8371898	1,26776248	7,06	FGF18	fibroblast growth factor 18
90316	8,53E-07	6,07E+00	4,58E-07	0,2514	5,0431966	1,26767623	54,55	TGIF2LX	TGFB induced factor homeobox 2 like X-linked
26784	4,64E-04	3,33E+00	2,97E-04	0,3503	3,6183318	1,26754887	29,64	SNORA64	small nucleolar RNA, H/ACA box 64
29028	4,08E-238	2,37E+02	3,46E-240	0,0383	33,0954388	1,26713799	13143,94	ATAD2	ATPase family AAA domain containing 2
6498	1,38E-65	6,49E+01	1,56E-66	0,0735	17,2309542	1,26670686	931,87	SKIL	SKI like proto-oncogene
81491	5,28E-18	1,73E+01	1,86E-18	0,1444	8,7652853	1,26608005	193,51	GPR63	G protein-coupled receptor 63
90634	4,40E-07	6,36E+00	2,33E-07	0,2448	5,1712766	1,26603842	60,14	N4BP2L1	NEDD4 binding protein 2 like 1
84945	1,30E-47	4,69E+01	2,17E-48	0,0865	14,6175478	1,26486689	625,06	ABHD13	abhydrolase domain containing 13
646024	7,61E-08	7,12E+00	3,86E-08	0,2299	5,4969146	1,2639238	65,18	RAET1K	retinoic acid early transcript 1K pseudogene
554251	8,18E-42	4,11E+01	1,58E-42	0,0925	13,6680098	1,26368368	452,14	FBXO48	F-box protein 48
105369828	5,48E-03	2,26E+00	3,83E-03	0,4369	2,8919598	1,26354826	18,2	LOC105369	uncharacterized LOC105369828
55284	3,48E-59	5,85E+01	4,53E-60	0,0773	16,3475757	1,26351838	912,64	UBE2W	ubiquitin conjugating enzyme E2 W
105373454	1,34E-02	1,87E+00	9,71E-03	0,4885	2,5859991	1,26334512	14,78	LOC105373	uncharacterized LOC105373454
201625	2,83E-03	2,55E+00	1,93E-03	0,4073	3,1013469	1,2633117	21,8	DNAH12	dynein axonemal heavy chain 12
83879	3,39E-64	6,35E+01	3,93E-65	0,0741	17,0431728	1,26217004	905,47	CDCA7	cell division cycle associated 7
126231	2,57E-10	9,59E+00	1,17E-10	0,1958	6,442811	1,26150136	91,72	ZNF573	zinc finger protein 573
1195	2,56E-104	1,04E+02	1,34E-105	0,0577	21,8250473	1,26015304	1846,31	CLK1	CDC like kinase 1
100507173	1,08E-04	3,97E+00	6,57E-05	0,3156	3,9914983	1,25972819	39,4	LINC01012	long intergenic non-protein coding RNA 1012
79675	4,35E-40	3,94E+01	8,69E-41	0,0941	13,3730149	1,25855797	491,35	FASTKD1	FAST kinase domains 1
23262	1,22E-145	1,45E+02	3,19E-147	0,0487	25,8394854	1,2585229	3208,98	PPIP5K2	diphosphoinositol pentakisphosphate kinase 2
93589	3,98E-33	3,24E+01	9,35E-34	0,1038	12,1099842	1,2572064	381,8	CACNA2D4	calcium voltage-gated channel auxiliary subunit alpha2delta 4
106699570	2,55E-03	2,59E+00	1,73E-03	0,4012	3,1332061	1,25719158	21,01	DYNC1LI2-D	DYNC1LI2 divergent transcript
3215	5,97E-02	1,22E+00	4,68E-02	0,6321	1,9883757	1,2567724	8,37	HOXB5	homeobox B5
3298	5,73E-90	8,92E+01	3,91E-91	0,0621	20,2452508	1,25648289	1378,59	HSF2	heat shock transcription factor 2
388906	1,79E-02	1,75E+00	1,32E-02	0,5065	2,4794611	1,25582859	13,22	OGFRP1	opioid growth factor receptor pseudogene 1
80218	8,75E-158	1,57E+02	1,92E-159	0,0467	26,9049858	1,2553334	6303,57	NAA50	N-alpha-acetyltransferase 50, NatE catalytic subunit
85319	2,79E-03	2,55E+00	1,90E-03	0,4042	3,1052802	1,25505798	21,68	BAGE2	BAGE family member 2, pseudogene
4179	1,47E-199	1,99E+02	1,92E-201	0,0414	30,2830256	1,25487614	8310,48	CD46	CD46 molecule
83744	6,26E-30	2,92E+01	1,59E-30	0,1093	11,4837702	1,25473532	313,93	ZNF484	zinc finger protein 484
83539	4,58E-05	4,34E+00	2,71E-05	0,2988	4,1962316	1,25365295	39,63	CHST9	carbohydrate sulfotransferase 9
105370550	9,55E-03	2,02E+00	6,84E-03	0,4635	2,7044383	1,25364212	16,69	GALNT16-AS	GALNT16 and EXD2 antisense RNA 1
494470	7,49E-05	4,13E+00	4,50E-05	0,3071	4,0799337	1,25299656	37,03	RNF165	ring finger protein 165
147947	8,32E-22	2,11E+01	2,62E-22	0,1289	9,71422	1,25246677	232,87	ZNF542P	zinc finger protein 542, pseudogene
105375363	6,15E-03	2,21E+00	4,32E-03	0,4388	2,8535043	1,25214494	17,34	LOC105375	uncharacterized LOC105375363
386593	7,39E-36	3,51E+01	1,63E-36	0,0992	12,6204882	1,25198761	399,03	CHKB-CPT1	CHKB-CPT1B readthrough (NMD candidate)
83990	4,00E-145	1,44E+02	1,05E-146	0,0485	25,7933472	1,25155653	2915,32	BRIP1	BRCA1 interacting helicase 1
51496	9,13E-104	1,03E+02	4,83E-105	0,0575	21,7663766	1,25135582	2075,03	CTDSPL2	CTD small phosphatase like 2
7188	6,32E-66	6,52E+01	7,05E-67	0,0724	17,2767063	1,25118104	836,57	TRAF5	TNF receptor associated factor 5
5311	5,94E-105	1,04E+02	3,07E-106	0,0571	21,8924435	1,25082709	1738,25	PKD2	polycystin 2, transient receptor potential cation channel
91664	9,45E-36	3,50E+01	2,09E-36	0,0992	12,6009356	1,24974915	408,19	ZNF845	zinc finger protein 845
2620	2,49E-02	1,60E+00	1,86E-02	0,5308	2,3538459	1,24932229	12,48	GAS2	growth arrest specific 2
101927027	2,36E-16	1,56E+01	8,78E-17	0,1501	8,3202718	1,24897882	186,75	CHROMR	cholesterol induced regulator of metabolism RNA
105371768	1,45E-03	2,84E+00	9,63E-04	0,3783	3,3012163	1,24895874	24,39	LOC105371	uncharacterized LOC105371768
87178	9,74E-120	1,19E+02	3,86E-121	0,0534	23,4043926	1,24895404	4304,24	PNPT1	polyribonucleotide nucleotidyltransferase 1
440248	4,36E-48	4,74E+01	7,24E-49	0,085	14,6921696	1,24875825	563,59	HERC2P9	HERC2 pseudogene 9
51715	1,48E-99	9,88E+01	8,46E-101	0,0586	21,3137943	1,24812846	1778,58	RAB23	RAB23, member RAS oncogene family
644100	5,15E-04	3,29E+00	3,30E-04	0,3476	3,5902659	1,24807979	28,52	ARL14EPL	ADP ribosylation factor like GTPase 14 effector protein like
760	1,38E-03	2,86E+00	9,14E-04	0,3763	3,3157044	1,24758914	26,26	CA2	carbonic anhydrase 2
781	6,26E-24	2,32E+01	1,87E-24	0,1222	10,2056322	1,24752893	272,35	CACNA2D1	calcium voltage-gated channel auxiliary subunit alpha2delta 1
55137	8,78E-51	5,01E+01	1,37E-51	0,0825	15,1111894	1,24621329	672,39	FIGN	fidgetin, microtubule severing factor
1105	6,25E-196	1,95E+02	8,31E-198	0,0415	30,0055282	1,24575001	5382,93	CHD1	chromodomain helicase DNA binding protein 1
4072	8,63E-48	4,71E+01	1,44E-48	0,0851	14,6455176	1,24565585	659,45	EPCAM	epithelial cell adhesion molecule
285636	1,79E-89	8,87E+01	1,23E-90	0,0617	20,1885948	1,24521691	1451,63	RIMOC1	RAB7A interacting MON1-CCZ1 complex subunit 1
105377283	5,46E-05	4,26E+00	3,25E-05	0,2996	4,1548561	1,24498728	38,15	LINC02562	long intergenic non-protein coding RNA 2562
3756	2,26E-03	2,65E+00	1,52E-03	0,3924	3,1702426	1,24392515	23,72	KCNH1	potassium voltage-gated channel subfamily H member 1
105374071	1,08E-03	2,97E+00	7,12E-04	0,3674	3,3850984	1,24361229	25	LOC105374	uncharacterized LOC105374071
730091	9,28E-14	1,30E+01	3,74E-14	0,1641	7,5698082	1,24246303	132,49	LINC00886	long intergenic non-protein coding RNA 886
4801	8,77E-83	8,21E+01	6,84E-84	0,064	19,4061947	1,24229564	1750,24	NFYB	nuclear transcription factor Y subunit beta
8790	6,34E-27	2,62E+01	1,74E-27	0,1143	10,8622521	1,24200872	298,31	FPGT	fucose-1-phosphate guanylyltransferase
84125	5,50E-05	4,26E+00	3,28E-05	0,299	4,1532116	1,24182419	39,34	LRRIQ1	leucine rich repeats and IQ motif containing 1
89837	1,83E-03	2,74E+00	1,23E-03	0,384	3,2318398	1,24102024	22,82	ULK4P3	ULK4 pseudogene 3
83856	7,87E-22	2,11E+01	2,48E-22	0,1276	9,7199117	1,23980163	267,15	FSD1L	fibronectin type III and SPRY domain containing 1 like
110599588	1,52E-46	4,58E+01	2,62E-47	0,0858	14,4468686	1,23965608	647,69	ASDURF	ASNSD1 upstream open reading frame
168451	9,43E-66	6,50E+01	1,06E-66	0,0718	17,253387	1,23892643	1216,04	THAP5	THAP domain containing 5
105372003	9,14E-02	1,04E+00	7,33E-02	0,6915	1,7906739	1,23831213	6,94	LOC105372	uncharacterized LOC105372003
9753	2,55E-56	5,56E+01	3,54E-57	0,0777	15,9364118	1,23820932	716,06	ZSCAN12	zinc finger and SCAN domain containing 12
84144	3,17E-23	2,25E+01	9,63E-24	0,1232	10,0453149	1,23792605	246,1	SYDE2	synapse defective Rho GTPase homolog 2
285989	1,32E-21	2,09E+01	4,18E-22	0,128	9,6666738	1,23756604	238,85	ZNF789	zinc finger protein 789
2957	1,85E-127	1,27E+02	6,36E-129	0,0512	24,1566057	1,23752229	3522,71	GTF2A1	general transcription factor IIA subunit 1
5367	4,41E-13	1,24E+01	1,82E-13	0,1679	7,3616094	1,2362452	122,17	PMCH	pro-melanin concentrating hormone
102723566	1,30E-04	3,89E+00	7,95E-05	0,3132	3,9459449	1,23597712	36,11	LOC102723	uncharacterized LOC102723566
5272	3,40E-104	1,03E+02	1,79E-105	0,0566	21,8119047	1,23538659	1744,09	SERPINB9	serpin family B member 9
101752400	6,39E-06	5,19E+00	3,60E-06	0,2665	4,6334022	1,23486014	47,5	CAPN10-DT	CAPN10 divergent transcript
280	1,30E-05	4,89E+00	7,50E-06	0,2756	4,479057	1,234549	47,1	AMY2B	amylase alpha 2B
10402	7,89E-67	6,61E+01	8,64E-68	0,071	17,3973856	1,23441374	947,61	ST3GAL6	ST3 beta-galactoside alpha-2,3-sialyltransferase 6
9201	5,76E-07	6,24E+00	3,06E-07	0,2411	5,1194869	1,23413565	64,45	DCLK1	doublecortin like kinase 1
641	5,51E-80	7,93E+01	4,56E-81	0,0647	19,0691539	1,23387238	1170,09	BLM	BLM RecQ like helicase
105369575	4,36E-03	2,36E+00	3,02E-03	0,4159	2,9658266	1,23362742	19,37	LOC105369	uncharacterized LOC105369575
1070	2,84E-119	1,19E+02	1,15E-120	0,0528	23,3578507	1,23348387	2477,32	CETN3	centrin 3
64430	4,53E-169	1,68E+02	8,46E-171	0,0442	27,8586754	1,23243163	8199,68	PCNX4	pecanex 4
945	1,77E-08	7,75E+00	8,75E-09	0,2141	5,7534227	1,23185997	75,89	CD33	CD33 molecule
100506599	6,61E-07	6,18E+00	3,53E-07	0,2418	5,0928369	1,23141533	63,89	PPP1R26-AS	PPP1R26 antisense RNA 1
2100	3,09E-06	5,51E+00	1,71E-06	0,2572	4,7851892	1,23078018	55,85	ESR2	estrogen receptor 2
401898	1,67E-05	4,78E+00	9,66E-06	0,2778	4,4246041	1,2290878	44,94	ZNF833P	zinc finger protein 833, pseudogene
341277	5,55E-07	6,26E+00	2,95E-07	0,2396	5,1268551	1,2284719	61,77	OVCH2	ovochymase 2
5884	1,03E-91	9,10E+01	6,83E-93	0,0601	20,4437711	1,22823703	2689,03	RAD17	RAD17 checkpoint clamp loader component
6309	7,79E-100	9,91E+01	4,43E-101	0,0575	21,344075	1,22774476	1854,53	SC5D	sterol-C5-desaturase
105379382	3,00E-04	3,52E+00	1,89E-04	0,3287	3,7328152	1,22684029	32,13	LOC105379	uncharacterized LOC105379382
4023	7,40E-03	2,13E+00	5,24E-03	0,4393	2,791878	1,2264604	19,1	LPL	lipoprotein lipase
285550	3,89E-66	6,54E+01	4,31E-67	0,0708	17,3049909	1,22553435	1337,89	FAM200B	family with sequence similarity 200 member B
55010	1,01E-80	8,00E+01	8,26E-82	0,064	19,1582597	1,22547998	1145,55	PARPBP	PARP1 binding protein
285331	1,69E-82	8,18E+01	1,33E-83	0,0632	19,3719356	1,22420746	1391,32	CCDC66	coiled-coil domain containing 66
10808	3,23E-161	1,60E+02	6,78E-163	0,045	27,1984319	1,22403647	9299,11	HSPH1	heat shock protein family H (Hsp110) member 1
100289574	8,25E-06	5,08E+00	4,68E-06	0,2673	4,5786508	1,22392822	47,41	HERC2P4	HERC2 pseudogene 4
57116	1,19E-09	8,92E+00	5,57E-10	0,1972	6,2020934	1,22327942	89,44	ZNF695	zinc finger protein 695
653857	4,09E-21	2,04E+01	1,32E-21	0,1281	9,5482518	1,22319922	219,44	ACTR3C	actin related protein 3C

162967	2,21E-69	6,87E+01	2,29E-70	0,0689	17,7339458	1,22221366	972,49	ZNF320	zinc finger protein 320
26084	1,08E-80	8,00E+01	8,85E-82	0,0638	19,1546798	1,22195488	1355,8	ARHGEF26	Rho guanine nucleotide exchange factor 26
79809	1,00E-44	4,40E+01	1,81E-45	0,0863	14,1521444	1,2218231	676,2	TTC21B	tetratricopeptide repeat domain 21B
130026	1,96E-09	8,71E+00	9,30E-10	0,1993	6,1209991	1,21977758	86,25	ICA1L	islet cell autoantigen 1 like
101927229	2,63E-36	3,56E+01	5,71E-37	0,096	12,7026846	1,21960176	434,97	LINC01929	long intergenic non-protein coding RNA 1929
100505576	7,00E-02	1,15E+00	5,53E-02	0,6363	1,9166582	1,21949546	8,26	LINC00672	long intergenic non-protein coding RNA 672
4110	1,82E-03	2,74E+00	1,22E-03	0,3769	3,2346773	1,21908145	24,03	MAGEA11	MAGE family member A11
200172	2,73E-04	3,56E+00	1,71E-04	0,3243	3,7581322	1,21874247	32,2	SLFNL1	schlafen like 1
101928631	9,14E-03	2,04E+00	6,54E-03	0,4481	2,7195182	1,21872969	17,17	LOC101928631	
55055	1,03E-92	9,20E+01	6,71E-94	0,0593	20,5566924	1,21871198	2489,75	ZWILCH	zwilch kinetochore protein
653080	7,73E-09	8,11E+00	3,75E-09	0,2065	5,8949162	1,21741318	80,91	GUSBP16	GUSB pseudogene 16
26575	4,55E-13	1,23E+01	1,88E-13	0,1654	7,3571869	1,21701753	126,57	RGS17	regulator of G protein signaling 17
9849	5,49E-50	4,93E+01	8,71E-51	0,0812	14,9886543	1,21700267	750,74	ZNF518A	zinc finger protein 518A
109617000	1,94E-03	2,71E+00	1,30E-03	0,3784	3,2152984	1,21676068	24,46	SNORA11F	small nucleolar RNA, H/ACA box 11F
105376058	6,10E-04	3,21E+00	3,94E-04	0,3431	3,5443803	1,2162439	30,2	LOC105376058	uncharacterized LOC105376058
105376533	2,67E-02	1,57E+00	2,00E-02	0,5228	2,3261303	1,21601625	12,28	LOC105376533	uncharacterized LOC105376533
26225	1,90E-67	6,67E+01	2,06E-68	0,0695	17,4792569	1,21527649	1321,79	ARL5A	ADP ribosylation factor like GTPase 5A
80704	1,43E-02	1,84E+00	1,04E-02	0,4744	2,5614646	1,21503647	15,1	SLC19A3	solute carrier family 19 member 3
81027	2,12E-03	2,67E+00	1,43E-03	0,3809	3,1892347	1,21490701	23,24	TUBB1	tubulin beta 1 class VI
5565	2,46E-72	7,16E+01	2,39E-73	0,067	18,1158114	1,21426619	1158,73	PRKAB2	protein kinase AMP-activated non-catalytic subunit beta 2
105376444	6,60E-02	1,18E+00	5,20E-02	0,6248	1,9429656	1,21403866	8,79	LINC02643	long intergenic non-protein coding RNA 2643
339883	1,00E-02	2,00E+00	7,20E-03	0,4516	2,6872352	1,21363961	16,46	APRG1	APRG1 tumor suppressor candidate
11062	1,80E-18	1,77E+01	6,24E-19	0,1365	8,8876282	1,21348759	208,3	DUS4L	dihydrouridine synthase 4 like
79718	3,70E-93	9,24E+01	2,39E-94	0,0589	20,6067375	1,21314718	3488,43	TBL1XR1	TBL1X/Y related 1
55214	4,34E-133	1,32E+02	1,34E-134	0,0491	24,6910307	1,21309038	3046,78	P3H2	prolyl 3-hydroxylase 2
1120	1,62E-20	1,98E+01	5,30E-21	0,129	9,403029	1,21291329	218,58	CHKB	choline kinase beta
51804	6,65E-68	6,72E+01	7,10E-69	0,0691	17,5399101	1,21272965	1097,37	SIX4	SIX homeobox 4
143686	1,23E-19	1,89E+01	4,13E-20	0,132	9,1845907	1,21199104	230,71	SESN3	sestrin 3
285268	1,18E-115	1,15E+02	5,08E-117	0,0527	22,9962584	1,21154878	2140,9	ZNF621	zinc finger protein 621
10208	9,17E-54	5,30E+01	1,35E-54	0,0779	15,5606921	1,2114375	699,3	USPL1	ubiquitin specific peptidase like 1
51701	1,44E-70	6,98E+01	1,46E-71	0,0677	17,8881932	1,21099196	1045,33	NLK	nemo like kinase
79767	8,38E-06	5,08E+00	4,76E-06	0,2647	4,5752392	1,21096056	51,17	ELMO3	engulfment and cell motility 3
57677	3,33E-16	1,55E+01	1,24E-16	0,1462	8,2791861	1,21056388	172,86	ZFP14	ZFP14 zinc finger protein
79072	3,96E-50	4,94E+01	6,26E-51	0,0806	15,0106104	1,20965784	843,04	FASTKD3	FAST kinase domains 3
105371998	1,45E-16	1,58E+01	5,34E-17	0,1444	8,3789969	1,20956332	176,19	LOC105371998	uncharacterized LOC105371998
112268016	4,03E-02	1,39E+00	3,09E-02	0,5602	2,158821	1,20946578	12,67	LOC112268016	collagen alpha-1(I) chain-like
79733	2,99E-80	7,95E+01	2,46E-81	0,0633	19,1014499	1,20902815	1332,62	E2F8	E2F transcription factor 8
28576	7,85E-05	4,11E+00	4,73E-05	0,2972	4,068513	1,20897559	40,91	TRBV12-4	T cell receptor beta variable 12-4
5208	3,77E-65	6,44E+01	4,27E-66	0,0704	17,1724193	1,20874829	898,97	PFKFB2	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 2
1583	1,01E-06	6,00E+00	5,45E-07	0,2411	5,0097149	1,20759913	60,02	CYP11A1	cytochrome P450 family 11 subfamily A member 1
51091	1,08E-35	3,50E+01	2,40E-36	0,0959	12,5899816	1,20719156	436,56	SEPSECS	Sep (O-phosphoserine) tRNA:Sec (selenocysteine) tRNA synthase
64431	9,17E-46	4,50E+01	1,61E-46	0,0842	14,3211207	1,20607301	1184,55	ACTR6	actin related protein 6
107984433	6,16E-02	1,21E+00	4,83E-02	0,6106	1,9746166	1,20570314	9,56	LOC107984433	uncharacterized LOC107984433
63982	3,83E-03	2,42E+00	2,64E-03	0,4009	3,0069864	1,20540026	20,98	ANO3	anoctamin 3
3663	1,14E-02	1,94E+00	8,21E-03	0,4559	2,6434494	1,20524047	16,34	IRF5	interferon regulatory factor 5
80298	1,32E-46	4,59E+01	2,26E-47	0,0833	14,4570409	1,20498145	689,86	MTERF2	mitochondrial transcription termination factor 2
54806	8,73E-64	6,31E+01	1,02E-64	0,0709	16,9871674	1,2046817	919,96	AHI1	Abelson helper integration site 1
29943	5,31E-07	6,27E+00	2,82E-07	0,2344	5,1351364	1,20348936	65,29	PADI1	peptidyl arginine deiminase 1
23074	2,99E-104	1,04E+02	1,57E-105	0,0552	21,8179397	1,20328108	2082,55	BLTP3B	bridge-like lipid transfer protein family member 3B
147687	1,05E-43	4,30E+01	1,94E-44	0,086	13,9846008	1,20281536	571,62	ZNF417	zinc finger protein 417
55704	1,78E-144	1,44E+02	4,74E-146	0,0467	25,7350736	1,20233785	5778,28	CCDC88A	coiled-coil domain containing 88A
105374816	2,25E-03	2,65E+00	1,52E-03	0,3789	3,1713173	1,20153508	23,65	LOC105374816	uncharacterized LOC105374816
7978	8,93E-31	3,00E+01	2,22E-31	0,1031	11,6526421	1,20150637	391,53	MTERF1	mitochondrial transcription termination factor 1
54793	1,46E-138	1,38E+02	4,18E-140	0,0477	25,1982803	1,20089636	4284,08	KCTD9	potassium channel tetramerization domain containing 9
56906	2,03E-19	1,87E+01	6,85E-20	0,1315	9,1300482	1,20034897	213,22	THAP10	THAP domain containing 10
106144529	7,90E-07	6,10E+00	4,23E-07	0,2373	5,0584119	1,20028729	63,3	GRPEL2-AS1	GRPEL2 antisense RNA 1
440482	2,33E-09	8,63E+00	1,11E-09	0,1969	6,0932779	1,20003997	87,67	ANKRD20A9	ankyrin repeat domain 20 family member A5, pseudogene
79725	2,27E-18	1,76E+01	7,92E-19	0,1354	8,8611875	1,19998248	200,39	THAP9	THAP domain containing 9
105379448	2,78E-02	1,56E+00	2,09E-02	0,5193	2,3104958	1,19994962	12,2	LOC105379448	uncharacterized LOC105379448
400931	5,07E-03	2,29E+00	3,53E-03	0,4112	2,917344	1,19973163	21,72	MIRLET7BHG	MIRLET7B host gene
339400	3,99E-15	1,44E+01	1,54E-15	0,1505	7,9733697	1,19964379	165,16	FLG-AS1	FLG antisense RNA 1
9595	2,21E-02	1,66E+00	1,63E-02	0,4996	2,4011255	1,19951079	13,45	CYTIP	cytohesin 1 interacting protein
693155	2,94E-03	2,53E+00	2,00E-03	0,3882	3,0899674	1,19947966	23,18	MIR570	microRNA 570
7569	3,85E-45	4,44E+01	6,87E-46	0,0843	14,2201698	1,19865951	584,92	ZNF182	zinc finger protein 182
283464	1,17E-79	7,89E+01	9,69E-81	0,063	19,0296288	1,19864272	1729,16	GXYLT1	glucoside xylosyltransferase 1
55236	1,89E-104	1,04E+02	9,86E-106	0,0549	21,839117	1,19857135	4291,64	UBA6	ubiquitin like modifier activating enzyme 6
50810	3,08E-103	1,03E+02	1,65E-104	0,0552	21,7101512	1,19855573	2325,96	HDGFL3	HDGF like 3
651	5,70E-02	1,24E+00	4,46E-02	0,5966	2,0088746	1,19854426	9,58	BMP3	bone morphogenetic protein 3
8099	1,51E-72	7,18E+01	1,46E-73	0,0661	18,1430494	1,19841368	2689,96	CDK2AP1	cyclin dependent kinase 2 associated protein 1
2181	7,63E-109	1,08E+02	3,65E-110	0,0537	22,3005655	1,19823301	5165,69	ACSL3	acyl-CoA synthetase long chain family member 3
84851	1,28E-44	4,39E+01	2,31E-45	0,0847	14,1350523	1,19773276	579,63	TRIM52	tripartite motif containing 52
50624	3,95E-03	2,40E+00	2,72E-03	0,3993	2,9975027	1,19684186	21,01	CUZD1	CUB and zona pellucida like domains 1
353500	5,95E-03	2,23E+00	4,18E-03	0,4176	2,8643005	1,19624543	19,59	BMP8A	bone morphogenetic protein 8a
101060321	1,57E-04	3,80E+00	9,70E-05	0,3069	3,8980121	1,1961816	37,41	TBC1D3G	TBC1 domain family member 3G
11201	8,89E-29	2,81E+01	2,33E-29	0,1063	11,2496139	1,19585911	393,94	POLI	DNA polymerase iota
11174	8,10E-36	3,51E+01	1,79E-36	0,0948	12,6131901	1,19526387	425,42	ADAMTS6	ADAM metallopeptidase with thrombospondin type 1 motif 6
101928234	2,87E-02	1,54E+00	2,16E-02	0,52	2,2976312	1,1948429	12,2	LOC101928234	uncharacterized LOC101928234
51014	1,05E-66	6,60E+01	1,15E-67	0,0687	17,3808726	1,19457492	2641,68	TMED7	transmembrane p24 trafficking protein 7
338799	1,10E-11	1,10E+01	4,76E-12	0,1728	6,9124304	1,19418564	119,98	LINC01089	long intergenic non-protein coding RNA 1089
8995	1,65E-02	1,78E+00	1,21E-02	0,4754	2,5092582	1,1927814	15,74	TNFSF18	TNF superfamily member 18
100129961	9,43E-06	5,03E+00	5,37E-06	0,262	4,549828	1,19225275	50,15	CCNT2-AS1	CCNT2 antisense RNA 1
107986246	5,69E-02	1,24E+00	4,45E-02	0,5933	2,0094317	1,19212947	9,54	LOC107986246	uncharacterized LOC107986246
440253	6,40E-05	4,19E+00	3,83E-05	0,2895	4,1173186	1,19204614	39,9	WHAMMP2	WHAMM pseudogene 2
102724776	2,61E-05	4,58E+00	1,52E-05	0,2756	4,3252796	1,19203383	43,89	MAP9-AS1	MAP9 antisense RNA 1
54507	3,39E-25	2,45E+01	9,78E-26	0,1136	10,4882327	1,19119107	314,35	ADAMTSL4	ADAMTS like 4
9648	2,77E-88	8,76E+01	1,95E-89	0,0594	20,05164	1,19116454	1438,55	GCC2	GRIP and coiled-coil domain containing 2
440515	1,45E-40	3,98E+01	2,86E-41	0,0885	13,4554799	1,19080118	500,75	ZNF506	zinc finger protein 506
374618	1,26E-12	1,19E+01	5,30E-13	0,165	7,2174898	1,190529	147,37	TEX9	testis expressed 9
22995	2,58E-81	8,06E+01	2,08E-82	0,0619	19,2299043	1,19050061	1298,62	CEP152	centrosomal protein 152
29841	3,39E-05	4,47E+00	1,99E-05	0,279	4,2656208	1,18994935	48,29	GRHL1	grainyhead like transcription factor 1
283755	4,57E-30	2,93E+01	1,16E-30	0,1033	11,5113347	1,1895123	350,98	HERC2P3	HERC2 pseudogene 3
266812	8,16E-13	1,21E+01	3,39E-13	0,1634	7,2778302	1,18940995	128,93	NAP1L5	nucleosome assembly protein 1 like 5
4050	2,40E-06	5,62E+00	1,32E-06	0,2458	4,8371889	1,18919778	56,8	LTB	lymphotoxin beta
197335	7,16E-31	3,01E+01	1,78E-31	0,1019	11,671597	1,18905974	410,92	WDR90	WD repeat domain 90
3575	8,17E-56	5,51E+01	1,15E-56	0,0749	15,8627722	1,18882921	766,64	IL7R	interleukin 7 receptor
105376204	2,28E-04	3,64E+00	1,42E-04	0,3125	3,8039597	1,1886096	34,55	LOC105376204	uncharacterized LOC105376204
283659	4,55E-37	3,63E+01	9,72E-38	0,0926	12,8405643	1,18853792	454,28	PRTG	protogenin
4883	7,15E-06	5,15E+00	4,04E-06	0,2577	4,609471	1,18803471	54,41	NPR3	natriuretic peptide receptor 3
81624	1,01E-133	1,33E+02	3,07E-135	0,048	24,7503906	1,1872038	4798,06	DIAPH3	diaphanous related formin 3
51427	2,62E-30	2,96E+01	6,60E-31	0,1026	11,559558	1,18658468	368,64	ZNF107	zinc finger protein 107
163081	6,73E-41	4,02E+01	1,32E-41	0,0878	13,5125728	1,18641413	528,48	ZNF567	zinc finger protein 567
112268092	8,09E-02	1,09E+00	6,44E-02	0,6416	1,8491477	1,18635508	8,9	LOC112268092	
7398	5,54E-128	1,27E+02	1,88E-129	0,049	24,2069321	1,18615951	8128,46	USP1	ubiquitin specific peptidase 1
23306	3,96E-128	1,27E+02	1,34E-129	0,049	24,2209457	1,18597369	2718,29	NEMP1	nuclear envelope integral membrane protein 1
101927999	1,39E-04	3,86E+00	8,55E-05	0,3016	3,9284229	1,18494138	36,94	LOC101927999	putative uncharacterized protein FLJ44672
643650	2,88E-13	1,25E+01	1,18E-13	0,1596	7,4191953	1,18377054	139,67	LINC00842	long intergenic non-protein coding RNA 842
114803	1,95E-30	2,97E+01	4,91E-31	0,1021	11,5850701	1,1833443	359,38	MYSM1	Myb like, SWIRM and MPN domains 1
57648	8,39E-46	4,51E+01	1,48E-46	0,0826	14,3274034	1,18315387	716,54	KIAA1522	KIAA1522
101928529	2,85E-02	1,55E+00	2,14E-02	0,5141	2,3011921	1,18313221	12,78	LOC101928529	uncharacterized LOC101928529
285429	3,06E-03	2,51E+00	2,09E-03	0,3843	3,0775926	1,18278648	23,45	DCAF4L1	DDB1 and CUL4 associated factor 4 like 1
54491	1,09E-52	5,20E+01	1,63E-53	0,0768	15,4001014	1,18274195	759,92	OTULINL	OTU deubiquitinase with linear linkage specificity like
29990	7,03E-16	1,52E+01	2,65E-16	0,1444	8,1882971	1,18240237	174,83	PILRB	paired immunoglobin like type 2 receptor beta
6059	8,49E-78	7,71E+01	7,38E-79	0,0629	18,8012197	1,18227689	11096,16	ABCE1	ATP binding cassette subfamily E member 1
7681	4,54E-09	8,34E+00	2,18E-09	0,1975	5,9838791	1,18175257	88,19	MKRN3	makorin ring finger protein 3
257144	4,69E-06	5,33E+00	2,62E-06	0,2514	4,6985168	1,18136985	53,6	GCSAM	germinal center associated signaling and motility
23037	9,97E-31	3,00E+01	2,49E-31	0,1014	11,6430515	1,18010535	428,64	PDZD2	PDZ domain containing 2
56890	4,42E-44	4,34E+01	8,09E-45	0,0839	14,0465596	1,17860442	627,07	MDM1	Mdm1 nuclear protein
116068	5,00E-64	6,33E+01	5,82E-65	0,0692	17,0201972	1,17820237	1450,64	LYSMD3	LysM domain containing 3
402569	2,83E-02	1,55E+00	2,13E-02	0,5113	2,3033053	1,17770222	12,82	KPNA7	karyopherin subunit alpha 7
80205	1,85E-104	1,04E+02	9,63E-106	0,0539	21,8402022	1,17733097	1992,1	CHD9	chromodomain helicase DNA binding protein 9

23566	4,35E-02	1,36E+00	3,34E-02	0,553	2,1270634	1,17627333	11,27	LPAR3	lysophosphatidic acid receptor 3
9583	2,83E-109	1,09E+02	1,35E-110	0,0526	22,3451449	1,17599641	2186,2	ENTPD4	ectonucleoside triphosphate diphosphohydrolase 4
222696	1,99E-06	5,70E+00	1,09E-06	0,2412	4,8747313	1,1759024	64,9	ZSCAN23	zinc finger and SCAN domain containing 23
55329	6,18E-26	2,52E+01	1,75E-26	0,1103	10,6498937	1,17504282	297,57	MNS1	meiosis specific nuclear structural 1
286148	3,47E-73	7,25E+01	3,31E-74	0,0645	18,224338	1,17494718	1100,73	DPY19L4	dpy-19 like 4
6096	2,27E-06	5,64E+00	1,25E-06	0,2423	4,8481495	1,17485106	60,09	RORB	RAR related orphan receptor B
57489	1,17E-85	8,49E+01	8,62E-87	0,0594	19,746355	1,17379634	1914,1	ODF2L	outer dense fiber of sperm tails 2 like
1829	2,41E-165	1,65E+02	4,74E-167	0,0426	27,5475394	1,17366887	7780,8	DSG2	desmoglein 2
22868	1,92E-83	8,27E+01	1,48E-84	0,0602	19,4847036	1,1735793	1921,42	FASTKD2	FAST kinase domains 2
10418	3,62E-02	1,44E+00	2,76E-02	0,5325	2,2035603	1,17349087	12,09	SPON1	spondin 1
100507487	6,05E-02	1,22E+00	4,74E-02	0,5917	1,9826416	1,17304557	9,93	LINC02615	long intergenic non-protein coding RNA 2615
26815	1,54E-17	1,68E+01	5,52E-18	0,1356	8,6420364	1,17212602	196,45	SNORD36A	small nucleolar RNA, C/D box 36A
80263	1,74E-17	1,68E+01	6,25E-18	0,1358	8,6279399	1,17171947	191,24	TRIM45	tripartite motif containing 45
729533	1,65E-64	6,38E+01	1,90E-65	0,0686	17,0856142	1,17146961	1063,74	FAM72A	family with sequence similarity 72 member A
152815	3,13E-48	4,75E+01	5,17E-49	0,0796	14,7149023	1,17115702	678,15	THAP6	THAP domain containing 6
9497	1,45E-99	9,88E+01	8,27E-101	0,0549	21,3148115	1,17113461	2050,96	SLC4A7	solute carrier family 4 member 7
378805	8,74E-26	2,51E+01	2,48E-26	0,1103	10,6170872	1,17060584	310,7	LINC-PINT	long intergenic non-protein coding RNA, p53 induced transcript
643699	8,90E-03	2,05E+00	6,35E-03	0,4288	2,7291997	1,170234	18,08	GOLGA8N	golgin A8 family member N
57683	2,66E-36	3,56E+01	5,77E-37	0,0921	12,7019243	1,17003893	457,88	ZDBF2	zinc finger DBF-type containing 2
114134	4,06E-20	1,94E+01	1,34E-20	0,1257	9,3047383	1,16988543	232,8	SLC2A13	solute carrier family 2 member 13
9465	2,56E-15	1,46E+01	9,83E-16	0,1457	8,0289891	1,16961411	168,91	AKAP7	A-kinase anchoring protein 7
286077	2,81E-24	2,36E+01	8,32E-25	0,1137	10,2839476	1,16943599	302,15	FAM83H	family with sequence similarity 83 member H
143888	3,67E-173	1,72E+02	6,40E-175	0,0414	28,1967766	1,16812885	6890,83	POGLUT3	protein O-glucosyltransferase 3
100616113	2,02E-03	2,69E+00	1,36E-03	0,3646	3,2030687	1,167995	26,19	MIR4680	microRNA 4680
9847	5,00E-93	9,23E+01	3,23E-94	0,0567	20,5920443	1,16797003	1783,33	C2CD5	C2 calcium dependent domain containing 5
101927813	2,35E-09	8,63E+00	1,12E-09	0,1917	6,0916517	1,16769088	92,8	HMMR-AS1	HMMR antisense RNA 1
145389	1,71E-15	1,48E+01	6,54E-16	0,1445	8,0787869	1,16753606	167,72	SLC38A6	solute carrier family 38 member 6
7429	9,83E-14	1,30E+01	3,96E-14	0,1544	7,5622015	1,16746913	154,45	VIL1	villin 1
53346	1,85E-05	4,73E+00	1,07E-05	0,265	4,4020033	1,16664536	47,98	TM6SF1	transmembrane 6 superfamily member 1
23325	4,48E-104	1,03E+02	2,37E-105	0,0535	21,7991135	1,16662172	4200,07	WASHC4	WASH complex subunit 4
23493	3,78E-02	1,42E+00	2,89E-02	0,5336	2,1850371	1,16591232	12,12	HEY2	hes related family bHLH transcription factor with YRPW motif 2
23322	1,45E-32	3,18E+01	3,44E-33	0,0971	12,0025696	1,16582279	448,17	RPGRIP1L	RPGRIP1 like
23089	2,85E-171	1,71E+02	5,10E-173	0,0416	28,0412972	1,16559585	7164,61	PEG10	paternally expressed 10
64863	1,83E-59	5,87E+01	2,36E-60	0,0711	16,3870985	1,16524442	977,99	METTL4	methyltransferase 4, N6-adenosine
5926	3,36E-70	6,95E+01	3,42E-71	0,0653	17,8405711	1,16521192	1338,96	ARID4A	AT-rich interaction domain 4A
112441434	3,75E-21	2,04E+01	1,21E-21	0,1219	9,5574838	1,1651703	240,06	SHLD3	shieldin complex subunit 3
140876	2,43E-04	3,61E+00	1,52E-04	0,3073	3,7871842	1,16389486	35,96	RIPOR3	RIPOR family member 3
728715	1,06E-03	2,97E+00	6,96E-04	0,3432	3,3910982	1,16388628	28,02	LOC728715	ovostatin homolog 2
105379383	1,93E-02	1,71E+00	1,42E-02	0,4747	2,4517335	1,16385155	14,68	LOC105379383	
3695	3,80E-03	2,42E+00	2,62E-03	0,3867	3,0096867	1,16382378	22	ITGB7	integrin subunit beta 7
1910	3,68E-13	1,24E+01	1,51E-13	0,1576	7,3858437	1,16377538	161,92	EDNRB	endothelin receptor type B
105377449	1,58E-03	2,80E+00	1,06E-03	0,3553	3,2750417	1,16374994	26,58	LOC105377449	
10793	7,74E-11	1,01E+01	3,46E-11	0,1756	6,6256803	1,16364325	111,98	ZNF273	zinc finger protein 273
285753	5,56E-52	5,13E+01	8,45E-53	0,0761	15,2934862	1,16354621	780,24	CEP57L1	centrosomal protein 57 like 1
390	2,50E-133	1,33E+02	7,69E-135	0,0471	24,7133514	1,16320158	4179,63	RND3	Rho family GTPase 3
107986087	1,03E-01	9,87E-01	8,34E-02	0,6718	1,7311807	1,16306119	7,39	LOC107986087	uncharacterized LOC107986087
105375541	1,92E-02	1,72E+00	1,42E-02	0,4741	2,4530753	1,16303764	16,17	LOC105375541	uncharacterized LOC105375541
675	1,05E-87	8,70E+01	7,46E-89	0,0582	19,9848852	1,16280903	1551,05	BRCA2	BRCA2 DNA repair associated
51095	1,10E-67	6,70E+01	1,19E-68	0,0663	17,5107279	1,16168695	1042,95	TRNT1	tRNA nucleotidyl transferase 1
389765	8,90E-12	1,11E+01	3,83E-12	0,1673	6,9432513	1,1616219	121,2	LOC389765	kinesin family member 27 pseudogene
105371554	8,97E-02	1,05E+00	7,19E-02	0,645	1,7998509	1,16096499	7,96	LOC105371554	uncharacterized LOC105371554
58155	1,32E-42	4,19E+01	2,49E-43	0,0841	13,8017925	1,16095827	700,51	PTBP2	polypyrimidine tract binding protein 2
283209	4,14E-47	4,64E+01	7,03E-48	0,0799	14,5373388	1,16087542	676	PGM2L1	phosphoglucomutase 2 like 1
106736475	1,51E-02	1,82E+00	1,10E-02	0,4564	2,5430916	1,16065045	15,91	PCF11-AS1	PCF11 antisense RNA 1
5898	1,24E-119	1,19E+02	4,94E-121	0,0496	23,3938087	1,16006812	4074,35	RALA	RAS like proto-oncogene A
100129836	3,94E-11	1,04E+01	1,74E-11	0,1725	6,7261457	1,16002645	125,07	COL4A2-AS2	COL4A2 antisense RNA 2
79768	6,86E-49	4,82E+01	1,12E-49	0,0783	14,8182849	1,15987605	848,12	KATNBL1	katanin regulatory subunit B1 like 1
692213	6,25E-15	1,42E+01	2,43E-15	0,1464	7,9171535	1,15891274	168,89	SNORD110	small nucleolar RNA, C/D box 110
84952	3,29E-04	3,48E+00	2,08E-04	0,3123	3,7096227	1,15859396	34,61	CGNL1	cingulin like 1
104355426	8,20E-04	3,09E+00	5,35E-04	0,3346	3,4628178	1,15852618	30,55	LENG8-AS1	LENG8 antisense RNA 1
54554	4,90E-17	1,63E+01	1,78E-17	0,1361	8,5073031	1,15825508	251,23	WDR5B	WD repeat domain 5B
105376214	2,69E-02	1,57E+00	2,01E-02	0,4983	2,3241435	1,15808008	13,28	LOC105376214	uncharacterized LOC105376214
548596	8,03E-04	3,10E+00	5,23E-04	0,3339	3,4685267	1,15797257	29,97	CKMT1A	creatine kinase, mitochondrial 1A
57139	7,53E-10	9,12E+00	3,50E-10	0,1845	6,2748828	1,15783199	99,7	RGL3	ral guanine nucleotide dissociation stimulator like 3
58480	3,69E-20	1,94E+01	1,22E-20	0,1243	9,3149487	1,15773669	279,14	RHOU	ras homolog family member U
441086	1,21E-01	9,17E-01	9,90E-02	0,7017	1,6496446	1,15760369	6,63	FAM169A-AS1	FAM169A antisense RNA 1
26807	4,64E-02	1,33E+00	3,58E-02	0,5514	2,0986887	1,15729883	11,28	SNORD43	small nucleolar RNA, C/D box 43
406928	1,28E-02	1,89E+00	9,29E-03	0,4446	2,6010478	1,15653855	16,57	MIR137	microRNA 137
102724660	2,83E-05	4,55E+00	1,66E-05	0,2685	4,3067168	1,15616526	49,36	HILPDA-AS1	HILPDA antisense RNA 1
112268118	1,50E-07	6,82E+00	7,72E-08	0,215	5,3735911	1,15542336	74,91	LOC112268118	uncharacterized LOC112268118
107984512	1,06E-02	1,97E+00	7,62E-03	0,433	2,6683176	1,15540489	18,07	LOC107984512	
26167	1,48E-05	4,83E+00	8,55E-06	0,2596	4,4509657	1,1552887	54	PCDHB5	protocadherin beta 5
107986583	1,96E-08	7,71E+00	9,68E-09	0,2014	5,7361922	1,15519639	88,22	LOC107986583	uncharacterized LOC107986583
64089	1,70E-34	3,38E+01	3,87E-35	0,0934	12,3685433	1,15517526	535,94	SNX16	sorting nexin 16
22989	1,32E-10	9,88E+00	5,96E-11	0,1764	6,5446623	1,1546453	112,99	MYH15	myosin heavy chain 15
5324	1,75E-24	2,38E+01	5,14E-25	0,1118	10,3303476	1,1544968	312,99	PLAG1	PLAG1 zinc finger
84140	5,12E-51	5,03E+01	7,92E-52	0,0762	15,1471181	1,15446239	749,37	FAM161A	FAM161 centrosomal protein A
53905	6,90E-06	5,16E+00	3,89E-06	0,25	4,6169649	1,15441256	55,46	DUOX1	dual oxidase 1
7556	3,23E-21	2,05E+01	1,04E-21	0,1206	9,5728867	1,1543164	249,64	ZNF10	zinc finger protein 10
337875	5,00E-06	5,30E+00	2,80E-06	0,2463	4,6849783	1,15384749	55,88	H2BP1	H2B histone pseudogene 1
283461	9,13E-02	1,04E+00	7,33E-02	0,644	1,7910393	1,15334987	7,99	C12orf40	chromosome 12 open reading frame 40
374987	2,28E-10	9,64E+00	1,04E-10	0,1785	6,461344	1,15311968	108,17	NEXN-AS1	NEXN antisense RNA 1
394	1,53E-136	1,36E+02	4,50E-138	0,0461	25,0122523	1,15287201	8586,48	ARHGAP5	Rho GTPase activating protein 5
101928337	2,47E-02	1,61E+00	1,84E-02	0,4889	2,3573883	1,15253978	13,96	PTCSC2	papillary thyroid carcinoma susceptibility candidate 2
112849	1,52E-50	4,98E+01	2,38E-51	0,0764	15,0745329	1,15226623	811,5	L3HYPDH	trans-L-3-hydroxyproline dehydratase
27303	8,74E-44	4,31E+01	1,61E-44	0,0823	13,9976943	1,15217336	622,42	RBMS3	RNA binding motif single stranded interacting protein 3
580	1,95E-53	5,27E+01	2,88E-54	0,0743	15,5120182	1,15215091	1029,61	BARD1	BRCA1 associated RING domain 1
102466747	1,24E-01	9,07E-01	1,02E-01	0,7037	1,6363371	1,15156116	6,69	MIR6840	microRNA 6840
105371492	1,85E-10	9,73E+00	8,37E-11	0,1773	6,4937771	1,1512819	108,73	CTNS-AS1	CTNS antisense RNA 1
10000	1,11E-106	1,06E+02	5,55E-108	0,0522	22,0745729	1,1512186	2034,7	AKT3	AKT serine/threonine kinase 3
23142	3,82E-90	8,94E+01	2,60E-91	0,0568	20,2653744	1,15121203	1656,91	DCUN1D4	defective in cullin neddylation 1 domain containing 4
653820	4,19E-71	7,04E+01	4,20E-72	0,0641	17,9574296	1,15070578	1225,13	FAM72B	family with sequence similarity 72 member B
399815	1,21E-07	6,92E+00	6,24E-08	0,2126	5,4118851	1,15067019	76,36	C10orf88B	C10orf88B (pseudogene)
53342	1,02E-08	7,99E+00	4,98E-09	0,1967	5,8478426	1,15037545	89,98	IL17D	interleukin 17D
105377604	1,52E-10	9,82E+00	6,88E-11	0,1763	6,5232491	1,15000202	109,13	LOC105377604	uncharacterized LOC105377604
100874029	7,83E-02	1,11E+00	6,22E-02	0,6165	1,8648037	1,14973432	8,59	CFAP44-AS1	CFAP44 antisense RNA 1
4642	5,41E-46	4,53E+01	9,44E-47	0,0801	14,3583774	1,14967649	620,77	MYO1D	myosin ID
10269	3,71E-120	1,19E+02	1,46E-121	0,049	23,4457497	1,14960412	4207,57	ZMPSTE24	zinc metallopeptidase STE24
33	5,02E-03	2,30E+00	3,50E-03	0,3936	2,9202414	1,14945958	23,28	ACADL	acyl-CoA dehydrogenase long chain
55540	4,95E-20	1,93E+01	1,64E-20	0,1238	9,2832381	1,14931039	237,2	IL17RB	interleukin 17 receptor B
130872	1,20E-60	5,99E+01	1,51E-61	0,0694	16,553441	1,14910934	925,5	AHSA2P	activator of HSP90 ATPase homolog 2, pseudogene
149483	8,31E-07	6,08E+00	4,46E-07	0,2276	5,0483134	1,14896923	76,83	CCDC17	coiled-coil domain containing 17
214	1,88E-170	1,70E+02	3,40E-172	0,0411	27,9736245	1,14890317	16946,18	ALCAM	activated leukocyte cell adhesion molecule
23347	8,24E-121	1,20E+02	3,23E-122	0,0489	23,5098761	1,14869904	4972,81	SMCHD1	structural maintenance of chromosomes flexible hinge domain containing 1
100499177	1,24E-89	8,89E+01	8,51E-91	0,0568	20,2069292	1,14860593	1539,3	THAP9-AS1	THAP9 antisense RNA 1
57120	1,23E-97	9,69E+01	7,32E-99	0,0544	21,1039496	1,14775469	1972,2	GOPC	golgi associated PDZ and coiled-coil motif containing
54914	1,34E-08	7,87E+00	6,60E-09	0,1978	5,8008883	1,14753052	90,34	FOCAD	focadhesin
651302	9,90E-06	5,00E+00	5,65E-06	0,2527	4,5391838	1,14724413	53,37	ZKSCAN8P1	ZKSCAN8 pseudogene 1
127396	1,31E-12	1,19E+01	5,48E-13	0,1591	7,2128102	1,1472382	136,39	ZNF684	zinc finger protein 684
80067	3,52E-59	5,85E+01	4,59E-60	0,0702	16,3467036	1,14722591	1081,87	DCAF17	DDB1 and CUL4 associated factor 17
115253422	9,01E-60	5,90E+01	1,16E-60	0,0698	16,4304018	1,14713821	1429,74	DUS4L-BCAP	DUS4L-BCAP29 readthrough
23253	7,77E-104	1,03E+02	4,11E-105	0,0527	21,7738032	1,14700222	2432,68	ANKRD12	ankyrin repeat domain 12
84914	2,43E-79	7,86E+01	2,03E-80	0,0604	18,9907389	1,14663515	1499,95	ZNF587	zinc finger protein 587
25913	2,37E-46	4,56E+01	4,11E-47	0,0795	14,4159294	1,14661065	1395,41	POT1	protection of telomeres 1
51380	1,73E-13	1,28E+01	7,05E-14	0,1531	7,4870066	1,14655065	145,44	CSAD	cysteine sulfinic acid decarboxylase
6876	2,86E-58	5,75E+01	3,80E-59	0,0707	16,2174613	1,14585811	850,33	TAGLN	transgelin
11001	4,62E-04	3,34E+00	2,95E-04	0,3165	3,619444	1,14557363	34,25	SLC27A2	solute carrier family 27 member 2
2686	8,96E-16	1,50E+01	3,39E-16	0,1404	8,1585828	1,14514086	181,43	GGT7	gamma-glutamyltransferase 7
7019	1,78E-94	9,37E+01	1,12E-95	0,0552	20,754341	1,14513333	3590,26	TFAM	transcription factor A, mitochondrial
84910	9,15E-76	7,50E+01	8,28E-77	0,0617	18,549152	1,14491045	2057,11	TMEM87B	transmembrane protein 87B

285203	7,97E-79	7,81E+01	6,75E-80	0,0605	18,9276748	1,1444528	1372,3	EOGT	EGF domain specific O-linked N-acetylglucosamine transferase
8835	3,74E-38	3,74E+01	7,80E-39	0,0878	13,0343521	1,14409861	551,13	SOCS2	suppressor of cytokine signaling 2
100288637	6,48E-46	4,52E+01	1,13E-46	0,0797	14,345657	1,14397524	682,73	LOC100288	OTU deubiquitinase 7A pseudogene
9318	7,96E-139	1,38E+02	2,28E-140	0,0453	25,2223008	1,14316737	4273	COPS2	COP9 signalosome subunit 2
221264	1,75E-30	2,98E+01	4,39E-31	0,0986	11,5945792	1,14286469	421,56	AK9	adenylate kinase 9
112268024	6,27E-02	1,20E+00	4,92E-02	0,5811	1,9666698	1,14275118	9,89	LOC112268	024
339483	6,52E-06	5,19E+00	3,68E-06	0,2469	4,6289462	1,14270948	56,96	MTMR9LP	myotubularin related protein 9 like, pseudogene
80184	7,08E-83	8,21E+01	5,51E-84	0,0588	19,417323	1,14240392	1482,23	CEP290	centrosomal protein 290
647946	4,13E-11	1,04E+01	1,82E-11	0,17	6,7194638	1,14226581	120,59	MIR924HG	MIR924 host gene
442590	2,40E-02	1,62E+00	1,78E-02	0,482	2,3690768	1,14199863	14,46	SPDYE5	speedy/RINGO cell cycle regulator family member E5
114823	1,23E-109	1,09E+02	5,84E-111	0,051	22,3823999	1,14161045	3669,11	LENG8	leukocyte receptor cluster member 8
145173	6,21E-49	4,82E+01	1,01E-49	0,077	14,8250038	1,14098799	759,8	B3GLCT	beta 3-glucosyltransferase
100507557	3,43E-05	4,46E+00	2,02E-05	0,2675	4,2625883	1,14037329	50,17	EPM2A-DT	EPM2A divergent transcript
9953	5,02E-47	4,63E+01	8,53E-48	0,0785	14,5240592	1,1403408	668,55	HS3ST3B1	heparan sulfate-glucosamine 3-sulfotransferase 3B1
107987147	3,76E-11	1,04E+01	1,66E-11	0,169	6,7330908	1,1381366	123,45	LOC107987	147
93986	1,64E-10	9,79E+00	7,42E-11	0,1748	6,5119386	1,1380131	112,62	FOXP2	forkhead box P2
57562	3,00E-22	2,15E+01	9,32E-23	0,1159	9,8190303	1,13762472	271,79	CEP126	centrosomal protein 126
79664	2,12E-63	6,27E+01	2,49E-64	0,0672	16,9348243	1,13725845	1671,22	ICE2	interactor of little elongation complex ELL subunit 2
105370135	6,44E-06	5,19E+00	3,63E-06	0,2455	4,631454	1,13719131	57,75	LOC105370	uncharacterized LOC105370135
857	8,24E-175	1,74E+02	1,41E-176	0,0401	28,331608	1,13714474	19887,38	CAV1	caveolin 1
107985306	2,73E-07	6,56E+00	1,43E-07	0,216	5,2616568	1,13654014	74,85	LOC107985	uncharacterized LOC107985306
677804	1,45E-03	2,84E+00	9,61E-04	0,3442	3,301821	1,13652083	27,63	SNORA17A	small nucleolar RNA, H/ACA box 17A
147138	4,55E-09	8,34E+00	2,18E-09	0,1898	5,983481	1,1355107	104,49	TMC8	transmembrane channel like 8
57053	1,96E-03	2,71E+00	1,32E-03	0,3535	3,2118207	1,13538409	27,06	CHRNA10	cholinergic receptor nicotinic alpha 10 subunit
107986973	1,83E-03	2,74E+00	1,23E-03	0,3511	3,2329671	1,13516381	27,51	LOC107986	973
102723316	2,92E-05	4,53E+00	1,72E-05	0,264	4,2990374	1,13496754	49,49	FRG1DP	FSHD region gene 1 family member D, pseudogene
158431	1,29E-18	1,79E+01	4,47E-19	0,1271	8,924597	1,13466492	221,44	ZNF782	zinc finger protein 782
51196	1,53E-62	6,18E+01	1,84E-63	0,0674	16,8167489	1,13414942	1091,01	PLCE1	phospholipase C epsilon 1
51290	5,49E-80	7,93E+01	4,54E-81	0,0595	19,0693434	1,13413164	2105,88	ERGIC2	ERGIC and golgi 2
100130771	9,79E-10	9,01E+00	4,57E-10	0,1819	6,2330831	1,13406536	107,23	EFCAB10	EF-hand calcium binding domain 10
284371	2,96E-50	4,95E+01	4,66E-51	0,0754	15,0300741	1,13397263	777,49	ZNF841	zinc finger protein 841
220164	1,14E-03	2,94E+00	7,53E-04	0,3365	3,369556	1,13393198	31,79	DOK6	docking protein 6
283742	2,50E-87	8,66E+01	1,80E-88	0,0568	19,940886	1,13329705	1818,86	FAM98B	family with sequence similarity 98 member B
646548	8,71E-02	1,06E+00	6,96E-02	0,6246	1,8142767	1,1331991	8,58	LOC646548	ADAM metallopeptidase domain 20 pseudogene
64151	1,67E-148	1,48E+02	4,19E-150	0,0434	26,0947025	1,13314282	9285,34	NCAPG	non-SMC condensin I complex subunit G
728233	3,69E-29	2,84E+01	9,56E-30	0,1	11,32775	1,13298135	397,95	PI4KAP1	phosphatidylinositol 4-kinase alpha pseudogene 1
143684	7,25E-63	6,21E+01	8,62E-64	0,0672	16,8616122	1,13258646	1186,33	FAM76B	family with sequence similarity 76 member B
101928103	1,11E-02	1,95E+00	8,00E-03	0,4269	2,6520366	1,13213942	18,96	SNHG31	small nucleolar RNA host gene 31
4897	1,74E-07	6,76E+00	9,04E-08	0,2118	5,3450561	1,13183734	80,75	NRCAM	neuronal cell adhesion molecule
403341	1,89E-40	3,97E+01	3,74E-41	0,0842	13,4356885	1,13180557	543,77	ZBTB34	zinc finger and BTB domain containing 34
286410	5,61E-79	7,83E+01	4,73E-80	0,0597	18,9463755	1,13175775	1701,63	ATP11C	ATPase phospholipid transporting 11C
8491	3,76E-106	1,05E+02	1,89E-107	0,0514	22,0191341	1,13146902	2182,09	MAP4K3	mitogen-activated protein kinase kinase kinase kinase 3
54454	3,38E-45	4,45E+01	6,02E-46	0,0795	14,2294122	1,13090444	666,56	ATAD2B	ATPase family AAA domain containing 2B
101059918	1,35E-02	1,87E+00	9,80E-03	0,4378	2,5828674	1,13082561	17,12	GOLGA8R	golgin A8 family member R
105379771	1,29E-03	2,89E+00	8,51E-04	0,339	3,3355502	1,13079891	28,78	LOC105379	uncharacterized LOC105379771
339500	1,09E-25	2,50E+01	3,11E-26	0,1067	10,5958871	1,13050989	363,24	ZNF678	zinc finger protein 678
51454	1,12E-52	5,20E+01	1,67E-53	0,0734	15,3986822	1,1302006	815,4	GULP1	GULP PTB domain containing engulfment adaptor 1
55208	5,73E-38	3,72E+01	1,20E-38	0,0868	13,0015176	1,12882908	553,32	DCUN1D2	defective in cullin neddylation 1 domain containing 2
1789	3,51E-59	5,85E+01	4,57E-60	0,069	16,3469674	1,12864363	999,97	DNMT3B	DNA methyltransferase 3 beta
165215	4,02E-30	2,94E+01	1,02E-30	0,0979	11,5223126	1,1285636	399,86	FAM171B	family with sequence similarity 171 member B
7768	4,38E-20	1,94E+01	1,45E-20	0,1213	9,2964765	1,12778092	251	ZNF225	zinc finger protein 225
50940	4,26E-14	1,34E+01	1,70E-14	0,1469	7,6715127	1,12727588	166,23	PDE11A	phosphodiesterase 11A
151011	1,95E-143	1,43E+02	5,27E-145	0,0439	25,641427	1,12687047	5416,08	SEPTIN10	septin 10
118788	4,33E-09	8,36E+00	2,08E-09	0,188	5,9917933	1,12661335	101,52	PIK3AP1	phosphoinositide-3-kinase adaptor protein 1
5286	9,82E-106	1,05E+02	5,01E-107	0,0513	21,9748737	1,12642925	2451,59	PIK3C2A	phosphatidylinositol-4-phosphate 3-kinase catalytic subunit type 2 alpha
642799	3,65E-11	1,04E+01	1,61E-11	0,1671	6,7378279	1,12618228	121,08	NPIPA2	nuclear pore complex interacting protein family member A2
55754	2,69E-89	8,86E+01	1,86E-90	0,0558	20,1682325	1,12556285	7902,04	TMEM30A	transmembrane protein 30A
140578	3,61E-03	2,44E+00	2,48E-03	0,372	3,0255399	1,12553794	24,14	CHODL	chondrolectin
83591	1,80E-10	9,74E+00	8,18E-11	0,1732	6,4972641	1,12531515	114,42	THAP2	THAP domain containing 2
343099	2,66E-62	6,16E+01	3,21E-63	0,067	16,7837886	1,12508976	1129,1	CCDC18	coiled-coil domain containing 18
441430	6,51E-02	1,19E+00	5,12E-02	0,577	1,9497739	1,12507664	9,79	ANKRD20A2	ankyrin repeat domain 20 family member A2, pseudogene
114908	1,70E-183	1,83E+02	2,58E-185	0,0388	29,0322233	1,12505064	21266,19	TMEM123	transmembrane protein 123
283208	8,63E-03	2,06E+00	6,15E-03	0,4102	2,7396276	1,1236614	19,55	P4HA3	prolyl 4-hydroxylase subunit alpha 3
10984	9,46E-07	6,02E+00	5,09E-07	0,2236	5,0228056	1,12312071	69,14	KCNQ1OT1	KCNQ1 opposite strand/antisense transcript 1
55451	5,50E-02	1,26E+00	4,28E-02	0,5545	2,0252171	1,12306901	11,05	LINC00216	long intergenic non-protein coding RNA 216
84832	1,12E-06	5,95E+00	6,05E-07	0,2249	4,9896388	1,12201002	66,83	ANKRD36B	ankyrin repeat domain 36B pseudogene 1
55247	1,67E-48	4,78E+01	2,74E-49	0,076	14,7577229	1,12116646	1024,26	NEIL3	nei like DNA glycosylase 3
23471	3,84E-14	1,34E+01	1,53E-14	0,1459	7,6848415	1,12110319	5372,94	TRAM1	translocation associated membrane protein 1
23162	4,12E-63	6,24E+01	4,88E-64	0,0663	16,8952403	1,12062919	1114,06	MAPK8IP3	mitogen-activated protein kinase 8 interacting protein 3
729218	2,81E-39	3,86E+01	5,73E-40	0,0847	13,2320921	1,12060715	577,86	LOC729218	uncharacterized LOC729218
84100	1,10E-33	3,30E+01	2,54E-34	0,0917	12,2163577	1,12057396	450,07	ARL6	ADP ribosylation factor like GTPase 6
730094	3,13E-30	2,95E+01	7,91E-31	0,0971	11,5440573	1,12046421	456,15	MOSMO	modulator of smoothened
80162	4,94E-19	1,83E+01	1,69E-19	0,124	9,031822	1,11995351	244,79	PGGHG	protein-glucosylgalactosylhydroxylysine glucosidase
105373835	1,11E-07	6,95E+00	5,71E-08	0,2062	5,4276109	1,11894618	80,16	LOC105373	uncharacterized LOC105373835
2264	9,47E-07	6,02E+00	5,10E-07	0,2227	5,0225411	1,11855849	71,53	FGFR4	fibroblast growth factor receptor 4
84312	1,40E-65	6,49E+01	1,57E-66	0,0649	17,2303963	1,11778432	1454,26	BRMS1L	BRMS1 like transcriptional repressor
26271	1,08E-96	9,60E+01	6,53E-98	0,0532	21,0002418	1,11759503	2086,32	FBXO5	F-box protein 5
1788	1,21E-24	2,39E+01	3,53E-25	0,1077	10,366207	1,11631622	322,35	DNMT3A	DNA methyltransferase 3 alpha
196394	5,18E-13	1,23E+01	2,14E-13	0,1521	7,3396835	1,11617105	153,62	AMN1	antagonist of mitotic exit network 1 homolog
56916	1,46E-77	7,68E+01	1,27E-78	0,0594	18,772203	1,11599698	2922,49	SMARCAD1	SWI/SNF-related, matrix-associated actin-dependent regulator of chromatin, subfamily a, containing DEAD/H box 1
900	6,15E-57	5,62E+01	8,40E-58	0,0696	16,0260758	1,11587657	2523,59	CCNG1	cyclin G1
105379352	3,93E-02	1,41E+00	3,01E-02	0,5145	2,1688243	1,1157856	13,11	LOC105379	uncharacterized LOC105379352
25843	1,11E-56	5,60E+01	1,52E-57	0,0698	15,9891885	1,11537395	1077,68	MOB4	MOB family member 4, phocein
54908	6,60E-147	1,46E+02	1,69E-148	0,043	25,9528477	1,1152234	5975,86	SPDL1	spindle apparatus coiled-coil protein 1
55757	4,07E-49	4,84E+01	6,58E-50	0,0751	14,8537453	1,11521446	907,51	UGGT2	UDP-glucose glycoprotein glucosyltransferase 2
440026	7,42E-66	6,51E+01	8,29E-67	0,0645	17,2673297	1,11433712	1123,01	TMEM41B	transmembrane protein 41B
6741	1,99E-151	1,51E+02	4,83E-153	0,0423	26,352322	1,11411405	8142,3	SSB	small RNA binding exonuclease protection factor La
105377103	5,20E-02	1,28E+00	4,04E-02	0,5434	2,0497736	1,113756	11,05	LOC105377	uncharacterized LOC105377103
23473	3,62E-74	7,34E+01	3,38E-75	0,0607	18,3487616	1,11349159	2279,23	CAPN7	calpain 7
1018	3,64E-07	6,44E+00	1,92E-07	0,2138	5,2072878	1,11342254	74,85	CDK3	cyclin dependent kinase 3
10620	5,05E-23	2,23E+01	1,54E-23	0,1113	9,9988801	1,11322217	313,25	ARID3B	AT-rich interaction domain 3B
54165	1,30E-64	6,39E+01	1,50E-65	0,0651	17,0995527	1,11306897	1704,62	DCUN1D1	defective in cullin neddylation 1 domain containing 1
64901	4,21E-23	2,24E+01	1,28E-23	0,1111	10,0171953	1,1130436	301,17	RANBP17	RAN binding protein 17
105375728	7,12E-13	1,21E+01	2,96E-13	0,1525	7,2962884	1,1128799	150,64	LOC105375	uncharacterized LOC105375728
64167	1,24E-36	3,59E+01	2,66E-37	0,0872	12,7622691	1,11282812	546,38	ERAP2	endoplasmic reticulum aminopeptidase 2
100379251	1,82E-11	1,07E+01	7,91E-12	0,1626	6,840149	1,11242146	129,73	NPPA-AS1	NPPA antisense RNA 1
9568	1,18E-01	9,28E-01	9,65E-02	0,6692	1,6621055	1,11231627	7,94	GABBR2	gamma-aminobutyric acid type B receptor subunit 2
1040	2,58E-07	6,59E+00	1,34E-07	0,211	5,2726886	1,11230696	79,74	CDS1	CDP-diacylglycerol synthase 1
6519	1,51E-21	2,08E+01	4,81E-22	0,1152	9,6522264	1,11174097	316,87	SLC3A1	solute carrier family 3 member 1
9107	2,09E-79	7,87E+01	1,75E-80	0,0585	18,9985995	1,11129707	2026,69	MTMR6	myotubularin related protein 6
90333	4,24E-49	4,84E+01	6,87E-50	0,0748	14,8508102	1,11078404	951,8	ZNF468	zinc finger protein 468
5934	2,31E-69	6,86E+01	2,41E-70	0,0626	17,7312526	1,11031682	1422,64	RBL2	RB transcriptional corepressor like 2
54517	2,85E-87	8,65E+01	2,05E-88	0,0557	19,9344077	1,11026676	1794,88	PUS7	pseudouridine synthase 7
63027	6,49E-08	7,19E+00	3,28E-08	0,2009	5,5256493	1,11010525	84,73	SLC22A23	solute carrier family 22 member 23
155370	1,14E-92	9,19E+01	7,42E-94	0,054	20,5517821	1,11003008	2645,12	SBDSP1	SBDS pseudogene 1
440295	4,26E-10	9,37E+00	1,96E-10	0,1743	6,3646774	1,10925521	114,11	GOLGA6L9	golgin A6 family like 9
6553	4,07E-20	1,94E+01	1,35E-20	0,1192	9,3044667	1,10905184	256,94	SLC9A5	solute carrier family 9 member A5
729096	1,58E-07	6,80E+00	8,17E-08	0,2068	5,3632682	1,10903362	77,9	BMS1P4	BMS1 pseudogene 4
79624	1,47E-58	5,78E+01	1,94E-59	0,0682	16,2587651	1,10830052	1244,75	ARMT1	acidic residue methyltransferase 1
284071	7,66E-05	4,12E+00	4,61E-05	0,2719	4,0744012	1,10771715	48,43	MEIOC	meiosis specific with coiled-coil domain
105371228	4,99E-02	1,30E+00	3,87E-02	0,5357	2,0678704	1,10770285	11,59	LINC02804	long intergenic non-protein coding RNA 2804
5366	1,05E-116	1,16E+02	4,42E-118	0,0479	23,1019949	1,10768129	4404,35	PMAIP1	phorbol-12-myristate-13-acetate-induced protein 1
55326	2,42E-66	6,56E+01	2,67E-67	0,0639	17,3325448	1,10755958	2022,3	AGPAT5	1-acylglycerol-3-phosphate O-acyltransferase 5
54822	4,49E-76	7,53E+01	4,04E-77	0,0596	18,5876985	1,10741468	1652,25	TRPM7	transient receptor potential cation channel subfamily M member 7
79839	1,38E-04	3,86E+00	8,45E-05	0,2816	3,9311731	1,10682989	41,53	CCDC102B	coiled-coil domain containing 102B
284254	8,08E-03	2,09E+00	5,74E-03	0,4007	2,7622306	1,10675044	22,77	DYNAP	dynactin associated protein
653390	3,08E-06	5,51E+00	1,70E-06	0,2313	4,7858651	1,10674948	63,08	RRN3P2	RRN3 pseudogene 2
596	1,59E-36	3,58E+01	3,42E-37	0,0868	12,7426956	1,10663148	567,76	BCL2	BCL2 apoptosis regulator
220930	8,27E-15	1,41E+01	3,23E-15	0,1404	7,8818028	1,10655707	182,03	ZEB1-AS1	ZEB1 antisense RNA 1
144453	6,34E-07	6,20E+00	3,38E-07	0,2169	5,1008848	1,10652588	70,69	BEST3	bestrophin 3

81611	5,49E-94	9,33E+01	3,49E-95	0,0535	20,6996441	1,10646531	9837,25	ANP32E	acidic nuclear phosphoprotein 32 family member E
79598	1,26E-71	7,09E+01	1,24E-72	0,0614	18,0251412	1,10585828	1634,46	CEP97	centrosomal protein 97
26002	1,03E-15	1,50E+01	3,92E-16	0,1358	8,1410242	1,10531846	194,26	MOXD1	monooxygenase DBH like 1
51764	1,30E-02	1,89E+00	9,44E-03	0,4257	2,5958695	1,10496797	18,77	GNG13	G protein subunit gamma 13
256356	6,97E-33	3,22E+01	1,65E-33	0,0915	12,0634062	1,10434656	483,88	GK5	glycerol kinase 5
101927365	2,99E-08	7,52E+00	1,49E-08	0,1949	5,6628863	1,10392506	98,65	PNISR-AS1	PNISR antisense RNA 1
105372579	5,32E-03	2,27E+00	3,71E-03	0,3801	2,9015687	1,10276821	23,25	LOC105372	uncharacterized LOC105372579
105377864	3,98E-02	1,40E+00	3,05E-02	0,5093	2,1637495	1,10205008	12,95	LOC105377	uncharacterized LOC105377864
9729	2,59E-13	1,26E+01	1,06E-13	0,1482	7,4337291	1,10160632	161,38	KIAA0408	KIAA0408
285672	3,49E-57	5,65E+01	4,75E-58	0,0686	16,0615546	1,10159152	1190,47	SREK1IP1	SREK1 interacting protein 1
107984428	9,16E-10	9,04E+00	4,27E-10	0,1764	6,243698	1,10142995	108,61	LOC107984	uncharacterized LOC107984428
84924	2,69E-31	3,06E+01	6,62E-32	0,0937	11,7554621	1,1013077	446,79	ZNF566	zinc finger protein 566
203228	8,40E-33	3,21E+01	1,99E-33	0,0914	12,0479145	1,10098658	582,72	C9orf72	C9orf72-SMCR8 complex subunit
195814	2,95E-20	1,95E+01	9,74E-21	0,1179	9,3388724	1,10088405	270,3	SDR16C5	short chain dehydrogenase/reductase family 16C member 5
9290	4,58E-02	1,34E+00	3,53E-02	0,523	2,104436	1,10056277	12,39	GPR55	G protein-coupled receptor 55
100289187	1,57E-47	4,68E+01	2,63E-48	0,0753	14,6045017	1,10033484	789,48	TMEM225B	transmembrane protein 225B
152519	9,13E-52	5,10E+01	1,39E-52	0,0721	15,2610338	1,10020894	857,98	NIPAL1	NIPA like domain containing 1
51315	3,56E-68	6,74E+01	3,78E-69	0,0626	17,575719	1,0998427	1328,19	KRCC1	lysine rich coiled-coil 1
158399	4,15E-03	2,38E+00	2,87E-03	0,3688	2,9811056	1,09930668	26,61	ZNF483	zinc finger protein 483
84874	7,80E-64	6,31E+01	9,10E-65	0,0647	16,9939659	1,09873044	1053,59	ZNF514	zinc finger protein 514
55657	2,98E-38	3,75E+01	6,21E-39	0,0842	13,05177	1,09838555	597,09	ZNF692	zinc finger protein 692
106635534	2,13E-59	5,87E+01	2,76E-60	0,067	16,3778012	1,09749086	1396,91	SNORA104	small nucleolar RNA, H/ACA box 104
22852	8,60E-61	6,01E+01	1,08E-61	0,0662	16,5735208	1,09736278	1102,52	ANKRD26	ankyrin repeat domain containing 26
146456	1,44E-04	3,84E+00	8,83E-05	0,2799	3,9205822	1,09731826	44,29	TMED6	transmembrane p24 trafficking protein 6
219790	1,16E-29	2,89E+01	2,96E-30	0,096	11,4300475	1,09726946	526,21	RTKN2	rhotekin 2
58484	3,85E-02	1,41E+00	2,94E-02	0,5034	2,1780307	1,09633441	12,91	NLRC4	NLR family CARD domain containing 4
400508	7,72E-02	1,11E+00	6,13E-02	0,5856	1,8715646	1,09597143	10,16	CRYM-AS1	CRYM antisense RNA 1
220729	6,24E-33	3,22E+01	1,47E-33	0,0908	12,0726127	1,09590871	479,52	SDHAP4	SDHA pseudogene 4
22832	7,71E-21	2,01E+01	2,51E-21	0,1156	9,481506	1,09577616	284,36	CEP162	centrosomal protein 162
105371129	1,02E-03	2,99E+00	6,72E-04	0,3222	3,4008435	1,09572962	36,98	LOC105371	uncharacterized LOC105371129
154007	2,06E-73	7,27E+01	1,95E-74	0,06	18,2532625	1,09559388	1377,71	SNRNP48	small nuclear ribonucleoprotein U11/U12 subunit 48
168850	2,45E-55	5,46E+01	3,48E-56	0,0693	15,793	1,09519217	973,69	ZNF800	zinc finger protein 800
51085	1,31E-02	1,88E+00	9,49E-03	0,422	2,5938129	1,09462962	18,68	MLXIPL	MLX interacting protein like
2123	2,44E-66	6,56E+01	2,69E-67	0,0631	17,3321139	1,0943748	1854,13	EVI2A	ecotropic viral integration site 2A
51166	9,32E-32	3,10E+01	2,26E-32	0,0924	11,8457795	1,09434158	479,08	AADAT	aminoadipate aminotransferase
29765	3,95E-03	2,40E+00	2,72E-03	0,3649	2,9974394	1,09388633	25,81	TMOD4	tropomodulin 4
105376070	1,29E-01	8,89E-01	1,06E-01	0,6766	1,616694	1,09377696	8,16	LOC105376	uncharacterized LOC105376070
728047	2,14E-03	2,67E+00	1,44E-03	0,3433	3,1857378	1,09373332	27,72	GOLGA8O	golgin A8 family member O
105378120	3,76E-04	3,42E+00	2,39E-04	0,2977	3,6741335	1,09372943	37,3	LOC105378	uncharacterized LOC105378120
129642	9,56E-52	5,10E+01	1,46E-52	0,0717	15,2580124	1,09337153	1377,85	MBOAT2	membrane bound O-acyltransferase domain containing 2
105369165	3,09E-02	1,51E+00	2,33E-02	0,4819	2,2682336	1,09311181	14,28	LOC105369	uncharacterized LOC105369165
105373310	7,40E-02	1,13E+00	5,87E-02	0,578	1,8906748	1,09279353	9,68	LOC105373	replaced by ID 112267910
153642	5,15E-35	3,43E+01	1,16E-35	0,0876	12,4651529	1,09254857	508,68	ARSK	arylsulfatase family member K
29966	1,10E-62	6,20E+01	1,32E-63	0,0649	16,8364413	1,09250405	1631,58	STRN3	striatin 3
137886	1,84E-50	4,97E+01	2,89E-51	0,0725	15,061711	1,0924639	884,07	UBXN2B	UBX domain protein 2B
84465	4,19E-09	8,38E+00	2,01E-09	0,1821	5,9970872	1,09182242	103,92	MEGF11	multiple EGF like domains 11
84515	4,13E-115	1,14E+02	1,80E-116	0,0476	22,941301	1,09152208	3515,85	MCM8	minichromosome maintenance 8 homologous recombination repair factor
10725	7,21E-101	1,00E+02	4,03E-102	0,0509	21,4558699	1,0913476	2678,65	NFAT5	nuclear factor of activated T cells 5
6508	4,62E-08	7,34E+00	2,32E-08	0,1952	5,5862004	1,09056209	90,87	SLC4A3	solute carrier family 4 member 3
100506658	5,15E-39	3,83E+01	1,05E-39	0,0827	13,1861602	1,0903355	601,67	OCLN	occludin
26046	2,17E-58	5,77E+01	2,87E-59	0,0672	16,2347053	1,0902912	1882,59	LTN1	listerin E3 ubiquitin protein ligase 1
4781	3,58E-52	5,14E+01	5,41E-53	0,0711	15,3224476	1,09015397	910,27	NFIB	nuclear factor I B
51430	4,43E-119	1,18E+02	1,79E-120	0,0467	23,3387515	1,0894975	4051,54	SUCO	SUN domain containing ossification factor
51029	1,71E-87	8,68E+01	1,22E-88	0,0546	19,9602352	1,08905328	3288,49	DESI2	desumoylating isopeptidase 2
57209	1,09E-43	4,30E+01	2,02E-44	0,0779	13,9816906	1,08890881	683,11	ZNF248	zinc finger protein 248
105372269	5,32E-02	1,27E+00	4,14E-02	0,5336	2,0394387	1,08828105	12,23	LOC105372	uncharacterized LOC105372269
101927157	6,93E-03	2,16E+00	4,89E-03	0,3866	2,8139336	1,08796029	21,86	LOC101927	uncharacterized LOC101927157
1292	2,13E-73	7,27E+01	2,02E-74	0,0596	18,2514181	1,08772479	2064,68	COL6A2	collagen type VI alpha 2 chain
6328	1,14E-01	9,43E-01	9,30E-02	0,6466	1,6797477	1,08617013	7,71	SCN3A	sodium voltage-gated channel alpha subunit 3
54819	1,47E-44	4,38E+01	2,66E-45	0,0769	14,1250728	1,08594635	743,42	ZCCHC10	zinc finger CCHC-type containing 10
105369364	3,11E-03	2,51E+00	2,12E-03	0,3533	3,0725204	1,08552256	27,55	LINC02701	long intergenic non-protein coding RNA 2701
101954278	5,82E-02	1,24E+00	4,55E-02	0,5427	1,9998177	1,08535008	11,61	RNU6-8	RNA, U6 small nuclear 8
100422885	1,20E-08	7,92E+00	5,86E-09	0,1864	5,8206972	1,08505072	865,55	MIR1244-2	microRNA 1244-2
55285	1,90E-67	6,67E+01	2,05E-68	0,0621	17,4794631	1,08469065	1243,65	RBM41	RNA binding motif protein 41
132241	4,82E-07	6,32E+00	2,55E-07	0,2104	5,1537716	1,08429057	77,52	RPL32P3	ribosomal protein L32 pseudogene 3
64282	2,05E-42	4,17E+01	3,90E-43	0,0787	13,7693061	1,08420007	669,09	TENT4B	terminal nucleotidyltransferase 4B
200894	7,22E-57	5,61E+01	9,89E-58	0,0677	16,015968	1,08363537	1393,76	ARL13B	ADP ribosylation factor like GTPase 13B
414764	6,22E-02	1,21E+00	4,88E-02	0,5499	1,9700878	1,08326209	10,88	HCG23	HLA complex group 23
51203	1,18E-117	1,17E+02	4,89E-119	0,0467	23,1969552	1,08306206	11536,5	NUSAP1	nucleolar and spindle associated protein 1
201725	6,54E-79	7,82E+01	5,53E-80	0,0572	18,9381869	1,08301787	1819,78	C4orf46	chromosome 4 open reading frame 46
81856	6,15E-33	3,22E+01	1,45E-33	0,0897	12,0738581	1,08298059	592,37	ZNF611	zinc finger protein 611
3156	3,65E-95	9,44E+01	2,27E-96	0,052	20,8309235	1,0825165	2869,35	HMGCR	3-hydroxy-3-methylglutaryl-CoA reductase
105376603	3,49E-11	1,05E+01	1,54E-11	0,1605	6,7442028	1,08228342	160,45	LINC02742	long intergenic non-protein coding RNA 2742
54622	1,55E-21	2,08E+01	4,93E-22	0,1121	9,6497898	1,08200033	297,41	ARL15	ADP ribosylation factor like GTPase 15
2086	2,02E-03	2,69E+00	1,36E-03	0,3378	3,2027418	1,08189813	32,91	ERV3-1	endogenous retrovirus group 3 member 1, envelope
23426	7,87E-12	1,11E+01	3,38E-12	0,1553	6,9608827	1,08079661	149,75	GRIP1	glutamate receptor interacting protein 1
120863	3,23E-10	9,49E+00	1,48E-10	0,1686	6,4077134	1,08059005	121,53	DEPDC4	DEP domain containing 4
54553	2,59E-09	8,59E+00	1,23E-09	0,1778	6,0761901	1,08017209	115,36	MIR4453HG	MIR4453 host gene
91661	2,15E-26	2,57E+01	6,00E-27	0,1005	10,7489201	1,07996498	455,15	ZNF765	zinc finger protein 765
3574	1,19E-07	6,92E+00	6,09E-08	0,1994	5,4161195	1,07986858	83,25	IL7	interleukin 7
222194	2,95E-34	3,35E+01	6,74E-35	0,0876	12,3238647	1,0798082	693,19	RSBN1L	round spermatid basic protein 1 like
9972	1,36E-158	1,58E+02	2,97E-160	0,04	26,9742223	1,07969024	10119,67	NUP153	nucleoporin 153
79684	2,62E-64	6,36E+01	3,03E-65	0,0633	17,0584425	1,07917455	1251,9	MSANTD2	Myb/SANT DNA binding domain containing 2
9920	1,01E-08	8,00E+00	4,94E-09	0,1843	5,8492886	1,07807986	101,96	KBTBD11	kelch repeat and BTB domain containing 11
84938	9,89E-36	3,50E+01	2,19E-36	0,0856	12,597296	1,07785451	672,03	ATG4C	autophagy related 4C cysteine peptidase
105372105	5,02E-02	1,30E+00	3,89E-02	0,5219	2,0651496	1,07783116	12,79	LOC105372	uncharacterized LOC105372105
147923	9,71E-22	2,10E+01	3,07E-22	0,1111	9,6982574	1,07782919	291,62	ZNF420	zinc finger protein 420
202915	6,01E-22	2,12E+01	1,89E-22	0,1106	9,7476884	1,07781518	309,42	TMEM184A	transmembrane protein 184A
90355	3,03E-46	4,55E+01	5,25E-47	0,0748	14,3990052	1,07772926	947,71	MACIR	macrophage immunometabolism regulator
79092	9,97E-03	2,00E+00	7,15E-03	0,4007	2,6896413	1,07768192	22,53	CARD14	caspase recruitment domain family member 14
389831	2,60E-13	1,26E+01	1,06E-13	0,145	7,4331876	1,07758339	167,08	LOC389831	uncharacterized LOC389831
125893	2,14E-17	1,67E+01	7,68E-18	0,1252	8,6043256	1,07740293	249,99	ZNF816	zinc finger protein 816
11320	5,36E-27	2,63E+01	1,47E-27	0,099	10,8776429	1,07693272	389,76	MGAT4A	alpha-1,3-mannosyl-glycoprotein 4-beta-N-acetylglucosaminyltransferase A
5925	2,43E-106	1,06E+02	1,22E-107	0,0489	22,0390746	1,07686676	4138,63	RB1	RB transcriptional corepressor 1
5988	1,88E-02	1,73E+00	1,38E-02	0,4375	2,4616317	1,07685917	17,22	RFPL1	ret finger protein like 1
25978	3,97E-63	6,24E+01	4,69E-64	0,0637	16,8975022	1,07674911	2186,59	CHMP2B	charged multivesicular body protein 2B
54813	2,35E-29	2,86E+01	6,07E-30	0,0947	11,3675686	1,07657908	440,94	KLHL28	kelch like family member 28
55740	6,58E-84	8,32E+01	5,04E-85	0,0551	19,5397625	1,07606427	2180,01	ENAH	ENAH actin regulator
79836	5,15E-58	5,73E+01	6,87E-59	0,0665	16,1809501	1,07550145	1025,29	LONRF3	LON peptidase N-terminal domain and ring finger 3
51377	1,55E-68	6,78E+01	1,63E-69	0,061	17,6232853	1,07548505	3263	UCHL5	ubiquitin C-terminal hydrolase L5
7627	1,87E-50	4,97E+01	2,94E-51	0,0714	15,0606317	1,07491903	848,02	ZNF75A	zinc finger protein 75a
102723360	2,40E-31	3,06E+01	5,90E-32	0,0913	11,7652025	1,07466293	489,34	LOC102723	uncharacterized LOC102723360
144608	3,03E-06	5,52E+00	1,67E-06	0,2244	4,7893361	1,07465657	65,82	C12orf60	chromosome 12 open reading frame 60
8847	3,64E-23	2,24E+01	1,11E-23	0,1071	10,0315909	1,07429665	324,57	DLEU2	deleted in lymphocytic leukemia 2
28779	5,91E-03	2,23E+00	4,15E-03	0,3747	2,8668082	1,07423521	23,52	IGLV5-52	immunoglobulin lambda variable 5-52
6726	2,51E-107	1,07E+02	1,24E-108	0,0485	22,1421498	1,07405152	6574,83	SRP9	signal recognition particle 9
253827	1,60E-102	1,02E+02	8,67E-104	0,0496	21,6336437	1,07329932	2491,47	MSRB3	methionine sulfoxide reductase B3
401320	8,50E-08	7,07E+00	4,33E-08	0,1959	5,4769023	1,07281567	88,03	GARS1-DT	GARS1 divergent transcript
23255	3,58E-119	1,18E+02	1,45E-120	0,0459	23,3479176	1,07264609	3545,54	MTCL1	microtubule crosslinking factor 1
728741	5,01E-04	3,30E+00	3,21E-04	0,2981	3,5976152	1,07259072	37,05	NPIPB6	nuclear pore complex interacting protein family member B6
2138	1,26E-01	9,00E-01	1,03E-01	0,6586	1,62848	1,07254067	7,73	EYA1	EYA transcriptional coactivator and phosphatase 1
1974	4,44E-121	1,20E+02	1,73E-122	0,0456	23,536509	1,07253439	20067,51	EIF4A2	eukaryotic translation initiation factor 4A2
5908	1,22E-60	5,99E+01	1,54E-61	0,0648	16,5524093	1,0721408	5252,57	RAP1B	RAP1B, member of RAS oncogene family
6936	3,79E-71	7,04E+01	3,78E-72	0,0597	17,9632106	1,07198438	1844,34	GCFC2	GC-rich sequence DNA-binding factor 2
3931	1,03E-11	1,10E+01	4,45E-12	0,1548	6,9220983	1,07187555	148,76	LCAT	lecithin-cholesterol acyltransferase
22875	3,83E-68	6,74E+01	4,07E-69	0,061	17,5715132	1,07170424	1544,24	ENPP4	ectonucleotide pyrophosphatase/phosphodiesterase 4
3422	5,75E-86	8,52E+01	4,23E-87	0,0541	19,7823053	1,07120409	2041,55	IDI1	isopentenyl-diphosphate delta isomerase 1
441155	1,38E-15	1,49E+01	5,26E-16	0,1322	8,1054396	1,07115562	212,67	ZC3H11C	zinc finger CCCH-type containing 11C
114805	2,13E-34	3,37E+01	4,86E-35	0,0867	12,3502278	1,07102959	528,07	GALNT13	polypeptide N-acetylgalactosaminyltransferase 13
107984026	2,48E-16	1,56E+01	9,21E-17	0,1288	8,3145838	1,07088257	211,83	LOC107984	replaced by ID 728005

153364	2,49E-34	3,36E+01	5,67E-35	0,0868	12,3377489	1,07082086	590,62	MBLAC2	metallo-beta-lactamase domain containing 2
107986084	5,53E-04	3,26E+00	3,56E-04	0,2996	3,5707862	1,06967607	39,11	LOC107986(	replaced by ID 7375
79609	2,68E-20	1,96E+01	8,84E-21	0,1144	9,3490932	1,06939957	315,06	VCPKMT	valosin containing protein lysine methyltransferase
84460	1,23E-09	8,91E+00	5,78E-10	0,1726	6,1963399	1,06937522	112,27	ZMAT1	zinc finger matrin-type 1
107986948	8,63E-02	1,06E+00	6,90E-02	0,5875	1,8186128	1,06840978	9,61	LOC107986948	
348174	1,08E-01	9,67E-01	8,76E-02	0,6253	1,7083469	1,06828756	8,33	CLEC18A	C-type lectin domain family 18 member A
6474	3,04E-30	2,95E+01	7,68E-31	0,0925	11,5465623	1,06822979	519,31	SHOX2	short stature homeobox 2
102465668	3,29E-02	1,48E+00	2,49E-02	0,4762	2,2425737	1,06795559	15,47	MIR7111	microRNA 7111
339745	1,90E-51	5,07E+01	2,90E-52	0,0701	15,212956	1,06705055	1193,79	SPOPL	speckle type BTB/POZ protein like
10125	5,39E-02	1,27E+00	4,19E-02	0,5242	2,0341786	1,06634745	12,69	RASGRP1	RAS guanyl releasing protein 1
79642	8,95E-86	8,50E+01	6,60E-87	0,054	19,7598601	1,066339	2647,35	ARSJ	arylsulfatase family member J
80310	9,72E-26	2,50E+01	2,76E-26	0,1005	10,6070359	1,06595035	376,34	PDGFD	platelet derived growth factor D
57161	3,33E-17	1,65E+01	1,20E-17	0,1245	8,5525677	1,06494911	229,94	PELI2	pellino E3 ubiquitin protein ligase family member 2
100287616	3,54E-46	4,55E+01	6,15E-47	0,074	14,3880067	1,06468366	904,83	LOXL1-AS1	LOXL1 antisense RNA 1
84955	7,90E-111	1,10E+02	3,65E-112	0,0473	22,5056484	1,06465214	6261,62	NUDCD1	NudC domain containing 1
6670	3,81E-108	1,07E+02	1,85E-109	0,0479	22,2278642	1,06426844	4242,75	SP3	Sp3 transcription factor
55728	1,17E-48	4,79E+01	1,91E-49	0,072	14,7821349	1,06408996	891,16	N4BP2	NEDD4 binding protein 2
105373296	1,17E-01	9,32E-01	9,53E-02	0,6375	1,6681658	1,06338804	8,33	LOC105373(	uncharacterized LOC105373296
55207	2,05E-69	6,87E+01	2,12E-70	0,0599	17,7382785	1,06335824	3223,87	ARL8B	ADP ribosylation factor like GTPase 8B
28638	7,30E-03	2,14E+00	5,17E-03	0,3801	2,7963122	1,0629096	22,88	TRBC2	T cell receptor beta constant 2
346157	1,30E-21	2,09E+01	4,13E-22	0,1099	9,6677506	1,06259016	399,73	ZNF391	zinc finger protein 391
284600	8,48E-02	1,07E+00	6,77E-02	0,5814	1,8268863	1,06223074	9,54	LOC284600	uncharacterized LOC284600
6867	1,88E-134	1,34E+02	5,68E-136	0,0428	24,8183915	1,06206872	8651,85	TACC1	transforming acidic coiled-coil containing protein 1
84451	8,12E-31	3,01E+01	2,02E-31	0,0911	11,660818	1,06181515	470,38	MAP3K21	mitogen-activated protein kinase kinase kinase 21
81493	3,10E-38	3,75E+01	6,46E-39	0,0813	13,0487172	1,06142596	1024,79	SYNC	syncoilin, intermediate filament protein
3187	2,95E-111	1,11E+02	1,35E-112	0,0471	22,5497205	1,06099609	24363,16	HNRNPH1	heterogeneous nuclear ribonucleoprotein H1
5801	1,13E-05	4,95E+00	6,48E-06	0,2352	4,510133	1,06074314	63,14	PTPRR	protein tyrosine phosphatase receptor type R
57563	4,26E-70	6,94E+01	4,36E-71	0,0595	17,8270874	1,0600301	1407,56	KLHL8	kelch like family member 8
400986	3,33E-21	2,05E+01	1,07E-21	0,1107	9,5699157	1,05978102	299,57	ANKRD36C	ankyrin repeat domain 36C
91862	1,30E-01	8,86E-01	1,06E-01	0,6558	1,6149339	1,05910651	7,59	MARVELD3	MARVEL domain containing 3
201562	5,68E-61	6,02E+01	7,13E-62	0,0638	16,5986567	1,05888845	1713,11	HACD2	3-hydroxyacyl-CoA dehydratase 2
102724951	2,86E-33	3,25E+01	6,71E-34	0,0872	12,1372293	1,05862515	580,87	LOC102724(	uncharacterized LOC102724951
1434	2,07E-20	1,97E+01	6,79E-21	0,1129	9,3769988	1,05824816	25261,28	CSE1L	chromosome segregation 1 like
114821	4,00E-12	1,14E+01	1,70E-12	0,1499	7,0568961	1,05815207	159,21	SCAND3	SCAN domain containing 3
10082	3,79E-27	2,64E+01	1,04E-27	0,097	10,9095637	1,05784814	465,38	GPC6	glypican 6
9069	3,30E-50	4,95E+01	5,21E-51	0,0704	15,0228068	1,05772174	2391,24	CLDN12	claudin 12
105375038	1,36E-01	8,66E-01	1,12E-01	0,6652	1,5899995	1,05770559	7,6	LOC105375(	uncharacterized LOC105375038
339318	1,69E-27	2,68E+01	4,58E-28	0,0963	10,9837044	1,05763095	447,53	ZNF181	zinc finger protein 181
339327	4,71E-11	1,03E+01	2,08E-11	0,1578	6,6999762	1,05715998	143,65	ZNF546	zinc finger protein 546
55521	4,36E-27	2,64E+01	1,19E-27	0,097	10,8967292	1,0569114	497,67	TRIM36	tripartite motif containing 36
329	1,37E-77	7,69E+01	1,19E-78	0,0563	18,775719	1,05674702	7589,66	BIRC2	baculoviral IAP repeat containing 2
100133315	2,22E-03	2,65E+00	1,50E-03	0,3328	3,1744556	1,05649886	30,55	XNDC1N	XRCC1 N-terminal domain containing 1, N-terminal like
154865	2,53E-02	1,60E+00	1,89E-02	0,4499	2,347682	1,05631069	17,86	IQUB	IQ motif and ubiquitin domain containing
57231	3,14E-09	8,50E+00	1,50E-09	0,1747	6,0442473	1,05607731	2623,26	SNX14	sorting nexin 14
126017	9,89E-18	1,70E+01	3,52E-18	0,1215	8,6932955	1,05587693	241,61	ZNF813	zinc finger protein 813
7571	3,14E-51	5,05E+01	4,83E-52	0,0695	15,1796041	1,05491334	917,74	ZNF23	zinc finger protein 23
85028	9,62E-30	2,90E+01	2,46E-30	0,0922	11,4461847	1,05478986	559,04	SNHG12	small nucleolar RNA host gene 12
6093	6,89E-136	1,35E+02	2,05E-137	0,0423	24,9516608	1,05456884	6401,54	ROCK1	Rho associated coiled-coil containing protein kinase 1
6502	2,02E-73	7,27E+01	1,91E-74	0,0578	18,2542299	1,0542259	1566,38	SKP2	S-phase kinase associated protein 2
107986305	7,03E-02	1,15E+00	5,55E-02	0,5505	1,9146719	1,05400074	10,83	LOC107986(	uncharacterized LOC107986305
165186	4,96E-08	7,30E+00	2,50E-08	0,189	5,5735487	1,05320988	95,14	TOGARAM2	TOG array regulator of axonemal microtubules 2
112268070	7,35E-04	3,13E+00	4,78E-04	0,3015	3,4930462	1,05320069	37,26	LOC112268(	uncharacterized LOC112268070
57121	1,93E-03	2,71E+00	1,30E-03	0,3273	3,2165258	1,05284382	31,48	LPAR5	lysophosphatidic acid receptor 5
54841	1,64E-43	4,28E+01	3,05E-44	0,0754	13,9521342	1,05247588	718,33	BIVM	basic, immunoglobulin-like variable motif containing
159371	4,70E-32	3,13E+01	1,13E-32	0,0884	11,9035974	1,05197209	512,74	SLC35G1	solute carrier family 35 member G1
1060	1,12E-64	6,40E+01	1,28E-65	0,0615	17,1086896	1,05158698	1304,69	CENPC	centromere protein C
8520	1,31E-09	8,88E+00	6,15E-10	0,1699	6,1864627	1,05100428	4123,81	HAT1	histone acetyltransferase 1
57546	1,53E-66	6,58E+01	1,68E-67	0,0605	17,3591744	1,05096447	1330,4	PDP2	pyruvate dehydrogenase phosphatase catalytic subunit 2
6458	1,52E-01	8,18E-01	1,26E-01	0,6866	1,5304238	1,05076929	7,01	SH3GL1P1	SH3 domain containing GRB2 like 1, endophilin A2 pseudogene 1
152926	2,27E-43	4,26E+01	4,23E-44	0,0754	13,9289507	1,05006645	758,86	PPM1K	protein phosphatase, Mg2+/Mn2+ dependent 1K
101928895	3,95E-07	6,40E+00	2,08E-07	0,2021	5,1919411	1,04947736	81,36	LINC01786	long intergenic non-protein coding RNA 1786
23433	4,74E-41	4,03E+01	9,26E-42	0,0775	13,5385354	1,04930236	1121,55	RHOQ	ras homolog family member Q
1385	2,53E-90	8,96E+01	1,71E-91	0,0517	20,2858922	1,04896549	2509,36	CREB1	cAMP responsive element binding protein 1
102724219	7,34E-37	3,61E+01	1,57E-37	0,0819	12,8031608	1,04891802	628,42	LOC102724(	uncharacterized LOC102724219
57700	1,43E-50	4,98E+01	2,24E-51	0,0696	15,0787293	1,04883099	1097,24	FHIP2A	FHF complex subunit HOOK interacting protein 2A
79884	1,61E-47	4,68E+01	2,70E-48	0,0718	14,6026025	1,04877782	935,82	MAP9	microtubule associated protein 9
101928063	1,66E-10	9,78E+00	7,50E-11	0,161	6,5102259	1,04842569	134,7	ZNF230-DT	ZNF230 divergent transcript
100137049	1,07E-03	2,97E+00	7,00E-04	0,3093	3,3894375	1,04833136	35,35	PLA2G4B	phospholipase A2 group IVB
664701	5,50E-17	1,63E+01	2,00E-17	0,1234	8,4936711	1,04827921	236,05	ZNF826P	zinc finger protein 826, pseudogene
253260	1,46E-80	7,98E+01	1,19E-81	0,0548	19,1390656	1,04811853	2478,69	RICTOR	RPTOR independent companion of MTOR complex 2
2770	5,42E-37	3,63E+01	1,16E-37	0,0817	12,8269247	1,04810525	687,75	GNAI1	G protein subunit alpha i1
79800	3,49E-11	1,05E+01	1,54E-11	0,1554	6,7443831	1,04778241	141,21	CARF	calcium responsive transcription factor
90624	3,85E-48	4,74E+01	6,38E-49	0,0713	14,7006852	1,04757308	886,49	LYRM7	LYR motif containing 7
5922	3,51E-55	5,45E+01	5,01E-56	0,0664	15,7699754	1,04674277	1121,73	RASA2	RAS p21 protein activator 2
1294	3,45E-51	5,05E+01	5,31E-52	0,069	15,1733552	1,04670716	1294,74	COL7A1	collagen type VII alpha 1 chain
105371967	1,56E-01	8,07E-01	1,29E-01	0,6895	1,5174995	1,04627779	6,97	LOC105371(	uncharacterized LOC105371967
5318	2,09E-92	9,17E+01	1,38E-93	0,051	20,5217864	1,04605004	2172,05	PKP2	plakophilin 2
9443	2,86E-37	3,65E+01	6,08E-38	0,0811	12,8767932	1,04459033	633,47	MED7	mediator complex subunit 7
85301	8,71E-33	3,21E+01	2,06E-33	0,0867	12,0448522	1,04403803	517,86	COL27A1	collagen type XXVII alpha 1 chain
105379549	9,85E-02	1,01E+00	7,94E-02	0,5951	1,7540198	1,04390485	9,49	LOC105379(	uncharacterized LOC105379549
221710	1,54E-99	9,88E+01	8,83E-101	0,049	21,311779	1,04375781	2618,36	SMIM13	small integral membrane protein 13
102724843	4,74E-43	4,23E+01	8,87E-44	0,0752	13,8759016	1,04359029	863,43	LOC102724(	uncharacterized LOC102724843
60592	4,48E-71	7,03E+01	4,49E-72	0,0581	17,9537528	1,04334227	2414,45	SCOC	short coiled-coil protein
55713	6,89E-03	2,16E+00	4,87E-03	0,3705	2,8158232	1,04331224	25,39	ZNF334	zinc finger protein 334
101927978	1,39E-02	1,86E+00	1,01E-02	0,4056	2,5723	1,04330967	22,03	ZFHX3-AS1	ZFHX3 antisense RNA 1
8620	1,08E-01	9,67E-01	8,74E-02	0,6104	1,7090273	1,04312947	8,79	NPFF	neuropeptide FF-amide peptide precursor
101927604	1,00E-01	1,00E+00	8,07E-02	0,597	1,7464986	1,04264461	9,51	LOC101927(	uncharacterized LOC101927604
106635532	2,97E-33	3,25E+01	6,97E-34	0,0859	12,1340591	1,04246877	674,04	SNORA100	small nucleolar RNA, H/ACA box 100
63979	8,92E-76	7,50E+01	8,07E-77	0,0561	18,550552	1,04152035	2009,57	FIGNL1	fidgetin like 1
54540	2,35E-44	4,36E+01	4,28E-45	0,0739	14,0916419	1,04134154	935,73	FAM193B	family with sequence similarity 193 member B
29957	2,24E-92	9,16E+01	1,48E-93	0,0507	20,518372	1,04125328	6530,16	SLC25A24	solute carrier family 25 member 24
440993	1,40E-05	4,85E+00	8,06E-06	0,2332	4,463661	1,04092081	61,5	MIR570HG	MIR570 host gene
105373754	1,08E-04	3,97E+00	6,58E-05	0,2608	3,9909567	1,04090682	54,31	LOC105373(	uncharacterized LOC105373754
339166	5,02E-04	3,30E+00	3,22E-04	0,2891	3,596882	1,03991667	40,21	LOC339166	uncharacterized LOC339166
90649	8,12E-36	3,51E+01	1,79E-36	0,0824	12,6130009	1,0396142	576,78	ZNF486	zinc finger protein 486
7572	1,30E-91	9,09E+01	8,59E-93	0,0509	20,4325601	1,03938645	3609,31	ZNF24	zinc finger protein 24
7733	1,33E-38	3,79E+01	2,75E-39	0,0793	13,1135972	1,03933066	696,92	ZNF180	zinc finger protein 180
23431	4,85E-48	4,73E+01	8,04E-49	0,0707	14,6850115	1,03888926	892,95	AP4E1	adaptor related protein complex 4 subunit epsilon 1
84671	2,08E-70	6,97E+01	2,11E-71	0,0581	17,8675827	1,0378158	1507,15	ZNF347	zinc finger protein 347
23230	9,35E-85	8,40E+01	7,03E-86	0,0528	19,6400752	1,03780969	2607,64	VPS13A	vacuolar protein sorting 13 homolog A
163049	1,43E-89	8,88E+01	9,82E-91	0,0514	20,1998348	1,03778962	2079,36	ZNF791	zinc finger protein 791
7582	8,93E-39	3,80E+01	1,84E-39	0,0789	13,1441819	1,0368443	682,34	ZNF33B	zinc finger protein 33B
25788	7,81E-47	4,61E+01	1,33E-47	0,0715	14,4933981	1,03637197	820,66	RAD54B	RAD54 homolog B
646851	5,03E-03	2,30E+00	3,51E-03	0,3548	2,9195038	1,03591708	27,64	FAM227A	family with sequence similarity 227 member A
126859	4,78E-02	1,32E+00	3,69E-02	0,4964	2,0864877	1,03567663	13,19	AXDND1	axonemal dynein light chain domain containing 1
55120	2,65E-42	4,16E+01	5,05E-43	0,0753	13,7506397	1,03565646	859,59	FANCL	FA complementation group L
85459	3,53E-76	7,55E+01	3,17E-77	0,0556	18,6007613	1,03490295	2065,8	CEP295	centrosomal protein 295
4194	4,81E-38	3,73E+01	1,01E-38	0,0795	13,0150141	1,03476172	799,89	MDM4	MDM4 regulator of p53
651746	1,86E-42	4,17E+01	3,52E-43	0,0751	13,7767024	1,03410255	980,52	ANKRD33B	ankyrin repeat domain 33B
4753	1,76E-04	3,75E+00	1,09E-04	0,2672	3,8699191	1,034011	50,11	NELL2	neural EGFL like 2
1906	6,61E-62	6,12E+01	8,08E-63	0,0618	16,7288706	1,03391803	1357,55	EDN1	endothelin 1
107985381	1,70E-07	6,77E+00	8,83E-08	0,1933	5,3493581	1,03383017	99,25	LOC107985381	
574042	9,94E-04	3,00E+00	6,52E-04	0,3031	3,4090757	1,03341562	35,12	SNORA10	small nucleolar RNA, H/ACA box 10
730198	1,02E-01	9,91E-01	8,27E-02	0,5956	1,7351546	1,03339127	9,4	MEIS1-AS3	MEIS1 antisense RNA 3
84698	4,17E-04	3,38E+00	2,66E-04	0,2834	3,6467312	1,0333583	42,93	CAPS2	calcyphosine 2
79866	1,81E-52	5,17E+01	2,71E-53	0,0672	15,3672861	1,03330952	1005,83	BORA	BORA aurora kinase A activator
9941	2,66E-40	3,96E+01	5,29E-41	0,077	13,4099444	1,03320203	670,69	EXOG	exo/endonuclease G
101927402	5,80E-02	1,24E+00	4,53E-02	0,516	2,0015379	1,0328254	12,5	AFTPH-DT	AFTPH divergent transcript
55023	7,84E-74	7,31E+01	7,36E-75	0,0564	18,3063705	1,03205145	2517,91	PHIP	pleckstrin homology domain interacting protein
7518	9,10E-43	4,20E+01	1,71E-43	0,0746	13,8285321	1,03172886	906,79	XRCC4	X-ray repair cross complementing 4

9859	5,98E-124	1,23E+02	2,23E-125	0,0433	23,8168957	1,03155711	7692,86	CEP170	centrosomal protein 170
105369299	8,47E-02	1,07E+00	6,76E-02	0,5642	1,8278043	1,03129541	10,55	LOC105369	uncharacterized LOC105369299
100852410	7,87E-02	1,10E+00	6,25E-02	0,5529	1,8625762	1,0298541	10,61	ZRANB2-DT	ZRANB2 divergent transcript
107984958	3,58E-02	1,45E+00	2,72E-02	0,4664	2,2082123	1,02981067	15,09	DHCR24-DT	DHCR24 divergent transcript
65008	9,36E-53	5,20E+01	1,40E-53	0,0668	15,4101615	1,02946801	1567,78	MRPL1	mitochondrial ribosomal protein L1
25842	1,59E-58	5,78E+01	2,10E-59	0,0633	16,25378	1,0294546	1152,39	ASF1A	anti-silencing function 1A histone chaperone
2124	5,09E-97	9,63E+01	3,06E-98	0,0489	21,0362559	1,02941872	2993,24	EVI2B	ecotropic viral integration site 2B
10198	1,31E-108	1,08E+02	6,30E-110	0,0462	22,2761417	1,02900322	3722,58	MPHOSPH9	M-phase phosphoprotein 9
101928419	7,02E-02	1,15E+00	5,55E-02	0,5372	1,9149816	1,02872845	11,3	LOC101928	uncharacterized LOC101928419
6877	1,96E-68	6,77E+01	2,07E-69	0,0584	17,6097551	1,02868531	1515,12	TAF5	TATA-box binding protein associated factor 5
26272	1,04E-46	4,60E+01	1,78E-47	0,071	14,4737291	1,02831437	1106,9	FBXO4	F-box protein 4
57786	4,47E-39	3,83E+01	9,14E-40	0,0779	13,1969296	1,02811997	726,44	RBAK	RB associated KRAB zinc finger
2820	1,30E-84	8,39E+01	9,76E-86	0,0524	19,6234088	1,02789453	2318,72	GPD2	glycerol-3-phosphate dehydrogenase 2
222236	2,68E-30	2,96E+01	6,77E-31	0,0889	11,5574914	1,02784701	556,98	NAPEPLD	N-acyl phosphatidylethanolamine phospholipase D
79582	7,18E-24	2,31E+01	2,15E-24	0,1008	10,1922452	1,02728344	389,02	SPAG16	sperm associated antigen 16
9530	4,86E-44	4,33E+01	8,91E-45	0,0732	14,0396674	1,02727476	851,12	BAG4	BAG cochaperone 4
9444	1,36E-99	9,89E+01	7,77E-101	0,0482	21,3177375	1,02695454	7102,07	QKI	QKI, KH domain containing RNA binding
677770	8,45E-10	9,07E+00	3,93E-10	0,1641	6,2567078	1,02657988	133,93	SCARNA22	small Cajal body-specific RNA 22
401207	1,42E-11	1,08E+01	6,16E-12	0,1493	6,8759103	1,0265045	158,83	C5orf63	chromosome 5 open reading frame 63
107985780	1,02E-02	1,99E+00	7,34E-03	0,3828	2,6810044	1,02640004	22,36	LOC107985	780
105376580	1,50E-01	8,24E-01	1,24E-01	0,6668	1,5392203	1,02629224	7,41	CSRP3-AS1	CSRP3 and E2F8 antisense RNA 1
373	3,21E-38	3,75E+01	6,68E-39	0,0786	13,0461837	1,0259601	813,91	TRIM23	tripartite motif containing 23
89839	2,48E-31	3,06E+01	6,10E-32	0,0872	11,7623973	1,02568912	621,8	ARHGAP11E	Rho GTPase activating protein 11B
112267942	3,18E-02	1,50E+00	2,40E-02	0,4543	2,2571345	1,02531478	16,33	LOC112267	uncharacterized LOC112267942
653653	3,12E-06	5,51E+00	1,72E-06	0,2143	4,7835554	1,02502305	86,25	LOC653653	adaptor related protein complex 1 subunit sigma 2 pseudogene
9603	1,26E-114	1,14E+02	5,52E-116	0,0448	22,8924699	1,02493854	9437,27	NFE2L3	NFE2 like bZIP transcription factor 3
107986127	2,10E-02	1,68E+00	1,55E-02	0,4234	2,4199578	1,02464698	18,17	LOC107986	uncharacterized LOC107986127
107984861	5,51E-02	1,26E+00	4,30E-02	0,5061	2,0239224	1,02435507	12,46	LOC107984	861
56605	7,98E-21	2,01E+01	2,60E-21	0,1081	9,4778385	1,02434955	312,9	ERO1B	endoplasmic reticulum oxidoreductase 1 beta
55156	8,64E-66	6,51E+01	9,67E-67	0,0593	17,2584354	1,02417209	1675,26	ARMC1	armadillo repeat containing 1
7697	1,49E-11	1,08E+01	6,46E-12	0,1491	6,8690172	1,02399767	158,74	ZNF138	zinc finger protein 138
7035	3,60E-87	8,64E+01	2,59E-88	0,0514	19,9226666	1,02369393	3572,22	TFPI	tissue factor pathway inhibitor
26098	1,20E-56	5,59E+01	1,65E-57	0,064	15,984013	1,023237	1343,19	EDRF1	erythroid differentiation regulatory factor 1
124739	6,95E-13	1,22E+01	2,88E-13	0,1401	7,2997109	1,02293686	193,87	USP43	ubiquitin specific peptidase 43
389668	2,47E-16	1,56E+01	9,15E-17	0,1228	8,31529	1,02143792	233,71	XKR9	XK related 9
7750	1,51E-70	6,98E+01	1,53E-71	0,0571	17,8855601	1,02143206	1818,99	ZMYM2	zinc finger MYM-type containing 2
126969	5,47E-02	1,26E+00	4,26E-02	0,5036	2,0276698	1,02121659	13,81	SLC44A3	solute carrier family 44 member 3
120379	2,10E-30	2,97E+01	5,29E-31	0,0882	11,5785365	1,02106218	614,62	PIH1D2	PIH1 domain containing 2
101929008	6,45E-03	2,19E+00	4,54E-03	0,3596	2,8376881	1,02039719	25,51	GTF2IP13	general transcription factor IIi pseudogene 13
283314	1,07E-08	7,97E+00	5,21E-09	0,1746	5,840247	1,01949091	110,86	C1RL-AS1	C1RL antisense RNA 1
23204	1,72E-81	8,08E+01	1,39E-82	0,053	19,2509262	1,01938756	11251,3	ARL6IP1	ADP ribosylation factor like GTPase 6 interacting protein 1
11259	1,72E-20	1,98E+01	5,64E-21	0,1084	9,3965964	1,01896135	362,12	FILIP1L	filamin A interacting protein 1 like
101929555	7,02E-05	4,15E+00	4,21E-05	0,2487	4,0955366	1,01855326	54,63	LOC101929	uncharacterized LOC101929555
112268035	1,75E-02	1,76E+00	1,29E-02	0,4094	2,4876266	1,01836718	19,29	LOC112268	035
54979	1,57E-01	8,04E-01	1,30E-01	0,6726	1,5135714	1,01797148	7,92	PLAAT2	phospholipase A and acyltransferase 2
152756	7,02E-04	3,15E+00	4,55E-04	0,2904	3,5059011	1,01796767	40,6	FAM218A	family with sequence similarity 218 member A
10443	5,89E-61	6,02E+01	7,40E-62	0,0613	16,5963918	1,01738202	1256,11	N4BP2L2	NEDD4 binding protein 2 like 2
112268301	3,83E-06	5,42E+00	2,13E-06	0,2145	4,7406255	1,01708003	72,6	LOC112268	301
11183	2,39E-114	1,14E+02	1,05E-115	0,0445	22,8644116	1,01659922	5070,16	MAP4K5	mitogen-activated protein kinase kinase kinase kinase 5
164781	6,79E-11	1,02E+01	3,02E-11	0,1529	6,6454596	1,01637451	144,69	DAW1	dynein assembly factor with WD repeats 1
4829	1,30E-01	8,86E-01	1,07E-01	0,63	1,6130014	1,0161362	8,04	NMBR	neuromedin B receptor
80007	6,28E-43	4,22E+01	1,18E-43	0,0733	13,8555293	1,01609145	765,21	C10orf88	chromosome 10 open reading frame 88
55299	1,21E-105	1,05E+02	6,17E-107	0,0462	21,9653836	1,01580192	4395,01	BRIX1	biogenesis of ribosomes BRX1
54718	1,61E-13	1,28E+01	6,55E-14	0,1354	7,4966583	1,01513878	193,73	BTN2A3P	butyrophilin subfamily 2 member A3, pseudogene
147339	4,02E-70	6,94E+01	4,11E-71	0,0569	17,8303569	1,0145692	1661,89	C18orf25	chromosome 18 open reading frame 25
8645	7,55E-02	1,12E+00	5,99E-02	0,5392	1,8813984	1,01440321	12,65	KCNK5	potassium two pore domain channel subfamily K member 5
388507	1,75E-61	6,08E+01	2,16E-62	0,0608	16,6700451	1,01420812	1406,5	ZNF788P	zinc finger family member 788, pseudogene
105370363	1,17E-01	9,32E-01	9,55E-02	0,6082	1,6670655	1,01393433	8,71	LOC105370	uncharacterized LOC105370363
29945	7,86E-56	5,51E+01	1,10E-56	0,0639	15,8652584	1,01392447	1643,2	ANAPC4	anaphase promoting complex subunit 4
83543	2,34E-32	3,16E+01	5,60E-33	0,0847	11,9623189	1,01380197	531,7	AIF1L	allograft inflammatory factor 1 like
23528	2,14E-73	7,27E+01	2,03E-74	0,0555	18,2510144	1,01356747	1803,13	ZNF281	zinc finger protein 281
285116	5,54E-39	3,83E+01	1,13E-39	0,0769	13,1806522	1,01344999	976,11	AHCTF1P1	AT-hook containing transcription factor 1 pseudogene 1
55732	1,89E-62	6,17E+01	2,28E-63	0,0603	16,8041256	1,01338756	1484,86	C1orf112	chromosome 1 open reading frame 112
2591	2,60E-83	8,26E+01	2,01E-84	0,052	19,4690372	1,01310719	2032,61	GALNT3	polypeptide N-acetylgalactosaminyltransferase 3
51175	1,22E-31	3,09E+01	2,98E-32	0,0857	11,8227585	1,01294982	532,29	TUBE1	tubulin epsilon 1
221150	6,99E-117	1,16E+02	2,93E-118	0,0438	23,1197711	1,0128582	3832,25	SKA3	spindle and kinetochore associated complex subunit 3
100132154	3,56E-22	2,14E+01	1,11E-22	0,1033	9,8013057	1,01273569	357,5	LOC100132	ankyrin repeat domain 30B pseudogene
80004	1,78E-42	4,17E+01	3,37E-43	0,0735	13,779801	1,01255299	861,12	ESRP2	epithelial splicing regulatory protein 2
84765	2,55E-13	1,26E+01	1,04E-13	0,1362	7,435862	1,01243997	196,21	ZNF577	zinc finger protein 577
105371314	4,21E-02	1,38E+00	3,23E-02	0,4728	2,1407652	1,01205385	14,28	LOC105371	314
26031	3,95E-119	1,18E+02	1,60E-120	0,0433	23,343656	1,01188379	4630,73	OSBPL3	oxysterol binding protein like 3
167153	1,09E-70	7,00E+01	1,10E-71	0,0565	17,904002	1,01187904	1754,95	TENT2	terminal nucleotidyltransferase 2
100506866	5,03E-06	5,30E+00	2,82E-06	0,216	4,6837441	1,01171525	71,28	TTN-AS1	TTN antisense RNA 1
23190	1,18E-124	1,24E+02	4,34E-126	0,0423	23,8854196	1,01082111	5732,14	UBXN4	UBX domain protein 4
9412	9,51E-45	4,40E+01	1,71E-45	0,0714	14,1560025	1,01051976	1325,18	MED21	mediator complex subunit 21
101926917	4,68E-11	1,03E+01	2,07E-11	0,1508	6,7006507	1,01045781	149,08	ANKRD18CI	ankyrin repeat domain 18C, pseudogene
107986182	8,09E-02	1,09E+00	6,44E-02	0,546	1,8491809	1,0096907	11,95	LOC107986	uncharacterized LOC107986182
80264	3,14E-22	2,15E+01	9,78E-23	0,1029	9,8142042	1,00946433	356,96	ZNF430	zinc finger protein 430
137695	1,24E-26	2,59E+01	3,43E-27	0,0935	10,8002237	1,00943089	475,98	TMEM68	transmembrane protein 68
55225	1,17E-33	3,29E+01	2,71E-34	0,0827	12,2112508	1,00934835	646,74	RAVER2	ribonucleoprotein, PTB binding 2
1290	4,31E-04	3,37E+00	2,75E-04	0,2775	3,6378289	1,00933738	43,76	COL5A2	collagen type V alpha 2 chain
54149	6,19E-29	2,82E+01	1,61E-29	0,0895	11,2818622	1,00919095	572,85	C21orf91	chromosome 21 open reading frame 91
101929512	1,36E-01	8,66E-01	1,12E-01	0,634	1,5913545	1,00896539	7,99	PSMD14-DT	PSMD14 divergent transcript
100874201	2,71E-05	4,57E+00	1,58E-05	0,2337	4,3166247	1,00894542	60,83	B4GALT4-AS	B4GALT4 antisense RNA 1
54014	6,66E-73	7,22E+01	6,38E-74	0,0555	18,1883487	1,00866749	2103,11	BRWD1	bromodomain and WD repeat domain containing 1
107985216	2,31E-03	2,64E+00	1,56E-03	0,3189	3,1632178	1,0086033	33,4	LOC107985	uncharacterized LOC107985216
7764	2,54E-105	1,05E+02	1,30E-106	0,046	21,9313921	1,00851437	3686,89	ZNF217	zinc finger protein 217
8065	2,86E-81	8,05E+01	2,30E-82	0,0525	19,2246085	1,00846264	2806,04	CUL5	cullin 5
28577	1,52E-01	8,18E-01	1,26E-01	0,6585	1,531365	1,0083972	7,49	TRBV12-3	T cell receptor beta variable 12-3
64895	6,07E-49	4,82E+01	9,86E-50	0,068	14,8265836	1,00807224	1015,87	PAPOLG	poly(A) polymerase gamma
2825	1,42E-33	3,28E+01	3,32E-34	0,0826	12,1947264	1,00782644	807,22	CMKLR2	chemerin chemokine-like receptor 2
51542	7,31E-54	5,31E+01	1,07E-54	0,0647	15,5754818	1,00754023	1515,8	VPS54	VPS54 subunit of GARP complex
100505636	1,34E-05	4,87E+00	7,67E-06	0,2252	4,4741133	1,00743443	65,76	MALINC1	mitosis associated long intergenic non-coding RNA 1
285172	1,37E-23	2,29E+01	4,14E-24	0,0995	10,1282371	1,00741112	486,86	HYCC2	hyccin PI4KA lipid kinase complex subunit 2
104	1,05E-50	5,00E+01	1,64E-51	0,0667	15,0990132	1,00737372	997,39	ADARB1	adenosine deaminase RNA specific B1
92822	9,10E-40	3,90E+01	1,83E-40	0,0756	13,3174049	1,0071007	770,26	ZNF276	zinc finger protein 276
25897	1,42E-68	6,78E+01	1,50E-69	0,0571	17,6282183	1,00704203	2145,36	RNF19A	ring finger protein 19A, RBR E3 ubiquitin protein ligase
55930	1,24E-71	7,09E+01	1,22E-72	0,0559	18,0260583	1,00698482	1873,11	MYO5C	myosin VC
107985209	1,90E-02	1,72E+00	1,40E-02	0,4096	2,4579261	1,00677439	19,13	ARHGEF2-A	ARHGEF2 antisense RNA 2
4356	1,49E-24	2,38E+01	4,37E-25	0,0973	10,3459134	1,00663951	435,55	MPP3	MAGUK p55 scaffold protein 3
10559	3,00E-32	3,15E+01	7,20E-33	0,0843	11,9413683	1,00642616	658,33	SLC35A1	solute carrier family 35 member A1
3977	5,51E-51	5,03E+01	8,55E-52	0,0665	15,1420541	1,00636648	1323,88	LIFR	LIF receptor subunit alpha
1002	5,90E-83	8,22E+01	4,59E-84	0,0518	19,4267409	1,00606844	2620,62	CDH4	cadherin 4
79772	3,46E-63	6,25E+01	4,09E-64	0,0595	16,9056335	1,00603536	1690,02	MCTP1	multiple C2 and transmembrane domain containing 1
5972	1,35E-01	8,70E-01	1,11E-01	0,6315	1,5930393	1,00595924	8,07	REN	renin
339535	3,30E-18	1,75E+01	1,16E-18	0,1141	8,8187738	1,00584025	293,04	LINC01139	long intergenic non-protein coding RNA 1139
58516	1,25E-79	7,89E+01	1,04E-80	0,0528	19,0259863	1,00530813	3211,17	SINHCAF	SIN3-HDAC complex associated factor
54816	9,52E-43	4,20E+01	1,80E-43	0,0727	13,8252244	1,00520337	769,38	ZNF280D	zinc finger protein 280D
100129917	7,92E-07	6,10E+00	4,24E-07	0,1987	5,0578094	1,00493207	84,27	PCGF3-AS1	PCGF3 antisense RNA 1
8706	4,07E-56	5,54E+01	5,68E-57	0,0631	15,9069035	1,00441962	1372,32	B3GALNT1	beta-1,3-N-acetylgalactosaminyltransferase 1 (globoside blood group)
27292	2,75E-77	7,66E+01	2,42E-78	0,0536	18,7380379	1,00438659	3443,67	DIMT1	DIM1 rRNA methyltransferase and ribosome maturation factor
445328	8,16E-11	1,01E+01	3,65E-11	0,1517	6,6177782	1,00398244	155,01	ARHGEF35	Rho guanine nucleotide exchange factor 35
80155	3,64E-62	6,14E+01	4,40E-63	0,0598	16,7649558	1,00325778	6603,16	NAA15	N-alpha-acetyltransferase 15, NatA auxiliary subunit
105374985	1,49E-07	6,83E+00	7,71E-08	0,1867	5,3739011	1,00320309	112,56	LOC105374	985
151556	1,93E-10	9,71E+00	8,75E-11	0,1546	6,4870845	1,00315266	153,23	GPR155	G protein-coupled receptor 155
262	1,07E-83	8,30E+01	8,25E-85	0,0514	19,5145824	1,00303909	5018,34	AMD1	adenosylmethionine decarboxylase 1
107985909	9,87E-02	1,01E+00	7,96E-02	0,5722	1,7528793	1,00303614	9,86	LOC107985	uncharacterized LOC107985909
9657	5,12E-37	3,63E+01	1,09E-37	0,0781	12,8314179	1,00276667	650,62	IQCB1	IQ motif containing B1
1295	1,19E-115	1,15E+02	5,11E-117	0,0436	22,9960493	1,00275859	8077,02	COL8A1	collagen type VIII alpha 1 chain
388572	4,63E-02	1,33E+00	3,57E-02	0,4774	2,1002736	1,00262157	14,21	LOC388572	replaced by ID 112268070

100526664	3,40E-33	3,25E+01	7,98E-34	0,0826	12,1229794	1,00146871	618,03	LY75-CD302	LY75-CD302 readthrough	
4999	8,10E-58	5,71E+01	1,09E-58	0,062	16,1527756	1,00125692	1263,68	ORC2	origin recognition complex subunit 2	
105370353	1,73E-04	3,76E+00	1,07E-04	0,2584	3,8736896	1,00111142	48,83	LOC105370	uncharacterized LOC105370353	
100505702	1,90E-06	5,72E+00	1,04E-06	0,2049	4,8840894	1,00096789	82,96	LINC01094	long intergenic non-protein coding RNA 1094	
130733	2,73E-04	3,56E+00	1,71E-04	0,2663	3,7577504	1,00076331	46,25	TMEM178A	transmembrane protein 178A	
102724701	8,92E-26	2,50E+01	2,53E-26	0,0941	10,615133	0,99901875	425,51	LOC102724	uncharacterized LOC102724701	
79810	2,97E-43	4,25E+01	5,55E-44	0,0718	13,9095137	0,99872616	798,51	PTCD2	pentatricopeptide repeat domain 2	
79862	1,59E-18	1,78E+01	5,53E-19	0,1122	8,9011165	0,99864696	334,65	ZNF669	zinc finger protein 669	
7576	7,81E-35	3,41E+01	1,76E-35	0,0803	12,4316212	0,99848511	671,3	ZNF28	zinc finger protein 28	
152742	9,79E-02	1,01E+00	7,89E-02	0,5682	1,756977	0,99829944	9,88	LINC01085	long intergenic non-protein coding RNA 1085	
5471	3,44E-80	7,95E+01	2,83E-81	0,0523	19,0940739	0,99819351	2056,51	PPAT	phosphoribosyl pyrophosphate amidotransferase	
64333	5,49E-04	3,26E+00	3,53E-04	0,2794	3,5728465	0,99815313	42,96	ARHGAP9	Rho GTPase activating protein 9	
10196	7,52E-68	6,71E+01	8,04E-69	0,0569	17,532855	0,99784319	2116,3	PRMT3	protein arginine methyltransferase 3	
79723	4,00E-44	4,34E+01	7,33E-45	0,071	14,0535649	0,99763488	1301,11	SUV39H2	SUV39H2 histone lysine methyltransferase	
55186	4,74E-69	6,83E+01	4,95E-70	0,0564	17,6906132	0,99706812	1843,57	SLC25A36	solute carrier family 25 member 36	
100616393	1,15E-05	4,94E+00	6,61E-06	0,2211	4,5058672	0,99631941	88,24	MIR4657	microRNA 4657	
9360	2,03E-69	6,87E+01	2,10E-70	0,0562	17,7388157	0,99617165	3825,68	PPIG	peptidylprolyl isomerase G	
8445	1,25E-34	3,39E+01	2,82E-35	0,0804	12,39384	0,99584847	695,71	DYRK2	dual specificity tyrosine phosphorylation regulated kinase 2	
10622	2,27E-47	4,66E+01	3,83E-48	0,0683	14,5788432	0,99548348	1443,96	POLR3G	RNA polymerase III subunit G	
8850	2,33E-57	5,66E+01	3,16E-58	0,0619	16,0867897	0,99526914	1465,88	KAT2B	lysine acetyltransferase 2B	
256643	1,10E-18	1,80E+01	3,80E-19	0,1113	8,9425247	0,99518305	305,75	BCLAF3	BCLAF1 and THRAP3 family member 3	
100131434	8,52E-03	2,07E+00	6,07E-03	0,3625	2,743979	0,99471766	24,66	EOLA1-DT	EOLA1 divergent transcript	
256471	9,25E-37	3,60E+01	1,99E-37	0,0778	12,7851008	0,99452965	747,54	MFSD8	major facilitator superfamily domain containing 8	
26035	3,00E-89	8,85E+01	2,08E-90	0,0493	20,1628119	0,99452817	2981,14	GLCE	glucuronic acid epimerase	
2984	3,64E-03	2,44E+00	2,51E-03	0,3289	3,0225707	0,99424776	31,3	GUCY2C	guanylate cyclase 2C	
169841	8,47E-09	8,07E+00	4,11E-09	0,1691	5,879589	0,99412317	134,2	ZNF169	zinc finger protein 169	
148266	3,11E-34	3,35E+01	7,12E-35	0,0807	12,3194041	0,99410655	628,25	ZNF569	zinc finger protein 569	
3842	1,12E-102	1,02E+02	6,07E-104	0,0459	21,650061	0,99378267	12719,9	TNPO1	transportin 1	
374354	8,03E-62	6,11E+01	9,84E-63	0,0594	16,7171006	0,99369982	1915	NHLRC2	NHL repeat containing 2	
54429	8,98E-02	1,05E+00	7,20E-02	0,552	1,7988631	0,99297689	10,48	TAS2R5	taste 2 receptor member 5	
148898	1,05E-05	4,98E+00	6,02E-06	0,2193	4,5255733	0,99264886	68,37	ZNF436-AS1	ZNF436 antisense RNA 1	
388272	5,37E-20	1,93E+01	1,79E-20	0,107	9,2743697	0,99213878	327,94	C16orf87	chromosome 16 open reading frame 87	
50511	1,11E-03	2,95E+00	7,28E-04	0,2936	3,3788001	0,99192308	38,09	SYCP3	synaptonemal complex protein 3	
6120	1,65E-55	5,48E+01	2,32E-56	0,0626	15,8183906	0,9909276	1264,38	RPE	ribulose-5-phosphate-3-epimerase	
6990	1,41E-41	4,09E+01	2,74E-42	0,0727	13,6277214	0,990457	1198,6	DYNLT3	dynein light chain Tctex-type 3	
112268415	4,67E-10	9,33E+00	2,15E-10	0,156	6,3501228	0,99044464	151,45	LOC112268	uncharacterized LOC112268415	
11103	8,97E-113	1,12E+02	4,02E-114	0,0436	22,7048111	0,99017776	4563,2	KRR1	KRR1 small subunit processome component homolog	
55608	3,08E-49	4,85E+01	4,96E-50	0,0666	14,8726206	0,99004681	1118,2	ANKRD10	ankyrin repeat domain 10	
23167	5,21E-111	1,10E+02	2,40E-112	0,0439	22,5243293	0,98921311	5268,8	EFR3A	EFR3 homolog A	
57018	3,00E-58	5,75E+01	3,97E-59	0,061	16,2146374	0,98900762	1344,65	CCNL1	cyclin L1	
11236	1,75E-22	2,18E+01	5,41E-23	0,1001	9,8737164	0,98883413	536,62	RNF139	ring finger protein 139	
27000	2,68E-42	4,16E+01	5,11E-43	0,0719	13,7497253	0,98876333	1380,43	DNAJC2	DnaJ heat shock protein family (Hsp40) member C2	
6197	1,58E-80	7,98E+01	1,29E-81	0,0517	19,1349273	0,98869129	3164,62	RPS6KA3	ribosomal protein S6 kinase A3	
337876	8,16E-23	2,21E+01	2,51E-23	0,0994	9,9505286	0,98865269	372,91	CHSY3	chondroitin sulfate synthase 3	
158747	9,21E-33	3,20E+01	2,19E-33	0,0821	12,0401352	0,98862261	636,03	MOSPD2	motile sperm domain containing 2	
100507066	5,57E-02	1,25E+00	4,34E-02	0,4895	2,019703	0,98858671	13,56	CLIP1-AS1	CLIP1 antisense RNA 1	
9787	6,10E-128	1,27E+02	2,07E-129	0,0408	24,2029277	0,98840184	12108,82	DLGAP5	DLG associated protein 5	
642636	3,61E-03	2,44E+00	2,48E-03	0,3266	3,0257286	0,98824252	31,33	RAD21L1	RAD21 cohesin complex component like 1	
101929467	1,25E-03	2,90E+00	8,28E-04	0,2955	3,3431373	0,98784163	42,54	LURAP1L-A	LURAP1L antisense RNA 1	
83449	7,66E-02	1,12E+00	6,08E-02	0,5267	1,8748474	0,98751957	11,7	PMFBP1	polyamine modulated factor 1 binding protein 1	
105372815	7,13E-03	2,15E+00	5,04E-03	0,352	2,8044301	0,98708345	27,1	LOC105372	uncharacterized LOC105372815	
23285	3,79E-10	9,42E+00	1,74E-10	0,1546	6,3829337	0,98664224	145,05	KIAA1107	replaced by ID 284697	
388561	5,06E-20	1,93E+01	1,68E-20	0,1063	9,2809002	0,98614263	314,79	ZNF761	zinc finger protein 761	
104909134	4,71E-06	5,33E+00	2,63E-06	0,2099	4,6976546	0,98600664	76,18	LINC02210-C	LINC02210-CRHR1 readthrough	
100750247	2,02E-35	3,47E+01	4,50E-36	0,0786	12,5401975	0,98564726	656,79	HIF1A-AS2	HIF1A antisense RNA 2	
84542	1,67E-26	2,58E+01	4,66E-27	0,0915	10,7721123	0,98552105	484,18	SANBR	SANT and BTB domain regulator of CSR	
29083	9,25E-35	3,40E+01	2,09E-35	0,0794	12,4179355	0,98549273	697,43	GTPBP8	GTP binding protein 8 (putative)	
23376	2,08E-49	4,87E+01	3,33E-50	0,0661	14,8992441	0,98534562	1034,07	UFL1	UFM1 specific ligase 1	
92126	1,18E-20	1,99E+01	3,86E-21	0,1044	9,4362948	0,98490279	344,08	DSEL	dermatan sulfate epimerase like	
9162	2,95E-03	2,53E+00	2,01E-03	0,3189	3,0883352	0,98476201	32,97	DGKI	diacylglycerol kinase iota	
4921	4,28E-06	5,37E+00	2,39E-06	0,2087	4,7176599	0,98453284	77,2	DDR2	discoidin domain receptor tyrosine kinase 2	
1536	1,63E-06	5,79E+00	8,92E-07	0,2003	4,9141877	0,98433609	85,05	CYBB	cytochrome b-245 beta chain	
55745	2,85E-61	6,05E+01	3,54E-62	0,0591	16,6405337	0,98313031	2097,91	AP5M1	adaptor related protein complex 5 subunit mu 1	
387921	8,56E-39	3,81E+01	1,76E-39	0,0747	13,1474392	0,98234555	723,09	NHLRC3	NHL repeat containing 3	
54443	2,90E-149	1,49E+02	7,19E-151	0,0375	26,1620469	0,98213935	34024,53	ANLN	anillin, actin binding protein	
576	1,14E-03	2,94E+00	7,49E-04	0,2913	3,3710177	0,98207296	40,9	ADGRB2	adhesion G protein-coupled receptor B2	
79572	1,55E-97	9,68E+01	9,22E-99	0,0466	21,0930062	0,98188366	7166,24	ATP13A3	ATPase 13A3	
169200	5,71E-42	4,12E+01	1,10E-42	0,0716	13,6944026	0,98116587	820,4	TMEM64	transmembrane protein 64	
56852	1,31E-78	7,79E+01	1,11E-79	0,0519	18,9013046	0,98077917	2220,75	RAD18	RAD18 E3 ubiquitin protein ligase	
112267914	3,65E-02	1,44E+00	2,78E-02	0,4456	2,2002133	0,98044892	17,28	LOC112267	uncharacterized LOC112267914	
7486	1,37E-44	4,39E+01	2,48E-45	0,0693	14,1301079	0,97984135	1030,26	WRN	WRN RecQ like helicase	
6619	7,90E-43	4,21E+01	1,49E-43	0,0708	13,8388373	0,97983025	865,04	SNAPC3	small nuclear RNA activating complex polypeptide 3	
55144	5,99E-80	7,92E+01	4,96E-81	0,0514	19,0647087	0,97970842	2101,52	LRRC8D	leucine rich repeat containing 8 VRAC subunit D	
729597	5,66E-03	2,25E+00	3,96E-03	0,3399	2,8810514	0,97924555	28,74	SPDYE6	speedy/RINGO cell cycle regulator family member E6	
27074	4,39E-08	7,36E+00	2,20E-08	0,175	5,5952823	0,97918215	121,75	LAMP3	lysosomal associated membrane protein 3	
110116772	1,16E-19	1,89E+01	3,89E-20	0,1065	9,1910405	0,97859897	313,04	ZNF765-ZNF	ZNF765-ZNF761 readthrough	
84255	1,65E-59	5,88E+01	2,13E-60	0,0597	16,3933556	0,97843328	1409,64	SLC37A3	solute carrier family 37 member 3	
5427	5,08E-62	6,13E+01	6,18E-63	0,0584	16,7448062	0,97812774	1965,04	POLE2	DNA polymerase epsilon 2, accessory subunit	
100288380	4,85E-04	3,31E+00	3,10E-04	0,2711	3,6065022	0,97761356	43,93	ULK4P2	ULK4 pseudogene 2	
6262	1,52E-05	4,82E+00	8,74E-06	0,2199	4,4461859	0,97755978	71,94	RYR2	ryanodine receptor 2	
81571	6,74E-03	2,17E+00	4,76E-03	0,3462	2,8231422	0,97737349	27,64	MIR600HG	MIR600 host gene	
162972	1,05E-19	1,90E+01	3,52E-20	0,1062	9,2017993	0,97703354	318,2	ZNF550	zinc finger protein 550	
55082	5,60E-68	6,73E+01	5,97E-69	0,0557	17,5498138	0,97702409	2447,07	ARGLU1	arginine and glutamate rich 1	
5966	1,62E-48	4,78E+01	2,65E-49	0,0662	14,7600682	0,97690587	1074,79	REL	REL proto-oncogene, NF-kB subunit	
25957	1,96E-61	6,07E+01	2,43E-62	0,0586	16,6631501	0,97663623	3330,72	PNISR	PNN interacting serine and arginine rich protein	
54664	4,13E-49	4,84E+01	6,68E-50	0,0657	14,852707	0,97653255	1481,41	TMEM106B	transmembrane protein 106B	
80006	4,26E-44	4,34E+01	7,80E-45	0,0695	14,0491023	0,97587214	1125,01	TRAPPC13	trafficking protein particle complex subunit 13	
143872	4,10E-63	6,24E+01	4,86E-64	0,0578	16,8954607	0,97573237	1899,55	ARHGAP42	Rho GTPase activating protein 42	
134353	3,40E-29	2,85E+01	8,78E-30	0,0861	11,3351942	0,97571511	569,22	LSM11	LSM11, U7 small nuclear RNA associated	
401145	2,29E-02	1,64E+00	1,70E-02	0,4087	2,3869504	0,97551496	20,27	CCSER1	coiled-coil serine rich protein 1	
387700	2,13E-02	1,67E+00	1,58E-02	0,404	2,4146505	0,97545867	20,27	SLC16A12	solute carrier family 16 member 12	
10927	2,06E-75	7,47E+01	1,87E-76	0,0527	18,5052207	0,97527119	4612,85	SPIN1	spindlin 1	
64398	3,91E-77	7,64E+01	3,45E-78	0,0521	18,7191892	0,97497071	4419,13	PALS1	protein associated with LIN7 1, MAGUK p55 family member	
147699	6,34E-03	2,20E+00	4,46E-03	0,3428	2,8433902	0,974763	27,95	PPM1N	protein phosphatase, Mg2+/Mn2+ dependent 1N (putative)	
23460	5,68E-02	1,25E+00	4,44E-02	0,4847	2,0106253	0,97457584	14,14	ABCA6	ATP binding cassette subfamily A member 6	
55322	2,61E-63	6,26E+01	3,08E-64	0,0576	16,9222691	0,97404095	1978,17	C5orf22	chromosome 5 open reading frame 22	
902	3,23E-80	7,95E+01	2,65E-81	0,051	19,0974692	0,97371599	3123,78	CCNH	cyclin H	
101927226	7,75E-02	1,11E+00	6,16E-02	0,5208	1,8693172	0,97357136	12,2	LOC101927	uncharacterized LOC101927226	
84896	1,60E-79	7,88E+01	1,33E-80	0,0512	19,0129927	0,97344817	2781,56	ATAD1	ATPase family AAA domain containing 1	
63967	3,41E-90	8,95E+01	2,32E-91	0,048	20,2710338	0,97342084	6241,08	CLSPN	claspin	
3280	1,96E-21	2,07E+01	6,26E-22	0,1011	9,6251984	0,97318661	364,69	HES1	hes family bHLH transcription factor 1	
2669	3,85E-44	4,34E+01	7,04E-45	0,0692	14,0563573	0,97310093	908,13	GEM	GTP binding protein overexpressed in skeletal muscle	
105372143	3,37E-02	1,47E+00	2,56E-02	0,4357	2,2326601	0,97284839	16,99	LOC105372	uncharacterized LOC105372143	
25909	1,81E-125	1,25E+02	6,50E-127	0,0406	23,9646783	0,97260636	7737,27	AHCTF1	AT-hook containing transcription factor 1	
100499484	7,25E-06	5,14E+00	4,10E-06	0,2111	4,606278	0,97235625	73,9	SUGT1P4-S	SUGT1P4-STRA6LP readthrough	
2027	1,74E-15	1,48E+01	6,64E-16	0,1203	8,0769465	0,97142128	283,78	ENO3	enolase 3	
81930	1,05E-73	7,30E+01	9,90E-75	0,0531	18,2902387	0,97140278	2569,2	KIF18A	kinesin family member 18A	
55293	1,02E-51	5,10E+01	1,56E-52	0,0637	15,2535844	0,97108134	1585,75	UEVLD	UEV and lactate/malate dehyrogenase domains	
100287896	3,49E-13	1,25E+01	1,43E-13	0,1313	7,3930789	0,97066558	209,7	LIPT2-AS1	LIPT2 antisense RNA 1	
80745	8,74E-30	2,91E+01	2,23E-30	0,0847	11,4546711	0,97063491	631,66	THUMPD2	THUMP domain containing 2	
55656	1,44E-60	5,98E+01	1,83E-61	0,0587	16,5420392	0,97040311	1472,62	INTS8	integrator complex subunit 8	
100506495	3,53E-02	1,45E+00	2,69E-02	0,4382	2,2134793	0,96991236	18,33	LIFR-AS1	LIFR antisense RNA 1	
10020	5,59E-100	9,93E+01	3,17E-101	0,0454	21,359698	0,96980225	3518,26	GNE	glucosamine (UDP-N-acetyl)-2-epimerase/N-acetylmannosamine kinase	
157695	1,96E-11	1,07E+01	8,54E-12	0,142	6,8292113	0,96953486	181,13	TDRP	testis development related protein	
147	4,98E-11	1,03E+01	2,21E-11	0,1449	6,6915726	0,96940895	159,95	ADRA1B	adrenoceptor alpha 1B	
342892	2,10E-29	2,87E+01	5,41E-30	0,0852	11,3776034	0,96912228	540	ZNF850	zinc finger protein 850	
641977	9,61E-26	2,50E+01	2,73E-26	0,0913	10,6081361	0,96896559	445,65	SEPTIN7P2	septin 7 pseudogene 2	
285237	8,56E-51	5,01E+01	1,33E-51	0,0641	15,1129019	0,96891034	1439,12	C3orf38	chromosome 3 open reading frame 38	
3987	2,22E-32	3,17E+01	5,30E-33	0,0809	11,9668651	0,96846642	1176,05	LIMS1	LIM zinc finger domain containing 1	
9196	1,14E-03	2,94E+00	7,54E-04	0,2874	3,3692366	0,96822207	38,99	KCNAB3	potassium voltage-gated channel subfamily A regulatory beta subunit 3	

55914	1,06E-121	1,21E+02	4,09E-123	0,041	23,5975055	0,96812449	7990,42	ERBIN	erbb2 interacting protein
4253	2,10E-60	5,97E+01	2,66E-61	0,0586	16,5193764	0,96776777	1707,16	MIA2	MIA SH3 domain ER export factor 2
10403	2,06E-119	1,19E+02	8,22E-121	0,0414	23,3720836	0,96751006	7291,5	NDC80	NDC80 kinetochore complex component
4647	3,00E-02	1,52E+00	2,26E-02	0,4239	2,2806491	0,96684935	18,26	MYO7A	myosin VIIA
84307	2,47E-44	4,36E+01	4,50E-45	0,0686	14,0880833	0,96678408	1007,17	ZNF397	zinc finger protein 397
7695	3,59E-18	1,74E+01	1,26E-18	0,1097	8,8091738	0,96670286	292,88	ZNF136	zinc finger protein 136
100507516	7,31E-31	3,01E+01	1,82E-31	0,0828	11,6697624	0,9666491	581,97	LINC02984	long intergenic non-protein coding RNA 2984
25862	4,74E-55	5,43E+01	6,77E-56	0,0613	15,7508912	0,96611796	1336,88	USP49	ubiquitin specific peptidase 49
5612	1,70E-90	8,98E+01	1,15E-91	0,0476	20,3054278	0,9659587	4686,3	THAP12	THAP domain containing 12
79669	1,96E-16	1,57E+01	7,24E-17	0,1158	8,3430859	0,96584536	295	C3orf52	chromosome 3 open reading frame 52
10314	5,40E-47	4,63E+01	9,19E-48	0,0665	14,5189462	0,96544615	1312,71	LANCL1	LanC like glutathione S-transferase 1
101929185	8,94E-20	1,90E+01	2,99E-20	0,1047	9,2194313	0,96522149	360,65	LOC101929	uncharacterized LOC101929185
10260	3,48E-50	4,95E+01	5,50E-51	0,0643	15,0192031	0,96508967	1238,66	DENND4A	DENN domain containing 4A
94163	1,03E-01	9,87E-01	8,31E-02	0,5569	1,7328884	0,96505745	10,31	SNORD38B	small nucleolar RNA, C/D box 38B
2966	9,85E-44	4,30E+01	1,82E-44	0,069	13,9891172	0,96503515	953,83	GTF2H2	general transcription factor IIH subunit 2
54566	4,40E-60	5,94E+01	5,62E-61	0,0586	16,4741937	0,96471362	1629,67	EPB41L4B	erythrocyte membrane protein band 4.1 like 4B
284273	9,35E-55	5,40E+01	1,34E-55	0,0614	15,7074963	0,96443693	1502,6	PTGR3	prostaglandin reductase 3
105369322	6,50E-02	1,19E+00	5,11E-02	0,4944	1,9505963	0,96430645	14,08	LOC105369	uncharacterized LOC105369322
105369373	4,03E-11	1,04E+01	1,78E-11	0,1434	6,7230814	0,96426874	164,41	LOC105369	uncharacterized LOC105369373
283299	1,12E-05	4,95E+00	6,43E-06	0,2137	4,5117871	0,96426449	81,1	LOC283299	uncharacterized LOC283299
114881	2,45E-20	1,96E+01	8,05E-21	0,103	9,35893	0,96413789	413,04	OSBPL7	oxysterol binding protein like 7
150962	5,83E-19	1,82E+01	2,00E-19	0,1069	9,0133382	0,96334495	308,63	PUS10	pseudouridine synthase 10
9666	9,27E-44	4,30E+01	1,71E-44	0,0688	13,9934652	0,96299928	1115,69	DZIP3	DAZ interacting zinc finger protein 3
8669	3,57E-81	8,04E+01	2,89E-82	0,0501	19,2129289	0,96226613	4640,37	EIF3J	eukaryotic translation initiation factor 3 subunit J
147657	2,83E-55	5,45E+01	4,02E-56	0,0609	15,7838613	0,96187302	1229,26	ZNF480	zinc finger protein 480
152518	6,73E-39	3,82E+01	1,38E-39	0,073	13,1657042	0,9611955	875,41	NFXL1	nuclear transcription factor, X-box binding like 1
5000	1,56E-41	4,08E+01	3,04E-42	0,0705	13,6202225	0,96031276	1294,4	ORC4	origin recognition complex subunit 4
5937	5,51E-90	8,93E+01	3,76E-91	0,0474	20,2472503	0,96023134	3041,04	RBMS1	RNA binding motif single stranded interacting protein 1
64848	1,68E-59	5,88E+01	2,17E-60	0,0586	16,3923498	0,96022584	2224,26	YTHDC2	YTH domain containing 2
91316	5,61E-09	8,25E+00	2,70E-09	0,1614	5,9486041	0,96004046	135,93	GUSBP11	GUSB pseudogene 11
90167	6,50E-04	3,19E+00	4,20E-04	0,272	3,5270406	0,9593926	45,29	FRMD7	FERM domain containing 7
51760	8,63E-10	9,06E+00	4,02E-10	0,1534	6,2531907	0,95934949	144,57	SYT17	synaptotagmin 17
493812	3,40E-13	1,25E+01	1,40E-13	0,1297	7,3966776	0,95923567	221,19	HCG11	HLA complex group 11
163087	1,11E-17	1,70E+01	3,94E-18	0,1105	8,6803717	0,95906989	298,57	ZNF383	zinc finger protein 383
257218	1,44E-24	2,38E+01	4,22E-25	0,0927	10,3492525	0,95892546	472,27	SHPRH	SNF2 histone linker PHD RING helicase
122769	7,53E-45	4,41E+01	1,35E-45	0,0677	14,1725606	0,958863	2287,49	LRR1	leucine rich repeat protein 1
1272	1,04E-04	3,98E+00	6,34E-05	0,2397	3,9999218	0,9588134	59,15	CNTN1	contactin 1
100189169	4,93E-02	1,31E+00	3,82E-02	0,4624	2,0731904	0,95871161	15,1	TRL-AAG3-1	tRNA-Leu (anticodon AAG) 3-1
9331	1,03E-55	5,50E+01	1,45E-56	0,0605	15,8481004	0,95860039	1289,88	B4GALT6	beta-1,4-galactosyltransferase 6
105378992	2,46E-03	2,61E+00	1,66E-03	0,3046	3,1443325	0,95768774	37,33	LINC02057	long intergenic non-protein coding RNA 2057
91120	1,66E-08	7,78E+00	8,20E-09	0,166	5,7643897	0,95672668	122,3	ZNF682	zinc finger protein 682
3936	1,33E-40	3,99E+01	2,62E-41	0,071	13,4619305	0,95628266	903,68	LCP1	lymphocyte cytosolic protein 1
22925	2,53E-08	7,60E+00	1,26E-08	0,168	5,6917139	0,95611907	117,89	PLA2R1	phospholipase A2 receptor 1
273	1,17E-09	8,93E+00	5,48E-10	0,154	6,2046122	0,95561309	149,22	AMPH	amphiphysin
375287	8,02E-09	8,10E+00	3,89E-09	0,1622	5,8888066	0,95499614	140,63	RBM43	RNA binding motif protein 43
105371611	4,28E-02	1,37E+00	3,29E-02	0,4476	2,1334611	0,95490862	15,73	LOC105371	uncharacterized LOC105371611
1783	2,47E-84	8,36E+01	1,87E-85	0,0487	19,5902246	0,9547755	5647,82	DYNC1LI2	dynein cytoplasmic 1 light intermediate chain 2
9760	4,39E-12	1,14E+01	1,87E-12	0,1355	7,0436857	0,95474871	186,08	TOX	thymocyte selection associated high mobility group box
105373490	5,43E-45	4,43E+01	9,72E-46	0,0672	14,1958506	0,95459067	924,68	LOC105373	uncharacterized LOC105373490
2016	1,43E-02	1,84E+00	1,04E-02	0,3725	2,5619765	0,95439669	26,75	EMX1	empty spiracles homeobox 1
9619	9,71E-13	1,20E+01	4,05E-13	0,1316	7,2538595	0,95434709	202,26	ABCG1	ATP binding cassette subfamily G member 1
150709	2,59E-07	6,59E+00	1,35E-07	0,181	5,2715882	0,95403177	104,32	ANKAR	ankyrin and armadillo repeat containing
163486	9,04E-22	2,10E+01	2,85E-22	0,0983	9,7056303	0,95398745	380,95	DENND1B	DENN domain containing 1B
64328	1,62E-58	5,78E+01	2,13E-59	0,0587	16,2528354	0,95387447	2058,82	XPO4	exportin 4
22824	1,37E-83	8,29E+01	1,05E-84	0,0489	19,5021696	0,95359047	3159,45	HSPA4L	heat shock protein family A (Hsp70) member 4 like
54893	3,01E-36	3,55E+01	6,54E-37	0,0751	12,6921201	0,95330327	826,05	MTMR10	myotubularin related protein 10
64786	9,84E-69	6,80E+01	1,04E-69	0,054	17,6490271	0,953182	1889,37	TBC1D15	TBC1 domain family member 15
6692	3,72E-15	1,44E+01	1,44E-15	0,1193	7,9823664	0,95269099	252,31	SPINT1	serine peptidase inhibitor, Kunitz type 1
11025	5,30E-02	1,28E+00	4,13E-02	0,4668	2,0408535	0,95267595	14,52	LILRB3	leukocyte immunoglobulin like receptor B3
5911	2,15E-57	5,67E+01	2,91E-58	0,0592	16,091852	0,95206411	1570,87	RAP2A	RAP2A, member of RAS oncogene family
9653	1,27E-72	7,19E+01	1,22E-73	0,0524	18,1527108	0,95205218	2379,74	HS2ST1	heparan sulfate 2-O-sulfotransferase 1
2218	7,14E-66	6,51E+01	7,97E-67	0,0551	17,269609	0,95166596	2031,37	FKTN	fukutin
693217	9,52E-12	1,10E+01	4,10E-12	0,1372	6,9336213	0,9512971	181	MIR632	microRNA 632
440823	1,22E-02	1,91E+00	8,84E-03	0,3633	2,6180118	0,95102111	24,71	MIAT	myocardial infarction associated transcript
140838	5,42E-37	3,63E+01	1,16E-37	0,0741	12,8269148	0,95068057	1052,5	NANP	N-acetylneuraminic acid phosphatase
644353	1,53E-07	6,82E+00	7,93E-08	0,177	5,368817	0,95050313	113,84	ZCCHC18	zinc finger CCHC-type containing 18
5638	2,57E-33	3,26E+01	6,02E-34	0,0782	12,1459943	0,94982738	661,24	PRRG1	proline rich and Gla domain 1
22874	7,62E-47	4,61E+01	1,30E-47	0,0655	14,4951277	0,94981127	1135,13	PLEKHA6	pleckstrin homology domain containing A6
129450	5,04E-25	2,43E+01	1,46E-25	0,0909	10,450258	0,94976388	482,29	TYW5	tRNA-yW synthesizing protein 5
107984261	1,03E-01	9,87E-01	8,30E-02	0,5478	1,7333425	0,94952219	10,91	LOC107984	261
119016	1,57E-08	7,80E+00	7,70E-09	0,1644	5,7748012	0,94949654	128,47	AGAP4	ArfGAP with GTPase domain, ankyrin repeat and PH domain 4
29967	5,15E-59	5,83E+01	6,73E-60	0,0582	16,3233762	0,94947515	2275,39	LRP12	LDL receptor related protein 12
54629	1,41E-34	3,39E+01	3,20E-35	0,0766	12,3837844	0,9491601	725,86	MINDY2	MINDY lysine 48 deubiquitinase 2
3930	1,98E-77	7,67E+01	1,74E-78	0,0506	18,7555274	0,9487355	4591	LBR	lamin B receptor
221687	2,05E-26	2,57E+01	5,72E-27	0,0882	10,7532763	0,94861562	491,86	RNF182	ring finger protein 182
113218502	3,54E-04	3,45E+00	2,24E-04	0,257	3,6900204	0,94832215	57,55	MIR10397	microRNA 10397
55175	1,27E-33	3,29E+01	2,95E-34	0,0777	12,2042161	0,94827571	656	KLHL11	kelch like family member 11
102724813	1,07E-02	1,97E+00	7,72E-03	0,3558	2,6642806	0,94781973	25,39	LOC102724	protein FRG1B
5932	3,87E-118	1,17E+02	1,59E-119	0,0407	23,2451045	0,94719672	5757,13	RBBP8	RB binding protein 8, endonuclease
6402	6,39E-03	2,19E+00	4,50E-03	0,3334	2,8410335	0,94716077	31,81	SELL	selectin L
2135	3,20E-43	4,25E+01	5,97E-44	0,0681	13,9042737	0,94711145	1390,19	EXTL2	exostosin like glycosyltransferase 2
105379163	1,18E-01	9,28E-01	9,61E-02	0,5691	1,6641153	0,94710617	10,33	LOC105379	uncharacterized LOC105379163
7711	2,87E-21	2,05E+01	9,22E-22	0,0988	9,585284	0,94694462	386,29	ZNF155	zinc finger protein 155
2553	5,33E-47	4,63E+01	9,07E-48	0,0652	14,5198864	0,94653235	1273,96	GABPB1	GA binding protein transcription factor subunit beta 1
57621	5,36E-56	5,53E+01	7,49E-57	0,0595	15,8895154	0,94602252	1536,45	ZBTB2	zinc finger and BTB domain containing 2
1101	5,33E-03	2,27E+00	3,73E-03	0,3261	2,9005113	0,94579899	30,6	CHAD	chondroadherin
105371749	1,35E-01	8,70E-01	1,11E-01	0,5935	1,5930581	0,94548146	8,97	LOC105371	uncharacterized LOC105371749
101928068	9,47E-03	2,02E+00	6,78E-03	0,3489	2,7075476	0,944701	26,5	LOC101928	uncharacterized LOC101928068
79834	9,78E-56	5,50E+01	1,37E-56	0,0596	15,8514113	0,94458731	1595,39	PEAK1	pseudopodium enriched atypical kinase 1
100652988	2,52E-03	2,60E+00	1,71E-03	0,3011	3,1366481	0,94445124	39,3	LINC00702	long intergenic non-protein coding RNA 702
23468	1,42E-81	8,08E+01	1,14E-82	0,049	19,2610706	0,94433838	3534,12	CBX5	chromobox 5
55676	2,04E-65	6,47E+01	2,30E-66	0,0549	17,2083871	0,94427637	2573,86	SLC30A6	solute carrier family 30 member 6
5562	4,37E-98	9,74E+01	2,57E-99	0,0446	21,1533125	0,94407249	4696,42	PRKAA1	protein kinase AMP-activated catalytic subunit alpha 1
8630	1,23E-06	5,91E+00	6,65E-07	0,1899	4,971249	0,94392571	90,36	HSD17B6	hydroxysteroid 17-beta dehydrogenase 6
1075	3,57E-102	1,01E+02	1,96E-103	0,0437	21,5959092	0,94379031	11231,53	CTSC	cathepsin C
105370461	1,35E-02	1,87E+00	9,80E-03	0,3652	2,5826723	0,94324609	24,63	LOC105370	uncharacterized LOC105370461
26226	1,11E-01	9,55E-01	9,02E-02	0,5567	1,6943459	0,94319302	10,18	FBXW4P1	F-box and WD repeat domain containing 4 pseudogene 1
5529	1,29E-79	7,89E+01	1,07E-80	0,0496	19,0243403	0,94311262	2924,99	PPP2R5E	protein phosphatase 2 regulatory subunit B'epsilon
6542	1,17E-56	5,59E+01	1,61E-57	0,059	15,9855888	0,94290042	1487,35	SLC7A2	solute carrier family 7 member 2
100128568	6,43E-02	1,19E+00	5,05E-02	0,4822	1,9554738	0,94286856	14,27	RANBP3-DT	RANBP3 divergent transcript
80143	1,76E-57	5,68E+01	2,38E-58	0,0585	16,1042543	0,94273269	2060,52	SIKE1	suppressor of IKBKE 1
130340	1,06E-56	5,60E+01	1,46E-57	0,0589	15,9917445	0,94224266	1376,55	AP1S3	adaptor related protein complex 1 subunit sigma 3
112267879	3,20E-02	1,49E+00	2,42E-02	0,4179	2,2542951	0,94208935	18,03	LOC112267	uncharacterized LOC112267879
55610	3,21E-36	3,55E+01	6,97E-37	0,0742	12,6870837	0,9419137	806,91	VPS50	VPS50 subunit of EARP/GARPII complex
22890	1,10E-55	5,50E+01	1,55E-56	0,0594	15,8437707	0,9416303	1696,91	ZBTB1	zinc finger and BTB domain containing 1
8745	1,86E-08	7,73E+00	9,18E-09	0,1639	5,7452836	0,94149008	128,6	ADAM23	ADAM metallopeptidase domain 23
79944	8,32E-49	4,81E+01	1,36E-49	0,0636	14,8052278	0,94148137	1184,77	L2HGDH	L-2-hydroxyglutarate dehydrogenase
132720	1,48E-25	2,48E+01	4,24E-26	0,0891	10,5669481	0,94146146	582,42	FAM241A	family with sequence similarity 241 member A
4659	2,14E-94	9,37E+01	1,35E-95	0,0453	20,7455211	0,94050839	5475,23	PPP1R12A	protein phosphatase 1 regulatory subunit 12A
55660	1,38E-129	1,29E+02	4,58E-131	0,0386	24,3596846	0,94038346	8519,37	PRPF40A	pre-mRNA processing factor 40 homolog A
55103	2,51E-71	7,06E+01	2,49E-72	0,0522	17,9863147	0,93960794	2235,56	RALGPS2	Ral GEF with PH domain and SH3 binding motif 2
79832	5,36E-87	8,63E+01	3,88E-88	0,0472	19,902371	0,93959014	4811,23	QSER1	glutamine and serine rich 1
5991	1,67E-09	8,78E+00	7,88E-10	0,1528	6,1472695	0,93915321	159,92	RFX3	regulatory factor X3
59345	2,41E-71	7,06E+01	2,38E-72	0,0522	17,9888371	0,93915002	4222,33	GNB4	G protein subunit beta 4
60558	2,90E-70	6,95E+01	2,95E-71	0,0526	17,8488973	0,93853766	3092,77	GUF1	GTP binding elongation factor GUF1
23642	4,55E-103	1,02E+02	2,44E-104	0,0433	21,6920218	0,93835069	4744,11	SNHG1	small nucleolar RNA host gene 1
84294	5,23E-59	5,83E+01	6,84E-60	0,0575	16,3223806	0,93814053	2093,36	UTP23	UTP23 small subunit processome component
6815	2,23E-45	4,47E+01	3,96E-46	0,0658	14,2586273	0,93809734	1153,83	STYX	serine/threonine/tyrosine interacting protein
105374838	1,54E-04	3,81E+00	9,47E-05	0,2402	3,9037422	0,93751505	58,42	LOC105374	838
692203	1,65E-03	2,78E+00	1,10E-03	0,2873	3,2625724	0,93747649	40,73	SNORD88B	small nucleolar RNA, C/D box 88B

25998	4,55E-84	8,33E+01	3,47E-85	0,0479	19,5587863	0,93739091	3860,58	IBTK	inhibitor of Bruton tyrosine kinase
51426	1,61E-55	5,48E+01	2,28E-56	0,0593	15,819652	0,93732805	1391,59	POLK	DNA polymerase kappa
55471	3,79E-47	4,64E+01	6,42E-48	0,0644	14,5434744	0,93719197	1275,6	NDUFAF7	NADH:ubiquinone oxidoreductase complex assembly factor 7
2996	6,89E-03	2,16E+00	4,87E-03	0,3327	2,8157663	0,93680644	29,53	GYPE	glycophorin E (MNS blood group)
107985440	7,48E-02	1,13E+00	5,93E-02	0,4966	1,8859955	0,93654174	13,21	LOC107985	uncharacterized LOC107985440
29842	3,44E-04	3,46E+00	2,18E-04	0,2532	3,6976705	0,93634795	53,24	TFCP2L1	transcription factor CP2 like 1
100289635	1,43E-27	2,68E+01	3,87E-28	0,0851	10,9988286	0,93598769	630,29	ZNF605	zinc finger protein 605
166824	3,01E-02	1,52E+00	2,27E-02	0,4108	2,2784258	0,93592402	19,16	RASSF6	Ras association domain family member 6
7042	3,92E-94	9,34E+01	2,49E-95	0,0452	20,71598	0,93562342	4399,5	TGFB2	transforming growth factor beta 2
51193	1,18E-65	6,49E+01	1,33E-66	0,0543	17,2400424	0,93552586	2223,86	ZNF639	zinc finger protein 639
100302691	6,56E-02	1,18E+00	5,16E-02	0,4805	1,9463754	0,93531077	15,36	LINC00184	long intergenic non-protein coding RNA 184
9824	2,08E-78	7,77E+01	1,78E-79	0,0495	18,8765111	0,93514528	4672,06	ARHGAP11A	Rho GTPase activating protein 11A
130827	6,08E-09	8,22E+00	2,94E-09	0,1576	5,9351697	0,93513905	141,48	TMEM182	transmembrane protein 182
81399	1,89E-01	7,24E-01	1,59E-01	0,6634	1,4081327	0,93414571	7,24	OR4F16	olfactory receptor family 4 subfamily F member 16
9515	1,86E-01	7,30E-01	1,56E-01	0,659	1,4175266	0,93408238	7,2	STXBP5L	syntaxin binding protein 5L
91137	1,21E-39	3,89E+01	2,45E-40	0,0702	13,2956821	0,93397389	2870,3	SLC25A46	solute carrier family 25 member 46
51444	1,69E-49	4,88E+01	2,71E-50	0,0626	14,9131564	0,93374364	1862,52	RNF138	ring finger protein 138
339105	7,72E-05	4,11E+00	4,65E-05	0,2291	4,0727488	0,93315817	64,4	PRSS53	serine protease 53
643155	4,28E-53	5,24E+01	6,37E-54	0,0604	15,4609133	0,93313295	3008,4	SMIM15	small integral membrane protein 15
112268272	4,28E-07	6,37E+00	2,26E-07	0,1802	5,1763007	0,93297164	109,19	LOC112268	uncharacterized LOC112268272
93594	7,75E-46	4,51E+01	1,36E-46	0,0651	14,3330348	0,93294046	1736,34	TBC1D31	TBC1 domain family member 31
652965	5,71E-02	1,24E+00	4,46E-02	0,4645	2,0084596	0,93292785	18,13	SNORA48	small nucleolar RNA, H/ACA box 48
3796	2,33E-94	9,36E+01	1,47E-95	0,0449	20,7412577	0,93223266	4308,64	KIF2A	kinesin family member 2A
64418	3,34E-34	3,35E+01	7,65E-35	0,0757	12,3136533	0,93207467	723,11	TMEM168	transmembrane protein 168
51575	5,25E-78	7,73E+01	4,53E-79	0,0495	18,8271258	0,93195736	3076,73	ESF1	ESF1 nucleolar pre-rRNA processing protein homolog
51742	5,26E-50	4,93E+01	8,34E-51	0,0622	14,9915461	0,93180033	2314,91	ARID4B	AT-rich interaction domain 4B
64799	1,02E-06	5,99E+00	5,48E-07	0,186	5,0087647	0,93170132	102,79	IQCH	IQ motif containing H
10265	2,85E-10	9,55E+00	1,30E-10	0,1449	6,4271238	0,93146493	165,63	IRX5	iroquois homeobox 5
53335	1,46E-03	2,84E+00	9,70E-04	0,2823	3,2990495	0,93145159	42,71	BCL11A	BCL11 transcription factor A
644128	1,20E-16	1,59E+01	4,42E-17	0,1108	8,4011795	0,9309531	308,57	RPL23AP53	ribosomal protein L23a pseudogene 53
56929	3,56E-46	4,54E+01	6,19E-47	0,0647	14,3875601	0,93059609	1537,46	FEM1C	fem-1 homolog C
9819	1,15E-39	3,89E+01	2,33E-40	0,07	13,2994096	0,93053677	859,72	TSC22D2	TSC22 domain family member 2
105371773	1,94E-02	1,71E+00	1,43E-02	0,3799	2,4491825	0,93036377	25,87	LOC105371	uncharacterized LOC105371773
8323	2,01E-78	7,77E+01	1,71E-79	0,0493	18,8784989	0,93030663	3770,51	FZD6	frizzled class receptor 6
55165	1,82E-104	1,04E+02	9,47E-106	0,0426	21,8409653	0,93009542	8216,09	CEP55	centrosomal protein 55
57657	2,02E-11	1,07E+01	8,83E-12	0,1363	6,8244498	0,93009069	211,41	HCN3	hyperpolarization activated cyclic nucleotide gated potassium channel 3
5584	1,39E-68	6,79E+01	1,46E-69	0,0527	17,6295512	0,92995743	3248,78	PRKCI	protein kinase C iota
10349	3,39E-05	4,47E+00	1,99E-05	0,218	4,2658244	0,92987593	68,09	ABCA10	ATP binding cassette subfamily A member 10
153443	6,26E-54	5,32E+01	9,13E-55	0,0596	15,5855527	0,9292538	1465,64	SRFBP1	serum response factor binding protein 1
387104	1,66E-15	1,48E+01	6,34E-16	0,1149	8,0826456	0,9288028	267,01	SOGA3	SOGA family member 3
440078	1,11E-01	9,55E-01	9,01E-02	0,548	1,6948089	0,92876664	10,67	FAM66C	family with sequence similarity 66 member C
80304	6,76E-40	3,92E+01	1,36E-40	0,0696	13,3398668	0,92813931	967,09	WDCP	WD repeat and coiled coil containing
55835	7,96E-43	4,21E+01	1,50E-43	0,067	13,8382214	0,92776439	1160,21	CENPJ	centromere protein J
107987300	6,73E-02	1,17E+00	5,31E-02	0,4796	1,9341173	0,92769681	13,81	LOC107987	uncharacterized LOC107987300
100313843	2,73E-02	1,56E+00	2,05E-02	0,4003	2,3172495	0,92762671	19,77	MIR711	microRNA 711
26230	2,84E-12	1,15E+01	1,20E-12	0,1306	7,1050063	0,92759906	211,61	TIAM2	TIAM Rac1 associated GEF 2
51571	4,63E-95	9,43E+01	2,89E-96	0,0445	20,8194005	0,9271821	5846,1	CYRIB	CYFIP related Rac1 interactor B
59338	4,11E-47	4,64E+01	6,96E-48	0,0638	14,5379627	0,92680612	1165,93	PLEKHA1	pleckstrin homology domain containing A1
9863	4,30E-04	3,37E+00	2,74E-04	0,2547	3,6383195	0,92672698	51,85	MAGI2	membrane associated guanylate kinase, WW and PDZ domain containing 2
107984449	1,22E-03	2,91E+00	8,07E-04	0,2766	3,3503661	0,92667189	44,19	LOC107984	uncharacterized LOC107984449
101060376	1,04E-06	5,98E+00	5,61E-07	0,1851	5,0042792	0,92615005	97,77	TBC1D3L	TBC1 domain family member 3L
1964	5,90E-52	5,12E+01	8,97E-53	0,0605	15,2895862	0,92509008	3894,97	EIF1AX	eukaryotic translation initiation factor 1A X-linked
7222	4,71E-04	3,33E+00	3,01E-04	0,2558	3,6142486	0,92461843	49,47	TRPC3	transient receptor potential cation channel subfamily C member 3
257194	8,05E-29	2,81E+01	2,10E-29	0,0821	11,2585566	0,92438104	633,66	NEGR1	neuronal growth regulator 1
7031	3,01E-03	2,52E+00	2,05E-03	0,2998	3,0827002	0,92416441	36,41	TFF1	trefoil factor 1
55279	1,15E-38	3,79E+01	2,37E-39	0,0704	13,1248477	0,92406061	897,78	ZNF654	zinc finger protein 654
55789	1,18E-62	6,19E+01	1,42E-63	0,0549	16,8320784	0,92342547	1684,46	DEPDC1B	DEP domain containing 1B
92092	9,49E-25	2,40E+01	2,77E-25	0,0889	10,3895919	0,92327936	466,44	ZC3HAV1L	zinc finger CCCH-type containing, antiviral 1 like
105369370	2,45E-41	4,06E+01	4,77E-42	0,0679	13,5872585	0,92307013	959,5	LOC105369	uncharacterized LOC105369370
286205	1,94E-19	1,87E+01	6,57E-20	0,101	9,1345901	0,92299258	381,09	SCAI	suppressor of cancer cell invasion
101929225	2,51E-02	1,60E+00	1,88E-02	0,3926	2,350358	0,92286385	20,8	MCM8-AS1	MCM8 antisense RNA 1
10092	4,46E-99	9,84E+01	2,59E-100	0,0434	21,2614131	0,92249506	10060,62	ARPC5	actin related protein 2/3 complex subunit 5
90576	2,20E-18	1,77E+01	7,66E-19	0,1041	8,8648709	0,92244553	338,11	ZNF799	zinc finger protein 799
89890	3,62E-31	3,04E+01	8,95E-32	0,0786	11,7300054	0,92237884	665,75	KBTBD6	kelch repeat and BTB domain containing 6
55366	1,22E-73	7,29E+01	1,15E-74	0,0504	18,2822116	0,92213802	3484,56	LGR4	leucine rich repeat containing G protein-coupled receptor 4
132789	1,07E-34	3,40E+01	2,43E-35	0,0743	12,4057462	0,92211393	784,47	GNPDA2	glucosamine-6-phosphate deaminase 2
116931	1,92E-06	5,72E+00	1,05E-06	0,1889	4,881737	0,92211	98,24	MED12L	mediator complex subunit 12L
100996758	2,11E-02	1,68E+00	1,56E-02	0,3814	2,4173717	0,92189958	21,96	NPY4R2	neuropeptide Y receptor Y4-2
5921	2,09E-100	9,97E+01	1,17E-101	0,043	21,4060568	0,92118585	4486,96	RASA1	RAS p21 protein activator 1
399669	3,83E-03	2,42E+00	2,64E-03	0,3063	3,0065536	0,92105006	34,41	ZNF321P	zinc finger protein 321, pseudogene
54851	7,92E-28	2,71E+01	2,13E-28	0,0833	11,0526642	0,92037941	597,53	ANKRD49	ankyrin repeat domain 49
11244	1,14E-64	6,39E+01	1,30E-65	0,0538	17,1075674	0,92026927	2048,68	ZHX1	zinc fingers and homeoboxes 1
100133331	5,21E-13	1,23E+01	2,15E-13	0,1254	7,3388409	0,92020396	261,51	LOC100133	replaced by ID 100288069
23446	1,91E-61	6,07E+01	2,36E-62	0,0552	16,6648738	0,92006515	2897,76	SLC44A1	solute carrier family 44 member 1
55233	2,16E-102	1,02E+02	1,18E-103	0,0426	21,6193749	0,91994981	7540,38	MOB1A	MOB kinase activator 1A
10087	1,30E-64	6,39E+01	1,50E-65	0,0538	17,0995121	0,91985037	2114,06	CERT1	ceramide transporter 1
727851	7,46E-25	2,41E+01	2,17E-25	0,0883	10,4127989	0,91976512	480,51	RGPD8	RANBP2 like and GRIP domain containing 8
284370	7,34E-16	1,51E+01	2,77E-16	0,1124	8,183071	0,91954171	299,44	ZNF615	zinc finger protein 615
57212	4,33E-41	4,04E+01	8,45E-42	0,0679	13,5452914	0,91948592	938,87	TP73-AS1	TP73 antisense RNA 1
51101	7,07E-17	1,62E+01	2,58E-17	0,1086	8,4640815	0,91916291	355,51	ZC2HC1A	zinc finger C2HC-type containing 1A
10390	6,88E-50	4,92E+01	1,09E-50	0,0614	14,973527	0,91877046	1310	CEPT1	choline/ethanolamine phosphotransferase 1
84138	2,15E-68	6,77E+01	2,28E-69	0,0522	17,6043367	0,91870488	2136,56	SLC7A6OS	solute carrier family 7 member 6 opposite strand
114822	5,38E-26	2,53E+01	1,52E-26	0,0862	10,6629469	0,918697	599,76	RHPN1	rhophilin Rho GTPase binding protein 1
9521	3,95E-55	5,44E+01	5,63E-56	0,0583	15,7625624	0,91863789	1779,54	EEF1E1	eukaryotic translation elongation factor 1 epsilon 1
102723320	5,87E-02	1,23E+00	4,59E-02	0,4602	1,9959256	0,91855081	19,8	CERS3-AS1	CERS3 antisense RNA 1
4751	2,49E-82	8,16E+01	1,97E-83	0,0475	19,35186	0,91846158	3071,74	NEK2	NIMA related kinase 2
10787	3,59E-16	1,54E+01	1,34E-16	0,1111	8,2698666	0,91845751	7124,73	NCKAP1	NCK associated protein 1
387990	6,88E-03	2,16E+00	4,86E-03	0,3261	2,8161485	0,91834226	31,54	TOMM20L	translocase of outer mitochondrial membrane 20 like
55167	6,33E-39	3,82E+01	1,30E-39	0,0697	13,1704397	0,9183185	921,76	MSL2	MSL complex subunit 2
5629	1,02E-03	2,99E+00	6,72E-04	0,27	3,4008024	0,91811713	45,68	PROX1	prospero homeobox 1
11177	1,11E-94	9,40E+01	6,98E-96	0,0442	20,7770413	0,91800499	5881,71	BAZ1A	bromodomain adjacent to zinc finger domain 1A
3157	1,95E-52	5,17E+01	2,93E-53	0,0598	15,3622746	0,91789955	1494,9	HMGCS1	3-hydroxy-3-methylglutaryl-CoA synthase 1
120227	2,59E-36	3,56E+01	5,63E-37	0,0723	12,7038526	0,91789138	1087,05	CYP2R1	cytochrome P450 family 2 subfamily R member 1
10592	7,79E-91	9,01E+01	5,22E-92	0,0451	20,3442901	0,91787157	7463,86	SMC2	structural maintenance of chromosomes 2
8540	8,40E-72	7,11E+01	8,23E-73	0,0508	18,0476608	0,9176719	3916,97	AGPS	alkylglycerone phosphate synthase
115795	4,79E-05	4,32E+00	2,85E-05	0,2192	4,185453	0,917351	70,73	FANCD2OS	FANCD2 opposite strand
146540	7,77E-08	7,11E+00	3,95E-08	0,167	5,4930674	0,91734726	125,71	ZNF785	zinc finger protein 785
153339	7,56E-45	4,41E+01	1,36E-45	0,0647	14,1722881	0,91719573	3286,35	TMEM167A	transmembrane protein 167A
11168	5,60E-49	4,83E+01	9,08E-50	0,0618	14,8321167	0,91715693	4220,82	PSIP1	PC4 and SRSF1 interacting protein 1
55288	8,35E-41	4,01E+01	1,64E-41	0,068	13,4966337	0,917132	1049,94	RHOT1	ras homolog family member T1
728841	1,86E-98	9,77E+01	1,09E-99	0,0432	21,1938359	0,91661009	4307,46	NBPF8	NBPF member 8
100302224	3,75E-02	1,43E+00	2,86E-02	0,4186	2,1883338	0,9160687	19,05	MIR2110	microRNA 2110
728591	6,49E-07	6,19E+00	3,46E-07	0,1796	5,0964649	0,91550997	114,31	CCDC169	coiled-coil domain containing 169
5446	1,49E-05	4,83E+00	8,57E-06	0,2056	4,4504521	0,91508799	80,86	PON3	paraoxonase 3
151987	1,28E-65	6,49E+01	1,43E-66	0,053	17,2357314	0,9141656	3923,84	PPP4R2	protein phosphatase 4 regulatory subunit 2
124930	2,29E-23	2,26E+01	6,95E-24	0,0907	10,0775257	0,91383273	536	ANKRD13B	ankyrin repeat domain 13B
727866	9,63E-25	2,40E+01	2,81E-25	0,0879	10,388154	0,91351992	542,66	FAM156B	family with sequence similarity 156 member B
2177	8,39E-65	6,41E+01	9,56E-66	0,0533	17,1256072	0,91341552	1966,34	FANCD2	FA complementation group D2
144766	4,87E-05	4,31E+00	2,89E-05	0,2184	4,1818806	0,91333067	69,71	LINC00355	long intergenic non-protein coding RNA 355
53616	2,46E-14	1,36E+01	9,76E-15	0,1179	7,7423911	0,91310718	281,96	ADAM22	ADAM metallopeptidase domain 22
9786	5,45E-62	6,13E+01	6,65E-63	0,0545	16,7404555	0,91287433	3160,36	KIAA0586	KIAA0586
143098	8,36E-09	8,08E+00	4,06E-09	0,1552	5,8818262	0,91265709	137,09	MPP7	MAGUK p55 scaffold protein 7
84206	4,73E-04	3,33E+00	3,03E-04	0,2526	3,6130775	0,91259867	50,93	MEX3B	mex-3 RNA binding family member B
54464	1,71E-46	4,58E+01	2,95E-47	0,0632	14,4387307	0,91229774	1129,61	XRN1	5'-3' exoribonuclease 1
440423	2,92E-25	2,45E+01	8,41E-26	0,0869	10,5025384	0,91220695	494,65	SUZ12P1	SUZ12 pseudogene 1
53339	1,52E-77	7,68E+01	1,34E-78	0,0486	18,769678	0,91195925	4261,21	BTBD1	BTB domain containing 1
127018	3,69E-23	2,24E+01	1,12E-23	0,0909	10,0303644	0,91173599	569,66	LYPLAL1	lysophospholipase like 1
107984427	9,80E-03	2,01E+00	7,02E-03	0,3382	2,6957013	0,91169735	27,91	ME3-DT	ME3 divergent transcript
4982	7,18E-38	3,71E+01	1,51E-38	0,0702	12,9840601	0,91115235	825,01	TNFRSF11B	TNF receptor superfamily member 11b
105372061	2,12E-02	1,67E+00	1,57E-02	0,377	2,4167514	0,91099603	22,57	LOC105372	uncharacterized LOC105372061

60496	2,77E-51	5,06E+01	4,25E-52	0,06	15,1879379	0,91090592	3161,84	AASDHPPT	aminoadipate-semialdehyde dehydrogenase-phosphopantetheinyl transferase
10640	8,98E-75	7,40E+01	8,27E-76	0,0494	18,4250309	0,91047766	4614,23	EXOC5	exocyst complex component 5
64757	8,27E-18	1,71E+01	2,93E-18	0,1045	8,7141131	0,91044624	390,37	MTARC1	mitochondrial amidoxime reducing component 1
157378	5,59E-30	2,93E+01	1,42E-30	0,0792	11,4936944	0,91041979	981,37	TMEM65	transmembrane protein 65
107987399	4,22E-02	1,37E+00	3,24E-02	0,4254	2,1399675	0,91031328	17,84	LOC107987	replaced by ID 101929819
49855	1,72E-26	2,58E+01	4,79E-27	0,0845	10,7695233	0,90980693	567,7	SCAPER	S-phase cyclin A associated protein in the ER
23657	1,62E-56	5,58E+01	2,23E-57	0,057	15,9652903	0,90967659	1548,71	SLC7A11	solute carrier family 7 member 11
10811	4,39E-08	7,36E+00	2,20E-08	0,1625	5,5951977	0,90933769	135,54	NOXA1	NADPH oxidase activator 1
92344	5,76E-26	2,52E+01	1,63E-26	0,0853	10,6564358	0,90892148	770,51	GORAB	golgin, RAB6 interacting
3146	1,20E-78	7,79E+01	1,02E-79	0,0481	18,9059698	0,90857843	20481,83	HMGB1	high mobility group box 1
57531	4,90E-27	2,63E+01	1,35E-27	0,0834	10,8858353	0,90839789	620,12	HACE1	HECT domain and ankyrin repeat containing E3 ubiquitin protein ligase 1
107984262	1,46E-04	3,84E+00	8,95E-05	0,2318	3,9174053	0,9078897	64,34	LOC107984	uncharacterized LOC107984262
100268168	2,44E-04	3,61E+00	1,53E-04	0,2397	3,7863765	0,90743184	56,74	RPL26L1-AS	RPL26L1 antisense RNA 1
101927293	9,62E-02	1,02E+00	7,74E-02	0,5139	1,7657207	0,90733872	13,18	LOC101927	uncharacterized LOC101927293
5290	2,37E-52	5,16E+01	3,57E-53	0,0591	15,3494631	0,90727427	1798,46	PIK3CA	phosphatidylinositol-4,5-bisphosphate 3-kinase catalytic subunit alpha
140707	4,60E-57	5,63E+01	6,27E-58	0,0565	16,0442632	0,90720643	1711,36	BRI3BP	BRI3 binding protein
4008	4,46E-77	7,64E+01	3,95E-78	0,0485	18,7120388	0,90676543	6948,11	LMO7	LIM domain 7
100130418	1,17E-02	1,93E+00	8,41E-03	0,344	2,635094	0,90653405	30,27	CECR7	cat eye syndrome chromosome region, candidate 7
79815	9,33E-18	1,70E+01	3,32E-18	0,1042	8,7000869	0,90614208	364,04	NIPAL2	NIPA like domain containing 2
9655	3,02E-48	4,75E+01	4,99E-49	0,0616	14,7173162	0,90606748	1466,35	SOCS5	suppressor of cytokine signaling 5
54332	6,66E-24	2,32E+01	1,99E-24	0,0888	10,1997261	0,90596598	466,29	GDAP1	ganglioside induced differentiation associated protein 1
151194	4,58E-17	1,63E+01	1,66E-17	0,1064	8,515212	0,90594465	455,69	METTL21A	methyltransferase 21A, HSPA lysine
6674	4,95E-54	5,33E+01	7,21E-55	0,058	15,6006446	0,90560013	1564,07	SPAG1	sperm associated antigen 1
643338	1,82E-03	2,74E+00	1,22E-03	0,2799	3,2336921	0,90521781	42,75	C15orf62	chromosome 15 open reading frame 62
5955	1,16E-82	8,19E+01	9,08E-84	0,0467	19,3916392	0,90495149	3811,37	RCN2	reticulocalbin 2
112268169	1,03E-03	2,99E+00	6,76E-04	0,266	3,3989676	0,90421619	44,93	LOC112268	uncharacterized LOC112268169
4124	4,55E-66	6,53E+01	5,07E-67	0,0523	17,2957107	0,90402054	6868,9	MAN2A1	mannosidase alpha class 2A member 1
2897	7,86E-02	1,10E+00	6,25E-02	0,4851	1,8627788	0,90368471	14,02	GRIK1	glutamate ionotropic receptor kainate type subunit 1
54962	2,74E-58	5,76E+01	3,63E-59	0,0557	16,2201784	0,90366014	1786,15	TIPIN	TIMELESS interacting protein
107984567	9,98E-02	1,00E+00	8,05E-02	0,517	1,7476839	0,90363836	11,8	LOC107984	LINE-1 retrotransposable element ORF2 protein-like
57547	3,23E-12	1,15E+01	1,37E-12	0,1275	7,0869647	0,90357552	215,68	ZNF624	zinc finger protein 624
107985508	1,55E-01	8,10E-01	1,29E-01	0,5942	1,5197086	0,90304599	8,9	LOC107985	uncharacterized LOC107985508
112268174	3,31E-02	1,48E+00	2,50E-02	0,4028	2,2406507	0,90244356	19,45	LOC112268	uncharacterized LOC112268174
169981	5,78E-22	2,12E+01	1,81E-22	0,0925	9,7516556	0,90221081	423,09	SPIN3	spindlin family member 3
165082	7,34E-05	4,13E+00	4,41E-05	0,2209	4,0849334	0,90216354	67,5	ADGRF3	adhesion G protein-coupled receptor F3
1875	6,47E-29	2,82E+01	1,68E-29	0,08	11,2780333	0,90216254	616,03	E2F5	E2F transcription factor 5
23232	2,24E-33	3,26E+01	5,23E-34	0,0742	12,157498	0,90169757	836,68	TBC1D12	TBC1 domain family member 12
54878	3,51E-55	5,45E+01	5,00E-56	0,0571	15,7700488	0,90114081	2050,74	DPP8	dipeptidyl peptidase 8
643836	4,01E-28	2,74E+01	1,07E-28	0,081	11,1141718	0,90058076	615,79	ZFP62	ZFP62 zinc finger protein
56704	9,07E-15	1,40E+01	3,54E-15	0,1144	7,8700515	0,90052087	277,09	JPH1	junctophilin 1
6558	1,61E-40	3,98E+01	3,18E-41	0,067	13,4475312	0,90036535	1450,01	SLC12A2	solute carrier family 12 member 2
22847	7,11E-62	6,11E+01	8,70E-63	0,0538	16,7244288	0,90031144	1849,82	ZNF507	zinc finger protein 507
84085	4,64E-38	3,73E+01	9,71E-39	0,0691	13,0176581	0,89993061	1013,88	FBXO30	F-box protein 30
6856	2,08E-64	6,37E+01	2,40E-65	0,0527	17,0719733	0,89973121	4048,25	SYPL1	synaptophysin like 1
6873	8,97E-75	7,40E+01	8,25E-76	0,0488	18,4251742	0,89963767	2844	TAF2	TATA-box binding protein associated factor 2
10301	1,13E-34	3,39E+01	2,55E-35	0,0725	12,4018356	0,89960739	861,8	DLEU1	deleted in lymphocytic leukemia 1
113939925	1,96E-09	8,71E+00	9,26E-10	0,1469	6,1217398	0,89898623	156,58	BMS1P4-AG	BMS1P4-AGAP5 readthrough
116064	5,93E-47	4,62E+01	1,01E-47	0,0619	14,5124776	0,89796169	1965,02	LRRC58	leucine rich repeat containing 58
100289124	9,40E-02	1,03E+00	7,56E-02	0,5051	1,7769493	0,89745174	12,4	FAM27E2	family with sequence similarity 27 member E2
728734	1,21E-02	1,92E+00	8,70E-03	0,342	2,6236261	0,89738098	27,11	NPIPB8	nuclear pore complex interacting protein family member B8
83699	3,54E-14	1,35E+01	1,41E-14	0,1166	7,6954648	0,89737669	278,92	SH3BGRL2	SH3 domain binding glutamate rich protein like 2
65250	1,17E-56	5,59E+01	1,61E-57	0,0561	15,9857382	0,89710964	1831,37	CPLANE1	ciliogenesis and planar polarity effector complex subunit 1
105370337	4,02E-10	9,40E+00	1,85E-10	0,1408	6,3736084	0,89708972	175,36	LOC105370	uncharacterized LOC105370337
6646	5,62E-56	5,53E+01	7,85E-57	0,0565	15,886542	0,89680603	6220,42	SOAT1	sterol O-acyltransferase 1
5610	2,04E-91	9,07E+01	1,36E-92	0,0439	20,4101901	0,89665576	5564,42	EIF2AK2	eukaryotic translation initiation factor 2 alpha kinase 2
100129387	1,47E-12	1,18E+01	6,18E-13	0,1246	7,1965376	0,89663186	217,76	GABPB1-AS	GABPB1 antisense RNA 1
130749	1,17E-08	7,93E+00	5,73E-09	0,1539	5,8243989	0,89650879	145,23	CPO	carboxypeptidase O
4238	5,87E-66	6,52E+01	6,54E-67	0,0519	17,2810053	0,89612501	2308,32	MFAP3	microfibril associated protein 3
481	2,19E-88	8,77E+01	1,55E-89	0,0447	20,0632864	0,89592598	12964,69	ATP1B1	ATPase Na+/K+ transporting subunit beta 1
1836	6,97E-58	5,72E+01	9,32E-59	0,0554	16,1621829	0,89574569	2004,62	SLC26A2	solute carrier family 26 member 2
101867536	8,94E-09	8,05E+00	4,34E-09	0,1526	5,870542	0,89561655	149,17	PRNCR1	prostate cancer associated non-coding RNA 1
84675	1,94E-01	7,12E-01	1,63E-01	0,6422	1,394542	0,89559516	7,64	TRIM55	tripartite motif containing 55
10692	7,89E-02	1,10E+00	6,27E-02	0,4801	1,8612317	0,89355865	14,04	RRH	retinal pigment epithelium-derived rhodopsin homolog
55773	4,70E-59	5,83E+01	6,13E-60	0,0547	16,3290493	0,89266975	2226,89	TBC1D23	TBC1 domain family member 23
105372321	2,55E-11	1,06E+01	1,12E-11	0,1314	6,790218	0,89228082	237,99	LOC105372	uncharacterized LOC105372321
105372824	1,83E-01	7,38E-01	1,54E-01	0,6255	1,4264109	0,89224704	8,29	LOC105372	uncharacterized LOC105372824
105375921	2,37E-01	6,25E-01	2,02E-01	0,6997	1,2751228	0,89222233	6,44	LOC105375	uncharacterized LOC105375921
80223	4,39E-57	5,64E+01	5,99E-58	0,0556	16,0471204	0,89216406	2148,09	RAB11FIP1	RAB11 family interacting protein 1
11073	4,92E-78	7,73E+01	4,24E-79	0,0474	18,8305763	0,89199661	3544,26	TOPBP1	DNA topoisomerase II binding protein 1
22889	2,73E-73	7,26E+01	2,59E-74	0,0489	18,2376814	0,89140056	2795,43	KHDC4	KH domain containing 4, pre-mRNA splicing factor
54931	2,99E-55	5,45E+01	4,25E-56	0,0565	15,7802803	0,8909245	1787,13	TRMT10C	tRNA methyltransferase 10C, mitochondrial RNase P subunit
29969	3,76E-28	2,74E+01	1,00E-28	0,0801	11,1200685	0,89090553	740,64	MDFIC	MyoD family inhibitor domain containing
221336	3,99E-10	9,40E+00	1,83E-10	0,1397	6,3747503	0,89064154	183,86	BEND6	BEN domain containing 6
23047	9,20E-61	6,00E+01	1,16E-61	0,0537	16,5693963	0,89008652	2122,23	PDS5B	PDS5 cohesin associated factor B
64225	3,97E-70	6,94E+01	4,06E-71	0,0499	17,831071	0,88994104	2903,76	ATL2	atlastin GTPase 2
8558	5,87E-43	4,22E+01	1,10E-43	0,0642	13,860345	0,88968445	1476,86	CDK10	cyclin dependent kinase 10
152185	1,63E-24	2,38E+01	4,79E-25	0,0861	10,3369732	0,88962055	502,94	SPICE1	spindle and centriole associated protein 1
1259	5,16E-05	4,29E+00	3,07E-05	0,2134	4,1684596	0,88958294	72,09	CNGA1	cyclic nucleotide gated channel subunit alpha 1
101928646	3,72E-08	7,43E+00	1,86E-08	0,1582	5,6246206	0,88954738	144,25	BMAL2-AS1	BMAL2 antisense RNA 1
107985297	4,09E-02	1,39E+00	3,13E-02	0,413	2,1528752	0,88913131	19,51	LOC107985	replaced by ID 10036
100335030	5,96E-02	1,22E+00	4,66E-02	0,4468	1,9897692	0,88901957	18,24	LOC100335	FGFR1 oncogene partner 2 pseudogene
26224	3,59E-40	3,94E+01	7,16E-41	0,0664	13,3874758	0,88893769	1492,2	FBXL3	F-box and leucine rich repeat protein 3
8564	1,99E-10	9,70E+00	9,04E-11	0,1371	6,4821951	0,8885208	179,41	KMO	kynurenine 3-monooxygenase
107987398	1,09E-03	2,96E+00	7,15E-04	0,2626	3,3838214	0,88843597	51,83	LOC107987	replaced by ID 101929819
91461	9,26E-05	4,03E+00	5,61E-05	0,2205	4,0285752	0,88817743	66,32	PKDCC	protein kinase domain containing, cytoplasmic
221078	1,95E-26	2,57E+01	5,44E-27	0,0825	10,7579308	0,88804317	629,7	NSUN6	NOP2/Sun RNA methyltransferase 6
221830	2,48E-51	5,06E+01	3,81E-52	0,0584	15,1951475	0,88783726	1678,18	POLR1F	RNA polymerase I subunit F
64844	2,73E-48	4,76E+01	4,52E-49	0,0603	14,7240452	0,88729988	3642,93	MARCHF7	membrane associated ring-CH-type finger 7
23102	5,91E-59	5,82E+01	7,74E-60	0,0544	16,3148424	0,8872997	1712,9	TBC1D2B	TBC1 domain family member 2B
9348	9,59E-03	2,02E+00	6,87E-03	0,3281	2,703061	0,88700043	31,81	NDST3	N-deacetylase and N-sulfotransferase 3
51389	3,74E-58	5,74E+01	4,97E-59	0,0547	16,2009231	0,88689824	2137,87	RWDD1	RWD domain containing 1
55266	1,06E-49	4,90E+01	1,69E-50	0,0593	14,9444802	0,88683684	1510,86	TMEM19	transmembrane protein 19
55664	1,87E-16	1,57E+01	6,90E-17	0,1062	8,3487367	0,88673647	318,67	CDC37L1	cell division cycle 37 like 1, HSP90 cochaperone
84220	2,60E-24	2,36E+01	7,67E-25	0,0862	10,2918126	0,8866625	495,98	RGPD5	RANBP2 like and GRIP domain containing 5
8500	4,68E-85	8,43E+01	3,49E-86	0,0451	19,6755639	0,88659215	4249,77	PPFIA1	PTPRF interacting protein alpha 1
257313	2,84E-02	1,55E+00	2,13E-02	0,385	2,3024163	0,88643126	22,41	UTS2B	urotensin 2B
2653	3,58E-04	3,45E+00	2,27E-04	0,2404	3,6873884	0,88638156	740,32	GCSH	glycine cleavage system protein H
29116	8,24E-34	3,31E+01	1,91E-34	0,0724	12,2396912	0,88626649	920,32	MYLIP	myosin regulatory light chain interacting protein
9254	1,29E-01	8,89E-01	1,06E-01	0,5479	1,6176922	0,88626493	11,08	CACNA2D2	calcium voltage-gated channel auxiliary subunit alpha2delta 2
23592	6,69E-34	3,32E+01	1,54E-34	0,0723	12,2568675	0,88617172	931,91	LEMD3	LEM domain containing 3
1787	5,70E-20	1,92E+01	1,90E-20	0,0956	9,2679537	0,88605682	536,94	TRDMT1	tRNA aspartic acid methyltransferase 1
10621	1,27E-39	3,89E+01	2,56E-40	0,0667	13,2924584	0,88602731	984,97	POLR3F	RNA polymerase III subunit F
105374746	2,72E-02	1,57E+00	2,04E-02	0,3819	2,3189023	0,88560903	22,33	LOC105374	uncharacterized LOC105374746
9767	1,33E-28	2,79E+01	3,48E-29	0,079	11,2139185	0,88558946	700,03	JADE3	jade family PHD finger 3
60561	1,97E-39	3,87E+01	4,00E-40	0,0668	13,2590812	0,8855391	1082,51	RINT1	RAD50 interactor 1
80119	1,49E-21	2,08E+01	4,74E-22	0,0917	9,653787	0,88525881	446,08	PIF1	PIF1 5'-to-3' DNA helicase
136263	1,27E-01	8,96E-01	1,04E-01	0,5441	1,6270555	0,88520681	10,58	SSMEM1	serine rich single-pass membrane protein 1
102	3,28E-102	1,01E+02	1,80E-103	0,0409	21,5998807	0,88399351	6564,78	ADAM10	ADAM metallopeptidase domain 10
284695	6,73E-46	4,52E+01	1,18E-46	0,0616	14,3430426	0,88317265	1923,99	ZNF326	zinc finger protein 326
57396	3,85E-28	2,74E+01	1,03E-28	0,0794	11,1180111	0,88286998	652,53	CLK4	CDC like kinase 4
55853	1,49E-11	1,08E+01	6,45E-12	0,1285	6,8692774	0,88276297	221,3	IDI2-AS1	IDI2 antisense RNA 1
131909	6,57E-02	1,18E+00	5,18E-02	0,4537	1,9451344	0,88255245	15,76	FAM172BP	family with sequence similarity 172 member B, pseudogene
5352	3,48E-98	9,75E+01	2,05E-99	0,0417	21,164086	0,88193909	8459,67	PLOD2	procollagen-lysine,2-oxoglutarate 5-dioxygenase 2
84188	6,11E-82	8,12E+01	4,86E-83	0,0457	19,30512	0,88185344	3866,57	FAR1	fatty acyl-CoA reductase 1
57590	3,47E-71	7,05E+01	3,46E-72	0,0491	17,9681189	0,88184878	3303,11	WDFY1	WD repeat and FYVE domain containing 1
26054	8,61E-68	6,71E+01	9,24E-69	0,0503	17,5249745	0,88183994	2870,91	SENP6	SUMO specific peptidase 6
4664	7,53E-57	5,61E+01	1,03E-57	0,055	16,0132322	0,88112341	2061,77	NAB1	NGFI-A binding protein 1
101928317	1,16E-02	1,94E+00	8,38E-03	0,3341	2,6364196	0,88089316	28,58	LOC101928	uncharacterized LOC101928317
112935969	6,86E-02	1,16E+00	5,42E-02	0,4575	1,9254945	0,88082233	16,5	SCAT8	S-phase cancer associated transcript 8
89832	1,78E-02	1,75E+00	1,31E-02	0,3549	2,4816244	0,88073463	25,89	CHRFAM7A	CHRNA7 (exons 5-10) and FAM7A (exons A-E) fusion

9856	5,20E-03	2,28E+00	3,62E-03	0,3027	2,9092657	0,88055995	35,58	KIAA0319	KIAA0319
1284	1,86E-95	9,47E+01	1,14E-96	0,0422	20,8637876	0,87999453	7466,17	COL4A2	collagen type IV alpha 2 chain
107986660	1,58E-01	8,01E-01	1,31E-01	0,583	1,5091657	0,87990459	9,34	LOC107986	uncharacterized LOC107986660
10045	5,07E-23	2,23E+01	1,55E-23	0,088	9,9984939	0,8798647	546,96	SH2D3A	SH2 domain containing 3A
729857	7,39E-04	3,13E+00	4,80E-04	0,252	3,4915395	0,87982673	50,33	RGPD2	RANBP2 like and GRIP domain containing 2
11179	2,25E-15	1,46E+01	8,62E-16	0,1094	8,0450994	0,87981325	483,84	ZNF277	zinc finger protein 277
105372836	1,69E-01	7,72E-01	1,41E-01	0,5972	1,4730697	0,87972097	8,75	LOC105372	uncharacterized LOC105372836
26586	6,30E-92	9,12E+01	4,17E-93	0,043	20,467851	0,87932294	7925,82	CKAP2	cytoskeleton associated protein 2
83852	8,37E-14	1,31E+01	3,37E-14	0,1159	7,583309	0,87872511	260,87	SETDB2	SET domain bifurcated histone lysine methyltransferase 2
340037	2,23E-03	2,65E+00	1,51E-03	0,2769	3,1731022	0,87862637	42,86	PRR7-AS1	PRR7 antisense RNA 1
9891	1,43E-70	6,98E+01	1,45E-71	0,0491	17,8886597	0,87838876	2423,67	NUAK1	NUAK family kinase 1
9821	5,74E-49	4,82E+01	9,32E-50	0,0592	14,8303782	0,87825281	2101,03	RB1CC1	RB1 inducible coiled-coil 1
100131997	1,19E-05	4,92E+00	6,82E-06	0,1952	4,4993163	0,87818828	88,88	FAM27E3	family with sequence similarity 27 member E3
5813	4,12E-58	5,74E+01	5,48E-59	0,0542	16,1948741	0,87818472	1864,64	PURA	purine rich element binding protein A
729540	3,50E-24	2,35E+01	1,04E-24	0,0856	10,2625225	0,87802513	504,6	RGPD6	RANBP2 like and GRIP domain containing 6
129531	9,36E-44	4,30E+01	1,73E-44	0,0627	13,9927345	0,87788171	1522,35	MITD1	microtubule interacting and trafficking domain containing 1
8702	9,47E-30	2,90E+01	2,42E-30	0,0767	11,447581	0,87747363	691,09	B4GALT4	beta-1,4-galactosyltransferase 4
100874195	1,02E-08	7,99E+00	4,98E-09	0,15	5,847985	0,87733383	150,96	DIAPH3-AS1	DIAPH3 antisense RNA 1
29057	1,70E-19	1,88E+01	5,74E-20	0,0959	9,149135	0,87709903	446,3	FAM156A	family with sequence similarity 156 member A
7690	7,57E-68	6,71E+01	8,10E-69	0,05	17,5324586	0,87648715	3254,08	ZNF131	zinc finger protein 131
255919	8,74E-24	2,31E+01	2,62E-24	0,0861	10,1729142	0,87581528	562,84	CNEP1R1	CTD nuclear envelope phosphatase 1 regulatory subunit 1
345462	3,53E-06	5,45E+00	1,96E-06	0,1841	4,7574842	0,87580316	103,43	ZNF879	zinc finger protein 879
2049	5,89E-03	2,23E+00	4,14E-03	0,3054	2,8676519	0,87564406	34,52	EPHB3	EPH receptor B3
100131998	9,58E-06	5,02E+00	5,46E-06	0,1926	4,5463652	0,87544928	91,34	RRN3P3	RRN3 pseudogene 3
84131	4,73E-62	6,13E+01	5,74E-63	0,0523	16,7492029	0,87540557	2749,26	CEP78	centrosomal protein 78
341640	6,31E-08	7,20E+00	3,19E-08	0,1582	5,5306663	0,87516257	135,57	FREM2	FRAS1 related extracellular matrix 2
144348	8,47E-103	1,02E+02	4,56E-104	0,0404	21,6632019	0,87483799	7752,54	ZNF664	zinc finger protein 664
79956	1,24E-24	2,39E+01	3,63E-25	0,0844	10,3634791	0,87457088	533,14	ERMP1	endoplasmic reticulum metallopeptidase 1
6814	3,44E-38	3,75E+01	7,17E-39	0,0671	13,0408012	0,87453118	1028,88	STXBP3	syntaxin binding protein 3
100642175	1,17E-01	9,32E-01	9,52E-02	0,5241	1,6685299	0,87447152	11,65	SPRY4-IT1	SPRY4 intronic transcript 1
55215	4,17E-76	7,54E+01	3,75E-77	0,047	18,5917364	0,87439907	4804	FANCI	FA complementation group I
203522	1,45E-14	1,38E+01	5,71E-15	0,1119	7,8102979	0,87433571	317,21	INTS6L	integrator complex subunit 6 like
9662	1,57E-46	4,58E+01	2,71E-47	0,0605	14,4447278	0,8742453	1534,04	CEP135	centrosomal protein 135
51122	2,42E-49	4,86E+01	3,89E-50	0,0587	14,8888661	0,87416154	1462,08	COMMD2	COMM domain containing 2
4361	1,17E-65	6,49E+01	1,31E-66	0,0507	17,240685	0,87398735	2759,99	MRE11	MRE11 homolog, double strand break repair nuclease
64327	9,75E-56	5,50E+01	1,37E-56	0,0551	15,8516186	0,87394257	2414,84	LMBR1	limb development membrane protein 1
84135	2,30E-56	5,56E+01	3,18E-57	0,0548	15,9431854	0,87328761	1827,58	UTP15	UTP15 small subunit processome component
132320	1,24E-45	4,49E+01	2,19E-46	0,061	14,2999161	0,87281017	1340,28	SCLT1	sodium channel and clathrin linker 1
29761	1,47E-61	6,08E+01	1,81E-62	0,0523	16,6807084	0,87258462	2488,3	USP25	ubiquitin specific peptidase 25
79661	9,46E-13	1,20E+01	3,94E-13	0,1202	7,2575062	0,87228252	245,15	NEIL1	nei like DNA glycosylase 1
57515	1,51E-96	9,58E+01	9,16E-98	0,0415	20,9841407	0,87155439	7863,58	SERINC1	serine incorporator 1
157567	4,96E-19	1,83E+01	1,70E-19	0,0965	9,0313064	0,87142132	451,44	ANKRD46	ankyrin repeat domain 46
112268239	2,11E-02	1,68E+00	1,56E-02	0,3604	2,4174366	0,87134402	24,47	LOC112268	uncharacterized LOC112268239
115426	4,17E-36	3,54E+01	9,10E-37	0,0688	12,6661804	0,87129702	946,07	UHRF2	ubiquitin like with PHD and ring finger domains 2
2069	3,01E-59	5,85E+01	3,92E-60	0,0533	16,3564051	0,8711771	2430,11	EREG	epiregulin
2005	1,95E-57	5,67E+01	2,63E-58	0,0541	16,0980998	0,87112558	2639,4	ELK4	ETS transcription factor ELK4
55356	1,58E-18	1,78E+01	5,47E-19	0,0978	8,9023492	0,87104827	397,78	SLC22A15	solute carrier family 22 member 15
57214	5,04E-70	6,93E+01	5,17E-71	0,0489	17,8175067	0,87073359	2542,98	CEMIP	cell migration inducing hyaluronidase 1
100505851	5,02E-02	1,30E+00	3,89E-02	0,4216	2,0652299	0,87063761	19,41	LOC100505	uncharacterized LOC100505851
105377486	4,67E-02	1,33E+00	3,60E-02	0,4151	2,0967731	0,87034288	19,05	FHIP1A-DT	FHIP1A divergent transcript
81616	1,24E-01	9,07E-01	1,01E-01	0,5314	1,6377254	0,87026198	11,04	ACSBG2	acyl-CoA synthetase bubblegum family member 2
57589	1,10E-34	3,40E+01	2,49E-35	0,0702	12,4037219	0,87013094	934,37	RIC1	RIC1 homolog, RAB6A GEF complex partner 1
89782	2,02E-48	4,77E+01	3,34E-49	0,059	14,744451	0,86954225	1533,89	LMLN	leishmanolysin like peptidase
400541	2,54E-05	4,60E+00	1,49E-05	0,2007	4,330859	0,86924993	81,33	LOC400541	uncharacterized LOC400541
2589	3,85E-84	8,34E+01	2,93E-85	0,0444	19,5674654	0,86893202	4710,98	GALNT1	polypeptide N-acetylgalactosaminyltransferase 1
9013	4,06E-29	2,84E+01	1,05E-29	0,0767	11,3194315	0,86869808	838,75	TAF1C	TATA-box binding protein associated factor, RNA polymerase I subunit C
8763	2,21E-59	5,87E+01	2,86E-60	0,053	16,3754662	0,86823578	2963,36	CD164	CD164 molecule
23259	1,47E-48	4,78E+01	2,41E-49	0,0588	14,7664562	0,86814283	1710,2	DDHD2	DDHD domain containing 2
11169	2,70E-80	7,96E+01	2,22E-81	0,0454	19,1068102	0,86781356	3663,96	WDHD1	WD repeat and HMG-box DNA binding protein 1
101927934	1,29E-01	8,89E-01	1,06E-01	0,537	1,615414	0,86747434	10,98	LINC01843	long intergenic non-protein coding RNA 1843
5001	7,15E-27	2,61E+01	1,97E-27	0,0799	10,8510155	0,86723229	1076,63	ORC5	origin recognition complex subunit 5
57728	3,86E-38	3,74E+01	8,06E-39	0,0665	13,0318485	0,8668828	1193,74	WDR19	WD repeat domain 19
79814	3,34E-15	1,45E+01	1,29E-15	0,1084	7,9956168	0,86679438	372,31	AGMAT	agmatinase
105375805	2,12E-01	6,74E-01	1,80E-01	0,6468	1,3399565	0,86664845	7,51	LOC105375	uncharacterized LOC105375805
3291	1,96E-02	1,71E+00	1,45E-02	0,3543	2,4454179	0,86635346	26,71	HSD11B2	hydroxysteroid 11-beta dehydrogenase 2
100507533	1,85E-02	1,73E+00	1,36E-02	0,3508	2,4687207	0,86600922	26,88	SOX21-AS1	SOX21 antisense divergent transcript 1
56889	7,24E-42	4,11E+01	1,39E-42	0,0633	13,6770361	0,86595129	7883,34	TM9SF3	transmembrane 9 superfamily member 3
100131211	4,04E-27	2,64E+01	1,11E-27	0,0794	10,9038024	0,86593392	618,58	NEMP2	nuclear envelope integral membrane protein 2
107986495	6,30E-02	1,20E+00	4,95E-02	0,4405	1,9644775	0,86530486	16,77	LOC107986	495
101929018	6,90E-02	1,16E+00	5,45E-02	0,4499	1,9227555	0,86495342	16,39	LOC101929	uncharacterized LOC101929018
54529	4,82E-41	4,03E+01	9,42E-42	0,0639	13,5372653	0,86467012	2163,87	ASNSD1	asparagine synthetase domain containing 1
199777	5,22E-17	1,63E+01	1,90E-17	0,1017	8,4998105	0,86450519	365,16	ZNF626	zinc finger protein 626
100506990	2,42E-09	8,62E+00	1,15E-09	0,142	6,0871477	0,86433218	182,39	FAM86B2-DT	FAM86B2 divergent transcript
101929340	2,09E-04	3,68E+00	1,30E-04	0,2259	3,8259339	0,86425202	65,12	ESAM-AS1	ESAM antisense RNA 1
26060	2,64E-70	6,96E+01	2,68E-71	0,0484	17,8541649	0,86410824	2791,38	APPL1	adaptor protein, phosphotyrosine interacting with PH domain and leucine zipper 1
26256	5,41E-09	8,27E+00	2,61E-09	0,1451	5,9546262	0,86398635	157,1	CABYR	calcium binding tyrosine phosphorylation regulated
26996	1,43E-10	9,84E+00	6,44E-11	0,1322	6,5331282	0,86389812	193,35	GPR160	G protein-coupled receptor 160
91749	2,67E-13	1,26E+01	1,09E-13	0,1162	7,429391	0,86347305	273,48	MFSD4B	major facilitator superfamily domain containing 4B
56204	3,13E-15	1,45E+01	1,21E-15	0,1079	8,0039398	0,86342149	347,06	ATOSA	atos homolog A
54799	3,44E-29	2,85E+01	8,89E-30	0,0762	11,3341132	0,86340044	720,88	MBTD1	mbt domain containing 1
100287082	1,74E-03	2,76E+00	1,17E-03	0,2658	3,2469797	0,86311341	47,33	GACAT2	gastric cancer associated transcript 2
157777	1,47E-03	2,83E+00	9,76E-04	0,2616	3,2974649	0,86260796	393,83	MCMDC2	minichromosome maintenance domain containing 2
113457	1,14E-01	9,43E-01	9,28E-02	0,5131	1,6810499	0,86257845	12,17	TUBA3D	tubulin alpha 3d
286749	2,53E-02	1,60E+00	1,88E-02	0,3672	2,3485882	0,8625166	23,22	STON1-GTF	STON1-GTF2A1L readthrough
55971	5,77E-26	2,52E+01	1,63E-26	0,0809	10,6563137	0,86247076	636,44	BAIAP2L1	BAR/IMD domain containing adaptor protein 2 like 1
23536	2,84E-59	5,85E+01	3,69E-60	0,0527	16,3599632	0,86240885	2000,98	ADAT1	adenosine deaminase tRNA specific 1
7871	7,12E-64	6,31E+01	8,30E-65	0,0507	16,9993399	0,86237244	2997,06	SLMAP	sarcolemma associated protein
89876	1,98E-01	7,03E-01	1,67E-01	0,6239	1,3818799	0,86217609	8,07	CFAP91	cilia and flagella associated protein 91
84455	8,95E-14	1,30E+01	3,61E-14	0,1138	7,5744256	0,8619721	266,4	EFCAB7	EF-hand calcium binding domain 7
7581	3,08E-56	5,55E+01	4,28E-57	0,0541	15,9245898	0,86196882	1882,06	ZNF33A	zinc finger protein 33A
172	4,64E-33	3,23E+01	1,09E-33	0,0712	12,0971672	0,8618101	933,38	AFG3L1P	AFG3 like matrix AAA peptidase subunit 1, pseudogene
2583	2,14E-12	1,17E+01	9,05E-13	0,1206	7,1443005	0,86163161	238,79	B4GALNT1	beta-1,4-N-acetyl-galactosaminyltransferase 1
55609	1,01E-17	1,70E+01	3,61E-18	0,0991	8,6904947	0,8614334	395,89	ZNF280C	zinc finger protein 280C
107985322	1,18E-02	1,93E+00	8,48E-03	0,3272	2,6321554	0,86137179	30,16	LOC107985	322
84128	1,26E-56	5,59E+01	1,74E-57	0,0539	15,9807465	0,86111184	3214,38	WDR75	WD repeat domain 75
101927111	8,31E-12	1,11E+01	3,57E-12	0,1238	6,9531298	0,86090017	220,83	SUCLG2-DT	SUCLG2 divergent transcript
27030	7,59E-28	2,71E+01	2,04E-28	0,0779	11,0564579	0,86083224	658,59	MLH3	mutL homolog 3
7638	1,72E-06	5,76E+00	9,38E-07	0,1755	4,9042208	0,86073348	108,69	ZNF221	zinc finger protein 221
10396	3,22E-19	1,85E+01	1,10E-19	0,0948	9,0788535	0,86050074	432,31	ATP8A1	ATPase phospholipid transporting 8A1
388182	6,77E-02	1,17E+00	5,34E-02	0,4454	1,9315227	0,86027958	17,77	SPATA41	spermatogenesis associated 41
29980	5,83E-58	5,72E+01	7,78E-59	0,0532	16,1733108	0,8601377	2487,58	DONSON	DNA replication fork stabilization factor DONSON
79752	2,82E-61	6,05E+01	3,51E-62	0,0517	16,6411843	0,86008143	2415,44	ZFAND1	zinc finger AN1-type containing 1
57102	3,28E-33	3,25E+01	7,70E-34	0,0709	12,1259107	0,85989384	1044,1	C12orf4	chromosome 12 open reading frame 4
103625684	6,43E-06	5,19E+00	3,62E-06	0,1856	4,63183	0,85963378	111,84	RNU6-2	RNA, U6 small nuclear 2
63908	7,04E-26	2,52E+01	1,99E-26	0,0808	10,6375003	0,85960684	605,14	NAPB	NSF attachment protein beta
4085	1,03E-56	5,60E+01	1,41E-57	0,0537	15,9937177	0,85885398	4452,52	MAD2L1	mitotic arrest deficient 2 like 1
107985184	1,29E-02	1,89E+00	9,36E-03	0,3305	2,598634	0,85881281	29,49	LOC107985	uncharacterized LOC107985184
6744	4,79E-85	8,43E+01	3,58E-86	0,0436	19,6743296	0,85844377	5916,79	ITPRID2	ITPR interacting domain containing 2
29887	8,61E-08	7,06E+00	4,39E-08	0,1568	5,4745755	0,85840121	151,91	SNX10	sorting nexin 10
79630	1,98E-01	7,03E-01	1,67E-01	0,6215	1,3811322	0,8583597	8,13	C1orf54	chromosome 1 open reading frame 54
107984308	5,04E-02	1,30E+00	3,91E-02	0,4159	2,0631242	0,85811883	19,04	LOC107984	uncharacterized LOC107984308
1718	8,21E-83	8,21E+01	6,40E-84	0,0442	19,4096366	0,8576555	8264,38	DHCR24	24-dehydrocholesterol reductase
100873947	1,19E-07	6,92E+00	6,09E-08	0,1583	5,4162092	0,85762173	139,39	LMLN-AS1	LMLN antisense RNA 1
170960	1,78E-35	3,47E+01	3,95E-36	0,0683	12,5505275	0,85748752	1022,51	ZNF721	zinc finger protein 721
160857	1,36E-12	1,19E+01	5,71E-13	0,119	7,2072376	0,85741137	246,13	CCDC122	coiled-coil domain containing 122
115308161	2,03E-01	6,93E-01	1,72E-01	0,6277	1,3657808	0,85732037	8,11	LOC115308	uncharacterized LOC115308161
79635	2,99E-04	3,52E+00	1,89E-04	0,2296	3,733917	0,85728494	67,38	CCDC121	coiled-coil domain containing 121
160851	2,44E-23	2,26E+01	7,41E-24	0,0851	10,0712067	0,85717178	540,68	DGKH	diacylglycerol kinase eta
160335	1,31E-20	1,99E+01	4,29E-21	0,0909	9,4252284	0,85713699	493,16	TMTC2	transmembrane O-mannosyltransferase targeting cadherins 2
102723704	6,10E-40	3,92E+01	1,22E-40	0,0642	13,3476213	0,85671731	1355,34	LOC102723	uncharacterized LOC102723704

100507431	9,75E-02	1,01E+00	7,85E-02	0,4869	1,759247	0,85661602	15,04	LINC02551	long intergenic non-protein coding RNA 2551
57587	2,37E-56	5,56E+01	3,28E-57	0,0537	15,9411422	0,85625936	2613,9	CFAP97	cilia and flagella associated protein 97
10068	4,13E-09	8,38E+00	1,98E-09	0,1426	5,9994026	0,85540689	164,24	IL18BP	interleukin 18 binding protein
51201	3,88E-58	5,74E+01	5,16E-59	0,0528	16,1986152	0,85538637	2408,34	ZDHHC2	zinc finger DHHC-type palmitoyltransferase 2
100505812	7,24E-18	1,71E+01	2,56E-18	0,098	8,7293318	0,8551033	373,34	CARD8-AS1	CARD8 antisense RNA 1
414189	1,88E-10	9,73E+00	8,51E-11	0,1316	6,4913207	0,85438452	194,23	AGAP6	ArfGAP with GTPase domain, ankyrin repeat and PH domain 6
285671	9,67E-07	6,01E+00	5,21E-07	0,1702	5,018384	0,85431356	119,16	RNF180	ring finger protein 180
4071	3,77E-86	8,54E+01	2,76E-87	0,0431	19,8038356	0,85411648	7661,79	TM4SF1	transmembrane 4 L six family member 1
83850	3,07E-04	3,51E+00	1,94E-04	0,2291	3,726832	0,85392746	63,65	ESYT3	extended synaptotagmin 3
107987027	1,07E-01	9,71E-01	8,64E-02	0,4979	1,7149277	0,85381535	12,69	LOC107987(	uncharacterized LOC107987027
4121	5,01E-18	1,73E+01	1,77E-18	0,0973	8,771303	0,85360341	433,85	MAN1A1	mannosidase alpha class 1A member 1
1102	5,33E-08	7,27E+00	2,69E-08	0,1535	5,5607221	0,85338878	150,41	RCBTB2	RCC1 and BTB domain containing protein 2
11039	2,92E-08	7,53E+00	1,46E-08	0,1506	5,6667467	0,85325678	145,56	GUSBP14	GUSB pseudogene 14
55088	8,57E-33	3,21E+01	2,03E-33	0,0708	12,0461989	0,8532488	956,29	CCDC186	coiled-coil domain containing 186
286102	1,45E-06	5,84E+00	7,88E-07	0,1728	4,9383351	0,85310306	124,81	TMED10P1	transmembrane p24 trafficking protein 10 pseudogene 1
55472	6,92E-03	2,16E+00	4,89E-03	0,3031	2,8144625	0,85297234	34,79	RBM12B-AS	RBM12B antisense RNA 1
113763	1,89E-12	1,17E+01	7,98E-13	0,1191	7,161537	0,8529398	239,01	ZBED10P	zinc finger BED-type containing 10, pseudogene
254251	1,08E-43	4,30E+01	1,99E-44	0,061	13,982698	0,85292613	2047,11	LCORL	ligand dependent nuclear receptor corepressor like
55172	6,72E-33	3,22E+01	1,59E-33	0,0707	12,0664698	0,85260014	1090,96	DNAAF2	dynein axonemal assembly factor 2
10059	6,43E-57	5,62E+01	8,80E-58	0,0532	16,0231851	0,85258556	4277,39	DNM1L	dynamin 1 like
7881	8,02E-67	6,61E+01	8,80E-68	0,049	17,3963349	0,85254015	2926,4	KCNAB1	potassium voltage-gated channel subfamily A regulatory beta subunit 1
94039	3,56E-21	2,04E+01	1,15E-21	0,0891	9,562893	0,8524505	527,98	ZNF101	zinc finger protein 101
161823	3,81E-28	2,74E+01	1,01E-28	0,0766	11,1189713	0,85222755	678,71	ADAL	adenosine deaminase like
4436	2,89E-62	6,15E+01	3,49E-63	0,0508	16,7787028	0,85191568	4957,26	MSH2	mutS homolog 2
57223	5,60E-77	7,63E+01	4,97E-78	0,0456	18,699822	0,85186906	3604,65	PPP4R3B	protein phosphatase 4 regulatory subunit 3B
56271	1,80E-01	7,45E-01	1,51E-01	0,5926	1,437202	0,85174544	9,78	BEX4	brain expressed X-linked 4
55159	1,56E-95	9,48E+01	9,58E-97	0,0408	20,8722163	0,85170873	5805	RFWD3	ring finger and WD repeat domain 3
23515	1,68E-53	5,28E+01	2,47E-54	0,0549	15,5217522	0,85146101	1972,04	MORC3	MORC family CW-type zinc finger 3
284837	1,61E-01	7,93E-01	1,34E-01	0,568	1,4988041	0,85128776	9,8	AATBC	apoptosis associated transcript in bladder cancer
100272228	2,41E-02	1,62E+00	1,80E-02	0,3596	2,3660485	0,85072934	25,23	EOLA2-DT	EOLA2 divergent transcript
84549	1,15E-45	4,49E+01	2,03E-46	0,0595	14,305236	0,85055386	1448,4	MAK16	MAK16 homolog
105370567	5,30E-03	2,28E+00	3,70E-03	0,293	2,9027734	0,85037644	37,51	LOC105370(	uncharacterized LOC105370567
54739	5,40E-13	1,23E+01	2,24E-13	0,1158	7,3339225	0,84960014	270,37	XAF1	XIAP associated factor 1
9933	8,90E-90	8,91E+01	6,10E-91	0,042	20,2233637	0,84913387	5868,46	PUM3	pumilio RNA binding family member 3
101927858	1,23E-03	2,91E+00	8,16E-04	0,2536	3,3472011	0,84872198	52,39	RNF32-AS1	RNF32 antisense RNA 1
9590	1,48E-35	3,48E+01	3,27E-36	0,0675	12,5653782	0,84835309	1989,61	AKAP12	A-kinase anchoring protein 12
100616394	5,51E-07	6,26E+00	2,92E-07	0,1654	5,1282659	0,84832057	963,44	MIR4444-1	microRNA 4444-1
1843	7,44E-41	4,01E+01	1,46E-41	0,0628	13,5051246	0,84821313	1684,97	DUSP1	dual specificity phosphatase 1
5412	3,79E-34	3,34E+01	8,68E-35	0,0689	12,3034147	0,84821181	1127,42	UBL3	ubiquitin like 3
9860	6,67E-40	3,92E+01	1,34E-40	0,0636	13,3409882	0,84819723	1117,94	LRIG2	leucine rich repeats and immunoglobulin like domains 2
100887750	1,06E-09	8,97E+00	4,97E-10	0,1363	6,2201701	0,84798738	187,1	MRPS31P5	mitochondrial ribosomal protein S31 pseudogene 5
25834	1,16E-01	9,36E-01	9,48E-02	0,5075	1,6705794	0,84784041	12,68	MGAT4C	MGAT4 family member C
100507433	6,42E-02	1,19E+00	5,05E-02	0,4334	1,9557108	0,84767711	16,74	ZNF571-AS1	ZNF571 antisense RNA 1
120103	8,74E-43	4,21E+01	1,65E-43	0,0613	13,8314724	0,84765229	2050,93	SLC36A4	solute carrier family 36 member 4
79811	4,53E-76	7,53E+01	4,08E-77	0,0456	18,5871298	0,84672867	7438,83	SLTM	SAFB like transcription modulator
51633	1,88E-32	3,17E+01	4,47E-33	0,0707	11,9808939	0,84667323	968,41	OTUD6B	OTU deubiquitinase 6B
23200	1,58E-67	6,68E+01	1,71E-68	0,0484	17,4900218	0,84632208	3851,42	ATP11B	ATPase phospholipid transporting 11B (putative)
4082	7,11E-55	5,41E+01	1,02E-55	0,0538	15,724958	0,84626813	5084,79	MARCKS	myristoylated alanine rich protein kinase C substrate
197021	8,73E-18	1,71E+01	3,09E-18	0,0972	8,7079501	0,84620926	390,3	LCTL	lactase like
123606	4,26E-46	4,54E+01	7,42E-47	0,0589	14,3750608	0,84611985	1552,19	NIPA1	NIPA magnesium transporter 1
286006	2,09E-02	1,68E+00	1,54E-02	0,3493	2,4220203	0,84607091	28,3	LSMEM1	leucine rich single-pass membrane protein 1
55037	4,98E-83	8,23E+01	3,86E-84	0,0435	19,4355823	0,84586358	5985,18	PTCD3	pentatricopeptide repeat domain 3
151649	5,61E-15	1,43E+01	2,18E-15	0,1066	7,9307868	0,84548303	333,64	PP2D1	protein phosphatase 2C like domain containing 1
7181	1,39E-36	3,59E+01	3,00E-37	0,0663	12,753083	0,84546483	1008,53	NR2C1	nuclear receptor subfamily 2 group C member 1
7003	7,00E-112	1,11E+02	3,17E-113	0,0374	22,6137526	0,84505546	10979,76	TEAD1	TEA domain transcription factor 1
221786	6,75E-19	1,82E+01	2,31E-19	0,0939	8,9972617	0,84493068	416,5	FAM200A	family with sequence similarity 200 member A
3845	8,32E-51	5,01E+01	1,29E-51	0,0559	15,1147708	0,8447795	1885,75	KRAS	KRAS proto-oncogene, GTPase
57403	3,51E-59	5,85E+01	4,58E-60	0,0517	16,3468352	0,84473879	4047,21	RAB22A	RAB22A, member RAS oncogene family
84295	2,73E-61	6,06E+01	3,40E-62	0,0508	16,6431042	0,84471112	2869,99	PHF6	PHD finger protein 6
29766	1,78E-93	9,27E+01	1,14E-94	0,0409	20,6423031	0,84467121	7721,06	TMOD3	tropomodulin 3
389206	5,59E-03	2,25E+00	3,91E-03	0,2926	2,8851121	0,84427269	38,13	BEND4	BEN domain containing 4
26258	6,89E-49	4,82E+01	1,12E-49	0,057	14,8179347	0,84420191	1911,74	BLOC1S6	biogenesis of lysosomal organelles complex 1 subunit 6
23678	9,71E-10	9,01E+00	4,53E-10	0,1353	6,2345323	0,84377642	188,83	SGK3	serum/glucocorticoid regulated kinase family member 3
105378499	4,55E-02	1,34E+00	3,50E-02	0,4001	2,1078776	0,84328346	19,48	HSPA12A-AS	HSPA12A antisense RNA 1
54741	2,15E-68	6,77E+01	2,28E-69	0,0479	17,6044352	0,84310893	3165,33	LEPROT	leptin receptor overlapping transcript
79074	3,20E-29	2,85E+01	8,27E-30	0,0743	11,3404774	0,84267507	1014,03	C2orf49	chromosome 2 open reading frame 49
27107	1,10E-53	5,30E+01	1,62E-54	0,0542	15,5487823	0,84256403	1726,33	ZBTB11	zinc finger and BTB domain containing 11
83849	1,70E-03	2,77E+00	1,13E-03	0,2588	3,2549547	0,84249351	48,62	SYT15	synaptotagmin 15
3658	1,14E-54	5,39E+01	1,64E-55	0,0537	15,6948243	0,84243398	2773,57	IREB2	iron responsive element binding protein 2
161436	1,28E-23	2,29E+01	3,86E-24	0,0831	10,1350434	0,84210053	570,78	EML5	EMAP like 5
105377359	3,74E-02	1,43E+00	2,85E-02	0,3844	2,1898718	0,84182146	23,96	LOC105377359	
9534	1,36E-16	1,59E+01	5,01E-17	0,1003	8,3865741	0,84135355	368,07	ZNF254	zinc finger protein 254
8674	7,02E-37	3,62E+01	1,50E-37	0,0657	12,8066831	0,84133711	1047,43	VAMP4	vesicle associated membrane protein 4
55605	1,70E-32	3,18E+01	4,04E-33	0,0702	11,9893394	0,841317	850,71	KIF21A	kinesin family member 21A
29931	1,55E-01	8,10E-01	1,29E-01	0,5536	1,5195141	0,84115997	10,34	LINC00312	long intergenic non-protein coding RNA 312
7705	7,41E-79	7,81E+01	6,27E-80	0,0444	18,9315536	0,8408419	5411,26	ZNF146	zinc finger protein 146
10600	7,15E-43	4,21E+01	1,34E-43	0,0607	13,8460952	0,84070033	3707,4	USP16	ubiquitin specific peptidase 16
2202	3,76E-68	6,74E+01	3,99E-69	0,0478	17,5726027	0,83991508	4836,69	EFEMP1	EGF containing fibulin extracellular matrix protein 1
5055	6,59E-10	9,18E+00	3,06E-10	0,1334	6,2959393	0,8396405	200,88	SERPINB2	serpin family B member 2
55359	5,37E-10	9,27E+00	2,48E-10	0,1327	6,3281524	0,839433	234,33	STYK1	serine/threonine/tyrosine kinase 1
221154	6,46E-40	3,92E+01	1,30E-40	0,0629	13,3433298	0,83895533	2902,66	MICU2	mitochondrial calcium uptake 2
100132923	3,05E-02	1,52E+00	2,30E-02	0,3689	2,2733231	0,83862967	26,04	FAM66D	family with sequence similarity 66 member D
101928376	1,20E-01	9,21E-01	9,81E-02	0,507	1,6539094	0,83854431	12,64	IL12A-AS1	IL12A antisense RNA 1
54839	3,76E-11	1,04E+01	1,66E-11	0,1245	6,7334646	0,83840844	265,6	LRRC49	leucine rich repeat containing 49
134510	9,21E-62	6,10E+01	1,13E-62	0,0502	16,7087955	0,83795423	2948,26	UBLCP1	ubiquitin like domain containing CTD phosphatase 1
10026	1,57E-66	6,58E+01	1,73E-67	0,0483	17,357599	0,83765251	2965,6	PIGK	phosphatidylinositol glycan anchor biosynthesis class K
10527	8,76E-65	6,41E+01	1,00E-65	0,0489	17,1229575	0,83732097	17780,35	IPO7	importin 7
5525	3,77E-29	2,84E+01	9,77E-30	0,0739	11,3259128	0,83722723	1121,55	PPP2R5A	protein phosphatase 2 regulatory subunit B'alpha
51119	4,87E-87	8,63E+01	3,52E-88	0,0421	19,9072163	0,83721473	8153,43	SBDS	SBDS ribosome maturation factor
643911	1,18E-09	8,93E+00	5,54E-10	0,1349	6,2029355	0,8367023	203,99	CRNDE	colorectal neoplasia differentially expressed
65975	7,07E-27	2,62E+01	1,95E-27	0,0771	10,8521376	0,83653008	709,65	STK33	serine/threonine kinase 33
646214	3,71E-02	1,43E+00	2,83E-02	0,3812	2,1931771	0,83607188	23,57	LOC646214	p21 (RAC1) activated kinase 2 pseudogene
6615	8,92E-03	2,05E+00	6,36E-03	0,3063	2,7283741	0,83579008	33,83	SNAI1	snail family transcriptional repressor 1
10776	6,57E-65	6,42E+01	7,48E-66	0,0487	17,1399053	0,83523673	5927,58	ARPP19	cAMP regulated phosphoprotein 19
25800	2,81E-92	9,16E+01	1,85E-93	0,0407	20,5073387	0,83516249	5787,96	SLC39A6	solute carrier family 39 member 6
145773	1,28E-04	3,89E+00	7,81E-05	0,2114	3,9502476	0,83503797	72,68	FAM81A	family with sequence similarity 81 member A
196528	1,88E-36	3,57E+01	4,07E-37	0,0656	12,7292828	0,83462881	1244,45	ARID2	AT-rich interaction domain 2
4015	1,66E-47	4,68E+01	2,80E-48	0,0572	14,6003094	0,83456789	2716,71	LOX	lysyl oxidase
72	5,03E-02	1,30E+00	3,90E-02	0,4043	2,0643471	0,8345215	19,99	ACTG2	actin gamma 2, smooth muscle
26820	7,31E-02	1,14E+00	5,78E-02	0,4397	1,8968672	0,83406191	17,09	SNORD24	small nucleolar RNA, C/D box 24
105377576	1,43E-06	5,84E+00	7,79E-07	0,1688	4,9405945	0,8340077	129,69	LOC105377(	uncharacterized LOC105377576
282679	8,88E-03	2,05E+00	6,34E-03	0,3055	2,7297995	0,83395046	34,97	AQP11	aquaporin 11
56169	1,09E-06	5,96E+00	5,88E-07	0,167	4,9949962	0,83394187	116,95	GSDMC	gasdermin C
5563	2,14E-25	2,47E+01	6,15E-26	0,0792	10,5319898	0,83381857	655,18	PRKAA2	protein kinase AMP-activated catalytic subunit alpha 2
4863	1,40E-53	5,29E+01	2,06E-54	0,0537	15,533505	0,83357827	2002,34	NPAT	nuclear protein, coactivator of histone transcription
105377887	4,58E-02	1,34E+00	3,53E-02	0,396	2,104855	0,83357148	20,08	LOC105377887	
102659353	5,57E-18	1,73E+01	1,96E-18	0,0951	8,759286	0,83331461	401,22	THRIL	TNF and HNRNPL related immunoregulatory long non-coding RNA
51012	2,62E-62	6,16E+01	3,15E-63	0,0496	16,7848261	0,83321102	6202,11	PRELID3B	PRELI domain containing 3B
105376617	3,06E-03	2,51E+00	2,09E-03	0,2707	3,0776893	0,8331853	45,86	LOC105376(	uncharacterized LOC105376617
103091864	6,83E-04	3,17E+00	4,43E-04	0,237	3,5132811	0,83267414	56,66	SNHG22	small nucleolar RNA host gene 22
133584	5,79E-02	1,24E+00	4,53E-02	0,4158	2,0023165	0,8326109	19,94	EGFLAM	EGF like, fibronectin type III and laminin G domains
8100	8,04E-24	2,31E+01	2,41E-24	0,0818	10,1811685	0,83260679	567,74	IFT88	intraflagellar transport 88
25914	2,34E-28	2,76E+01	6,20E-29	0,0746	11,1628108	0,8324568	755,83	RTTN	rotatin
545	1,57E-44	4,38E+01	2,84E-45	0,059	14,1204288	0,83240051	1899,44	ATR	ATR serine/threonine kinase
642402	7,75E-02	1,11E+00	6,16E-02	0,445	1,8693915	0,83197146	16,02	GOLGA6L17	golgin A6 family like 17, pseudogene
81627	5,13E-40	3,93E+01	1,03E-40	0,0623	13,3605332	0,83173679	1426,54	TRMT1L	tRNA methyltransferase 1 like
64946	8,66E-20	1,91E+01	2,89E-20	0,0902	9,222909	0,83144883	530,32	CENPH	centromere protein H
5756	7,49E-58	5,71E+01	1,00E-58	0,0514	16,157661	0,83123085	4459,77	TWF1	twinfilin actin binding protein 1
50804	9,77E-41	4,00E+01	1,92E-41	0,0616	13,4849081	0,83102395	1344,54	MYEF2	myelin expression factor 2
79912	6,56E-29	2,82E+01	1,71E-29	0,0737	11,2768069	0,83089302	824,27	PYROXD1	pyridine nucleotide-disulphide oxidoreductase domain 1

283140	1,33E-01	8,76E-01	1,09E-01	0,5187	1,6015634	0,83072932	11,97	LINC02762	long intergenic non-protein coding RNA 2762
56624	1,61E-16	1,58E+01	5,94E-17	0,0993	8,3663241	0,83065356	373,73	ASAH2	N-acylsphingosine amidohydrolase 2
7592	8,21E-29	2,81E+01	2,15E-29	0,0738	11,25676	0,8305772	848,83	ZNF41	zinc finger protein 41
441425	1,63E-01	7,88E-01	1,36E-01	0,5567	1,4908706	0,82999478	10,33	ANKRD20A3	ankyrin repeat domain 20 family member A3, pseudogene
157769	5,30E-67	6,63E+01	5,78E-68	0,0476	17,4203321	0,82994317	5053,06	FAM91A1	family with sequence similarity 91 member A1
7337	6,63E-54	5,32E+01	9,69E-55	0,0533	15,5817547	0,82992853	4019,44	UBE3A	ubiquitin protein ligase E3A
105371756	2,32E-07	6,63E+00	1,21E-07	0,1568	5,2922101	0,8298362	133,06	LOC105371	uncharacterized LOC105371756
55607	1,74E-14	1,38E+01	6,87E-15	0,1066	7,7867695	0,82982086	311,82	PPP1R9A	protein phosphatase 1 regulatory subunit 9A
122945	3,02E-02	1,52E+00	2,28E-02	0,3644	2,2773719	0,82979658	23,95	NOXRED1	NADP dependent oxidoreductase domain containing 1
440590	1,06E-16	1,60E+01	3,89E-17	0,0986	8,4162139	0,82945087	372,25	ZYG11A	zyg-11 family member A, cell cycle regulator
154043	2,85E-33	3,25E+01	6,67E-34	0,0683	12,1376872	0,82924936	993,22	CNKSR3	CNKSR family member 3
105377616	1,50E-12	1,18E+01	6,28E-13	0,1152	7,1941586	0,82887077	264,68	LOC105377	uncharacterized LOC105377616
55863	1,43E-48	4,78E+01	2,35E-49	0,0561	14,7682325	0,82874532	1979,73	TMEM126B	transmembrane protein 126B
4049	1,30E-01	8,86E-01	1,07E-01	0,5135	1,6134649	0,82852061	12,01	LTA	lymphotoxin alpha
22908	9,73E-58	5,70E+01	1,31E-58	0,0513	16,1413641	0,8282172	2480,28	SACM1L	SAC1 like phosphatidylinositide phosphatase
399474	3,76E-22	2,14E+01	1,17E-22	0,0845	9,7957054	0,82818708	604,61	TMEM200B	transmembrane protein 200B
285346	6,79E-06	5,17E+00	3,83E-06	0,1792	4,6205195	0,82811297	113,3	ZNF852	zinc finger protein 852
121536	1,51E-28	2,78E+01	3,98E-29	0,0739	11,2020834	0,82785552	907,45	AEBP2	AE binding protein 2
55119	5,74E-38	3,72E+01	1,20E-38	0,0637	13,0013461	0,82758519	4440,51	PRPF38B	pre-mRNA processing factor 38B
7336	5,71E-58	5,72E+01	7,62E-59	0,0512	16,174584	0,82741262	2726,3	UBE2V2	ubiquitin conjugating enzyme E2 V2
142910	6,19E-02	1,21E+00	4,86E-02	0,4194	1,9725174	0,82732177	18,27	LIPJ	lipase family member J
525	1,23E-01	9,10E-01	1,00E-01	0,5036	1,6429531	0,82731597	13,07	ATP6V1B1	ATPase H+ transporting V1 subunit B1
105374013	3,60E-04	3,44E+00	2,28E-04	0,2245	3,6858674	0,82730864	66,62	LOC105374	013
7168	3,08E-60	5,95E+01	3,93E-61	0,0501	16,4957999	0,82713138	3571,86	TPM1	tropomyosin 1
55151	1,34E-23	2,29E+01	4,04E-24	0,0816	10,1306066	0,82701956	921,23	TMEM38B	transmembrane protein 38B
9984	1,23E-50	4,99E+01	1,92E-51	0,0548	15,0887192	0,82669675	2421,2	THOC1	THO complex subunit 1
100499227	4,73E-02	1,33E+00	3,65E-02	0,3952	2,0909044	0,82637785	22,47	USP2-AS1	USP2 antisense RNA 1
57703	1,51E-52	5,18E+01	2,27E-53	0,0537	15,3788413	0,82635769	2012,43	CWC22	CWC22 spliceosome associated protein homolog
65986	3,41E-23	2,25E+01	1,04E-23	0,0823	10,038183	0,82613407	643,98	ZBTB10	zinc finger and BTB domain containing 10
2259	9,26E-03	2,03E+00	6,63E-03	0,3043	2,7151024	0,82612232	34,23	FGF14	fibroblast growth factor 14
65124	7,02E-24	2,32E+01	2,10E-24	0,081	10,1944887	0,82546665	827,92	SOWAHC	sosondowah ankyrin repeat domain family member C
10153	9,81E-66	6,50E+01	1,10E-66	0,0478	17,2510378	0,82540304	5093,02	CEBPZ	CCAAT enhancer binding protein zeta
782	1,81E-16	1,57E+01	6,71E-17	0,0988	8,352101	0,82485727	387,16	CACNB1	calcium voltage-gated channel auxiliary subunit beta 1
8813	8,02E-50	4,91E+01	1,28E-50	0,0551	14,9632167	0,82413422	2815,75	DPM1	dolichyl-phosphate mannosyltransferase subunit 1, catalytic
339451	1,24E-20	1,99E+01	4,06E-21	0,0874	9,4311241	0,8239494	596,98	KLHL17	kelch like family member 17
56978	6,98E-46	4,52E+01	1,22E-46	0,0575	14,3403888	0,823883	1604,9	PRDM8	PR/SET domain 8
7465	7,24E-43	4,21E+01	1,36E-43	0,0595	13,8451667	0,82387048	1580,35	WEE1	WEE1 G2 checkpoint kinase
11056	9,79E-69	6,80E+01	1,03E-69	0,0467	17,6493291	0,82356911	3365,02	DDX52	DExD-box helicase 52
9263	4,07E-46	4,54E+01	7,10E-47	0,0573	14,3781548	0,82348799	2694,14	STK17A	serine/threonine kinase 17a
23517	8,23E-47	4,61E+01	1,41E-47	0,0568	14,4898066	0,8233385	2370,02	MTREX	Mtr4 exosome RNA helicase
9039	3,32E-73	7,25E+01	3,16E-74	0,0452	18,2267786	0,82332544	3832,15	UBA3	ubiquitin like modifier activating enzyme 3
4090	6,57E-45	4,42E+01	1,18E-45	0,058	14,1822852	0,82326685	2937,44	SMAD5	SMAD family member 5
100287497	9,71E-05	4,01E+00	5,89E-05	0,2049	4,0172091	0,82319038	76,37	SEPTIN7P13	septin 7 pseudogene 13
26033	1,31E-11	1,09E+01	5,67E-12	0,1195	6,8876853	0,82296578	242,09	ATRNL1	attractin like 1
6491	2,50E-85	8,46E+01	1,86E-86	0,0417	19,7074907	0,82262325	5329,59	STIL	STIL centriolar assembly protein
8908	2,64E-05	4,58E+00	1,55E-05	0,1903	4,3218984	0,82235261	100,99	GYG2	glycogenin 2
343521	2,61E-02	1,58E+00	1,95E-02	0,3521	2,3352066	0,82215658	26,09	DYNLT4	dynein light chain Tctex-type 4
503637	3,19E-17	1,65E+01	1,15E-17	0,0961	8,5574838	0,82208583	514,55	DUXAP8	double homeobox A pseudogene 8
7570	4,75E-56	5,53E+01	6,63E-57	0,0517	15,8972081	0,82187213	2864,95	ZNF22	zinc finger protein 22
100507336	1,32E-01	8,79E-01	1,09E-01	0,5121	1,6048927	0,82185913	11,99	LOC100507	uncharacterized LOC100507336
3434	4,65E-50	4,93E+01	7,35E-51	0,0548	14,9998896	0,82178732	3053,45	IFIT1	interferon induced protein with tetratricopeptide repeats 1
81575	3,60E-12	1,14E+01	1,53E-12	0,1162	7,071614	0,82168314	282,43	APOLD1	apolipoprotein L domain containing 1
283446	1,77E-02	1,75E+00	1,30E-02	0,3307	2,4843223	0,82152644	30	MYO1H	myosin IH
8562	1,41E-77	7,69E+01	1,24E-78	0,0437	18,7738514	0,82133495	11738,15	DENR	density regulated re-initiation and release factor
100132247	8,83E-46	4,51E+01	1,56E-46	0,0573	14,3237432	0,82132955	2068,24	NPIPB5	nuclear pore complex interacting protein family member B5
55629	4,81E-65	6,43E+01	5,47E-66	0,0479	17,1580552	0,82122153	4929,08	PNRC2	proline rich nuclear receptor coactivator 2
84216	8,72E-04	3,06E+00	5,70E-04	0,2383	3,4456168	0,82115984	59,22	TMEM117	transmembrane protein 117
127253	4,41E-51	5,04E+01	6,81E-52	0,0541	15,1570086	0,82055947	1910,28	TYW3	tRNA-yW synthesizing protein 3 homolog
79634	1,67E-27	2,68E+01	4,54E-28	0,0747	10,9845082	0,82024427	909,21	SCRN3	secernin 3
23586	1,28E-74	7,39E+01	1,18E-75	0,0445	18,4057087	0,81979083	5497,16	RIGI	RNA sensor RIG-I
574040	5,40E-02	1,27E+00	4,21E-02	0,4031	2,0329997	0,81950309	22,86	SNORA6	small nucleolar RNA, H/ACA box 6
51136	5,66E-11	1,02E+01	2,51E-11	0,1227	6,6726267	0,81906316	257,31	RNFT1	ring finger protein, transmembrane 1
799	1,28E-01	8,93E-01	1,05E-01	0,5053	1,6209793	0,81904931	12,5	CALCR	calcitonin receptor
55892	2,22E-38	3,77E+01	4,61E-39	0,0626	13,0745065	0,81903144	1125,55	MYNN	myoneurin
100129518	2,06E-04	3,69E+00	1,28E-04	0,2139	3,8298487	0,81901847	72,73	SOD2-OT1	SOD2 overlapping transcript 1
7738	8,39E-27	2,61E+01	2,32E-27	0,0756	10,8363357	0,81893604	729,8	ZNF184	zinc finger protein 184
4645	1,57E-11	1,08E+01	6,83E-12	0,1193	6,8611788	0,81859968	252,23	MYO5B	myosin VB
56895	4,48E-21	2,03E+01	1,45E-21	0,0858	9,5387136	0,81835618	630,55	AGPAT4	1-acylglycerol-3-phosphate O-acyltransferase 4
80167	7,90E-26	2,51E+01	2,24E-26	0,077	10,6266831	0,81834864	655,52	ABHD18	abhydrolase domain containing 18
112840	4,05E-24	2,34E+01	1,20E-24	0,0797	10,2484358	0,81700455	984,28	WDR89	WD repeat domain 89
9213	1,52E-50	4,98E+01	2,38E-51	0,0542	15,0745871	0,81667239	2007,82	XPR1	xenotropic and polytropic retrovirus receptor 1
51251	3,39E-28	2,75E+01	9,02E-29	0,0734	11,1294725	0,81656338	1181,34	NT5C3A	5'-nucleotidase, cytosolic IIIA
342908	1,62E-02	1,79E+00	1,19E-02	0,3245	2,5161329	0,81655375	30,77	ZNF404	zinc finger protein 404
55589	9,95E-63	6,20E+01	1,19E-63	0,0485	16,8425219	0,81607214	2717,82	BMP2K	BMP2 inducible kinase
92342	2,39E-11	1,06E+01	1,05E-11	0,12	6,7999271	0,81580642	279,34	METTL18	methyltransferase like 18
345079	1,46E-01	8,36E-01	1,21E-01	0,5255	1,5522823	0,81574847	11,34	SOWAHB	sosondowah ankyrin repeat domain family member B
83875	1,29E-01	8,89E-01	1,06E-01	0,5048	1,6159178	0,81566414	12,42	BCO2	beta-carotene oxygenase 2
112479	3,82E-16	1,54E+01	1,43E-16	0,0987	8,2624371	0,81532357	382,12	ERI2	ERI1 exoribonuclease family member 2
23398	5,43E-57	5,63E+01	7,42E-58	0,0508	16,0338261	0,81527625	2417,35	PPWD1	peptidylprolyl isomerase domain and WD repeat containing 1
146198	2,83E-35	3,45E+01	6,31E-36	0,0652	12,5134176	0,81527464	1061,35	ZFP90	ZFP90 zinc finger protein
414059	4,74E-02	1,32E+00	3,66E-02	0,39	2,0899688	0,81505554	20,5	TBC1D3B	TBC1 domain family member 3B
53344	6,35E-17	1,62E+01	2,31E-17	0,0961	8,4768314	0,81502229	410,25	CHIC1	cysteine rich hydrophobic domain 1
7099	6,63E-57	5,62E+01	9,07E-58	0,0509	16,0213249	0,81477916	3062,02	TLR4	toll like receptor 4
80010	3,16E-54	5,35E+01	4,59E-55	0,0521	15,629387	0,81465456	2862,45	RMI1	RecQ mediated genome instability 1
91750	2,84E-30	2,95E+01	7,18E-31	0,0704	11,5524052	0,8138588	861,47	LIN52	lin-52 DREAM MuvB core complex component
109864269	2,42E-23	2,26E+01	7,33E-24	0,0808	10,0721663	0,81385605	608,29	MIR302CHG	miR-302/367 cluster host gene
1356	2,13E-11	1,07E+01	9,33E-12	0,1194	6,8164606	0,81374678	242,51	CP	ceruloplasmin
55646	8,75E-66	6,51E+01	9,80E-67	0,0472	17,257682	0,81370495	4951,62	LYAR	Ly1 antibody reactive
165631	4,59E-06	5,34E+00	2,56E-06	0,1729	4,7029207	0,81336444	114,3	PARP15	poly(ADP-ribose) polymerase family member 15
4012	2,31E-69	6,86E+01	2,40E-70	0,0459	17,7314757	0,81326726	3875,52	LNPEP	leucyl and cystinyl aminopeptidase
51735	2,39E-54	5,36E+01	3,47E-55	0,0519	15,647287	0,8118103	2193,58	RAPGEF6	Rap guanine nucleotide exchange factor 6
92241	1,37E-41	4,09E+01	2,65E-42	0,0595	13,6300303	0,8116306	1378,36	RCSD1	RCSD domain containing 1
101929580	2,28E-02	1,64E+00	1,70E-02	0,3399	2,3875362	0,81162153	27,29	GTF2IP23	general transcription factor IIi pseudogene 23
100505767	1,60E-01	7,96E-01	1,33E-01	0,5405	1,5015228	0,8115757	10,75	SPDYE18	speedy/RINGO cell cycle regulator family member E18
113251	1,15E-78	7,79E+01	9,74E-80	0,0429	18,9083518	0,81149659	4489,22	LARP4	La ribonucleoprotein 4
10486	3,71E-61	6,04E+01	4,64E-62	0,0488	16,6244415	0,8110481	3672,18	CAP2	cyclase associated actin cytoskeleton regulatory protein 2
346007	6,58E-03	2,18E+00	4,63E-03	0,2863	2,8314592	0,8106766	38,44	EYS	eyes shut homolog
121456	1,06E-01	9,75E-01	8,55E-02	0,4712	1,719784	0,81040535	15,76	SLC9A7P1	solute carrier family 9 member 7 pseudogene 1
285141	1,87E-04	3,73E+00	1,16E-04	0,2102	3,8543875	0,81037607	83,81	ERICH2	glutamate rich 2
90627	5,90E-40	3,92E+01	1,18E-40	0,0607	13,3501582	0,80972686	1306,75	STARD13	StAR related lipid transfer domain containing 13
57576	3,59E-02	1,44E+00	2,74E-02	0,3669	2,2064611	0,80951492	23,79	KIF17	kinesin family member 17
647859	1,59E-04	3,80E+00	9,79E-05	0,2077	3,8958157	0,8092391	75,81	OCLNP1	OCLN pseudogene 1
5994	3,17E-09	8,50E+00	1,51E-09	0,1339	6,0428159	0,80919918	198,22	RFXAP	regulatory factor X associated protein
107985678	9,89E-02	1,00E+00	7,98E-02	0,4617	1,752033	0,8089847	15,82	LOC107985678	
56992	3,82E-46	4,54E+01	6,65E-47	0,0562	14,3826067	0,80888344	3363,81	KIF15	kinesin family member 15
285782	9,22E-02	1,04E+00	7,41E-02	0,4528	1,7861778	0,80883563	15,3	CAGE1	cancer antigen 1
151449	6,53E-02	1,19E+00	5,14E-02	0,4151	1,9482642	0,8087158	18,68	GDF7	growth differentiation factor 7
257203	1,58E-01	8,01E-01	1,31E-01	0,5359	1,5089243	0,80865955	10,77	DSCR9	Down syndrome critical region 9
4752	1,68E-07	6,77E+00	8,71E-08	0,1511	5,3517332	0,80858583	165,02	NEK3	NIMA related kinase 3
150275	4,02E-48	4,74E+01	6,66E-49	0,055	14,6978281	0,8084942	1746,27	CCDC117	coiled-coil domain containing 117
105374764	8,90E-02	1,05E+00	7,13E-02	0,4481	1,8034164	0,80804821	15,78	LOC105374	uncharacterized LOC105374764
4683	3,78E-47	4,64E+01	6,41E-48	0,0556	14,5436241	0,80796667	2903,62	NBN	nibrin
200539	1,54E-03	2,81E+00	1,03E-03	0,2461	3,2823358	0,80785328	55,06	ANKRD23	ankyrin repeat domain 23
134957	2,36E-28	2,76E+01	6,25E-29	0,0724	11,162131	0,8077397	878,86	STXBP5	syntaxin binding protein 5
5876	5,10E-43	4,23E+01	9,56E-44	0,0582	13,8705076	0,8074109	3608,29	RABGGTB	Rab geranylgeranyltransferase subunit beta
23205	1,35E-20	1,99E+01	4,41E-21	0,0857	9,4223817	0,80729062	601,83	ACSBG1	acyl-CoA synthetase bubblegum family member 1
80311	9,52E-28	2,70E+01	2,56E-28	0,0732	11,0359326	0,80728872	1004,74	KLHL15	kelch like family member 15
9631	9,68E-65	6,40E+01	1,11E-65	0,0471	17,1170139	0,8070671	5203,78	NUP155	nucleoporin 155
107986488	3,97E-04	3,40E+00	2,52E-04	0,2204	3,6598158	0,80674203	70,16	LOC107986	488
22858	1,65E-55	5,48E+01	2,33E-56	0,051	15,8183226	0,80643537	2510,26	CILK1	ciliogenesis associated kinase 1

182	1,66E-92	9,18E+01	1,09E-93	0,0393	20,5332455	0,80641834	8438,79	JAG1	jagged canonical Notch ligand 1
197342	1,91E-02	1,72E+00	1,40E-02	0,3282	2,4560643	0,80614181	29,51	EME2	essential meiotic structure-specific endonuclease subunit 2
55327	8,52E-28	2,71E+01	2,29E-28	0,073	11,0460823	0,80613838	1284,26	LIN7C	lin-7 homolog C, crumbs cell polarity complex component
6713	9,36E-25	2,40E+01	2,73E-25	0,0775	10,3908671	0,80527148	772,37	SQLE	squalene epoxidase
9456	2,21E-34	3,37E+01	5,04E-35	0,0652	12,3472634	0,80466286	1073,61	HOMER1	homer scaffold protein 1
114882	1,23E-58	5,79E+01	1,61E-59	0,0495	16,270005	0,80460616	4334,37	OSBPL8	oxysterol binding protein like 8
5590	1,89E-19	1,87E+01	6,38E-20	0,088	9,1377678	0,80457397	521,1	PRKCZ	protein kinase C zeta
144402	3,96E-31	3,04E+01	9,80E-32	0,0686	11,722296	0,80433813	953,81	CPNE8	copine 8
201595	4,12E-43	4,24E+01	7,69E-44	0,0579	13,8860752	0,80394523	13564,38	STT3B	STT3 oligosaccharyltransferase complex catalytic subunit B
4139	8,87E-14	1,31E+01	3,57E-14	0,1061	7,5757386	0,80388714	314,1	MARK1	microtubule affinity regulating kinase 1
701	4,43E-68	6,74E+01	4,72E-69	0,0458	17,5631742	0,80378508	6039,19	BUB1B	BUB1 mitotic checkpoint serine/threonine kinase B
728463	1,23E-08	7,91E+00	6,03E-09	0,1382	5,8159607	0,80354487	173,82	TGFB2-AS1	TGFB2 antisense RNA 1 (head to head)
8554	1,14E-44	4,39E+01	2,07E-45	0,0568	14,1428891	0,80348917	1841,71	PIAS1	protein inhibitor of activated STAT 1
85313	3,48E-49	4,85E+01	5,61E-50	0,054	14,8643839	0,80319972	1899,46	PPIL4	peptidylprolyl isomerase like 4
151254	4,16E-05	4,38E+00	2,46E-05	0,1904	4,2180745	0,80312464	90,04	C2CD6	C2 calcium dependent domain containing 6
51018	5,37E-41	4,03E+01	1,05E-41	0,0594	13,5292845	0,80304526	2805,74	RRP15	ribosomal RNA processing 15 homolog
284406	8,97E-21	2,00E+01	2,92E-21	0,0848	9,4655356	0,80292285	573,21	ZFP82	ZFP82 zinc finger protein
114004351	7,89E-10	9,10E+00	3,67E-10	0,1281	6,2675696	0,80288945	204,27	PARGP1-AG	PARGP1-AGAP4 readthrough
51001	1,60E-25	2,48E+01	4,57E-26	0,076	10,5599664	0,80284199	858,25	MTERF3	mitochondrial transcription termination factor 3
100133612	2,75E-02	1,56E+00	2,06E-02	0,3469	2,3144501	0,80280157	26,39	LINC01134	long intergenic non-protein coding RNA 1134
5064	2,14E-03	2,67E+00	1,44E-03	0,2519	3,1862151	0,80275688	50,39	PALM	paralemmin
203328	1,15E-07	6,94E+00	5,87E-08	0,148	5,4226234	0,80239743	160,35	SUSD3	sushi domain containing 3
253782	8,05E-44	4,31E+01	1,48E-44	0,0573	14,0035704	0,80186342	1572,17	CERS6	ceramide synthase 6
23350	2,19E-73	7,27E+01	2,08E-74	0,0439	18,2498405	0,80165816	5177,61	U2SURP	U2 snRNP associated SURP domain containing
4763	4,03E-35	3,44E+01	9,04E-36	0,0642	12,4848037	0,80157987	1099,65	NF1	neurofibromin 1
105371630	1,43E-02	1,84E+00	1,04E-02	0,3127	2,5619083	0,80109217	32,92	LOC105371	uncharacterized LOC105371630
105372436	1,93E-01	7,14E-01	1,63E-01	0,5741	1,3952267	0,80101152	9,62	LOC105372	uncharacterized LOC105372436
29068	4,20E-58	5,74E+01	5,60E-59	0,0495	16,1935906	0,8007794	2447,44	ZBTB44	zinc finger and BTB domain containing 44
206412	1,18E-01	9,28E-01	9,61E-02	0,481	1,6640315	0,80047912	13,5	C6orf163	chromosome 6 open reading frame 163
4212	5,48E-25	2,43E+01	1,59E-25	0,0767	10,4422816	0,80045373	660,83	MEIS2	Meis homeobox 2
29110	7,51E-39	3,81E+01	1,54E-39	0,0608	13,1574386	0,79999413	1679,49	TBK1	TANK binding kinase 1
23594	2,27E-32	3,16E+01	5,42E-33	0,0669	11,96495	0,79992152	1323,83	ORC6	origin recognition complex subunit 6
400966	1,15E-03	2,94E+00	7,62E-04	0,2375	3,3662937	0,79962645	58,25	RGPD1	RANBP2 like and GRIP domain containing 1
9991	9,50E-62	6,10E+01	1,17E-62	0,0479	16,7068939	0,79944755	5596,67	PTBP3	polypyrimidine tract binding protein 3
653238	2,33E-27	2,66E+01	6,33E-28	0,0729	10,9544001	0,79893257	891,22	GTF2H2B	general transcription factor IIH subunit 2B (pseudogene)
124359	6,12E-32	3,12E+01	1,48E-32	0,0672	11,8812882	0,79891907	1036,81	CDYL2	chromodomain Y like 2
378108	4,33E-17	1,64E+01	1,57E-17	0,0937	8,5218049	0,79881101	408,8	TRIM74	tripartite motif containing 74
3034	1,52E-01	8,18E-01	1,26E-01	0,5221	1,5293125	0,79845413	13,72	HAL	histidine ammonia-lyase
6383	9,55E-33	3,20E+01	2,27E-33	0,0663	12,037132	0,79833068	1004,62	SDC2	syndecan 2
1780	2,29E-05	4,64E+00	1,33E-05	0,1833	4,3545125	0,79827614	98,46	DYNC1I1	dynein cytoplasmic 1 intermediate chain 1
3572	1,06E-90	9,00E+01	7,13E-92	0,0393	20,328984	0,7982724	18357,43	IL6ST	interleukin 6 cytokine family signal transducer
54675	2,56E-06	5,59E+00	1,41E-06	0,1655	4,8235542	0,79807009	1153,18	CRLS1	cardiolipin synthase 1
65056	2,11E-72	7,17E+01	2,05E-73	0,044	18,1242466	0,79776806	4374,31	GPBP1	GC-rich promoter binding protein 1
100506895	1,29E-02	1,89E+00	9,34E-03	0,3068	2,5995085	0,79748948	34,18	LUARIS	lncRNA upregulator of antiviral response interferon signaling
326340	2,34E-09	8,63E+00	1,11E-09	0,1309	6,0921568	0,79717483	207,28	ZAR1	zygote arrest 1
160140	4,27E-05	4,37E+00	2,53E-05	0,1892	4,2121125	0,79694596	90,64	C11orf65	chromosome 11 open reading frame 65
3895	7,01E-84	8,32E+01	5,38E-85	0,0408	19,5364293	0,79680071	21908,21	KTN1	kinectin 1
100506302	4,63E-06	5,33E+00	2,59E-06	0,1694	4,7012656	0,79651556	120,39	RBM33-DT	RBM33 divergent transcript
5097	3,52E-09	8,45E+00	1,69E-09	0,1322	6,0254999	0,79650858	202,81	PCDH1	protocadherin 1
23150	1,53E-07	6,82E+00	7,92E-08	0,1483	5,3688493	0,79643603	151,16	FRMD4B	FERM domain containing 4B
102723390	4,89E-02	1,31E+00	3,79E-02	0,3835	2,0764422	0,79626314	21,43	FRG1EP	FSHD region gene 1 family member E, pseudogene
79465	7,55E-23	2,21E+01	2,32E-23	0,0799	9,9584233	0,79574911	614,91	ULBP3	UL16 binding protein 3
28557	1,77E-01	7,52E-01	1,48E-01	0,5506	1,4450425	0,79566955	10,58	TRBV30	T cell receptor beta variable 30
7748	3,17E-26	2,55E+01	8,90E-27	0,0743	10,7124198	0,79554745	785,28	ZNF195	zinc finger protein 195
122060	3,01E-19	1,85E+01	1,02E-19	0,0875	9,0863304	0,79548397	530,92	SLAIN1	SLAIN motif family member 1
55901	5,86E-03	2,23E+00	4,11E-03	0,2772	2,8697687	0,7954215	45,2	THSD1	thrombospondin type 1 domain containing 1
23595	2,78E-43	4,26E+01	5,18E-44	0,0572	13,914381	0,79536454	2192,96	ORC3	origin recognition complex subunit 3
51379	5,02E-43	4,23E+01	9,40E-44	0,0573	13,871683	0,79530973	1554,06	CRLF3	cytokine receptor like factor 3
105378260	6,66E-02	1,18E+00	5,25E-02	0,41	1,9390358	0,79494593	19,28	LOC105378	replaced by ID 85319
54532	4,43E-45	4,44E+01	7,92E-46	0,0559	14,2102364	0,79484174	1736,82	USP53	ubiquitin specific peptidase 53
100533105	1,17E-09	8,93E+00	5,48E-10	0,128	6,2047365	0,79441863	207,06	C8orf44-SG	C8orf44-SGK3 readthrough
107986641	1,98E-01	7,03E-01	1,67E-01	0,5751	1,3813236	0,79433633	9,58	LOC107986641	
10217	1,90E-57	5,67E+01	2,57E-58	0,0493	16,0995308	0,79431115	2342,53	CTDSPL	CTD small phosphatase like
200933	3,67E-38	3,74E+01	7,66E-39	0,0609	13,0357294	0,79428023	1867,05	FBXO45	F-box protein 45
100287314	9,90E-22	2,10E+01	3,13E-22	0,0819	9,6962497	0,79427634	659,03	LINC00941	long intergenic non-protein coding RNA 941
23116	1,71E-26	2,58E+01	4,76E-27	0,0737	10,7701155	0,79417398	745,84	TOGARAM1	TOG array regulator of axonemal microtubules 1
830	2,33E-43	4,26E+01	4,33E-44	0,057	13,9272179	0,79414453	2861,79	CAPZA2	capping actin protein of muscle Z-line subunit alpha 2
5885	3,14E-88	8,75E+01	2,22E-89	0,0396	20,0452793	0,79397211	26057,72	RAD21	RAD21 cohesin complex component
376940	4,14E-04	3,38E+00	2,64E-04	0,2176	3,6486819	0,79396707	73,57	ZC3H6	zinc finger CCCH-type containing 6
1286	7,65E-06	5,12E+00	4,33E-06	0,1728	4,5947047	0,79396672	107,59	COL4A4	collagen type IV alpha 4 chain
7174	3,87E-56	5,54E+01	5,40E-57	0,0499	15,9100702	0,79384424	2751,08	TPP2	tripeptidyl peptidase 2
22891	1,38E-01	8,60E-01	1,14E-01	0,5022	1,5807698	0,79379626	12,38	ZNF365	zinc finger protein 365
159	6,10E-45	4,42E+01	1,09E-45	0,0559	14,187602	0,79352484	4721,19	ADSS2	adenylosuccinate synthase 2
11235	5,63E-61	6,02E+01	7,07E-62	0,0478	16,5991662	0,79319727	3191,5	PDCD10	programmed cell death 10
1296	5,95E-02	1,23E+00	4,66E-02	0,3984	1,9899321	0,79287869	19,66	COL8A2	collagen type VIII alpha 2 chain
9169	1,77E-65	6,48E+01	2,00E-66	0,046	17,2165235	0,79277987	4850,4	SCAF11	SR-related CTD associated factor 11
2776	5,32E-44	4,33E+01	9,77E-45	0,0565	14,033149	0,79240305	1756,12	GNAQ	G protein subunit alpha q
3839	4,00E-49	4,84E+01	6,47E-50	0,0533	14,8548626	0,79237085	3586,23	KPNA3	karyopherin subunit alpha 3
160298	2,38E-03	2,62E+00	1,61E-03	0,2509	3,1546933	0,79165935	51,48	C11orf42	chromosome 11 open reading frame 42
51276	9,89E-06	5,00E+00	5,64E-06	0,1744	4,5395349	0,79161751	112,74	ZNF571	zinc finger protein 571
139886	2,62E-20	1,96E+01	8,63E-21	0,0846	9,3515958	0,79127403	618,04	SPIN4	spindlin family member 4
5984	3,71E-57	5,64E+01	5,05E-58	0,0493	16,0576777	0,79123115	3501,4	RFC4	replication factor C subunit 4
306	3,60E-81	8,04E+01	2,91E-82	0,0412	19,2124999	0,79101886	8815,38	ANXA3	annexin A3
91151	1,54E-21	2,08E+01	4,91E-22	0,0819	9,6501329	0,79035272	638,52	TIGD7	tigger transposable element derived 7
83989	1,47E-28	2,78E+01	3,86E-29	0,0705	11,2047711	0,79015715	868,59	FAM172A	family with sequence similarity 172 member A
7620	3,78E-14	1,34E+01	1,51E-14	0,1028	7,6869799	0,78995969	341,92	ZNF69	zinc finger protein 69
50808	1,83E-31	3,07E+01	4,48E-32	0,067	11,7883461	0,78981741	1303,05	AK3	adenylate kinase 3
728485	2,98E-03	2,53E+00	2,03E-03	0,256	3,085655	0,78978563	52,75	LOC728485	uncharacterized LOC728485
1386	3,68E-44	4,34E+01	6,71E-45	0,0561	14,0597342	0,78936652	2014,63	ATF2	activating transcription factor 2
83594	1,76E-18	1,78E+01	6,11E-19	0,0888	8,8899699	0,78903228	461,83	NUDT12	nudix hydrolase 12
105373682	1,17E-01	9,32E-01	9,53E-02	0,4728	1,6681821	0,78875554	14,52	LOC105373	uncharacterized LOC105373682
7782	2,22E-11	1,07E+01	9,74E-12	0,1158	6,8103653	0,78870888	262,33	SLC30A4	solute carrier family 30 member 4
9926	5,72E-55	5,42E+01	8,20E-56	0,0501	15,7387557	0,78815178	2610,8	LPGAT1	lysophosphatidylglycerol acyltransferase 1
93556	1,84E-01	7,35E-01	1,54E-01	0,5533	1,4241891	0,78801706	10,78	EGFEM1P	EGF like and EMI domain containing 1, pseudogene
100132062	1,02E-05	4,99E+00	5,80E-06	0,1738	4,5335526	0,78789517	111,33	LOC100132	uncharacterized LOC100132062
112268244	2,17E-03	2,66E+00	1,46E-03	0,2476	3,1817239	0,78781948	53,42	LOC112268	uncharacterized LOC112268244
100101467	4,55E-22	2,13E+01	1,43E-22	0,0805	9,7761491	0,78744978	695,4	ZSCAN30	zinc finger and SCAN domain containing 30
115752	5,18E-48	4,73E+01	8,60E-49	0,0536	14,6804917	0,78739774	1860,61	DIS3L	DIS3 like exosome 3'-5' exoribonuclease
53981	1,41E-71	7,09E+01	1,39E-72	0,0437	18,0185412	0,78733502	6964,6	CPSF2	cleavage and polyadenylation specific factor 2
85025	6,01E-15	1,42E+01	2,33E-15	0,0994	7,9221953	0,78720542	528,9	TMEM60	transmembrane protein 60
619279	3,20E-21	2,05E+01	1,03E-21	0,0822	9,5739214	0,78699585	560,4	ZNF704	zinc finger protein 704
7480	2,61E-02	1,58E+00	1,95E-02	0,337	2,3352999	0,78693973	28,74	WNT10B	Wnt family member 10B
284217	4,21E-08	7,38E+00	2,11E-08	0,1404	5,6027524	0,78665813	168,58	LAMA1	laminin subunit alpha 1
100288152	1,20E-04	3,92E+00	7,32E-05	0,1983	3,9657168	0,78657442	86,98	SLC9A3-AS1	SLC9A3 antisense RNA 1
9914	6,79E-04	3,17E+00	4,40E-04	0,2238	3,5151101	0,78657378	69,62	ATP2C2	ATPase secretory pathway Ca2+ transporting 2
105373567	2,29E-01	6,40E-01	1,96E-01	0,6076	1,294464	0,78652662	9,58	LOC105373	uncharacterized LOC105373567
9173	9,79E-02	1,01E+00	7,89E-02	0,4476	1,7570771	0,78645154	15,67	IL1RL1	interleukin 1 receptor like 1
9156	1,19E-59	5,89E+01	1,53E-60	0,0479	16,4135739	0,7857389	2750,8	EXO1	exonuclease 1
11131	4,28E-05	4,37E+00	2,53E-05	0,1865	4,2119491	0,78571718	99,43	CAPN11	calpain 11
55854	1,34E-67	6,69E+01	1,44E-68	0,0449	17,4995909	0,78554066	4256,03	ZC3H15	zinc finger CCCH-type containing 15
107986136	2,27E-13	1,26E+01	9,26E-14	0,1054	7,4510015	0,78538307	317,68	IL20RB-AS1	IL20RB antisense RNA 1
221914	2,54E-01	5,95E-01	2,18E-01	0,6381	1,2308629	0,78536738	7,95	GPC2	glypican 2
800	3,70E-44	4,34E+01	6,75E-45	0,0559	14,0593176	0,7853054	4282,11	CALD1	caldesmon 1
80350	1,19E-04	3,92E+00	7,24E-05	0,1977	3,9683469	0,78469331	87,08	LPAL2	lipoprotein(a) like 2, pseudogene
57532	1,14E-76	7,59E+01	1,02E-77	0,042	18,6615601	0,78447205	7816,81	NUFIP2	nuclear FMR1 interacting protein 2
29798	1,60E-10	9,80E+00	7,23E-11	0,1204	6,5157085	0,78445427	261,36	C2orf27A	chromosome 2 open reading frame 27A
347716	1,82E-03	2,74E+00	1,22E-03	0,2426	3,2335885	0,78441454	55,54	USP32P3	ubiquitin specific peptidase 32 pseudogene 3
107984242	1,59E-05	4,80E+00	9,21E-06	0,1766	4,4349931	0,78335371	105,85	LOC107984	uncharacterized LOC107984242
129881	7,57E-02	1,12E+00	6,01E-02	0,4166	1,8804081	0,78334336	18,44	CFAP210	cilia and flagella associated protein 210
84546	7,84E-03	2,11E+00	5,56E-03	0,2825	2,7724202	0,78330533	54,89	SNORD35B	small nucleolar RNA, C/D box 35B

84869	2,01E-34	3,37E+01	4,57E-35	0,0633	12,3550477	0,78245857	1384,87	CBR4	carbonyl reductase 4
9818	4,72E-70	6,93E+01	4,84E-71	0,0439	17,8212085	0,78244012	4682,54	NUP58	nucleoporin 58
56925	3,34E-19	1,85E+01	1,14E-19	0,0862	9,075134	0,78197323	509,19	LXN	latexin
10915	1,19E-70	6,99E+01	1,20E-71	0,0437	17,8992031	0,78171862	5857,35	TCERG1	transcription elongation regulator 1
388284	1,76E-01	7,54E-01	1,48E-01	0,5393	1,4482724	0,78110023	10,61	C16orf86	chromosome 16 open reading frame 86
727909	1,77E-01	7,52E-01	1,48E-01	0,5397	1,4471823	0,78097713	10,6	GOLGA8Q	golgin A8 family member Q
9321	5,21E-52	5,13E+01	7,90E-53	0,051	15,29783	0,78034978	2765,63	TRIP11	thyroid hormone receptor interactor 11
6296	2,41E-05	4,62E+00	1,41E-05	0,1797	4,3426045	0,78015284	108,22	ACSM3	acyl-CoA synthetase medium chain family member 3
9581	6,77E-43	4,22E+01	1,27E-43	0,0563	13,8499907	0,78013857	1571,26	PREPL	prolyl endopeptidase like
57134	1,51E-02	1,82E+00	1,10E-02	0,3066	2,5427029	0,77955448	34,58	MAN1C1	mannosidase alpha class 1C member 1
158046	1,67E-01	7,77E-01	1,39E-01	0,5269	1,4793176	0,77943529	11,6	NXNL2	nucleoredoxin like 2
1407	5,15E-49	4,83E+01	8,35E-50	0,0525	14,8377882	0,77917671	2336,51	CRY1	cryptochrome circadian regulator 1
5501	2,47E-61	6,06E+01	3,07E-62	0,0468	16,6491635	0,77906606	10840,79	PPP1CC	protein phosphatase 1 catalytic subunit gamma
84240	1,75E-40	3,98E+01	3,46E-41	0,058	13,4413046	0,77898623	1704,88	ZCCHC9	zinc finger CCHC-type containing 9
29843	7,25E-39	3,81E+01	1,49E-39	0,0592	13,16008	0,77841925	1892,97	SENP1	SUMO specific peptidase 1
158358	8,59E-19	1,81E+01	2,96E-19	0,0868	8,9703405	0,77836875	540,7	KIAA2026	KIAA2026
105369865	3,49E-04	3,46E+00	2,21E-04	0,2107	3,6938865	0,77827664	78,91	PPP1R12A-A	PPP1R12A antisense RNA 1
1595	3,34E-42	4,15E+01	6,37E-43	0,0567	13,7337667	0,77825968	1846,76	CYP51A1	cytochrome P450 family 51 subfamily A member 1
5775	3,50E-14	1,35E+01	1,39E-14	0,1011	7,6971865	0,77801168	410,46	PTPN4	protein tyrosine phosphatase non-receptor type 4
107986718	2,89E-05	4,54E+00	1,69E-05	0,1808	4,302068	0,77799178	99,28	LOC107986	replaced by ID 105375535
122773	8,84E-04	3,05E+00	5,77E-04	0,226	3,4420743	0,77780016	65,09	KLHDC1	kelch domain containing 1
107985675	8,88E-03	2,05E+00	6,33E-03	0,2849	2,7299984	0,77774887	43,03	LOC107985	uncharacterized LOC107985675
105369663	5,63E-06	5,25E+00	3,16E-06	0,1669	4,659995	0,77761198	127,98	LOC105369	uncharacterized LOC105369663
201965	4,31E-33	3,24E+01	1,01E-33	0,0642	12,1033922	0,77739984	1412,38	RWDD4	RWD domain containing 4
29984	1,92E-06	5,72E+00	1,05E-06	0,1592	4,8818228	0,77739628	139,72	RHOD	ras homolog family member D
27094	6,32E-04	3,20E+00	4,08E-04	0,2199	3,5346707	0,77738912	72,9	KCNMB3	potassium calcium-activated channel subfamily M regulatory beta subunit 3
89970	2,24E-43	4,26E+01	4,16E-44	0,0558	13,9300945	0,77718204	1596,26	RSPRY1	ring finger and SPRY domain containing 1
55106	3,39E-30	2,95E+01	8,58E-31	0,0673	11,537018	0,77675026	1097,94	SLFN12	schlafen family member 12
4214	1,85E-40	3,97E+01	3,65E-41	0,0578	13,4373453	0,77674103	1579,16	MAP3K1	mitogen-activated protein kinase kinase kinase 1
54916	2,69E-19	1,86E+01	9,13E-20	0,0853	9,0988138	0,77652301	557,97	TMEM260	transmembrane protein 260
54892	1,43E-79	7,88E+01	1,19E-80	0,0408	19,0187921	0,77644142	8589,03	NCAPG2	non-SMC condensin II complex subunit G2
122786	2,91E-79	7,85E+01	2,45E-80	0,0409	18,9810267	0,77641455	11027,21	FRMD6	FERM domain containing 6
117177	1,10E-29	2,90E+01	2,83E-30	0,0679	11,4339962	0,7763577	1170,62	RAB3IP	RAB3A interacting protein
51184	1,10E-31	3,10E+01	2,68E-32	0,0656	11,8316375	0,77624966	2120,25	GPN3	GPN-loop GTPase 3
255119	3,09E-02	1,51E+00	2,33E-02	0,342	2,2685822	0,77585127	28,4	CFAP299	cilia and flagella associated protein 299
80014	5,15E-50	4,93E+01	8,16E-51	0,0517	14,992967	0,7758222	2690,99	WWC2	WW and C2 domain containing 2
55000	7,37E-86	8,51E+01	5,44E-87	0,0392	19,7696427	0,77569712	7761,9	TUG1	taurine up-regulated 1
9668	1,79E-13	1,27E+01	7,29E-14	0,1037	7,4825332	0,7755802	325,4	ZNF432	zinc finger protein 432
1456	5,60E-48	4,73E+01	9,32E-49	0,0528	14,6750423	0,77524313	2186,91	CSNK1G3	casein kinase 1 gamma 3
57189	4,57E-34	3,33E+01	1,05E-34	0,0631	12,2881096	0,7752399	1137,17	DENND11	DENN domain containing 11
9975	3,83E-56	5,54E+01	5,33E-57	0,0487	15,9107918	0,77498044	3373,79	NR1D2	nuclear receptor subfamily 1 group D member 2
26278	2,14E-55	5,47E+01	3,04E-56	0,049	15,8014903	0,77473772	3834,69	SACS	sacsin molecular chaperone
26009	2,34E-56	5,56E+01	3,24E-57	0,0486	15,9420606	0,77470509	4305,63	ZZZ3	zinc finger ZZ-type containing 3
57162	5,13E-23	2,23E+01	1,57E-23	0,0774	9,9972022	0,77410762	656,09	PELI1	pellino E3 ubiquitin protein ligase 1
84437	4,08E-34	3,34E+01	9,35E-35	0,0629	12,297414	0,7739524	1339,3	MSANTD4	Myb/SANT DNA binding domain containing 4 with coiled-coils
8905	7,45E-38	3,71E+01	1,56E-38	0,0596	12,9812053	0,77386196	1823,1	AP1S2	adaptor related protein complex 1 subunit sigma 2
2059	1,36E-44	4,39E+01	2,47E-45	0,0547	14,1303178	0,77334142	1905,5	EPS8	epidermal growth factor receptor pathway substrate 8
7082	1,33E-58	5,79E+01	1,75E-59	0,0475	16,2648897	0,77312465	4757,91	TJP1	tight junction protein 1
80318	4,21E-16	1,54E+01	1,57E-16	0,0936	8,2507747	0,7724194	408,24	GKAP1	G kinase anchoring protein 1
201627	1,41E-54	5,39E+01	2,03E-55	0,0493	15,6813336	0,77234917	2600,79	DENND6A	DENN domain containing 6A
148268	9,91E-13	1,20E+01	4,14E-13	0,1065	7,2510435	0,77226416	340,65	ZNF570	zinc finger protein 570
200576	2,30E-49	4,86E+01	3,69E-50	0,0519	14,8923846	0,77222772	2067,31	PIKFYVE	phosphoinositide kinase, FYVE-type zinc finger containing
50999	3,25E-40	3,95E+01	6,47E-41	0,0576	13,3949153	0,77212252	3584,15	TMED5	transmembrane p24 trafficking protein 5
23360	2,81E-55	5,46E+01	4,00E-56	0,0489	15,7841428	0,77202939	3753,18	FNBP4	formin binding protein 4
55814	4,52E-44	4,33E+01	8,28E-45	0,055	14,0448934	0,77192342	4003,01	BDP1	B double prime 1, subunit of RNA polymerase III transcription initiation factor IIIB
619423	5,22E-02	1,28E+00	4,06E-02	0,3769	2,0478894	0,77175451	22,4	FAM85A	family with sequence similarity 85 member A
84524	6,30E-18	1,72E+01	2,23E-18	0,0882	8,7452069	0,77160028	476,05	ZC3H8	zinc finger CCCH-type containing 8
10179	2,35E-33	3,26E+01	5,49E-34	0,0635	12,1536213	0,77144107	2376,02	RBM7	RNA binding motif protein 7
79848	8,54E-28	2,71E+01	2,30E-28	0,0698	11,045773	0,77143573	941,24	CSPP1	centrosome and spindle pole associated protein 1
51347	1,88E-63	6,27E+01	2,21E-64	0,0455	16,9417662	0,77137194	4531,61	TAOK3	TAO kinase 3
51463	4,73E-27	2,63E+01	1,30E-27	0,0708	10,8891857	0,77129529	1024,18	GPR89B	G protein-coupled receptor 89B
64864	6,54E-36	3,52E+01	1,44E-36	0,0611	12,6304162	0,7711405	1344,14	RFX7	regulatory factor X7
688	1,29E-32	3,19E+01	3,06E-33	0,0642	12,0123483	0,77081848	1357,76	KLF5	KLF transcription factor 5
51274	6,83E-45	4,42E+01	1,23E-45	0,0543	14,179513	0,77063548	1743,3	KLF3	KLF transcription factor 3
10818	3,74E-31	3,04E+01	9,24E-32	0,0657	11,7272636	0,77022965	1200,61	FRS2	fibroblast growth factor receptor substrate 2
105375631	6,59E-02	1,18E+00	5,19E-02	0,3961	1,9442341	0,7701782	20,67	LOC105375	LINE-1 retrotransposable element ORF2 protein-like
10438	3,16E-26	2,55E+01	8,86E-27	0,0718	10,7128356	0,76965446	1034,24	C1D	C1D nuclear receptor corepressor
65251	2,22E-12	1,17E+01	9,37E-13	0,1078	7,1394472	0,76946373	323,11	ZNF649	zinc finger protein 649
339192	6,65E-03	2,18E+00	4,69E-03	0,2721	2,8278162	0,76939537	43,38	FMNL1-DT	FMNL1 divergent transcript
55197	2,87E-51	5,05E+01	4,41E-52	0,0506	15,185496	0,769117	3056,35	RPRD1A	regulation of nuclear pre-mRNA domain containing 1A
8548	3,18E-36	3,55E+01	6,92E-37	0,0606	12,6876328	0,76904956	1322,4	BLZF1	basic leucine zipper nuclear factor 1
201973	1,40E-20	1,99E+01	4,57E-21	0,0816	9,4186425	0,7688603	574,94	PRIMPOL	primase and DNA directed polymerase
388558	2,54E-11	1,06E+01	1,11E-11	0,1132	6,7909995	0,76880668	291,84	ZNF808	zinc finger protein 808
107983971	5,12E-02	1,29E+00	3,97E-02	0,3734	2,056662	0,76799594	23,45	LOC107983971	
55355	3,55E-64	6,34E+01	4,12E-65	0,0451	17,0403163	0,76776372	6095,77	HJURP	Holliday junction recognition protein
1185	1,53E-26	2,58E+01	4,25E-27	0,0712	10,780543	0,76747386	814,04	CLCN6	chloride voltage-gated channel 6
54431	4,16E-61	6,04E+01	5,21E-62	0,0462	16,6174644	0,76728294	6663,91	DNAJC10	DnaJ heat shock protein family (Hsp40) member C10
344595	5,62E-17	1,63E+01	2,05E-17	0,0904	8,4909981	0,76722141	476,97	DUBR	DPPA2 upstream binding RNA
54619	1,61E-23	2,28E+01	4,85E-24	0,0759	10,1127724	0,76720493	680,69	CCNJ	cyclin J
9702	2,42E-58	5,76E+01	3,20E-59	0,0473	16,2279249	0,76707021	3910,37	CEP57	centrosomal protein 57
162073	2,80E-52	5,16E+01	4,23E-53	0,05	15,33853	0,76664814	2645,91	ITPRIPL2	ITPRIP like 2
23012	8,82E-35	3,41E+01	1,99E-35	0,0617	12,42177	0,76654395	1303,46	STK38L	serine/threonine kinase 38 like
51099	3,21E-57	5,65E+01	4,36E-58	0,0477	16,0667643	0,76653245	2863,03	ABHD5	abhydrolase domain containing 5, lysophosphatidic acid acyltransferase
6687	1,21E-37	3,69E+01	2,55E-38	0,0592	12,9437088	0,76640074	1621,98	SPG7	SPG7 matrix AAA peptidase subunit, paraplegin
399975	1,77E-14	1,38E+01	7,00E-15	0,0984	7,7845628	0,76636578	404,71	LOC399975	uncharacterized LOC399975
10659	9,88E-27	2,60E+01	2,73E-27	0,0708	10,8211394	0,76605724	1001,49	CELF2	CUGBP Elav-like family member 2
9917	4,35E-63	6,24E+01	5,15E-64	0,0453	16,891992	0,76603959	5128,63	FAM20B	FAM20B glycosaminoglycan xylosylkinase
54823	2,25E-11	1,06E+01	9,85E-12	0,1125	6,8087332	0,7660227	292,64	SWT1	SWT1 RNA endoribonuclease homolog
154214	2,39E-14	1,36E+01	9,45E-15	0,0989	7,7464504	0,76587994	426,32	RNF217	ring finger protein 217
7617	2,31E-05	4,64E+00	1,35E-05	0,176	4,352328	0,76587878	107,15	ZNF66	zinc finger protein 66
157773	2,35E-05	4,63E+00	1,37E-05	0,176	4,3492588	0,76546376	106,15	C8orf48	chromosome 8 open reading frame 48
25926	8,20E-68	6,71E+01	8,77E-69	0,0437	17,5279058	0,76544245	5292,82	NOL11	nucleolar protein 11
54957	6,82E-22	2,12E+01	2,15E-22	0,0786	9,7345795	0,76523233	717,75	TXNL4B	thioredoxin like 4B
253650	2,02E-15	1,47E+01	7,74E-16	0,0949	8,0581787	0,76491912	406,26	ANKRD18A	ankyrin repeat domain 18A
100129973	1,07E-03	2,97E+00	7,03E-04	0,2257	3,3884987	0,76480997	62,3	CERNA1	competing endogenous lncRNA 1 for miR-4707-5p and miR-4767
26783	5,43E-02	1,27E+00	4,23E-02	0,3765	2,0303736	0,7644785	23,36	SNORA65	small nucleolar RNA, H/ACA box 65
115294	1,20E-12	1,19E+01	5,01E-13	0,1058	7,2250311	0,76434595	313	PCMTD1	protein-L-isoaspartate (D-aspartate) O-methyltransferase domain containing 1
23411	1,25E-30	2,99E+01	3,14E-31	0,0658	11,6233694	0,76427528	1221,68	SIRT1	sirtuin 1
105371374	2,74E-04	3,56E+00	1,72E-04	0,2034	3,7566537	0,76418994	77,65	ATP2C2-AS1	ATP2C2 antisense RNA 1
137994	3,76E-22	2,14E+01	1,17E-22	0,078	9,7957643	0,76412661	760,15	LETM2	leucine zipper and EF-hand containing transmembrane protein 2
23318	3,52E-54	5,35E+01	5,12E-55	0,0489	15,6224619	0,7640681	3042,23	TUT4	terminal uridylyl transferase 4
54762	5,15E-10	9,29E+00	2,38E-10	0,1206	6,3347174	0,76385479	242,91	GRAMD1C	GRAM domain containing 1C
3612	2,11E-35	3,47E+01	4,69E-36	0,0609	12,5369121	0,76358382	1345,16	IMPA1	inositol monophosphatase 1
728215	1,97E-13	1,27E+01	7,99E-14	0,1022	7,4704163	0,76353269	362,17	NALF1	NALCN channel auxiliary factor 1
5978	7,22E-45	4,41E+01	1,30E-45	0,0539	14,1755564	0,76344072	2042,7	REST	RE1 silencing transcription factor
65084	4,47E-23	2,23E+01	1,36E-23	0,0762	10,010969	0,7632714	764,59	TMEM135	transmembrane protein 135
163589	7,91E-02	1,10E+00	6,29E-02	0,4103	1,8599841	0,76322587	19,44	TDRD5	tudor domain containing 5
107985399	1,18E-01	9,28E-01	9,61E-02	0,4585	1,664236	0,76309818	16,29	LOC107985399	
54874	1,31E-48	4,79E+01	2,14E-49	0,0516	14,774337	0,76290136	2161,94	FNBP1L	formin binding protein 1 like
51710	2,02E-24	2,37E+01	5,96E-25	0,0739	10,3160253	0,76262508	810,81	ZNF44	zinc finger protein 44
23556	7,59E-21	2,01E+01	2,46E-21	0,0804	9,4832491	0,76198632	697,07	PIGN	phosphatidylinositol glycan anchor biosynthesis class N
4240	2,65E-40	3,96E+01	5,26E-41	0,0568	13,4103834	0,76174611	2879,08	MFGE8	milk fat globule EGF and factor V/VIII domain containing
112267985	1,79E-01	7,47E-01	1,50E-01	0,5283	1,4406335	0,76113234	11,07	LOC112267985	
115111	5,77E-03	2,24E+00	4,04E-03	0,2647	2,8749371	0,76109202	46,93	SLC26A7	solute carrier family 26 member 7
105374894	9,57E-02	1,02E+00	7,70E-02	0,4304	1,7684058	0,76109144	17,89	LOC105374	uncharacterized LOC105374894
27332	2,92E-60	5,95E+01	3,73E-61	0,0461	16,499068	0,76108974	4252,98	ZNF638	zinc finger protein 638
6645	5,01E-40	3,93E+01	1,00E-40	0,0569	13,3624609	0,76076071	1503,49	SNTB2	syntrophin beta 2
9749	7,10E-34	3,31E+01	1,64E-34	0,0621	12,2519343	0,76029397	2488,51	PHACTR2	phosphatase and actin regulator 2
10472	1,90E-38	3,77E+01	3,94E-39	0,0581	13,0862978	0,76003885	1639,06	ZBTB18	zinc finger and BTB domain containing 18
57695	9,35E-29	2,80E+01	2,45E-29	0,0675	11,2451907	0,75903408	1015,38	USP37	ubiquitin specific peptidase 37

734	6,05E-29	2,82E+01	1,57E-29	0,0673	11,2839848	0,7589493	1401,32	OSGIN2	oxidative stress induced growth inhibitor family member 2
105376333	2,82E-03	2,55E+00	1,92E-03	0,2446	3,1020236	0,75885219	53,24	LOC105376	uncharacterized LOC105376333
387882	1,09E-56	5,60E+01	1,50E-57	0,0475	15,9901846	0,75883024	4057,94	C12orf75	chromosome 12 open reading frame 75
55619	1,21E-19	1,89E+01	4,07E-20	0,0826	9,1861358	0,75868815	603,84	DOCK10	dedicator of cytokinesis 10
23272	3,62E-45	4,44E+01	6,44E-46	0,0533	14,2246718	0,75868547	3648,63	TASOR	transcription activation suppressor
101927730	2,18E-04	3,66E+00	1,36E-04	0,1988	3,8155591	0,75860134	83,57	SERPINB9-A	SERPINB9 antisense RNA 1
26022	5,31E-10	9,27E+00	2,45E-10	0,1198	6,3300955	0,75847214	235,88	TMEM98	transmembrane protein 98
5277	2,98E-24	2,35E+01	8,84E-25	0,0738	10,2782026	0,75840383	896,08	PIGA	phosphatidylinositol glycan anchor biosynthesis class A
105375304	4,02E-02	1,40E+00	3,07E-02	0,351	2,1604304	0,7582553	25,92	SNX10-AS1	SNX10 antisense RNA 1
107985567	4,11E-06	5,39E+00	2,29E-06	0,1604	4,7259674	0,75822318	149,84	LOC107985	protein LLP homolog
203414	6,81E-03	2,17E+00	4,81E-03	0,2687	2,8197713	0,7577412	44,18	LINC01560	long intergenic non-protein coding RNA 1560
57092	1,60E-58	5,78E+01	2,11E-59	0,0466	16,2536298	0,75769324	7276,9	PCNP	PEST proteolytic signal containing nuclear protein
27347	3,22E-37	3,65E+01	6,86E-38	0,0588	12,8675263	0,75673272	1997,66	STK39	serine/threonine kinase 39
23435	8,85E-72	7,11E+01	8,69E-73	0,0419	18,04469	0,7565231	9074,86	TARDBP	TAR DNA binding protein
100874203	2,32E-05	4,63E+00	1,35E-05	0,1738	4,3515386	0,75639792	108,06	COL4A2-AS	COL4A2 antisense RNA 1
107986281	2,53E-01	5,97E-01	2,17E-01	0,6125	1,2339196	0,75581701	8,37	LOC107986	uncharacterized LOC107986281
11127	4,49E-25	2,43E+01	1,30E-25	0,0722	10,46125	0,75579521	1305,27	KIF3A	kinesin family member 3A
494143	3,33E-17	1,65E+01	1,20E-17	0,0883	8,5524563	0,75554391	577,81	CHAC2	ChaC glutathione specific gamma-glutamylcyclotransferase 2
55435	7,74E-34	3,31E+01	1,79E-34	0,0617	12,2448966	0,75517268	1420,55	AP1AR	adaptor related protein complex 1 associated regulatory protein
9848	1,61E-15	1,48E+01	6,15E-16	0,0934	8,0863263	0,75495448	414,89	MFAP3L	microfibril associated protein 3 like
5592	8,45E-06	5,07E+00	4,80E-06	0,1651	4,573514	0,75492085	126,51	PRKG1	protein kinase cGMP-dependent 1
51028	5,56E-33	3,23E+01	1,31E-33	0,0625	12,0822044	0,75485827	1345,44	VPS36	vacuolar protein sorting 36 homolog
388536	4,07E-12	1,14E+01	1,74E-12	0,107	7,0542234	0,75462948	296,29	ZNF790	zinc finger protein 790
100533483	1,94E-38	3,77E+01	4,01E-39	0,0577	13,0849758	0,75460339	1447,99	DNAAF4-CC	DNAAF4-CCPG1 readthrough (NMD candidate)
730051	2,19E-08	7,66E+00	1,09E-08	0,132	5,7168681	0,75439619	201,48	ZNF814	zinc finger protein 814
55787	5,27E-48	4,73E+01	8,76E-49	0,0514	14,6791824	0,75434645	2066,93	TXLNG	taxilin gamma
54969	3,76E-23	2,24E+01	1,14E-23	0,0752	10,02831	0,7542708	874,73	HPF1	histone PARylation factor 1
101928450	1,33E-01	8,76E-01	1,09E-01	0,4707	1,6020455	0,75409737	16,78	LOC101928	uncharacterized LOC101928450
10728	8,63E-44	4,31E+01	1,59E-44	0,0539	13,998632	0,75404697	13725,37	PTGES3	prostaglandin E synthase 3
4931	1,66E-30	2,98E+01	4,18E-31	0,065	11,5988592	0,75373914	1884,71	NVL	nuclear VCP like
101059938	8,74E-08	7,06E+00	4,45E-08	0,1377	5,4718868	0,75370735	178,96	NPIPA7	nuclear pore complex interacting protein family member A7
22894	2,24E-46	4,56E+01	3,88E-47	0,0523	14,4199636	0,75367637	3895,8	DIS3	DIS3 homolog, exosome endoribonuclease and 3'-5' exoribonuclease
8395	6,30E-02	1,20E+00	4,95E-02	0,3836	1,9644052	0,75356603	21	PIP5K1B	phosphatidylinositol-4-phosphate 5-kinase type 1 beta
100506282	2,13E-06	5,67E+00	1,17E-06	0,155	4,8612636	0,75344221	150,07	ANKRD42-D	ANKRD42 divergent transcript
23527	1,17E-40	3,99E+01	2,31E-41	0,0559	13,4712994	0,75344089	2259,06	ACAP2	ArfGAP with coiled-coil, ankyrin repeat and PH domains 2
283922	1,30E-06	5,89E+00	7,07E-07	0,1519	4,9593076	0,75341615	146,42	PDPR2P	pyruvate dehydrogenase phosphatase regulatory subunit 2, pseudogene
79728	1,41E-31	3,09E+01	3,44E-32	0,0638	11,810722	0,75334038	1269,25	PALB2	partner and localizer of BRCA2
51397	5,03E-25	2,43E+01	1,46E-25	0,0721	10,4504627	0,75330367	786,73	COMMD10	COMM domain containing 10
54845	2,00E-01	6,99E-01	1,69E-01	0,5478	1,3746326	0,75296675	10,54	ESRP1	epithelial splicing regulatory protein 1
22981	1,76E-12	1,18E+01	7,40E-13	0,105	7,1718935	0,75287395	333,04	NINL	ninein like
283431	1,47E-37	3,68E+01	3,10E-38	0,0582	12,9287252	0,75277754	1645,37	GAS2L3	growth arrest specific 2 like 3
114294	3,42E-39	3,85E+01	6,98E-40	0,0569	13,2172405	0,75270767	1808,29	LACTB	lactamase beta
64710	2,10E-81	8,07E+01	1,69E-82	0,0391	19,2405535	0,75265353	29013,81	NUCKS1	nuclear casein kinase and cyclin dependent kinase substrate 1
9493	1,30E-62	6,19E+01	1,56E-63	0,0447	16,8264617	0,75253661	8950,74	KIF23	kinesin family member 23
91057	1,09E-39	3,90E+01	2,21E-40	0,0565	13,3035169	0,75227126	1543,06	CCDC34	coiled-coil domain containing 34
79003	8,79E-39	3,81E+01	1,81E-39	0,0572	13,1454486	0,75225302	2125,09	MIS12	MIS12 kinetochore complex component
4193	1,80E-53	5,27E+01	2,65E-54	0,0485	15,5171859	0,75204596	2851,4	MDM2	MDM2 proto-oncogene
6885	1,14E-41	4,09E+01	2,20E-42	0,0551	13,6438816	0,75202811	2023,21	MAP3K7	mitogen-activated protein kinase kinase kinase 7
102723753	1,51E-02	1,82E+00	1,10E-02	0,2958	2,5418801	0,75194499	35,79	LOC102723	HECT and RLD domain containing E3 ubiquitin protein ligase 2 pseudogene
728340	5,65E-27	2,62E+01	1,55E-27	0,0692	10,8727645	0,75186731	937,53	GTF2H2C	GTF2H2 family member C
9014	1,15E-45	4,49E+01	2,03E-46	0,0525	14,3053029	0,75171404	2355,61	TAF1B	TATA-box binding protein associated factor, RNA polymerase I subunit B
7078	7,84E-84	8,31E+01	6,03E-85	0,0385	19,530645	0,7516825	28755,61	TIMP3	TIMP metallopeptidase inhibitor 3
338739	3,51E-03	2,45E+00	2,41E-03	0,2477	3,0339571	0,75166283	52,97	CSTF3-DT	CSTF3 divergent transcript
1147	2,09E-45	4,47E+01	3,70E-46	0,0527	14,2633654	0,75162191	1861,03	CHUK	component of inhibitor of nuclear factor kappa B kinase complex
253832	3,57E-51	5,04E+01	5,50E-52	0,0495	15,1710721	0,75152504	3778,95	ZDHHC20	zinc finger DHHC-type palmitoyltransferase 20
92591	2,80E-04	3,55E+00	1,76E-04	0,2003	3,7509929	0,75123186	85,18	ASB16	ankyrin repeat and SOCS box containing 16
137872	2,27E-02	1,64E+00	1,69E-02	0,3144	2,3895823	0,7512219	32,61	ADHFE1	alcohol dehydrogenase iron containing 1
51130	1,58E-12	1,18E+01	6,65E-13	0,1045	7,1863751	0,75105476	324,81	ASB3	ankyrin repeat and SOCS box containing 3
51562	8,12E-31	3,01E+01	2,02E-31	0,0644	11,6607713	0,75095941	1205,14	MBIP	MAP3K12 binding inhibitory protein 1
283629	1,61E-03	2,79E+00	1,07E-03	0,2295	3,2710951	0,75061615	60,77	TSSK4	testis specific serine kinase 4
10199	8,20E-54	5,31E+01	1,20E-54	0,0482	15,5679286	0,75052845	2676,62	MPHOSPH1	M-phase phosphoprotein 10
1486	2,38E-25	2,46E+01	6,85E-26	0,0713	10,5219244	0,75028518	998,9	CTBS	chitobiase
23270	1,59E-20	1,98E+01	5,21E-21	0,0798	9,4048856	0,75023744	773,43	TSPYL4	TSPY like 4
85349	6,81E-10	9,17E+00	3,16E-10	0,1192	6,2906727	0,75015804	247,3	KRT87P	keratin 87, pseudogene
100527978	9,39E-08	7,03E+00	4,80E-08	0,1373	5,458719	0,74943604	177,76	TLCD4-RWD	TLCD4-RWDD3 readthrough
11335	4,58E-53	5,23E+01	6,81E-54	0,0485	15,4566111	0,74934867	9488,85	CBX3	chromobox 3
643783	2,89E-03	2,54E+00	1,97E-03	0,242	3,0950274	0,74908173	61,8	USP46-DT	USP46 divergent transcript
25932	2,63E-64	6,36E+01	3,04E-65	0,0439	17,0581241	0,74901472	16733,24	CLIC4	chloride intracellular channel 4
100505912	2,50E-01	6,02E-01	2,15E-01	0,604	1,2400172	0,74900849	8,73	LOC100505	uncharacterized LOC100505912
643382	3,21E-02	1,49E+00	2,43E-02	0,3325	2,2526525	0,74896063	28,1	TMEM253	transmembrane protein 253
26212	9,75E-02	1,01E+00	7,86E-02	0,4257	1,7589383	0,74880198	17,14	OR2B6	olfactory receptor family 2 subfamily B member 6
55681	7,06E-38	3,72E+01	1,48E-38	0,0577	12,9854478	0,74874646	2328,15	SCYL2	SCY1 like pseudokinase 2
9205	2,61E-17	1,66E+01	9,41E-18	0,0872	8,5809908	0,74854474	496,1	ZMYM5	zinc finger MYM-type containing 5
7342	1,35E-63	6,29E+01	1,58E-64	0,0441	16,9615557	0,74844525	5517,2	UBP1	upstream binding protein 1
200728	8,55E-05	4,07E+00	5,16E-05	0,1849	4,0480995	0,74830988	101,58	TMEM17	transmembrane protein 17
255967	6,31E-36	3,52E+01	1,38E-36	0,0592	12,6332228	0,74789396	1608,42	PAN3	poly(A) specific ribonuclease subunit PAN3
100302652	3,95E-12	1,14E+01	1,68E-12	0,1059	7,0584695	0,74740284	317,14	GPR75-ASB	GPR75-ASB3 readthrough
26092	7,98E-67	6,61E+01	8,75E-68	0,043	17,3966624	0,74737945	4447,19	TOR1AIP1	torsin 1A interacting protein 1
157753	1,57E-07	6,80E+00	8,13E-08	0,1393	5,3642777	0,74720411	192,55	TMEM74	transmembrane protein 74
51388	1,33E-48	4,79E+01	2,18E-49	0,0506	14,7731352	0,7471957	3538,48	NIP7	nucleolar pre-rRNA processing protein NIP7
100507599	3,88E-05	4,41E+00	2,29E-05	0,1764	4,2347898	0,74709793	106,57	TFIP11-DT	TFIP11 divergent transcript
6584	9,81E-20	1,90E+01	3,28E-20	0,0811	9,2092939	0,74683862	571,12	SLC22A5	solute carrier family 22 member 5
6732	6,42E-96	9,52E+01	3,92E-97	0,0357	20,9148311	0,74659069	20190,17	SRPK1	SRSF protein kinase 1
51696	1,28E-18	1,79E+01	4,41E-19	0,0836	8,9260792	0,74638501	669,84	HECA	hdc homolog, cell cycle regulator
153830	4,20E-69	6,84E+01	4,39E-70	0,0422	17,6974588	0,74623228	5166,26	RNF145	ring finger protein 145
57696	3,24E-49	4,85E+01	5,21E-50	0,0502	14,869323	0,74618395	2876,53	DDX55	DEAD-box helicase 55
145694	4,71E-19	1,83E+01	1,61E-19	0,0825	9,0371694	0,74579504	552,11	KIF23-AS1	KIF23 and PAQR5 antisense RNA 1
9439	1,41E-34	3,39E+01	3,19E-35	0,0602	12,3839593	0,74535006	1341,11	MED23	mediator complex subunit 23
85378	2,19E-20	1,97E+01	7,18E-21	0,0795	9,3710388	0,74522312	731,73	TUBGCP6	tubulin gamma complex associated protein 6
123283	7,49E-11	1,01E+01	3,34E-11	0,1124	6,6306898	0,74496286	271,42	TARS3	threonyl-tRNA synthetase 3
92283	1,66E-04	3,78E+00	1,02E-04	0,1918	3,8849941	0,74495091	108,66	ZNF461	zinc finger protein 461
10221	1,26E-24	2,39E+01	3,70E-25	0,0719	10,361881	0,74489997	822,39	TRIB1	tribbles pseudokinase 1
100130855	5,20E-07	6,28E+00	2,76E-07	0,1448	5,1394321	0,74444476	158,57	USP3-AS1	USP3 antisense RNA 1
63939	8,50E-31	3,01E+01	2,12E-31	0,0638	11,6568479	0,7442477	1410,66	FAM217B	family with sequence similarity 217 member B
138639	1,08E-29	2,90E+01	2,77E-30	0,065	11,4359355	0,74390201	1018,49	PTPDC1	protein tyrosine phosphatase domain containing 1
282809	1,17E-39	3,89E+01	2,38E-40	0,0559	13,298076	0,7438867	1695,7	POC1B	POC1 centriolar protein B
10762	1,25E-54	5,39E+01	1,80E-55	0,0474	15,6888191	0,74378667	4459,98	NUP50	nucleoporin 50
286190	4,45E-12	1,14E+01	1,90E-12	0,1056	7,0415671	0,74378155	307,55	LACTB2-AS	LACTB2 antisense RNA 1
10009	5,69E-36	3,52E+01	1,25E-36	0,0588	12,641564	0,74374477	1550,83	ZBTB33	zinc finger and BTB domain containing 33
123228	1,54E-09	8,81E+00	7,28E-10	0,1207	6,1598617	0,74372599	245,37	SENP8	SUMO peptidase family member, NEDD8 specific
3998	2,97E-54	5,35E+01	4,31E-55	0,0476	15,6334174	0,74372209	9967,83	LMAN1	lectin, mannose binding 1
5167	1,68E-48	4,78E+01	2,76E-49	0,0504	14,7573383	0,74371548	2871,47	ENPP1	ectonucleotide pyrophosphatase/phosphodiesterase 1
55161	3,41E-49	4,85E+01	5,49E-50	0,05	14,8658279	0,7434027	3544	TMEM33	transmembrane protein 33
374986	2,13E-30	2,97E+01	5,35E-31	0,0642	11,5775854	0,7432816	1199,54	MIGA1	mitoguardin 1
80342	4,13E-02	1,38E+00	3,17E-02	0,3458	2,1487436	0,74309131	27,74	TRAF3IP3	TRAF3 interacting protein 3
103352539	2,48E-04	3,61E+00	1,55E-04	0,1964	3,7821963	0,7429842	88,27	LINC01410	long intergenic non-protein coding RNA 1410
11010	1,71E-66	6,58E+01	1,89E-67	0,0428	17,3526011	0,74297629	4517,72	GLIPR1	GLI pathogenesis related 1
100310846	8,57E-02	1,07E+00	6,85E-02	0,4076	1,821924	0,74253694	21,8	ANKRD61	ankyrin repeat domain 61
127255	7,06E-03	2,15E+00	4,99E-03	0,2644	2,8074436	0,74228817	45,59	LRRIQ3	leucine rich repeats and IQ motif containing 3
221756	1,82E-01	7,40E-01	1,53E-01	0,5188	1,4303362	0,74211379	11,63	SERPINB9P	serpin family B member 9 pseudogene 1
154807	1,99E-45	4,47E+01	3,53E-46	0,052	14,2667001	0,74189879	2380,38	VKORC1L1	vitamin K epoxide reductase complex subunit 1 like 1
90799	1,21E-36	3,59E+01	2,61E-37	0,0581	12,7639698	0,74174072	1501,9	CEP95	centrosomal protein 95
221037	2,83E-63	6,25E+01	3,34E-64	0,0438	16,9174887	0,74165179	3939,76	JMJD1C	jumonji domain containing 1C
149371	1,65E-24	2,38E+01	4,86E-25	0,0717	10,3357061	0,7414692	865,05	EXOC8	exocyst complex component 8
10079	1,06E-07	6,97E+00	5,41E-08	0,1363	5,4373708	0,74125157	184	ATP9A	ATPase phospholipid transporting 9A (putative)
112267872	1,14E-02	1,94E+00	8,18E-03	0,2802	2,6445744	0,74108812	42,01	LOC112267872	
26808	2,87E-01	5,42E-01	2,49E-01	0,6435	1,1516769	0,74107811	7,8	SNORD42B	small nucleolar RNA, C/D box 42B
94101	7,45E-42	4,11E+01	1,43E-42	0,0542	13,6749631	0,74057493	1835,32	ORMDL1	ORMDL sphingolipid biosynthesis regulator 1
4621	2,33E-10	9,63E+00	1,06E-10	0,1146	6,4581832	0,74042808	259,74	MYH3	myosin heavy chain 3
22869	1,31E-28	2,79E+01	3,45E-29	0,066	11,2146872	0,74028285	1170,73	ZNF510	zinc finger protein 510

129401	9,13E-30	2,90E+01	2,33E-30	0,0646	11,4507231	0,74014437	1057,02	NUP35	nucleoporin 35
1161	4,39E-23	2,24E+01	1,34E-23	0,0739	10,012744	0,74011646	808,06	ERCC8	ERCC excision repair 8, CSA ubiquitin ligase complex subunit
170506	3,95E-50	4,94E+01	6,25E-51	0,0493	15,0107284	0,73999051	2715,67	DHX36	DEAH-box helicase 36
84815	7,18E-14	1,31E+01	2,89E-14	0,0973	7,6033776	0,73962978	371,99	MGC12916	uncharacterized protein MGC12916
7444	2,35E-42	4,16E+01	4,46E-43	0,0537	13,7596111	0,73929878	1933,79	VRK2	VRK serine/threonine kinase 2
7347	5,10E-29	2,83E+01	1,33E-29	0,0654	11,2990853	0,73865502	2724,9	UCHL3	ubiquitin C-terminal hydrolase L3
79101	1,36E-52	5,19E+01	2,03E-53	0,048	15,3859414	0,73795535	3974,28	TAF1D	TATA-box binding protein associated factor, RNA polymerase I subunit D
85457	3,40E-27	2,65E+01	9,29E-28	0,0676	10,9196087	0,73766412	947,21	CIPC	CLOCK interacting pacemaker
10114	2,01E-40	3,97E+01	3,98E-41	0,0549	13,4310745	0,73763272	1871,56	HIPK3	homeodomain interacting protein kinase 3
63977	5,10E-18	1,73E+01	1,80E-18	0,0841	8,7693832	0,73754987	546,71	PRDM15	PR/SET domain 15
11064	1,85E-31	3,07E+01	4,53E-32	0,0626	11,7875028	0,73743247	2054,49	CNTRL	centriolin
54680	6,92E-46	4,52E+01	1,21E-46	0,0514	14,3410625	0,73703196	3110,66	ZNHIT6	zinc finger HIT-type containing 6
5150	2,83E-16	1,55E+01	1,05E-16	0,0888	8,2986171	0,73691753	475,99	PDE7A	phosphodiesterase 7A
107984328	2,21E-12	1,17E+01	9,35E-13	0,1032	7,1397286	0,73674684	345,31	LOC107984	uncharacterized LOC107984328
10116	3,43E-36	3,55E+01	7,46E-37	0,0581	12,6817702	0,73625972	2075,55	FEM1B	fem-1 homolog B
102465669	1,55E-01	8,10E-01	1,28E-01	0,4843	1,5201949	0,73624778	13,12	MIR7113	microRNA 7113
102724749	2,45E-01	6,11E-01	2,10E-01	0,587	1,2540577	0,73614086	9,34	LOC102724	uncharacterized LOC102724749
101928373	1,81E-01	7,42E-01	1,51E-01	0,5131	1,4345216	0,73611754	12,12	LOC101928	uncharacterized LOC101928373
100505746	2,96E-09	8,53E+00	1,41E-09	0,1216	6,0540772	0,73608916	230,56	ITGB2-AS1	ITGB2 antisense RNA 1
139231	9,75E-29	2,80E+01	2,55E-29	0,0655	11,2413483	0,73579172	1522,15	FAM199X	family with sequence similarity 199, X-linked
284161	9,18E-05	4,04E+00	5,56E-05	0,1824	4,0306666	0,73537872	110,87	GDPD1	glycerophosphodiester phosphodiesterase domain containing 1
440345	9,35E-15	1,40E+01	3,66E-15	0,0935	7,8661265	0,73523256	429,23	NPIPB4	nuclear pore complex interacting protein family member B4
107986303	5,33E-09	8,27E+00	2,57E-09	0,1234	5,9571743	0,73489689	229,36	LOC107986	303
23041	1,17E-29	2,89E+01	3,01E-30	0,0643	11,4286144	0,73485896	1349,22	MON2	MON2 homolog, regulator of endosome-to-Golgi trafficking
107985259	2,76E-04	3,56E+00	1,73E-04	0,1957	3,7549332	0,73485334	84,89	LOC107985	uncharacterized LOC107985259
54557	3,76E-19	1,84E+01	1,28E-19	0,0811	9,0621253	0,73471769	741,82	SGTB	small glutamine rich tetratricopeptide repeat co-chaperone beta
26827	2,13E-04	3,67E+00	1,32E-04	0,1922	3,8219812	0,73449415	98,71	RNU6-1	RNA, U6 small nuclear 1
253558	3,68E-34	3,34E+01	8,42E-35	0,0597	12,3058452	0,73411849	1456,46	LCLAT1	lysocardiolipin acyltransferase 1
106635540	1,65E-13	1,28E+01	6,69E-14	0,098	7,4937553	0,73401396	487,37	SNORA105E	small nucleolar RNA, H/ACA box 105B
347736	9,28E-05	4,03E+00	5,62E-05	0,1822	4,0280654	0,73388077	97,67	NME9	NME/NM23 family member 9
79854	5,41E-03	2,27E+00	3,78E-03	0,2534	2,8961812	0,73386069	51,17	LINC00115	long intergenic non-protein coding RNA 115
112268143	9,85E-03	2,01E+00	7,07E-03	0,2724	2,6937498	0,73385239	44,93	LOC112268	uncharacterized LOC112268143
107984836	1,43E-02	1,84E+00	1,04E-02	0,2863	2,5632215	0,73378407	39,03	KCTD13-DT	KCTD13 divergent transcript
57150	7,04E-06	5,15E+00	3,97E-06	0,1591	4,6127343	0,73377468	133,7	SMIM8	small integral membrane protein 8
8556	3,94E-15	1,44E+01	1,52E-15	0,092	7,9752631	0,73368045	433,29	CDC14A	cell division cycle 14A
7567	9,54E-05	4,02E+00	5,78E-05	0,1824	4,0215889	0,73353864	105,89	ZNF19	zinc finger protein 19
7741	1,62E-31	3,08E+01	3,95E-32	0,0622	11,799083	0,73337714	1152,41	ZSCAN26	zinc finger and SCAN domain containing 26
10746	1,08E-43	4,30E+01	2,00E-44	0,0524	13,9822638	0,73325615	2368,92	MAP3K2	mitogen-activated protein kinase kinase kinase 2
100996724	5,14E-26	2,53E+01	1,45E-26	0,0687	10,6671442	0,73307093	896,13	PDE4DIPP2	PDE4DIP pseudogene 2
91147	4,48E-07	6,35E+00	2,37E-07	0,1418	5,1675585	0,73298643	191,56	TMEM67	transmembrane protein 67
79973	1,80E-05	4,74E+00	1,04E-05	0,1663	4,4081873	0,73295222	117,51	ZNF442	zinc finger protein 442
25896	2,88E-54	5,35E+01	4,18E-55	0,0469	15,6353881	0,73266311	3716,27	INTS7	integrator complex subunit 7
9227	1,58E-02	1,80E+00	1,15E-02	0,29	2,526738	0,73264164	37,91	LRAT	lecithin retinol acyltransferase
124411	3,42E-09	8,47E+00	1,63E-09	0,1215	6,0305352	0,73258533	247,51	KRBOX5	KRAB box domain containing 5
8732	2,57E-36	3,56E+01	5,57E-37	0,0577	12,7046984	0,73256182	1524,21	RNGTT	RNA guanylyltransferase and 5'-phosphatase
57678	1,32E-26	2,59E+01	3,66E-27	0,0678	10,7943808	0,73233196	990,05	GPAM	glycerol-3-phosphate acyltransferase, mitochondrial
23333	2,83E-37	3,65E+01	6,01E-38	0,0569	12,877745	0,73230774	2139,96	DPY19L1	dpy-19 like C-mannosyltransferase 1
107985410	2,66E-01	5,75E-01	2,29E-01	0,6088	1,2022927	0,73200652	8,87	LOC107985	uncharacterized LOC107985410
6018	2,22E-31	3,07E+01	5,46E-32	0,0622	11,7717686	0,73176093	1867,34	RLF	RLF zinc finger
23252	1,05E-23	2,30E+01	3,14E-24	0,0721	10,1552872	0,73174842	781,56	OTUD3	OTU deubiquitinase 3
5523	5,46E-44	4,33E+01	1,00E-44	0,0521	14,0313029	0,73135673	2021,04	PPP2R3A	protein phosphatase 2 regulatory subunit B"alpha
79663	1,26E-13	1,29E+01	5,10E-14	0,0971	7,529219	0,73129786	401,89	HSPBAP1	HSPB1 associated protein 1
64599	6,67E-35	3,42E+01	1,50E-35	0,0587	12,44438	0,73097962	1359,55	GIGYF1	GRB10 interacting GYF protein 1
996	6,77E-70	6,92E+01	6,96E-71	0,0411	17,8008694	0,73087646	10860,7	CDC27	cell division cycle 27
23366	5,36E-32	3,13E+01	1,29E-32	0,0615	11,8925578	0,73080566	1421,88	MATCAP2	microtubule associated tyrosine carboxypeptidase 2
57511	1,65E-26	2,58E+01	4,59E-27	0,0678	10,7735898	0,73053938	982,43	COG6	component of oligomeric golgi complex 6
56603	2,92E-21	2,05E+01	9,36E-22	0,0762	9,5836876	0,73038903	742,3	CYP26B1	cytochrome P450 family 26 subfamily B member 1
28962	3,21E-25	2,45E+01	9,25E-26	0,0696	10,4934992	0,7303458	1096,8	OSTM1	osteoclastogenesis associated transmembrane protein 1
55623	5,38E-44	4,33E+01	9,88E-45	0,052	14,0323897	0,73033316	2163,87	THUMPD1	THUMP domain containing 1
80821	3,72E-35	3,44E+01	8,31E-36	0,0585	12,4914261	0,73029674	1419,03	DDHD1	DDHD domain containing 1
1871	1,12E-45	4,50E+01	1,97E-46	0,051	14,3071553	0,73014971	3651,58	E2F3	E2F transcription factor 3
107984347	1,18E-13	1,29E+01	4,78E-14	0,0968	7,5378794	0,72985169	381,51	LOC107984	replaced by ID 121233926
51527	6,61E-19	1,82E+01	2,27E-19	0,0811	8,9994962	0,72948163	628,82	GSKIP	GSK3B interacting protein
253635	9,84E-37	3,60E+01	2,11E-37	0,0571	12,7802598	0,72940724	2321,43	GPATCH11	G-patch domain containing 11
8803	1,09E-31	3,10E+01	2,66E-32	0,0616	11,8321877	0,72933462	1475,97	SUCLA2	succinate-CoA ligase ADP-forming subunit beta
1073	8,09E-36	3,51E+01	1,78E-36	0,0578	12,6132638	0,72932139	4816,48	CFL2	cofilin 2
7584	2,35E-18	1,76E+01	8,22E-19	0,0823	8,8570536	0,72922445	623,8	ZNF35	zinc finger protein 35
55671	7,99E-54	5,31E+01	1,17E-54	0,0468	15,5696081	0,72908693	5463,77	PPP4R3A	protein phosphatase 4 regulatory subunit 3A
9562	1,32E-16	1,59E+01	4,87E-17	0,0868	8,3898254	0,72845273	1090,99	MINPP1	multiple inositol-polyphosphate phosphatase 1
25950	5,08E-09	8,29E+00	2,45E-09	0,1221	5,9650274	0,72842809	254,8	RWDD3	RWD domain containing 3
100130476	1,98E-01	7,03E-01	1,67E-01	0,5263	1,3825909	0,72772485	11,98	WAKMAR2	wound and keratinocyte migration associated lncRNA 2
653121	9,28E-16	1,50E+01	3,51E-16	0,0892	8,1543749	0,72767041	538,67	ZBTB8A	zinc finger and BTB domain containing 8A
647979	7,01E-46	4,52E+01	1,23E-46	0,0507	14,340114	0,72765345	17280,13	NORAD	non-coding RNA activated by DNA damage
153129	1,22E-23	2,29E+01	3,68E-24	0,0718	10,1398697	0,72761435	935,72	SLC38A9	solute carrier family 38 member 9
9833	1,56E-74	7,38E+01	1,45E-75	0,0395	18,394816	0,72725414	8223,35	MELK	maternal embryonic leucine zipper kinase
84527	4,31E-20	1,94E+01	1,43E-20	0,0782	9,2982756	0,72717641	811,91	ZNF559	zinc finger protein 559
80856	1,89E-30	2,97E+01	4,74E-31	0,0627	11,5880738	0,72697324	1558,4	LNPK	lunapark, ER junction formation factor
54968	1,98E-15	1,47E+01	7,57E-16	0,0901	8,0608988	0,72621074	640,13	TMEM70	transmembrane protein 70
54438	3,12E-19	1,85E+01	1,06E-19	0,0799	9,082451	0,72563966	584,55	GFOD1	glucose-fructose oxidoreductase domain containing 1
91947	1,46E-09	8,84E+00	6,89E-10	0,1176	6,1685215	0,72563743	268,81	ARRDC4	arrestin domain containing 4
57475	4,11E-11	1,04E+01	1,82E-11	0,108	6,7201494	0,72558127	308,83	PLEKHH1	pleckstrin homology, MyTH4 and FERM domain containing H1
219285	1,76E-24	2,38E+01	5,18E-25	0,0702	10,3294676	0,72532398	979,88	SAMD9L	sterile alpha motif domain containing 9 like
9937	4,25E-33	3,24E+01	1,00E-33	0,0599	12,1044184	0,72486602	1395,94	DCLRE1A	DNA cross-link repair 1A
100128288	8,67E-02	1,06E+00	6,93E-02	0,399	1,8165678	0,72482333	20,15	LOC100128	uncharacterized LOC100128288
389834	9,01E-06	5,05E+00	5,12E-06	0,1589	4,5596641	0,72474266	130,25	LOC389834	ankyrin repeat domain 57 pseudogene
727	9,52E-06	5,02E+00	5,42E-06	0,1593	4,5477487	0,7245013	126,62	C5	complement C5
10806	3,16E-34	3,35E+01	7,22E-35	0,0588	12,3183159	0,7243631	1453,79	SDCCAG8	SHH signaling and ciliogenesis regulator SDCCAG8
401233	1,31E-37	3,69E+01	2,77E-38	0,056	12,9374046	0,72424587	1640,18	HTATSF1P2	HIV-1 Tat specific factor 1 pseudogene 2
285847	2,34E-01	6,31E-01	2,00E-01	0,5651	1,281493	0,72419672	9,79	LOC285847	uncharacterized LOC285847
134430	1,05E-40	4,00E+01	2,07E-41	0,0537	13,4792459	0,72411026	3071,72	WDR36	WD repeat domain 36
10644	1,03E-56	5,60E+01	1,41E-57	0,0453	15,9938505	0,72381951	5049,84	IGF2BP2	insulin like growth factor 2 mRNA binding protein 2
55347	4,22E-37	3,64E+01	9,01E-38	0,0563	12,8464066	0,7236978	1822,1	ABHD10	abhydrolase domain containing 10, depalmitoylase
7766	2,63E-09	8,58E+00	1,25E-09	0,1191	6,0731603	0,72358516	257,56	ZNF223	zinc finger protein 223
146050	1,62E-25	2,48E+01	4,65E-26	0,0685	10,558328	0,72318145	976,64	ZSCAN29	zinc finger and SCAN domain containing 29
79957	6,39E-03	2,19E+00	4,50E-03	0,2545	2,8410322	0,72315291	51,03	PAQR6	progestin and adipoQ receptor family member 6
442578	2,73E-06	5,56E+00	1,51E-06	0,1503	4,8104107	0,72304708	144,75	STAG3L3	stromal antigen 3-like 3 (pseudogene)
107986642	4,58E-02	1,34E+00	3,53E-02	0,3433	2,104934	0,72259213	26,25	LOC107986	uncharacterized LOC107986642
8347	3,65E-05	4,44E+00	2,15E-05	0,17	4,248438	0,72212826	111,83	H2BC4	H2B clustered histone 4
255520	6,60E-29	2,82E+01	1,72E-29	0,064	11,2762475	0,72206755	1118,61	ELMOD2	ELMO domain containing 2
7779	2,84E-19	1,85E+01	9,66E-20	0,0794	9,0927138	0,72188284	1253,3	SLC30A1	solute carrier family 30 member 1
105378678	4,52E-02	1,34E+00	3,48E-02	0,342	2,1105633	0,72179024	27,13	LOC105378	uncharacterized LOC105378678
105372457	4,70E-02	1,33E+00	3,63E-02	0,3447	2,0937174	0,72178534	26,29	MYADM-AS1	MYADM antisense RNA 1
5313	1,58E-01	8,01E-01	1,31E-01	0,4781	1,5094119	0,72162408	13,71	PKLR	pyruvate kinase L/R
254042	1,53E-13	1,28E+01	6,22E-14	0,0961	7,5032739	0,7212092	399,38	METAP1D	methionyl aminopeptidase type 1D, mitochondrial
4123	3,96E-22	2,14E+01	1,24E-22	0,0737	9,7903849	0,72120837	808,6	MAN2C1	mannosidase alpha class 2C member 1
4058	1,64E-03	2,79E+00	1,10E-03	0,2207	3,2647759	0,72046556	76,78	LTK	leukocyte receptor tyrosine kinase
221656	6,49E-36	3,52E+01	1,42E-36	0,057	12,6310499	0,72045423	1661,11	KDM1B	lysine demethylase 1B
163882	1,34E-30	2,99E+01	3,35E-31	0,062	11,6177371	0,72043332	1245,29	CNST	consortin, connexin sorting protein
23032	4,88E-45	4,43E+01	8,72E-46	0,0507	14,2034421	0,72012144	3167,23	USP33	ubiquitin specific peptidase 33
64924	1,41E-37	3,69E+01	2,97E-38	0,0557	12,9318886	0,72011942	2257,83	SLC30A5	solute carrier family 30 member 5
137492	5,87E-31	3,02E+01	1,46E-31	0,0616	11,6886878	0,71992673	1444,24	VPS37A	VPS37A subunit of ESCRT-I
7320	3,52E-36	3,55E+01	7,67E-37	0,0568	12,679652	0,71970477	1735,75	UBE2B	ubiquitin conjugating enzyme E2 B
203274	2,41E-05	4,62E+00	1,41E-05	0,1657	4,3429286	0,71969513	116,44	LINC00537	long intergenic non-protein coding RNA 537
8654	3,98E-05	4,40E+00	2,35E-05	0,1701	4,2287909	0,7195049	113,72	PDE5A	phosphodiesterase 5A
56983	7,32E-28	2,71E+01	1,96E-28	0,0651	11,0599035	0,71948679	1046,22	POGLUT1	protein O-glucosyltransferase 1
10389	5,53E-18	1,73E+01	1,95E-18	0,0821	8,7601452	0,71937695	613,84	SCML2	Scm polycomb group protein like 2
10678	1,42E-25	2,48E+01	4,06E-26	0,068	10,5709927	0,71934273	1089,31	B3GNT2	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 2
54876	1,45E-52	5,18E+01	2,17E-53	0,0468	15,3817007	0,7193011	3401,12	DCAF16	DDB1 and CUL4 associated factor 16
80705	2,31E-08	7,64E+00	1,15E-08	0,126	5,7076257	0,71922578	207,82	TSGA10	testis specific 10
541473	9,61E-02	1,02E+00	7,73E-02	0,4071	1,7664038	0,71916188	18,97	LOC541473	FKBP prolyl isomerase 6 pseudogene

84456	6,40E-12	1,12E+01	2,74E-12	0,1028	6,9903496	0,71891164	367,67	L3MBTL3	L3MBTL histone methyl-lysine binding protein 3
3908	3,74E-03	2,43E+00	2,57E-03	0,2384	3,0148119	0,71879194	55,5	LAMA2	laminin subunit alpha 2
2175	8,30E-38	3,71E+01	1,75E-38	0,0554	12,9727449	0,71877296	2222,41	FANCA	FA complementation group A
80152	7,42E-34	3,31E+01	1,71E-34	0,0587	12,2483804	0,71852579	1562,65	CENPT	centromere protein T
55601	5,70E-18	1,72E+01	2,01E-18	0,082	8,7566536	0,7182001	815,68	DDX60	DExD/H-box helicase 60
255812	4,78E-13	1,23E+01	1,97E-13	0,0977	7,3506799	0,71809825	385,37	SDHAP1	SDHA pseudogene 1
23301	2,44E-56	5,56E+01	3,38E-57	0,045	15,9393352	0,71800691	3761,18	EHBP1	EH domain binding protein 1
100528032	2,34E-01	6,31E-01	2,00E-01	0,5602	1,2813216	0,71785934	9,75	KLRC4-KLRI	KLRC4-KLRK1 readthrough
9306	2,80E-23	2,26E+01	8,50E-24	0,0713	10,0576474	0,71749908	865,39	SOCS6	suppressor of cytokine signaling 6
120	1,58E-43	4,28E+01	2,93E-44	0,0514	13,9550577	0,71741861	2446,95	ADD3	adducin 3
11342	4,62E-28	2,73E+01	1,23E-28	0,0646	11,1015007	0,71721014	1245,41	RNF13	ring finger protein 13
64434	6,66E-45	4,42E+01	1,20E-45	0,0506	14,1812874	0,71716807	2731,81	NOM1	nucleolar protein with MIF4G domain 1
400027	7,97E-08	7,10E+00	4,06E-08	0,1307	5,488383	0,71712706	202,79	LINC00938	long intergenic non-protein coding RNA 938
100506939	3,22E-03	2,49E+00	2,20E-03	0,2342	3,0617326	0,71696078	57,06	PRKG1-AS1	PRKG1 antisense RNA 1
10799	3,18E-22	2,15E+01	9,91E-23	0,073	9,8128557	0,71682868	845,01	RPP40	ribonuclease P/MRP subunit p40
51371	6,84E-34	3,32E+01	1,58E-34	0,0585	12,2549998	0,71668261	5066,45	POMP	proteasome maturation protein
636	4,85E-20	1,93E+01	1,61E-20	0,0772	9,2853951	0,71652115	696,44	BICD1	BICD cargo adaptor 1
93183	1,17E-15	1,49E+01	4,43E-16	0,0882	8,1262331	0,7164612	480,42	PIGM	phosphatidylinositol glycan anchor biosynthesis class M
5577	1,78E-09	8,75E+00	8,41E-10	0,1167	6,1370323	0,71642775	259,74	PRKAR2B	protein kinase cAMP-dependent type II regulatory subunit beta
10513	4,98E-29	2,83E+01	1,29E-29	0,0634	11,3012074	0,7160833	2036,84	APPBP2	amyloid beta precursor protein binding protein 2
9419	8,19E-16	1,51E+01	3,09E-16	0,0876	8,1696535	0,71598456	583,84	CRIPT	CXXC repeat containing interactor of PDZ3 domain
54700	1,36E-29	2,89E+01	3,49E-30	0,0627	11,4156727	0,71570977	1839,49	RRN3	RRN3 homolog, RNA polymerase I transcription factor
102723385	7,70E-03	2,11E+00	5,46E-03	0,2575	2,7784414	0,71552646	47,87	COQ7-DT	COQ7 divergent transcript
25994	5,23E-64	6,33E+01	6,09E-65	0,042	17,0175426	0,71545894	7181,03	HIGD1A	HIG1 hypoxia inducible domain family member 1A
472	8,76E-49	4,81E+01	1,43E-49	0,0483	14,8016078	0,71476991	3350,1	ATM	ATM serine/threonine kinase
55180	1,38E-10	9,86E+00	6,24E-11	0,1093	6,5378557	0,71472068	295,48	LINS1	lines homolog 1
8690	1,76E-28	2,78E+01	4,66E-29	0,0639	11,1882407	0,71450087	1086,01	JRKL	JRK like
100533111	1,10E-02	1,96E+00	7,88E-03	0,2689	2,6569989	0,71438461	44,21	ZNF670-ZNF	ZNF670-ZNF695 readthrough (NMD candidate)
26064	2,34E-49	4,86E+01	3,75E-50	0,048	14,8913911	0,71415649	9831,54	RAI14	retinoic acid induced 14
153241	3,70E-31	3,04E+01	9,15E-32	0,0609	11,7281284	0,71386772	1439,72	CEP120	centrosomal protein 120
9651	2,91E-02	1,54E+00	2,19E-02	0,3112	2,2929421	0,71362477	33,06	PLCH2	phospholipase C eta 2
105378688	2,09E-01	6,80E-01	1,78E-01	0,5292	1,3484591	0,71358086	11,36	LINC02918	long intergenic non-protein coding RNA 2918
407	2,80E-01	5,53E-01	2,42E-01	0,6101	1,169182	0,71329942	8,71	ARR3	arrestin 3
149013	5,64E-29	2,82E+01	1,47E-29	0,0632	11,290149	0,7130255	1517,6	NBPF12	NBPF member 12
4154	1,65E-54	5,38E+01	2,38E-55	0,0455	15,671081	0,71292469	7090,81	MBNL1	muscleblind like splicing regulator 1
100131193	6,04E-03	2,22E+00	4,25E-03	0,2492	2,8593289	0,71252393	52,3	CCDC183-A	CCDC183 antisense RNA 1
100507118	7,36E-30	2,91E+01	1,87E-30	0,0621	11,4696619	0,71251201	2075,32	PRC1-AS1	PRC1 antisense RNA 1
79682	5,46E-46	4,53E+01	9,53E-47	0,0496	14,3577098	0,71223925	4752,71	CENPU	centromere protein U
57639	3,84E-08	7,42E+00	1,92E-08	0,1267	5,6189065	0,71209563	217,6	CCDC146	coiled-coil domain containing 146
105371312	1,24E-08	7,91E+00	6,06E-09	0,1224	5,8151004	0,71192681	294,68	LOC105371	uncharacterized LOC105371312
81792	3,08E-54	5,35E+01	4,48E-55	0,0455	15,6310017	0,71180743	3839,32	ADAMTS12	ADAM metallopeptidase with thrombospondin type 1 motif 12
441027	4,72E-03	2,33E+00	3,28E-03	0,2421	2,9398845	0,71163534	54,16	TMEM150C	transmembrane protein 150C
656	1,81E-07	6,74E+00	9,40E-08	0,1333	5,3380022	0,71150927	199,34	BMP8B	bone morphogenetic protein 8b
54441	2,81E-08	7,55E+00	1,40E-08	0,1254	5,6734151	0,71124916	240,5	STAG3L1	stromal antigen 3-like 1 (pseudogene)
257044	2,86E-02	1,54E+00	2,15E-02	0,3093	2,2995132	0,71115556	33,92	CATSPERE	catsper channel auxiliary subunit epsilon
23137	2,74E-53	5,26E+01	4,06E-54	0,0459	15,4899291	0,71102804	3723,83	SMC5	structural maintenance of chromosomes 5
134359	1,04E-21	2,10E+01	3,29E-22	0,0734	9,6909837	0,71098821	1160,7	POC5	POC5 centriolar protein
100775104	1,41E-01	8,51E-01	1,16E-01	0,4523	1,5718362	0,71093072	15,79	KLHL7-DT	KLHL7 divergent transcript
100846999	2,22E-12	1,17E+01	9,39E-13	0,0995	7,1391886	0,71036542	458,78	MIR4444-2	microRNA 4444-2
55028	1,22E-37	3,69E+01	2,58E-38	0,0549	12,9429241	0,7102408	2099,52	C17orf80	chromosome 17 open reading frame 80
10206	1,31E-19	1,89E+01	4,42E-20	0,0774	9,1773108	0,7102175	743,54	TRIM13	tripartite motif containing 13
442524	6,63E-02	1,18E+00	5,22E-02	0,3658	1,9412218	0,71012093	24,05	DPY19L2P3	DPY19L2 pseudogene 3
57045	2,89E-52	5,15E+01	4,37E-53	0,0463	15,3363946	0,70972196	3902,64	TWSG1	twisted gastrulation BMP signaling modulator 1
8091	2,51E-46	4,56E+01	4,34E-47	0,0492	14,4121467	0,70966057	3526,53	HMGA2	high mobility group AT-hook 2
286144	1,50E-19	1,88E+01	5,04E-20	0,0774	9,1631976	0,70961872	693,09	TRIQK	triple QxxK/R motif containing
55300	2,57E-31	3,06E+01	6,31E-32	0,0603	11,7595015	0,70948713	2146,98	PI4K2B	phosphatidylinositol 4-kinase type 2 beta
124751	4,76E-06	5,32E+00	2,66E-06	0,1511	4,6954899	0,70933663	148,28	KRBA2	KRAB-A domain containing 2
84911	9,00E-03	2,05E+00	6,43E-03	0,26	2,7251759	0,70864856	55,35	ZNF382	zinc finger protein 382
23122	5,22E-45	4,43E+01	9,33E-46	0,0499	14,1987201	0,70846779	3280,06	CLASP2	cytoplasmic linker associated protein 2
10236	1,47E-46	4,58E+01	2,53E-47	0,049	14,4493393	0,70841019	19303,67	HNRNPR	heterogeneous nuclear ribonucleoprotein R
80173	4,53E-28	2,73E+01	1,21E-28	0,0638	11,1033285	0,70836064	1236,59	IFT74	intraflagellar transport 74
6738	1,02E-31	3,10E+01	2,48E-32	0,0598	11,8379784	0,70797389	1798,64	RO60	Ro60, Y RNA binding protein
9617	2,79E-11	1,06E+01	1,23E-11	0,1044	6,7769379	0,7077874	337,92	MTRF1	mitochondrial translation release factor 1
101928352	2,08E-01	6,82E-01	1,76E-01	0,5231	1,3527385	0,70766813	12,02	LOC101928	uncharacterized LOC101928352
7696	8,62E-03	2,06E+00	6,14E-03	0,2582	2,7402357	0,70746483	46,61	ZNF137P	zinc finger protein 137, pseudogene
124152	1,22E-09	8,91E+00	5,72E-10	0,1141	6,1980897	0,70728567	279,21	IQCK	IQ motif containing K
27031	1,68E-09	8,77E+00	7,91E-10	0,115	6,146762	0,70676031	261,02	NPHP3	nephrocystin 3
57482	5,30E-09	8,28E+00	2,55E-09	0,1186	5,9582245	0,70637905	260,6	CRACD	capping protein inhibiting regulator of actin dynamics
100130890	1,43E-04	3,84E+00	8,80E-05	0,1801	3,9214106	0,70634952	107,11	TSTD3	thiosulfate sulfurtransferase like domain containing 3
85363	1,81E-20	1,97E+01	5,94E-21	0,0752	9,3910874	0,70623374	1019,48	TRIM5	tripartite motif containing 5
51495	1,55E-67	6,68E+01	1,67E-68	0,0404	17,491165	0,70619421	6736,93	HACD3	3-hydroxyacyl-CoA dehydratase 3
34	1,87E-48	4,77E+01	3,08E-49	0,0479	14,7499851	0,70617276	3240,93	ACADM	acyl-CoA dehydrogenase medium chain
339005	2,06E-03	2,69E+00	1,39E-03	0,2208	3,1967624	0,70580993	68,72	WHAMMP3	WHAMM pseudogene 3
1139	1,76E-01	7,54E-01	1,47E-01	0,4864	1,4504659	0,70548916	13,63	CHRNA7	cholinergic receptor nicotinic alpha 7 subunit
10979	1,00E-57	5,70E+01	1,35E-58	0,0437	16,1394642	0,70539495	6589,34	FERMT2	FERM domain containing kindlin 2
57335	4,45E-26	2,54E+01	1,25E-26	0,066	10,6807919	0,70525075	937,04	ZNF286A	zinc finger protein 286A
51110	3,49E-16	1,55E+01	1,30E-16	0,0852	8,2732525	0,70507986	757,02	LACTB2	lactamase beta 2
261726	1,15E-39	3,89E+01	2,32E-40	0,053	13,2996786	0,70498534	4075,6	TIPRL	TOR signaling pathway regulator
101927911	5,41E-02	1,27E+00	4,21E-02	0,3468	2,0324283	0,70486214	26,07	LOC101927	uncharacterized LOC101927911
7368	9,43E-24	2,30E+01	2,83E-24	0,0693	10,1655009	0,70478895	953,98	UGT8	UDP glycosyltransferase 8
107984814	2,58E-02	1,59E+00	1,93E-02	0,3011	2,3405306	0,70478384	35,15	LOC107984	replaced by ID 101927978
259217	1,36E-11	1,09E+01	5,91E-12	0,1024	6,881825	0,70464504	324,66	HSPA12A	heat shock protein family A (Hsp70) member 12A
26263	2,72E-28	2,76E+01	7,21E-29	0,0632	11,1493693	0,70445336	1130,28	FBXO22	F-box protein 22
341	1,25E-04	3,90E+00	7,60E-05	0,178	3,9565811	0,70434576	107,13	APOC1	apolipoprotein C1
8808	2,52E-03	2,60E+00	1,71E-03	0,2245	3,1368944	0,70422706	62,79	IL1RL2	interleukin 1 receptor like 2
54757	1,01E-48	4,80E+01	1,65E-49	0,0476	14,7918376	0,7041393	3313,66	FAM20A	FAM20A golgi associated secretory pathway pseudokinase
101927768	3,66E-02	1,44E+00	2,79E-02	0,3202	2,1982121	0,70393847	32,95	HDAC2-AS2	HDAC2 and HS3ST5 antisense RNA 2
134728	1,17E-03	2,93E+00	7,69E-04	0,2092	3,3635415	0,70367779	75,47	IRAK1BP1	interleukin 1 receptor associated kinase 1 binding protein 1
23683	7,56E-53	5,21E+01	1,13E-53	0,0456	15,4240081	0,70362149	4297,45	PRKD3	protein kinase D3
152687	1,42E-11	1,08E+01	6,13E-12	0,1023	6,876515	0,70326386	383,52	ZNF595	zinc finger protein 595
4775	1,67E-39	3,88E+01	3,38E-40	0,053	13,2715738	0,70314971	1986,98	NFATC3	nuclear factor of activated T cells 3
51385	4,05E-17	1,64E+01	1,47E-17	0,0824	8,5297051	0,70313584	575,49	ZNF589	zinc finger protein 589
4591	2,79E-53	5,26E+01	4,14E-54	0,0454	15,4886481	0,70306482	3921,28	TRIM37	tripartite motif containing 37
130355	5,78E-07	6,24E+00	3,08E-07	0,1373	5,1187274	0,7030526	174,88	C2orf76	chromosome 2 open reading frame 76
8450	5,58E-47	4,63E+01	9,49E-48	0,0484	14,5167221	0,70293417	6419,1	CUL4B	cullin 4B
105378248	2,12E-01	6,74E-01	1,80E-01	0,5239	1,3415782	0,70286925	11,31	LOC105378	uncharacterized LOC105378248
28977	1,05E-32	3,20E+01	2,49E-33	0,0584	12,0294332	0,70263626	3175,46	MRPL42	mitochondrial ribosomal protein L42
9236	1,32E-35	3,49E+01	2,93E-36	0,0559	12,5742323	0,7025684	1612,37	CCPG1	cell cycle progression 1
6655	2,17E-40	3,97E+01	4,29E-41	0,0523	13,4253959	0,70243583	2232,04	SOS2	SOS Ras/Rho guanine nucleotide exchange factor 2
1621	1,19E-02	1,92E+00	8,62E-03	0,2672	2,6268272	0,70201952	43,28	DBH	dopamine beta-hydroxylase
57122	7,31E-54	5,31E+01	1,07E-54	0,0451	15,5754532	0,70196668	4444,43	NUP107	nucleoporin 107
83932	7,27E-26	2,51E+01	2,06E-26	0,066	10,6345739	0,70182214	1041,91	SPRTN	SprT-like N-terminal domain
110354863	5,82E-12	1,12E+01	2,49E-12	0,1001	7,0037424	0,70131771	375,33	ZNF660-ZNF	ZNF660-ZNF197 readthrough
8930	1,48E-31	3,08E+01	3,62E-32	0,0594	11,8064056	0,70104795	1372,69	MBD4	methyl-CpG binding domain 4, DNA glycosylase
84340	8,84E-45	4,41E+01	1,59E-45	0,0495	14,161131	0,70100581	2743,06	GFM2	GTP dependent ribosome recycling factor mitochondrial 2
100507401	1,17E-01	9,32E-01	9,57E-02	0,4206	1,6659808	0,70063851	17,83	LRP4-AS1	LRP4 antisense RNA 1
107986596	1,59E-03	2,80E+00	1,06E-03	0,214	3,2739592	0,70058211	73,56	LOC107986	uncharacterized LOC107986596
100652772	7,83E-15	1,41E+01	3,05E-15	0,0887	7,8886767	0,70008427	708,73	NNT-AS1	NNT antisense RNA 1
353274	5,32E-24	2,33E+01	1,59E-24	0,0685	10,2216432	0,69999157	1194,32	ZNF445	zinc finger protein 445
29117	6,07E-45	4,42E+01	1,09E-45	0,0493	14,1879432	0,69990549	4205,48	BRD7	bromodomain containing 7
84068	6,38E-14	1,32E+01	2,56E-14	0,0919	7,6188862	0,69990132	469,47	SLC10A7	solute carrier family 10 member 7
80790	1,06E-55	5,50E+01	1,49E-56	0,0442	15,846499	0,6998361	5380,23	CMIP	c-Maf inducing protein
55109	2,87E-44	4,35E+01	5,24E-45	0,0497	14,0773045	0,69983005	2613,35	AGGF1	angiogenic factor with G-patch and FHA domains 1
89849	3,54E-22	2,15E+01	1,11E-22	0,0714	9,8018526	0,69970132	801,72	ATG16L2	autophagy related 16 like 2
93164	1,30E-06	5,89E+00	7,03E-07	0,141	4,9605501	0,69957815	166,58	HTR7P1	5-hydroxytryptamine receptor 7 pseudogene 1
11227	8,90E-39	3,81E+01	1,83E-39	0,0532	13,1444389	0,69957741	3000,71	GALNT5	polypeptide N-acetylgalactosaminyltransferase 5
100861513	8,12E-04	3,09E+00	5,30E-04	0,2016	3,4653688	0,69864065	78,25	ZMYM4-AS1	ZMYM4 antisense RNA 1
22823	1,77E-29	2,88E+01	4,54E-30	0,0613	11,3927796	0,69861873	1422,02	MTF2	metal response element binding transcription factor 2
1017	1,13E-56	5,59E+01	1,55E-57	0,0437	15,9880209	0,69838538	4231,04	CDK2	cyclin dependent kinase 2
79959	4,39E-23	2,24E+01	1,34E-23	0,0697	10,012759	0,69835513	956,17	CEP76	centrosomal protein 76

105369293	1,75E-01	7,57E-01	1,46E-01	0,4806	1,4530522	0,69829039	13,94	LOC105369	uncharacterized LOC105369293
9694	1,06E-32	3,20E+01	2,52E-33	0,058	12,0285537	0,69802571	2066	EMC2	ER membrane protein complex subunit 2
1299	2,97E-01	5,27E-01	2,59E-01	0,6178	1,1294958	0,69775077	8,12	COL9A3	collagen type IX alpha 3 chain
8411	3,13E-40	3,95E+01	6,23E-41	0,0521	13,3977685	0,69763695	2522,21	EEA1	early endosome antigen 1
6102	5,27E-25	2,43E+01	1,53E-25	0,0667	10,4459588	0,69714481	1621,8	RP2	RP2 activator of ARL3 GTPase
10903	2,23E-25	2,47E+01	6,40E-26	0,0662	10,5282944	0,69706024	954,11	MTMR11	myotubularin related protein 11
80110	6,71E-21	2,02E+01	2,18E-21	0,0734	9,4961307	0,69705608	733,96	ZNF614	zinc finger protein 614
762	3,02E-05	4,52E+00	1,77E-05	0,1624	4,2917237	0,69697532	134,24	CA4	carbonic anhydrase 4
10168	8,59E-12	1,11E+01	3,70E-12	0,1002	6,9483351	0,69645431	374,51	ZNF197	zinc finger protein 197
130574	2,57E-18	1,76E+01	8,99E-19	0,0786	8,8470479	0,69572193	694,59	LYPD6	LY6/PLAUR domain containing 6
105371275	1,17E-01	9,32E-01	9,56E-02	0,4174	1,6667096	0,69571282	18,84	LOC105371	uncharacterized LOC105371275
283487	1,35E-03	2,87E+00	8,92E-04	0,2094	3,3225502	0,69559467	77,8	PRECSIT	p53 regulated carcinoma associated Stat3 activating long intergenic non-protein coding transcript
338323	1,00E-01	1,00E+00	8,09E-02	0,3983	1,7456796	0,69523672	19,85	NLRP14	NLR family pyrin domain containing 14
8805	1,67E-28	2,78E+01	4,42E-29	0,0621	11,192894	0,69481808	1422	TRIM24	tripartite motif containing 24
107985917	1,76E-04	3,75E+00	1,09E-04	0,1796	3,8692728	0,69477216	100,62	LOC107985	917
11076	2,93E-02	1,53E+00	2,21E-02	0,3033	2,2894012	0,6943738	35,01	TPPP	tubulin polymerization promoting protein
100294145	2,08E-39	3,87E+01	4,23E-40	0,0524	13,2548185	0,69435264	1989,67	LOC100294	uncharacterized LOC100294145
5764	2,28E-08	7,64E+00	1,13E-08	0,1216	5,7096701	0,69426886	240,56	PTN	pleiotrophin
57708	1,03E-39	3,90E+01	2,08E-40	0,0522	13,3079466	0,69419363	2364,22	MIER1	MIER1 transcriptional regulator
29079	8,82E-27	2,61E+01	2,44E-27	0,0641	10,8316817	0,69418252	1664,16	MED4	mediator complex subunit 4
100529855	8,05E-07	6,09E+00	4,31E-07	0,1373	5,0546444	0,69415931	193,62	ZNF625-ZNF	ZNF625-ZNF20 readthrough (NMD candidate)
22807	1,16E-12	1,19E+01	4,85E-13	0,096	7,2293065	0,69412567	432,35	IKZF2	IKAROS family zinc finger 2
51209	2,19E-08	7,66E+00	1,08E-08	0,1214	5,7170603	0,69402168	233,05	RAB9B	RAB9B, member RAS oncogene family
55832	1,95E-32	3,17E+01	4,64E-33	0,0579	11,9777988	0,69386437	6617,18	CAND1	cullin associated and neddylation dissociated 1
23099	3,82E-29	2,84E+01	9,90E-30	0,0613	11,3246755	0,69377059	1233,83	ZBTB43	zinc finger and BTB domain containing 43
105375821	2,53E-01	5,97E-01	2,17E-01	0,5621	1,2341128	0,69364785	10,13	LOC105375	uncharacterized LOC105375821
85865	9,56E-26	2,50E+01	2,72E-26	0,0654	10,6086461	0,69351562	1084,23	GTPBP10	GTP binding protein 10
121457	1,13E-46	4,59E+01	1,94E-47	0,0479	14,4676716	0,69348018	4777,08	IKBIP	IKBKB interacting protein
7075	3,63E-09	8,44E+00	1,74E-09	0,1151	6,0205152	0,69318036	267,82	TIE1	tyrosine kinase with immunoglobulin like and EGF like domains 1
1001	5,45E-02	1,26E+00	4,24E-02	0,3416	2,0292255	0,69308302	28,77	CDH3	cadherin 3
54329	1,84E-01	7,35E-01	1,55E-01	0,4871	1,4226144	0,69297607	12,92	GPR85	G protein-coupled receptor 85
63901	1,77E-52	5,18E+01	2,65E-53	0,0451	15,3687283	0,69296577	3677,72	FAM111A	FAM111 trypsin like peptidase A
503638	1,86E-26	2,57E+01	5,18E-27	0,0644	10,7624699	0,6928567	1032,69	DUXAP9	double homeobox A pseudogene 9
101930275	2,14E-01	6,70E-01	1,82E-01	0,5185	1,3360722	0,6926916	11,77	MTUS1-DT	MTUS1 divergent transcript
26232	8,28E-03	2,08E+00	5,89E-03	0,2514	2,753967	0,69247273	53,41	FBXO2	F-box protein 2
56650	4,54E-70	6,93E+01	4,66E-71	0,0388	17,8233622	0,69238293	7564,57	CLDND1	claudin domain containing 1
100293516	8,61E-10	9,06E+00	4,01E-10	0,1107	6,2537276	0,69199494	292,1	ZNF587B	zinc finger protein 587B
63899	1,25E-19	1,89E+01	4,20E-20	0,0753	9,1829168	0,69191675	676,14	NSUN3	NOP2/Sun RNA methyltransferase 3
25816	2,80E-24	2,36E+01	8,29E-25	0,0672	10,2843884	0,69146859	1277,75	TNFAIP8	TNF alpha induced protein 8
10512	4,53E-38	3,73E+01	9,47E-39	0,0531	13,0195485	0,69127917	4537,8	SEMA3C	semaphorin 3C
285315	1,75E-04	3,76E+00	1,08E-04	0,1785	3,8719275	0,69118216	107,95	C3orf33	chromosome 3 open reading frame 33
79674	8,92E-13	1,20E+01	3,71E-13	0,0951	7,2655899	0,6908585	402,46	VEPH1	ventricular zone expressed PH domain containing 1
92270	2,07E-07	6,68E+00	1,07E-07	0,13	5,31365	0,6906884	195,49	ATP6AP1L	ATPase H+ transporting accessory protein 1 like (pseudogene)
54505	3,16E-52	5,15E+01	4,78E-53	0,045	15,3305315	0,69063633	4075,33	DHX29	DExH-box helicase 29
10565	5,08E-44	4,33E+01	9,32E-45	0,0492	14,0364838	0,68999495	2604,91	ARFGEF1	ADP ribosylation factor guanine nucleotide exchange factor 1
60559	3,21E-37	3,65E+01	6,83E-38	0,0536	12,8678603	0,68985551	4962,45	SPCS3	signal peptidase complex subunit 3
54386	8,06E-38	3,71E+01	1,69E-38	0,0532	12,9750705	0,68983429	3123,89	TERF2IP	TERF2 interacting protein
8727	2,37E-10	9,63E+00	1,08E-10	0,1068	6,4557457	0,68968062	15316,79	CTNNAL1	catenin alpha like 1
65009	6,01E-06	5,22E+00	3,38E-06	0,1484	4,6461875	0,68949097	165,55	NDRG4	NDRG family member 4
692108	2,09E-01	6,80E-01	1,77E-01	0,5106	1,3499895	0,68931409	12,26	SNORD67	small nucleolar RNA, C/D box 67
8322	2,10E-27	2,67E+01	5,70E-28	0,0629	10,9638612	0,68913737	1119,17	FZD4	frizzled class receptor 4
55749	9,19E-55	5,40E+01	1,32E-55	0,0439	15,7085915	0,6891067	7864,11	CCAR1	cell division cycle and apoptosis regulator 1
23117	1,49E-16	1,58E+01	5,51E-17	0,0823	8,3753513	0,68903081	604,42	NPIPB3	nuclear pore complex interacting protein family member B3
23584	2,30E-04	3,64E+00	1,44E-04	0,1812	3,8013055	0,68886015	98,17	VSIG2	V-set and immunoglobulin domain containing 2
51249	3,90E-41	4,04E+01	7,61E-42	0,0508	13,552928	0,68865693	2978,89	TMEM69	transmembrane protein 69
105369781	3,38E-01	4,71E-01	2,98E-01	0,6618	1,0405216	0,68860604	7	LOC105369	uncharacterized LOC105369781
57552	2,68E-71	7,06E+01	2,66E-72	0,0383	17,9828141	0,68851648	16497,45	NCEH1	neutral cholesterol ester hydrolase 1
1810	4,91E-30	2,93E+01	1,25E-30	0,0598	11,5048761	0,68796341	3309,14	DR1	down-regulator of transcription 1
653308	3,29E-18	1,75E+01	1,15E-18	0,078	8,8191943	0,68787268	710,13	ASAH2B	N-acylsphingosine amidohydrolase 2B
341676	2,79E-01	5,54E-01	2,42E-01	0,5873	1,1712291	0,68782084	9,58	NEK5	NIMA related kinase 5
84614	1,33E-15	1,49E+01	5,04E-16	0,0848	8,1105204	0,68759877	512,98	ZBTB37	zinc finger and BTB domain containing 37
9310	1,13E-04	3,95E+00	6,91E-05	0,1728	3,9795162	0,68759827	113,03	ZNF235	zinc finger protein 235
54812	1,86E-38	3,77E+01	3,84E-39	0,0525	13,0882285	0,68743537	2177,54	AFTPH	aftiphilin
101928146	2,54E-02	1,60E+00	1,89E-02	0,2929	2,3470668	0,68737991	36,64	LOC101928	uncharacterized LOC101928146
6782	8,79E-46	4,51E+01	1,55E-46	0,048	14,3241433	0,68719659	4767,13	HSPA13	heat shock protein family A (Hsp70) member 13
10111	5,68E-44	4,32E+01	1,05E-44	0,0489	14,0283873	0,68664972	2955,23	RAD50	RAD50 double strand break repair protein
101927983	1,70E-02	1,77E+00	1,25E-02	0,2747	2,4978377	0,68626692	42,45	EDRF1-AS1	EDRF1 antisense RNA 1
148867	4,58E-27	2,63E+01	1,26E-27	0,063	10,8921046	0,68619298	1183,02	SLC30A7	solute carrier family 30 member 7
9147	1,10E-35	3,50E+01	2,44E-36	0,0545	12,58858	0,68597698	4093,98	NEMF	nuclear export mediator factor
107985304	2,04E-35	3,47E+01	4,53E-36	0,0547	12,5396779	0,68595024	1652,2	LOC107985	uncharacterized LOC107985304
440288	1,03E-03	2,99E+00	6,79E-04	0,2019	3,3979736	0,68591666	81,84	UBL7-DT	UBL7 divergent transcript
64766	3,67E-33	3,24E+01	8,62E-34	0,0566	12,116647	0,68584091	1631,86	S100PBP	S100P binding protein
79366	1,55E-04	3,81E+00	9,55E-05	0,1758	3,9018523	0,68578326	702,39	HMGN5	high mobility group nucleosome binding domain 5
79627	2,39E-46	4,56E+01	4,14E-47	0,0476	14,4153563	0,68576046	7055,17	OGFRL1	opioid growth factor receptor like 1
256021	9,90E-02	1,00E+00	7,99E-02	0,3916	1,7512164	0,68573419	20,93	LINC01619	long intergenic non-protein coding RNA 1619
23022	4,83E-43	4,23E+01	9,03E-44	0,0494	13,8746001	0,68565897	3977,19	PALLD	palladin, cytoskeletal associated protein
4091	8,51E-14	1,31E+01	3,43E-14	0,0904	7,5810984	0,6854795	481,12	SMAD6	SMAD family member 6
56990	1,07E-26	2,60E+01	2,95E-27	0,0634	10,8141361	0,68539325	1848,32	CDC42SE2	CDC42 small effector 2
100507283	7,96E-02	1,10E+00	6,33E-02	0,369	1,8569932	0,68520122	24,44	MSANTD2-A	MSANTD2 antisense RNA 1
79930	4,24E-07	6,37E+00	2,24E-07	0,1322	5,178096	0,68467697	215,44	DOK3	docking protein 3
163859	3,03E-20	1,95E+01	1,00E-20	0,0733	9,3359426	0,68442678	1528,71	SDE2	SDE2 telomere maintenance homolog
54665	1,79E-24	2,37E+01	5,28E-25	0,0663	10,3277221	0,6842755	1168,66	RSBN1	round spermatid basic protein 1
105371036	1,95E-01	7,10E-01	1,65E-01	0,4923	1,3899028	0,68424601	12,81	LOC105371	replaced by ID 58986
2925	1,40E-01	8,54E-01	1,16E-01	0,4347	1,5738853	0,68416134	17,88	GRPR	gastrin releasing peptide receptor
374899	3,22E-11	1,05E+01	1,42E-11	0,1012	6,7561487	0,6838366	340,93	ZNF829	zinc finger protein 829
7781	1,22E-01	9,14E-01	1,00E-01	0,4156	1,6447412	0,68347392	18,11	SLC30A3	solute carrier family 30 member 3
22977	1,14E-01	9,43E-01	9,25E-02	0,4061	1,6825948	0,68334296	18,7	AKR7A3	aldo-keto reductase family 7 member A3
84280	5,05E-46	4,53E+01	8,81E-47	0,0476	14,363169	0,68331851	4359,14	BTBD10	BTB domain containing 10
105376483	1,46E-01	8,36E-01	1,20E-01	0,44	1,5529233	0,68321473	17,23	LOC105376	uncharacterized LOC105376483
26080	9,75E-02	1,01E+00	7,86E-02	0,3882	1,7591171	0,68291133	22,93	FAM230C	family with sequence similarity 230 member C
5825	9,01E-31	3,00E+01	2,24E-31	0,0586	11,6518871	0,68279062	3148,3	ABCD3	ATP binding cassette subfamily D member 3
79577	5,73E-38	3,72E+01	1,20E-38	0,0525	13,001422	0,68272997	2525,82	CDC73	cell division cycle 73
728343	1,85E-01	7,33E-01	1,56E-01	0,4805	1,4200007	0,68236723	13,33	NXF2B	nuclear RNA export factor 2B
400818	6,73E-49	4,82E+01	1,09E-49	0,046	14,819617	0,68200649	3322,21	NBPF9	NBPF member 9
100526837	3,78E-40	3,94E+01	7,55E-41	0,051	13,3834924	0,68198834	2110,3	EEF1E1-BL	EEF1E1-BLOC1S5 readthrough (NMD candidate)
55074	3,23E-41	4,05E+01	6,30E-42	0,0502	13,5668668	0,68144089	2386,5	OXR1	oxidation resistance 1
100529240	4,83E-03	2,32E+00	3,36E-03	0,2323	2,9328339	0,68135057	58,22	ZNF816-ZNF	ZNF816-ZNF321P readthrough
55364	2,42E-29	2,86E+01	6,23E-30	0,0599	11,3652484	0,68130162	1381,08	IMPACT	impact RWD domain protein
55032	6,35E-36	3,52E+01	1,39E-36	0,0539	12,632716	0,68119823	2027,03	SLC35A5	solute carrier family 35 member A5
5189	1,42E-25	2,48E+01	4,04E-26	0,0644	10,5714275	0,6811592	1023,86	PEX1	peroxisomal biogenesis factor 1
54951	1,39E-15	1,49E+01	5,28E-16	0,084	8,1049354	0,6811351	737,58	COMMD8	COMM domain containing 8
51053	5,41E-51	5,03E+01	8,39E-52	0,045	15,1433087	0,68089643	4347,36	GMNN	geminin DNA replication inhibitor
28990	4,99E-11	1,03E+01	2,21E-11	0,1017	6,6911863	0,68057329	357,08	ASTE1	asteroid homolog 1
22862	4,56E-39	3,83E+01	9,32E-40	0,0515	13,1954217	0,68010976	2835,3	FNDC3A	fibronectin type III domain containing 3A
143884	4,24E-23	2,24E+01	1,29E-23	0,0679	10,0163524	0,68010645	1023,4	CWF19L2	CWF19 like cell cycle control factor 2
55196	3,05E-27	2,65E+01	8,32E-28	0,0622	10,9296141	0,68000515	1241,15	RESF1	retroelement silencing factor 1
9958	2,35E-39	3,86E+01	4,78E-40	0,0513	13,245591	0,67988103	2462,46	USP15	ubiquitin specific peptidase 15
25782	2,74E-44	4,36E+01	5,00E-45	0,0483	14,0806048	0,67948785	2973,38	RAB3GAP2	RAB3 GTPase activating non-catalytic protein subunit 2
105377276	7,23E-07	6,14E+00	3,86E-07	0,1339	5,075541	0,67944377	201,47	LOC105377	uncharacterized LOC105377276
132949	1,64E-17	1,68E+01	5,88E-18	0,0787	8,6348887	0,67933085	825,55	AASDH	aminoadipate-semialdehyde dehydrogenase
27327	1,24E-43	4,29E+01	2,29E-44	0,0486	13,9726952	0,67915442	2396,69	TNRC6A	trinucleotide repeat containing adaptor 6A
90589	6,65E-05	4,18E+00	3,99E-05	0,1652	4,1083124	0,67870671	126,02	ZNF625	zinc finger protein 625
345275	2,65E-01	5,77E-01	2,28E-01	0,5631	1,2045899	0,67831022	9,65	HSD17B13	hydroxysteroid 17-beta dehydrogenase 13
30832	3,56E-18	1,74E+01	1,25E-18	0,077	8,8101701	0,67821151	664,46	ZNF354C	zinc finger protein 354C
80817	1,62E-19	1,88E+01	5,48E-20	0,074	9,1541481	0,67767818	723,32	CEP44	centrosomal protein 44
100873965	2,23E-11	1,07E+01	9,77E-12	0,0995	6,8097794	0,67727324	365,73	MED4-AS1	MED4 antisense RNA 1
51194	2,61E-40	3,96E+01	5,17E-41	0,0505	13,411587	0,67699581	2674,54	IPO11	importin 11
101929240	7,54E-06	5,12E+00	4,27E-06	0,1472	4,5979866	0,67699046	150,02	LOC101929	U5 small nuclear ribonucleoprotein 200 kDa helicase-like
3516	5,58E-55	5,43E+01	8,00E-56	0,043	15,7403477	0,67690214	6894,59	RBPJ	recombination signal binding protein for immunoglobulin kappa J region
118429	1,38E-61	6,09E+01	1,71E-62	0,0406	16,6842623	0,67686057	15633,25	ANTXR2	ANTXR cell adhesion molecule 2

10973	7,64E-46	4,51E+01	1,34E-46	0,0472	14,3340354	0,67651969	3890,31	ASCC3	activating signal cointegrator 1 complex subunit 3
284565	1,15E-46	4,59E+01	1,97E-47	0,0467	14,4665538	0,67615381	3248,32	NBPF15	NBPF member 15
23178	4,34E-10	9,36E+00	2,00E-10	0,1063	6,3615187	0,67614022	317,63	PASK	PAS domain containing serine/threonine kinase
83714	8,82E-02	1,05E+00	7,06E-02	0,3739	1,8080021	0,67597961	21,95	NRIP2	nuclear receptor interacting protein 2
10947	1,31E-33	3,29E+01	3,04E-34	0,0554	12,2018535	0,67583521	1669,25	AP3M2	adaptor related protein complex 3 subunit mu 2
144132	1,30E-18	1,79E+01	4,49E-19	0,0757	8,9242466	0,67572632	728,14	DNHD1	dynein heavy chain domain 1
164	1,84E-51	5,07E+01	2,81E-52	0,0444	15,2151415	0,67559404	5173,7	AP1G1	adaptor related protein complex 1 subunit gamma 1
8539	3,38E-67	6,65E+01	3,68E-68	0,0387	17,4462202	0,67525781	7702,31	API5	apoptosis inhibitor 5
100129361	1,41E-23	2,29E+01	4,26E-24	0,0666	10,1254485	0,67430431	1142,54	SMIM10L1	small integral membrane protein 10 like 1
645455	4,61E-08	7,34E+00	2,32E-08	0,1207	5,5865181	0,67410538	233,35	CEP170P1	centrosomal protein 170 pseudogene 1
4144	8,40E-59	5,81E+01	1,10E-59	0,0414	16,2932196	0,67387281	13737,44	MAT2A	methionine adenosyltransferase 2A
154743	4,72E-08	7,33E+00	2,37E-08	0,1207	5,5824882	0,67386019	253,86	BMT2	base methyltransferase of 25S rRNA 2 homolog
9532	2,60E-43	4,26E+01	4,85E-44	0,0484	13,9190639	0,67355545	2823,95	BAG2	BAG cochaperone 2
107985879	7,69E-05	4,11E+00	4,63E-05	0,1653	4,0734584	0,67333028	123,19	LINC01833	long intergenic non-protein coding RNA 1833
126731	1,27E-18	1,79E+01	4,40E-19	0,0754	8,9263032	0,67329913	751,67	CCSAP	centriole, cilia and spindle associated protein
2803	4,25E-54	5,34E+01	6,19E-55	0,0431	15,6103531	0,67329861	8038,5	GOLGA4	golgin A4
55027	3,81E-26	2,54E+01	1,07E-26	0,063	10,6953503	0,67329164	1256,25	HEATR3	HEAT repeat containing 3
4671	2,15E-06	5,67E+00	1,18E-06	0,1385	4,8595141	0,67327387	172,43	NAIP	NLR family apoptosis inhibitory protein
7756	6,97E-69	6,82E+01	7,31E-70	0,0381	17,6686719	0,67309799	7673,55	ZNF207	zinc finger protein 207
100132074	3,06E-02	1,51E+00	2,31E-02	0,2962	2,2724242	0,67306834	36,25	FOXO6	forkhead box O6
102465976	3,32E-01	4,79E-01	2,93E-01	0,6392	1,0526474	0,67288279	7,45	MIR6807	microRNA 6807
9575	2,23E-46	4,57E+01	3,86E-47	0,0466	14,4202589	0,67248348	3283,07	CLOCK	clock circadian regulator
4750	3,74E-24	2,34E+01	1,11E-24	0,0656	10,2561405	0,67239516	1033,63	NEK1	NIMA related kinase 1
9913	2,50E-41	4,06E+01	4,86E-42	0,0495	13,5858	0,67208718	2697,07	SUPT7L	SPT7 like, STAGA complex subunit gamma
440944	1,19E-13	1,29E+01	4,79E-14	0,0891	7,5374163	0,67169267	495,1	THUMPD3-A	THUMPD3 antisense RNA 1
96459	6,20E-26	2,52E+01	1,75E-26	0,063	10,649568	0,67137416	1636,69	FNIP1	folliculin interacting protein 1
92285	2,54E-18	1,76E+01	8,89E-19	0,0758	8,8482459	0,67113507	697,39	ZNF585B	zinc finger protein 585B
7062	2,17E-01	6,64E-01	1,84E-01	0,5049	1,3287226	0,67088962	12,32	TCHH	trichohyalin
200765	1,28E-08	7,89E+00	6,30E-09	0,1155	5,8086424	0,6707685	273,93	TIGD1	tigger transposable element derived 1
196074	2,60E-18	1,76E+01	9,09E-19	0,0758	8,8457612	0,67074276	671,37	METTL15	methyltransferase like 15
729978	1,10E-01	9,59E-01	8,88E-02	0,3942	1,7015028	0,67070634	20,24	NPIPB2	nuclear pore complex interacting protein family member B2
51460	1,54E-22	2,18E+01	4,77E-23	0,0678	9,8864398	0,67062004	1261,59	SFMBT1	Scm like with four mbt domains 1
23036	4,50E-28	2,73E+01	1,20E-28	0,0604	11,1038955	0,67060128	1231,52	ZNF292	zinc finger protein 292
200030	1,36E-23	2,29E+01	4,09E-24	0,0662	10,1294063	0,67046766	964,68	NBPF11	NBPF member 11
1901	8,61E-03	2,06E+00	6,14E-03	0,2446	2,7404422	0,67042455	51,75	S1PR1	sphingosine-1-phosphate receptor 1
9284	9,83E-06	5,01E+00	5,61E-06	0,1476	4,5407636	0,67039801	147,02	NPIPA1	nuclear pore complex interacting protein family member A1
284098	1,15E-29	2,89E+01	2,95E-30	0,0586	11,4302436	0,67000987	1310,03	PIGW	phosphatidylinositol glycan anchor biosynthesis class W
107984120	4,69E-02	1,33E+00	3,62E-02	0,3197	2,0941899	0,66960566	29,85	LOC107984	120
23731	3,53E-67	6,65E+01	3,84E-68	0,0384	17,4437101	0,66952525	9174,17	TMEM245	transmembrane protein 245
1977	5,64E-34	3,32E+01	1,30E-34	0,0545	12,2709001	0,6692974	4148,76	EIF4E	eukaryotic translation initiation factor 4E
644150	2,06E-01	6,86E-01	1,74E-01	0,4921	1,359499	0,66905114	13,29	WIPF3	WAS/WASL interacting protein family member 3
65997	3,33E-01	4,78E-01	2,93E-01	0,6362	1,0515054	0,66891962	7,5	RASL11B	RAS like family 11 member B
55561	1,80E-04	3,74E+00	1,11E-04	0,1731	3,8646667	0,66885681	106,18	CDC42BPG	CDC42 binding protein kinase gamma
11228	2,97E-24	2,35E+01	8,79E-25	0,0651	10,2787387	0,66871341	1291,04	RASSF8	Ras association domain family member 8
89874	4,64E-04	3,33E+00	2,96E-04	0,1848	3,6184831	0,66863935	92,55	SLC25A21	solute carrier family 25 member 21
9804	2,36E-44	4,36E+01	4,30E-45	0,0474	14,0912783	0,66851364	12206,54	TOMM20	translocase of outer mitochondrial membrane 20
6801	5,80E-36	3,52E+01	1,27E-36	0,0529	12,6399875	0,66831108	2866,95	STRN	striatin
25898	6,62E-21	2,02E+01	2,15E-21	0,0704	9,4976797	0,66818611	1150,41	RCHY1	ring finger and CHY zinc finger domain containing 1
3624	5,22E-22	2,13E+01	1,64E-22	0,0684	9,7620903	0,66808575	979,63	INHBA	inhibin subunit beta A
55251	8,04E-28	2,71E+01	2,16E-28	0,0604	11,0513414	0,66783166	1662,17	PCMTD2	protein-L-isoaspartate (D-aspartate) O-methyltransferase domain containing 2
10825	1,61E-21	2,08E+01	5,13E-22	0,0692	9,6455297	0,66773448	931,95	NEU3	neuraminidase 3
4690	2,62E-20	1,96E+01	8,62E-21	0,0714	9,3517105	0,66767349	904,62	NCK1	NCK adaptor protein 1
4485	8,07E-03	2,09E+00	5,73E-03	0,2416	2,7625837	0,6674472	58,83	MST1	macrophage stimulating 1
154860	1,68E-05	4,77E+00	9,74E-06	0,1509	4,4229448	0,66722172	172,47	FEZF1-AS1	FEZF1 antisense RNA 1
51528	1,28E-05	4,89E+00	7,36E-06	0,1488	4,4830115	0,66701925	2778,77	JKAMP	JNK1/MAPK8 associated membrane protein
54811	2,37E-37	3,66E+01	5,03E-38	0,0517	12,8914292	0,66676662	2056,28	ZNF562	zinc finger protein 562
102724708	3,20E-01	4,95E-01	2,81E-01	0,6178	1,0790247	0,66666371	8,62	ARFGEF1-D	ARFGEF1 divergent transcript
7554	5,58E-14	1,33E+01	2,23E-14	0,0873	7,6363667	0,66659609	585,59	ZNF8	zinc finger protein 8
80018	3,73E-53	5,24E+01	5,54E-54	0,0431	15,4699392	0,66651218	4032,25	NAA25	N-alpha-acetyltransferase 25, NatB auxiliary subunit
22909	6,12E-23	2,22E+01	1,88E-23	0,0668	9,9794185	0,66634341	1044,05	FAN1	FANCD2 and FANCI associated nuclease 1
107985272	3,35E-01	4,75E-01	2,96E-01	0,6371	1,0457299	0,66627633	7,49	LOC107985272	
109286553	2,57E-18	1,76E+01	8,97E-19	0,0752	8,8471915	0,66570855	683,74	ARHGAP27F	ARHGAP27P1-BPTFP1-KPNA2P3 readthrough, transcribed pseudogene
727956	4,48E-09	8,35E+00	2,15E-09	0,1112	5,9858526	0,66557583	279,25	SDHAP2	SDHA pseudogene 2
983	2,18E-53	5,27E+01	3,22E-54	0,0429	15,5047466	0,66553545	6105,96	CDK1	cyclin dependent kinase 1
728407	2,81E-04	3,55E+00	1,77E-04	0,1775	3,7502199	0,66551237	103,57	PARGP1	poly(ADP-ribose) glycohydrolase pseudogene 1
8139	1,37E-08	7,86E+00	6,74E-09	0,1148	5,7973976	0,6654998	275,88	GAN	gigaxonin
84912	2,80E-28	2,76E+01	7,44E-29	0,0597	11,146612	0,66532072	1531,05	SLC35B4	solute carrier family 35 member B4
25934	3,97E-25	2,44E+01	1,15E-25	0,0635	10,4731566	0,66526667	1720,56	NIPSNAP3A	nipsnap homolog 3A
5980	1,27E-26	2,59E+01	3,51E-27	0,0616	10,7981311	0,66520051	1404,54	REV3L	REV3 like, DNA directed polymerase zeta catalytic subunit
8851	2,30E-08	7,64E+00	1,14E-08	0,1165	5,7081298	0,66517154	258,33	CDK5R1	cyclin dependent kinase 5 regulatory subunit 1
51582	1,84E-29	2,87E+01	4,73E-30	0,0584	11,3892726	0,66465507	10513,96	AZIN1	antizyme inhibitor 1
440028	8,39E-03	2,08E+00	5,97E-03	0,2417	2,749472	0,66456258	57,63	LINC02709	long intergenic non-protein coding RNA 2709
7915	2,18E-15	1,47E+01	8,34E-16	0,0825	8,0490753	0,66413927	637,58	ALDH5A1	aldehyde dehydrogenase 5 family member A1
2296	9,53E-18	1,70E+01	3,39E-18	0,0763	8,6976736	0,66397861	685,99	FOXC1	forkhead box C1
101928021	9,90E-02	1,00E+00	7,99E-02	0,3791	1,7513009	0,66397377	21,87	HELZ-AS1	HELZ antisense RNA 1
6259	4,05E-37	3,64E+01	8,64E-38	0,0517	12,8496219	0,66396363	2577,67	RYK	receptor like tyrosine kinase
22881	2,01E-08	7,70E+00	9,95E-09	0,1158	5,7316053	0,66390724	248,64	ANKRD6	ankyrin repeat domain 6
81539	2,15E-67	6,67E+01	2,33E-68	0,038	17,4722382	0,66381182	13101,79	SLC38A1	solute carrier family 38 member 1
2739	6,66E-46	4,52E+01	1,17E-46	0,0462	14,3437139	0,66338262	11971,45	GLO1	glyoxalase I
8766	1,62E-34	3,38E+01	3,69E-35	0,0536	12,3722834	0,66301939	4934,15	RAB11A	RAB11A, member RAS oncogene family
5583	2,93E-08	7,53E+00	1,46E-08	0,117	5,6663735	0,66301682	261,98	PRKCH	protein kinase C eta
142940	2,21E-15	1,47E+01	8,47E-16	0,0824	8,047286	0,66299219	875,4	TRUB1	TruB pseudouridine synthase family member 1
4573	3,23E-11	1,05E+01	1,42E-11	0,0981	6,7554278	0,66298206	390,74	TRNR	tRNA-Arg
7013	2,08E-21	2,07E+01	6,66E-22	0,0689	9,6188113	0,66288972	973,15	TERF1	telomeric repeat binding factor 1
101928762	3,50E-02	1,46E+00	2,66E-02	0,2989	2,2167772	0,66267858	37,33	LOC101928	uncharacterized LOC101928762
26576	1,96E-01	7,08E-01	1,65E-01	0,4772	1,3885186	0,66261979	15,97	SRPK3	SRSF protein kinase 3
440145	3,05E-20	1,95E+01	1,01E-20	0,0709	9,3354568	0,66230855	1273	MZT1	mitotic spindle organizing protein 1
147011	1,07E-01	9,71E-01	8,70E-02	0,3869	1,7114584	0,66223717	21,18	PROCA1	protein interacting with cyclin A1
51360	3,72E-21	2,04E+01	1,20E-21	0,0693	9,5582589	0,66217298	1467,01	MBTPS2	membrane bound transcription factor peptidase, site 2
7769	4,02E-17	1,64E+01	1,46E-17	0,0776	8,5305982	0,66214628	621,34	ZNF226	zinc finger protein 226
23300	9,96E-40	3,90E+01	2,01E-40	0,0497	13,3106006	0,66213958	2481,91	ATMIN	ATM interactor
142686	9,30E-09	8,03E+00	4,52E-09	0,1129	5,8637871	0,6620957	282,5	ASB14	ankyrin repeat and SOCS box containing 14
26108	4,96E-15	1,43E+01	1,92E-15	0,0833	7,9462006	0,66208281	617,43	PYGO1	pygopus family PHD finger 1
105369782	4,29E-02	1,37E+00	3,30E-02	0,3104	2,1323246	0,6618465	32,39	LOC105369	uncharacterized LOC105369782
55762	5,97E-13	1,22E+01	2,47E-13	0,0904	7,3203449	0,6617756	441,21	ZNF701	zinc finger protein 701
112487	1,42E-19	1,88E+01	4,77E-20	0,0721	9,1691433	0,66154292	767,15	DTD2	D-aminoacyl-tRNA deacylase 2
92597	4,49E-29	2,83E+01	1,16E-29	0,0585	11,310473	0,6612668	1852,42	MOB1B	MOB kinase activator 1B
653519	4,58E-22	2,13E+01	1,44E-22	0,0676	9,7753552	0,66106528	1249,53	GPR89A	G protein-coupled receptor 89A
29080	3,53E-40	3,95E+01	7,03E-41	0,0494	13,3887733	0,66094072	2311,91	CCDC59	coiled-coil domain containing 59
5557	1,93E-24	2,37E+01	5,68E-25	0,064	10,3206439	0,66054875	1488,43	PRIM1	DNA primase subunit 1
152137	4,64E-40	3,93E+01	9,29E-41	0,0494	13,3681178	0,66049151	7868,2	CCDC50	coiled-coil domain containing 50
79691	2,44E-30	2,96E+01	6,14E-31	0,0571	11,5657529	0,66048154	1768,14	QTRT2	queuine tRNA-ribosyltransferase accessory subunit 2
257396	1,91E-13	1,27E+01	7,78E-14	0,0883	7,4739779	0,66029727	507,98	MOCS2-DT	MOCS2 divergent transcript
8577	2,04E-06	5,69E+00	1,12E-06	0,1356	4,8691894	0,66010396	184,51	TMEFF1	transmembrane protein with EGF like and two follistatin like domains 1
3231	3,01E-06	5,52E+00	1,66E-06	0,1378	4,7908972	0,65997209	183,61	HOXD1	homeobox D1
25836	1,61E-44	4,38E+01	2,92E-45	0,0467	14,1185127	0,65994049	4412,28	NIPBL	NIPBL cohesin loading factor
178	6,64E-26	2,52E+01	1,88E-26	0,062	10,6430945	0,65986713	1435,64	AGL	amylo-alpha-1, 6-glucosidase, 4-alpha-glucanotransferase
51809	5,00E-37	3,63E+01	1,07E-37	0,0514	12,833292	0,65972877	2900,27	GALNT7	polypeptide N-acetylgalactosaminyltransferase 7
105376037	1,94E-01	7,12E-01	1,64E-01	0,4733	1,3931383	0,65937101	14,86	LOC105376	uncharacterized LOC105376037
55336	1,88E-03	2,73E+00	1,26E-03	0,2045	3,2239112	0,65930005	77,68	FBXL8	F-box and leucine rich repeat protein 8
55105	2,01E-16	1,57E+01	7,43E-17	0,079	8,3399333	0,65921986	711,47	GPATCH2	G-patch domain containing 2
51000	1,42E-22	2,18E+01	4,40E-23	0,0666	9,8944845	0,65893645	1081,02	SLC35B3	solute carrier family 35 member B3
148046	3,17E-02	1,50E+00	2,39E-02	0,2917	2,2580624	0,65860701	39,31	CIRBP-AS1	CIRBP antisense RNA 1
84154	1,35E-39	3,89E+01	2,73E-40	0,0496	13,2877143	0,65860511	2434,72	RPF2	ribosome production factor 2 homolog
284293	1,07E-09	8,97E+00	5,01E-10	0,1059	6,2189124	0,65841805	311,94	HMSD	histocompatibility minor serpin domain containing
3641	1,54E-01	8,12E-01	1,28E-01	0,4321	1,5237096	0,65839387	18,29	INSL4	insulin like 4
80255	1,34E-32	3,19E+01	3,19E-33	0,0548	12,0088472	0,65831944	1747,25	SLC35F5	solute carrier family 35 member F5
344787	4,92E-14	1,33E+01	1,97E-14	0,086	7,652688	0,65802459	489,18	ZNF860	zinc finger protein 860
1740	7,55E-03	2,12E+00	5,35E-03	0,2362	2,7850597	0,65771766	56,31	DLG2	discs large MAGUK scaffold protein 2
4200	1,72E-31	3,08E+01	4,20E-32	0,0558	11,7937957	0,65754397	2063,09	ME2	malic enzyme 2

9774	7,67E-60	5,91E+01	9,85E-61	0,04	16,4402543	0,65734644	9271,38	BCLAF1	BCL2 associated transcription factor 1
7189	4,65E-16	1,53E+01	1,74E-16	0,0798	8,2386093	0,65732386	789,64	TRAF6	TNF receptor associated factor 6
10914	7,93E-70	6,91E+01	8,16E-71	0,0369	17,7919266	0,65728162	11575,12	PAPOLA	poly(A) polymerase alpha
23329	6,17E-07	6,21E+00	3,29E-07	0,1287	5,1061081	0,65710885	208,43	TBC1D30	TBC1 domain family member 30
285282	2,99E-21	2,05E+01	9,58E-22	0,0686	9,5812827	0,65706739	918,71	RABL3	RAB, member of RAS oncogene family like 3
29915	3,71E-17	1,64E+01	1,34E-17	0,0769	8,5399975	0,65704297	726,86	HCFC2	host cell factor C2
414149	1,43E-15	1,48E+01	5,43E-16	0,0811	8,1015146	0,65701379	605,1	ACBD7	acyl-CoA binding domain containing 7
92	6,16E-10	9,21E+00	2,85E-10	0,1041	6,3065724	0,65671331	328,22	ACVR2A	activin A receptor type 2A
105370165	3,00E-03	2,52E+00	2,05E-03	0,213	3,0835345	0,6566812	71,51	LOC105370165	
54861	2,56E-18	1,76E+01	8,96E-19	0,0742	8,8473497	0,65666248	872,89	SNRK	SNF related kinase
51534	4,87E-35	3,43E+01	1,09E-35	0,0527	12,4695655	0,65660315	2524,08	VTA1	vesicle trafficking 1
101929798	3,01E-01	5,21E-01	2,63E-01	0,5859	1,1203046	0,65640017	9,64	PDE4DIPP4	PDE4DIP pseudogene 4
106633814	1,78E-06	5,75E+00	9,73E-07	0,134	4,89712	0,65626234	1861,54	SNORA86	small nucleolar RNA, H/ACA box 86
123872	1,28E-04	3,89E+00	7,82E-05	0,166	3,9499325	0,65585444	116,89	DNAAF1	dynein axonemal assembly factor 1
55014	9,37E-30	2,90E+01	2,39E-30	0,0573	11,4485195	0,6554964	1701,35	STX17	syntaxin 17
55796	1,78E-20	1,97E+01	5,85E-21	0,0698	9,3926663	0,65529172	838,58	MBNL3	muscleblind like splicing regulator 3
6241	5,42E-67	6,63E+01	5,92E-68	0,0376	17,4190039	0,65523711	21239,08	RRM2	ribonucleotide reductase regulatory subunit M2
204010	2,39E-04	3,62E+00	1,50E-04	0,1728	3,7915133	0,65517373	107,86	RPSAP52	ribosomal protein SA pseudogene 52
200844	2,11E-04	3,68E+00	1,31E-04	0,1712	3,8243762	0,65489239	124,01	CFAP20DC	CFAP20 domain containing
246181	1,05E-01	9,79E-01	8,50E-02	0,3798	1,7224565	0,65427424	23,39	AKR7L	aldo-keto reductase family 7 like (gene/pseudogene)
619571	4,71E-09	8,33E+00	2,27E-09	0,1095	5,9775499	0,65425266	368,39	SNORD96A	small nucleolar RNA, C/D box 96A
105375284	6,30E-03	2,20E+00	4,43E-03	0,2298	2,8456067	0,6540615	60,85	LOC105375284	uncharacterized LOC105375284
105376266	5,54E-02	1,26E+00	4,32E-02	0,3235	2,0219186	0,65403708	32,97	LOC105376266	uncharacterized LOC105376266
101060171	4,79E-02	1,32E+00	3,70E-02	0,3136	2,0854599	0,65400119	32,77	ODAD2P1	outer dynein arm docking complex subunit 2 pseudogene 1
8087	9,92E-65	6,40E+01	1,14E-65	0,0382	17,1155848	0,65386339	10010,8	FXR1	FMR1 autosomal homolog 1
105374651	1,62E-08	7,79E+00	7,96E-09	0,1133	5,7692206	0,65379669	263,87	LOC105374651	uncharacterized LOC105374651
27131	6,14E-32	3,12E+01	1,49E-32	0,055	11,8810264	0,65361832	5023,49	SNX5	sorting nexin 5
7707	7,03E-27	2,62E+01	1,94E-27	0,0602	10,8526273	0,65325056	1696,22	ZNF148	zinc finger protein 148
2013	2,11E-44	4,37E+01	3,84E-45	0,0463	14,0991591	0,65319294	3064,44	EMP2	epithelial membrane protein 2
731275	1,86E-02	1,73E+00	1,37E-02	0,2649	2,4656395	0,65313336	44,59	LINC01347	long intergenic non-protein coding RNA 1347
64853	9,62E-33	3,20E+01	2,28E-33	0,0543	12,0365132	0,65311533	3865,26	AIDA	axin interactor, dorsalization associated
5274	6,69E-08	7,17E+00	3,39E-08	0,1183	5,5201365	0,65297405	254,06	SERPINI1	serpin family I member 1
100507419	6,88E-02	1,16E+00	5,44E-02	0,3392	1,9239334	0,65267333	27,1	MMP25-AS1	MMP25 antisense RNA 1
56267	1,77E-19	1,88E+01	5,97E-20	0,0714	9,1448683	0,65249707	1290,23	KYAT3	kynurenine aminotransferase 3
79968	2,51E-36	3,56E+01	5,43E-37	0,0513	12,7066905	0,65247451	2005,08	WDR76	WD repeat domain 76
105377102	4,13E-06	5,38E+00	2,30E-06	0,138	4,7248887	0,65188272	183,11	LOC105377102	uncharacterized LOC105377102
3475	9,65E-26	2,50E+01	2,75E-26	0,0615	10,6076677	0,65184671	2613,16	IFRD1	interferon related developmental regulator 1
26038	2,81E-01	5,51E-01	2,44E-01	0,5595	1,1649329	0,65182896	10,16	CHD5	chromodomain helicase DNA binding protein 5
353497	1,49E-02	1,83E+00	1,09E-02	0,2559	2,5473705	0,65174635	48,68	POLN	DNA polymerase nu
109729161	5,34E-02	1,27E+00	4,16E-02	0,3196	2,0376586	0,65123851	31,08	LNCSRLR	lncRNA sorafenib resistance in renal cell carcinoma associated
1739	3,87E-64	6,34E+01	4,49E-65	0,0382	17,0353703	0,65111148	9992,74	DLG1	discs large MAGUK scaffold protein 1
55795	2,72E-32	3,16E+01	6,53E-33	0,0545	11,9495625	0,65089634	1638,24	PCID2	PCI domain containing 2
222643	5,10E-03	2,29E+00	3,55E-03	0,223	2,9152584	0,64996032	75,26	UNC5CL	unc-5 family C-terminal like
112268260	5,88E-02	1,23E+00	4,60E-02	0,3257	1,9954403	0,64988159	29,12	LOC112268260	uncharacterized LOC112268260
65078	2,89E-01	5,39E-01	2,51E-01	0,566	1,1482299	0,64986674	9,46	RTN4R	reticulon 4 receptor
51167	1,20E-25	2,49E+01	3,42E-26	0,0614	10,5870932	0,64985445	1449,29	CYB5R4	cytochrome b5 reductase 4
102724881	2,23E-01	6,52E-01	1,90E-01	0,4953	1,3111668	0,6494203	12,74	LOC102724881	
10910	1,34E-31	3,09E+01	3,26E-32	0,055	11,8150933	0,6494018	2115,7	SUGT1	SGT1 homolog, MIS12 kinetochore complex assembly cochaperone
284900	1,36E-08	7,87E+00	6,66E-09	0,112	5,7992944	0,64929415	275,11	TTC28-AS1	TTC28 antisense RNA 1
100996419	2,47E-02	1,61E+00	1,84E-02	0,2754	2,3565062	0,649032	41,83	MRNIP-DT	MRNIP divergent transcript
10558	3,33E-46	4,55E+01	5,78E-47	0,0451	14,3923047	0,64878666	3728,5	SPTLC1	serine palmitoyltransferase long chain base subunit 1
402483	4,69E-19	1,83E+01	1,60E-19	0,0718	9,037563	0,64876893	797,44	LINC01000	long intergenic non-protein coding RNA 1000
154089	3,25E-01	4,88E-01	2,86E-01	0,6079	1,0670193	0,64864805	8,87	LINC01312	long intergenic non-protein coding RNA 1312
168090	2,15E-01	6,68E-01	1,83E-01	0,4868	1,331839	0,64831608	14,21	C6orf118	chromosome 6 open reading frame 118
388115	2,29E-48	4,76E+01	3,77E-49	0,044	14,7362537	0,6481333	4161,17	CCDC9B	coiled-coil domain containing 9B
414241	1,02E-04	3,99E+00	6,22E-05	0,1619	4,0044641	0,64812315	122,08	SHLD2P1	shieldin complex subunit 2 pseudogene 1
55213	1,04E-22	2,20E+01	3,19E-23	0,0653	9,9265608	0,64808761	1029,16	RCBTB1	RCC1 and BTB domain containing protein 1
91860	7,04E-08	7,15E+00	3,57E-08	0,1176	5,51094	0,64806724	253,06	CALML4	calmodulin like 4
115560	7,13E-08	7,15E+00	3,61E-08	0,1176	5,5087432	0,64801618	248,81	ZNF501	zinc finger protein 501
105373265	2,65E-01	5,77E-01	2,29E-01	0,5382	1,2037505	0,64788802	10,61	LOC105373265	uncharacterized LOC105373265
10890	4,29E-52	5,14E+01	6,50E-53	0,0423	15,310566	0,64785266	7521,85	RAB10	RAB10, member RAS oncogene family
441457	1,86E-01	7,30E-01	1,57E-01	0,4574	1,4158836	0,64762117	15,48	NUTM2G	NUT family member 2G
153684	2,32E-02	1,63E+00	1,72E-02	0,2718	2,3817742	0,64746139	42,8	ANXA2R-AS	ANXA2R antisense RNA 1
57679	7,07E-29	2,82E+01	1,84E-29	0,0574	11,2700857	0,64736497	1535,1	ALS2	alsin Rho guanine nucleotide exchange factor ALS2
115548	2,01E-29	2,87E+01	5,19E-30	0,0569	11,3812475	0,64713225	1506,63	FCHO2	FCH and mu domain containing endocytic adaptor 2
10466	1,20E-26	2,59E+01	3,34E-27	0,0599	10,8028843	0,64687178	1978,93	COG5	component of oligomeric golgi complex 5
54943	1,61E-03	2,79E+00	1,07E-03	0,1978	3,2706496	0,64684318	102,72	DNAJC28	DnaJ heat shock protein family (Hsp40) member C28
154091	5,86E-05	4,23E+00	3,50E-05	0,1563	4,1384513	0,64680027	137,02	SLC2A12	solute carrier family 2 member 12
260294	1,15E-06	5,94E+00	6,24E-07	0,1298	4,983553	0,64675133	200,44	NSUN5P2	NSUN5 pseudogene 2
22943	8,46E-51	5,01E+01	1,32E-51	0,0428	15,1136943	0,64667961	8816,15	DKK1	dickkopf WNT signaling pathway inhibitor 1
84033	5,73E-04	3,24E+00	3,69E-04	0,1816	3,5610336	0,6465477	97,95	OBSCN	obscurin, cytoskeletal calmodulin and titin-interacting RhoGEF
401588	7,21E-10	9,14E+00	3,35E-10	0,1029	6,2818482	0,64648462	332,01	ZNF674-AS1	ZNF674 antisense RNA 1 (head to head)
100130887	1,31E-01	8,83E-01	1,08E-01	0,4018	1,6089069	0,64638206	20,05	ATE1-AS1	ATE1 antisense RNA 1
728262	1,47E-07	6,83E+00	7,56E-08	0,1202	5,3772904	0,64624176	254,55	FAM157A	family with sequence similarity 157 member A
55142	6,83E-27	2,62E+01	1,88E-27	0,0595	10,8553679	0,64622553	1900,85	HAUS2	HAUS augmin like complex subunit 2
8545	2,36E-37	3,66E+01	5,01E-38	0,0501	12,8916939	0,64611185	4169,95	CGGBP1	CGG triplet repeat binding protein 1
85458	5,90E-08	7,23E+00	2,98E-08	0,1166	5,5425713	0,64604437	288,77	DIXDC1	DIX domain containing 1
23271	9,06E-42	4,10E+01	1,75E-42	0,0473	13,6604413	0,64603191	4340,87	CAMSAP2	calmodulin regulated spectrin associated protein family member 2
4289	3,27E-36	3,55E+01	7,12E-37	0,0509	12,6854152	0,64595009	2381,58	MKLN1	muskelin 1
10190	1,34E-33	3,29E+01	3,13E-34	0,0529	12,1995377	0,64588527	3312,99	TXNDC9	thioredoxin domain containing 9
23545	3,38E-38	3,75E+01	7,04E-39	0,0495	13,0422359	0,64575391	2602,4	ATP6V0A2	ATPase H+ transporting V0 subunit a2
441394	5,97E-03	2,22E+00	4,19E-03	0,2255	2,8632506	0,64572378	62,94	SUGT1P1	SUGT1 pseudogene 1
7539	2,69E-07	6,57E+00	1,40E-07	0,1226	5,2649947	0,64568882	226,4	ZFP37	ZFP37 zinc finger protein
79621	1,05E-11	1,10E+01	4,55E-12	0,0933	6,918912	0,64566987	871,01	RNASEH2B	ribonuclease H2 subunit B
6397	5,29E-53	5,23E+01	7,89E-54	0,0418	15,4471462	0,64538999	7833,67	SEC14L1	SEC14 like lipid binding 1
151507	3,15E-21	2,05E+01	1,01E-21	0,0674	9,5755859	0,64515149	977,05	MSL3P1	MSL complex subunit 3 pseudogene 1
199704	1,02E-15	1,50E+01	3,87E-16	0,0792	8,1424462	0,6450243	610,37	ZNF585A	zinc finger protein 585A
23244	4,10E-58	5,74E+01	5,46E-59	0,0398	16,1951074	0,64490472	8214,78	PDS5A	PDS5 cohesin associated factor A
11077	1,68E-05	4,77E+00	9,74E-06	0,1458	4,4229419	0,64489032	153,79	HSF2BP	heat shock transcription factor 2 binding protein
8028	6,08E-32	3,12E+01	1,47E-32	0,0542	11,8818834	0,64449992	1817,13	MLLT10	MLLT10 histone lysine methyltransferase DOT1L cofactor
79161	2,11E-13	1,27E+01	8,59E-14	0,0864	7,4609571	0,64437879	502,78	TMEM243	transmembrane protein 243
7153	1,98E-68	6,77E+01	2,09E-69	0,0366	17,6092477	0,6443494	42101,86	TOP2A	DNA topoisomerase II alpha
64283	2,20E-51	5,07E+01	3,37E-52	0,0424	15,2031253	0,64404302	6283,95	ARHGEF28	Rho guanine nucleotide exchange factor 28
57456	6,73E-42	4,12E+01	1,29E-42	0,047	13,6823903	0,6437248	2886,73	KIAA1143	KIAA1143
8504	2,28E-22	2,16E+01	7,08E-23	0,0653	9,8467202	0,64340708	1142,15	PEX3	peroxisomal biogenesis factor 3
55296	2,66E-06	5,58E+00	1,47E-06	0,1336	4,8159057	0,64329276	191,13	TBC1D19	TBC1 domain family member 19
100507564	1,64E-01	7,85E-01	1,37E-01	0,4324	1,4872488	0,64304738	17,49	MAGOH-DT	MAGOH divergent transcript
105371993	2,07E-02	1,68E+00	1,53E-02	0,2649	2,4258392	0,64250964	45,82	LOC105371993	uncharacterized LOC105371993
91523	8,32E-05	4,08E+00	5,02E-05	0,1584	4,0545876	0,642415	127,87	PCED1B	PC-esterase domain containing 1B
112267915	2,74E-01	5,62E-01	2,37E-01	0,5427	1,1833747	0,64221876	10,93	LOC112267915	uncharacterized LOC112267915
51602	7,12E-51	5,01E+01	1,11E-51	0,0425	15,1251415	0,64216603	6116,9	NOP58	NOP58 ribonucleoprotein
9779	6,44E-35	3,42E+01	1,45E-35	0,0516	12,4472432	0,64215582	1935,75	TBC1D5	TBC1 domain family member 5
53938	4,57E-24	2,33E+01	1,36E-24	0,0627	10,2366326	0,64191018	1076,13	PPIL3	peptidylprolyl isomerase like 3
728888	2,62E-04	3,58E+00	1,64E-04	0,1703	3,7684598	0,64167839	111,28	NPIPB11	nuclear pore complex interacting protein family member B11
7095	8,89E-33	3,21E+01	2,11E-33	0,0533	12,0431244	0,64166097	5815,54	SEC62	SEC62 homolog, preprotein translocation factor
105376615	7,47E-04	3,13E+00	4,86E-04	0,1839	3,4884952	0,641575	93,12	LOC105376615	uncharacterized LOC105376615
91298	3,41E-26	2,55E+01	9,58E-27	0,0599	10,7056292	0,64138053	1494,01	C12orf29	chromosome 12 open reading frame 29
80071	1,75E-17	1,68E+01	6,28E-18	0,0742	8,627405	0,64057991	725,61	CCDC15	coiled-coil domain containing 15
101926969	1,15E-02	1,94E+00	8,30E-03	0,2426	2,6395279	0,64042408	53,26	LOC101926969	
692093	2,23E-02	1,65E+00	1,66E-02	0,2672	2,3964077	0,64029067	50,99	SNORD62B	small nucleolar RNA, C/D box 62B
84870	1,89E-01	7,24E-01	1,59E-01	0,4548	1,4077932	0,64027567	14,8	RSPO3	R-spondin 3
343990	7,00E-02	1,15E+00	5,53E-02	0,3341	1,9162192	0,64027096	28,99	CRACDL	CRACD like
102724329	3,34E-01	4,76E-01	2,94E-01	0,6099	1,0494607	0,64010877	8,47	ATF6-DT	ATF6 divergent transcript
105375913	2,38E-01	6,23E-01	2,04E-01	0,5038	1,2704658	0,64006963	12,12	LOC105375913	uncharacterized LOC105375913
100505876	3,62E-31	3,04E+01	8,93E-32	0,0545	11,7301307	0,63986435	2160,24	CEBPZOS	CEBPZ opposite strand
10526	3,09E-37	3,65E+01	6,57E-38	0,0497	12,8708566	0,63963814	3156,18	IPO8	importin 8
107985869	3,38E-01	4,71E-01	2,98E-01	0,6146	1,0405709	0,63957702	8,4	LOC107985869	uncharacterized LOC107985869
5782	2,88E-61	6,05E+01	3,58E-62	0,0384	16,6398943	0,63954515	10479,86	PTPN12	protein tyrosine phosphatase non-receptor type 12
29902	2,50E-25	2,46E+01	7,18E-26	0,0608	10,517394	0,63950418	1305,24	FAM216A	family with sequence similarity 216 member A
27032	5,69E-37	3,62E+01	1,22E-37	0,0499	12,8230996	0,63947896	4555,96	ATP2C1	ATPase secretory pathway Ca2+ transporting 1

440354	1,20E-07	6,92E+00	6,15E-08	0,1181	5,4143995	0,63942884	294,23	SMG1P2	SMG1 pseudogene 2
375611	1,82E-03	2,74E+00	1,22E-03	0,1977	3,2336081	0,63935971	85,98	SLC26A5	solute carrier family 26 member 5
5810	1,43E-32	3,18E+01	3,41E-33	0,0533	12,0033956	0,63935662	2096,87	RAD1	RAD1 checkpoint DNA exonuclease
80095	2,16E-08	7,67E+00	1,07E-08	0,1117	5,7194177	0,63860883	287,52	ZNF606	zinc finger protein 606
133686	2,80E-20	1,96E+01	9,22E-21	0,0683	9,3446017	0,63839352	972,92	NADK2	NAD kinase 2, mitochondrial
8507	3,58E-60	5,94E+01	4,57E-61	0,0387	16,486751	0,63828164	8503,91	ENC1	ectodermal-neural cortex 1
56034	4,28E-40	3,94E+01	8,56E-41	0,0477	13,3742125	0,63810547	3085,09	PDGFC	platelet derived growth factor C
3091	3,04E-58	5,75E+01	4,03E-59	0,0394	16,213786	0,63809235	17159,62	HIF1A	hypoxia inducible factor 1 subunit alpha
1047	7,52E-28	2,71E+01	2,02E-28	0,0577	11,0573259	0,63808865	2486,87	CLGN	calmegin
10054	3,16E-45	4,45E+01	5,62E-46	0,0448	14,2342375	0,63798175	5332,58	UBA2	ubiquitin like modifier activating enzyme 2
55206	3,40E-44	4,35E+01	6,21E-45	0,0454	14,0652767	0,63794437	6920,73	SBNO1	strawberry notch homolog 1
23251	5,22E-05	4,28E+00	3,11E-05	0,1531	4,1655516	0,63790491	158,81	MINAR1	membrane integral NOTCH2 associated receptor 1
595101	9,47E-08	7,02E+00	4,84E-08	0,1169	5,4571274	0,63790425	264,16	SMG1P5	SMG1 pseudogene 5
653268	3,51E-03	2,45E+00	2,41E-03	0,2101	3,0347647	0,63770897	72,59	AGAP7P	ArfGAP with GTPase domain, ankyrin repeat and PH domain 7, pseudogene
729737	8,58E-13	1,21E+01	3,57E-13	0,0877	7,2709308	0,63755273	519,45	LOC729737	uncharacterized LOC729737
93145	2,17E-01	6,64E-01	1,85E-01	0,4804	1,3269473	0,63750189	14,66	OLFM2	olfactomedin 2
7568	6,33E-05	4,20E+00	3,79E-05	0,1546	4,1201508	0,63715749	139,22	ZNF20	zinc finger protein 20
10923	5,73E-23	2,22E+01	1,75E-23	0,0638	9,986031	0,63714843	7532,6	SUB1	SUB1 regulator of transcription
11017	4,08E-24	2,34E+01	1,21E-24	0,0621	10,2476027	0,63671531	1539,1	SNRNP27	small nuclear ribonucleoprotein U4/U6.U5 subunit 27
171177	6,56E-02	1,18E+00	5,16E-02	0,3271	1,9461933	0,63659225	29,01	RHOV	ras homolog family member V
101927703	9,17E-02	1,04E+00	7,36E-02	0,3558	1,7889091	0,63658027	24,7	FOXCUT	FOXC1 upstream transcript
8555	4,61E-29	2,83E+01	1,20E-29	0,0563	11,308147	0,63627016	1556,16	CDC14B	cell division cycle 14B
100288842	5,65E-13	1,22E+01	2,34E-13	0,0868	7,3278127	0,6362609	479,82	B3GALT9	beta-1,3-galactosyltransferase 9
85315	5,42E-09	8,27E+00	2,61E-09	0,1068	5,9541837	0,63601629	357,16	PAQR8	progestin and adipoQ receptor family member 8
1176	2,40E-25	2,46E+01	6,91E-26	0,0604	10,5210649	0,6358734	3343,79	AP3S1	adaptor related protein complex 3 subunit sigma 1
5357	4,69E-28	2,73E+01	1,25E-28	0,0573	11,1001436	0,63578995	1783,93	PLS1	plastin 1
79886	6,18E-24	2,32E+01	1,84E-24	0,0623	10,2070067	0,63577413	1255,01	CAAP1	caspase activity and apoptosis inhibitor 1
105375532	3,56E-01	4,49E-01	3,15E-01	0,6332	1,0037532	0,63559314	7,93	LOC105375	uncharacterized LOC105375532
79819	2,86E-01	5,44E-01	2,48E-01	0,5504	1,1547109	0,63551085	10,02	DNAI4	dynein axonemal intermediate chain 4
54852	1,54E-17	1,68E+01	5,50E-18	0,0735	8,6424089	0,63536433	884,33	PAQR5	progestin and adipoQ receptor family member 5
55786	5,13E-08	7,29E+00	2,58E-08	0,1141	5,5676367	0,63518229	265,65	ZNF415	zinc finger protein 415
80254	3,17E-31	3,05E+01	7,80E-32	0,0541	11,7415759	0,63498867	1692,74	CEP63	centrosomal protein 63
80746	2,87E-19	1,85E+01	9,75E-20	0,0698	9,0917388	0,6349379	825,57	TSEN2	tRNA splicing endonuclease subunit 2
120526	3,30E-18	1,75E+01	1,16E-18	0,072	8,8188416	0,63464199	971,2	DNAJC24	DnaJ heat shock protein family (Hsp40) member C24
23554	1,11E-07	6,95E+00	5,69E-08	0,1169	5,428171	0,63462827	244,73	TSPAN12	tetraspanin 12
2624	1,18E-11	1,09E+01	5,12E-12	0,0919	6,9022311	0,63462067	436,73	GATA2	GATA binding protein 2
7541	1,11E-13	1,30E+01	4,49E-14	0,084	7,545928	0,63408734	512,12	ZBTB14	zinc finger and BTB domain containing 14
148362	4,22E-26	2,54E+01	1,19E-26	0,0593	10,6856193	0,63404368	2188,56	BROX	BRO1 domain and CAAX motif containing
157313	2,30E-36	3,56E+01	4,98E-37	0,0498	12,7133742	0,63354682	2593,53	CDCA2	cell division cycle associated 2
5868	3,49E-49	4,85E+01	5,64E-50	0,0426	14,8641145	0,63352174	4838,42	RAB5A	RAB5A, member RAS oncogene family
64400	6,02E-21	2,02E+01	1,95E-21	0,0666	9,5076025	0,63335278	927,76	AKTIP	AKT interacting protein
729082	2,18E-38	3,77E+01	4,52E-39	0,0484	13,0759494	0,63313958	3061,54	OIP5-AS1	OIP5 antisense RNA 1
100289019	7,53E-04	3,12E+00	4,90E-04	0,1815	3,4864219	0,63272499	97,22	SLC25A25-A	SLC25A25 antisense RNA 1
103695435	3,22E-01	4,92E-01	2,83E-01	0,5894	1,0734513	0,63269633	8,87	BBOX1-AS1	BBOX1 antisense RNA 1
84503	1,27E-08	7,90E+00	6,24E-09	0,1089	5,8102499	0,63255849	319,32	ZNF527	zinc finger protein 527
728819	2,76E-03	2,56E+00	1,88E-03	0,2034	3,1090055	0,63223375	80,73	C1GALT1C1	C1GALT1 specific chaperone 1 like
342931	1,38E-07	6,86E+00	7,08E-08	0,1173	5,389147	0,63222066	256,26	RFPL4A	ret finger protein like 4A
102724488	2,28E-03	2,64E+00	1,54E-03	0,1995	3,1668989	0,63192739	79,71	SYT15B	synaptotagmin 15B
51592	5,85E-39	3,82E+01	1,20E-39	0,048	13,1763651	0,63186643	3495,98	TRIM33	tripartite motif containing 33
28981	1,09E-18	1,80E+01	3,75E-19	0,0706	8,9441632	0,6317764	901,03	IFT81	intraflagellar transport 81
57539	5,34E-38	3,73E+01	1,12E-38	0,0486	13,0069595	0,63175928	2975,47	WDR35	WD repeat domain 35
54058	1,02E-13	1,30E+01	4,12E-14	0,0836	7,5570907	0,6316843	575,97	C21orf58	chromosome 21 open reading frame 58
89790	3,24E-01	4,89E-01	2,84E-01	0,5897	1,0710575	0,63160774	9,53	SIGLEC10	sialic acid binding Ig like lectin 10
23596	3,39E-11	1,05E+01	1,49E-11	0,0935	6,7486441	0,63124266	403,33	OPN3	opsin 3
7357	5,09E-30	2,93E+01	1,29E-30	0,0549	11,5017926	0,63112817	4766,81	UGCG	UDP-glucose ceramide glucosyltransferase
100130357	1,29E-01	8,89E-01	1,06E-01	0,3898	1,6176811	0,63064435	21,05	LOC100130	uncharacterized LOC100130357
105369315	1,04E-01	9,83E-01	8,39E-02	0,3649	1,7282897	0,63057693	24,19	LOC105369	uncharacterized LOC105369315
10257	2,48E-28	2,76E+01	6,56E-29	0,0565	11,1577528	0,63044732	1765,48	ABCC4	ATP binding cassette subfamily C member 4
100996442	1,05E-02	1,98E+00	7,57E-03	0,236	2,6706623	0,63029804	56,85	LOC100996	WAS protein family homolog 2-like
101928076	2,98E-05	4,53E+00	1,75E-05	0,1467	4,2947565	0,63004444	161,65	DSP-AS1	DSP antisense RNA 1
101927761	3,12E-04	3,51E+00	1,97E-04	0,1692	3,7231331	0,63000267	118,05	TH2LCRR	T helper type 2 locus control region associated RNA
11116	3,48E-24	2,35E+01	1,03E-24	0,0614	10,2631959	0,62996414	1281,86	CEP43	centrosomal protein 43
91392	4,12E-08	7,39E+00	2,07E-08	0,1123	5,606448	0,62984203	297,25	ZNF502	zinc finger protein 502
57509	7,48E-19	1,81E+01	2,57E-19	0,0701	8,9857343	0,62967028	841,7	MTUS1	microtubule associated scaffold protein 1
55133	7,66E-29	2,81E+01	2,00E-29	0,0559	11,2630305	0,62964452	1776,43	SRBD1	S1 RNA binding domain 1
79829	1,11E-25	2,50E+01	3,15E-26	0,0594	10,594833	0,62963343	1396,54	NAA40	N-alpha-acetyltransferase 40, NatD catalytic subunit
4038	1,25E-09	8,90E+00	5,87E-10	0,1017	6,1939512	0,62961632	357,35	LRP4	LDL receptor related protein 4
65117	1,11E-27	2,70E+01	3,00E-28	0,0571	11,0217085	0,62955796	7693,61	RSRC2	arginine and serine rich coiled-coil 2
7442	2,44E-06	5,61E+00	1,34E-06	0,1301	4,8339033	0,62900795	199,57	TRPV1	transient receptor potential cation channel subfamily V member 1
3953	1,40E-11	1,09E+01	6,07E-12	0,0914	6,8778973	0,62897866	451,66	LEPR	leptin receptor
990	1,43E-46	4,58E+01	2,46E-47	0,0435	14,4513779	0,62875124	6237,56	CDC6	cell division cycle 6
5172	3,18E-02	1,50E+00	2,40E-02	0,2786	2,2566036	0,6287293	42,05	SLC26A4	solute carrier family 26 member 4
23484	1,13E-26	2,59E+01	3,14E-27	0,0582	10,8084763	0,62863599	1375,88	LEPROTL1	leptin receptor overlapping transcript like 1
124540	1,81E-33	3,27E+01	4,23E-34	0,0516	12,1748787	0,62843627	1941,87	MSI2	musashi RNA binding protein 2
222234	4,73E-07	6,33E+00	2,50E-07	0,1218	5,1574563	0,62811429	246,49	FAM185A	family with sequence similarity 185 member A
5520	5,36E-27	2,63E+01	1,47E-27	0,0577	10,8777367	0,62810646	3286,77	PPP2R2A	protein phosphatase 2 regulatory subunit Balpha
57551	6,33E-46	4,52E+01	1,11E-46	0,0438	14,3473777	0,62788319	5927,41	TAOK1	TAO kinase 1
9113	1,69E-28	2,78E+01	4,47E-29	0,0561	11,1919412	0,62764863	1490,6	LATS1	large tumor suppressor kinase 1
105370274	1,15E-01	9,39E-01	9,40E-02	0,3747	1,6748216	0,62759435	22,55	LOC105370	uncharacterized LOC105370274
55205	9,17E-31	3,00E+01	2,28E-31	0,0538	11,6503597	0,62724958	1762,27	ZNF532	zinc finger protein 532
55297	1,17E-19	1,89E+01	3,94E-20	0,0682	9,1897324	0,62715781	999,48	CCDC91	coiled-coil domain containing 91
54520	1,44E-29	2,88E+01	3,70E-30	0,0549	11,4106226	0,62696993	2567,06	CCDC93	coiled-coil domain containing 93
128346	2,16E-04	3,67E+00	1,34E-04	0,1642	3,8181853	0,62693374	118,21	C1orf162	chromosome 1 open reading frame 162
107983979	3,77E-02	1,42E+00	2,88E-02	0,2866	2,1867867	0,62672753	37,59	LOC107983	979
63915	1,44E-15	1,48E+01	5,50E-16	0,0774	8,0999581	0,6266244	661,84	BLOC1S5	biogenesis of lysosomal organelles complex 1 subunit 5
60481	3,94E-50	4,94E+01	6,23E-51	0,0417	15,0108611	0,62633739	10093,55	ELOVL5	ELOVL fatty acid elongase 5
105378645	3,02E-01	5,20E-01	2,64E-01	0,5605	1,1171098	0,62611933	9,88	TFAP2E-AS1	TFAP2E antisense RNA 1
692201	2,24E-18	1,76E+01	7,80E-19	0,0706	8,862804	0,62609871	976	SNORD86	small nucleolar RNA, C/D box 86
54542	2,79E-40	3,96E+01	5,55E-41	0,0467	13,4063553	0,62594692	4143,76	RC3H2	ring finger and CCCH-type domains 2
11215	7,40E-33	3,21E+01	1,75E-33	0,0519	12,0583761	0,6258915	2757,25	AKAP11	A-kinase anchoring protein 11
7037	1,61E-39	3,88E+01	3,27E-40	0,0472	13,2741365	0,62587866	19738,37	TFRC	transferrin receptor
25827	3,46E-13	1,25E+01	1,42E-13	0,0846	7,394517	0,62581493	535,3	FBXL2	F-box and leucine rich repeat protein 2
105379395	2,90E-02	1,54E+00	2,18E-02	0,2727	2,2936391	0,62549967	41,75	LOC105379	uncharacterized LOC105379395
132660	2,55E-28	2,76E+01	6,77E-29	0,0561	11,1549285	0,62538567	1804,58	LIN54	lin-54 DREAM MuvB core complex component
56938	3,00E-47	4,65E+01	5,08E-48	0,043	14,559531	0,62533833	4191,2	BMAL2	basic helix-loop-helix ARNT like 2
642475	7,74E-05	4,11E+00	4,66E-05	0,1535	4,0720572	0,62524857	172,97	MROH6	maestro heat like repeat family member 6
80022	2,72E-02	1,57E+00	2,03E-02	0,2694	2,3198528	0,62499983	42,87	MYO15B	myosin XVB
80204	6,86E-33	3,22E+01	1,62E-33	0,0518	12,0646955	0,62494226	3752,76	FBXO11	F-box protein 11
105372165	1,99E-02	1,70E+00	1,47E-02	0,2561	2,4401471	0,62488127	47,96	LOC105372	uncharacterized LOC105372165
105378973	5,42E-07	6,27E+00	2,88E-07	0,1218	5,1311342	0,62487264	232,47	LOC105378	uncharacterized LOC105378973
6917	5,11E-43	4,23E+01	9,59E-44	0,045	13,8703174	0,62479896	4651,4	TCEA1	transcription elongation factor A1
100873941	9,21E-07	6,04E+00	4,95E-07	0,1243	5,0282607	0,62476637	222,68	OPA1-AS1	OPA1 antisense RNA 1
84210	2,31E-01	6,36E-01	1,97E-01	0,4848	1,2887659	0,62476525	13,03	ANKRD20A1	ankyrin repeat domain 20 family member A1
84060	1,74E-12	1,18E+01	7,32E-13	0,087	7,173309	0,62442698	522,63	RBM48	RNA binding motif protein 48
7746	7,41E-15	1,41E+01	2,89E-15	0,0791	7,895658	0,62440514	894,97	ZSCAN9	zinc finger and SCAN domain containing 9
9488	1,20E-08	7,92E+00	5,86E-09	0,1073	5,820753	0,6243187	402,82	PIGB	phosphatidylinositol glycan anchor biosynthesis class B
10307	9,45E-10	9,02E+00	4,41E-10	0,1	6,2387798	0,62396324	349,78	APBB3	amyloid beta precursor protein binding family B member 3
54536	5,18E-19	1,83E+01	1,77E-19	0,0691	9,026668	0,62391069	881,54	EXOC6	exocyst complex component 6
22900	8,31E-19	1,81E+01	2,86E-19	0,0695	8,9740293	0,6236119	893,94	CARD8	caspase recruitment domain family member 8
93134	9,47E-28	2,70E+01	2,55E-28	0,0564	11,036425	0,62263413	1841,77	ZNF561	zinc finger protein 561
79901	1,12E-31	3,10E+01	2,72E-32	0,0526	11,8304984	0,6225172	3398,78	CYBRD1	cytochrome b reductase 1
51574	3,37E-33	3,25E+01	7,91E-34	0,0513	12,1236612	0,62238243	3332,62	LARP7	La ribonucleoprotein 7, transcriptional regulator
10200	8,85E-24	2,31E+01	2,65E-24	0,0612	10,1716955	0,62235107	1630,1	MPHOSPH6	M-phase phosphoprotein 6
64841	2,40E-37	3,66E+01	5,10E-38	0,0483	12,8904056	0,62215779	5427,71	GNPNAT1	glucosamine-phosphate N-acetyltransferase 1
144535	5,34E-02	1,27E+00	4,16E-02	0,3053	2,0374587	0,6220785	34,95	CFAP54	cilia and flagella associated protein 54
22795	5,44E-02	1,26E+00	4,24E-02	0,3064	2,029461	0,62174802	34,29	NID2	nidogen 2
56660	1,14E-02	1,94E+00	8,24E-03	0,2353	2,6419909	0,6216592	58,54	KCNK12	potassium two pore domain channel subfamily K member 12
653489	2,26E-04	3,65E+00	1,41E-04	0,1633	3,8065915	0,6215202	120,98	RGPD3	RANBP2 like and GRIP domain containing 3
29922	4,04E-23	2,24E+01	1,23E-23	0,062	10,0211113	0,62132647	1924,42	NME7	NME/NM23 family member 7
7587	2,63E-29	2,86E+01	6,78E-30	0,0547	11,3577802	0,62130029	1662,66	ZNF37A	zinc finger protein 37A

79801	4,06E-35	3,44E+01	9,10E-36	0,0498	12,4842167	0,62120519	3706,55	SHCBP1	SHC binding and spindle associated 1
3600	4,57E-04	3,34E+00	2,92E-04	0,1715	3,6223355	0,62105629	109,91	IL15	interleukin 15
54941	1,20E-05	4,92E+00	6,91E-06	0,1381	4,4965749	0,62086331	176,7	RNF125	ring finger protein 125
105370956	2,39E-01	6,22E-01	2,04E-01	0,4888	1,2689658	0,62031649	12,99	LOC105370	uncharacterized LOC105370956
100128386	5,64E-02	1,25E+00	4,40E-02	0,3081	2,0136731	0,62031493	32,34	ARHGAP42-	ARHGAP42 antisense RNA 1
9841	7,05E-14	1,32E+01	2,83E-14	0,0815	7,605783	0,61981349	650,4	ZBTB24	zinc finger and BTB domain containing 24
51727	2,09E-32	3,17E+01	4,99E-33	0,0518	11,9718133	0,61979753	7475,93	CMPK1	cytidine/uridine monophosphate kinase 1
110117499	4,33E-10	9,36E+00	1,99E-10	0,0974	6,3621138	0,61962872	378,45	P3R3URF-PI	P3R3URF-PIK3R3 readthrough
9522	4,10E-20	1,94E+01	1,36E-20	0,0666	9,3035971	0,61959008	1633,06	SCAMP1	secretory carrier membrane protein 1
1057	3,15E-01	5,02E-01	2,77E-01	0,5693	1,0882019	0,6194832	9,39	CELP	carboxyl ester lipase pseudogene
6745	3,12E-46	4,55E+01	5,42E-47	0,043	14,3968301	0,61940123	15488,86	SSR1	signal sequence receptor subunit 1
1203	1,38E-16	1,59E+01	5,09E-17	0,0739	8,3847035	0,61936966	807,39	CLN5	CLN5 intracellular trafficking protein
29883	1,46E-36	3,58E+01	3,15E-37	0,0486	12,7491074	0,61899422	3775,51	CNOT7	CCR4-NOT transcription complex subunit 7
349114	1,54E-05	4,81E+00	8,88E-06	0,1393	4,4427995	0,61892563	181,59	LINC00265	long intergenic non-protein coding RNA 265
100529241	1,18E-33	3,29E+01	2,74E-34	0,0507	12,2101806	0,61890752	4681,55	HSPE1-MOE	HSPE1-MOB4 readthrough
4563	2,27E-08	7,64E+00	1,12E-08	0,1083	5,7111226	0,61872026	341,45	TRNG	tRNA-Gly
8910	2,59E-28	2,76E+01	6,88E-29	0,0555	11,1535617	0,61852	2307,03	SGCE	sarcoglycan epsilon
7068	1,47E-07	6,83E+00	7,57E-08	0,115	5,377023	0,61844099	255,69	THRB	thyroid hormone receptor beta
220869	2,07E-20	1,97E+01	6,78E-21	0,0659	9,3770658	0,61800788	1082,5	ZNG1E	Zn regulated GTPase metalloprotein activator 1E
653464	1,29E-28	2,79E+01	3,38E-29	0,0551	11,2166257	0,61774289	1787,67	SRGAP2C	SLIT-ROBO Rho GTPase activating protein 2C
3638	3,04E-23	2,25E+01	9,21E-24	0,0615	10,0497527	0,6177163	1315,68	INSIG1	insulin induced gene 1
107985404	6,75E-04	3,17E+00	4,37E-04	0,1756	3,5166341	0,61747174	107,5	LOC107985	uncharacterized LOC107985404
79573	2,01E-31	3,07E+01	4,92E-32	0,0524	11,7805653	0,61739005	2846,5	TTC13	tetratricopeptide repeat domain 13
105374773	2,92E-01	5,35E-01	2,54E-01	0,5409	1,1411352	0,6172726	10,38	LOC105374	uncharacterized LOC105374773
26816	2,31E-01	6,36E-01	1,97E-01	0,4787	1,2892158	0,61717089	13,61	SNORD35A	small nucleolar RNA, C/D box 35A
161582	2,92E-03	2,53E+00	1,99E-03	0,1996	3,0916599	0,61699876	79,83	DNAAF4	dynein axonemal assembly factor 4
122830	7,39E-16	1,51E+01	2,79E-16	0,0754	8,1822328	0,61690196	1113,5	NAA30	N-alpha-acetyltransferase 30, NatC catalytic subunit
105375213	1,49E-02	1,83E+00	1,09E-02	0,2422	2,5468009	0,61689909	54,04	LOC105375	213
26235	1,72E-15	1,48E+01	6,57E-16	0,0763	8,0782456	0,61649358	842,67	FBXL4	F-box and leucine rich repeat protein 4
1123	8,56E-16	1,51E+01	3,23E-16	0,0755	8,1642872	0,61645592	675,6	CHN1	chimerin 1
170688	1,65E-14	1,38E+01	6,51E-15	0,0791	7,7937071	0,61644286	652,22	NUDT4P2	nudix hydrolase 4 pseudogene 2
574036	3,15E-07	6,50E+00	1,65E-07	0,1177	5,2349248	0,61639177	263,58	SERTAD4-AS	SERTAD4 antisense RNA 1
100874094	2,56E-01	5,92E-01	2,21E-01	0,5029	1,2246458	0,61592652	12,38	ZNF197-AS1	ZNF197 antisense RNA 1
93166	2,55E-02	1,59E+00	1,90E-02	0,2625	2,3452885	0,61569384	48,95	PRDM6	PR/SET domain 6
10672	6,81E-25	2,42E+01	1,98E-25	0,059	10,4214984	0,61535613	4242,89	GNA13	G protein subunit alpha 13
117143	2,69E-15	1,46E+01	1,03E-15	0,0766	8,0229365	0,61485675	691,87	TADA1	transcriptional adaptor 1
2146	7,21E-44	4,31E+01	1,33E-44	0,0438	14,0114439	0,61409258	4627,69	EZH2	enhancer of zeste 2 polycomb repressive complex 2 subunit
55669	3,10E-34	3,35E+01	7,08E-35	0,0498	12,3198264	0,61398438	2638,49	MFN1	mitofusin 1
91801	9,46E-24	2,30E+01	2,84E-24	0,0604	10,1651631	0,61397728	1238,2	ALKBH8	alkB homolog 8, tRNA methyltransferase
51105	3,24E-34	3,35E+01	7,41E-35	0,0498	12,3161664	0,61394293	3974,36	PHF20L1	PHD finger protein 20 like 1
5567	1,99E-16	1,57E+01	7,36E-17	0,0736	8,3411544	0,61362059	889,08	PRKACB	protein kinase cAMP-activated catalytic subunit beta
663	8,88E-32	3,11E+01	2,16E-32	0,0518	11,8498689	0,6132965	3251,57	BNIP2	BCL2 interacting protein 2
57168	3,79E-03	2,42E+00	2,61E-03	0,2037	3,0104461	0,61317703	74,93	ASPHD2	aspartate beta-hydroxylase domain containing 2
100505678	4,05E-05	4,39E+00	2,40E-05	0,1451	4,2244035	0,6131174	166,05	STARD4-AS	STARD4 antisense RNA 1
330	3,45E-37	3,65E+01	7,35E-38	0,0477	12,8622057	0,61299176	7261,83	BIRC3	baculoviral IAP repeat containing 3
107986298	4,61E-07	6,34E+00	2,44E-07	0,1187	5,1622278	0,61296708	252,89	LOC107986	uncharacterized LOC107986298
9584	1,67E-55	5,48E+01	2,36E-56	0,0388	15,8174646	0,61296049	13723,01	RBM39	RNA binding motif protein 39
100996425	3,46E-01	4,61E-01	3,06E-01	0,599	1,023329	0,61295545	9,99	ARLNC1	androgen receptor regulated long noncoding RNA 1
6044	3,59E-02	1,44E+00	2,73E-02	0,2778	2,2065338	0,61294989	39,97	SNORA62	small nucleolar RNA, H/ACA box 62
100132287	4,34E-07	6,36E+00	2,29E-07	0,1185	5,1738411	0,61284847	279,03	LOC100132	uncharacterized LOC100132287
440672	1,04E-15	1,50E+01	3,93E-16	0,0752	8,1405851	0,61216925	733,02	NUDT4B	nudix hydrolase 4B
4698	6,72E-06	5,17E+00	3,79E-06	0,1324	4,6226456	0,61198216	1810,92	NDUFA5	NADH:ubiquinone oxidoreductase subunit A5
100505616	8,37E-04	3,08E+00	5,46E-04	0,177	3,4569888	0,61187866	100,28	SNHG21	small nucleolar RNA host gene 21
100287049	2,56E-05	4,59E+00	1,49E-05	0,1412	4,3298557	0,61130771	176,04	DCAF8-DT	DCAF8 divergent transcript
200845	1,33E-14	1,39E+01	5,22E-15	0,0781	7,8215688	0,61115027	642,69	KCTD6	potassium channel tetramerization domain containing 6
55312	6,85E-18	1,72E+01	2,42E-18	0,0699	8,735786	0,61105988	1329,26	RFK	riboflavin kinase
84253	1,11E-03	2,95E+00	7,31E-04	0,1809	3,3775217	0,6109811	110,38	GARNL3	GTPase activating Rap/RanGAP domain like 3
58490	1,85E-34	3,37E+01	4,21E-35	0,0494	12,361671	0,61080718	3195,43	RPRD1B	regulation of nuclear pre-mRNA domain containing 1B
151742	5,12E-08	7,29E+00	2,58E-08	0,1097	5,5681038	0,6106713	303,92	PPM1L	protein phosphatase, Mg2+/Mn2+ dependent 1L
145748	6,69E-10	9,17E+00	3,10E-10	0,097	6,2936429	0,6106338	380,06	LYSMD4	LysM domain containing 4
7761	1,58E-04	3,80E+00	9,76E-05	0,1567	3,8964452	0,61047272	133,53	ZNF214	zinc finger protein 214
5814	2,57E-37	3,66E+01	5,46E-38	0,0474	12,885045	0,61041719	3699,33	PURB	purine rich element binding protein B
7804	3,62E-37	3,64E+01	7,72E-38	0,0475	12,8583892	0,61041483	2699,69	LRP8	LDL receptor related protein 8
3690	3,28E-06	5,48E+00	1,82E-06	0,1279	4,7727949	0,61032873	197,93	ITGB3	integrin subunit beta 3
81671	1,68E-41	4,08E+01	3,27E-42	0,0448	13,6147897	0,60994296	6571,15	VMP1	vacuole membrane protein 1
126069	3,75E-03	2,43E+00	2,58E-03	0,2024	3,0134066	0,60992608	90,67	ZNF491	zinc finger protein 491
339559	4,66E-06	5,33E+00	2,60E-06	0,1297	4,6997894	0,60967458	208,21	ZFP69	ZFP69 zinc finger protein
84888	4,79E-21	2,03E+01	1,55E-21	0,064	9,5317299	0,60965023	2115,62	SPPL2A	signal peptide peptidase like 2A
8487	1,53E-18	1,78E+01	5,30E-19	0,0684	8,9059019	0,60957045	885,95	GEMIN2	gem nuclear organelle associated protein 2
9319	2,23E-34	3,37E+01	5,09E-35	0,0494	12,3464208	0,60953218	2384,05	TRIP13	thyroid hormone receptor interactor 13
55726	1,52E-33	3,28E+01	3,55E-34	0,05	12,1891993	0,60937757	2203,48	INTS13	integrator complex subunit 13
2241	4,91E-28	2,73E+01	1,31E-28	0,0549	11,0960874	0,60923045	2735,15	FER	FER tyrosine kinase
4088	1,67E-51	5,08E+01	2,55E-52	0,04	15,2213855	0,60920673	10424,62	SMAD3	SMAD family member 3
10254	5,23E-22	2,13E+01	1,64E-22	0,0624	9,7619641	0,6092029	1324,46	STAM2	signal transducing adaptor molecule 2
101101772	9,08E-03	2,04E+00	6,49E-03	0,2236	2,7219437	0,60861569	70,3	LINC00601	long intergenic non-protein coding RNA 601
9874	1,03E-32	3,20E+01	2,44E-33	0,0506	12,0308938	0,608391	2263,05	TLK1	tousled like kinase 1
124808	8,56E-26	2,51E+01	2,43E-26	0,0573	10,6191041	0,60836514	1854,78	CCDC43	coiled-coil domain containing 43
11163	5,21E-28	2,73E+01	1,39E-28	0,0548	11,0906886	0,60827852	2632,62	NUDT4	nudix hydrolase 4
388815	2,39E-01	6,22E-01	2,05E-01	0,4795	1,2683763	0,60820243	13,52	MIR99AHG	mir-99a-let-7c cluster host gene
286076	2,24E-01	6,50E-01	1,91E-01	0,4645	1,3090523	0,60806715	14,56	LINC02878	long intergenic non-protein coding RNA 2878
154075	1,48E-01	8,30E-01	1,23E-01	0,3935	1,5443301	0,60763852	21,76	SAMD3	sterile alpha motif domain containing 3
56132	1,05E-01	9,79E-01	8,53E-02	0,353	1,7208087	0,60748844	24,96	PCDHB3	protocadherin beta 3
9923	2,10E-29	2,87E+01	5,40E-30	0,0534	11,3777448	0,60747968	1823,71	ZBTB40	zinc finger and BTB domain containing 40
23161	2,90E-15	1,45E+01	1,11E-15	0,0758	8,0136459	0,60740176	763,07	SNX13	sorting nexin 13
100506207	4,56E-02	1,34E+00	3,51E-02	0,2882	2,1072019	0,60737097	37,34	LOC100506	uncharacterized LOC100506207
83732	7,93E-38	3,71E+01	1,67E-38	0,0468	12,9763484	0,60719528	3003,85	RIOK1	RIO kinase 1
55737	1,81E-50	4,97E+01	2,84E-51	0,0403	15,0629951	0,6065067	8725,43	VPS35	VPS35 retromer complex component
10561	1,88E-21	2,07E+01	6,01E-22	0,063	9,6294055	0,60641031	1316,69	IFI44	interferon induced protein 44
101927497	8,18E-03	2,09E+00	5,82E-03	0,2199	2,7578835	0,60637608	64,8	CDK6-AS1	CDK6 antisense RNA 1
79871	1,79E-25	2,47E+01	5,12E-26	0,0575	10,5491677	0,60630171	1554,92	RPAP2	RNA polymerase II associated protein 2
10329	5,47E-19	1,83E+01	1,87E-19	0,0672	9,0206453	0,60622894	1062,36	RXYLT1	ribitol xylosyltransferase 1
8676	2,37E-03	2,63E+00	1,60E-03	0,1921	3,1554797	0,60614677	90,77	STX11	syntaxin 11
2039	9,69E-03	2,01E+00	6,95E-03	0,2245	2,6994476	0,60595181	66,2	DMTN	dematin actin binding protein
91526	1,74E-08	7,76E+00	8,59E-09	0,1052	5,7564661	0,60580719	314,35	ANKRD44	ankyrin repeat domain 44
10625	5,63E-39	3,82E+01	1,15E-39	0,046	13,1794465	0,60579641	3895,72	IVNS1ABP	influenza virus NS1A binding protein
102157402	1,21E-27	2,69E+01	3,28E-28	0,055	11,0137646	0,60560907	1752,88	AK6	adenylate kinase 6
130507	4,56E-22	2,13E+01	1,43E-22	0,0619	9,775902	0,60517653	1514,8	UBR3	ubiquitin protein ligase E3 component n-recognin 3
81542	5,09E-43	4,23E+01	9,53E-44	0,0436	13,8707586	0,60469606	4851,27	TMX1	thioredoxin related transmembrane protein 1
677826	2,29E-01	6,40E-01	1,96E-01	0,4672	1,2940185	0,60456267	14,05	SNORA3B	small nucleolar RNA, H/ACA box 3B
11037	3,32E-02	1,48E+00	2,52E-02	0,27	2,2389679	0,6044874	41,97	STON1	stonin 1
55680	5,28E-31	3,03E+01	1,31E-31	0,0517	11,6978264	0,60442536	2389,84	RUFY2	RUN and FYVE domain containing 2
106478957	6,45E-03	2,19E+00	4,54E-03	0,213	2,8378301	0,60434215	72,83	DDX39B-AS	DDX39B antisense RNA 1
10988	3,99E-40	3,94E+01	7,98E-41	0,0452	13,3794189	0,60425825	11038,56	METAP2	methionyl aminopeptidase 2
8233	1,23E-10	9,91E+00	5,52E-11	0,0921	6,5563215	0,60404865	625,51	ZRSR2	zinc finger CCCH-type, RNA binding motif and serine/arginine rich 2
64421	1,39E-22	2,19E+01	4,30E-23	0,061	9,8966656	0,6039606	1270,43	DCLRE1C	DNA cross-link repair 1C
80219	2,90E-15	1,45E+01	1,12E-15	0,0753	8,0133514	0,60364132	1102,26	COQ10B	coenzyme Q10B
4148	5,42E-05	4,27E+00	3,23E-05	0,1452	4,1567	0,60344046	152,7	MATN3	matrilin 3
220988	6,10E-39	3,82E+01	1,25E-39	0,0458	13,173299	0,60340983	18790,08	HNRNPA3	heterogeneous nuclear ribonucleoprotein A3
6683	1,37E-15	1,49E+01	5,23E-16	0,0744	8,1061112	0,60340952	983,06	SPAST	spastin
113510	9,46E-14	1,30E+01	3,81E-14	0,0797	7,5672298	0,60303699	683,76	HELQ	helicase, POLQ like
57496	6,09E-17	1,62E+01	2,22E-17	0,0711	8,4816353	0,60292283	1035,1	MRTFB	myocardin related transcription factor B
207107	1,01E-14	1,40E+01	3,94E-15	0,0767	7,8568486	0,602899	675,98	SFTA1P	surfactant associated 1, lncRNA
1645	5,37E-05	4,27E+00	3,20E-05	0,1449	4,1589025	0,60255543	160,75	AKR1C1	aldo-keto reductase family 1 member C1
55781	1,10E-24	2,40E+01	3,21E-25	0,0581	10,3753961	0,60245864	2031,38	RIOK2	RIO kinase 2
10413	8,93E-43	4,20E+01	1,68E-43	0,0436	13,8298825	0,60242283	8619,33	YAP1	Yes1 associated transcriptional regulator
57182	5,52E-34	3,33E+01	1,27E-34	0,0491	12,2726006	0,60210457	2821,9	ANKRD50	ankyrin repeat domain containing 50
6935	5,59E-31	3,03E+01	1,38E-31	0,0515	11,6929515	0,60205706	3639,35	ZEB1	zinc finger E-box binding homeobox 1
202018	3,17E-19	1,85E+01	1,08E-19	0,0663	9,080667	0,60198802	967,1	TAPT1	transmembrane anterior posterior transformation 1
9683	2,20E-25	2,47E+01	6,31E-26	0,0571	10,5296565	0,60141463	1585,83	N4BP1	NEDD4 binding protein 1
80829	3,47E-46	4,55E+01	6,04E-47	0,0418	14,3893262	0,60117251	8566,31	ZFP91	ZFP91 zinc finger protein, atypical E3 ubiquitin ligase

54439	2,17E-33	3,27E+01	5,06E-34	0,0494	12,1602218	0,60115946	2992,73	RBM27	RNA binding motif protein 27
120534	1,49E-17	1,68E+01	5,33E-18	0,0695	8,6461277	0,60107391	1278,68	ARL14EP	ADP ribosylation factor like GTPase 14 effector protein
3267	3,72E-24	2,34E+01	1,11E-24	0,0586	10,2565687	0,60106121	2944,95	AGFG1	ArfGAP with FG repeats 1
55195	3,08E-01	5,11E-01	2,70E-01	0,5441	1,1040575	0,60077087	10,34	CCDC198	coiled-coil domain containing 198
105375336	2,22E-01	6,54E-01	1,89E-01	0,4569	1,3147513	0,600703	15,11	LOC105375	uncharacterized LOC105375336
55125	1,14E-33	3,29E+01	2,64E-34	0,0492	12,2133472	0,60066498	2949,31	CEP192	centrosomal protein 192
10138	1,73E-09	8,76E+00	8,15E-10	0,0978	6,1418965	0,60045823	401,8	YAF2	YY1 associated factor 2
55031	1,09E-32	3,20E+01	2,60E-33	0,0499	12,0258392	0,60030733	4209,37	USP47	ubiquitin specific peptidase 47
51265	1,20E-08	7,92E+00	5,85E-09	0,1031	5,8209065	0,59997981	361	CDKL3	cyclin dependent kinase like 3
11193	7,75E-19	1,81E+01	2,66E-19	0,0668	8,9818497	0,59974594	1342,86	WBP4	WW domain binding protein 4
150082	1,63E-01	7,88E-01	1,35E-01	0,4015	1,4930523	0,59945961	19,74	LCA5L	lebercilin LCA5 like
57583	6,96E-28	2,72E+01	1,87E-28	0,0542	11,0644178	0,59938217	1772,97	TMEM181	transmembrane protein 181
767558	7,74E-38	3,71E+01	1,62E-38	0,0461	12,9782768	0,59888168	3953,1	LUZP6	leucine zipper protein 6
136319	7,74E-38	3,71E+01	1,62E-38	0,0461	12,9782768	0,59888168	3953,1	MTPN	myotrophin
27252	2,24E-22	2,16E+01	6,96E-23	0,0608	9,8484945	0,59887286	1270,4	KLHL20	kelch like family member 20
253430	1,06E-11	1,10E+01	4,58E-12	0,0865	6,9181126	0,59861799	492,81	IPMK	inositol polyphosphate multikinase
10735	5,00E-42	4,13E+01	9,59E-43	0,0437	13,7041308	0,59854489	6625,23	STAG2	stromal antigen 2
23369	4,34E-42	4,14E+01	8,30E-43	0,0436	13,7146136	0,59850149	5839,71	PUM2	pumilio RNA binding family member 2
205564	3,87E-30	2,94E+01	9,78E-31	0,0519	11,5258023	0,59833584	2011,83	SENP5	SUMO specific peptidase 5
105371954	2,20E-01	6,58E-01	1,87E-01	0,4537	1,3185884	0,59829337	15,64	LOC105371	uncharacterized LOC105371954
57508	1,07E-21	2,10E+01	3,38E-22	0,0617	9,6883414	0,59776271	1818,8	INTS2	integrator complex subunit 2
83737	3,03E-46	4,55E+01	5,25E-47	0,0415	14,3989441	0,59735099	5723,55	ITCH	itchy E3 ubiquitin protein ligase
8629	2,79E-22	2,16E+01	8,69E-23	0,0608	9,8261782	0,5973189	1207,39	JRK	Jrk helix-turn-helix protein
102724642	2,99E-07	6,52E+00	1,57E-07	0,1139	5,2446388	0,59730465	259,95	LOC102724	anaphase-promoting complex subunit 1-like
105374556	6,19E-02	1,21E+00	4,86E-02	0,3027	1,9722811	0,59695667	37,01	LOC105374	uncharacterized LOC105374556
647309	3,52E-01	4,53E-01	3,12E-01	0,5903	1,0112408	0,59691472	8,73	GMNC	geminin coiled-coil domain containing
6760	9,28E-48	4,70E+01	1,55E-48	0,0408	14,6404983	0,5967936	7948,57	SS18	SS18 subunit of BAF chromatin remodeling complex
55553	3,26E-02	1,49E+00	2,47E-02	0,2657	2,2461076	0,59673997	44,35	SOX6	SRY-box transcription factor 6
55194	1,97E-02	1,71E+00	1,45E-02	0,2441	2,4441432	0,59656544	56,01	EVA1B	eva-1 homolog B
80351	2,91E-29	2,85E+01	7,51E-30	0,0526	11,3489396	0,59651014	2680,56	TNKS2	tankyrase 2
388324	1,57E-02	1,80E+00	1,14E-02	0,2358	2,5293875	0,59649089	57,27	INCA1	inhibitor of CDK, cyclin A1 interacting protein 1
51455	4,45E-32	3,14E+01	1,07E-32	0,0501	11,908153	0,59629881	2369,64	REV1	REV1 DNA directed polymerase
80267	1,76E-36	3,58E+01	3,80E-37	0,0468	12,7345551	0,59621742	3455,49	EDEM3	ER degradation enhancing alpha-mannosidase like protein 3
1160	7,41E-02	1,13E+00	5,87E-02	0,3154	1,8901469	0,596089	33,43	CKMT2	creatine kinase, mitochondrial 2
374443	2,02E-08	7,69E+00	1,00E-08	0,104	5,7307333	0,59606469	324,75	LOC374443	C-type lectin domain family 2 member D pseudogene
5870	8,57E-40	3,91E+01	1,72E-40	0,0447	13,3220166	0,59602087	7184,26	RAB6A	RAB6A, member RAS oncogene family
22843	1,58E-04	3,80E+00	9,73E-05	0,1529	3,8972698	0,59589856	149,61	PPM1E	protein phosphatase, Mg2+/Mn2+ dependent 1E
441601	2,32E-01	6,35E-01	1,98E-01	0,4628	1,2873089	0,59572334	15,1	SEPTIN7P11	septin 7 pseudogene 11
100381270	1,18E-19	1,89E+01	3,97E-20	0,0648	9,1887982	0,59555821	1471,13	ZBED6	zinc finger BED-type containing 6
29899	2,84E-41	4,05E+01	5,53E-42	0,0439	13,5763209	0,59550606	3748,46	GPSM2	G protein signaling modulator 2
90826	1,68E-16	1,58E+01	6,20E-17	0,0712	8,3614329	0,59526536	893,92	PRMT9	protein arginine methyltransferase 9
196403	1,23E-09	8,91E+00	5,78E-10	0,096	6,1964249	0,59471734	435,56	DTX3	deltex E3 ubiquitin ligase 3
101927178	5,74E-11	1,02E+01	2,55E-11	0,0891	6,6706121	0,59446586	472,84	LOC101927	uncharacterized LOC101927178
10795	2,55E-15	1,46E+01	9,77E-16	0,074	8,0296798	0,59440165	965,98	ZNF268	zinc finger protein 268
8774	2,99E-24	2,35E+01	8,87E-25	0,0578	10,2778088	0,59421989	2232,76	NAPG	NSF attachment protein gamma
51567	2,61E-36	3,56E+01	5,67E-37	0,0468	12,7033275	0,59418464	3128,94	TDP2	tyrosyl-DNA phosphodiesterase 2
7673	9,60E-06	5,02E+00	5,47E-06	0,1307	4,546042	0,594098	203,21	ZNF222	zinc finger protein 222
84376	5,18E-24	2,33E+01	1,54E-24	0,0581	10,2242487	0,59402108	1487,58	HOOK3	hook microtubule tethering protein 3
27436	6,35E-47	4,62E+01	1,08E-47	0,0409	14,5076808	0,59394063	4942,35	EML4	EMAP like 4
338391	3,64E-02	1,44E+00	2,77E-02	0,2697	2,2008081	0,59364587	42,41	H2BP2	H2B histone pseudogene 2
65109	2,13E-26	2,57E+01	5,94E-27	0,0552	10,7498351	0,59353993	2064,75	UPF3B	UPF3B regulator of nonsense mediated mRNA decay
7803	5,17E-52	5,13E+01	7,84E-53	0,0388	15,2983561	0,59334453	9482,92	PTP4A1	protein tyrosine phosphatase 4A1
56913	1,99E-24	2,37E+01	5,87E-25	0,0575	10,3175102	0,59291549	2196,06	C1GALT1	core 1 synthase, glycoprotein-N-acetylgalactosamine 3-beta-galactosyltransferase 1
348094	5,86E-02	1,23E+00	4,58E-02	0,2969	1,9970866	0,59287519	35,49	ANKDD1A	ankyrin repeat and death domain containing 1A
8723	5,45E-19	1,83E+01	1,86E-19	0,0657	9,0210328	0,59276644	1247,67	SNX4	sorting nexin 4
100271835	7,77E-02	1,11E+00	6,17E-02	0,3172	1,8682588	0,59269665	30,92	LIMS3-LOC4	LIMS3-LOC440895 readthrough
196527	2,28E-28	2,76E+01	6,04E-29	0,0531	11,1651079	0,59267345	2708,82	ANO6	anoctamin 6
731656	3,63E-01	4,40E-01	3,22E-01	0,5977	0,9905271	0,59204885	8,67	LINC01348	long intergenic non-protein coding RNA 1348
107986838	5,62E-07	6,25E+00	2,99E-07	0,1154	5,1243157	0,59158737	292,3	LOC107986	uncharacterized LOC107986838
55638	1,26E-05	4,90E+00	7,25E-06	0,1319	4,4862194	0,59155672	188,2	SYBU	syntabulin
26127	2,78E-19	1,86E+01	9,43E-20	0,065	9,0952737	0,59150183	1214,16	FGFR1OP2	FGFR1 oncogene partner 2
79876	1,61E-18	1,78E+01	5,57E-19	0,0665	8,9003195	0,59147087	1069,05	UBA5	ubiquitin like modifier activating enzyme 5
7321	1,75E-11	1,08E+01	7,60E-12	0,0863	6,8459129	0,59108416	666,2	UBE2D1	ubiquitin conjugating enzyme E2 D1
57698	1,98E-14	1,37E+01	7,84E-15	0,0761	7,7701972	0,59099776	1566,84	SHTN1	shootin 1
8502	1,95E-39	3,87E+01	3,96E-40	0,0446	13,2597456	0,59086899	4522,39	PKP4	plakophilin 4
7525	3,80E-28	2,74E+01	1,01E-28	0,0531	11,1190881	0,59082819	6008,24	YES1	YES proto-oncogene 1, Src family tyrosine kinase
8438	7,84E-23	2,21E+01	2,41E-23	0,0593	9,9546492	0,59042139	1320,79	RAD54L	RAD54 like
56122	2,22E-04	3,65E+00	1,38E-04	0,1549	3,8112867	0,5902538	146,91	PCDHB14	protocadherin beta 14
9880	4,79E-12	1,13E+01	2,05E-12	0,0839	7,0313163	0,59017165	537,04	ZBTB39	zinc finger and BTB domain containing 39
1606	1,36E-13	1,29E+01	5,51E-14	0,0785	7,5191377	0,59014984	605,97	DGKA	diacylglycerol kinase alpha
389941	2,02E-02	1,69E+00	1,49E-02	0,2423	2,4346422	0,5898349	55,44	C1QL3	complement C1q like 3
79962	4,80E-05	4,32E+00	2,85E-05	0,1409	4,1853075	0,58970854	172,21	DNAJC22	DnaJ heat shock protein family (Hsp40) member C22
645121	9,49E-02	1,02E+00	7,64E-02	0,3327	1,7721809	0,58968721	27,3	CCNI2	cyclin I family member 2
285440	1,98E-18	1,77E+01	6,88E-19	0,0664	8,8768758	0,5894184	1003,83	CYP4V2	cytochrome P450 family 4 subfamily V member 2
23097	6,03E-16	1,52E+01	2,27E-16	0,0718	8,2071023	0,58939099	782,45	CDK19	cyclin dependent kinase 19
145482	2,45E-21	2,06E+01	7,86E-22	0,0614	9,6017146	0,58922701	1226,57	PTGR2	prostaglandin reductase 2
100329109	1,40E-02	1,85E+00	1,02E-02	0,2292	2,5704217	0,58916473	60,81	GCSHP3	GCSH pseudogene 3
3964	1,29E-46	4,59E+01	2,21E-47	0,0407	14,4586395	0,58913722	6828,28	LGALS8	galectin 8
642852	8,27E-14	1,31E+01	3,33E-14	0,0777	7,5849646	0,58912827	702,95	LINC00205	long intergenic non-protein coding RNA 205
404281	5,95E-05	4,23E+00	3,55E-05	0,1425	4,1347697	0,5891154	160,12	YY2	YY2 transcription factor
101060684	8,35E-28	2,71E+01	2,25E-28	0,0533	11,04783	0,5890468	1961,14	NBPF26	NBPF member 26
51312	1,71E-48	4,78E+01	2,80E-49	0,0399	14,7563049	0,58899623	6499,52	SLC25A37	solute carrier family 25 member 37
93627	4,62E-12	1,13E+01	1,97E-12	0,0837	7,0362683	0,58889122	546,01	TBCK	TBC1 domain containing kinase
5718	3,29E-27	2,65E+01	8,98E-28	0,0539	10,9226824	0,58856149	7724,03	PSMD12	proteasome 26S subunit, non-ATPase 12
22976	3,77E-22	2,14E+01	1,18E-22	0,0601	9,7955021	0,58854897	1736,03	PAXIP1	PAX interacting protein 1
440934	1,78E-01	7,50E-01	1,49E-01	0,4079	1,4426943	0,58845272	19,77	CT75	cancer/testis associated transcript 75
107986655	2,39E-01	6,22E-01	2,04E-01	0,4637	1,2689026	0,58844751	14,48	HIVEP2-DT	HIVEP2 divergent transcript
23607	3,69E-25	2,44E+01	1,07E-25	0,0561	10,4800357	0,58838425	6027,34	CD2AP	CD2 associated protein
9055	1,09E-36	3,60E+01	2,34E-37	0,046	12,7724167	0,58816841	12714,45	PRC1	protein regulator of cytokinesis 1
100132057	2,08E-01	6,82E-01	1,77E-01	0,4348	1,3515966	0,58771506	16,89	PDE4DIPP6	PDE4DIP pseudogene 6
5552	4,60E-26	2,53E+01	1,29E-26	0,055	10,6776637	0,58766666	6447,8	SRGN	serglycin
8493	2,28E-15	1,46E+01	8,75E-16	0,073	8,0432956	0,58716011	990,92	PPM1D	protein phosphatase, Mg2+/Mn2+ dependent 1D
1629	2,98E-23	2,25E+01	9,03E-24	0,0584	10,051652	0,58712151	1476,59	DBT	dihydrolipoamide branched chain transacylase E2
55531	5,00E-02	1,30E+00	3,87E-02	0,284	2,0669498	0,58702556	38,54	ELMOD1	ELMO domain containing 1
3655	7,56E-56	5,51E+01	1,06E-56	0,037	15,8678075	0,58670014	35641,16	ITGA6	integrin subunit alpha 6
23768	2,38E-22	2,16E+01	7,40E-23	0,0596	9,8423452	0,58650225	1237,53	FLRT2	fibronectin leucine rich transmembrane protein 2
260425	1,30E-19	1,89E+01	4,37E-20	0,0639	9,178539	0,58643747	1206,74	MAGI3	membrane associated guanylate kinase, WW and PDZ domain containing 3
23314	1,26E-18	1,79E+01	4,37E-19	0,0657	8,9271464	0,58619458	1167,84	SATB2	SATB homeobox 2
100132356	3,01E-02	1,52E+00	2,27E-02	0,2573	2,2781301	0,58619025	46,32	LOC100132	uncharacterized LOC100132356
4040	2,07E-32	3,17E+01	4,94E-33	0,0489	11,9727354	0,58604178	3505,75	LRP6	LDL receptor related protein 6
203238	2,22E-03	2,65E+00	1,50E-03	0,1846	3,175351	0,5860361	93,16	CCDC171	coiled-coil domain containing 171
30001	1,03E-36	3,60E+01	2,22E-37	0,0459	12,7765042	0,58600633	10047,01	ERO1A	endoplasmic reticulum oxidoreductase 1 alpha
6198	4,34E-32	3,14E+01	1,04E-32	0,0492	11,9103989	0,5858332	3098,83	RPS6KB1	ribosomal protein S6 kinase B1
10426	5,95E-28	2,72E+01	1,59E-28	0,0529	11,0786906	0,58578218	2128,98	TUBGCP3	tubulin gamma complex associated protein 3
54881	5,95E-20	1,92E+01	1,98E-20	0,0632	9,2632517	0,58577302	3751,03	TEX10	testis expressed 10
101927701	9,39E-02	1,03E+00	7,55E-02	0,3294	1,7774821	0,58547427	30,07	LINC01812	long intergenic non-protein coding RNA 1812
56907	1,47E-38	3,78E+01	3,04E-39	0,0446	13,1059481	0,58501369	3803,69	SPIRE1	spire type actin nucleation factor 1
5168	3,15E-01	5,02E-01	2,76E-01	0,537	1,0887041	0,5845966	10,82	ENPP2	ectonucleotide pyrophosphatase/phosphodiesterase 2
23456	7,20E-19	1,81E+01	2,47E-19	0,065	8,9899901	0,58457574	991,01	ABCB10	ATP binding cassette subfamily B member 10
613037	1,76E-04	3,75E+00	1,09E-04	0,151	3,8698938	0,58430451	139,25	NPIPB13	nuclear pore complex interacting protein family, member B13
348808	2,29E-01	6,40E-01	1,95E-01	0,4509	1,2958849	0,58427038	15,43	NPHP3-AS1	NPHP3 antisense RNA 1
2037	2,65E-30	2,96E+01	6,68E-31	0,0505	11,5585665	0,58415776	7629,27	EPB41L2	erythrocyte membrane protein band 4.1 like 2
389170	2,33E-01	6,33E-01	1,99E-01	0,4549	1,2839116	0,5841081	16,48	LEKR1	leucine, glutamate and lysine rich 1
202181	1,82E-02	1,74E+00	1,34E-02	0,2361	2,4733181	0,58406223	56,95	LOC202181	SUMO interacting motifs containing 1 pseudogene
23108	3,31E-13	1,25E+01	1,36E-13	0,0789	7,4003142	0,58392899	690,69	RAP1GAP2	RAP1 GTPase activating protein 2
169270	2,49E-03	2,60E+00	1,69E-03	0,1859	3,1406644	0,58385083	91,61	ZNF596	zinc finger protein 596
84947	1,35E-09	8,87E+00	6,36E-10	0,0944	6,1811493	0,58373256	399,7	SERAC1	serine active site containing 1
100996716	1,87E-05	4,73E+00	1,08E-05	0,1326	4,3998285	0,58361361	197,55	SEC22B2P	SEC22 homolog B2, pseudogene
29267	5,49E-08	7,26E+00	2,77E-08	0,105	5,5555882	0,58339781	311,03	TMOD2	tropomodulin 2
375189	9,88E-02	1,01E+00	7,97E-02	0,3327	1,7525587	0,58314319	28,89	PFN4	profilin family member 4

57669	1,43E-13	1,28E+01	5,79E-14	0,0776	7,512681	0,58312987	644,35	EPB41L5	erythrocyte membrane protein band 4.1 like 5
29126	2,34E-25	2,46E+01	6,74E-26	0,0554	10,5234143	0,58293946	1744,34	CD274	CD274 molecule
80319	1,22E-02	1,91E+00	8,84E-03	0,2226	2,618313	0,5829272	63,1	CXXC4	CXXC finger protein 4
26052	1,21E-05	4,92E+00	6,96E-06	0,1297	4,4948972	0,58279518	222,48	DNM3	dynamin 3
26036	3,04E-25	2,45E+01	8,78E-26	0,0555	10,4984654	0,58267875	2444,42	ZNF451	zinc finger protein 451
55752	1,17E-42	4,19E+01	2,21E-43	0,0422	13,8101261	0,58262653	11576,85	SEPTIN11	septin 11
401546	1,38E-01	8,60E-01	1,13E-01	0,368	1,5830816	0,58256381	22,57	C9orf152	chromosome 9 open reading frame 152
641298	1,09E-07	6,96E+00	5,58E-08	0,1071	5,4319099	0,58200214	295,49	SMG1P1	SMG1 pseudogene 1
102724748	4,89E-16	1,53E+01	1,83E-16	0,0707	8,2324862	0,58196428	791,62	LOC102724748	
201931	1,89E-26	2,57E+01	5,26E-27	0,0541	10,7609469	0,58174755	1636,64	TMEM192	transmembrane protein 192
105370485	2,48E-01	6,06E-01	2,13E-01	0,4669	1,2458386	0,58164367	13,91	LOC105370485	uncharacterized LOC105370485
1738	8,22E-35	3,41E+01	1,85E-35	0,0468	12,4275401	0,58161422	5262,98	DLD	dihydrolipoamide dehydrogenase
80034	2,95E-02	1,53E+00	2,22E-02	0,2543	2,2873281	0,58160397	49,8	CSRNP3	cysteine and serine rich nuclear protein 3
5420	1,41E-39	3,89E+01	2,86E-40	0,0438	13,284095	0,58134963	11205,11	PODXL	podocalyxin like
57556	2,14E-03	2,67E+00	1,44E-03	0,1824	3,1865047	0,58120466	100,01	SEMA6A	semaphorin 6A
5737	1,23E-02	1,91E+00	8,86E-03	0,222	2,6175689	0,58115314	65,24	PTGFR	prostaglandin F receptor
7693	4,17E-16	1,54E+01	1,56E-16	0,0704	8,251931	0,58109898	1234,12	ZNF134	zinc finger protein 134
100996517	7,75E-05	4,11E+00	4,67E-05	0,1427	4,0716032	0,58105383	169,57	SEC22B3P	SEC22 homolog B3, pseudogene
5330	1,22E-01	9,14E-01	9,95E-02	0,3528	1,6470932	0,58102577	25,63	PLCB2	phospholipase C beta 2
829	6,10E-42	4,12E+01	1,17E-42	0,0424	13,6896532	0,58098584	10079,93	CAPZA1	capping actin protein of muscle Z-line subunit alpha 1
84108	9,71E-17	1,60E+01	3,55E-17	0,0689	8,4267193	0,58058618	1029,97	PCGF6	polycomb group ring finger 6
7172	1,49E-17	1,68E+01	5,34E-18	0,0671	8,6458969	0,58056321	1104,54	TPMT	thiopurine S-methyltransferase
401093	5,05E-08	7,30E+00	2,54E-08	0,1042	5,5702496	0,58052302	327,15	MBNL1-AS1	MBNL1 antisense RNA 1
105373974	9,74E-02	1,01E+00	7,84E-02	0,3298	1,7598252	0,58036164	29,84	LOC105373974	uncharacterized LOC105373974
105378913	2,81E-01	5,51E-01	2,44E-01	0,4976	1,1662489	0,58033337	12,76	LOC105378913	
56648	1,57E-22	2,18E+01	4,87E-23	0,0587	9,8842929	0,58021488	1942,03	EIF5A2	eukaryotic translation initiation factor 5A2
7163	8,77E-19	1,81E+01	3,02E-19	0,0647	8,9680931	0,57991745	1907,56	TPD52	tumor protein D52
9101	4,07E-31	3,04E+01	1,01E-31	0,0495	11,7199906	0,57988978	2525,64	USP8	ubiquitin specific peptidase 8
1429	1,67E-23	2,28E+01	5,06E-24	0,0574	10,1086989	0,57980444	1547,83	CRYZ	crystallin zeta
440353	4,51E-06	5,35E+00	2,52E-06	0,1232	4,7067864	0,5797419	231,38	NPIPB12	nuclear pore complex interacting protein family member B12
51195	2,74E-05	4,56E+00	1,60E-05	0,1344	4,3143177	0,57969476	185,29	RAPGEFL1	Rap guanine nucleotide exchange factor like 1
7155	6,63E-49	4,82E+01	1,08E-49	0,0391	14,8205673	0,57963171	7969,74	TOP2B	DNA topoisomerase II beta
10892	1,42E-26	2,58E+01	3,96E-27	0,0537	10,7871963	0,57955415	2291,59	MALT1	MALT1 paracaspase
9204	2,10E-17	1,67E+01	7,53E-18	0,0673	8,6065429	0,5793207	1119,7	ZMYM6	zinc finger MYM-type containing 6
84930	4,95E-39	3,83E+01	1,01E-39	0,0439	13,1891541	0,57926748	3963,42	MASTL	microtubule associated serine/threonine kinase like
27244	6,01E-07	6,22E+00	3,20E-07	0,1132	5,1112299	0,57874321	313,6	SESN1	sestrin 1
57393	3,48E-02	1,46E+00	2,65E-02	0,2607	2,2195178	0,57873093	48,35	CLTRN	collectrin, amino acid transport regulator
105370174	8,78E-02	1,06E+00	7,03E-02	0,3197	1,8099409	0,57861264	30,16	LOC105370174	uncharacterized LOC105370174
8503	5,06E-10	9,30E+00	2,33E-10	0,0913	6,3375307	0,57851997	437,48	PIK3R3	phosphoinositide-3-kinase regulatory subunit 3
57226	2,77E-28	2,76E+01	7,37E-29	0,0519	11,1474448	0,57844524	2096,38	LYRM2	LYR motif containing 2
140545	1,17E-04	3,93E+00	7,11E-05	0,1456	3,9726513	0,57844213	152,49	RNF32	ring finger protein 32
8301	5,48E-50	4,93E+01	8,68E-51	0,0386	14,9888519	0,57830931	13090,5	PICALM	phosphatidylinositol binding clathrin assembly protein
8334	7,82E-15	1,41E+01	3,05E-15	0,0733	7,8887472	0,57821091	787,3	H2AC6	H2A clustered histone 6
3832	2,63E-40	3,96E+01	5,23E-41	0,0431	13,4107982	0,57804587	8465,09	KIF11	kinesin family member 11
79412	1,28E-01	8,93E-01	1,05E-01	0,356	1,6233357	0,57798023	25,74	KREMEN2	kringle containing transmembrane protein 2
126272	1,08E-04	3,97E+00	6,60E-05	0,1448	3,990287	0,57785846	170,79	EID2B	EP300 interacting inhibitor of differentiation 2B
92906	1,78E-24	2,37E+01	5,24E-25	0,0559	10,3285059	0,57784842	1919,25	HNRNPLL	heterogeneous nuclear ribonucleoprotein L like
58489	3,89E-22	2,14E+01	1,22E-22	0,059	9,7921975	0,57783211	1842,03	ABHD17C	abhydrolase domain containing 17C, depalmitoylase
25852	1,32E-22	2,19E+01	4,06E-23	0,0583	9,9024709	0,57749506	1711,86	ARMC8	armadillo repeat containing 8
285267	2,66E-08	7,58E+00	1,32E-08	0,1016	5,6828325	0,57749039	357,86	ZNF619	zinc finger protein 619
26496	9,18E-02	1,04E+00	7,37E-02	0,3229	1,7882604	0,57743174	32,3	OR10A3	olfactory receptor family 10 subfamily A member 3
92797	6,22E-02	1,21E+00	4,88E-02	0,293	1,970565	0,57732031	39,7	HELB	DNA helicase B
2122	1,01E-31	3,10E+01	2,45E-32	0,0488	11,8392071	0,57719452	2763,59	MECOM	MDS1 and EVI1 complex locus
8811	1,83E-01	7,38E-01	1,54E-01	0,4046	1,4259152	0,57696811	19,59	GALR2	galanin receptor 2
26548	3,82E-01	4,18E-01	3,41E-01	0,6053	0,9530957	0,5769013	8,83	ITGB1BP2	integrin subunit beta 1 binding protein 2
55802	5,11E-22	2,13E+01	1,60E-22	0,0591	9,7642886	0,57675527	1637,36	DCP1A	decapping mRNA 1A
6249	8,53E-26	2,51E+01	2,42E-26	0,0543	10,619452	0,57667616	8154,23	CLIP1	CAP-Gly domain containing linker protein 1
129831	6,77E-08	7,17E+00	3,43E-08	0,1045	5,5179618	0,57658866	382,47	RBM45	RNA binding motif protein 45
51068	2,91E-25	2,45E+01	8,38E-26	0,0549	10,5028993	0,5765815	2218,99	NMD3	NMD3 ribosome export adaptor
154141	1,88E-09	8,73E+00	8,91E-10	0,0941	6,1278732	0,57646655	397,34	MBOAT1	membrane bound O-acyltransferase domain containing 1
1056	3,25E-02	1,49E+00	2,46E-02	0,2563	2,2476526	0,57609343	46,66	CEL	carboxyl ester lipase
24146	1,11E-05	4,95E+00	6,37E-06	0,1276	4,5138274	0,57604518	209,99	CLDN15	claudin 15
23414	2,92E-05	4,53E+00	1,71E-05	0,1339	4,2997215	0,57586654	186,26	ZFPM2	zinc finger protein, FOG family member 2
3214	3,09E-01	5,10E-01	2,71E-01	0,5225	1,1018357	0,57573828	11,36	HOXB4	homeobox B4
55722	4,12E-13	1,24E+01	1,70E-13	0,0781	7,3708588	0,57563761	770,16	CEP72	centrosomal protein 72
153562	1,04E-04	3,98E+00	6,30E-05	0,1438	4,0013877	0,5754158	175	MARVELD2	MARVEL domain containing 2
90806	1,94E-19	1,87E+01	6,55E-20	0,063	9,13484	0,57531053	1285,07	ANGEL2	angel homolog 2
2838	2,01E-04	3,70E+00	1,25E-04	0,1499	3,8365552	0,57519562	161,51	GPR15	G protein-coupled receptor 15
50484	2,17E-19	1,87E+01	7,35E-20	0,063	9,1223825	0,57494765	1251,7	RRM2B	ribonucleotide reductase regulatory TP53 inducible subunit M2B
100505933	9,61E-03	2,02E+00	6,89E-03	0,2127	2,7023283	0,57485411	71,55	ADD3-AS1	ADD3 antisense RNA 1
23118	2,81E-40	3,96E+01	5,60E-41	0,0429	13,4057234	0,57469971	5203,78	TAB2	TGF-beta activated kinase 1 (MAP3K7) binding protein 2
56623	2,61E-11	1,06E+01	1,15E-11	0,0847	6,7867879	0,57460803	744,75	INPP5E	inositol polyphosphate-5-phosphatase E
22841	9,57E-18	1,70E+01	3,41E-18	0,0661	8,6970613	0,57455475	972,85	RAB11FIP2	RAB11 family interacting protein 2
81847	1,06E-18	1,80E+01	3,65E-19	0,0642	8,9471462	0,5743864	1144,11	RNF146	ring finger protein 146
100132707	8,19E-08	7,09E+00	4,17E-08	0,1047	5,4835662	0,5743589	339,89	PAXIP1-AS2	PAXIP1 antisense RNA 2
570	3,97E-01	4,01E-01	3,55E-01	0,6212	0,9243717	0,57422682	8,18	BAAT	bile acid-CoA:amino acid N-acyltransferase
6009	2,22E-27	2,67E+01	6,05E-28	0,0524	10,9585449	0,57392689	6577,43	RHEB	Ras homolog, mTORC1 binding
107986121	3,64E-01	4,39E-01	3,24E-01	0,5814	0,9870847	0,57390394	9,71	LOC107986121	uncharacterized LOC107986121
105374454	2,53E-01	5,97E-01	2,17E-01	0,4653	1,2333163	0,57390089	14,7	RASGRP3-AS1	RASGRP3 antisense RNA 1
150353	1,39E-01	8,57E-01	1,15E-01	0,3636	1,5780067	0,57383802	23,7	DNAJB7	DnaJ heat shock protein family (Hsp40) member B7
135114	3,45E-14	1,35E+01	1,37E-14	0,0745	7,69884	0,57380582	746,14	HINT3	histidine triad nucleotide binding protein 3
4084	3,18E-15	1,45E+01	1,23E-15	0,0717	8,0018864	0,5737534	801,97	MXD1	MAX dimerization protein 1
148156	8,14E-18	1,71E+01	2,88E-18	0,0658	8,7158898	0,5737121	987,84	ZNF558	zinc finger protein 558
1663	2,26E-21	2,06E+01	7,22E-22	0,0597	9,610467	0,57370506	1609,82	DDX11	DEAD/H-box helicase 11
100131096	1,48E-03	2,83E+00	9,84E-04	0,174	3,2951933	0,57346264	105,63	TNRC6C-AS1	replaced by ID 11322
105369745	1,10E-01	9,59E-01	8,89E-02	0,337	1,7014618	0,57341645	27,58	LOC105369745	uncharacterized LOC105369745
91687	2,82E-20	1,95E+01	9,30E-21	0,0614	9,3436915	0,57333956	1323,21	CENPL	centromere protein L
105379028	3,60E-02	1,44E+00	2,74E-02	0,2599	2,2054552	0,573123	47,93	LOC105379028	uncharacterized LOC105379028
105370459	5,66E-04	3,25E+00	3,64E-04	0,1608	3,5648206	0,57308186	127,39	LOC105370459	uncharacterized LOC105370459
4147	4,45E-16	1,54E+01	1,67E-16	0,0695	8,2439915	0,5730798	1120,1	MATN2	matrilin 2
9044	3,13E-25	2,45E+01	9,02E-26	0,0546	10,4958665	0,57285786	2576,75	BTAF1	B-TFIID TATA-box binding protein associated factor 1
50618	2,20E-30	2,97E+01	5,55E-31	0,0495	11,5744967	0,57282843	2514,89	ITSN2	intersectin 2
9208	5,12E-21	2,03E+01	1,65E-21	0,0601	9,5247634	0,57259517	6987,6	LRRFIP1	LRR binding FLII interacting protein 1
116150	1,43E-24	2,38E+01	4,19E-25	0,0553	10,3499238	0,57247097	2718,49	NUS1	NUS1 dehydrodolichyl diphosphate synthase subunit
729288	1,86E-05	4,73E+00	1,08E-05	0,1301	4,4003775	0,57245371	200,11	ZNF286B	zinc finger protein 286B (pseudogene)
93081	3,21E-16	1,55E+01	1,20E-16	0,0691	8,2833495	0,57197091	900,12	TEX30	testis expressed 30
84981	7,81E-15	1,41E+01	3,05E-15	0,0724	7,8890114	0,57149034	787,35	MIR22HG	MIR22 host gene
55342	4,58E-18	1,73E+01	1,61E-18	0,0651	8,781594	0,5713821	992,94	STRBP	spermatid perinuclear RNA binding protein
79666	6,10E-10	9,21E+00	2,82E-10	0,0905	6,3082423	0,57083358	502,1	PLEKHF2	pleckstrin homology and FYVE domain containing 2
65266	1,47E-03	2,83E+00	9,81E-04	0,1731	3,2959588	0,57064828	111,66	WNK4	WNK lysine deficient protein kinase 4
165324	2,11E-23	2,27E+01	6,37E-24	0,0566	10,0860408	0,57038323	1866,89	UBXN2A	UBX domain protein 2A
105372308	3,09E-01	5,10E-01	2,71E-01	0,5177	1,1014114	0,57020428	11,23	LOC105372308	uncharacterized LOC105372308
9637	3,61E-36	3,54E+01	7,87E-37	0,045	12,6776369	0,56993209	4396,45	FEZ2	fasciculation and elongation protein zeta 2
105379364	5,65E-02	1,25E+00	4,41E-02	0,2831	2,0130696	0,56990826	38,98	LOC105379364	uncharacterized LOC105379364
11260	7,80E-37	3,61E+01	1,67E-37	0,0445	12,7984136	0,56978286	9333,49	XPOT	exportin for tRNA
2339	1,87E-16	1,57E+01	6,93E-17	0,0682	8,3482306	0,56927891	1542,93	FNTA	farnesyltransferase, CAAX box, alpha
2149	3,07E-29	2,85E+01	7,92E-30	0,0502	11,3442251	0,56927075	2729,83	F2R	coagulation factor II thrombin receptor
4686	8,48E-40	3,91E+01	1,71E-40	0,0427	13,3228177	0,5688086	4539,25	NCBP1	nuclear cap binding protein subunit 1
6635	3,01E-17	1,65E+01	1,09E-17	0,0664	8,564503	0,56870892	2790,28	SNRPE	small nuclear ribonucleoprotein polypeptide E
1622	8,17E-27	2,61E+01	2,25E-27	0,0524	10,8388206	0,56848724	4316,85	DBI	diazepam binding inhibitor, acyl-CoA binding protein
390980	2,04E-08	7,69E+00	1,01E-08	0,0992	5,7293587	0,56845452	356,39	ZNF805	zinc finger protein 805
101928571	9,35E-02	1,03E+00	7,52E-02	0,3192	1,779479	0,56800737	30,71	ZNF649-AS1	ZNF649 antisense RNA 1
23429	1,09E-25	2,50E+01	3,10E-26	0,0536	10,5964363	0,56768762	1998,75	RYBP	RING1 and YY1 binding protein
57620	2,19E-20	1,97E+01	7,20E-21	0,0606	9,3707826	0,56768099	1220,79	STIM2	stromal interaction molecule 2
100874291	2,80E-02	1,55E+00	2,10E-02	0,2458	2,3079947	0,56733905	55,41	ALMS1-IT1	ALMS1 intronic transcript 1
102724528	1,10E-02	1,96E+00	7,90E-03	0,2136	2,6561418	0,56732965	73,72	LOC102724528	uncharacterized LOC102724528
442582	1,37E-06	5,86E+00	7,47E-07	0,1146	4,9486952	0,56722875	249,81	STAG3L2	stromal antigen 3-like 2 (pseudogene)
440072	3,63E-01	4,40E-01	3,22E-01	0,5728	0,9899811	0,56706822	9,22	PRDM10-DT	PRDM10 divergent transcript
105372902	3,77E-01	4,24E-01	3,36E-01	0,589	0,9624889	0,5669093	9,75	LOC105372902	uncharacterized LOC105372902
54518	1,58E-26	2,58E+01	4,39E-27	0,0526	10,7776148	0,56675109	1921,46	APBB1IP	amyloid beta precursor protein binding family B member 1 interacting protein

115703	4,46E-07	6,35E+00	2,36E-07	0,1096	5,1687559	0,56625068	318,69	ARHGAP33	Rho GTPase activating protein 33
27098	1,07E-01	9,71E-01	8,64E-02	0,3302	1,7149411	0,5662494	28,05	CLUL1	clusterin like 1
10333	2,68E-07	6,57E+00	1,40E-07	0,1075	5,265408	0,56613004	301,57	TLR6	toll like receptor 6
10099	1,58E-26	2,58E+01	4,40E-27	0,0525	10,777518	0,56610649	6969,66	TSPAN3	tetraspanin 3
890	6,93E-36	3,52E+01	1,53E-36	0,0448	12,6256319	0,56601026	9428,49	CCNA2	cyclin A2
23279	6,73E-36	3,52E+01	1,48E-36	0,0448	12,6280118	0,56593136	5007,28	NUP160	nucleoporin 160
5965	1,13E-23	2,29E+01	3,40E-24	0,0558	10,1475818	0,5658554	2641,56	RECQL	RecQ like helicase
85460	2,74E-13	1,26E+01	1,12E-13	0,0762	7,4259761	0,5657127	785,95	ZNF518B	zinc finger protein 518B
445372	1,47E-11	1,08E+01	6,38E-12	0,0823	6,8709409	0,5656849	550,82	TRIM6-TRIM	TRIM6-TRIM34 readthrough
10231	3,65E-03	2,44E+00	2,51E-03	0,1872	3,0216939	0,56564538	94,82	RCAN2	regulator of calcineurin 2
107985400	2,81E-01	5,51E-01	2,43E-01	0,4847	1,1668692	0,56556738	13,22	LOC107985	uncharacterized LOC107985400
105377294	8,83E-03	2,05E+00	6,30E-03	0,2069	2,7318817	0,56511933	82,45	LOC105377	uncharacterized LOC105377294
114112	1,21E-07	6,92E+00	6,23E-08	0,1044	5,4121758	0,56501669	365,24	TXNRD3	thioredoxin reductase 3
11329	5,64E-53	5,22E+01	8,41E-54	0,0366	15,4429859	0,56487906	10982,08	STK38	serine/threonine kinase 38
105378728	5,15E-03	2,29E+00	3,59E-03	0,194	2,9121277	0,56484729	84,11	LOC105378	uncharacterized LOC105378728
1479	2,55E-34	3,36E+01	5,83E-35	0,0458	12,3355554	0,56467977	3276,28	CSTF3	cleavage stimulation factor subunit 3
57534	4,03E-26	2,54E+01	1,14E-26	0,0528	10,6898893	0,56462929	3319,7	MIB1	MIB E3 ubiquitin protein ligase 1
101928767	2,96E-01	5,29E-01	2,57E-01	0,4984	1,1327629	0,56461182	12,21	LINC02328	long intergenic non-protein coding RNA 2328
57645	1,24E-37	3,69E+01	2,61E-38	0,0436	12,9419056	0,56460281	3927,94	POGK	pogo transposable element derived with KRAB domain
112268222	3,96E-19	1,84E+01	1,35E-19	0,0623	9,0561384	0,56418584	1824,44	LOC112268	222
7294	3,88E-08	7,41E+00	1,94E-08	0,1004	5,6169142	0,56403561	345,32	TXK	TXK tyrosine kinase
84289	6,61E-19	1,82E+01	2,27E-19	0,0627	8,9995741	0,56398478	1198,18	ING5	inhibitor of growth family member 5
4976	4,10E-41	4,04E+01	8,00E-42	0,0416	13,5492611	0,56398301	6185,64	OPA1	OPA1 mitochondrial dynamin like GTPase
57412	8,81E-02	1,06E+00	7,05E-02	0,3116	1,8083814	0,56354996	31,14	AS3MT	arsenite methyltransferase
9445	3,48E-17	1,65E+01	1,26E-17	0,0659	8,5475515	0,56295611	4012,59	ITM2B	integral membrane protein 2B
892	9,85E-21	2,00E+01	3,21E-21	0,0595	9,4555774	0,56239838	1811,38	CCNC	cyclin C
284390	6,10E-03	2,21E+00	4,28E-03	0,1968	2,856569	0,56221611	88,7	ZNF763	zinc finger protein 763
55763	1,52E-27	2,68E+01	4,11E-28	0,0511	10,9933714	0,56202597	2020,24	EXOC1	exocyst complex component 1
10693	7,34E-03	2,13E+00	5,20E-03	0,2011	2,7945695	0,56201874	76,84	CCT6B	chaperonin containing TCP1 subunit 6B
56980	4,65E-15	1,43E+01	1,80E-15	0,0707	7,9542233	0,56199693	791,96	PRDM10	PR/SET domain 10
10286	3,55E-18	1,74E+01	1,25E-18	0,0638	8,8103223	0,56196424	2752,28	BCAS2	BCAS2 pre-mRNA processing factor
100129480	8,60E-02	1,07E+00	6,87E-02	0,3086	1,8201618	0,56174622	32,16	MKRN2OS	MKRN2 opposite strand
22863	7,58E-19	1,81E+01	2,60E-19	0,0625	8,9842873	0,5616524	1331	ATG14	autophagy related 14
113263	5,56E-06	5,25E+00	3,12E-06	0,1204	4,6626671	0,56133626	224,97	GLCCI1	glucocorticoid induced 1
100288332	5,62E-05	4,25E+00	3,35E-05	0,1353	4,1481755	0,56125864	175,29	NPIPA5	nuclear pore complex interacting protein family member A5
8490	1,42E-05	4,85E+00	8,16E-06	0,1258	4,4610327	0,56121775	217,07	RGS5	regulator of G protein signaling 5
112840933	2,23E-01	6,52E-01	1,90E-01	0,4283	1,3101173	0,5611556	16,84	ZKSCAN7-A	ZKSCAN7 ZNF cluster antisense RNA 1
100532724	5,31E-09	8,27E+00	2,56E-09	0,0942	5,9578332	0,56114408	431,94	NPHP3-ACA	NPHP3-ACAD11 readthrough (NMD candidate)
147694	7,50E-09	8,12E+00	3,63E-09	0,0951	5,9000955	0,5608147	392,5	ZNF548	zinc finger protein 548
989	9,22E-43	4,20E+01	1,74E-43	0,0406	13,8275598	0,56076102	10623,67	SEPTIN7	septin 7
729681	2,35E-01	6,29E-01	2,01E-01	0,4384	1,2784394	0,56051842	16,35	LOC729681	uncharacterized LOC729681
84529	8,22E-14	1,31E+01	3,31E-14	0,0739	7,5856932	0,56046429	714,83	CDIN1	CDAN1 interacting nuclease 1
84142	1,61E-18	1,78E+01	5,58E-19	0,063	8,9000282	0,56038638	1777,93	ABRAXAS1	abraxas 1, BRCA1 A complex subunit
3714	1,03E-02	1,99E+00	7,37E-03	0,209	2,6796431	0,56009762	73,44	JAG2	jagged canonical Notch ligand 2
80321	1,42E-12	1,18E+01	5,96E-13	0,0777	7,2014806	0,55969999	692,77	CEP70	centrosomal protein 70
7257	1,79E-24	2,37E+01	5,27E-25	0,0542	10,3278843	0,55962705	1895,67	TSNAX	translin associated factor X
138241	2,16E-10	9,67E+00	9,83E-11	0,0865	6,4696008	0,55953423	595,53	C9orf85	chromosome 9 open reading frame 85
27185	3,12E-06	5,51E+00	1,72E-06	0,117	4,7834826	0,55944845	239,76	DISC1	DISC1 scaffold protein
101927556	3,27E-26	2,55E+01	9,17E-27	0,0522	10,70962	0,55932425	2013,98	LOC101927	uncharacterized LOC101927556
51174	1,32E-09	8,88E+00	6,22E-10	0,0904	6,184676	0,55932331	498,3	TUBD1	tubulin delta 1
22911	2,48E-18	1,76E+01	8,68E-19	0,0632	8,8509799	0,55916079	1188,21	WDR47	WD repeat domain 47
5771	3,32E-29	2,85E+01	8,58E-30	0,0493	11,3372213	0,55911828	3301,78	PTPN2	protein tyrosine phosphatase non-receptor type 2
79699	1,06E-21	2,10E+01	3,34E-22	0,0577	9,6895503	0,55910767	1678,22	ZYG11B	zyg-11 family member B, cell cycle regulator
51191	2,01E-27	2,67E+01	5,46E-28	0,051	10,967692	0,55907586	2283,58	HERC5	HECT and RLD domain containing E3 ubiquitin protein ligase 5
55425	1,73E-19	1,88E+01	5,83E-20	0,0611	9,147395	0,55889295	1451,39	GPALPP1	GPALPP motifs containing 1
10930	3,11E-01	5,07E-01	2,72E-01	0,5087	1,0983385	0,55873234	11,69	APOBEC2	apolipoprotein B mRNA editing enzyme catalytic subunit 2
55193	1,96E-42	4,17E+01	3,71E-43	0,0405	13,7728135	0,55837548	6245,73	PBRM1	polybromo 1
108949267	9,86E-02	1,01E+00	7,95E-02	0,3183	1,7534041	0,55813416	31,33	ACBD7-DCL	ACBD7-DCLRE1CP1 readthrough
80135	1,98E-24	2,37E+01	5,84E-25	0,0541	10,3179672	0,55804668	3663,07	RPF1	ribosome production factor 1 homolog
7773	2,46E-06	5,61E+00	1,35E-06	0,1155	4,8315395	0,55797394	253,21	ZNF230	zinc finger protein 230
55254	2,71E-18	1,76E+01	9,50E-19	0,0631	8,8408688	0,55788767	1317,63	TMEM39A	transmembrane protein 39A
8880	7,58E-32	3,11E+01	1,84E-32	0,047	11,863245	0,55784179	3183,51	FUBP1	far upstream element binding protein 1
5108	2,37E-40	3,96E+01	4,70E-41	0,0416	13,4186305	0,55761719	6203,43	PCM1	pericentriolar material 1
79183	1,41E-26	2,59E+01	3,91E-27	0,0517	10,7882392	0,55760087	2081,06	TTPAL	alpha tocopherol transfer protein like
116966	1,09E-03	2,96E+00	7,15E-04	0,1647	3,3838365	0,55736428	118,29	WDR17	WD repeat domain 17
90737	7,45E-12	1,11E+01	3,20E-12	0,0799	6,9688222	0,55713609	948,93	PAGE5	PAGE family member 5
387707	1,18E-02	1,93E+00	8,52E-03	0,2118	2,6305981	0,55711127	72,51	CC2D2B	coiled-coil and C2 domain containing 2B
444	5,40E-27	2,63E+01	1,48E-27	0,0512	10,8770171	0,55693694	12512,87	ASPH	aspartate beta-hydroxylase
645212	9,11E-07	6,04E+00	4,90E-07	0,1107	5,0302793	0,55663528	273,5	EIF3J-DT	EIF3J divergent transcript
414777	1,29E-30	2,99E+01	3,24E-31	0,0479	11,620567	0,55659057	2730,55	HCG18	HLA complex group 18
56001	2,97E-01	5,27E-01	2,59E-01	0,4926	1,1296571	0,55642349	12,63	NXF2	nuclear RNA export factor 2
140688	1,74E-08	7,76E+00	8,59E-09	0,0966	5,7564042	0,55626821	377,83	NOL4L	nucleolar protein 4 like
5933	5,49E-27	2,63E+01	1,51E-27	0,0511	10,8753961	0,55622058	2881,56	RBL1	RB transcriptional corepressor like 1
1756	6,95E-11	1,02E+01	3,10E-11	0,0837	6,6418702	0,55594655	542,31	DMD	dystrophin
266971	2,57E-06	5,59E+00	1,41E-06	0,1153	4,8233626	0,55593282	255,45	PIPSL	PIP5K1A and PSMD4 like (pseudogene)
25871	9,41E-20	1,90E+01	3,15E-20	0,0603	9,2138382	0,55584583	1747,9	NEPRO	nucleolus and neural progenitor protein
648987	3,58E-02	1,45E+00	2,73E-02	0,2517	2,2075539	0,55557967	48,33	ANXA2R-OT	ANXA2R overlapping transcript
3433	1,58E-35	3,48E+01	3,50E-36	0,0442	12,5601471	0,55551048	4227,8	IFIT2	interferon induced protein with tetratricopeptide repeats 2
107984019	3,26E-02	1,49E+00	2,47E-02	0,2472	2,246684	0,55543416	51,82	LOC107984	uncharacterized LOC107984019
2908	2,98E-31	3,05E+01	7,33E-32	0,0473	11,7468238	0,55540194	6144,36	NR3C1	nuclear receptor subfamily 3 group C member 1
55035	1,84E-27	2,67E+01	4,99E-28	0,0506	10,975922	0,55533773	2785,65	NOL8	nucleolar protein 8
54965	2,44E-20	1,96E+01	8,04E-21	0,0593	9,3590983	0,55528372	1283,65	PIGX	phosphatidylinositol glycan anchor biosynthesis class X
9403	8,14E-34	3,31E+01	1,88E-34	0,0454	12,2407723	0,555251	7628,91	SELENOF	selenoprotein F
96626	6,59E-02	1,18E+00	5,19E-02	0,2855	1,9436561	0,55494628	37,55	LIMS3	LIM zinc finger domain containing 3
5711	7,03E-35	3,42E+01	1,58E-35	0,0446	12,440079	0,55463	4178,28	PSMD5	proteasome 26S subunit, non-ATPase 5
102725021	5,16E-02	1,29E+00	4,01E-02	0,2701	2,0527503	0,55451735	43,22	ARHGAP11E	ARHGAP11B divergent transcript
8187	1,33E-08	7,88E+00	6,52E-09	0,0956	5,80278	0,55449852	438,87	ZNF239	zinc finger protein 239
105369755	1,15E-04	3,94E+00	7,02E-05	0,1395	3,9757751	0,55443705	181,33	LOC105369	uncharacterized LOC105369755
728609	2,61E-02	1,58E+00	1,95E-02	0,2373	2,3356847	0,55427561	58,01	SDHAP3	SDHA pseudogene 3
100861402	7,61E-09	8,12E+00	3,69E-09	0,094	5,8976036	0,55415756	467,85	CERS6-AS1	CERS6 antisense RNA 1
7096	3,65E-02	1,44E+00	2,78E-02	0,2519	2,1995765	0,55404309	50,76	TLR1	toll like receptor 1
200558	5,70E-10	9,24E+00	2,64E-10	0,0877	6,3187179	0,55390224	489,98	APLF	aprataxin and PNKP like factor
133022	9,54E-03	2,02E+00	6,83E-03	0,2047	2,7050489	0,55381938	80,2	TRAM1L1	translocation associated membrane protein 1 like 1
286046	5,23E-03	2,28E+00	3,65E-03	0,1905	2,9067267	0,55359427	95,41	XKR6	XK related 6
678	3,55E-16	1,54E+01	1,33E-16	0,0669	8,2712453	0,55352973	1312,66	ZFP36L2	ZFP36 ring finger protein like 2
285761	3,04E-18	1,75E+01	1,06E-18	0,0627	8,8281346	0,55329402	1215,88	DCBLD1	discoidin, CUB and LCCL domain containing 1
93380	3,18E-16	1,55E+01	1,18E-16	0,0668	8,2846839	0,55325732	1815,07	MMGT1	membrane magnesium transporter 1
5581	8,22E-19	1,81E+01	2,83E-19	0,0616	8,9751904	0,55319846	1175,65	PRKCE	protein kinase C epsilon
6788	1,15E-15	1,49E+01	4,38E-16	0,0681	8,1276222	0,55318927	937,51	STK3	serine/threonine kinase 3
641339	6,59E-06	5,18E+00	3,71E-06	0,1195	4,6268488	0,55313079	228,74	ZNF674	zinc finger protein 674
375748	1,87E-23	2,27E+01	5,64E-24	0,0548	10,097956	0,55310475	1676,31	ERCC6L2	ERCC excision repair 6 like 2
100529207	2,03E-13	1,27E+01	8,27E-14	0,0741	7,4660089	0,55299811	734,44	RAD51L3-RF	RAD51L3-RFFL readthrough
60488	1,16E-21	2,09E+01	3,69E-22	0,0571	9,6794378	0,55288257	2210,82	MRPS35	mitochondrial ribosomal protein S35
6772	3,11E-32	3,15E+01	7,47E-33	0,0463	11,9383658	0,55286882	4815,9	STAT1	signal transducer and activator of transcription 1
730234	2,94E-01	5,32E-01	2,56E-01	0,487	1,1350878	0,55276106	13,67	LOC730234	uncharacterized LOC730234
114825	4,09E-20	1,94E+01	1,36E-20	0,0594	9,3037721	0,552689	1272,4	PWWP2A	PWWP domain containing 2A
55270	4,52E-25	2,43E+01	1,31E-25	0,0528	10,4606635	0,55262161	2620,35	NUDT15	nudix hydrolase 15
3224	8,84E-02	1,05E+00	7,08E-02	0,3058	1,8068092	0,55259824	34,54	HOXC8	homeobox C8
84071	6,82E-03	2,17E+00	4,81E-03	0,1959	2,8193989	0,55231431	87,84	ARMC2	armadillo repeat containing 2
65243	1,12E-10	9,95E+00	5,05E-11	0,0841	6,5695528	0,55223464	551,45	ZFP69B	ZFP69 zinc finger protein B
100288695	1,22E-02	1,91E+00	8,83E-03	0,2109	2,6187184	0,55216958	71,49	LIMS4	LIM zinc finger domain containing 4
80232	8,04E-36	3,51E+01	1,77E-36	0,0438	12,6137751	0,55215573	6775,53	WDR26	WD repeat domain 26
285955	7,30E-02	1,14E+00	5,78E-02	0,2911	1,8969861	0,55214611	38,79	SPDYE1	speedy/RINGO cell cycle regulator family member E1
29078	2,82E-12	1,15E+01	1,20E-12	0,0777	7,105932	0,55209634	836,77	NDUFAF4	NADH:ubiquinone oxidoreductase complex assembly factor 4
27141	1,09E-11	1,10E+01	4,69E-12	0,0798	6,9147865	0,55206863	583,79	CIDEB	cell death inducing DFFA like effector b
51569	2,18E-26	2,57E+01	6,10E-27	0,0514	10,7473952	0,55206657	3103,04	UFM1	ubiquitin fold modifier 1
340706	1,96E-01	7,08E-01	1,65E-01	0,3978	1,3876882	0,55201726	21,19	VWA2	von Willebrand factor A domain containing 2
5599	2,76E-27	2,66E+01	7,52E-28	0,0504	10,9387443	0,55184579	2501,59	MAPK8	mitogen-activated protein kinase 8
116937	2,64E-01	5,78E-01	2,27E-01	0,4569	1,2072794	0,55163927	15,24	SNORD83A	small nucleolar RNA, C/D box 83A
55127	8,78E-34	3,31E+01	2,03E-34	0,0451	12,2344794	0,55162983	4000,24	HEATR1	HEAT repeat containing 1

219736	2,60E-03	2,59E+00	1,77E-03	0,1764	3,1269455	0,5514829	104,21	STOX1	storkhead box 1
84343	2,16E-19	1,87E+01	7,33E-20	0,0604	9,1226737	0,55130465	2130,03	HPS3	HPS3 biogenesis of lysosomal organelles complex 2 subunit 1
8615	3,94E-30	2,94E+01	9,97E-31	0,0478	11,5241188	0,55127106	6994,62	USO1	USO1 vesicle transport factor
107984343	3,99E-01	3,99E-01	3,57E-01	0,5989	0,9205018	0,55125618	8,64	LOC107984	uncharacterized LOC107984343
2072	2,30E-11	1,06E+01	1,01E-11	0,081	6,8056176	0,5512506	609,81	ERCC4	ERCC excision repair 4, endonuclease catalytic subunit
2960	5,15E-14	1,33E+01	2,06E-14	0,0721	7,6469231	0,55116355	843,22	GTF2E1	general transcription factor IIE subunit 1
107984043	5,28E-03	2,28E+00	3,68E-03	0,1898	2,9040282	0,55107832	94,53	LOC107984	formin-2-like
84622	1,18E-07	6,93E+00	6,03E-08	0,1017	5,417939	0,55100432	353,88	ZNF594	zinc finger protein 594
100616439	7,47E-02	1,13E+00	5,93E-02	0,292	1,8863248	0,55085586	37,15	MIR4658	microRNA 4658
858	6,04E-22	2,12E+01	1,90E-22	0,0565	9,7471615	0,55081806	3271,01	CAV2	caveolin 2
54627	1,23E-09	8,91E+00	5,78E-10	0,0889	6,1962749	0,55072853	453,36	MAP10	microtubule associated protein 10
5706	2,38E-44	4,36E+01	4,34E-45	0,0391	14,0906539	0,5506039	7116,09	PSMC6	proteasome 26S subunit, ATPase 6
100132618	5,57E-08	7,25E+00	2,81E-08	0,0991	5,5529574	0,55021857	367,51	ZRANB2-AS	ZRANB2 antisense RNA 1
81034	1,00E-23	2,30E+01	3,01E-24	0,0541	10,1593611	0,5500479	3054,74	SLC25A32	solute carrier family 25 member 32
5887	6,06E-46	4,52E+01	1,06E-46	0,0383	14,3503871	0,55003331	12898,87	RAD23B	RAD23 homolog B, nucleotide excision repair protein
79887	1,52E-10	9,82E+00	6,87E-11	0,0843	6,5234076	0,55002013	508,5	PLBD1	phospholipase B domain containing 1
84057	2,88E-20	1,95E+01	9,50E-21	0,0589	9,3414397	0,54988695	1325,92	MND1	meiotic nuclear divisions 1
5645	2,21E-02	1,66E+00	1,64E-02	0,229	2,4008529	0,54974913	58,35	PRSS2	serine protease 2
107985343	8,84E-03	2,05E+00	6,31E-03	0,2012	2,7313323	0,54955328	82,01	LINC01836	long intergenic non-protein coding RNA 1836
55319	1,76E-17	1,68E+01	6,32E-18	0,0637	8,6266396	0,54952506	1518,81	TMA16	translation machinery associated 16 homolog
23169	5,98E-16	1,52E+01	2,25E-16	0,0669	8,2081267	0,54926892	1148	SLC35D1	solute carrier family 35 member D1
7637	7,08E-15	1,41E+01	2,76E-15	0,0695	7,9015086	0,5492634	867,04	ZNF84	zinc finger protein 84
9652	2,92E-27	2,65E+01	7,97E-28	0,0502	10,9334876	0,54919299	4653,95	SKIC3	SKI3 subunit of superkiller complex
101929494	1,92E-09	8,72E+00	9,10E-10	0,0897	6,124367	0,54914124	484,99	LOC101929	uncharacterized LOC101929494
252995	3,83E-01	4,17E-01	3,42E-01	0,5781	0,9496323	0,5489866	9,08	FNDC5	fibronectin type III domain containing 5
55667	1,41E-18	1,79E+01	4,90E-19	0,0616	8,9144854	0,54892718	1290,04	DENND4C	DENN domain containing 4C
101927179	1,81E-03	2,74E+00	1,22E-03	0,1697	3,2353239	0,54890096	113,53	LOC101927	uncharacterized LOC101927179
123016	1,87E-18	1,77E+01	6,51E-19	0,0618	8,8829939	0,54874642	1225,38	TTC8	tetratricopeptide repeat domain 8
139420	1,30E-01	8,86E-01	1,06E-01	0,3398	1,6143229	0,54851712	30,05	PPP4R3C	protein phosphatase 4 regulatory subunit 3C
100128594	2,07E-02	1,68E+00	1,53E-02	0,2261	2,4258502	0,54849709	66,49	TMSB15B-A	TMSB15B antisense RNA 1
221468	3,95E-07	6,40E+00	2,08E-07	0,1056	5,1917124	0,54831558	301,45	TMEM217	transmembrane protein 217
80306	5,72E-25	2,42E+01	1,66E-25	0,0525	10,4381546	0,54826279	1874,32	MED28	mediator complex subunit 28
157657	1,92E-04	3,72E+00	1,19E-04	0,1425	3,8481845	0,54825324	166,67	CFAP418	cilia and flagella associated protein 418
3150	3,59E-31	3,04E+01	8,85E-32	0,0467	11,7309397	0,54819988	11633,95	HMGN1	high mobility group nucleosome binding domain 1
64412	3,44E-17	1,65E+01	1,24E-17	0,0641	8,5487042	0,54814062	1075,85	GZF1	GDNF inducible zinc finger protein 1
5281	3,10E-10	9,51E+00	1,42E-10	0,0855	6,4140811	0,54809141	537,81	PIGF	phosphatidylinositol glycan anchor biosynthesis class F
440738	3,93E-01	4,06E-01	3,51E-01	0,5878	0,9322931	0,54797025	8,61	MAP1LC3C	microtubule associated protein 1 light chain 3 gamma
2635	2,89E-26	2,55E+01	8,09E-27	0,0511	10,7212229	0,54795322	3922,1	GBP3	guanylate binding protein 3
26515	8,95E-16	1,50E+01	3,39E-16	0,0672	8,1587415	0,54791703	984,12	TIMM10B	translocase of inner mitochondrial membrane 10B
101927872	3,21E-03	2,49E+00	2,20E-03	0,1789	3,0624563	0,54791207	99,67	LOC101927	uncharacterized LOC101927872
9782	4,57E-37	3,63E+01	9,75E-38	0,0427	12,8403347	0,5478608	23211,1	MATR3	matrin 3
3454	1,35E-29	2,89E+01	3,47E-30	0,048	11,4161193	0,54770533	3795,58	IFNAR1	interferon alpha and beta receptor subunit 1
84174	6,54E-04	3,18E+00	4,23E-04	0,1554	3,5251372	0,54765963	172,18	SLA2	Src like adaptor 2
64645	4,69E-29	2,83E+01	1,22E-29	0,0484	11,3066424	0,54760822	3039,18	MFSD14A	major facilitator superfamily domain containing 14A
105375785	4,55E-06	5,34E+00	2,54E-06	0,1164	4,7049278	0,54752418	242,76	LOC105375	uncharacterized LOC105375785
6747	1,11E-31	3,10E+01	2,71E-32	0,0463	11,8305918	0,54730534	8107,55	SSR3	signal sequence receptor subunit 3
2308	3,08E-08	7,51E+00	1,54E-08	0,0967	6,5574967	0,54730248	424,39	FOXO1	forkhead box O1
5111	6,60E-36	3,52E+01	1,45E-36	0,0433	12,6295967	0,54721183	9793,82	PCNA	proliferating cell nuclear antigen
55679	7,34E-06	5,13E+00	4,15E-06	0,1188	4,6038488	0,5471034	278,27	LIMS2	LIM zinc finger domain containing 2
55699	6,00E-35	3,42E+01	1,35E-35	0,0439	12,4528925	0,5467377	9346,8	IARS2	isoleucyl-tRNA synthetase 2, mitochondrial
101927864	7,42E-06	5,13E+00	4,19E-06	0,1188	4,6015413	0,54665215	237,73	LOC101927	uncharacterized LOC101927864
79898	1,44E-07	6,84E+00	7,41E-08	0,1016	5,3809281	0,54660493	360,84	ZNF613	zinc finger protein 613
285704	3,76E-35	3,44E+01	8,41E-36	0,0438	12,4905401	0,54659868	5482,19	RGMB	repulsive guidance molecule BMP co-receptor b
51326	6,66E-10	9,18E+00	3,09E-10	0,0868	6,2942801	0,54649753	531,07	ARL17A	ADP ribosylation factor like GTPase 17A
4059	1,39E-12	1,19E+01	5,84E-13	0,0759	7,2041388	0,54648343	682,46	BCAM	basal cell adhesion molecule (Lutheran blood group)
29066	2,07E-28	2,77E+01	5,48E-29	0,0489	11,1737164	0,54640416	2692,41	ZC3H7A	zinc finger CCCH-type containing 7A
5495	2,24E-25	2,46E+01	6,43E-26	0,0519	10,5278993	0,54635676	2722,49	PPM1B	protein phosphatase, Mg2+/Mn2+ dependent 1B
107985014	2,87E-01	5,42E-01	2,49E-01	0,4741	1,1522311	0,54631668	13,6	LOC107985	uncharacterized LOC107985014
10905	3,55E-23	2,24E+01	1,08E-23	0,0544	10,0340879	0,54630538	2863,24	MAN1A2	mannosidase alpha class 1A member 2
84272	2,16E-18	1,77E+01	7,54E-19	0,0616	8,8666165	0,54626462	1594,06	YIPF4	Yip1 domain family member 4
647135	2,22E-20	1,97E+01	7,29E-21	0,0583	9,3694707	0,54607244	1611,59	SRGAP2B	SLIT-ROBO Rho GTPase activating protein 2B
25820	8,48E-25	2,41E+01	2,47E-25	0,0525	10,4004079	0,5460022	2403,78	ARIH1	ariadne RBR E3 ubiquitin protein ligase 1
5229	1,53E-14	1,38E+01	6,02E-15	0,0699	7,8035627	0,54571976	1098,59	PGGT1B	protein geranylgeranyltransferase type I subunit beta
10210	1,75E-27	2,68E+01	4,75E-28	0,0497	10,9804112	0,54557486	2879,08	TOPORS	TOP1 binding arginine/serine rich protein, E3 ubiquitin ligase
90488	1,49E-26	2,58E+01	4,13E-27	0,0506	10,7831746	0,54545318	2650,01	TMEM263	transmembrane protein 263
8036	4,64E-25	2,43E+01	1,34E-25	0,0522	10,4581783	0,54545296	1955,64	SHOC2	SHOC2 leucine rich repeat scaffold protein
653234	7,96E-02	1,10E+00	6,33E-02	0,2935	1,8567839	0,54491478	35,46	AGAP10P	ArfGAP with GTPase domain, ankyrin repeat and PH domain 10, pseudogene
100507098	1,70E-01	7,70E-01	1,42E-01	0,3707	1,4694519	0,54473251	22,26	ADAMTS9-A	ADAMTS9 antisense RNA 2
23637	1,54E-33	3,28E+01	3,59E-34	0,0447	12,188187	0,54469144	3640,31	RABGAP1	RAB GTPase activating protein 1
79158	2,80E-23	2,26E+01	8,48E-24	0,0541	10,0579322	0,54454767	2123,73	GNPTAB	N-acetylglucosamine-1-phosphate transferase subunits alpha and beta
55421	3,38E-27	2,65E+01	9,22E-28	0,0499	10,9202514	0,54451789	2854,25	NCBP3	nuclear cap binding subunit 3
7059	2,62E-04	3,58E+00	1,64E-04	0,1445	3,7681072	0,54445997	156,95	THBS3	thrombospondin 3
100302285	1,28E-04	3,89E+00	7,84E-05	0,1378	3,9492493	0,54431071	2110,7	MIR1244-1	microRNA 1244-1
54534	9,47E-23	2,20E+01	2,92E-23	0,0548	9,9355329	0,54429926	2138,83	MRPL50	mitochondrial ribosomal protein L50
10845	2,00E-27	2,67E+01	5,42E-28	0,0496	10,9684267	0,54414266	2346,95	CLPX	caseinolytic mitochondrial matrix peptidase chaperone subunit X
4882	6,18E-04	3,21E+00	3,99E-04	0,1537	3,5406898	0,54408929	138,77	NPR2	natriuretic peptide receptor 2
4735	2,31E-49	4,86E+01	3,70E-50	0,0365	14,8921817	0,54408714	20797,64	SEPTIN2	septin 2
220134	1,67E-21	2,08E+01	5,32E-22	0,0564	9,6418981	0,5439998	1479,34	SKA1	spindle and kinetochore associated complex subunit 1
257106	2,91E-03	2,54E+00	1,98E-03	0,1759	3,0930664	0,54397569	102,37	ARHGAP30	Rho GTPase activating protein 30
730102	4,29E-07	6,37E+00	2,27E-07	0,1051	5,1761129	0,54379559	327,44	CRYZL2P	crystallin zeta like 2, pseudogene
727764	5,75E-03	2,24E+00	4,03E-03	0,189	2,8756689	0,54355407	98,84	MAFIP	MAFF interacting protein (pseudogene)
3781	6,49E-02	1,19E+00	5,11E-02	0,2786	1,9509466	0,54351165	43,98	KCNN2	potassium calcium-activated channel subfamily N member 2
84267	3,63E-21	2,04E+01	1,17E-21	0,0568	9,5608075	0,54329376	1562,27	C9orf64	chromosome 9 open reading frame 64
130013	3,08E-01	5,11E-01	2,69E-01	0,4914	1,1055011	0,54329207	12,65	ACMSD	aminocarboxymuconate semialdehyde decarboxylase
79977	4,47E-01	3,50E-01	4,05E-01	0,653	0,8318518	0,54320219	7,06	GRHL2	grainyhead like transcription factor 2
439949	4,37E-03	2,36E+00	3,02E-03	0,1832	2,9652753	0,54315357	97,33	PRKCQ-AS1	PRKCQ antisense RNA 1
6571	1,68E-04	3,77E+00	1,04E-04	0,1399	3,8814889	0,54312898	184,67	SLC18A2	solute carrier family 18 member A2
100506994	2,98E-07	6,53E+00	1,56E-07	0,1034	5,2454676	0,54258159	337,95	PTPRG-AS1	PTPRG antisense RNA 1
154881	1,06E-09	8,97E+00	4,96E-10	0,0872	6,2202548	0,54252808	497,28	KCTD7	potassium channel tetramerization domain containing 7
158135	2,76E-17	1,66E+01	9,97E-18	0,0633	8,5743347	0,54243957	1166,38	TTLL11	tubulin tyrosine ligase like 11
2967	1,35E-33	3,29E+01	3,15E-34	0,0445	12,1988701	0,5423541	5185,88	GTF2H3	general transcription factor IIH subunit 3
27165	1,57E-01	8,04E-01	1,31E-01	0,3588	1,5111994	0,54215425	23,85	GLS2	glutaminase 2
100505915	4,67E-02	1,33E+00	3,61E-02	0,2586	2,0960668	0,54213738	45,42	LOC100505	uncharacterized LOC100505915
223082	3,14E-06	5,50E+00	1,74E-06	0,1134	4,781632	0,54211043	255,28	ZNRF2	zinc and ring finger 2
29121	2,21E-03	2,66E+00	1,49E-03	0,1707	3,1760688	0,54202803	116,02	CLEC2D	C-type lectin domain family 2 member D
10492	8,47E-42	4,11E+01	1,63E-42	0,0397	13,6653938	0,54202143	16036,77	SYNCRIP	synaptotagmin binding cytoplasmic RNA interacting protein
100507495	7,27E-04	3,14E+00	4,72E-04	0,155	3,4960676	0,54191726	151,67	SDCBP2-AS	SDCBP2 antisense RNA 1
102723786	1,47E-01	8,33E-01	1,22E-01	0,3499	1,5480042	0,54170154	25,25	LOC102723	uncharacterized LOC102723786
51474	4,28E-47	4,64E+01	7,27E-48	0,0373	14,5349984	0,54157736	10005,16	LIMA1	LIM domain and actin binding 1
9801	1,06E-21	2,10E+01	3,34E-22	0,0559	9,689572	0,5414446	2513,46	MRPL19	mitochondrial ribosomal protein L19
2114	1,44E-24	2,38E+01	4,22E-25	0,0523	10,3493039	0,5413627	1931,44	ETS2	ETS proto-oncogene 2, transcription factor
105373095	1,14E-05	4,94E+00	6,54E-06	0,1201	4,5080949	0,54130452	233,38	SELENOO-A	SELENOO antisense RNA 1
26190	5,98E-36	3,52E+01	1,31E-36	0,0428	12,6374679	0,54120078	4573,28	FBXW2	F-box and WD repeat domain containing 2
440068	2,11E-01	6,76E-01	1,78E-01	0,4021	1,3455813	0,54109439	19,24	CARD17P	caspase recruitment domain family member 17, pseudogene
27039	8,32E-05	4,08E+00	5,02E-05	0,1334	4,0546055	0,54087831	203,84	PKD2L2	polycystin 2 like 2, transient receptor potential cation channel
6596	9,31E-29	2,80E+01	2,44E-29	0,0481	11,2455605	0,54071136	3194,63	HLTF	helicase like transcription factor
92346	2,30E-03	2,64E+00	1,55E-03	0,1709	3,1645909	0,54068568	116,34	C1orf105	chromosome 1 open reading frame 105
8434	3,03E-08	7,52E+00	1,51E-08	0,0955	5,6602923	0,54056783	417,16	RECK	reversion inducing cysteine rich protein with kazal motifs
9519	2,46E-12	1,16E+01	1,04E-12	0,0758	7,1250852	0,54040286	743,81	TBPL1	TATA-box binding protein like 1
1303	6,04E-35	3,42E+01	1,36E-35	0,0434	12,4522843	0,5403562	8180,57	COL12A1	collagen type XII alpha 1 chain
79053	3,18E-16	1,55E+01	1,19E-16	0,0652	8,2845913	0,54035313	4046,71	ALG8	ALG8 alpha-1,3-glucosyltransferase
222950	1,14E-01	9,43E-01	9,27E-02	0,3213	1,6813498	0,54017622	32,52	NYAP1	neuronal tyrosine phosphorylated phosphoinositide-3-kinase adaptor 1
286101	7,74E-16	1,51E+01	2,92E-16	0,0661	8,1764996	0,54014204	1054,43	ZNF252P	zinc finger protein 252, pseudogene
113218477	1,16E-07	6,94E+00	5,94E-08	0,0996	5,4205054	0,53986021	349,89	TIMM23B-A	TIMM23B-AGAP6 readthrough (NMD candidate)
202020	1,83E-01	7,38E-01	1,54E-01	0,3783	1,4267725	0,53981463	21,69	TAPT1-AS1	TAPT1 antisense RNA 1 (head to head)
9674	1,35E-01	8,70E-01	1,11E-01	0,3383	1,5954329	0,53978585	28,85	KIAA0040	KIAA0040
55596	1,12E-27	2,70E+01	3,03E-28	0,049	11,0209842	0,53969686	2430,28	ZCCHC8	zinc finger CCHC-type containing 8
222235	7,74E-05	4,11E+00	4,66E-05	0,1325	4,0721402	0,53940555	181,78	FBXL13	F-box and leucine rich repeat protein 13
9976	1,31E-04	3,88E+00	8,01E-05	0,1367	3,9439901	0,53910167	196,84	CLEC2B	C-type lectin domain family 2 member B
100616139	1,02E-02	1,99E+00	7,30E-03	0,201	2,6827101	0,53909875	79,34	MIR4741	microRNA 4741

51088	2,48E-40	3,96E+01	4,92E-41	0,0401	13,4152762	0,53840916	6646,42	KLHL5	kelch like family member 5
26512	7,33E-23	2,21E+01	2,25E-23	0,054	9,961468	0,53832603	1871,21	INTS6	integrator complex subunit 6
84436	2,65E-12	1,16E+01	1,12E-12	0,0756	7,1147567	0,53820144	678,15	ZNF528	zinc finger protein 528
107984397	1,63E-01	7,88E-01	1,36E-01	0,3606	1,4921241	0,53804425	23,65	LOC107984	replaced by ID 9854
150468	2,57E-25	2,46E+01	7,41E-26	0,0511	10,5144737	0,53766133	5699,7	CKAP2L	cytoskeleton associated protein 2 like
728642	2,59E-21	2,06E+01	8,30E-22	0,056	9,5960814	0,53743045	2012,91	CDK11A	cyclin dependent kinase 11A
83464	6,25E-09	8,20E+00	3,02E-09	0,0906	5,9305548	0,53730414	455,1	APH1B	aph-1 homolog B, gamma-secretase subunit
23143	9,76E-18	1,70E+01	3,48E-18	0,0618	8,6947573	0,53723458	1315,25	LRCH1	leucine rich repeats and calponin homology domain containing 1
166614	5,08E-06	5,29E+00	2,84E-06	0,1147	4,6817362	0,53717837	254,77	DCLK2	doublecortin like kinase 2
55056	6,35E-05	4,20E+00	3,80E-05	0,1304	4,1195182	0,53707144	198,81	GABPB1-IT1	GABPB1 intronic transcript
11218	1,57E-25	2,48E+01	4,50E-26	0,0508	10,5613577	0,53699907	2117,86	DDX20	DEAD-box helicase 20
3419	2,77E-20	1,96E+01	9,13E-21	0,0574	9,3456727	0,53674287	1650,7	IDH3A	isocitrate dehydrogenase (NAD(+)) 3 catalytic subunit alpha
8622	1,22E-04	3,91E+00	7,42E-05	0,1354	3,9625568	0,53666152	174,15	PDE8B	phosphodiesterase 8B
100506710	6,23E-16	1,52E+01	2,34E-16	0,0654	8,203192	0,53653012	1949,02	EBLN3P	endogenous Bornavirus like nucleoprotein 3, pseudogene
79646	1,17E-27	2,69E+01	3,17E-28	0,0487	11,0169504	0,53640707	5329,91	PANK3	pantothenate kinase 3
123811	7,17E-24	2,31E+01	2,14E-24	0,0526	10,1924835	0,5363653	2783,62	CEP20	centrosomal protein 20
5903	1,27E-30	2,99E+01	3,18E-31	0,0461	11,6221031	0,53622693	6667,29	RANBP2	RAN binding protein 2
8718	6,82E-02	1,17E+00	5,39E-02	0,278	1,9278875	0,53585791	39,29	TNFRSF25	TNF receptor superfamily member 25
2696	1,68E-01	7,75E-01	1,40E-01	0,3627	1,4766698	0,5356559	23,11	GIPR	gastric inhibitory polypeptide receptor
9209	3,93E-21	2,04E+01	1,27E-21	0,056	9,5524353	0,53540808	3842,34	LRRFIP2	LRR binding FLII interacting protein 2
23548	3,91E-12	1,14E+01	1,66E-12	0,0758	7,0601244	0,53522264	879,73	TTC33	tetratricopeptide repeat domain 33
64854	2,48E-14	1,36E+01	9,82E-15	0,0691	7,7415642	0,53518626	934,74	USP46	ubiquitin specific peptidase 46
84946	1,35E-23	2,29E+01	4,06E-24	0,0528	10,1301653	0,53494	3082,79	LTV1	LTV1 ribosome biogenesis factor
347344	4,05E-06	5,39E+00	2,26E-06	0,1131	4,7289401	0,53490408	316,51	ZNF81	zinc finger protein 81
54537	5,37E-25	2,43E+01	1,56E-25	0,0512	10,4440952	0,53475941	2777,49	SHLD2	shieldin complex subunit 2
90874	1,44E-13	1,28E+01	5,85E-14	0,0712	7,5114611	0,53473903	1320,97	ZNF697	zinc finger protein 697
7326	2,07E-19	1,87E+01	7,02E-20	0,0586	9,1273339	0,53471443	2412,84	UBE2G1	ubiquitin conjugating enzyme E2 G1
6392	2,08E-27	2,67E+01	5,64E-28	0,0488	10,9648746	0,53465444	3997,93	SDHD	succinate dehydrogenase complex subunit D
105379219	2,83E-01	5,48E-01	2,46E-01	0,4602	1,1608653	0,53425992	14,14	FAM85B	family with sequence similarity 85 member B
27333	9,99E-24	2,30E+01	3,00E-24	0,0526	10,1598218	0,53409792	3439,61	GOLIM4	golgi integral membrane protein 4
6428	1,03E-40	4,00E+01	2,03E-41	0,0396	13,4806546	0,53395888	14437,56	SRSF3	serine and arginine rich splicing factor 3
54879	1,13E-19	1,89E+01	3,78E-20	0,0581	9,1940945	0,53391386	1455,12	ST7L	suppression of tumorigenicity 7 like
400743	8,05E-02	1,09E+00	6,41E-02	0,2883	1,8515803	0,53378177	36,68	LINC02783	long intergenic non-protein coding RNA 2783
107986364	3,21E-01	4,93E-01	2,82E-01	0,4955	1,0768143	0,53360425	13,11	LOC107986	364
102723458	2,16E-05	4,67E+00	1,25E-05	0,1221	4,3679239	0,53349116	225,64	LOC102723	uncharacterized LOC102723458
80315	1,25E-16	1,59E+01	4,61E-17	0,0635	8,3962312	0,53329515	1282,77	CPEB4	cytoplasmic polyadenylation element binding protein 4
57158	3,63E-04	3,44E+00	2,31E-04	0,1448	3,6829808	0,53325887	158,85	JPH2	junctophilin 2
54830	1,95E-03	2,71E+00	1,31E-03	0,1659	3,213019	0,53290708	113,35	NUP62CL	nucleoporin 62 C-terminal like
6875	7,38E-18	1,71E+01	2,61E-18	0,061	8,727196	0,53270316	1185,64	TAF4B	TATA-box binding protein associated factor 4b
10605	3,81E-26	2,54E+01	1,07E-26	0,0498	10,6953093	0,53265609	5071,63	PAIP1	poly(A) binding protein interacting protein 1
23327	1,06E-43	4,30E+01	1,96E-44	0,0381	13,9837427	0,53221942	13749,23	NEDD4L	NEDD4 like E3 ubiquitin protein ligase
6426	1,82E-38	3,77E+01	3,76E-39	0,0407	13,0899077	0,53212513	14443,32	SRSF1	serine and arginine rich splicing factor 1
55733	2,99E-07	6,52E+00	1,57E-07	0,1014	5,2445287	0,53184617	357,27	HHAT	hedgehog acyltransferase
1983	2,69E-38	3,76E+01	5,59E-39	0,0407	13,0597448	0,53180887	18920,69	EIF5	eukaryotic translation initiation factor 5
440138	1,38E-12	1,19E+01	5,80E-13	0,0738	7,205064	0,53174878	885,77	ALG11	ALG11 alpha-1,2-mannosyltransferase
100506119	4,00E-01	3,98E-01	3,59E-01	0,5792	0,9177653	0,53161357	9,6	LINC01503	long intergenic non-protein coding RNA 1503
401251	1,81E-01	7,42E-01	1,52E-01	0,3711	1,4321779	0,53148457	22,1	SAPCD1	suppressor APC domain containing 1
128710	4,26E-08	7,37E+00	2,13E-08	0,0949	5,60074	0,53139453	392,02	SLX4IP	SLX4 interacting protein
51144	4,37E-32	3,14E+01	1,05E-32	0,0446	11,9098017	0,53104804	3700,44	HSD17B12	hydroxysteroid 17-beta dehydrogenase 12
8418	3,93E-02	1,41E+00	3,01E-02	0,2448	2,1688237	0,5309537	52,64	CMAHP	cytidine monophospho-N-acetylneuraminic acid hydroxylase, pseudogene
10878	3,55E-01	4,50E-01	3,15E-01	0,528	1,0053335	0,53078947	11,06	CFHR3	complement factor H related 3
6675	1,75E-40	3,98E+01	3,47E-41	0,0395	13,4412282	0,53027477	7949,27	UAP1	UDP-N-acetylglucosamine pyrophosphorylase 1
9140	1,78E-21	2,07E+01	5,69E-22	0,055	9,634987	0,53023983	1984,49	ATG12	autophagy related 12
4213	1,22E-08	7,91E+00	5,98E-09	0,0911	5,8174425	0,53021387	427,61	MEIS3P1	Meis homeobox 3 pseudogene 1
105379490	1,01E-01	9,96E-01	8,12E-02	0,304	1,7438065	0,53019137	33,14	LOC105379	490
728622	6,81E-02	1,17E+00	5,37E-02	0,2748	1,9291145	0,5301882	42,98	SKP1P2	S-phase kinase associated protein 1 pseudogene 2
57721	5,26E-21	2,03E+01	1,70E-21	0,0557	9,52183	0,53012619	1862,78	METTL14	methyltransferase 14, N6-adenosine-methyltransferase subunit
5500	1,44E-24	2,38E+01	4,23E-25	0,0512	10,3488937	0,53011821	7213,06	PPP1CB	protein phosphatase 1 catalytic subunit beta
23023	4,24E-11	1,04E+01	1,88E-11	0,0789	6,7154078	0,52998993	673,53	TMCC1	transmembrane and coiled-coil domain family 1
677810	3,28E-01	4,84E-01	2,89E-01	0,4991	1,0613513	0,52966782	12,12	SNORA26	small nucleolar RNA, H/ACA box 26
58517	1,51E-06	5,82E+00	8,23E-07	0,1074	4,9299102	0,52962879	10739,86	RBM25	RNA binding motif protein 25
10778	4,56E-20	1,93E+01	1,51E-20	0,0569	9,2921225	0,52890855	1855,52	ZNF271P	zinc finger protein 271, pseudogene
105371260	1,54E-16	1,58E+01	5,68E-17	0,0632	8,3716728	0,52878828	2476,43	LIX1L-AS1	LIX1L antisense RNA 1
729974	2,14E-04	3,67E+00	1,34E-04	0,1384	3,819717	0,52861466	169,34	RFPL4AL1	ret finger protein like 4A like 1
55066	1,51E-27	2,68E+01	4,10E-28	0,0481	10,9936172	0,52839023	2779,27	PDPR	pyruvate dehydrogenase phosphatase regulatory subunit
100526835	3,41E-02	1,47E+00	2,59E-02	0,2369	2,2282869	0,52790085	57,07	FPGT-TNNI3	FPGT-TNNI3K readthrough
1654	2,47E-39	3,86E+01	5,04E-40	0,0399	13,2417451	0,52770264	25963,1	DDX3X	DEAD-box helicase 3 X-linked
51015	2,26E-14	1,36E+01	8,92E-15	0,0681	7,7537299	0,52767271	1161,42	ISOC1	isochorismatase domain containing 1
7565	7,87E-08	7,10E+00	4,00E-08	0,0961	5,4907502	0,52766449	381,33	ZNF17	zinc finger protein 17
84660	2,01E-01	6,97E-01	1,70E-01	0,3846	1,3717193	0,52755549	23,81	CCDC62	coiled-coil domain containing 62
84641	6,20E-31	3,02E+01	1,54E-31	0,0452	11,6839597	0,5275418	4263,54	MFSD14B	major facilitator superfamily domain containing 14B
27430	4,54E-19	1,83E+01	1,55E-19	0,0583	9,0412502	0,52711455	3667,98	MAT2B	methionine adenosyltransferase 2B
100132215	1,40E-06	5,85E+00	7,61E-07	0,1066	4,9451619	0,52701195	297,83	EHBP1-AS1	EHBP1 antisense RNA 1
9255	1,81E-27	2,67E+01	4,91E-28	0,048	10,977351	0,52699226	3009,85	AIMP1	aminoacyl tRNA synthetase complex interacting multifunctional protein 1
55314	4,90E-05	4,31E+00	2,91E-05	0,126	4,1805158	0,52674253	206,73	TMEM144	transmembrane protein 144
11101	8,02E-21	2,01E+01	2,61E-21	0,0556	9,4773408	0,52672029	1933,55	ATE1	arginyltransferase 1
105374334	5,39E-02	1,27E+00	4,20E-02	0,2589	2,0336736	0,52659033	46,74	LOC105374	uncharacterized LOC105374334
56479	1,21E-18	1,79E+01	4,18E-19	0,0589	8,9320668	0,52629956	1324,31	KCNQ5	potassium voltage-gated channel subfamily Q member 5
64795	2,44E-23	2,26E+01	7,39E-24	0,0522	10,0714683	0,52620241	2473,74	RMND5A	required for meiotic nuclear division 5 homolog A
26275	1,57E-11	1,08E+01	6,83E-12	0,0767	6,8612654	0,52601037	702,97	HIBCH	3-hydroxyisobutyryl-CoA hydrolase
23029	6,26E-23	2,22E+01	1,92E-23	0,0527	9,9772757	0,5259544	2622,9	RBM34	RNA binding motif protein 34
205428	8,12E-07	6,09E+00	4,35E-07	0,1041	5,052914	0,52579517	362,14	DIPK2A	divergent protein kinase domain 2A
642236	1,29E-04	3,89E+00	7,91E-05	0,1332	3,947233	0,52572978	194,83	FRG1JP	FSHD region gene 1 family member J, pseudogene
254128	6,55E-13	1,22E+01	2,72E-13	0,0719	7,3077616	0,5256099	866,28	NIFK-AS1	NIFK antisense RNA 1
65062	2,38E-20	1,96E+01	7,84E-21	0,0561	9,3617524	0,52540792	1638,14	TMEM237	transmembrane protein 237
54556	2,97E-10	9,53E+00	1,36E-10	0,0818	6,4205935	0,52530146	564,44	ING3	inhibitor of growth family member 3
79828	6,58E-15	1,42E+01	2,56E-15	0,0664	7,9106555	0,5250643	1017	METTL8	methyltransferase 8, methylcytidine
3646	3,91E-17	1,64E+01	1,42E-17	0,0615	8,5337156	0,52505245	18849,24	EIF3E	eukaryotic translation initiation factor 3 subunit E
10282	2,68E-10	9,57E+00	1,22E-10	0,0816	6,436765	0,52497103	614,03	BET1	Bet1 golgi vesicular membrane trafficking protein
25894	1,60E-11	1,08E+01	6,95E-12	0,0765	6,8585912	0,52486716	817,59	PLEKHG4	pleckstrin homology and RhoGEF domain containing G4
388327	3,12E-02	1,51E+00	2,36E-02	0,2319	2,26365	0,52483417	65,73	C17orf100	chromosome 17 open reading frame 100
25904	1,53E-19	1,88E+01	5,16E-20	0,0573	9,1605759	0,52457647	1839,31	CNOT10	CCR4-NOT transcription complex subunit 10
126006	2,77E-01	5,58E-01	2,40E-01	0,4455	1,1762283	0,5239847	15,54	PCP2	Purkinje cell protein 2
10142	1,84E-22	2,17E+01	5,70E-23	0,0531	9,8686007	0,52393049	2249,13	AKAP9	A-kinase anchoring protein 9
79918	1,20E-16	1,59E+01	4,41E-17	0,0624	8,4014971	0,52391702	1073,82	SETD6	SET domain containing 6, protein lysine methyltransferase
375593	3,52E-01	4,53E-01	3,12E-01	0,517	1,0119371	0,52312698	12,09	TRIM73	tripartite motif containing 73
103695436	1,23E-01	9,10E-01	1,01E-01	0,3185	1,642202	0,52306732	32,51	LINC01269	long intergenic non-protein coding RNA 1269
219333	3,79E-22	2,14E+01	1,18E-22	0,0534	9,7949387	0,52306302	2784,44	USP12	ubiquitin specific peptidase 12
728339	2,98E-01	5,26E-01	2,60E-01	0,4645	1,1259343	0,5229925	15,04	FRG1-DT	FRG1 divergent transcript
23127	6,42E-14	1,32E+01	2,57E-14	0,0686	7,6181652	0,52297279	851,21	COLGALT2	collagen beta(1-O)galactosyltransferase 2
112268021	4,83E-05	4,32E+00	2,87E-05	0,125	4,1836817	0,52292919	215,24	LOC112268	021
80008	1,43E-21	2,08E+01	4,55E-22	0,0541	9,6580051	0,52289529	2014,96	TMEM156	transmembrane protein 156
166929	4,96E-21	2,03E+01	1,60E-21	0,0549	9,5281176	0,5228547	2109,06	SGMS2	sphingomyelin synthase 2
55744	5,92E-32	3,12E+01	1,43E-32	0,044	11,8841501	0,52267418	5454,3	COA1	cytochrome c oxidase assembly factor 1
57717	1,88E-02	1,73E+00	1,39E-02	0,2123	2,4608526	0,52253161	74,99	PCDHB16	protocadherin beta 16
439965	9,98E-13	1,20E+01	4,17E-13	0,0721	7,2500525	0,52252887	1101,18	SHLD2P3	shieldin complex subunit 2 pseudogene 3
4331	1,21E-25	2,49E+01	3,45E-26	0,0493	10,5863293	0,52214058	2521,23	MNAT1	MNAT1 component of CDK activating kinase
7110	6,97E-28	2,72E+01	1,87E-28	0,0472	11,0642995	0,52175753	3207	TMF1	TATA element modulatory factor 1
6884	2,49E-17	1,66E+01	8,97E-18	0,0608	8,5864779	0,52172163	1322,31	TAF13	TATA-box binding protein associated factor 13
5930	4,25E-31	3,04E+01	1,05E-31	0,0445	11,7163499	0,52132501	3644,01	RBBP6	RB binding protein 6, ubiquitin ligase
51135	1,29E-13	1,29E+01	5,24E-14	0,0693	7,5258363	0,52123326	873,89	IRAK4	interleukin 1 receptor associated kinase 4
10656	4,49E-17	1,63E+01	1,63E-17	0,0612	8,5174599	0,52112708	1525,66	KHDRBS3	KH RNA binding domain containing, signal transduction associated 3
10473	5,51E-28	2,73E+01	1,47E-28	0,047	11,0856575	0,52072713	5279,5	HMGN4	high mobility group nucleosomal binding domain 4
56946	9,88E-19	1,80E+01	3,41E-19	0,0581	8,954707	0,52053778	2191,31	EMSY	EMSY transcriptional repressor, BRCA2 interacting
79648	8,78E-15	1,41E+01	3,43E-15	0,0661	7,8741791	0,52022848	948,84	MCPH1	microcephalin 1
150472	3,16E-13	1,25E+01	1,30E-13	0,0702	7,4065985	0,52012892	855,04	ZNG1B	Zn regulated GTPase metalloprotein activator 1B
101926996	2,00E-01	6,99E-01	1,69E-01	0,378	1,3750257	0,51981662	21,98	RUNDC3A-A	RUNDC3A antisense RNA 1
1824	5,58E-09	8,25E+00	2,69E-09	0,0873	5,9495229	0,51960364	473,92	DSC2	desmocollin 2
9768	9,21E-20	1,90E+01	3,08E-20	0,0564	9,2162122	0,51945071	2547,79	PCLAF	PCNA clamp associated factor
84978	6,65E-14	1,32E+01	2,67E-14	0,0682	7,6135872	0,51933906	949,21	FRMD5	FERM domain containing 5

84224	1,46E-14	1,38E+01	5,75E-15	0,0664	7,8092787	0,51875028	999,8	NBPF3	NBPF member 3
9633	1,09E-03	2,96E+00	7,21E-04	0,1534	3,3815927	0,51868141	140,26	TESMIN	testis expressed metallothionein like protein
7993	1,12E-08	7,95E+00	5,47E-09	0,0889	5,8320925	0,51866285	486,31	UBXN8	UBX domain protein 8
729920	2,61E-03	2,58E+00	1,77E-03	0,1658	3,1262596	0,51843142	117,04	CRPPA	CDP-L-ribitol pyrophosphorylase A
80150	5,59E-04	3,25E+00	3,60E-04	0,1452	3,567953	0,51794416	154,37	ASRGL1	asparaginase and isoaspartyl peptidase 1
699	6,31E-44	4,32E+01	1,16E-44	0,0369	14,0209355	0,5178553	9497,87	BUB1	BUB1 mitotic checkpoint serine/threonine kinase
57570	1,10E-19	1,90E+01	3,67E-20	0,0563	9,1972157	0,51773555	1737,05	TRMT5	tRNA methyltransferase 5
641372	1,84E-01	7,35E-01	1,54E-01	0,3631	1,4250464	0,51750443	23,95	ACOT6	acyl-CoA thioesterase 6
79893	2,70E-30	2,96E+01	6,82E-31	0,0448	11,5568039	0,51743201	4683,5	GGNBP2	gametogenetin binding protein 2
1196	3,96E-17	1,64E+01	1,44E-17	0,0606	8,5322216	0,51737939	1210,95	CLK2	CDC like kinase 2
100303453	4,47E-15	1,43E+01	1,73E-15	0,065	7,9592782	0,51717	999,99	TSNAX-DISC	TSNAX-DISC1 readthrough (NMD candidate)
84928	8,50E-15	1,41E+01	3,32E-15	0,0656	7,8781831	0,51708254	1143,13	TMEM209	transmembrane protein 209
134145	8,49E-09	8,07E+00	4,12E-09	0,0879	5,8791705	0,51662406	466,91	ATPSCKMT	ATP synthase c subunit lysine N-methyltransferase
53354	2,61E-07	6,58E+00	1,36E-07	0,098	5,2700262	0,51658288	421,09	PANK1	pantothenate kinase 1
105371622	3,48E-02	1,46E+00	2,65E-02	0,2326	2,2195293	0,51620124	59,43	LOC105371	uncharacterized LOC105371622
55130	7,38E-06	5,13E+00	4,17E-06	0,1121	4,6026688	0,51617401	289,65	ODAD2	outer dynein arm docking complex subunit 2
30819	2,33E-01	6,33E-01	1,99E-01	0,4017	1,2842319	0,51593722	18,53	KCNIP2	potassium voltage-gated channel interacting protein 2
55616	8,59E-12	1,11E+01	3,70E-12	0,0742	6,9483476	0,51584384	873,91	ASAP3	ArfGAP with SH3 domain, ankyrin repeat and PH domain 3
8886	2,77E-35	3,46E+01	6,18E-36	0,0412	12,5150239	0,51550324	5514,3	DDX18	DEAD-box helicase 18
9525	2,14E-23	2,27E+01	6,48E-24	0,0511	10,0843989	0,5152645	2751,25	VPS4B	vacuolar protein sorting 4 homolog B
64426	8,64E-23	2,21E+01	2,66E-23	0,0518	9,9448179	0,51526123	2323,89	SUDS3	SDS3 homolog, SIN3A corepressor complex component
9475	2,73E-26	2,56E+01	7,65E-27	0,048	10,7264176	0,51511021	5469,7	ROCK2	Rho associated coiled-coil containing protein kinase 2
101927795	1,25E-10	9,90E+00	5,63E-11	0,0786	6,5531491	0,51509087	837,67	BZW1-AS1	BZW1 antisense RNA 1
10556	3,85E-22	2,14E+01	1,21E-22	0,0525	9,7931352	0,51440282	2500,32	RPP30	ribonuclease P/MRP subunit p30
10463	8,03E-26	2,51E+01	2,28E-26	0,0484	10,6251323	0,51406182	3394,22	SLC30A9	solute carrier family 30 member 9
84640	4,29E-18	1,74E+01	1,51E-18	0,0585	8,7891912	0,51402003	1764,35	USP38	ubiquitin specific peptidase 38
256329	6,33E-03	2,20E+00	4,45E-03	0,1806	2,8442353	0,51375025	104,18	LMNTD2	lamin tail domain containing 2
374928	9,27E-02	1,03E+00	7,44E-02	0,2879	1,7840502	0,51369705	43,32	ZNF773	zinc finger protein 773
57415	1,43E-11	1,08E+01	6,20E-12	0,0747	6,8749204	0,51366267	859,01	C3orf14	chromosome 3 open reading frame 14
6789	7,82E-33	3,21E+01	1,85E-33	0,0426	12,0538466	0,513557	5057,39	STK4	serine/threonine kinase 4
10128	3,67E-22	2,14E+01	1,14E-22	0,0524	9,7983878	0,51350375	11542,96	LRPPRC	leucine rich pentatricopeptide repeat containing
222389	1,72E-20	1,98E+01	5,64E-21	0,0546	9,3964351	0,51344473	1727,52	BEND7	BEN domain containing 7
1021	9,65E-27	2,60E+01	2,67E-27	0,0474	10,8234169	0,51342403	3262,08	CDK6	cyclin dependent kinase 6
9060	4,88E-26	2,53E+01	1,38E-26	0,0481	10,6720459	0,51333216	2909,02	PAPSS2	3'-phosphoadenosine 5'-phosphosulfate synthase 2
9487	2,03E-09	8,69E+00	9,60E-10	0,0839	6,1158894	0,51307746	607,08	PIGL	phosphatidylinositol glycan anchor biosynthesis class L
55602	6,50E-16	1,52E+01	2,44E-16	0,0626	8,1980494	0,51296462	1136,74	CDKN2AIP	CDKN2A interacting protein
50944	2,56E-01	5,92E-01	2,20E-01	0,4186	1,2254435	0,5129272	18,11	SHANK1	SH3 and multiple ankyrin repeat domains 1
399818	1,35E-13	1,29E+01	5,48E-14	0,0682	7,5199179	0,51284538	857,6	EEF1AKMT2	EEF1A lysine methyltransferase 2
79160	2,12E-01	6,74E-01	1,80E-01	0,382	1,3413744	0,51241092	26,3	LINC01711	long intergenic non-protein coding RNA 1711
23254	2,47E-06	5,61E+00	1,36E-06	0,106	4,8308723	0,51230018	315,92	KAZN	kazrin, periplakin interacting protein
835	2,04E-16	1,57E+01	7,56E-17	0,0614	8,33798	0,51212817	1187,33	CASP2	caspase 2
254531	8,06E-20	1,91E+01	2,69E-20	0,0555	9,2306604	0,51187563	1910,07	LPCAT4	lysophosphatidylcholine acyltransferase 4
171586	5,48E-10	9,26E+00	2,53E-10	0,0807	6,3248927	0,51058746	686,65	ABHD3	abhydrolase domain containing 3, phospholipase
137075	2,07E-03	2,68E+00	1,40E-03	0,1598	3,1956352	0,51054445	127,35	CLDN23	claudin 23
55184	3,41E-04	3,47E+00	2,16E-04	0,138	3,6995384	0,51047945	168,74	DZANK1	double zinc ribbon and ankyrin repeat domains 1
4437	2,13E-16	1,57E+01	7,90E-17	0,0613	8,3327866	0,51046332	1454,92	MSH3	mutS homolog 3
84871	2,89E-01	5,39E-01	2,52E-01	0,4449	1,1465112	0,51007689	16,51	AGBL4	AGBL carboxypeptidase 4
80012	4,09E-19	1,84E+01	1,39E-19	0,0563	9,0527551	0,50994503	1642,79	PHC3	polyhomeotic homolog 3
80723	2,28E-09	8,64E+00	1,08E-09	0,0836	6,0969293	0,50979672	858,48	SLC35G2	solute carrier family 35 member G2
54904	3,29E-27	2,65E+01	8,97E-28	0,0467	10,9227606	0,50968767	3359,3	NSD3	nuclear receptor binding SET domain protein 3
146223	3,61E-15	1,44E+01	1,39E-15	0,0638	7,985952	0,50961044	1089,07	CMTM4	CKLF like MARVEL transmembrane domain containing 4
2171	1,01E-14	1,40E+01	3,95E-15	0,0649	7,8564011	0,50959108	1727,5	FABP5	fatty acid binding protein 5
84925	4,88E-09	8,31E+00	2,35E-09	0,0853	5,9717556	0,50941568	793,6	SLC49A4	solute carrier family 49 member 4
3799	9,95E-38	3,70E+01	2,10E-38	0,0393	12,9587948	0,50922092	17262,62	KIF5B	kinesin family member 5B
54778	1,64E-14	1,38E+01	6,48E-15	0,0653	7,7942074	0,5091134	1325,2	RNF111	ring finger protein 111
7341	9,77E-25	2,40E+01	2,85E-25	0,049	10,3867648	0,50909317	5342,68	SUMO1	small ubiquitin like modifier 1
6326	3,69E-01	4,33E-01	3,29E-01	0,521	0,9769008	0,50900959	11,81	SCN2A	sodium voltage-gated channel alpha subunit 2
6496	6,21E-02	1,21E+00	4,87E-02	0,2582	1,9713032	0,50898401	46,36	SIX3	SIX homeobox 3
728613	4,53E-03	2,34E+00	3,15E-03	0,1723	2,9530178	0,50886702	111,14	PDCD6P1	PDCD6 pseudogene 1
388650	6,87E-15	1,42E+01	2,67E-15	0,0644	7,9052354	0,50885214	1150,98	DIPK1A	divergent protein kinase domain 1A
219902	1,35E-09	8,87E+00	6,37E-10	0,0823	6,1809676	0,50870115	614,59	TLCD5	TLC domain containing 5
583	1,28E-17	1,69E+01	4,57E-18	0,0587	8,663644	0,50862267	1598,81	BBS2	Bardet-Biedl syndrome 2
27230	1,65E-18	1,78E+01	5,73E-19	0,0572	8,8970999	0,5085445	2943,66	SERP1	stress associated endoplasmic reticulum protein 1
7247	6,29E-18	1,72E+01	2,22E-18	0,0581	8,7454581	0,50839618	3766,31	TSN	translin
4211	8,93E-03	2,05E+00	6,37E-03	0,1863	2,727935	0,50834037	97,98	MEIS1	Meis homeobox 1
83941	1,11E-11	1,10E+01	4,80E-12	0,0735	6,9114128	0,50829323	916,71	TM2D1	TM2 domain containing 1
8771	4,42E-02	1,35E+00	3,40E-02	0,2397	2,1199289	0,50824544	53,8	TNFRSF6B	TNF receptor superfamily member 6b
104326058	3,58E-02	1,45E+00	2,72E-02	0,2299	2,2083365	0,50759044	58,63	SMAD1-AS1	SMAD1 antisense RNA 1
51362	2,96E-17	1,65E+01	1,07E-17	0,0592	8,566455	0,5073876	1271,7	CDC40	cell division cycle 40
101927919	8,39E-02	1,08E+00	6,69E-02	0,2769	1,8321904	0,50734691	43,25	LOC101927	uncharacterized LOC101927919
107984129	3,52E-01	4,53E-01	3,11E-01	0,5013	1,0120873	0,50732163	12,38	LOC107984	129
107986800	4,11E-01	3,86E-01	3,70E-01	0,5658	0,8965755	0,50731406	9,4	LOC107986	putative uncharacterized protein FLJ44672
101929160	5,01E-04	3,30E+00	3,21E-04	0,141	3,5977821	0,50728528	169,41	LOC101929	160
389677	6,58E-13	1,22E+01	2,73E-13	0,0694	7,307259	0,50727418	1069,29	RBM12B	RNA binding motif protein 12B
2736	6,63E-03	2,18E+00	4,67E-03	0,1792	2,8286833	0,50691547	102,9	GLI2	GLI family zinc finger 2
112267866	2,33E-01	6,33E-01	1,99E-01	0,3945	1,2843115	0,50666441	22,46	LOC112267	866
497661	9,74E-11	1,00E+01	4,36E-11	0,0768	6,5912524	0,50647455	643,46	C18orf32	chromosome 18 open reading frame 32
158405	1,37E-13	1,29E+01	5,54E-14	0,0674	7,5186256	0,50640444	922,98	KIAA1958	KIAA1958
5308	3,79E-01	4,21E-01	3,37E-01	0,5278	0,9591895	0,50625469	10,93	PITX2	paired like homeodomain 2
6868	3,98E-28	2,74E+01	1,06E-28	0,0455	11,1149692	0,50592597	3338,42	ADAM17	ADAM metallopeptidase domain 17
58493	4,25E-16	1,54E+01	1,59E-16	0,0613	8,2496242	0,50585095	1236,57	INIP	INTS3 and NABP interacting protein
284996	6,60E-17	1,62E+01	2,41E-17	0,0597	8,472224	0,50582814	1690,3	RNF149	ring finger protein 149
231	9,19E-31	3,00E+01	2,29E-31	0,0434	11,6501499	0,50575567	8245,37	AKR1B1	aldo-keto reductase family 1 member B
729092	2,24E-02	1,65E+00	1,66E-02	0,2112	2,3948567	0,50574263	68,63	AGAP5	ArfGAP with GTPase domain, ankyrin repeat and PH domain 5
23506	7,70E-14	1,31E+01	3,10E-14	0,0666	7,5942494	0,50568937	1299,69	BICRAL	BICRA like chromatin remodeling complex associated protein
11216	7,39E-16	1,51E+01	2,79E-16	0,0618	8,1822611	0,50565377	1809,28	AKAP10	A-kinase anchoring protein 10
105370689	7,05E-02	1,15E+00	5,57E-02	0,2642	1,9131725	0,50553625	46,56	LOC105370	uncharacterized LOC105370689
92667	2,56E-24	2,36E+01	7,56E-25	0,0491	10,2932765	0,50517188	2772,34	MGME1	mitochondrial genome maintenance exonuclease 1
400720	1,09E-09	8,96E+00	5,11E-10	0,0813	6,2155735	0,50515571	555,82	ZNF772	zinc finger protein 772
3233	8,70E-09	8,06E+00	4,23E-09	0,0858	5,8751215	0,50417752	494,22	HOXD4	homeobox D4
339804	5,74E-10	9,24E+00	2,66E-10	0,0798	6,317622	0,50409805	612,52	C2orf74	chromosome 2 open reading frame 74
81537	2,53E-08	7,60E+00	1,26E-08	0,0885	5,6919634	0,50390036	841,35	SGPP1	sphingosine-1-phosphate phosphatase 1
51714	7,37E-17	1,61E+01	2,69E-17	0,0596	8,4592459	0,50389232	3356,49	SELENOT	selenoprotein T
10855	2,96E-12	1,15E+01	1,25E-12	0,071	7,0993235	0,50389229	1111,51	HPSE	heparanase
9689	9,99E-30	2,90E+01	2,55E-30	0,044	11,4428687	0,50375067	20277,63	BZW1	basic leucine zipper and W2 domains 1
101927420	8,06E-02	1,09E+00	6,42E-02	0,2721	1,8507098	0,50363085	42,19	DMTF1-AS1	DMTF1 antisense RNA 1
5376	1,42E-28	2,78E+01	3,75E-29	0,0449	11,2074446	0,50290663	3249,72	PMP22	peripheral myelin protein 22
9969	9,64E-34	3,30E+01	2,23E-34	0,0411	12,2268404	0,50280322	4817,06	MED13	mediator complex subunit 13
100996579	5,06E-06	5,30E+00	2,84E-06	0,1074	4,6823838	0,50275487	307,88	LINC01806	long intergenic non-protein coding RNA 1806
101927746	2,41E-04	3,62E+00	1,51E-04	0,1326	3,7897853	0,50259543	193,25	EMSLR	E2F1 mRNA stabilizing lncRNA
1121	9,40E-18	1,70E+01	3,34E-18	0,0578	8,6993218	0,50245122	1661,24	CHM	CHM Rab escort protein
836	2,55E-18	1,76E+01	8,93E-19	0,0567	8,8478021	0,50198313	2445,25	CASP3	caspase 3
4122	8,37E-20	1,91E+01	2,79E-20	0,0544	9,2266096	0,50153584	1918,48	MAN2A2	mannosidase alpha class 2A member 2
101928118	4,34E-01	3,63E-01	3,92E-01	0,5863	0,8553378	0,50150068	9,01	RWDD3-DT	RWDD3 divergent transcript
3673	1,44E-37	3,68E+01	3,05E-38	0,0388	12,9299823	0,50143175	20804,92	ITGA2	integrin subunit alpha 2
101060200	4,20E-03	2,38E+00	2,91E-03	0,1682	2,9772974	0,50082756	110,7	ZNF891	zinc finger protein 891
57571	4,04E-01	3,94E-01	3,63E-01	0,5504	0,9097403	0,50067635	9,96	CARNS1	carnosine synthase 1
106480334	3,76E-01	4,25E-01	3,35E-01	0,5188	0,9647612	0,50053235	11,54	BMS1P22	BMS1 pseudogene 22
55668	2,05E-24	2,37E+01	6,04E-25	0,0485	10,3147614	0,50033301	2627,25	GPATCH2L	G-patch domain containing 2 like
84318	5,85E-16	1,52E+01	2,20E-16	0,0609	8,2107577	0,50018878	1229,09	CCDC77	coiled-coil domain containing 77
3570	5,54E-02	1,26E+00	4,32E-02	0,2472	2,0217419	0,49980355	52,83	IL6R	interleukin 6 receptor
51185	2,57E-15	1,46E+01	9,86E-16	0,0622	8,0286034	0,49961956	1179,74	CRBN	cereblon
25945	1,17E-27	2,69E+01	3,14E-28	0,0453	11,0175971	0,49958386	3869,35	NECTIN3	nectin cell adhesion molecule 3
647174	5,64E-03	2,25E+00	3,95E-03	0,1733	2,8822418	0,49954883	111,59	SERPINE3	serpin family E member 3
84102	3,59E-09	8,44E+00	1,72E-09	0,0829	6,0223037	0,49951818	563,57	SLC41A2	solute carrier family 41 member 2
143666	5,82E-02	1,24E+00	4,55E-02	0,2497	2,0000995	0,49943302	51,85	LOC143666	uncharacterized LOC143666
56942	3,01E-15	1,45E+01	1,16E-15	0,0623	8,0086901	0,49914358	1470,68	CMC2	C-X9-C motif containing 2
64762	1,74E-06	5,76E+00	9,50E-07	0,1018	4,9016228	0,49901742	359,13	GAREM1	GRB2 associated regulator of MAPK1 subtype 1
218	8,80E-02	1,06E+00	7,04E-02	0,2758	1,8091255	0,49898652	43,18	ALDH3A1	aldehyde dehydrogenase 3 family member A1
4089	1,07E-21	2,10E+01	3,39E-22	0,0515	9,6879111	0,49863692	2097,51	SMAD4	SMAD family member 4

102724687	3,00E-01	5,23E-01	2,62E-01	0,4439	1,1218858	0,49799355	16,55	LOC102724687	uncharacterized LOC102724687
9669	3,32E-19	1,85E+01	1,13E-19	0,0548	9,0757348	0,49773849	18470,96	EIF5B	eukaryotic translation initiation factor 5B
252983	2,19E-08	7,66E+00	1,08E-08	0,087	5,717268	0,49766359	490,04	STXBP4	syntaxin binding protein 4
100505549	1,46E-03	2,84E+00	9,70E-04	0,1508	3,2991027	0,49751984	141,06	ATP8B1-AS1	ATP8B1 antisense RNA 1
105378841	4,38E-01	3,59E-01	3,97E-01	0,5872	0,8470293	0,49734887	9,04	LOC105378	uncharacterized LOC105378841
81688	2,08E-25	2,47E+01	5,98E-26	0,0472	10,5347001	0,49700782	7571,89	C6orf62	chromosome 6 open reading frame 62
85461	1,67E-15	1,48E+01	6,37E-16	0,0615	8,0820285	0,49695636	1276,05	TANC1	tetratricopeptide repeat, ankyrin repeat and coiled-coil containing 1
84826	3,70E-04	3,43E+00	2,35E-04	0,1351	3,6780309	0,49688003	176,43	SFT2D3	SFT2 domain containing 3
56952	2,09E-10	9,68E+00	9,51E-11	0,0767	6,4744977	0,49683734	670,12	PRTFDC1	phosphoribosyl transferase domain containing 1
27067	9,89E-17	1,60E+01	3,62E-17	0,059	8,4244854	0,49682829	1346,72	STAU2	staufen double-stranded RNA binding protein 2
54872	4,16E-17	1,64E+01	1,51E-17	0,0582	8,5265803	0,49660715	1593,09	PIGG	phosphatidylinositol glycan anchor biosynthesis class G
106633804	1,57E-02	1,80E+00	1,14E-02	0,1964	2,5289686	0,49660626	84,27	SNORD135	small nucleolar RNA, C/D box 135
285598	2,22E-05	4,65E+00	1,29E-05	0,1138	4,3612658	0,4964906	263,35	ARL10	ADP ribosylation factor like GTPase 10
112267932	2,56E-01	5,92E-01	2,20E-01	0,4052	1,2252677	0,49648323	19,36	LOC112267	uncharacterized LOC112267932
10057	2,09E-20	1,97E+01	6,87E-21	0,053	9,3757354	0,49645984	1876,06	ABCC5	ATP binding cassette subfamily C member 5
149837	7,07E-03	2,15E+00	5,00E-03	0,1768	2,8073325	0,49635526	100,68	LINC00654	long intergenic non-protein coding RNA 654
54865	2,14E-19	1,87E+01	7,23E-20	0,0544	9,1241346	0,49616976	3243	GPATCH4	G-patch domain containing 4 (gene/pseudogene)
55578	1,75E-20	1,98E+01	5,73E-21	0,0528	9,3948627	0,49610182	2302,48	SUPT20H	SPT20 homolog, SAGA complex component
151188	1,50E-14	1,38E+01	5,91E-15	0,0636	7,8058023	0,4960793	1284,99	ARL6IP6	ADP ribosylation factor like GTPase 6 interacting protein 6
54942	2,85E-13	1,25E+01	1,17E-13	0,0668	7,4206292	0,49602777	1028,75	ABITRAM	actin binding transcription modulator
813	8,34E-35	3,41E+01	1,88E-35	0,0399	12,4263271	0,49601919	27495,91	CALU	calumenin
9126	2,90E-31	3,05E+01	7,14E-32	0,0422	11,7491294	0,49592703	10794,22	SMC3	structural maintenance of chromosomes 3
101929768	3,33E-01	4,78E-01	2,93E-01	0,4715	1,0516443	0,49583095	14,91	OSMR-DT	OSMR divergent transcript
26777	2,62E-01	5,82E-01	2,26E-01	0,4094	1,2108371	0,49568823	18,39	SNORA71A	small nucleolar RNA, H/ACA box 71A
4780	1,39E-26	2,59E+01	3,86E-27	0,0459	10,7895695	0,49557194	5551,18	NFE2L2	NFE2 like bZIP transcription factor 2
993	1,99E-21	2,07E+01	6,35E-22	0,0515	9,6236625	0,49532549	1983,23	CDC25A	cell division cycle 25A
100506714	5,57E-07	6,25E+00	2,96E-07	0,0966	5,1260358	0,49528967	413,33	NUP50-DT	NUP50 divergent transcript
79712	1,31E-09	8,88E+00	6,14E-10	0,08	6,1867799	0,49512303	567,95	GTDC1	glycosyltransferase like domain containing 1
80303	9,85E-06	5,01E+00	5,62E-06	0,109	4,5402613	0,49509678	313,49	EFHD1	EF-hand domain family member D1
3075	3,46E-19	1,85E+01	1,18E-19	0,0546	9,0712605	0,49492072	1695,2	CFH	complement factor H
56919	3,30E-26	2,55E+01	9,26E-27	0,0462	10,7087986	0,49454208	3426,44	DHX33	DEAH-box helicase 33
5519	2,89E-19	1,85E+01	9,82E-20	0,0544	9,0909407	0,49449686	2132,73	PPP2R1B	protein phosphatase 2 scaffold subunit Abeta
150577	2,80E-01	5,53E-01	2,43E-01	0,4235	1,167161	0,49429559	18,19	LINC01104	long intergenic non-protein coding RNA 1104
10955	2,56E-37	3,66E+01	5,43E-38	0,0384	12,8855851	0,49424071	13865,87	SERINC3	serine incorporator 3
10175	1,05E-21	2,10E+01	3,33E-22	0,051	9,6898918	0,49405693	6257,82	CNIH1	cornichon family AMPA receptor auxiliary protein 1
5423	2,38E-08	7,62E+00	1,18E-08	0,0866	5,7025982	0,49390746	479,81	POLB	DNA polymerase beta
107984485	5,02E-02	1,30E+00	3,89E-02	0,2391	2,0653139	0,493776	53,93	LOC107984	485
64403	5,12E-09	8,29E+00	2,46E-09	0,0828	5,9638124	0,49367363	542,68	CDH24	cadherin 24
162993	1,09E-02	1,96E+00	7,81E-03	0,1855	2,6603881	0,49356936	97,84	ZNF846	zinc finger protein 846
55805	1,70E-04	3,77E+00	1,05E-04	0,1272	3,8787865	0,49343289	201,96	LRP2BP	LRP2 binding protein
256051	5,17E-07	6,29E+00	2,74E-07	0,096	5,1405073	0,49332563	421,89	ZNF549	zinc finger protein 549
7844	2,04E-15	1,47E+01	7,79E-16	0,0612	8,057414	0,49298995	1204,48	RNF103	ring finger protein 103
55276	2,66E-26	2,56E+01	7,45E-27	0,0459	10,7288369	0,49276865	3574,48	PGM2	phosphoglucomutase 2
105369362	3,91E-01	4,08E-01	3,49E-01	0,5266	0,9356816	0,4927668	10,91	CHKA-DT	CHKA divergent transcript
84809	2,11E-04	3,68E+00	1,31E-04	0,1288	3,8242546	0,49243824	220,29	CROCCP2	CROCC pseudogene 2
5570	3,24E-02	1,49E+00	2,45E-02	0,2189	2,2494577	0,49243014	66,74	PKIB	cAMP-dependent protein kinase inhibitor beta
11245	1,39E-13	1,29E+01	5,64E-14	0,0655	7,5160975	0,49233543	1020,52	GPR176	G protein-coupled receptor 176
26985	1,09E-28	2,80E+01	2,85E-29	0,0438	11,2315615	0,49223146	3848,13	AP3M1	adaptor related protein complex 3 subunit mu 1
100289137	5,59E-03	2,25E+00	3,91E-03	0,1706	2,8851247	0,49219042	113,65	FAM95C	family with sequence similarity 95 member C
389641	2,03E-04	3,69E+00	1,26E-04	0,1283	3,8334355	0,49173743	204,07	TNFRSF10A	TNFRSF10A divergent transcript
8444	1,37E-16	1,59E+01	5,05E-17	0,0586	8,3855083	0,49172049	1493,86	DYRK3	dual specificity tyrosine phosphorylation regulated kinase 3
91408	4,13E-21	2,04E+01	1,33E-21	0,0515	9,5472197	0,49145872	2966,96	BTF3L4	basic transcription factor 3 like 4
100533107	3,31E-12	1,15E+01	1,41E-12	0,0693	7,0832436	0,49079535	908,61	RTEL1-TNFF	RTEL1-TNFRSF6B readthrough (NMD candidate)
79858	4,53E-06	5,34E+00	2,53E-06	0,1042	4,7056842	0,49035555	345,46	NEK11	NIMA related kinase 11
126374	2,90E-05	4,54E+00	1,70E-05	0,114	4,3013652	0,49028826	289,5	WTIP	WT1 interacting protein
105372279	1,10E-01	9,59E-01	8,91E-02	0,2883	1,7001947	0,49018649	38,14	LOC105372	uncharacterized LOC105372279
100506472	3,13E-01	5,04E-01	2,74E-01	0,4479	1,0937506	0,48988438	15,3	LOC100506	uncharacterized LOC100506472
23312	2,14E-12	1,17E+01	9,02E-13	0,0686	7,1446629	0,48983972	867,81	DMXL2	Dmx like 2
503639	2,53E-10	9,60E+00	1,15E-10	0,076	6,445723	0,48983205	649,23	DUXAP10	double homeobox A pseudogene 10
9886	6,37E-05	4,20E+00	3,81E-05	0,1189	4,1186415	0,48975074	286,91	RHOBTB1	Rho related BTB domain containing 1
100505538	5,93E-03	2,23E+00	4,16E-03	0,1709	2,865792	0,4897143	115,57	RBM26-AS1	RBM26 antisense RNA 1
105370876	2,59E-01	5,87E-01	2,23E-01	0,4016	1,2188923	0,48951442	19,26	LINC02896	long intergenic non-protein coding RNA 2896
571	1,00E-18	1,80E+01	3,46E-19	0,0547	8,9528741	0,48950811	2528,88	BACH1	BTB domain and CNC homolog 1
5601	1,95E-23	2,27E+01	5,89E-24	0,0485	10,093728	0,48923409	2674,31	MAPK9	mitogen-activated protein kinase 9
947	2,94E-02	1,53E+00	2,21E-02	0,2138	2,2881439	0,48922431	80,12	CD34	CD34 molecule
101928173	1,42E-01	8,48E-01	1,17E-01	0,3122	1,5666427	0,48914253	32,08	LINC01943	long intergenic non-protein coding RNA 1943
101929163	4,19E-01	3,78E-01	3,77E-01	0,5541	0,8827491	0,4891243	9,85	TSBP1-AS1	TSBP1 and BTNL2 antisense RNA 1
221035	1,10E-19	1,90E+01	3,69E-20	0,0532	9,1966188	0,48902347	2711,11	REEP3	receptor accessory protein 3
375298	1,33E-01	8,76E-01	1,09E-01	0,3053	1,6016671	0,48900512	32,71	CERKL	ceramide kinase like
101929004	2,22E-01	6,54E-01	1,89E-01	0,3719	1,3142406	0,48879321	22,71	LOC101929	uncharacterized LOC101929004
112268131	1,56E-04	3,81E+00	9,63E-05	0,1253	3,8996437	0,48863146	218,43	LOC112268	131
51750	1,99E-11	1,07E+01	8,70E-12	0,0716	6,8265698	0,48856445	878,78	RTEL1	regulator of telomere elongation helicase 1
25801	6,64E-06	5,18E+00	3,74E-06	0,1056	4,6250567	0,48849629	316,99	GCA	grancalcin
100500808	9,13E-03	2,04E+00	6,52E-03	0,1796	2,7201758	0,48847242	1849,16	MIR3917	microRNA 3917
107985885	4,18E-01	3,79E-01	3,77E-01	0,5525	0,8840376	0,48840597	9,87	PPP4R3B-D	PPP4R3B divergent transcript
4773	1,40E-14	1,39E+01	5,50E-15	0,0625	7,8149165	0,48831637	1103,27	NFATC2	nuclear factor of activated T cells 2
259230	2,18E-16	1,57E+01	8,11E-17	0,0586	8,3296803	0,4881581	1615,22	SGMS1	sphingomyelin synthase 1
54677	5,73E-06	5,24E+00	3,22E-06	0,1048	4,6565155	0,4880453	319,36	CROT	carnitine O-octanoyltransferase
100129924	3,51E-01	4,55E-01	3,11E-01	0,4817	1,0131867	0,48801168	13,77	TMEM269	transmembrane protein 269
5627	6,30E-15	1,42E+01	2,45E-15	0,0616	7,9161399	0,48766179	1221,51	PROS1	protein S
90233	6,36E-06	5,20E+00	3,58E-06	0,1052	4,6342994	0,48760925	363,41	ZNF551	zinc finger protein 551
144455	6,17E-30	2,92E+01	1,57E-30	0,0425	11,4850984	0,48757803	5164,59	E2F7	E2F transcription factor 7
10664	2,77E-19	1,86E+01	9,41E-20	0,0536	9,095588	0,48744267	4046,93	CTCF	CCCTC-binding factor
25948	8,94E-23	2,20E+01	2,75E-23	0,049	9,94133	0,487403	2910,43	KBTBD2	kelch repeat and BTB domain containing 2
220064	1,02E-13	1,30E+01	4,12E-14	0,0645	7,55702	0,48736258	1017,4	LTO1	LTO1 maturation factor of ABCE1
51585	2,65E-21	2,06E+01	8,51E-22	0,0508	9,593592	0,48730048	2146,63	PCF11	PCF11 cleavage and polyadenylation factor subunit
148789	4,89E-20	1,93E+01	1,63E-20	0,0525	9,2844553	0,48722096	2145,03	B3GALNT2	beta-1,3-N-acetylgalactosaminyltransferase 2
105376156	5,19E-03	2,28E+00	3,62E-03	0,1674	2,9093589	0,48698151	111,05	LOC105376	uncharacterized LOC105376156
57472	1,93E-17	1,67E+01	6,92E-18	0,0565	8,6162415	0,48690085	2618,58	CNOT6	CCR4-NOT transcription complex subunit 6
51097	7,27E-14	1,31E+01	2,92E-14	0,064	7,6018488	0,48676265	3373,96	SCCPDH	saccharopine dehydrogenase (putative)
1665	6,39E-34	3,32E+01	1,47E-34	0,0397	12,2606101	0,48667224	14084,46	DHX15	DEAH-box helicase 15
64065	3,51E-16	1,55E+01	1,31E-16	0,0588	8,2727635	0,48646955	2748,69	PERP	p53 apoptosis effector related to PMP22
10606	1,98E-45	4,47E+01	3,51E-46	0,0341	14,2669999	0,48645454	23409,31	PAICS	phosphoribosylaminoimidazole carboxylase and phosphoribosylaminoimidazolesuccinocarboxamide synthase
724102	3,55E-10	9,45E+00	1,63E-10	0,0761	6,3931311	0,48632423	668,09	SNHG4	small nucleolar RNA host gene 4
9529	1,37E-24	2,39E+01	4,01E-25	0,0469	10,3539904	0,4859924	3102,12	BAG5	BAG cochaperone 5
92400	5,63E-19	1,82E+01	1,93E-19	0,0539	9,017309	0,48571666	1831,44	RBM18	RNA binding motif protein 18
8452	6,14E-30	2,92E+01	1,56E-30	0,0423	11,4855907	0,48570474	4839,69	CUL3	cullin 3
2743	3,87E-07	6,41E+00	2,04E-07	0,0935	5,1958975	0,48563296	432,51	GLRB	glycine receptor beta
355	7,30E-07	6,14E+00	3,90E-07	0,0957	5,0737019	0,48545428	372,28	FAS	Fas cell surface death receptor
7799	6,10E-15	1,42E+01	2,37E-15	0,0613	7,9202502	0,48513047	1494,66	PRDM2	PR/SET domain 2
3597	2,51E-22	2,16E+01	7,80E-23	0,0493	9,8369561	0,48503493	4288,1	IL13RA1	interleukin 13 receptor subunit alpha 1
4170	2,02E-26	2,57E+01	5,65E-27	0,0451	10,7544478	0,48494126	14885,65	MCL1	MCL1 apoptosis regulator, BCL2 family member
9188	8,81E-39	3,81E+01	1,81E-39	0,0369	13,1452371	0,48478632	19398,4	DDX21	DExD-box helicase 21
81788	2,63E-05	4,58E+00	1,54E-05	0,1121	4,3228734	0,48459413	276,52	NUAK2	NUAK family kinase 2
55008	1,97E-11	1,07E+01	8,58E-12	0,0709	6,8285565	0,4844358	1012,11	HERC6	HECT and RLD domain containing E3 ubiquitin protein ligase family member 6
55855	4,40E-07	6,36E+00	2,33E-07	0,0937	5,1712067	0,48443375	493,74	DENND10P1	DENND10 pseudogene 1
7608	2,54E-01	5,95E-01	2,18E-01	0,3932	1,231592	0,48428444	19,86	ZNF56P	zinc finger protein 56, pseudogene
26751	1,11E-05	4,95E+00	6,36E-06	0,1072	4,5141269	0,48408307	299,58	SH3YL1	SH3 and SYLF domain containing 1
9778	2,04E-19	1,87E+01	6,90E-20	0,053	9,1291472	0,48400995	2025,46	KIAA0232	KIAA0232
3398	2,62E-01	5,82E-01	2,25E-01	0,3993	1,2121261	0,48397192	19,94	ID2	inhibitor of DNA binding 2
56985	3,89E-07	6,41E+00	2,05E-07	0,0931	5,1949147	0,48374902	450,68	ADPRM	ADP-ribose/CDP-alcohol diphosphatase, manganese dependent
65983	2,88E-18	1,75E+01	1,01E-18	0,0548	8,8340994	0,48370019	1855,18	GRAMD2B	GRAM domain containing 2B
101926941	5,96E-02	1,22E+00	4,67E-02	0,2432	1,989026	0,48369387	56,07	SPRY4-AS1	SPRY4 antisense RNA 1
64801	1,21E-09	8,92E+00	5,67E-10	0,078	6,1992034	0,48353496	655,83	ARV1	ARV1 homolog, fatty acid homeostasis modulator
23155	7,28E-19	1,81E+01	2,50E-19	0,0537	8,9887782	0,48295194	2191,45	CLCC1	chloride channel CLIC like 1
727676	3,87E-01	4,12E-01	3,46E-01	0,5126	0,9420552	0,48287669	11,81	SNORD118	small nucleolar RNA, C/D box 118
51124	6,70E-16	1,52E+01	2,52E-16	0,0589	8,1941957	0,48281191	2015,63	IER3IP1	immediate early response 3 interacting protein 1
84081	1,49E-13	1,28E+01	6,06E-14	0,0643	7,5067805	0,48271201	4280,66	NSRP1	nuclear speckle splicing regulatory protein 1
79807	2,06E-12	1,17E+01	8,69E-13	0,0675	7,1498116	0,48256054	948,2	GSTCD	glutathione S-transferase C-terminal domain containing
90268	6,18E-19	1,82E+01	2,12E-19	0,0536	9,0070371	0,48254922	1943,75	OTULIN	OTU deubiquitinase with linear linkage specificity

9100	5,67E-26	2,52E+01	1,60E-26	0,0453	10,6579223	0,48249343	5063,15	USP10	ubiquitin specific peptidase 10
4205	2,45E-14	1,36E+01	9,69E-15	0,0623	7,7432557	0,48230607	1684,21	MEF2A	myocyte enhancer factor 2A
586	1,97E-19	1,87E+01	6,66E-20	0,0528	9,1330444	0,48229516	4151,87	BCAT1	branched chain amino acid transaminase 1
7957	3,99E-05	4,40E+00	2,36E-05	0,1141	4,2277821	0,48221535	265,74	EPM2A	EPM2A glucan phosphatase, laforin
284656	7,39E-02	1,13E+00	5,85E-02	0,2549	1,8916834	0,48211768	50,97	EPHA10	EPH receptor A10
10010	5,42E-17	1,63E+01	1,97E-17	0,0567	8,4953366	0,4820798	1611,11	TANK	TRAF family member associated NFKB activator
817	1,39E-12	1,19E+01	5,81E-13	0,0669	7,2047676	0,48200071	1316,42	CAMK2D	calcium/calmodulin dependent protein kinase II delta
10053	4,26E-12	1,14E+01	1,82E-12	0,0684	7,0479388	0,48197181	880,81	AP1M2	adaptor related protein complex 1 subunit mu 2
118490	1,81E-01	7,42E-01	1,52E-01	0,3363	1,4327643	0,48190571	27,69	MSS51	MSS51 mitochondrial translational activator
729683	4,01E-01	3,97E-01	3,59E-01	0,5256	0,9167641	0,48188388	11,42	LOC729683	uncharacterized LOC729683
143903	8,66E-17	1,61E+01	3,17E-17	0,0571	8,4402788	0,4816461	2321,55	LAYN	layilin
114885	6,85E-14	1,32E+01	2,75E-14	0,0633	7,6096286	0,48156367	1327,69	OSBPL11	oxysterol binding protein like 11
100288846	3,22E-01	4,92E-01	2,83E-01	0,4482	1,0742593	0,4815272	14,77	MIA2-AS1	MIA2 antisense RNA 1
8649	5,25E-12	1,13E+01	2,24E-12	0,0686	7,018428	0,48147087	1054,95	LAMTOR3	late endosomal/lysosomal adaptor, MAPK and MTOR activator 3
79899	1,42E-06	5,85E+00	7,70E-07	0,0974	4,9429206	0,48142747	370,23	PRR5L	proline rich 5 like
100271836	1,15E-07	6,94E+00	5,89E-08	0,0887	5,4221752	0,48120486	448,1	SMG1P3	SMG1 pseudogene 3
10650	4,84E-03	2,32E+00	3,37E-03	0,1641	2,9322519	0,48115742	126,9	PRELID3A	PRELI domain containing 3A
115004	2,82E-16	1,55E+01	1,05E-16	0,058	8,2993371	0,48097704	1889,86	CGAS	cyclic GMP-AMP synthase
105371026	1,76E-01	7,54E-01	1,48E-01	0,332	1,448293	0,48087013	27,63	LOC10537102	uncharacterized LOC105371026
153770	2,05E-01	6,88E-01	1,73E-01	0,3529	1,3624646	0,48079743	26,19	PLAC8L1	PLAC8 like 1
81790	3,28E-10	9,48E+00	1,50E-10	0,075	6,4055019	0,48071683	705,5	RNF170	ring finger protein 170
101926967	1,20E-01	9,21E-01	9,83E-02	0,2908	1,6531312	0,4806685	38,39	ATXN7L3-AS	ATXN7L3 antisense RNA 1
2531	8,65E-21	2,01E+01	2,82E-21	0,0507	9,4693642	0,48052432	2789,49	KDSR	3-ketodihydrosphingosine reductase
84940	3,68E-02	1,43E+00	2,81E-02	0,2188	2,196182	0,48041699	69,78	CORO6	coronin 6
79989	3,15E-09	8,50E+00	1,51E-09	0,0795	6,0437636	0,48027305	630,81	TTC26	tetratricopeptide repeat domain 26
6654	5,08E-23	2,23E+01	1,55E-23	0,048	9,9983236	0,47958734	3076,07	SOS1	SOS Ras/Rac guanine nucleotide exchange factor 1
752014	3,29E-02	1,48E+00	2,49E-02	0,2138	2,242506	0,47950076	67,96	CEMP1	cementum protein 1
107985082	6,06E-02	1,22E+00	4,74E-02	0,2419	1,9823014	0,47947945	52,24	LOC107985082	
26091	2,20E-24	2,37E+01	6,49E-25	0,0465	10,3078361	0,47944451	3916,2	HERC4	HECT and RLD domain containing E3 ubiquitin protein ligase 4
57486	9,33E-24	2,30E+01	2,80E-24	0,0471	10,1664915	0,47930803	2977,07	NLN	neurolysin
121506	4,67E-01	3,31E-01	4,26E-01	0,6016	0,7966703	0,47927913	9,8	ERP27	endoplasmic reticulum protein 27
83544	1,03E-10	9,99E+00	4,63E-11	0,0728	6,5822161	0,47913295	887,05	DNAL1	dynein axonemal light chain 1
30836	1,73E-22	2,18E+01	5,37E-23	0,0485	9,8745593	0,47909773	7306,89	DNTTIP2	deoxynucleotidyltransferase terminal interacting protein 2
107984006	8,28E-02	1,08E+00	6,60E-02	0,2606	1,8382253	0,4790596	45,87	LOC107984006	uncharacterized LOC107984006
119	2,71E-02	1,57E+00	2,03E-02	0,2064	2,3207152	0,47905815	73,94	ADD2	adducin 2
8821	7,52E-20	1,91E+01	2,51E-20	0,0518	9,2382246	0,47880084	2808,19	INPP4B	inositol polyphosphate-4-phosphatase type II B
4128	3,03E-14	1,35E+01	1,20E-14	0,062	7,7156175	0,47875179	1270,55	MAOA	monoamine oxidase A
548645	3,40E-08	7,47E+00	1,70E-08	0,0848	5,6402917	0,47823751	596,76	DNAJC25	DnaJ heat shock protein family (Hsp40) member C25
528	1,57E-24	2,38E+01	4,62E-25	0,0462	10,3405842	0,47800374	4901,32	ATP6V1C1	ATPase H+ transporting V1 subunit C1
166378	1,23E-14	1,39E+01	4,82E-15	0,061	7,8314482	0,47787654	1237,82	SPATA5	spermatogenesis associated 5
107985423	3,79E-01	4,21E-01	3,38E-01	0,4983	0,9588359	0,4778179	13,11	LOC107985423	uncharacterized LOC107985423
9097	3,14E-23	2,25E+01	9,52E-24	0,0476	10,0464413	0,47771291	7971,83	USP14	ubiquitin specific peptidase 14
91603	1,19E-09	8,92E+00	5,61E-10	0,077	6,2011309	0,47754937	702,83	ZNF830	zinc finger protein 830
102466854	2,29E-01	6,40E-01	1,95E-01	0,3685	1,2959391	0,47749276	23,87	MIR7705	microRNA 7705
85415	2,70E-12	1,16E+01	1,14E-12	0,0671	7,1122541	0,47747723	970,3	RHPN2	rhophilin Rho GTPase binding protein 2
100775107	5,86E-04	3,23E+00	3,78E-04	0,1343	3,5550133	0,4774191	183,29	RBM5-AS1	RBM5 antisense RNA 1
100616323	3,86E-01	4,13E-01	3,45E-01	0,5048	0,9450489	0,47708704	11,75	MIR4482	microRNA 4482
55758	4,03E-15	1,44E+01	1,56E-15	0,0598	7,9722885	0,47701348	1330,01	RCOR3	REST corepressor 3
57577	1,15E-02	1,94E+00	8,31E-03	0,1805	2,6394058	0,47645514	102,13	CCDC191	coiled-coil domain containing 191
4233	7,74E-26	2,51E+01	2,19E-26	0,0448	10,6286635	0,4764289	9501,86	MET	MET proto-oncogene, receptor tyrosine kinase
1832	5,46E-21	2,03E+01	1,77E-21	0,05	9,5179278	0,47631893	10928,99	DSP	desmoplakin
4800	1,16E-24	2,39E+01	3,40E-25	0,0459	10,3699362	0,47631569	5375,81	NFYA	nuclear transcription factor Y subunit alpha
100874255	2,92E-01	5,35E-01	2,54E-01	0,4174	1,1409772	0,47626444	17,74	RNASEH2B-A	RNASEH2B antisense RNA 1
54499	5,08E-24	2,33E+01	1,51E-24	0,0466	10,2261584	0,47605696	4270,5	TMCO1	transmembrane and coiled-coil domains 1
100421746	6,68E-01	1,75E-01	6,32E-01	0,9932	0,4793039	0,47603941	19,91	LOC100421	PAGE family member 5 pseudogene
414245	6,95E-03	2,16E+00	4,91E-03	0,1691	2,813	0,47566951	111,82	DNAJC9-AS	DNAJC9 and MRPS16 antisense RNA 1
199221	2,42E-03	2,62E+00	1,63E-03	0,151	3,1496885	0,4754846	145,73	DZIP1L	DAZ interacting zinc finger protein 1 like
114818	9,68E-15	1,40E+01	3,79E-15	0,0605	7,8618101	0,47542156	1252,4	KLHL29	kelch like family member 29
119395	3,94E-01	4,05E-01	3,53E-01	0,5115	0,9290603	0,47524304	12,41	CALHM3	calcium homeostasis modulator 3
22800	3,54E-17	1,65E+01	1,28E-17	0,0556	8,545433	0,47524078	2235,65	RRAS2	RAS related 2
7507	5,48E-10	9,26E+00	2,53E-10	0,0751	6,3250424	0,47496019	715,2	XPA	XPA, DNA damage recognition and repair factor
105377286	4,27E-01	3,70E-01	3,86E-01	0,5475	0,8673957	0,4748629	10,72	LOC10537728	uncharacterized LOC105377286
23774	1,63E-11	1,08E+01	7,11E-12	0,0693	6,8555192	0,47484705	842,55	BRD1	bromodomain containing 1
142891	2,25E-17	1,66E+01	8,11E-18	0,0552	8,5980688	0,47472015	2034,7	SAMD8	sterile alpha motif domain containing 8
2312	1,53E-07	6,82E+00	7,89E-08	0,0884	5,3697338	0,47468198	498,97	FLG	filaggrin
90338	3,11E-13	1,25E+01	1,28E-13	0,0641	7,408731	0,47462046	1082,76	ZNF160	zinc finger protein 160
9282	2,75E-27	2,66E+01	7,49E-28	0,0434	10,9391066	0,47457982	4225,23	MED14	mediator complex subunit 14
2054	9,81E-21	2,00E+01	3,20E-21	0,0502	9,4560573	0,47447101	2187,58	STX2	syntaxin 2
79872	7,55E-14	1,31E+01	3,04E-14	0,0624	7,5967438	0,47426813	1689,28	CBLL1	Cbl proto-oncogene like 1
105371870	2,03E-01	6,93E-01	1,71E-01	0,3468	1,3674701	0,47419746	25,07	LOC10537187	uncharacterized LOC105371870
54760	1,36E-01	8,66E-01	1,12E-01	0,2982	1,5890523	0,4739345	36,43	PCSK4	proprotein convertase subtilisin/kexin type 4
159090	1,68E-18	1,78E+01	5,83E-19	0,0533	8,8951533	0,47377103	1890	PABIR2	PABIR family member 2
83693	2,18E-13	1,27E+01	8,90E-14	0,0635	7,4563111	0,47371079	1153,58	HSDL1	hydroxysteroid dehydrogenase like 1
6248	1,15E-06	5,94E+00	6,22E-07	0,095	4,9843539	0,47367729	438,48	RSC1A1	regulator of solute carriers 1
107986862	4,58E-01	3,39E-01	4,17E-01	0,5833	0,8119413	0,47356603	8,81	LOC107986862	
6443	1,64E-22	2,18E+01	5,07E-23	0,0479	9,8803401	0,47354671	3152,08	SGCB	sarcoglycan beta
101929200	2,81E-02	1,55E+00	2,11E-02	0,2052	2,3068849	0,47348506	74,27	LOC10192920	uncharacterized LOC101929200
53371	6,44E-22	2,12E+01	2,03E-22	0,0486	9,7404995	0,47322916	3684,56	NUP54	nucleoporin 54
105377211	4,82E-01	3,17E-01	4,40E-01	0,6128	0,7721777	0,47321754	7,88	LOC10537721	uncharacterized LOC105377211
54103	3,76E-06	5,42E+00	2,09E-06	0,0997	4,7443887	0,47295784	409,35	GSAP	gamma-secretase activating protein
6421	1,15E-19	1,89E+01	3,84E-20	0,0514	9,1924629	0,47279479	19800,71	SFPQ	splicing factor proline and glutamine rich
11167	2,14E-32	3,17E+01	5,12E-33	0,0395	11,9697474	0,47258826	11906,09	FSTL1	follistatin like 1
79736	4,75E-10	9,32E+00	2,19E-10	0,0744	6,3474092	0,47238398	715,11	TEFM	transcription elongation factor, mitochondrial
8467	1,24E-25	2,49E+01	3,54E-26	0,0446	10,5839239	0,47232975	8275,65	SMARCA5	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 5
25780	1,68E-05	4,77E+00	9,71E-06	0,1068	4,4234693	0,47230444	295,11	RASGRP3	RAS guanyl releasing protein 3
92912	4,48E-16	1,53E+01	1,68E-16	0,0573	8,2432052	0,47227867	1562,52	UBE2Q2	ubiquitin conjugating enzyme E2 Q2
101927905	3,66E-01	4,37E-01	3,26E-01	0,4801	0,9831904	0,4720098	13,28	LINC02449	long intergenic non-protein coding RNA 2449
4299	6,68E-21	2,02E+01	2,17E-21	0,0497	9,4967276	0,47172811	3530,16	AFF1	ALF transcription elongation factor 1
56124	1,02E-01	9,91E-01	8,23E-02	0,2714	1,7373937	0,47160234	42,33	PCDHB12	protocadherin beta 12
3093	3,28E-27	2,65E+01	8,96E-28	0,0432	10,9228515	0,47138332	5653,07	UBE2K	ubiquitin conjugating enzyme E2 K
145781	8,65E-12	1,11E+01	3,72E-12	0,0678	6,9474297	0,47130009	897,75	GCOM1	GCOM1, MYZAP-POLR2M combined locus
80333	8,54E-02	1,07E+00	6,81E-02	0,2583	1,8240457	0,47109996	45,64	KCNIP4	potassium voltage-gated channel interacting protein 4
100132352	9,75E-07	6,01E+00	5,25E-07	0,0939	5,0168235	0,47109673	430,64	FRG1HP	FSHD region gene 1 family member H, pseudogene
51002	1,39E-10	9,86E+00	6,25E-11	0,072	6,5375258	0,47064517	1830,07	TPRKB	TP53RK binding protein
56899	8,04E-06	5,09E+00	4,56E-06	0,1026	4,5842322	0,47049292	348,32	ANKS1B	ankyrin repeat and sterile alpha motif domain containing 1B
101927155	1,55E-06	5,81E+00	8,45E-07	0,0955	4,9247464	0,47039563	380,66	LMO7-AS1	LMO7 antisense RNA 1
9375	6,12E-21	2,02E+01	1,98E-21	0,0495	9,5059867	0,47021021	5922,39	TM9SF2	transmembrane 9 superfamily member 2
85236	9,55E-17	1,60E+01	3,49E-17	0,0558	8,4287397	0,4701212	5235	H2BC12	H2B clustered histone 12
81555	1,74E-21	2,08E+01	5,56E-22	0,0488	9,6374048	0,47005057	2890,67	YIPF5	Yip1 domain family member 5
163126	3,75E-09	8,43E+00	1,80E-09	0,0781	6,0152897	0,46994803	713,97	EID2	EP300 interacting inhibitor of differentiation 2
389602	3,83E-09	8,42E+00	1,84E-09	0,0781	6,0117167	0,46980472	624,24	LOC389602	uncharacterized LOC389602
51306	4,29E-21	2,04E+01	1,38E-21	0,0492	9,5432466	0,46971865	2798,97	FAM13B	family with sequence similarity 13 member B
54843	4,84E-08	7,32E+00	2,43E-08	0,0841	5,5779688	0,4691769	519,8	SYTL2	synaptotagmin like 2
10371	8,01E-18	1,71E+01	2,84E-18	0,0538	8,7177409	0,46859808	2089,79	SEMA3A	semaphorin 3A
9184	2,88E-36	3,55E+01	6,25E-37	0,0369	12,6956075	0,46859	13984,96	BUB3	BUB3 mitotic checkpoint protein
8417	1,76E-17	1,68E+01	6,31E-18	0,0543	8,6267075	0,46850077	2193,94	STX7	syntaxin 7
1119	1,95E-11	1,07E+01	8,49E-12	0,0686	6,830074	0,46848657	2018,57	CHKA	choline kinase alpha
162962	2,02E-04	3,69E+00	1,25E-04	0,1221	3,8351819	0,46846674	246,56	ZNF836	zinc finger protein 836
81533	9,68E-16	1,50E+01	3,66E-16	0,0574	8,1492127	0,46785594	2284,6	ITFG1	integrin alpha FG-GAP repeat containing 1
84886	3,90E-17	1,64E+01	1,41E-17	0,0548	8,5341093	0,46776876	1690,56	C1orf198	chromosome 1 open reading frame 198
100506881	3,35E-03	2,47E+00	2,29E-03	0,1534	3,0492289	0,46766628	133,22	MKLN1-AS	MKLN1 antisense RNA
10520	9,46E-13	1,20E+01	3,94E-13	0,0644	7,2574778	0,46758479	1083,53	ZNF211	zinc finger protein 211
1956	9,64E-37	3,60E+01	2,07E-37	0,0366	12,7818627	0,46733909	18770,98	EGFR	epidermal growth factor receptor
84771	2,30E-01	6,38E-01	1,96E-01	0,3615	1,2926775	0,46730108	24,3	DDX11L2	DEAD/H-box helicase 11 like 2 (pseudogene)
89848	8,61E-13	1,21E+01	3,58E-13	0,0643	7,2703785	0,46713404	1022,71	FCHSD1	FCH and double SH3 domains 1
55711	2,74E-02	1,56E+00	2,05E-02	0,2016	2,316978	0,46711492	79,03	FAR2	fatty acyl-CoA reductase 2
5194	7,91E-13	1,21E+01	3,29E-13	0,0641	7,2819995	0,46708634	1115,26	PEX13	peroxisomal biogenesis factor 13
7596	3,03E-15	1,45E+01	1,16E-15	0,0583	8,0080984	0,46693794	1324,69	ZNF45	zinc finger protein 45
9187	1,31E-08	7,88E+00	6,44E-09	0,0804	5,8049758	0,46689435	637,76	SLC24A1	solute carrier family 24 member 1
348235	9,64E-25	2,40E+01	2,81E-25	0,0449	10,3880013	0,46649249	4885,48	SKA2	spindle and kinetochore associated complex subunit 2

222484	3,05E-08	7,52E+00	1,52E-08	0,0824	5,6594141	0,46640965	562,53	LNX2	ligand of numb-protein X 2
6996	2,25E-19	1,86E+01	7,61E-20	0,0511	9,1186513	0,46638807	2211,15	TDG	thymine DNA glycosylase
51127	4,67E-01	3,31E-01	4,25E-01	0,5845	0,7974092	0,46606546	8,82	TRIM17	tripartite motif containing 17
65110	4,45E-20	1,94E+01	1,48E-20	0,0501	9,2945896	0,46559495	2943,06	UPF3A	UPF3A regulator of nonsense mediated mRNA decay
9474	5,12E-16	1,53E+01	1,92E-16	0,0566	8,2269656	0,46558754	1732,72	ATG5	autophagy related 5
7447	5,97E-02	1,22E+00	4,68E-02	0,2341	1,9883037	0,46549998	57,72	VSNL1	visinin like 1
8476	1,83E-24	2,37E+01	5,38E-25	0,0451	10,3259327	0,46539346	7175,84	CDC42BPA	CDC42 binding protein kinase alpha
90693	6,48E-04	3,19E+00	4,19E-04	0,1319	3,5279668	0,46526745	228,74	CCDC126	coiled-coil domain containing 126
100652736	1,68E-01	7,75E-01	1,40E-01	0,3154	1,4750515	0,46519614	30,91	LINC01311	long intergenic non-protein coding RNA 1311
102724262	3,56E-02	1,45E+00	2,71E-02	0,2103	2,2105378	0,46481271	70,61	LOC102724262	uncharacterized LOC102724262
84236	6,10E-12	1,12E+01	2,62E-12	0,0664	6,9969843	0,46473084	1010,7	RHBDD1	rhomboid domain containing 1
100507398	3,35E-01	4,75E-01	2,95E-01	0,4434	1,04738	0,46445522	15,76	INTS6-AS1	INTS6 antisense RNA 1
84288	1,08E-07	6,97E+00	5,52E-08	0,0855	5,4335754	0,4644478	520,79	EFCAB2	EF-hand calcium binding domain 2
2823	4,69E-01	3,29E-01	4,27E-01	0,5845	0,7944153	0,46437426	9,62	GPM6A	glycoprotein M6A
7743	2,02E-09	8,69E+00	9,55E-10	0,0759	6,1166985	0,46409594	673,54	ZNF189	zinc finger protein 189
100505641	9,17E-31	3,00E+01	2,29E-31	0,0398	11,6503389	0,46408276	6772,63	FGD5-AS1	FGD5 antisense RNA 1
6045	7,35E-14	1,31E+01	2,95E-14	0,061	7,6003657	0,46383347	1263,87	RNF2	ring finger protein 2
7112	1,09E-20	2,00E+01	3,56E-21	0,0491	9,4447214	0,46349371	15037,51	TMPO	thymopoietin
10283	7,43E-20	1,91E+01	2,48E-20	0,0502	9,2394605	0,46341831	2454,93	CWC27	CWC27 spliceosome associated cyclophilin
5685	1,27E-23	2,29E+01	3,82E-24	0,0457	10,1362256	0,46327504	7778,03	PSMA4	proteasome 20S subunit alpha 4
643749	2,74E-03	2,56E+00	1,86E-03	0,1489	3,1117884	0,46323634	142,26	TRAF3IP2-A	TRAF3IP2 antisense RNA 1
7334	9,84E-23	2,20E+01	3,03E-23	0,0466	9,9317226	0,46308073	6508,61	UBE2N	ubiquitin conjugating enzyme E2 N
23173	3,10E-23	2,25E+01	9,41E-24	0,0461	10,0475897	0,4630478	3290,78	METAP1	methionyl aminopeptidase 1
105372709	1,20E-01	9,21E-01	9,78E-02	0,2797	1,6557124	0,4630446	41,25	LOC105372	uncharacterized LOC105372709
6938	4,05E-21	2,04E+01	1,31E-21	0,0485	9,549255	0,4629072	2927,68	TCF12	transcription factor 12
59285	2,91E-01	5,36E-01	2,53E-01	0,4049	1,1429736	0,46276989	18,14	CACNG6	calcium voltage-gated channel auxiliary subunit gamma 6
54462	5,05E-21	2,03E+01	1,63E-21	0,0486	9,5260678	0,4626345	2567,01	CCSER2	coiled-coil serine rich protein 2
340485	1,86E-02	1,73E+00	1,36E-02	0,1874	2,4666464	0,46236499	89,82	ACER2	alkaline ceramidase 2
152006	2,53E-13	1,26E+01	1,03E-13	0,0622	7,4369437	0,46231303	1204,39	RNF38	ring finger protein 38
8724	2,27E-24	2,36E+01	6,70E-25	0,0449	10,3047728	0,46228019	3772,12	SNX3	sorting nexin 3
105372275	4,37E-02	1,36E+00	3,36E-02	0,2175	2,124832	0,46220524	64,08	LOC105372275	
9728	7,14E-15	1,41E+01	2,78E-15	0,0585	7,9003958	0,4618426	1653,67	SECISBP2L	SECIS binding protein 2 like
643977	1,15E-01	9,39E-01	9,35E-02	0,2753	1,6770224	0,46170357	41,47	FLJ32255	uncharacterized LOC643977
51738	4,44E-01	3,53E-01	4,03E-01	0,5515	0,8371318	0,46169467	9,75	GHRL	ghrelin and obestatin prepropeptide
101928290	3,33E-01	4,78E-01	2,93E-01	0,4389	1,0516435	0,46154791	16,01	PLBD1-AS1	PLBD1 antisense RNA 1
10651	4,00E-15	1,44E+01	1,55E-15	0,0579	7,9731456	0,46146482	2304,11	MTX2	metaxin 2
9865	2,11E-01	6,76E-01	1,79E-01	0,3434	1,3439059	0,46144403	26,71	TRIL	TLR4 interactor with leucine rich repeats
266727	6,97E-04	3,16E+00	4,52E-04	0,1315	3,5077826	0,46125571	210,36	MDGA1	MAM domain containing glycosylphosphatidylinositol anchor 1
728712	6,35E-02	1,20E+00	4,99E-02	0,2351	1,9612485	0,46107062	57,45	SPANXA2	SPANX family member A2
8777	2,20E-14	1,37E+01	8,72E-15	0,0594	7,756708	0,46106678	1451,39	MPDZ	multiple PDZ domain crumbs cell polarity complex component
3301	8,35E-23	2,21E+01	2,57E-23	0,0463	9,9482074	0,46093789	20114,29	DNAJA1	DnaJ heat shock protein family (Hsp40) member A1
101929003	1,52E-01	8,18E-01	1,26E-01	0,3012	1,5295117	0,46061718	36,29	LOC101929(	uncharacterized LOC101929003
79963	7,80E-07	6,11E+00	4,17E-07	0,091	5,0608935	0,46050397	430,7	ABCA11P	ATP binding cassette subfamily A member 11, pseudogene
84301	9,65E-19	1,80E+01	3,33E-19	0,0514	8,957347	0,46032337	2169,44	DDI2	DNA damage inducible 1 homolog 2
1942	5,95E-04	3,23E+00	3,84E-04	0,1296	3,5509584	0,46012757	200,71	EFNA1	ephrin A1
441094	3,55E-06	5,45E+00	1,97E-06	0,0967	4,7560834	0,4599429	513,15	NR2F1-AS1	NR2F1 antisense RNA 1
3189	8,36E-18	1,71E+01	2,96E-18	0,0528	8,7128864	0,45992141	11603,92	HNRNPH3	heterogeneous nuclear ribonucleoprotein H3
55750	4,39E-20	1,94E+01	1,46E-20	0,0495	9,2961787	0,45989502	2331,5	AGK	acylglycerol kinase
2332	2,99E-15	1,45E+01	1,15E-15	0,0574	8,00958	0,45988427	1999,18	FMR1	fragile X messenger ribonucleoprotein 1
84450	8,55E-20	1,91E+01	2,86E-20	0,0498	9,2242314	0,45980139	2604,62	ZNF512	zinc finger protein 512
81488	6,39E-10	9,19E+00	2,96E-10	0,0729	6,3009102	0,45959555	740,23	POLR2M	RNA polymerase II subunit M
105373511	3,97E-05	4,40E+00	2,35E-05	0,1087	4,229079	0,45949139	291,68	LOC105373	uncharacterized LOC105373511
4065	1,63E-05	4,79E+00	9,39E-06	0,1037	4,4306549	0,45940445	311,21	LY75	lymphocyte antigen 75
389247	2,26E-01	6,46E-01	1,93E-01	0,3525	1,3031209	0,45939367	23,99	ING2-DT	ING2 divergent transcript
133746	9,27E-11	1,00E+01	4,15E-11	0,0696	6,5986078	0,45908693	948,95	JMY	junction mediating and regulatory protein, p53 cofactor
11231	1,08E-22	2,20E+01	3,34E-23	0,0463	9,9218842	0,45889322	5364,12	SEC63	SEC63 homolog, protein translocation regulator
107984852	4,04E-01	3,94E-01	3,63E-01	0,5039	0,910507	0,45882787	12,23	LOC107984	uncharacterized LOC107984852
105374771	2,57E-01	5,90E-01	2,21E-01	0,3747	1,22398	0,45866401	21,43	LGALSL-DT	LGALSL divergent transcript
3281	2,83E-24	2,35E+01	8,38E-25	0,0446	10,2832796	0,45821737	4650,97	HSBP1	heat shock factor binding protein 1
8867	6,08E-12	1,12E+01	2,60E-12	0,0655	6,9975862	0,45801037	1058,79	SYNJ1	synaptojanin 1
51605	2,23E-21	2,07E+01	7,14E-22	0,0476	9,6116966	0,45791965	2743,44	TRMT6	tRNA methyltransferase 6 non-catalytic subunit
5244	1,69E-01	7,72E-01	1,41E-01	0,3111	1,471735	0,45790927	31,8	ABCB4	ATP binding cassette subfamily B member 4
57614	2,12E-14	1,37E+01	8,37E-15	0,059	7,7618106	0,45786192	1406,43	RELCH	RAB11 binding and LisH domain, coiled-coil and HEAT repeat containing
4189	9,07E-08	7,04E+00	4,62E-08	0,0838	5,4651822	0,45785485	600,22	DNAJB9	DnaJ heat shock protein family (Hsp40) member B9
7046	4,92E-18	1,73E+01	1,73E-18	0,0522	8,7734681	0,45763624	3868,14	TGFBR1	transforming growth factor beta receptor 1
85013	5,64E-10	9,25E+00	2,61E-10	0,0724	6,3204847	0,45756424	901,38	TMEM128	transmembrane protein 128
26065	6,35E-22	2,12E+01	2,00E-22	0,047	9,7419617	0,457502	5730,37	LSM14A	LSM14A mRNA processing body assembly factor
105378991	5,68E-02	1,25E+00	4,44E-02	0,2275	2,0106126	0,45750173	60,79	ERCC8-AS1	ERCC8 antisense RNA 1
8453	3,48E-13	1,25E+01	1,43E-13	0,0619	7,3934426	0,45743598	3318,97	CUL2	cullin 2
101928100	2,20E-01	6,58E-01	1,87E-01	0,3467	1,3193192	0,45736547	27,1	KLRK1-AS1	KLRK1 antisense RNA 1
96764	1,16E-13	1,29E+01	4,70E-14	0,0606	7,5398959	0,45710901	1334,7	TGS1	trimethylguanosine synthase 1
6418	1,80E-28	2,77E+01	4,76E-29	0,0408	11,1863009	0,45688502	29568,23	SET	SET nuclear proto-oncogene
23035	6,56E-12	1,12E+01	2,81E-12	0,0653	6,9867918	0,45643329	960,95	PHLPP2	PH domain and leucine rich repeat protein phosphatase 2
41	4,78E-04	3,32E+00	3,06E-04	0,1264	3,6101789	0,45638296	213,72	ASIC1	acid sensing ion channel subunit 1
100287098	2,47E-04	3,61E+00	1,55E-04	0,1206	3,7836951	0,45627171	261,81	TONSL-AS1	TONSL antisense RNA 1
101927352	3,56E-01	4,49E-01	3,15E-01	0,454	1,0043876	0,45596695	15,15	PLS3-AS1	PLS3 antisense RNA 1
101929959	7,06E-02	1,15E+00	5,59E-02	0,2384	1,9122026	0,45588833	55,85	BMS1P14	BMS1 pseudogene 14
55274	2,36E-20	1,96E+01	7,76E-21	0,0487	9,3629099	0,45586921	2473,35	PHF10	PHD finger protein 10
90317	4,86E-06	5,31E+00	2,72E-06	0,0972	4,6907236	0,45581723	374,92	ZNF616	zinc finger protein 616
114899	8,32E-02	1,08E+00	6,64E-02	0,2482	1,835793	0,45568583	55,81	C1QTNF3	C1q and TNF related 3
9949	7,58E-09	8,12E+00	3,67E-09	0,0772	5,8982704	0,4555422	952,97	AMMECR1	AMMECR nuclear protein 1
728377	4,25E-03	2,37E+00	2,94E-03	0,1532	2,9739692	0,4554726	141,65	ARHGEF34F	Rho guanine nucleotide exchange factor 34, pseudogene
158586	5,51E-07	6,26E+00	2,93E-07	0,0888	5,128188	0,4552831	541,3	ZXDB	zinc finger X-linked duplicated B
10745	7,21E-16	1,51E+01	2,72E-16	0,0556	8,1852261	0,45526007	2070,86	PHTF1	putative homeodomain transcription factor 1
105378268	1,74E-01	7,59E-01	1,46E-01	0,3128	1,455116	0,45513431	31,56	LOC105378	uncharacterized LOC105378268
3336	7,90E-19	1,81E+01	2,72E-19	0,0506	8,9796127	0,45466217	3792,89	HSPE1	heat shock protein family E (Hsp10) member 1
57187	7,25E-24	2,31E+01	2,17E-24	0,0446	10,1913496	0,45448529	5828,31	THOC2	THO complex subunit 2
5530	6,26E-18	1,72E+01	2,21E-18	0,0519	8,7460052	0,45429472	2955,86	PPP3CA	protein phosphatase 3 catalytic subunit alpha
100526761	5,31E-02	1,27E+00	4,13E-02	0,2226	2,0406399	0,45424222	61,99	CCDC169-S	CCDC169-SOHLH2 readthrough
89846	3,38E-01	4,71E-01	2,98E-01	0,4365	1,0403504	0,45408527	15,65	FGD3	FYVE, RhoGEF and PH domain containing 3
3455	1,56E-10	9,81E+00	7,07E-11	0,0697	6,5191435	0,45406054	886,24	IFNAR2	interferon alpha and beta receptor subunit 2
114118903	8,89E-15	1,41E+01	3,47E-15	0,0577	7,872625	0,45404219	1672,38	ARHGAP11A	ARHGAP11A-SCG5 readthrough
2162	1,39E-01	8,57E-01	1,15E-01	0,2875	1,5772865	0,45341915	42,51	F13A1	coagulation factor XIII A chain
131076	1,10E-10	9,96E+00	4,93E-11	0,0689	6,5730371	0,45302455	926,3	MIX23	mitochondrial matrix import factor 23
3840	3,51E-21	2,05E+01	1,13E-21	0,0473	9,5643452	0,45283834	5082,47	KPNA4	karyopherin subunit alpha 4
4568	3,24E-03	2,49E+00	2,22E-03	0,148	3,0596092	0,45272856	178,14	TRNL2	tRNA-Leu
79731	2,37E-08	7,63E+00	1,17E-08	0,0794	5,7033963	0,45268368	675,79	NARS2	asparaginyl-tRNA synthetase 2, mitochondrial
105379173	2,28E-04	3,64E+00	1,42E-04	0,1189	3,8038658	0,45242766	234,04	LOC105379	uncharacterized LOC105379173
105370458	1,49E-03	2,83E+00	9,94E-04	0,1374	3,2923122	0,4523053	188,42	SEC23A-AS	SEC23A antisense RNA 1
111064646	4,53E-03	2,34E+00	3,14E-03	0,1531	2,9536642	0,45208857	141,43	TPM1-AS	TPM1 antisense RNA
283578	8,30E-15	1,41E+01	3,24E-15	0,0574	7,8812992	0,45201039	1632,14	TMED8	transmembrane p24 trafficking protein family member 8
105370041	6,08E-03	2,22E+00	4,27E-03	0,1582	2,8573263	0,45194454	127,37	LOC105370(	uncharacterized LOC105370041
445571	3,48E-10	9,46E+00	1,60E-10	0,0707	6,3959591	0,4518835	784,86	ZNG1C	Zn regulated GTPase metalloprotein activator 1C
58533	7,28E-22	2,11E+01	2,29E-22	0,0464	9,727881	0,45185811	4936,16	SNX6	sorting nexin 6
28316	4,70E-01	3,28E-01	4,28E-01	0,5701	0,7923951	0,45174982	9,29	CDH20	cadherin 20
105370560	4,84E-05	4,32E+00	2,87E-05	0,108	4,1831879	0,45170608	312,77	RBM25-AS1	RBM25 antisense RNA 1
404201	5,96E-03	2,22E+00	4,18E-03	0,1577	2,8639527	0,45159987	147,8	WDFY3-AS2	WDFY3 antisense RNA 2
8470	2,88E-07	6,54E+00	1,51E-07	0,086	5,2518686	0,45141772	548,35	SORBS2	sorbin and SH3 domain containing 2
55556	1,41E-27	2,69E+01	3,82E-28	0,041	10,9999222	0,45140594	5055,67	ENOSF1	enolase superfamily member 1
11232	2,18E-07	6,66E+00	1,13E-07	0,085	5,3038257	0,45104582	490,36	POLG2	DNA polymerase gamma 2, accessory subunit
3459	1,30E-16	1,59E+01	4,78E-17	0,0537	8,391937	0,45095374	2167,73	IFNGR1	interferon gamma receptor 1
50619	8,50E-08	7,07E+00	4,33E-08	0,0823	5,4768647	0,4508304	575,72	DEF6	DEF6 guanine nucleotide exchange factor
26273	6,25E-15	1,42E+01	2,43E-15	0,0569	7,9171932	0,45081439	1557,3	FBXO3	F-box protein 3
84890	7,35E-12	1,11E+01	3,16E-12	0,0647	6,9706013	0,45077084	1356,08	ADO	2-aminoethanethiol dioxygenase
100302174	4,39E-01	3,58E-01	3,97E-01	0,5324	0,8465574	0,45072234	10,71	MIR1307	microRNA 1307
105378698	1,50E-01	8,24E-01	1,24E-01	0,2933	1,5363606	0,45061052	36,39	LOC105378(	uncharacterized LOC105378698
22998	7,23E-18	1,71E+01	2,56E-18	0,0516	8,729493	0,45054759	7239,63	LIMCH1	LIM and calponin homology domains 1
10767	2,86E-18	1,75E+01	1,00E-18	0,051	8,8348837	0,45027949	2808,88	HBS1L	HBS1 like translational GTPase
9337	1,25E-16	1,59E+01	4,61E-17	0,0536	8,3962234	0,45002518	2651,13	CNOT8	CCR4-NOT transcription complex subunit 8
4352	3,79E-01	4,21E-01	3,38E-01	0,4695	0,9585714	0,45000297	14,14	MPL	MPL proto-oncogene, thrombopoietin receptor

3652	3,44E-06	5,46E+00	1,91E-06	0,0945	4,7629897	0,44993697	394,51	IPP	intracisternal A particle-promoted polypeptide
100287902	4,87E-05	4,31E+00	2,90E-05	0,1076	4,1815515	0,44991618	377,62	LGALS8-AS1	LGALS8 antisense RNA 1
8754	1,62E-27	2,68E+01	4,40E-28	0,0409	10,9872393	0,4498983	13320,98	ADAM9	ADAM metallopeptidase domain 9
401022	4,38E-12	1,14E+01	1,87E-12	0,0639	7,0438483	0,44979723	1138,5	HAGLR	HOXD antisense growth-associated long non-coding RNA
54708	5,00E-10	9,30E+00	2,30E-10	0,0709	6,3395621	0,44925174	1524,9	MARCHF5	membrane associated ring-CH-type finger 5
55571	1,49E-15	1,48E+01	5,66E-16	0,0555	8,0963664	0,44913029	1716,56	CNOT11	CCR4-NOT transcription complex subunit 11
101059953	2,63E-02	1,58E+00	1,97E-02	0,1925	2,3327068	0,44901362	84,72	NPIPA8	nuclear pore complex interacting protein family member A8
374900	9,65E-04	3,02E+00	6,32E-04	0,1314	3,4174746	0,44900783	192,46	ZNF568	zinc finger protein 568
219899	4,07E-15	1,44E+01	1,57E-15	0,0563	7,9709183	0,44898765	1920,85	TBCEL	tubulin folding cofactor E like
80317	6,00E-08	7,22E+00	3,04E-08	0,081	5,5393998	0,4484409	576,18	ZKSCAN3	zinc finger with KRAB and SCAN domains 3
400761	3,43E-01	4,65E-01	3,03E-01	0,4355	1,0296092	0,44834355	16,52	LRRC8C-DT	LRRC8C divergent transcript
101927263	4,62E-01	3,35E-01	4,21E-01	0,5568	0,8048544	0,4481511	10,27	LOC101927	uncharacterized LOC101927263
29081	8,42E-13	1,21E+01	3,50E-13	0,0616	7,2734894	0,44807048	1716,96	METTL5	methyltransferase 5, N6-adenosine
7098	1,55E-03	2,81E+00	1,04E-03	0,1366	3,2805087	0,44805391	239,7	TLR3	toll like receptor 3
4166	3,60E-01	4,44E-01	3,19E-01	0,4498	0,9960736	0,44800471	15,13	CHST6	carbohydrate sulfotransferase 6
55677	8,75E-16	1,51E+01	3,31E-16	0,0549	8,1616342	0,44779927	2742,49	IWS1	interacts with SUPT6H, CTD assembly factor 1
55573	3,87E-31	3,04E+01	9,57E-32	0,0382	11,7243288	0,44752189	10367,49	CDV3	CDV3 homolog
9851	5,65E-11	1,02E+01	2,51E-11	0,067	6,6728469	0,44740345	1146,84	KIAA0753	KIAA0753
107985939	1,58E-01	8,01E-01	1,31E-01	0,2962	1,5101183	0,44733911	36,51	LOC107985	uncharacterized LOC107985939
348995	3,88E-20	1,94E+01	1,28E-20	0,048	9,3096681	0,44713834	2741,85	NUP43	nucleoporin 43
317	4,10E-14	1,34E+01	1,64E-14	0,0582	7,6764355	0,4470368	1419,4	APAF1	apoptotic peptidase activating factor 1
51030	2,97E-11	1,05E+01	1,31E-11	0,0661	6,7678998	0,44702127	1320,64	TVP23B	trans-golgi network vesicle protein 23 homolog B
57380	7,07E-15	1,42E+01	2,75E-15	0,0566	7,9015515	0,44700938	1993,17	MRS2	magnesium transporter MRS2
8505	1,73E-17	1,68E+01	6,19E-18	0,0518	8,6290321	0,44687338	1916,75	PARG	poly(ADP-ribose) glycohydrolase
2935	6,65E-29	2,82E+01	1,73E-29	0,0396	11,2754709	0,44684737	9224,86	GSPT1	G1 to S phase transition 1
107985523	6,93E-02	1,16E+00	5,47E-02	0,2326	1,9208941	0,44682518	57,36	LOC107985523	
3988	1,58E-21	2,08E+01	5,02E-22	0,0463	9,6477458	0,44666701	4066,42	LIPA	lipase A, lysosomal acid type
145508	5,09E-09	8,29E+00	2,45E-09	0,0749	5,9648892	0,44653892	844,01	CEP128	centrosomal protein 128
23287	4,48E-19	1,83E+01	1,53E-19	0,0494	9,0425451	0,44634714	3516,78	AGTPBP1	ATP/GTP binding carboxypeptidase 1
118460	5,63E-14	1,32E+01	2,26E-14	0,0584	7,6351196	0,44617269	1414,16	EXOSC6	exosome component 6
93517	2,01E-09	8,70E+00	9,53E-10	0,0729	6,1170782	0,44594022	815,77	SDR42E1	short chain dehydrogenase/reductase family 42E, member 1
54205	1,10E-13	1,30E+01	4,42E-14	0,059	7,5479186	0,44547615	6532,92	CYCS	cytochrome c, somatic
7984	8,04E-05	4,09E+00	4,85E-05	0,1096	4,0628724	0,44545398	297,43	ARHGEF5	Rho guanine nucleotide exchange factor 5
51422	1,87E-16	1,57E+01	6,92E-17	0,0533	8,3484685	0,44512969	2200,93	PRKAG2	protein kinase AMP-activated non-catalytic subunit gamma 2
390940	9,73E-02	1,01E+00	7,84E-02	0,2529	1,7600843	0,44510815	47,09	PINLYP	phospholipase A2 inhibitor and LY6/PLAUR domain containing
79745	3,82E-19	1,84E+01	1,30E-19	0,0491	9,0600825	0,44510618	2439,93	CLIP4	CAP-Gly domain containing linker protein family member 4
6671	6,64E-05	4,18E+00	3,98E-05	0,1083	4,1085759	0,44491319	316,95	SP4	Sp4 transcription factor
144715	2,57E-06	5,59E+00	1,41E-06	0,0922	4,8230114	0,44478991	434,93	RAD9B	RAD9 checkpoint clamp component B
23063	7,71E-23	2,21E+01	2,37E-23	0,0447	9,9563529	0,4447013	4783,28	WAPL	WAPL cohesin release factor
84129	3,08E-04	3,51E+00	1,94E-04	0,1193	3,7264394	0,44442429	234,46	ACAD11	acyl-CoA dehydrogenase family member 11
2043	7,28E-09	8,14E+00	3,53E-09	0,0752	5,9050575	0,44432884	659,86	EPHA4	EPH receptor A4
100287290	3,21E-01	4,93E-01	2,82E-01	0,4128	1,0763038	0,44431316	19,55	LOC100287	uncharacterized LOC100287290
6643	2,05E-19	1,87E+01	6,92E-20	0,0487	9,1289661	0,44419704	3648,53	SNX2	sorting nexin 2
261729	1,01E-02	2,00E+00	7,26E-03	0,1654	2,6847094	0,44401313	116,62	STEAP2	STEAP2 metalloreductase
285605	9,33E-05	4,03E+00	5,65E-05	0,1102	4,0268955	0,44389908	280,99	DTWD2	DTW domain containing 2
102465133	3,26E-02	1,49E+00	2,47E-02	0,1976	2,2462991	0,44382323	81,3	MIR6125	microRNA 6125
84899	2,97E-07	6,53E+00	1,55E-07	0,0846	5,2459748	0,44379152	538,39	TMTC4	transmembrane O-mannosyltransferase targeting cadherins 4
390963	1,13E-02	1,95E+00	8,14E-03	0,1677	2,6462278	0,44374884	112,95	ZNF818P	zinc finger protein 818, pseudogene
196792	1,05E-04	3,98E+00	6,37E-05	0,1109	3,9987444	0,44351124	296,87	FAM24B	family with sequence similarity 24 member B
9021	3,42E-10	9,47E+00	1,56E-10	0,0693	6,3989363	0,44329413	1035,02	SOCS3	suppressor of cytokine signaling 3
10097	2,27E-20	1,96E+01	7,47E-21	0,0473	9,3669035	0,44324852	19000,47	ACTR2	actin related protein 2
5151	2,05E-19	1,87E+01	6,94E-20	0,0485	9,1286475	0,44308415	2871,59	PDE8A	phosphodiesterase 8A
64789	2,55E-09	8,59E+00	1,21E-09	0,0729	6,0783451	0,44296076	717,4	EXO5	exonuclease 5
401321	1,69E-03	2,77E+00	1,13E-03	0,136	3,2560214	0,44292375	178,21	LINC00997	long intergenic non-protein coding RNA 997
9837	1,54E-14	1,38E+01	6,09E-15	0,0567	7,8021475	0,4427523	1851,41	GINS1	GINS complex subunit 1
150786	7,84E-02	1,11E+00	6,23E-02	0,2374	1,8644102	0,44264116	82,39	RAB6D	RAB6D, member RAS oncogene family
27020	9,10E-19	1,80E+01	3,13E-19	0,0494	8,9639025	0,44240539	3957,63	NPTN	neuroplastin
105374363	5,75E-04	3,24E+00	3,70E-04	0,1242	3,5603931	0,44223756	210,24	GTF3C2-AS2	GTF3C2 antisense RNA 2
7702	3,29E-10	9,48E+00	1,51E-10	0,069	6,4046078	0,44200169	1127,57	ZNF143	zinc finger protein 143
324	2,61E-18	1,76E+01	9,12E-19	0,05	8,8453554	0,44190014	2902,47	APC	APC regulator of WNT signaling pathway
197131	1,55E-14	1,38E+01	6,12E-15	0,0566	7,8015253	0,44178094	1677,72	UBR1	ubiquitin protein ligase E3 component n-recognin 1
27109	1,26E-09	8,90E+00	5,93E-10	0,0713	6,1923982	0,44149789	785,58	DMAC2L	distal membrane arm assembly component 2 like
245711	7,86E-02	1,10E+00	6,25E-02	0,2369	1,8628877	0,44138074	56,98	SPDYA	speedy/RINGO cell cycle regulator family member A
6341	9,01E-18	1,70E+01	3,20E-18	0,0507	8,7042484	0,44121206	2672,7	SCO1	synthesis of cytochrome C oxidase 1
9364	1,79E-12	1,17E+01	7,55E-13	0,0615	7,1691097	0,44118427	1337,12	RAB28	RAB28, member RAS oncogene family
254170	1,23E-10	9,91E+00	5,56E-11	0,0673	6,5552325	0,44102829	1229,98	FBXO33	F-box protein 33
348093	3,15E-02	1,50E+00	2,38E-02	0,195	2,2606764	0,44081973	88,42	RBPMS2	RNA binding protein, mRNA processing factor 2
3232	8,22E-02	1,09E+00	6,56E-02	0,2393	1,8414481	0,44061647	55,49	HOXD3	homeobox D3
100129029	6,35E-03	2,20E+00	4,47E-03	0,155	2,8430457	0,44058655	132,51	PKP4-AS1	PKP4 antisense RNA 1
9262	1,14E-12	1,19E+01	4,79E-13	0,0609	7,2311926	0,44046831	1381,79	STK17B	serine/threonine kinase 17b
474170	3,66E-05	4,44E+00	2,16E-05	0,1037	4,2475379	0,44041905	353,07	LRRC37A2	leucine rich repeat containing 37 member A2
344405	1,03E-01	9,87E-01	8,32E-02	0,2541	1,7323541	0,44017954	48,07	PRORSD1P	prolyl-tRNA synthetase associated domain containing 1, pseudogene
142680	2,41E-01	6,18E-01	2,06E-01	0,348	1,2642176	0,4400105	26,91	SLC34A3	solute carrier family 34 member 3
286437	2,58E-02	1,59E+00	1,92E-02	0,1879	2,3408305	0,43987487	95,62	LOC286437	uncharacterized LOC286437
1183	1,50E-14	1,38E+01	5,92E-15	0,0563	7,8056771	0,43982525	2159,59	CLCN4	chloride voltage-gated channel 4
105370532	3,81E-01	4,19E-01	3,40E-01	0,4602	0,9550906	0,43956528	15,13	LOC105370	uncharacterized LOC105370532
84365	2,55E-17	1,66E+01	9,19E-18	0,0512	8,5836986	0,43952162	2224	NIFK	nucleolar protein interacting with the FHA domain of MKI67
10299	4,85E-18	1,73E+01	1,71E-18	0,0501	8,7750058	0,43951785	4823,47	MARCHF6	membrane associated ring-CH-type finger 6
384	2,50E-11	1,06E+01	1,10E-11	0,0647	6,7933595	0,43935922	1142,05	ARG2	arginase 2
64682	8,46E-23	2,21E+01	2,60E-23	0,0442	9,9469133	0,43931677	3426,62	ANAPC1	anaphase promoting complex subunit 1
4925	3,43E-22	2,15E+01	1,07E-22	0,0448	9,8051638	0,43911951	4075,88	NUCB2	nucleobindin 2
6752	1,73E-03	2,76E+00	1,16E-03	0,1351	3,2486579	0,43877353	184,1	SSTR2	somatostatin receptor 2
160760	1,01E-12	1,20E+01	4,23E-13	0,0605	7,2481211	0,43865983	1851,99	PPTC7	protein phosphatase targeting COQ7
9135	2,39E-23	2,26E+01	7,22E-24	0,0435	10,0736462	0,43851896	5211,17	RABEP1	rabaptin, RAB GTPase binding effector protein 1
6920	9,79E-10	9,01E+00	4,57E-10	0,0703	6,2331119	0,43826527	1392,66	TCEA3	transcription elongation factor A3
80144	1,40E-17	1,69E+01	5,01E-18	0,0506	8,6532091	0,43825403	2477,1	FRAS1	Fraser extracellular matrix complex subunit 1
54726	3,65E-20	1,94E+01	1,21E-20	0,047	9,3161646	0,43821247	5741,42	OTUD4	OTU deubiquitinase 4
112268147	6,41E-02	1,19E+00	5,03E-02	0,2237	1,9570192	0,43785254	61,53	LOC112268	147
51115	9,28E-15	1,40E+01	3,63E-15	0,0556	7,8671271	0,43764966	1620,77	RMDN1	regulator of microtubule dynamics 1
79071	2,28E-21	2,06E+01	7,30E-22	0,0455	9,6093415	0,43750435	5068,61	ELOVL6	ELOVL fatty acid elongase 6
9589	1,98E-16	1,57E+01	7,34E-17	0,0524	8,3415059	0,43742053	3210,1	WTAP	WT1 associated protein
105370384	6,89E-03	2,16E+00	4,87E-03	0,1553	2,8157773	0,43739045	134,08	LOC105370	uncharacterized LOC105370384
105378513	7,30E-02	1,14E+00	5,78E-02	0,2304	1,8972389	0,43720769	58,28	LOC105378	uncharacterized LOC105378513
100874260	1,72E-02	1,76E+00	1,26E-02	0,1752	2,4948519	0,4371148	102,37	UBE2CP5	ubiquitin conjugating enzyme E2 C pseudogene 5
101927750	3,13E-02	1,50E+00	2,37E-02	0,1932	2,2627582	0,43707443	86,46	ATP6V1B1-A	ATP6V1B1 antisense RNA 1
90987	1,34E-09	8,87E+00	6,29E-10	0,0707	6,1830502	0,43691836	882,55	ZNF251	zinc finger protein 251
101928794	1,88E-01	7,26E-01	1,58E-01	0,3093	1,4120553	0,43681854	32,81	MAST4-AS1	MAST4 antisense RNA 1
51111	4,52E-12	1,13E+01	1,93E-12	0,0621	7,0395977	0,4368079	1566,95	KMT5B	lysine methyltransferase 5B
105372273	2,04E-01	6,90E-01	1,72E-01	0,3201	1,3643192	0,43678485	30,95	LOC105372	uncharacterized LOC105372273
102724364	3,34E-04	3,48E+00	2,11E-04	0,1178	3,7053243	0,43654829	244,03	SEC22B4P	SEC22 homolog B4, pseudogene
29094	6,11E-06	5,21E+00	3,44E-06	0,094	4,6427843	0,43638647	402,12	LGALSL	galectin like
6581	1,24E-06	5,91E+00	6,72E-07	0,0878	4,9693518	0,43633193	509,08	SLC22A3	solute carrier family 22 member 3
81609	2,77E-12	1,16E+01	1,18E-12	0,0613	7,1082165	0,43603663	1210,61	SNX27	sorting nexin 27
100506161	5,26E-02	1,28E+00	4,09E-02	0,2131	2,0448433	0,43571579	66,73	TAF1A-AS1	TAF1A antisense RNA 1
220213	3,12E-07	6,51E+00	1,63E-07	0,0832	5,2367243	0,43563496	620,63	OTUD1	OTU deubiquitinase 1
2004	3,75E-24	2,34E+01	1,11E-24	0,0425	10,2558589	0,43561573	7505,18	ELK3	ETS transcription factor ELK3
55839	5,28E-23	2,23E+01	1,61E-23	0,0436	9,9943011	0,43536642	4017,1	CENPN	centromere protein N
100131827	3,95E-04	3,40E+00	2,51E-04	0,1189	3,661175	0,43535239	231,52	ZNF717	zinc finger protein 717
148229	1,08E-04	3,97E+00	6,57E-05	0,109	3,9914178	0,43511063	323,6	ATP8B3	ATPase phospholipid transporting 8B3
23424	8,77E-13	1,21E+01	3,65E-13	0,0599	7,2679282	0,43507277	1329,24	TDRD7	tudor domain containing 7
51765	1,71E-11	1,08E+01	7,46E-12	0,0635	6,8484913	0,43497666	1093,16	STK26	serine/threonine kinase 26
105371441	1,42E-01	8,48E-01	1,18E-01	0,2778	1,5652409	0,4347681	41,26	LOC105371	441
345651	2,02E-01	6,95E-01	1,71E-01	0,3174	1,3691199	0,43452302	31,22	ACTBL2	actin beta like 2
8726	4,49E-15	1,43E+01	1,74E-15	0,0546	7,9586772	0,43420669	2050,18	EED	embryonic ectoderm development
25936	5,98E-11	1,02E+01	2,66E-11	0,0652	6,6643103	0,43418915	1288,25	NSL1	NSL1 component of MIS12 kinetochore complex
54765	4,12E-30	2,94E+01	1,04E-30	0,0377	11,5203136	0,43415238	9150,88	TRIM44	tripartite motif containing 44
5613	4,95E-07	6,31E+00	2,62E-07	0,0843	5,1487882	0,43414135	539,33	PRKX	protein kinase cAMP-dependent X-linked catalytic subunit
102465249	3,67E-01	4,35E-01	3,27E-01	0,4425	0,98097	0,4340891	15,58	MIR6502	microRNA 6502
101928279	2,80E-01	5,53E-01	2,43E-01	0,3715	1,1680146	0,43389583	23,86	LOC101928	uncharacterized LOC101928279
55033	2,01E-11	1,07E+01	8,76E-12	0,0636	6,8255585	0,43389471	1132,32	FKBP14	FKBP prolyl isomerase 14

101928979	2,84E-01	5,47E-01	2,46E-01	0,374	1,1592767	0,43360697	21,77	LINC01719	long intergenic non-protein coding RNA 1719
55228	4,25E-13	1,24E+01	1,75E-13	0,0588	7,3666918	0,43329879	1276,72	PNMA8A	PNMA family member 8A
8697	5,98E-22	2,12E+01	1,88E-22	0,0444	9,7481772	0,43295361	4318,1	CDC23	cell division cycle 23
79786	3,48E-10	9,46E+00	1,59E-10	0,0677	6,3963491	0,43272813	905,49	KLHL36	kelch like family member 36
9352	1,86E-15	1,47E+01	7,09E-16	0,0536	8,0689096	0,43260679	4490,05	TXNL1	thioredoxin like 1
254013	1,52E-02	1,82E+00	1,11E-02	0,1703	2,540611	0,43254844	110,47	ETFBKMT	electron transfer flavoprotein subunit beta lysine methyltransferase
80777	5,38E-21	2,03E+01	1,74E-21	0,0454	9,5195341	0,43252373	4862,83	CYB5B	cytochrome b5 type B
254048	1,62E-06	5,79E+00	8,83E-07	0,088	4,9159832	0,43244352	476,24	UBN2	ubinuclein 2
54821	1,27E-17	1,69E+01	4,53E-18	0,0499	8,6646564	0,43228369	2475,53	ERCC6L	ERCC excision repair 6 like, spindle assembly checkpoint helicase
284001	6,34E-11	1,02E+01	2,82E-11	0,0649	6,655695	0,43177174	1146,45	CCDC57	coiled-coil domain containing 57
10529	9,59E-02	1,02E+00	7,72E-02	0,2443	1,7671096	0,43176207	60,54	NEBL	nebulette
105371427	3,40E-01	4,69E-01	3,00E-01	0,4169	1,0357232	0,43176102	17,81	LOC105371	replaced by ID 56957
105373424	1,41E-02	1,85E+00	1,02E-02	0,1682	2,5675467	0,43174859	114,74	LOC105373	uncharacterized LOC105373424
221895	6,71E-05	4,17E+00	4,02E-05	0,1051	4,1062922	0,43171622	312,97	JAZF1	JAZF zinc finger 1
192669	3,95E-10	9,40E+00	1,81E-10	0,0677	6,3763812	0,43161965	1000,74	AGO3	argonaute RISC catalytic component 3
5602	5,09E-01	2,93E-01	4,67E-01	0,593	0,7277673	0,4315297	9,78	MAPK10	mitogen-activated protein kinase 10
7411	9,95E-18	1,70E+01	3,54E-18	0,0496	8,6925325	0,43150764	2713,96	VBP1	VHL binding protein 1
340156	3,42E-11	1,05E+01	1,51E-11	0,064	6,7473547	0,43150695	1039,4	MYLK4	myosin light chain kinase family member 4
105378672	4,11E-01	3,86E-01	3,70E-01	0,4809	0,8971371	0,43141661	14,76	EXO5-DT	EXO5 divergent transcript
55917	5,56E-15	1,43E+01	2,16E-15	0,0544	7,9319876	0,43140604	2077,01	CTTNBP2NL	CTTNBP2 N-terminal like
149428	4,70E-01	3,28E-01	4,28E-01	0,5442	0,7926892	0,43134982	10,72	BNIPL	BCL2 interacting protein like
3074	5,72E-23	2,22E+01	1,75E-23	0,0432	9,9862064	0,43133038	5269,44	HEXB	hexosaminidase subunit beta
5939	1,55E-21	2,08E+01	4,94E-22	0,0447	9,6495513	0,43123213	7388,3	RBMS2	RNA binding motif single stranded interacting protein 2
23119	5,14E-03	2,29E+00	3,58E-03	0,148	2,9126033	0,43117181	160,29	HIC2	HIC ZBTB transcriptional repressor 2
84959	1,06E-24	2,40E+01	3,08E-25	0,0415	10,3792734	0,43115146	6829,6	UBASH3B	ubiquitin associated and SH3 domain containing B
8394	2,20E-27	2,67E+01	5,97E-28	0,0393	10,959654	0,43047355	6441,13	PIP5K1A	phosphatidylinositol-4-phosphate 5-kinase type 1 alpha
101927124	5,21E-01	2,83E-01	4,79E-01	0,6082	0,7076807	0,43041839	8,2	HEATR5A-D	HEATR5A divergent transcript
197187	1,98E-01	7,03E-01	1,67E-01	0,3115	1,3813786	0,43029757	32,41	SNAI3-AS1	SNAI3 antisense RNA 1
55746	1,06E-16	1,60E+01	3,89E-17	0,0511	8,4160555	0,43023496	3722,8	NUP133	nucleoporin 133
51318	2,61E-22	2,16E+01	8,11E-23	0,0437	9,8330927	0,42996026	3913,47	MRPL35	mitochondrial ribosomal protein L35
10771	2,85E-16	1,55E+01	1,06E-16	0,0518	8,2980956	0,42978621	3842,11	ZMYND11	zinc finger MYND-type containing 11
157506	3,36E-04	3,47E+00	2,13E-04	0,116	3,7034096	0,42963858	247,27	RDH10	retinol dehydrogenase 10
102724580	3,22E-01	4,92E-01	2,83E-01	0,4	1,0740219	0,4296375	18,81	LOC102724	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 1 like pseudogene
51141	1,03E-09	8,99E+00	4,83E-10	0,069	6,224386	0,42947349	995,6	INSIG2	insulin induced gene 2
153222	1,86E-05	4,73E+00	1,08E-05	0,0976	4,4010526	0,42942883	521,97	CREBRF	CREB3 regulatory factor
55916	1,04E-05	4,98E+00	5,94E-06	0,0948	4,5283562	0,42934477	469,44	NXT2	nuclear transport factor 2 like export factor 2
100996492	5,07E-01	2,95E-01	4,65E-01	0,5877	0,7304001	0,42923622	8,74	CTXND1	cortexin domain containing 1
10521	8,24E-25	2,41E+01	2,40E-25	0,0412	10,4031811	0,429052	6174,61	DDX17	DEAD-box helicase 17
9868	1,76E-18	1,78E+01	6,10E-19	0,0483	8,8902122	0,42900106	6016,31	TOMM70	translocase of outer mitochondrial membrane 70
51010	1,55E-10	9,81E+00	7,02E-11	0,0658	6,5201796	0,42871164	1658,54	EXOSC3	exosome component 3
9197	4,24E-09	8,37E+00	2,03E-09	0,0715	5,9951507	0,42864261	1085,21	SLC33A1	solute carrier family 33 member 1
9925	6,53E-11	1,02E+01	2,91E-11	0,0644	6,6512919	0,42857199	1060,76	ZBTB5	zinc finger and BTB domain containing 5
55771	1,20E-21	2,09E+01	3,81E-22	0,0443	9,6759804	0,42853439	13434,46	PRR11	proline rich 11
387712	6,34E-04	3,20E+00	4,10E-04	0,1212	3,5336169	0,42836541	228,94	ENO4	enolase 4
101927167	3,97E-02	1,40E+00	3,04E-02	0,1978	2,1654138	0,42832694	79,35	GATA2-AS1	GATA2 antisense RNA 1
54955	9,68E-15	1,40E+01	3,79E-15	0,0545	7,8616984	0,42823489	1637,73	C1orf109	chromosome 1 open reading frame 109
100996712	1,13E-09	8,95E+00	5,29E-10	0,069	6,2103996	0,42820931	969,54	SRGAP2D	SLIT-ROBO Rho GTPase activating protein 2D (pseudogene)
29911	2,97E-08	7,53E+00	1,48E-08	0,0756	5,6640298	0,4282071	727,7	HOOK2	hook microtubule tethering protein 2
112268223	1,57E-01	8,04E-01	1,30E-01	0,2829	1,5131155	0,42802952	40,27	CDC42-AS1	CDC42 antisense RNA 1
105371709	5,12E-02	1,29E+00	3,97E-02	0,208	2,0565759	0,42783558	73,77	LOC105371	uncharacterized LOC105371709
148254	9,92E-04	3,00E+00	6,50E-04	0,1254	3,4096597	0,42761683	218,58	ZNF555	zinc finger protein 555
100506757	4,12E-01	3,85E-01	3,71E-01	0,4777	0,8948174	0,42742737	13,53	LINC00629	long intergenic non-protein coding RNA 629
1315	2,10E-13	1,27E+01	8,54E-14	0,0573	7,4616824	0,42726494	14648,97	COPB1	COPI coat complex subunit beta 1
54996	4,80E-05	4,32E+00	2,85E-05	0,1021	4,1853307	0,42712294	356,02	MTARC2	mitochondrial amidoxime reducing component 2
105373148	4,27E-01	3,70E-01	3,86E-01	0,4923	0,8670649	0,42681276	12,54	LOC105373	uncharacterized LOC105373148
2287	4,79E-21	2,03E+01	1,55E-21	0,0448	9,5318224	0,42680153	3836,26	FKBP3	FKBP prolyl isomerase 3
1207	3,80E-19	1,84E+01	1,30E-19	0,0471	9,0606743	0,42675485	4617,65	CLNS1A	chloride nucleotide-sensitive channel 1A
51663	3,28E-27	2,65E+01	8,97E-28	0,0391	10,9228176	0,42655436	11019,49	ZFR	zinc finger RNA binding protein
9330	8,26E-12	1,11E+01	3,55E-12	0,0613	6,9540239	0,42645292	1467,05	GTF3C3	general transcription factor IIIC subunit 3
552891	5,61E-10	9,25E+00	2,59E-10	0,0674	6,3214177	0,4263608	1069,48	DNAJC25-GI	DNAJC25-GNG10 readthrough
101928764	3,83E-01	4,17E-01	3,42E-01	0,4486	0,9503811	0,42633518	14,95	LOC101928	coiled-coil domain-containing protein 144B
11171	1,42E-18	1,78E+01	4,92E-19	0,0478	8,9140072	0,42614347	6901,31	STRAP	serine/threonine kinase receptor associated protein
55888	2,44E-02	1,61E+00	1,82E-02	0,1804	2,3614401	0,42595344	97,17	ZKSCAN7	zinc finger with KRAB and SCAN domains 7
100874261	5,04E-01	2,98E-01	4,62E-01	0,5789	0,7357467	0,42594904	9,59	CCDC200	coiled-coil domain containing 200
2790	7,72E-10	9,11E+00	3,59E-10	0,0678	6,2709665	0,42547356	1056,77	GNG10	G protein subunit gamma 10
29102	1,70E-21	2,08E+01	5,41E-22	0,0441	9,6401499	0,42522758	4941,9	DROSHA	drosha ribonuclease III
85403	1,85E-15	1,47E+01	7,08E-16	0,0527	8,0691124	0,42521792	1928,22	EAF1	ELL associated factor 1
5747	4,86E-30	2,93E+01	1,23E-30	0,0369	11,5058493	0,42494322	9537,12	PTK2	protein tyrosine kinase 2
285220	1,14E-01	9,43E-01	9,26E-02	0,2525	1,6820796	0,42472507	52,9	EPHA6	EPH receptor A6
58500	1,65E-07	6,78E+00	8,53E-08	0,0793	5,3555523	0,42460456	662,82	ZNF250	zinc finger protein 250
8881	4,38E-17	1,64E+01	1,59E-17	0,0498	8,5205941	0,42448607	3023,8	CDC16	cell division cycle 16
8675	1,17E-15	1,49E+01	4,43E-16	0,0522	8,1261036	0,42447873	2955,69	STX16	syntaxin 16
57835	5,30E-02	1,28E+00	4,13E-02	0,208	2,0407993	0,42444238	81,21	SLC4A5	solute carrier family 4 member 5
107986934	1,41E-02	1,85E+00	1,03E-02	0,1653	2,567133	0,42437199	113,67	LOC107986	uncharacterized LOC107986934
107984251	2,60E-02	1,59E+00	1,94E-02	0,1815	2,337516	0,42417072	99,55	LOC107984	uncharacterized LOC107984251
353088	1,51E-02	1,82E+00	1,10E-02	0,1667	2,5437041	0,42406625	122,58	ZNF429	zinc finger protein 429
105377920	4,64E-02	1,33E+00	3,58E-02	0,2019	2,0993605	0,42394749	81,9	LOC105377	920
80853	5,63E-03	2,25E+00	3,94E-03	0,147	2,8827314	0,42381635	164,16	KDM7A	lysine demethylase 7A
6560	1,78E-11	1,07E+01	7,75E-12	0,0619	6,8430351	0,42352585	1899,71	SLC12A4	solute carrier family 12 member 4
55370	1,23E-05	4,91E+00	7,07E-06	0,0943	4,4916856	0,42342037	452,36	PPP4R1L	protein phosphatase 4 regulatory subunit 1 like (pseudogene)
57460	7,09E-04	3,15E+00	4,60E-04	0,1208	3,502838	0,42328586	239,42	PPM1H	protein phosphatase, Mg2+/Mn2+ dependent 1H
57484	1,79E-01	7,47E-01	1,50E-01	0,2939	1,4401615	0,42321371	40,34	RNF150	ring finger protein 150
100526833	4,45E-01	3,52E-01	4,04E-01	0,5067	0,8349872	0,42309621	11,52	SEPT5-GP1I	SEPT5-GP1BB readthrough
129880	1,57E-03	2,80E+00	1,05E-03	0,1291	3,2769386	0,42295258	191,38	BBS5	Bardet-Biedl syndrome 5
8936	1,00E-10	1,00E+01	4,48E-11	0,0642	6,5871218	0,42285716	1101,5	WASF1	WASP family member 1
4173	3,15E-28	2,75E+01	8,38E-29	0,0379	11,1360263	0,42247527	10211,09	MCM4	minichromosome maintenance complex component 4
54888	1,01E-25	2,50E+01	2,89E-26	0,0398	10,6030196	0,42226962	7657,03	NSUN2	NOP2/Sun RNA methyltransferase 2
134218	2,19E-17	1,67E+01	7,88E-18	0,0491	8,6012848	0,42224799	2882,51	DNAJC21	DnaJ heat shock protein family (Hsp40) member C21
100131897	7,39E-17	1,61E+01	2,70E-17	0,0499	8,4589302	0,42218775	2177,43	INSYN2B	inhibitory synaptic factor family member 2B
286451	2,09E-17	1,67E+01	7,50E-18	0,049	8,6070032	0,42185871	2601,67	YIPF6	Yip1 domain family member 6
1837	4,82E-09	8,32E+00	2,32E-09	0,0706	5,9738326	0,42184575	857,78	DTNA	dystrobrevin alpha
6049	8,14E-17	1,61E+01	2,98E-17	0,0499	8,4474299	0,42171403	2859,45	RNF6	ring finger protein 6
151760	5,05E-01	2,97E-01	4,63E-01	0,5752	0,7331311	0,42169957	9,77	LOC151760	putative uncharacterized protein LOC151760
654841	2,43E-01	6,14E-01	2,08E-01	0,335	1,2586837	0,42162814	29,97	MFF-DT	MFF divergent transcript
115271120	4,16E-05	4,38E+00	2,46E-05	0,0999	4,2182813	0,42153908	412,54	LDLR-AS1	LDLR antisense RNA 1
8976	5,29E-15	1,43E+01	2,05E-15	0,0531	7,9382289	0,42148405	1944,83	WASL	WASP like actin nucleation promoting factor
55012	3,09E-09	8,51E+00	1,48E-09	0,0697	6,0470025	0,421379	1575,28	PPP2R3C	protein phosphatase 2 regulatory subunit B"gamma
9884	3,19E-03	2,50E+00	2,18E-03	0,1374	3,0639957	0,42106928	170,59	LRRC37A	leucine rich repeat containing 37A
101928555	5,21E-01	2,83E-01	4,80E-01	0,5959	0,706574	0,42103183	9,19	LINC01537	long intergenic non-protein coding RNA 1537
55751	1,24E-10	9,91E+00	5,56E-11	0,0642	6,5551166	0,42096673	1826,26	TMEM184C	transmembrane protein 184C
246243	1,29E-17	1,69E+01	4,60E-18	0,0486	8,6629669	0,42094525	2633,62	RNASEH1	ribonuclease H1
6632	5,10E-14	1,33E+01	2,04E-14	0,055	7,648057	0,42088859	8872,69	SNRPD1	small nuclear ribonucleoprotein D1 polypeptide
51077	1,30E-19	1,89E+01	4,36E-20	0,0458	9,1786938	0,4208127	3557,94	FCF1	FCF1 rRNA-processing protein
5534	7,14E-19	1,81E+01	2,45E-19	0,0468	8,9910169	0,42051635	5054,85	PPP3R1	protein phosphatase 3 regulatory subunit B, alpha
93622	1,38E-05	4,86E+00	7,93E-06	0,094	4,4670001	0,42000324	468,85	LOC93622	Morf4 family associated protein 1 like 1
10363	1,57E-14	1,38E+01	6,17E-15	0,0538	7,8003267	0,41997786	1697,68	HMG20A	high mobility group 20A
112268289	3,29E-01	4,83E-01	2,89E-01	0,3962	1,0597342	0,41983955	19,27	LOC112268	uncharacterized LOC112268289
128338	4,99E-06	5,30E+00	2,79E-06	0,0896	4,6853927	0,41981761	899,34	DRAM2	DNA damage regulated autophagy modulator 2
11034	2,50E-11	1,06E+01	1,10E-11	0,0618	6,7933601	0,41975886	12943,54	DSTN	destrin, actin depolymerizing factor
1795	2,40E-04	3,62E+00	1,50E-04	0,1107	3,7909937	0,41967207	281,54	DOCK3	dedicator of cytokinesis 3
101928236	4,15E-02	1,38E+00	3,18E-02	0,1954	2,1470577	0,41944423	92,58	LOC101928	uncharacterized LOC101928236
23160	4,66E-25	2,43E+01	1,35E-25	0,0401	10,4577537	0,41937857	6380,86	WDR43	WD repeat domain 43
115361	2,06E-08	7,69E+00	1,02E-08	0,0732	5,7277641	0,41933222	757,74	GBP4	guanylate binding protein 4
100101148	4,30E-01	3,67E-01	3,88E-01	0,486	0,8626181	0,41919526	12,48	LOC100101	FKBP prolyl isomerase 6 pseudogene
51263	1,83E-20	1,97E+01	6,02E-21	0,0446	9,3897054	0,41918283	3586,76	MRPL30	mitochondrial ribosomal protein L30
1515	8,38E-04	3,08E+00	5,47E-04	0,1212	3,4567609	0,41904551	245,07	CTSV	cathepsin V
100500832	7,62E-03	2,12E+00	5,40E-03	0,1505	2,7820395	0,41880987	161,55	MIR3658	microRNA 3658
10048	1,18E-20	1,99E+01	3,86E-21	0,0444	9,4362924	0,41872557	5443,43	RANBP9	RAN binding protein 9
644019	1,27E-08	7,90E+00	6,20E-09	0,072	5,8112013	0,41857205	746,78	ZNG1F	Zn regulated GTPase metalloprotein activator 1F
100506275	4,78E-02	1,32E+00	3,70E-02	0,2005	2,0858143	0,41824114	78,34	KRBOX1-AS	KRBOX1 antisense RNA 1

54516	5,97E-11	1,02E+01	2,65E-11	0,0627	6,6646432	0,41813867	1208,07	MTRF1L	mitochondrial translation release factor 1 like
105373925	1,51E-01	8,21E-01	1,25E-01	0,2723	1,5348979	0,41798	41,23	LOC105373	uncharacterized LOC105373925
132989	1,74E-01	7,59E-01	1,45E-01	0,2867	1,4571383	0,41773344	36,94	C4orf36	chromosome 4 open reading frame 36
138948	1,98E-02	1,70E+00	1,46E-02	0,171	2,4424035	0,41770817	105,67	DBH-AS1	DBH antisense RNA 1
100507250	4,33E-01	3,64E-01	3,91E-01	0,4871	0,8572231	0,41756706	12,51	LOC100507	uncharacterized LOC100507250
84919	5,23E-21	2,03E+01	1,69E-21	0,0438	9,5224043	0,41743209	3793,17	PPP1R15B	protein phosphatase 1 regulatory subunit 15B
26043	1,28E-20	1,99E+01	4,18E-21	0,0443	9,4281148	0,41736724	3826,12	UBXN7	UBX domain protein 7
222161	4,77E-02	1,32E+00	3,69E-02	0,1999	2,0869625	0,41717146	79,48	DKFZP586I1	uncharacterized protein DKFZp586I1420
5537	1,67E-17	1,68E+01	5,99E-18	0,0483	8,6326683	0,41708194	4604,66	PPP6C	protein phosphatase 6 catalytic subunit
221178	2,95E-08	7,53E+00	1,47E-08	0,0736	5,6653244	0,41705686	709,2	SPATA13	spermatogenesis associated 13
4893	7,65E-16	1,51E+01	2,89E-16	0,051	8,177938	0,41694558	6091,31	NRAS	NRAS proto-oncogene, GTPase
3320	6,26E-22	2,12E+01	1,97E-22	0,0428	9,7433873	0,4169104	128951,67	HSP90AA1	heat shock protein 90 alpha family class A member 1
139341	4,09E-08	7,39E+00	2,05E-08	0,0743	5,6079002	0,41676297	839,71	FUNDC1	FUN14 domain containing 1
1054	4,84E-12	1,13E+01	2,07E-12	0,0593	7,0299248	0,41657729	1946,94	CEBPG	CCAAT enhancer binding protein gamma
117584	6,98E-11	1,02E+01	3,11E-11	0,0627	6,641069	0,41640531	1109,47	RFFL	ring finger and FYVE like domain containing E3 ubiquitin protein ligase
7323	2,56E-16	1,56E+01	9,52E-17	0,0501	8,3106569	0,41637861	10420,84	UBE2D3	ubiquitin conjugating enzyme E2 D3
101927018	4,44E-01	3,53E-01	4,03E-01	0,4974	0,8369571	0,41633254	11,97	LOC101927	uncharacterized LOC101927018
101929147	6,62E-05	4,18E+00	3,97E-05	0,1012	4,1094272	0,41601508	349,35	WARS2-AS1	WARS2 antisense RNA 1
1601	1,05E-15	1,50E+01	3,98E-16	0,0511	8,1390602	0,41600489	2071,89	DAB2	DAB adaptor protein 2
100130691	6,89E-02	1,16E+00	5,44E-02	0,2162	1,9238604	0,41593164	71,82	LOC100130	Putative uncharacterized protein FLJ44553
7976	4,99E-03	2,30E+00	3,48E-03	0,1423	2,9220143	0,41577408	163,05	FZD3	frizzled class receptor 3
55714	8,03E-19	1,81E+01	2,76E-19	0,0463	8,9777958	0,41566243	3461,03	TENM3	teneurin transmembrane protein 3
84950	2,20E-18	1,77E+01	7,66E-19	0,0469	8,8648541	0,41560796	3366,4	PRPF38A	pre-mRNA processing factor 38A
147372	6,63E-13	1,22E+01	2,75E-13	0,0569	7,306076	0,41550273	1584,24	CCBE1	collagen and calcium binding EGF domains 1
26149	1,85E-03	2,73E+00	1,24E-03	0,1286	3,229038	0,41532566	191,1	ZNF658	zinc finger protein 658
757	1,81E-12	1,17E+01	7,63E-13	0,0579	7,1676645	0,4151566	1349,32	TMEM50B	transmembrane protein 50B
1009	4,84E-14	1,33E+01	1,93E-14	0,0542	7,6550464	0,41506297	12896,83	CDH11	cadherin 11
112268063	3,07E-01	5,13E-01	2,68E-01	0,3745	1,1074404	0,41475957	22,26	LOC112268	uncharacterized LOC112268063
3148	1,03E-14	1,40E+01	4,03E-15	0,0528	7,8538806	0,41443881	12846,07	HMGB2	high mobility group box 2
4552	2,80E-16	1,56E+01	1,04E-16	0,0499	8,299995	0,41436003	2894,46	MTRR	5-methyltetrahydrofolate-homocysteine methyltransferase reductase
101926994	3,28E-01	4,84E-01	2,88E-01	0,3902	1,0614493	0,41420314	20,82	LOC101926	uncharacterized LOC101926994
8578	5,22E-02	1,28E+00	4,06E-02	0,2023	2,0474197	0,41418634	80,61	SCARF1	scavenger receptor class F member 1
23171	9,91E-09	8,00E+00	4,82E-09	0,0708	5,8531573	0,41413709	1141,83	GPD1L	glycerol-3-phosphate dehydrogenase 1 like
23741	1,01E-13	1,30E+01	4,09E-14	0,0547	7,5581886	0,41351971	5268,6	EID1	EP300 interacting inhibitor of differentiation 1
80224	3,05E-06	5,52E+00	1,69E-06	0,0863	4,7878039	0,413423	486,19	NUBPL	NUBP iron-sulfur cluster assembly factor, mitochondrial
84916	2,19E-25	2,47E+01	6,28E-26	0,0392	10,5299792	0,41286107	6176,75	UTP4	UTP4 small subunit processome component
255252	4,02E-12	1,14E+01	1,71E-12	0,0585	7,0559179	0,41285495	1278,99	LRRC57	leucine rich repeat containing 57
64116	1,14E-03	2,94E+00	7,54E-04	0,1225	3,369144	0,41272116	2603,89	SLC39A8	solute carrier family 39 member 8
116369	2,59E-01	5,87E-01	2,23E-01	0,3386	1,2185026	0,41260665	26,49	SLC26A8	solute carrier family 26 member 8
100506730	3,11E-03	2,51E+00	2,12E-03	0,1343	3,0723517	0,41256052	185,51	LOC100506	uncharacterized LOC100506730
57103	1,15E-07	6,94E+00	5,90E-08	0,076	5,4216675	0,41218238	735,98	TIGAR	TP53 induced glycolysis regulatory phosphatase
143458	1,05E-13	1,30E+01	4,24E-14	0,0546	7,5534152	0,41213755	1658,19	LDLRAD3	low density lipoprotein receptor class A domain containing 3
116228	3,95E-15	1,44E+01	1,53E-15	0,0517	7,9747151	0,41193453	2222,21	COX20	cytochrome c oxidase assembly factor COX20
64753	2,07E-02	1,68E+00	1,53E-02	0,1697	2,4258862	0,41162889	108,05	CCDC136	coiled-coil domain containing 136
1903	2,79E-06	5,55E+00	1,54E-06	0,0856	4,8062574	0,41122259	576,93	S1PR3	sphingosine-1-phosphate receptor 3
27229	1,19E-11	1,09E+01	5,16E-12	0,0596	6,9011949	0,41119157	1419,52	TUBGCP4	tubulin gamma complex associated protein 4
9877	1,35E-20	1,99E+01	4,42E-21	0,0436	9,4221127	0,41113746	7272,93	ZC3H11A	zinc finger CCCH-type containing 11A
7770	4,46E-08	7,35E+00	2,24E-08	0,0735	5,5926809	0,41101249	761,94	ZNF227	zinc finger protein 227
492303	1,23E-01	9,10E-01	1,01E-01	0,2503	1,6412997	0,41085263	49,82	GEMIN8P4	gem nuclear organelle associated protein 8 pseudogene 4
50859	1,38E-01	8,60E-01	1,14E-01	0,2595	1,5821988	0,41063468	51,82	SPOCK3	SPARC (osteonectin), cwcv and kazal like domains proteoglycan 3
100874042	2,49E-01	6,04E-01	2,14E-01	0,3304	1,2427251	0,41059431	28,42	HM13-AS1	HM13 antisense RNA 1
6809	2,02E-14	1,37E+01	7,98E-15	0,0528	7,767865	0,41045692	3428,1	STX3	syntaxin 3
51106	9,62E-07	6,02E+00	5,18E-07	0,0817	5,0194954	0,41029379	568,62	TFB1M	transcription factor B1, mitochondrial
221442	1,64E-02	1,79E+00	1,20E-02	0,1633	2,5124398	0,41024399	124,06	ADCY10P1	ADCY10 pseudogene 1
11042	8,50E-02	1,07E+00	6,79E-02	0,2246	1,8257182	0,41004315	65,35	GUSBP15	GUSB pseudogene 15
9252	8,51E-07	6,07E+00	4,57E-07	0,0811	5,0436831	0,40901834	577,35	RPS6KA5	ribosomal protein S6 kinase A5
8900	5,22E-04	3,28E+00	3,35E-04	0,114	3,5865119	0,40890041	280,21	CCNA1	cyclin A1
113115	7,23E-08	7,14E+00	3,67E-08	0,0741	5,506177	0,40824449	758,82	MTFR2	mitochondrial fission regulator 2
9462	3,40E-20	1,95E+01	1,12E-20	0,0438	9,3238292	0,40820981	4107,01	RASAL2	RAS protein activator like 2
254394	6,76E-06	5,17E+00	3,81E-06	0,0883	4,6212821	0,4078416	482,71	MCM9	minichromosome maintenance 9 homologous recombination repair factor
2065	7,44E-04	3,13E+00	4,83E-04	0,1168	3,4898269	0,4075359	246,32	ERBB3	erb-b2 receptor tyrosine kinase 3
81846	2,66E-15	1,46E+01	1,02E-15	0,0508	8,0241942	0,40745726	2635,53	SBF2	SET binding factor 2
51143	3,57E-20	1,94E+01	1,18E-20	0,0437	9,3183644	0,40724415	4315,94	DYNC1LI1	dynein cytoplasmic 1 light intermediate chain 1
219844	8,64E-11	1,01E+01	3,86E-11	0,0616	6,6092434	0,4071776	2594,33	HYLS1	HYLS1 centriolar and ciliogenesis associated
55761	3,03E-18	1,75E+01	1,06E-18	0,0461	8,8284161	0,40702902	4407,74	TTC17	tetratricopeptide repeat domain 17
55454	2,79E-18	1,76E+01	9,76E-19	0,046	8,837781	0,40661927	4149,1	CSGALNAC	chondroitin sulfate N-acetylgalactosaminyltransferase 2
3621	4,71E-07	6,33E+00	2,49E-07	0,0788	5,1582392	0,4065764	633,01	ING1	inhibitor of growth family member 1
133383	1,04E-04	3,98E+00	6,32E-05	0,1016	4,0004224	0,40640759	339,97	SETD9	SET domain containing 9
1266	1,68E-15	1,48E+01	6,42E-16	0,0503	8,0811014	0,40623324	13030,18	CNN3	calponin 3
100874246	4,28E-01	3,69E-01	3,86E-01	0,4686	0,8667435	0,40613046	13,87	ARHGAP31-	ARHGAP31 antisense RNA 1
56130	7,14E-02	1,15E+00	5,65E-02	0,2129	1,9071988	0,40612618	67,4	PCDHB6	protocadherin beta 6
80145	5,69E-19	1,82E+01	1,95E-19	0,045	9,0161835	0,4058896	3475,55	THOC7	THO complex subunit 7
3269	1,54E-14	1,38E+01	6,06E-15	0,052	7,8027199	0,40588049	2157,32	HRH1	histamine receptor H1
105374811	1,40E-01	8,54E-01	1,16E-01	0,258	1,5728232	0,4058592	45,83	LOC105374	uncharacterized LOC105374811
84513	1,88E-06	5,73E+00	1,03E-06	0,083	4,8863863	0,40576014	622,47	PLPP5	phospholipid phosphatase 5
10933	2,42E-25	2,46E+01	6,95E-26	0,0386	10,5204629	0,40571145	12234,53	MORF4L1	mortality factor 4 like 1
1950	5,20E-02	1,28E+00	4,04E-02	0,1979	2,0495053	0,40559959	79,72	EGF	epidermal growth factor
79857	4,18E-01	3,79E-01	3,77E-01	0,4588	0,8836561	0,40546308	15,43	FLJ13224	uncharacterized LOC79857
347442	1,28E-01	8,93E-01	1,05E-01	0,2499	1,6212487	0,40522435	55,32	DCAF8L2	DDB1 and CUL4 associated factor 8 like 2
11275	2,64E-12	1,16E+01	1,12E-12	0,0569	7,1153799	0,40510554	1444,17	KLHL2	kelch like family member 2
100288198	2,30E-05	4,64E+00	1,34E-05	0,093	4,3532519	0,40501446	457,49	HMGN3-AS1	HMGN3 antisense RNA 1
3066	5,20E-28	2,73E+01	1,39E-28	0,0365	11,0908359	0,40498745	10358,67	HDAC2	histone deacetylase 2
23219	1,51E-11	1,08E+01	6,55E-12	0,059	6,8671104	0,40495444	3625,36	FBXO28	F-box protein 28
10440	2,50E-12	1,16E+01	1,06E-12	0,0568	7,1225033	0,40468764	3524,54	TIMM17A	translocase of inner mitochondrial membrane 17A
101930112	1,94E-01	7,12E-01	1,64E-01	0,2904	1,3929982	0,40453674	39,19	LOC101930	uncharacterized LOC101930112
64983	9,52E-12	1,10E+01	4,10E-12	0,0583	6,9335392	0,40446377	2303,12	MRPL32	mitochondrial ribosomal protein L32
10618	4,18E-30	2,94E+01	1,06E-30	0,0351	11,519053	0,40434421	17047,16	TGOLN2	trans-golgi network protein 2
4287	2,04E-10	9,69E+00	9,26E-11	0,0624	6,4785236	0,40433132	1257,04	ATXN3	ataxin 3
3308	7,26E-22	2,11E+01	2,29E-22	0,0415	9,728194	0,40409552	15410,69	HSPA4	heat shock protein family A (Hsp70) member 4
105376373	1,27E-01	8,96E-01	1,04E-01	0,2485	1,6257551	0,40404602	62,93	LOC105376	uncharacterized LOC105376373
8621	5,28E-18	1,73E+01	1,86E-18	0,0461	8,7654381	0,40394074	3238,25	CDK13	cyclin dependent kinase 13
105371354	3,87E-01	4,12E-01	3,46E-01	0,4285	0,9420886	0,40371398	18,33	LOC105371	uncharacterized LOC105371354
2581	1,89E-15	1,47E+01	7,22E-16	0,05	8,066716	0,4036932	2434,36	GALC	galactosylceramidase
285382	1,52E-01	8,18E-01	1,26E-01	0,2637	1,5306392	0,40359101	46,84	C3orf70	chromosome 3 open reading frame 70
100288911	2,72E-02	1,57E+00	2,04E-02	0,1739	2,3198024	0,40338225	105,55	CRIM1-DT	CRIM1 divergent transcript
134492	2,48E-07	6,61E+00	1,29E-07	0,0764	5,2797202	0,40319873	1495,17	NUDCD2	NudC domain containing 2
246175	3,91E-10	9,41E+00	1,79E-10	0,0632	6,3780371	0,4029452	1159,11	CNOT6L	CCR4-NOT transcription complex subunit 6 like
51552	4,86E-16	1,53E+01	1,82E-16	0,0489	8,2332989	0,4029107	5042,03	RAB14	RAB14, member RAS oncogene family
113540	1,34E-01	8,73E-01	1,10E-01	0,2519	1,5993478	0,40286166	49,79	CMTM1	CKLF like MARVEL transmembrane domain containing 1
25961	1,56E-02	1,81E+00	1,14E-02	0,1592	2,5303998	0,40285523	132,81	NUDT13	nudix hydrolase 13
10434	2,39E-14	1,36E+01	9,44E-15	0,052	7,7465452	0,40278709	2069,87	LYPLA1	lysophospholipase 1
4771	8,16E-05	4,09E+00	4,92E-05	0,0992	4,0594564	0,40277418	348,14	NF2	NF2, moesin-ezrin-radixin like (MERLIN) tumor suppressor
51188	2,44E-06	5,61E+00	1,34E-06	0,0833	4,8337933	0,40250076	626,51	SS18L2	SS18 like 2
503542	9,66E-02	1,02E+00	7,78E-02	0,2279	1,7634615	0,40181897	58,15	SPRN	shadow of prion protein
51109	8,47E-21	2,01E+01	2,76E-21	0,0424	9,4716321	0,40172061	4790,6	RDH11	retinol dehydrogenase 11
9440	1,36E-11	1,09E+01	5,90E-12	0,0583	6,8819534	0,40132396	3441,16	MED17	mediator complex subunit 17
908	4,51E-24	2,33E+01	1,34E-24	0,0392	10,2377252	0,40130145	30089,51	CCT6A	chaperonin containing TCP1 subunit 6A
107303344	4,60E-05	4,34E+00	2,73E-05	0,0956	4,1951773	0,40123077	406,37	SETDB2-PH	SETDB2-PHF11 readthrough
107985873	8,23E-03	2,08E+00	5,85E-03	0,1456	2,7559128	0,40119533	174,89	LOC107985873	
100216545	1,04E-01	9,83E-01	8,44E-02	0,2324	1,7257546	0,401077	56,5	KMT2E-AS1	KMT2E antisense RNA 1
84056	2,36E-09	8,63E+00	1,12E-09	0,0658	6,0911181	0,40090544	1312,66	KATNAL1	katanin catalytic subunit A1 like 1
23002	1,95E-09	8,71E+00	9,23E-10	0,0655	6,1221218	0,40090113	1231,5	DAAM1	dishevelled associated activator of morphogenesis 1
29979	7,67E-25	2,41E+01	2,23E-25	0,0385	10,4100043	0,40089625	10530,75	UBQLN1	ubiquilin 1
6715	1,90E-11	1,07E+01	8,30E-12	0,0586	6,8332355	0,40067887	1422,8	SRD5A1	steroid 5 alpha-reductase 1
123688	1,64E-01	7,85E-01	1,37E-01	0,2694	1,4873966	0,40066158	47,48	HYKK	hydroxylysine kinase
54923	1,70E-03	2,77E+00	1,13E-03	0,1231	3,2549948	0,40062349	225,04	LIME1	Lck interacting transmembrane adaptor 1
63933	7,15E-16	1,51E+01	2,69E-16	0,0489	8,1862541	0,40057046	4918,57	MCUR1	mitochondrial calcium uniporter regulator 1
9814	9,71E-07	6,01E+00	5,23E-07	0,0798	5,0176795	0,40036835	625,56	SFI1	SFI1 centrin binding protein
83787	2,43E-07	6,61E+00	1,26E-07	0,0757	5,2839751	0,40002611	964,41	ARMC10	armadillo repeat containing 10
9908	1,35E-24	2,39E+01	3,95E-25	0,0386	10,3554635	0,39984592	13034,18	G3BP2	G3BP stress granule assembly factor 2

140612	4,21E-07	6,38E+00	2,22E-07	0,0772	5,1798249	0,39976458	616,63	ZFP28	ZFP28 zinc finger protein
55815	1,74E-01	7,59E-01	1,46E-01	0,2749	1,4541374	0,39975683	40,53	TSNAXIP1	translin associated factor X interacting protein 1
54468	1,38E-08	7,86E+00	6,77E-09	0,069	5,7966524	0,39970382	1011,73	MIOS	meiosis regulator for oocyte development
84168	2,02E-22	2,17E+01	6,27E-23	0,0405	9,8589137	0,39966957	6739,28	ANTXR1	ANTXR cell adhesion molecule 1
343578	6,83E-07	6,17E+00	3,65E-07	0,0786	5,0864684	0,39966215	583,18	ARHGAP40	Rho GTPase activating protein 40
100507299	3,12E-01	5,06E-01	2,73E-01	0,3646	1,0960194	0,3996367	24,83	SMC5-DT	SMC5 divergent transcript
1041	2,80E-01	5,53E-01	2,42E-01	0,3417	1,1693482	0,3996044	28,79	CDSN	corneodesmosin
1316	5,58E-24	2,33E+01	1,66E-24	0,0391	10,2169984	0,39925666	9311,24	KLF6	KLF transcription factor 6
136332	4,62E-01	3,35E-01	4,21E-01	0,496	0,8048948	0,39919511	14,52	LRGUK	leucine rich repeats and guanylate kinase domain containing
55788	1,08E-06	5,97E+00	5,84E-07	0,0798	4,9964954	0,3986729	778,46	LMBRD1	LMBR1 domain containing 1
105379499	3,26E-01	4,87E-01	2,86E-01	0,3739	1,0659422	0,39853187	22,31	LOC105379	uncharacterized LOC105379499
55157	2,72E-16	1,56E+01	1,01E-16	0,048	8,3035604	0,39848931	2543,6	DARS2	aspartyl-tRNA synthetase 2, mitochondrial
51601	7,50E-04	3,12E+00	4,88E-04	0,1143	3,487345	0,39846679	264,56	LIPT1	lipoyltransferase 1
57343	4,25E-08	7,37E+00	2,13E-08	0,0711	5,6010976	0,39841143	768,98	ZNF304	zinc finger protein 304
101930370	1,32E-02	1,88E+00	9,59E-03	0,1538	2,5901723	0,39833284	131,52	GALNT7-DT	GALNT7 divergent transcript
51322	5,39E-23	2,23E+01	1,65E-23	0,0398	9,9922506	0,39812631	8839,75	WAC	WW domain containing adaptor with coiled-coil
9678	5,25E-11	1,03E+01	2,33E-11	0,0596	6,6836828	0,39805642	2398	PHF14	PHD finger protein 14
39	2,50E-15	1,46E+01	9,57E-16	0,0495	8,0322035	0,39798819	3599,06	ACAT2	acetyl-CoA acetyltransferase 2
100506540	4,25E-03	2,37E+00	2,94E-03	0,1338	2,9737771	0,3979361	177,9	MISFA	mitochondrial sheath formation associated
105374732	4,48E-01	3,49E-01	4,06E-01	0,4788	0,8309815	0,39787136	13,28	LOC105374	uncharacterized LOC105374732
8204	3,18E-14	1,35E+01	1,26E-14	0,0516	7,7097196	0,397831	2188,21	NRIP1	nuclear receptor interacting protein 1
114791	1,84E-10	9,74E+00	8,35E-11	0,0612	6,4940997	0,39767845	1225,03	TUBGCP5	tubulin gamma complex associated protein 5
164312	1,20E-02	1,92E+00	8,64E-03	0,1514	2,6261594	0,3975594	139,97	LRRN4	leucine rich repeat neuronal 4
9710	5,51E-09	8,26E+00	2,66E-09	0,0668	5,9514084	0,39734595	943	GARRE1	granule associated Rac and RHOG effector 1
151477	4,27E-01	3,70E-01	3,85E-01	0,4574	0,8685309	0,39728892	14,69	LINC00471	long intergenic non-protein coding RNA 471
730268	1,45E-07	6,84E+00	7,46E-08	0,0738	5,3796162	0,39716866	692,15	ANAPC1P4	ANAPC1 pseudogene 4
10352	4,22E-08	7,37E+00	2,12E-08	0,0709	5,6020755	0,39712518	896,4	WARS2	tryptophanyl tRNA synthetase 2, mitochondrial
4199	3,28E-07	6,48E+00	1,72E-07	0,076	5,2273454	0,39708088	704,3	ME1	malic enzyme 1
9604	2,08E-11	1,07E+01	9,10E-12	0,0582	6,8201078	0,39691267	2545,5	RNF14	ring finger protein 14
648	1,24E-10	9,91E+00	5,57E-11	0,0605	6,5548267	0,39685641	1882,98	BMI1	BMI1 proto-oncogene, polycomb ring finger
112935892	4,28E-01	3,69E-01	3,86E-01	0,4582	0,8660267	0,39683919	15,35	LINC02605	long intergenic non-protein coding RNA 2605
101929072	2,76E-04	3,56E+00	1,73E-04	0,1056	3,7548117	0,39650235	294,82	MICA-AS1	MICA antisense RNA 1
10411	3,70E-04	3,43E+00	2,35E-04	0,1077	3,6784533	0,39632919	291,29	RAPGEF3	Rap guanine nucleotide exchange factor 3
84932	9,75E-09	8,01E+00	4,74E-09	0,0677	5,8559314	0,39628941	900,24	RAB2B	RAB2B, member RAS oncogene family
65977	5,31E-07	6,27E+00	2,82E-07	0,0772	5,1351623	0,39625495	774,62	PLEKHA3	pleckstrin homology domain containing A3
29933	3,94E-01	4,05E-01	3,53E-01	0,4262	0,9297137	0,39621196	20,06	GPR132	G protein-coupled receptor 132
23405	3,46E-18	1,75E+01	1,21E-18	0,045	8,8135027	0,39617704	3338,13	DICER1	dicer 1, ribonuclease III
149041	1,56E-06	5,81E+00	8,53E-07	0,0805	4,922806	0,39604944	758,64	RC3H1	ring finger and CCCH-type domains 1
56987	7,58E-16	1,51E+01	2,86E-16	0,0484	8,1791476	0,39587463	6790,5	BBX	BBX high mobility group box domain containing
286411	4,84E-01	3,15E-01	4,42E-01	0,5147	0,7684323	0,39554661	11,89	LINC00632	long intergenic non-protein coding RNA 632
27101	1,58E-17	1,68E+01	5,67E-18	0,0458	8,6390687	0,39544171	9773,85	CACYBP	calcyclin binding protein
7543	7,39E-11	1,01E+01	3,30E-11	0,0596	6,6327395	0,39543935	1231,85	ZFX	zinc finger protein X-linked
672	2,06E-14	1,37E+01	8,15E-15	0,0509	7,7652531	0,39533661	2102,32	BRCA1	BRCA1 DNA repair associated
9111	1,29E-08	7,89E+00	6,34E-09	0,068	5,8076359	0,39508608	897,4	NMI	N-myc and STAT interactor
112267909	3,33E-01	4,78E-01	2,93E-01	0,3756	1,0511089	0,39476616	21,9	LOC112267	uncharacterized LOC112267909
11044	1,04E-16	1,60E+01	3,80E-17	0,0469	8,4190017	0,39462199	2654,39	TENT4A	terminal nucleotidyltransferase 4A
100506286	4,12E-01	3,85E-01	3,70E-01	0,4401	0,8956761	0,39418444	15,8	TBC1D8-AS	TBC1D8 antisense RNA 1
5896	4,54E-01	3,43E-01	4,12E-01	0,4807	0,8199978	0,39415077	13,43	RAG1	recombination activating 1
26610	1,18E-06	5,93E+00	6,39E-07	0,0792	4,9790834	0,39411685	950,05	ELP4	elongator acetyltransferase complex subunit 4
100527964	1,87E-01	7,28E-01	1,58E-01	0,2788	1,413448	0,39404701	38,99	LHX4-AS1	LHX4 antisense RNA 1
10741	4,44E-13	1,24E+01	1,83E-13	0,0535	7,3605491	0,3936757	3069,85	RBBP9	RB binding protein 9, serine hydrolase
2295	1,60E-04	3,80E+00	9,86E-05	0,101	3,8940137	0,39330619	340,04	FOXF2	forkhead box F2
342132	4,24E-02	1,37E+00	3,25E-02	0,184	2,1379801	0,39328982	99,99	ZNF774	zinc finger protein 774
54848	5,22E-01	2,82E-01	4,81E-01	0,5575	0,7051594	0,39315086	9,9	ARHGEF38	Rho guanine nucleotide exchange factor 38
23011	1,25E-12	1,19E+01	5,22E-13	0,0544	7,219399	0,39294695	2526,17	RAB21	RAB21, member RAS oncogene family
100996506	4,46E-01	3,51E-01	4,05E-01	0,4715	0,8334282	0,39293093	14,3	LOC100996506	
55777	8,16E-05	4,09E+00	4,92E-05	0,0967	4,0591829	0,39254786	407,26	MBD5	methyl-CpG binding domain protein 5
10234	4,46E-01	3,51E-01	4,05E-01	0,4712	0,8328851	0,39243026	13,33	LRRC17	leucine rich repeat containing 17
25972	2,39E-09	8,62E+00	1,14E-09	0,0644	6,0890286	0,39241307	1197,26	UNC50	unc-50 inner nuclear membrane RNA binding protein
80262	9,32E-09	8,03E+00	4,53E-09	0,0669	5,8634522	0,39225486	1023,94	PHAF1	phagosome assembly factor 1
100130701	1,44E-03	2,84E+00	9,58E-04	0,1188	3,3026264	0,39223837	229,72	LRRC58-DT	LRRC58 divergent transcript
100286938	3,66E-01	4,37E-01	3,25E-01	0,3984	0,98355	0,39181527	20,53	VPS13A-AS	VPS13A antisense RNA 1
10781	8,69E-12	1,11E+01	3,74E-12	0,0564	6,9467132	0,39174812	1926,67	ZNF266	zinc finger protein 266
6731	1,21E-21	2,09E+01	3,85E-22	0,0405	9,6751551	0,39174282	11625,36	SRP72	signal recognition particle 72
6431	9,98E-22	2,10E+01	3,15E-22	0,0404	9,6954793	0,39158689	9432,58	SRSF6	serine and arginine rich splicing factor 6
5893	8,14E-06	5,09E+00	4,62E-06	0,0855	4,58141	0,39151721	494,48	RAD52	RAD52 homolog, DNA repair protein
442421	5,17E-01	2,87E-01	4,76E-01	0,5489	0,7131563	0,39146077	11	PTGER4P2-	PTGER4P2-CDK2AP2P2 readthrough, transcribed pseudogene
203547	5,70E-12	1,12E+01	2,44E-12	0,0559	7,0067984	0,39138398	2242,8	VMA21	vacuolar ATPase assembly factor VMA21
83666	2,81E-06	5,55E+00	1,55E-06	0,0814	4,8047073	0,39114756	592,55	PARP9	poly(ADP-ribose) polymerase family member 9
84865	5,08E-04	3,29E+00	3,26E-04	0,1088	3,593998	0,39106475	308,5	CCDC142	coiled-coil domain containing 142
51808	3,41E-14	1,35E+01	1,36E-14	0,0507	7,7005166	0,3906373	3806,53	PHAX	phosphorylated adaptor for RNA export
127841	4,85E-01	3,14E-01	4,43E-01	0,5095	0,7663043	0,39045844	12,67	LINC00628	long intergenic non-protein coding RNA 628
84918	1,63E-10	9,79E+00	7,39E-11	0,0599	6,512543	0,39035443	1245,99	LRP11	LDL receptor related protein 11
100533184	1,03E-04	3,99E+00	6,22E-05	0,0975	4,0041419	0,39023106	365,3	ARHGAP19-	ARHGAP19-SLIT1 readthrough (NMD candidate)
105374676	3,11E-01	5,07E-01	2,72E-01	0,3551	1,0988912	0,39016183	27,72	LINC02241	long intergenic non-protein coding RNA 2241
222256	3,23E-01	4,91E-01	2,83E-01	0,3631	1,073125	0,38964712	24,44	CDHR3	cadherin related family member 3
53842	3,13E-01	5,04E-01	2,74E-01	0,3563	1,0934794	0,38964281	24,23	CLDN22	claudin 22
8106	1,09E-15	1,50E+01	4,15E-16	0,0479	8,1341853	0,38949571	3102,4	PABPN1	poly(A) binding protein nuclear 1
81610	1,68E-15	1,48E+01	6,40E-16	0,0482	8,0813896	0,38934466	4161,98	FAM83D	family with sequence similarity 83 member D
388566	1,56E-05	4,81E+00	9,00E-06	0,0877	4,4399241	0,38916765	534,76	ZNF470	zinc finger protein 470
440926	3,42E-12	1,15E+01	1,45E-12	0,055	7,0788985	0,38900654	2193,11	H3P6	H3 histone pseudogene 6
5918	4,74E-01	3,24E-01	4,33E-01	0,4956	0,7847403	0,38891847	12,91	RARRES1	retinoic acid receptor responder 1
107986334	3,59E-01	4,45E-01	3,18E-01	0,3896	0,9982754	0,3889017	19,46	LOC107986	uncharacterized LOC107986334
56180	2,25E-08	7,65E+00	1,11E-08	0,0681	5,7123475	0,38880592	1177,26	MOSPD1	motile sperm domain containing 1
80169	4,25E-10	9,37E+00	1,95E-10	0,0611	6,3648992	0,38869745	1313,87	CTC1	CST telomere replication complex component 1
90321	3,06E-05	4,51E+00	1,80E-05	0,0906	4,2885485	0,3884909	473,94	ZNF766	zinc finger protein 766
9512	1,39E-12	1,19E+01	5,81E-13	0,0539	7,2048833	0,38816778	3285,32	PMPCB	peptidase, mitochondrial processing subunit beta
7752	9,15E-05	4,04E+00	5,54E-05	0,0963	4,0315854	0,38809714	445,41	ZNF200	zinc finger protein 200
150776	8,42E-07	6,07E+00	4,52E-07	0,0769	5,0457714	0,38807016	697	SMPD4BP	sphingomyelin phosphodiesterase 4B, pseudogene
84191	4,14E-10	9,38E+00	1,90E-10	0,0609	6,3689892	0,3880657	1747,91	CIAO2A	cytosolic iron-sulfur assembly component 2A
5291	3,55E-13	1,24E+01	1,46E-13	0,0525	7,3908981	0,38806465	2020,8	PIK3CB	phosphatidylinositol-4,5-bisphosphate 3-kinase catalytic subunit beta
100507171	4,14E-02	1,38E+00	3,17E-02	0,1806	2,1477763	0,38787297	96,21	BOLA3-DT	BOLA3 divergent transcript
22931	6,62E-13	1,22E+01	2,75E-13	0,0531	7,3062574	0,3877725	2833,05	RAB18	RAB18, member RAS oncogene family
79818	3,34E-04	3,48E+00	2,11E-04	0,1046	3,7053848	0,38769116	333,04	ZNF552	zinc finger protein 552
64393	4,21E-07	6,38E+00	2,22E-07	0,0748	5,1796075	0,38763199	732,45	ZMAT3	zinc finger matrin-type 3
9422	4,15E-07	6,38E+00	2,19E-07	0,0748	5,1825536	0,38745329	676,76	ZNF264	zinc finger protein 264
105373793	3,10E-01	5,09E-01	2,71E-01	0,3519	1,100667	0,38735446	25,22	LOC105373	uncharacterized LOC105373793
10658	2,41E-21	2,06E+01	7,73E-22	0,0403	9,603499	0,3867359	5378,98	CELF1	CUGBP Elav-like family member 1
23175	5,31E-14	1,33E+01	2,12E-14	0,0506	7,6429321	0,38655708	2049,9	LPIN1	lipin 1
10484	7,64E-18	1,71E+01	2,70E-18	0,0443	8,7232282	0,3865561	6202,18	SEC23A	SEC23 homolog A, COPII coat complex component
54477	1,11E-10	9,95E+00	5,00E-11	0,0588	6,5710549	0,38606897	2214,05	PLEKHA5	pleckstrin homology domain containing A5
1998	7,24E-10	9,14E+00	3,36E-10	0,0614	6,2811548	0,38596191	1427,29	ELF2	E74 like ETS transcription factor 2
406	7,06E-06	5,15E+00	3,99E-06	0,0836	4,6121493	0,38578207	530,8	BMAL1	basic helix-loop-helix ARNT like 1
400658	3,35E-01	4,75E-01	2,95E-01	0,3681	1,0472844	0,38551827	22,37	ZNF516-DT	ZNF516 divergent transcript
107986268	3,99E-01	3,99E-01	3,58E-01	0,4185	0,9196288	0,38487932	18,42	LOC107986	uncharacterized LOC107986268
105376287	2,70E-01	5,69E-01	2,33E-01	0,3226	1,1927789	0,38482384	28,89	LOC105376	replaced by ID 100506080
22941	2,86E-04	3,54E+00	1,80E-04	0,1027	3,7459899	0,38471216	339,07	SHANK2	SH3 and multiple ankyrin repeat domains 2
387640	2,19E-01	6,60E-01	1,86E-01	0,2911	1,3216859	0,38470443	35,72	SKIDA1	SKI/DACH domain containing 1
100289178	2,16E-01	6,66E-01	1,83E-01	0,2889	1,3314307	0,38462101	37,08	GNG12-AS1	GNG12, DIRAS3 and WLS antisense RNA 1
27004	5,23E-01	2,81E-01	4,81E-01	0,5458	0,7046098	0,38459736	9,97	TCL6	T cell leukemia/lymphoma 6
391059	3,79E-02	1,42E+00	2,89E-02	0,176	2,1846212	0,38451624	107,43	FRRS1	ferric chelate reductase 1
55124	2,43E-01	6,14E-01	2,08E-01	0,3054	1,2580614	0,38427087	32,77	PIWIL2	piwi like RNA-mediated gene silencing 2
258010	1,84E-07	6,74E+00	9,55E-08	0,072	5,3350704	0,38423223	1091,98	SVIP	small VCP interacting protein
7027	4,24E-20	1,94E+01	1,40E-20	0,0413	9,3000686	0,38420966	7914,38	TFDP1	transcription factor Dp-1
100287765	7,83E-04	3,11E+00	5,10E-04	0,1105	3,4755452	0,38409723	289,04	LINC00630	long intergenic non-protein coding RNA 630
7175	7,70E-16	1,51E+01	2,90E-16	0,047	8,1772601	0,38402596	15621,25	TPR	translocated promoter region, nuclear basket protein
9942	1,77E-04	3,75E+00	1,09E-04	0,0992	3,8688632	0,38378554	421,29	XYLB	xylulokinase
27248	1,18E-18	1,79E+01	4,09E-19	0,0429	8,9345983	0,3831095	4122,02	ERLEC1	endoplasmic reticulum lectin 1
53840	7,75E-05	4,11E+00	4,67E-05	0,0941	4,0717806	0,38302363	385,71	TRIM34	tripartite motif containing 34
6095	7,08E-02	1,15E+00	5,60E-02	0,2004	1,9109026	0,38289707	78,42	RORA	RAR related orphan receptor A

284958	1,97E-04	3,71E+00	1,23E-04	0,0996	3,8409555	0,38248827	363,71	NT5DC4	5'-nucleotidase domain containing 4
105370928	3,41E-01	4,67E-01	3,01E-01	0,3698	1,0334852	0,38214281	22,85	LOC105370928	uncharacterized LOC105370928
54585	3,26E-06	5,49E+00	1,81E-06	0,08	4,7739716	0,38207825	736,27	LZTFL1	leucine zipper transcription factor like 1
105373989	4,05E-01	3,93E-01	3,64E-01	0,4205	0,9084851	0,38202818	18,35	LOC105373	putative cuticle collagen 91
165918	4,01E-10	9,40E+00	1,84E-10	0,0599	6,3740429	0,38202213	2003,8	RNF168	ring finger protein 168
284434	3,12E-01	5,06E-01	2,73E-01	0,3483	1,0957458	0,38163975	26,8	NWD1	NACHT and WD repeat domain containing 1
9170	1,39E-02	1,86E+00	1,01E-02	0,1483	2,572671	0,38163135	153,54	LPAR2	lysophosphatidic acid receptor 2
5573	5,09E-17	1,63E+01	1,85E-17	0,0449	8,5027801	0,38152655	11641,44	PRKAR1A	protein kinase cAMP-dependent type I regulatory subunit alpha
50640	2,83E-10	9,55E+00	1,29E-10	0,0593	6,4282923	0,38132066	1560,26	PNPLA8	patatin like phospholipase domain containing 8
5080	2,79E-01	5,54E-01	2,42E-01	0,3256	1,1707939	0,38124844	29,41	PAX6	paired box 6
64900	2,95E-05	4,53E+00	1,73E-05	0,0887	4,2969309	0,38104287	538,02	LPIN3	lipin 3
166793	1,27E-03	2,90E+00	8,41E-04	0,114	3,3387983	0,3806801	262,95	ZBTB49	zinc finger and BTB domain containing 49
112268269	4,88E-03	2,31E+00	3,39E-03	0,1299	2,929574	0,38051662	196,44	LOC1122682	uncharacterized LOC112268269
200879	1,65E-08	7,78E+00	8,13E-09	0,066	5,7658306	0,38036598	1074,18	LIPH	lipase H
26146	3,25E-07	6,49E+00	1,70E-07	0,0727	5,2292171	0,38034566	885,58	TRAF3IP1	TRAF3 interacting protein 1
55721	1,36E-04	3,87E+00	8,32E-05	0,0966	3,935028	0,38012802	372,54	IQCC	IQ motif containing C
105372589	5,23E-01	2,81E-01	4,81E-01	0,5392	0,7046236	0,37994195	10,97	BCL2L1-AS1	BCL2L1 antisense RNA 1
107984307	4,64E-02	1,33E+00	3,58E-02	0,1809	2,0990133	0,37962867	97,59	LOC107984	uncharacterized LOC107984307
100874034	1,55E-01	8,10E-01	1,29E-01	0,2499	1,5190671	0,3795474	54,73	UBXN7-AS1	UBXN7 antisense RNA 1
5597	1,56E-15	1,48E+01	5,95E-16	0,0469	8,0903773	0,37925432	3899,31	MAPK6	mitogen-activated protein kinase 6
221584	4,55E-01	3,42E-01	4,13E-01	0,4636	0,8180083	0,37919438	14,68	ZSCAN12P1	zinc finger and SCAN domain containing 12 pseudogene 1
79269	6,37E-09	8,20E+00	3,08E-09	0,064	5,9272269	0,3791225	1879,36	DCAF10	DDB1 and CUL4 associated factor 10
2444	7,64E-02	1,12E+00	6,06E-02	0,202	1,8762974	0,37899434	77,78	FRK	fyn related Src family tyrosine kinase
102724916	4,51E-02	1,35E+00	3,48E-02	0,1795	2,1112101	0,37894485	100,75	LOC102724	uncharacterized LOC102724916
644660	1,06E-03	2,97E+00	6,94E-04	0,1116	3,3920244	0,37870614	275,21	RAD21-AS1	RAD21 antisense RNA 1
953	1,65E-10	9,78E+00	7,49E-11	0,0582	6,5105457	0,3786975	1405,45	ENTPD1	ectonucleoside triphosphate diphosphohydrolase 1
131965	1,77E-08	7,75E+00	8,75E-09	0,0658	5,7533408	0,37863211	1189,05	METTL6	methyltransferase 6, methylcytidine
3709	3,34E-09	8,48E+00	1,60E-09	0,0627	6,034169	0,37855893	1172,47	ITPR2	inositol 1,4,5-trisphosphate receptor type 2
7776	2,17E-06	5,66E+00	1,19E-06	0,0779	4,8574878	0,37823298	664,5	ZNF236	zinc finger protein 236
23078	3,53E-07	6,45E+00	1,86E-07	0,0725	5,2131173	0,37814694	819,62	VWA8	von Willebrand factor A domain containing 8
57600	5,67E-08	7,25E+00	2,86E-08	0,0681	5,5497301	0,37803739	919,71	FNIP2	folliculin interacting protein 2
25837	2,99E-01	5,24E-01	2,60E-01	0,3358	1,1254264	0,37787332	26,47	RAB26	RAB26, member RAS oncogene family
81691	1,77E-03	2,75E+00	1,18E-03	0,1165	3,2425439	0,37774649	257,24	REXO5	RNA exonuclease 5
79066	5,21E-12	1,13E+01	2,23E-12	0,0538	7,019439	0,37771535	1734,52	METTL16	methyltransferase 16, N6-methyladenosine
64411	1,41E-09	8,85E+00	6,64E-10	0,0612	6,1744237	0,37768882	1557,55	ARAP3	ArfGAP with RhoGAP domain, ankyrin repeat and PH domain 3
10971	9,23E-18	1,70E+01	3,28E-18	0,0434	8,7013394	0,37767135	22157,68	YWHAQ	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein theta
441478	9,03E-02	1,04E+00	7,24E-02	0,2102	1,7962831	0,37763463	68,14	NRARP	NOTCH regulated ankyrin repeat protein
9736	2,53E-15	1,46E+01	9,71E-16	0,047	8,0305238	0,37754725	5534,02	USP34	ubiquitin specific peptidase 34
728411	3,15E-03	2,50E+00	2,15E-03	0,123	3,0685534	0,37738206	244,23	GUSBP1	GUSB pseudogene 1
55778	2,41E-08	7,62E+00	1,20E-08	0,0662	5,7003395	0,37737932	1006,65	ZNF839	zinc finger protein 839
23518	3,36E-13	1,25E+01	1,38E-13	0,051	7,3982941	0,37723329	2376,63	R3HDM1	R3H domain containing 1
64839	3,82E-07	6,42E+00	2,01E-07	0,0725	5,1984603	0,37708693	769,87	FBXL17	F-box and leucine rich repeat protein 17
3887	2,73E-10	9,56E+00	1,25E-10	0,0586	6,4335623	0,37706253	2381,74	KRT81	keratin 81
65055	5,07E-03	2,29E+00	3,53E-03	0,1292	2,9170907	0,37696694	189,6	REEP1	receptor accessory protein 1
55110	3,07E-07	6,51E+00	1,61E-07	0,0719	5,2398903	0,3769238	745	MAGOHB	mago homolog B, exon junction complex subunit
10902	3,08E-15	1,45E+01	1,19E-15	0,0471	8,0059804	0,37678556	5936,27	BRD8	bromodomain containing 8
373509	3,46E-01	4,61E-01	3,05E-01	0,3675	1,0247324	0,37663286	22,64	USP50	ubiquitin specific peptidase 50
9202	7,42E-14	1,31E+01	2,98E-14	0,0496	7,5990316	0,37660139	4090,79	ZMYM4	zinc finger MYM-type containing 4
107987001	1,83E-01	7,38E-01	1,53E-01	0,2635	1,4277155	0,37620981	45,87	FAM27E4	family with sequence similarity 27 member E4
2526	1,81E-04	3,74E+00	1,12E-04	0,0973	3,8632827	0,37597757	378,36	FUT4	fucosyltransferase 4
7182	2,89E-13	1,25E+01	1,18E-13	0,0507	7,4186931	0,3758927	2012,72	NR2C2	nuclear receptor subfamily 2 group C member 2
399844	1,18E-02	1,93E+00	8,48E-03	0,1428	2,6324636	0,37581888	170,96	LINC01002	long intergenic non-protein coding RNA 1002
9990	7,83E-12	1,11E+01	3,36E-12	0,054	6,9616902	0,37577687	1782,7	SLC12A6	solute carrier family 12 member 6
11234	2,98E-10	9,53E+00	1,36E-10	0,0585	6,4201827	0,3753126	1786,05	HPS5	HPS5 biogenesis of lysosomal organelles complex 2 subunit 2
26984	3,89E-05	4,41E+00	2,30E-05	0,0886	4,2337001	0,37528122	687,42	SEC22A	SEC22 homolog A, vesicle trafficking protein
79896	1,28E-05	4,89E+00	7,33E-06	0,0837	4,483947	0,37525019	526,26	THNSL1	threonine synthase like 1
26790	6,81E-04	3,17E+00	4,41E-04	0,1068	3,5142504	0,37522522	312,42	SNORD58B	small nucleolar RNA, C/D box 58B
199731	2,26E-02	1,65E+00	1,68E-02	0,1569	2,3910259	0,37519034	136,39	CADM4	cell adhesion molecule 4
26122	4,89E-10	9,31E+00	2,25E-10	0,0591	6,3430374	0,37476956	1238,52	EPC2	enhancer of polycomb homolog 2
441242	5,25E-02	1,28E+00	4,08E-02	0,1832	2,0453784	0,37468723	95,23	LINC03006	long intergenic non-protein coding RNA 3006
23075	2,61E-18	1,76E+01	9,15E-19	0,0423	8,8450689	0,37454432	5275,31	SWAP70	switching B cell complex subunit SWAP70
23039	6,40E-17	1,62E+01	2,33E-17	0,0442	8,475929	0,37452101	5841,93	XPO7	exportin 7
83607	1,06E-11	1,10E+01	4,56E-12	0,0541	6,9186554	0,37448093	1794,69	AMMECR1L	AMMECR1 like
2310	2,37E-03	2,63E+00	1,60E-03	0,1187	3,1551145	0,374411	232,72	FOXO3B	forkhead box O3B
5428	2,91E-15	1,45E+01	1,12E-15	0,0467	8,0128038	0,37429174	2950,8	POLG	DNA polymerase gamma, catalytic subunit
60485	7,21E-11	1,01E+01	3,22E-11	0,0564	6,6363052	0,37409989	2472,29	SAV1	salvador family WW domain containing protein 1
10081	9,12E-10	9,04E+00	4,25E-10	0,0599	6,2443818	0,37392459	1396,17	PDCD7	programmed cell death 7
123720	1,94E-06	5,71E+00	1,06E-06	0,0766	4,8794242	0,37381773	644,42	WHAMM	WASP homolog associated with actin, golgi membranes and microtubules
140733	3,89E-01	4,10E-01	3,47E-01	0,3977	0,9397603	0,37378711	19,75	MACROD2	mono-ADP ribosylhydrolase 2
54758	3,30E-06	5,48E+00	1,83E-06	0,0783	4,7712548	0,37359382	609,68	KLHDC4	kelch domain containing 4
4036	3,59E-01	4,45E-01	3,18E-01	0,3742	0,9982311	0,37356583	22,15	LRP2	LDL receptor related protein 2
401466	5,65E-09	8,25E+00	2,73E-09	0,0628	5,9473394	0,37355782	1771,17	RBIS	ribosomal biogenesis factor
105371912	2,17E-01	6,64E-01	1,84E-01	0,2813	1,3277144	0,37348633	40,96	LOC105371	uncharacterized LOC105371912
84064	1,27E-06	5,90E+00	6,88E-07	0,0752	4,964757	0,37341733	820,68	HDHD2	haloacid dehalogenase like hydrolase domain containing 2
84668	3,79E-13	1,24E+01	1,56E-13	0,0506	7,3818818	0,37323426	2416,96	HYCC1	hyccin PI4KA lipid kinase complex subunit 1
105369435	5,57E-01	2,54E-01	5,17E-01	0,575	0,648618	0,37297043	9,75	LOC105369	uncharacterized LOC105369435
9557	1,39E-12	1,19E+01	5,83E-13	0,0518	7,2044098	0,37292769	2343,4	CHD1L	chromodomain helicase DNA binding protein 1 like
126549	1,78E-01	7,50E-01	1,49E-01	0,2585	1,4420323	0,37269952	46,75	ANKLE1	ankyrin repeat and LEM domain containing 1
83891	5,49E-08	7,26E+00	2,77E-08	0,0671	5,5553871	0,37251683	993,15	SNX25	sorting nexin 25
115106	2,88E-12	1,15E+01	1,22E-12	0,0524	7,1027026	0,37251564	1943,67	HAUS1	HAUS augmin like complex subunit 1
51678	1,18E-07	6,93E+00	6,06E-08	0,0687	5,4171599	0,3723081	955,57	PALS2	protein associated with LIN7 2, MAGUK p55 family member
6342	4,62E-16	1,53E+01	1,73E-16	0,0451	8,2394363	0,37183611	4496,95	SCP2	sterol carrier protein 2
150465	7,15E-18	1,71E+01	2,53E-18	0,0426	8,7307922	0,3716865	4961,77	TTL	tubulin tyrosine ligase
6606	2,79E-13	1,26E+01	1,14E-13	0,0501	7,4232499	0,37158584	2679,74	SMN1	survival of motor neuron 1, telomeric
201626	3,78E-12	1,14E+01	1,61E-12	0,0526	7,0646388	0,3715678	2597,58	PDE12	phosphodiesterase 12
285190	4,31E-02	1,37E+00	3,31E-02	0,1743	2,1305814	0,37140767	102,84	RGPD4	RANBP2 like and GRIP domain containing 4
5516	2,44E-12	1,16E+01	1,03E-12	0,0521	7,126025	0,37125786	3581,72	PPP2CB	protein phosphatase 2 catalytic subunit beta
124961	2,45E-01	6,11E-01	2,10E-01	0,2962	1,2533265	0,37119805	37,45	ZFP3	ZFP3 zinc finger protein
4703	3,68E-01	4,34E-01	3,28E-01	0,3791	0,9788885	0,37114287	22,62	NEB	nebulin
10873	1,18E-08	7,93E+00	5,78E-09	0,0637	5,8228679	0,3710174	1312,05	ME3	malic enzyme 3
105374191	2,79E-01	5,54E-01	2,42E-01	0,3168	1,1710353	0,37098956	30,55	LOC105374	uncharacterized LOC105374191
6314	5,88E-11	1,02E+01	2,61E-11	0,0556	6,6668479	0,37064615	1832,26	ATXN7	ataxin 7
66036	1,32E-06	5,88E+00	7,14E-07	0,0747	4,9575109	0,37052279	803,13	MTMR9	myotubularin related protein 9
166815	1,26E-06	5,90E+00	6,81E-07	0,0746	4,9668037	0,37042561	895,24	TIGD2	tigger transposable element derived 2
79649	7,44E-15	1,41E+01	2,90E-15	0,0469	7,8951823	0,37038146	6285,3	MAP7D3	MAP7 domain containing 3
55132	3,77E-09	8,42E+00	1,80E-09	0,0616	6,0144854	0,37027749	1358,13	LARP1B	La ribonucleoprotein 1B
5515	1,35E-15	1,49E+01	5,14E-16	0,0457	8,1081316	0,37021392	10696,42	PPP2CA	protein phosphatase 2 catalytic subunit alpha
22936	1,01E-15	1,50E+01	3,82E-16	0,0455	8,1440406	0,37016994	4069,97	ELL2	elongation factor for RNA polymerase II 2
54467	8,89E-13	1,21E+01	3,70E-13	0,0509	7,2659607	0,36996636	2570,34	ANKIB1	ankyrin repeat and IBR domain containing 1
91746	7,94E-17	1,61E+01	2,90E-17	0,0437	8,4504139	0,36967526	4909,82	YTHDC1	YTH domain containing 1
1676	8,77E-19	1,81E+01	3,02E-19	0,0412	8,9680345	0,36959308	4656,75	DFFA	DNA fragmentation factor subunit alpha
23760	8,69E-18	1,71E+01	3,08E-18	0,0424	8,7083797	0,36935948	4878,94	PITPNB	phosphatidylinositol transfer protein beta
7128	1,00E-09	9,00E+00	4,68E-10	0,0593	6,229422	0,36935706	1644,93	TNFAIP3	TNF alpha induced protein 3
90381	1,33E-08	7,88E+00	6,53E-09	0,0636	5,8025736	0,369222	1325,67	TICRR	TOPBP1 interacting checkpoint and replication regulator
100128885	2,82E-01	5,50E-01	2,45E-01	0,3174	1,1625418	0,36903562	33,58	LOC100128	uncharacterized LOC100128885
105370705	5,21E-01	2,83E-01	4,79E-01	0,5216	0,7071594	0,36888855	11,33	LOC105370	collagen alpha-2(I) chain-like
55871	2,75E-10	9,56E+00	1,26E-10	0,0573	6,4324946	0,36882194	2202,37	ZNG1A	Zn regulated GTPase metalloprotein activator 1A
6477	3,03E-05	4,52E+00	1,78E-05	0,0859	4,2912524	0,36869265	485,97	SIAH1	siah E3 ubiquitin protein ligase 1
9258	4,29E-07	6,37E+00	2,27E-07	0,0712	5,175835	0,36843112	995,74	MFHAS1	multifunctional ROCO family signaling regulator 1
54780	3,47E-12	1,15E+01	1,48E-12	0,052	7,076704	0,36809722	2129,45	NSMCE4A	NSE4 homolog A, SMC5-SMC6 complex component
8458	1,00E-10	1,00E+01	4,50E-11	0,0559	6,5866121	0,36800368	2424,2	TTF2	transcription termination factor 2
64773	2,42E-06	5,62E+00	1,33E-06	0,0761	4,8355273	0,36781277	828,47	PCED1A	PC-esterase domain containing 1A
8681	1,25E-01	9,03E-01	1,03E-01	0,2252	1,6325647	0,36758146	70,49	JMJD7-PLA2	JMJD7-PLA2G4B readthrough
9724	1,22E-05	4,91E+00	6,97E-06	0,0818	4,4946547	0,36748534	717,38	UTP14C	UTP14C small subunit processome component
101928424	2,43E-01	6,14E-01	2,08E-01	0,2918	1,258888	0,36737966	34,86	TMEM123-D	TMEM123 divergent transcript
116840	2,78E-13	1,26E+01	1,14E-13	0,0495	7,4240741	0,36717057	3346,11	CNTROB	centrobin, centriole duplication and spindle assembly protein
177	3,40E-02	1,47E+00	2,58E-02	0,1647	2,2297358	0,36715944	128,04	AGER	advanced glycosylation end-product specific receptor
22898	1,82E-10	9,74E+00	8,24E-11	0,0565	6,4961877	0,36714394	1491,3	DENND3	DENN domain containing 3
51719	1,19E-15	1,49E+01	4,53E-16	0,0452	8,1236023	0,36704344	5225,65	CAB39	calcium binding protein 39
84791	3,57E-04	3,45E+00	2,26E-04	0,0995	3,6875145	0,36694898	363,17	LINC00467	long intergenic non-protein coding RNA 467

51200	9,37E-08	7,03E+00	4,79E-08	0,0672	5,4591044	0,36693614	918,51	CPA4	carboxypeptidase A4
84986	2,74E-10	9,56E+00	1,25E-10	0,057	6,4329939	0,3667151	1639,93	ARHGAP19	Rho GTPase activating protein 19
11120	4,39E-16	1,54E+01	1,64E-16	0,0445	8,2456923	0,36656687	3789,13	BTN2A1	butyrophilin subfamily 2 member A1
728034	1,66E-03	2,78E+00	1,11E-03	0,1123	3,2613168	0,3662268	269,61	BMS1P23	BMS1 pseudogene 23
199692	1,47E-05	4,83E+00	8,48E-06	0,0822	4,4525726	0,3660161	554,57	ZNF627	zinc finger protein 627
2035	6,76E-08	7,17E+00	3,43E-08	0,0663	5,5181926	0,36585562	1081,2	EPB41	erythrocyte membrane protein band 4.1
3603	4,66E-01	3,32E-01	4,25E-01	0,458	0,798588	0,36574699	14,13	IL16	interleukin 16
29035	2,26E-12	1,16E+01	9,57E-13	0,0512	7,1365478	0,36561775	1989,61	HAPSTR1	HUWE1 associated protein modifying stress responses
23243	1,60E-19	1,88E+01	5,40E-20	0,0399	9,1556786	0,36554609	5757,21	ANKRD28	ankyrin repeat domain 28
23007	4,37E-03	2,36E+00	3,03E-03	0,1233	2,9646587	0,36545268	228,34	PLCH1	phospholipase C eta 1
90407	5,56E-08	7,25E+00	2,80E-08	0,0658	5,553339	0,36532373	1796,18	TMEM41A	transmembrane protein 41A
54891	3,47E-05	4,46E+00	2,04E-05	0,0857	4,2601054	0,36506023	495,65	INO80D	INO80 complex subunit D
5774	5,53E-11	1,03E+01	2,46E-11	0,0547	6,6760257	0,36504494	1668,03	PTPN3	protein tyrosine phosphatase non-receptor type 3
51199	2,26E-12	1,16E+01	9,55E-13	0,0511	7,1368935	0,36450484	6296,24	NIN	ninein
245972	3,06E-01	5,14E-01	2,68E-01	0,3286	1,1086113	0,36431535	29,84	ATP6V0D2	ATPase H+ transporting V0 subunit d2
84078	2,13E-03	2,67E+00	1,43E-03	0,1142	3,1879206	0,36406133	248,27	KBTBD7	kelch repeat and BTB domain containing 7
55013	7,07E-08	7,15E+00	3,58E-08	0,0661	5,5101809	0,36399368	1659,82	MCUB	mitochondrial calcium uniporter dominant negative subunit beta
60526	4,33E-05	4,36E+00	2,56E-05	0,0864	4,2091194	0,36364434	564,71	LDAH	lipid droplet associated hydrolase
109729141	9,17E-02	1,04E+00	7,36E-02	0,2032	1,7892833	0,36361146	73,85	TDRKH-AS1	TDRKH antisense RNA 1
5558	1,40E-12	1,19E+01	5,89E-13	0,0505	7,2029312	0,36349308	2569,41	PRIM2	DNA primase subunit 2
7732	3,64E-01	4,39E-01	3,23E-01	0,3675	0,9881486	0,36317523	24,66	RNF112	ring finger protein 112
5413	5,19E-01	2,85E-01	4,78E-01	0,5114	0,7100135	0,36313034	11,25	SEPTIN5	septin 5
105377319	5,05E-01	2,97E-01	4,63E-01	0,4949	0,7336471	0,36306694	12,83	LOC105377	uncharacterized LOC105377319
147929	3,20E-02	1,49E+00	2,42E-02	0,161	2,2535996	0,36277455	123,86	ZNF565	zinc finger protein 565
54093	4,19E-06	5,38E+00	2,34E-06	0,0768	4,7219534	0,36276205	636,72	SETD4	SET domain containing 4
6591	1,39E-09	8,86E+00	6,53E-10	0,0587	6,1769745	0,36274839	1350,41	SNAI2	snail family transcriptional repressor 2
10959	1,19E-18	1,79E+01	4,12E-19	0,0406	8,9336475	0,36263838	18133,82	TMED2	transmembrane p24 trafficking protein 2
253943	1,62E-09	8,79E+00	7,63E-10	0,0589	6,1523808	0,36259776	2457,01	YTHDF3	YTH N6-methyladenosine RNA binding protein 3
105370579	3,35E-01	4,75E-01	2,96E-01	0,3465	1,045905	0,36244362	25,28	LOC105370	uncharacterized LOC105370579
100288798	6,76E-02	1,17E+00	5,33E-02	0,1873	1,9326349	0,36204425	89,93	SLC38A4-AS	SLC38A4 antisense RNA 1
171024	2,79E-01	5,54E-01	2,42E-01	0,3092	1,170835	0,36202262	31,95	SYNPO2	synaptopodin 2
466	5,39E-08	7,27E+00	2,72E-08	0,0651	5,5588271	0,36193042	1356,47	ATF1	activating transcription factor 1
150759	1,04E-01	9,83E-01	8,40E-02	0,2095	1,7278686	0,36191068	86,18	LINC00342	long intergenic non-protein coding RNA 342
253039	2,69E-06	5,57E+00	1,48E-06	0,0751	4,8134502	0,3616609	748,78	CUTALP	cutA divalent cation tolerance like, pseudogene
51691	4,42E-09	8,35E+00	2,12E-09	0,0604	5,9881369	0,36156685	1821,34	LSM8	LSM8 homolog, U6 small nuclear RNA associated
5862	3,54E-12	1,15E+01	1,51E-12	0,0511	7,0739855	0,36155264	2583,42	RAB2A	RAB2A, member RAS oncogene family
101927789	1,69E-01	7,72E-01	1,41E-01	0,2453	1,4732894	0,36136404	53,06	FAUP4	FAU pseudogene 4
107986997	7,50E-02	1,12E+00	5,95E-02	0,1915	1,8846144	0,36085178	82,75	LOC107986	uncharacterized LOC107986997
3181	5,65E-16	1,52E+01	2,12E-16	0,0439	8,2149661	0,36068676	79737,56	HNRNPA2B	heterogeneous nuclear ribonucleoprotein A2/B1
10042	1,67E-08	7,78E+00	8,22E-09	0,0625	5,7638562	0,36050245	2063,31	HMGXB4	HMG-box containing 4
11097	6,32E-05	4,20E+00	3,78E-05	0,0875	4,1203961	0,36048814	634,12	NUP42	nucleoporin 42
84777	1,96E-01	7,08E-01	1,65E-01	0,2593	1,3876378	0,35987495	45,09	DLGAP1-AS	DLGAP1 antisense RNA 2
9873	1,18E-10	9,93E+00	5,31E-11	0,0548	6,5618346	0,35983767	1784,26	FCHSD2	FCH and double SH3 domains 2
650623	1,04E-01	9,83E-01	8,45E-02	0,2084	1,7248957	0,35955083	72,62	BEND3P3	BEN domain containing 3 pseudogene 3
9401	4,39E-10	9,36E+00	2,02E-10	0,0565	6,3596914	0,35952952	2237,65	RECQL4	RecQ like helicase 4
22903	1,33E-07	6,88E+00	6,87E-08	0,0666	5,3946599	0,35910228	1301,99	BTBD3	BTB domain containing 3
29105	1,11E-11	1,10E+01	4,78E-12	0,0519	6,9118592	0,35902005	2521,27	CFAP20	cilia and flagella associated protein 20
222255	4,38E-04	3,36E+00	2,79E-04	0,0988	3,6337214	0,35900424	355,47	ATXN7L1	ataxin 7 like 1
9455	1,95E-05	4,71E+00	1,13E-05	0,0817	4,3904407	0,35860696	602,38	HOMER2	homer scaffold protein 2
647070	2,89E-04	3,54E+00	1,82E-04	0,0957	3,7432456	0,35836088	521,06	DHX9-AS1	DHX9 antisense RNA 1
3992	1,57E-20	1,98E+01	5,14E-21	0,0381	9,4062829	0,35818321	10477,15	FADS1	fatty acid desaturase 1
5962	3,11E-12	1,15E+01	1,32E-12	0,0505	7,0922401	0,35793317	6343,24	RDX	radixin
28998	9,90E-13	1,20E+01	4,13E-13	0,0493	7,2512328	0,3577721	3599,9	MRPL13	mitochondrial ribosomal protein L13
54940	6,39E-14	1,32E+01	2,56E-14	0,047	7,6186897	0,35773431	5871,83	OCIAD1	OCIA domain containing 1
653188	2,84E-01	5,47E-01	2,46E-01	0,3084	1,159739	0,35769241	31,52	GUSBP3	GUSB pseudogene 3
4628	2,17E-16	1,57E+01	8,06E-17	0,0429	8,3303732	0,35762714	4937,55	MYH10	myosin heavy chain 10
594	5,27E-05	4,28E+00	3,13E-05	0,0859	4,1634434	0,35747379	539,36	BCKDHB	branched chain keto acid dehydrogenase E1 subunit beta
57132	1,30E-11	1,09E+01	5,62E-12	0,0519	6,8890316	0,35744227	2750,41	CHMP1B	charged multivesicular body protein 1B
64750	8,05E-22	2,11E+01	2,54E-22	0,0368	9,7175497	0,35721532	12377,01	SMURF2	SMAD specific E3 ubiquitin protein ligase 2
1719	3,74E-15	1,44E+01	1,44E-15	0,0447	7,9816592	0,35717049	7278,5	DHFR	dihydrofolate reductase
27	4,33E-18	1,74E+01	1,52E-18	0,0406	8,7880801	0,35661438	7242,26	ABL2	ABL proto-oncogene 2, non-receptor tyrosine kinase
728294	1,23E-02	1,91E+00	8,87E-03	0,1361	2,6171756	0,3560893	174,36	D2HGDH	D-2-hydroxyglutarate dehydrogenase
646817	2,75E-01	5,61E-01	2,38E-01	0,3016	1,1806122	0,35602792	34,13	SETSIP	SET like protein
29063	2,28E-07	6,64E+00	1,18E-07	0,0672	5,2958677	0,3557564	904,4	ZCCHC4	zinc finger CCHC-type containing 4
107984969	5,43E-01	2,65E-01	5,02E-01	0,5298	0,6714519	0,35575562	10,81	TMEM11-DT	TMEM11 divergent transcript
55907	6,47E-09	8,19E+00	3,13E-09	0,06	5,924631	0,35570738	1706,58	CMAS	cytidine monophosphate N-acetylneuraminic acid synthetase
652276	9,68E-03	2,01E+00	6,93E-03	0,1315	2,6999684	0,3551092	195,96	LOC652276	potassium channel tetramerization domain containing 5 pseudogene
79879	2,59E-06	5,59E+00	1,43E-06	0,0736	4,8214565	0,35490431	750,41	CCDC134	coiled-coil domain containing 134
9987	1,17E-15	1,49E+01	4,43E-16	0,0436	8,1260783	0,35469459	17114,76	HNRNPDL	heterogeneous nuclear ribonucleoprotein D like
59084	2,78E-01	5,56E-01	2,41E-01	0,3022	1,1726776	0,35440774	32,91	ENPP5	ectonucleotide pyrophosphatase/phosphodiesterase family member 5
100288730	2,05E-01	6,88E-01	1,74E-01	0,2605	1,3604134	0,35437807	44,45	PAN3-AS1	PAN3 antisense RNA 1
90639	7,35E-05	4,13E+00	4,42E-05	0,0867	4,0844502	0,35427617	607,75	COX19	cytochrome c oxidase assembly factor COX19
7274	2,49E-01	6,04E-01	2,14E-01	0,2849	1,2432437	0,35420432	37,35	TTPA	alpha tocopherol transfer protein
5429	1,20E-13	1,29E+01	4,84E-14	0,047	7,5361657	0,35415699	3076,23	POLH	DNA polymerase eta
494115	9,99E-13	1,20E+01	4,17E-13	0,0488	7,249994	0,35401957	2262,61	RBMXL1	RBMX like 1
10920	2,12E-12	1,17E+01	8,95E-13	0,0495	7,1456896	0,35391858	2854,08	COPS8	COP9 signalosome subunit 8
7026	3,16E-12	1,15E+01	1,34E-12	0,0499	7,0898155	0,35381724	5759,66	NR2F2	nuclear receptor subfamily 2 group F member 2
10154	7,50E-03	2,12E+00	5,31E-03	0,1269	2,7874706	0,35376235	206,32	PLXNC1	plexin C1
23317	3,99E-13	1,24E+01	1,64E-13	0,048	7,375166	0,3536569	3561,2	DNAJC13	DnaJ heat shock protein family (Hsp40) member C13
401541	7,36E-07	6,13E+00	3,93E-07	0,0696	5,0720854	0,35324175	841,34	CENPP	centromere protein P
6103	1,37E-06	5,86E+00	7,44E-07	0,0713	4,9494177	0,35303363	862,42	RPGR	retinitis pigmentosa GTPase regulator
5928	1,05E-16	1,60E+01	3,86E-17	0,0419	8,4170901	0,35303064	5820,87	RBBP4	RB binding protein 4, chromatin remodeling factor
83940	2,83E-08	7,55E+00	1,41E-08	0,0622	5,6725664	0,35300684	1221,03	TATDN1	TatD DNase domain containing 1
284391	5,20E-05	4,28E+00	3,09E-05	0,0847	4,1664596	0,35273477	523,92	ZNF844	zinc finger protein 844
51514	2,02E-14	1,37E+01	8,00E-15	0,0454	7,7676129	0,35263022	3586,9	DTL	denticleless E3 ubiquitin protein ligase homolog
51132	5,84E-13	1,22E+01	2,42E-13	0,0481	7,3234306	0,35247403	3558,09	RLIM	ring finger protein, LIM domain interacting
26010	1,99E-16	1,57E+01	7,36E-17	0,0422	8,3410305	0,35239238	6267,99	SPATS2L	spermatogenesis associated serine rich 2 like
645158	3,71E-01	4,31E-01	3,31E-01	0,3622	0,9726298	0,35226854	24,75	CBX3P2	CBX3 pseudogene 2
83548	2,05E-08	7,69E+00	1,01E-08	0,0614	5,7287539	0,35193266	1425,19	COG3	component of oligomeric golgi complex 3
5494	5,14E-14	1,33E+01	2,06E-14	0,046	7,6470547	0,35184919	3271,09	PPM1A	protein phosphatase, Mg2+/Mn2+ dependent 1A
91179	6,77E-02	1,17E+00	5,34E-02	0,1821	1,9318564	0,35178416	118,65	SCARF2	scavenger receptor class F member 2
197259	2,10E-08	7,68E+00	1,04E-08	0,0615	5,7239654	0,35173929	1274,33	MLKL	mixed lineage kinase domain like pseudokinase
100133204	5,20E-03	2,28E+00	3,63E-03	0,1209	2,9088738	0,35156963	219	HSDL2-AS1	HSDL2 antisense RNA 1
54503	7,87E-06	5,10E+00	4,46E-06	0,0766	4,5886199	0,35139284	652,33	ZDHHC13	zinc finger DHHC-type palmitoyltransferase 13
100507217	9,81E-07	6,01E+00	5,29E-07	0,07	5,015596	0,35131248	991,73	CHASERR	CHD2 adjacent suppressive regulatory RNA
102724826	5,48E-03	2,26E+00	3,83E-03	0,1215	2,8919898	0,35130231	217,94	ZNF337-AS1	ZNF337 antisense RNA 1
4338	2,89E-12	1,15E+01	1,23E-12	0,0494	7,1022472	0,35109872	3521,81	MOCS2	molybdenum cofactor synthesis 2
5019	7,25E-11	1,01E+01	3,23E-11	0,0529	6,6355668	0,35103307	1894,01	OXCT1	3-oxoacid CoA-transferase 1
29104	6,18E-05	4,21E+00	3,70E-05	0,0851	4,1256977	0,35098765	531,82	N6AMT1	N-6 adenine-specific DNA methyltransferase 1
23379	1,04E-13	1,30E+01	4,18E-14	0,0464	7,5551276	0,35060409	3458,62	ICE1	interactor of little elongation complex ELL subunit 1
5828	1,49E-10	9,83E+00	6,73E-11	0,0537	6,5266177	0,35055601	1839,69	PEX2	peroxisomal biogenesis factor 2
105370479	3,84E-01	4,16E-01	3,43E-01	0,3692	0,9491054	0,3503997	24,07	LINC02303	long intergenic non-protein coding RNA 2303
221294	3,32E-08	7,48E+00	1,66E-08	0,0621	5,6444018	0,35033025	1155,76	NT5DC1	5'-nucleotidase domain containing 1
375061	5,79E-03	2,24E+00	4,06E-03	0,1219	2,8734002	0,35026617	226,6	FAM89A	family with sequence similarity 89 member A
23469	4,06E-19	1,84E+01	1,38E-19	0,0387	9,0535209	0,3501837	8597,59	PHF3	PHD finger protein 3
107984316	1,56E-01	8,07E-01	1,30E-01	0,231	1,5152241	0,35006524	60,92	LOC107984	replaced by ID 374383
55291	1,63E-16	1,58E+01	6,03E-17	0,0418	8,3646226	0,34992704	6753,73	PPP6R3	protein phosphatase 6 regulatory subunit 3
4774	3,53E-05	4,45E+00	2,08E-05	0,0822	4,2559107	0,34987002	566,66	NFIA	nuclear factor I A
26156	1,24E-13	1,29E+01	5,00E-14	0,0465	7,5318109	0,34986871	10080,42	RSL1D1	ribosomal L1 domain containing 1
23355	3,89E-07	6,41E+00	2,05E-07	0,0673	5,1948619	0,34981639	1013,21	VPS8	VPS8 subunit of CORVET complex
57184	9,88E-07	6,01E+00	5,32E-07	0,0697	5,014262	0,34936224	855,18	FAM219B	family with sequence similarity 219 member B
342357	3,66E-05	4,44E+00	2,16E-05	0,0822	4,2476535	0,34923364	563,18	ZKSCAN2	zinc finger with KRAB and SCAN domains 2
283440	2,46E-01	6,09E-01	2,11E-01	0,2792	1,250263	0,34902453	39,51	ITFG2-AS1	ITFG2 antisense RNA 1
257177	1,36E-02	1,87E+00	9,89E-03	0,1351	2,5795157	0,34860433	183,87	CFAP126	cilia and flagella associated protein 126
5013	1,30E-01	8,86E-01	1,06E-01	0,2158	1,6147941	0,34843849	67,58	OTX1	orthodenticle homeobox 1
898	5,64E-05	4,25E+00	3,36E-05	0,084	4,1474643	0,34842376	583,25	CCNE1	cyclin E1
6495	2,49E-08	7,60E+00	1,24E-08	0,0612	5,6943038	0,34841	1439,63	SIX1	SIX homeobox 1
100289333	3,15E-01	5,02E-01	2,76E-01	0,3194	1,0892091	0,34788862	29,81	LOC100289	uncharacterized LOC100289333
84263	8,61E-14	1,31E+01	3,46E-14	0,0459	7,57966	0,34780053	3852,43	HSDL2	hydroxysteroid dehydrogenase like 2
22887	6,89E-17	1,62E+01	2,52E-17	0,0411	8,4671222	0,34776181	4770,16	FOXJ3	forkhead box J3

27125	3,97E-14	1,34E+01	1,58E-14	0,0453	7,6806421	0,34771926	8131,96	AFF4	ALF transcription elongation factor 4
114814	2,73E-07	6,56E+00	1,43E-07	0,0661	5,2614547	0,34762029	923,51	GNRHR2	gonadotropin releasing hormone receptor 2 (pseudogene)
84248	4,07E-11	1,04E+01	1,80E-11	0,0517	6,7214903	0,34742667	3732,39	FYTTD1	forty-two-three domain containing 1
8895	2,54E-13	1,26E+01	1,04E-13	0,0467	7,4363377	0,34726427	4190,77	CPNE3	copine 3
116143	9,23E-08	7,03E+00	4,71E-08	0,0636	5,4619005	0,34717876	1192,86	DNAAF10	dynein axonemal assembly factor 10
147948	2,10E-01	6,78E-01	1,78E-01	0,2576	1,3474524	0,34709554	46,98	ZNF582	zinc finger protein 582
9508	3,08E-02	1,51E+00	2,32E-02	0,1528	2,2695529	0,34686626	146,75	ADAMTS3	ADAM metallopeptidase with thrombospondin type 1 motif 3
107984773	1,76E-01	7,54E-01	1,47E-01	0,2393	1,4496588	0,34684206	54,66	LINC01852	long intergenic non-protein coding RNA 1852
26292	4,10E-06	5,39E+00	2,29E-06	0,0733	4,7263994	0,34660299	836,2	MYCBP	MYC binding protein
53944	3,11E-08	7,51E+00	1,55E-08	0,0613	5,6556599	0,3465813	1321,65	CSNK1G1	casein kinase 1 gamma 1
109703458	1,09E-06	5,96E+00	5,86E-07	0,0694	4,9957963	0,3465126	809,96	HTD2	hydroxyacyl-thioester dehydratase type 2
6845	5,76E-10	9,24E+00	2,66E-10	0,0549	6,3172412	0,34650866	2950,25	VAMP7	vesicle associated membrane protein 7
91419	5,86E-03	2,23E+00	4,11E-03	0,1207	2,8694584	0,34641082	238,36	ATP23	ATP23 metallopeptidase and ATP synthase assembly factor homolog
84923	1,78E-10	9,75E+00	8,07E-11	0,0533	6,4992094	0,3461819	2632,74	FAM104A	family with sequence similarity 104 member A
22876	5,97E-11	1,02E+01	2,66E-11	0,0519	6,6645092	0,34597791	1835,25	INPP5F	inositol polyphosphate-5-phosphatase F
55001	4,12E-01	3,85E-01	3,71E-01	0,3864	0,8949048	0,34579158	21,71	TTC22	tetratricopeptide repeat domain 22
100189028	5,12E-01	2,91E-01	4,71E-01	0,4789	0,7216513	0,34559287	13,08	TRI-TAT2-2	tRNA-Ile (anticodon TAT) 2-2
100527950	4,50E-06	5,35E+00	2,51E-06	0,0734	4,7072403	0,34551541	840,53	GJA9-MYCB	GJA9-MYCBP readthrough
84298	6,20E-08	7,21E+00	3,13E-08	0,0624	5,5337389	0,34537472	2760,42	LLPH	LLP homolog, long-term synaptic facilitation factor
5193	1,64E-04	3,79E+00	1,01E-04	0,0888	3,8875189	0,34532172	523,45	PEX12	peroxisomal biogenesis factor 12
503693	4,39E-01	3,58E-01	3,98E-01	0,4085	0,845234	0,34525935	18,95	LOH12CR2	loss of heterozygosity on chromosome 12, region 2
114883	8,42E-16	1,51E+01	3,18E-16	0,0423	8,1662742	0,34520556	5436,89	OSBPL9	oxysterol binding protein like 9
8887	1,84E-15	1,47E+01	7,04E-16	0,0428	8,0698469	0,34505095	7313,66	TAX1BP1	Tax1 binding protein 1
55153	6,52E-16	1,52E+01	2,45E-16	0,0421	8,1976058	0,34486751	4719,21	SDAD1	SDA1 domain containing 1
79647	1,06E-12	1,20E+01	4,43E-13	0,0476	7,2416092	0,344789	3638,75	AKIRIN1	akirin 1
673	1,16E-07	6,94E+00	5,95E-08	0,0636	5,4203922	0,34460739	1147,53	BRAF	B-Raf proto-oncogene, serine/threonine kinase
200895	5,49E-03	2,26E+00	3,84E-03	0,1191	2,8912629	0,34437161	248,66	DHFR2	dihydrofolate reductase 2
9166	3,63E-08	7,44E+00	1,81E-08	0,0612	5,6288081	0,34433294	1142,31	EBAG9	estrogen receptor binding site associated antigen 9
105375044	4,02E-01	3,96E-01	3,61E-01	0,3768	0,9137663	0,34428959	20,99	LOC105375(	uncharacterized LOC105375044
5981	1,46E-14	1,38E+01	5,76E-15	0,0441	7,8090753	0,34424704	4877,2	RFC1	replication factor C subunit 1
23240	3,25E-06	5,49E+00	1,80E-06	0,072	4,7744431	0,34389462	726,28	TMEM131L	transmembrane 131 like
9839	2,89E-05	4,54E+00	1,69E-05	0,0799	4,3017226	0,34363562	750,69	ZEB2	zinc finger E-box binding homeobox 2
6386	1,51E-16	1,58E+01	5,58E-17	0,041	8,3737321	0,34361279	12064,45	SDCBP	syndecan binding protein
64432	2,30E-11	1,06E+01	1,01E-11	0,0505	6,8051419	0,3435262	2495,29	MRPS25	mitochondrial ribosomal protein S25
253512	1,29E-08	7,89E+00	6,32E-09	0,0591	5,8081244	0,34321305	1330,49	SLC25A30	solute carrier family 25 member 30
55858	5,25E-13	1,23E+01	2,17E-13	0,0468	7,3378006	0,34320012	4882,16	TMEM165	transmembrane protein 165
55246	9,80E-10	9,01E+00	4,58E-10	0,055	6,2329571	0,3430995	1853,53	CCDC25	coiled-coil domain containing 25
22861	1,33E-06	5,88E+00	7,22E-07	0,0692	4,9554744	0,34271648	1018,19	NLRP1	NLR family pyrin domain containing 1
3364	9,40E-06	5,03E+00	5,35E-06	0,0753	4,5506636	0,34266977	742,39	HUS1	HUS1 checkpoint clamp component
5358	3,01E-19	1,85E+01	1,02E-19	0,0377	9,0862687	0,34249591	20779,65	PLS3	plastin 3
81929	3,62E-16	1,54E+01	1,35E-16	0,0414	8,2688057	0,34219808	5921,14	SEH1L	SEH1 like nucleoporin
246269	3,55E-04	3,45E+00	2,25E-04	0,0928	3,6890036	0,34218184	408,99	AFG1L	AFG1 like ATPase
23286	2,70E-15	1,46E+01	1,04E-15	0,0427	8,022539	0,34217429	4325,43	WWC1	WW and C2 domain containing 1
257068	1,11E-01	9,55E-01	9,04E-02	0,2019	1,6934253	0,34196642	87,14	PLCXD2	phosphatidylinositol specific phospholipase C X domain containing 2
107985139	2,62E-04	3,58E+00	1,64E-04	0,0907	3,7685231	0,34191646	456,39	LOC107985	139
8975	3,45E-12	1,15E+01	1,47E-12	0,0483	7,0775719	0,34179666	3150,97	USP13	ubiquitin specific peptidase 13
9477	5,44E-11	1,03E+01	2,41E-11	0,0512	6,6784789	0,34176728	2708,31	MED20	mediator complex subunit 20
107985367	6,98E-04	3,16E+00	4,53E-04	0,0973	3,5071245	0,3411755	363,08	LOC107985	367
86	2,06E-16	1,57E+01	7,64E-17	0,0409	8,3366917	0,34104698	7804,94	ACTL6A	actin like 6A
2289	1,72E-13	1,28E+01	6,99E-14	0,0455	7,4879694	0,3410387	3537,81	FKBP5	FKBP prolyl isomerase 5
65267	4,40E-04	3,36E+00	2,81E-04	0,0938	3,632303	0,34062353	413,82	WNK3	WNK lysine deficient protein kinase 3
100129460	1,35E-01	8,70E-01	1,11E-01	0,2139	1,5925813	0,34062046	67,81	DPY19L1P1	DPY19L1 pseudogene 1
9476	4,04E-01	3,94E-01	3,62E-01	0,374	0,9107218	0,34060127	22	NAPSA	napsin A aspartic peptidase
107985263	5,00E-02	1,30E+00	3,88E-02	0,1647	2,0666436	0,3403552	125,14	LOC107985	263
29789	2,48E-15	1,46E+01	9,50E-16	0,0423	8,0331635	0,34018552	7642,22	OLA1	Obg like ATPase 1
107985325	2,39E-01	6,22E-01	2,05E-01	0,2683	1,2676448	0,34016314	42,76	GP6-AS1	GP6 antisense RNA 1
54756	6,77E-07	6,17E+00	3,61E-07	0,0668	5,0884158	0,34014326	991,27	IL17RD	interleukin 17 receptor D
9527	2,28E-13	1,26E+01	9,30E-14	0,0456	7,4504516	0,33972359	3164,36	GOSR1	golgi SNAP receptor complex member 1
8446	4,38E-09	8,36E+00	2,10E-09	0,0567	5,9899452	0,33950228	1833,66	DUSP11	dual specificity phosphatase 11
4856	9,24E-08	7,03E+00	4,72E-08	0,0622	5,4617083	0,33948156	1433,63	CCN3	cellular communication network factor 3
100506930	2,74E-02	1,56E+00	2,06E-02	0,1466	2,3160396	0,33946999	150,84	LINC00665	long intergenic non-protein coding RNA 665
60468	4,51E-02	1,35E+00	3,47E-02	0,1607	2,1117812	0,33937695	134,11	BACH2	BTB domain and CNC homolog 2
5509	3,63E-04	3,44E+00	2,30E-04	0,0921	3,683388	0,33932853	433,74	PPP1R3D	protein phosphatase 1 regulatory subunit 3D
205717	1,96E-07	6,71E+00	1,02E-07	0,0637	5,3238213	0,33931368	1040,76	USF3	upstream transcription factor family member 3
26778	8,66E-02	1,06E+00	6,92E-02	0,1867	1,8171693	0,33922972	91,58	SNORA70	small nucleolar RNA, H/ACA box 70
657	1,17E-08	7,93E+00	5,70E-09	0,0582	5,8253807	0,3390842	1395,17	BMPR1A	bone morphogenetic protein receptor type 1A
8218	2,64E-04	3,58E+00	1,65E-04	0,09	3,7668288	0,33891846	445,61	CLTCL1	clathrin heavy chain like 1
55604	8,38E-09	8,08E+00	4,07E-09	0,0576	5,8814862	0,33872467	1528,85	CARMIL1	capping protein regulator and myosin 1 linker 1
8731	1,86E-11	1,07E+01	8,10E-12	0,0495	6,8367222	0,33863994	3022,61	RNMT	RNA guanine-7 methyltransferase
10250	1,11E-08	7,95E+00	5,40E-09	0,058	5,834267	0,338432	7485,41	SRRM1	serine and arginine repetitive matrix 1
57798	4,09E-08	7,39E+00	2,05E-08	0,0602	5,6077555	0,33763677	1208,16	GATAD1	GATA zinc finger domain containing 1
113	8,44E-07	6,07E+00	4,53E-07	0,0669	5,045289	0,33758407	880,89	ADCY7	adenylate cyclase 7
6728	2,65E-11	1,06E+01	1,16E-11	0,0498	6,7848867	0,33755067	3790,46	SRP19	signal recognition particle 19
51202	8,62E-13	1,21E+01	3,59E-13	0,0464	7,2702064	0,3374856	4894,75	DDX47	DEAD-box helicase 47
10172	6,30E-02	1,20E+00	4,95E-02	0,1717	1,9643366	0,33732666	107,37	ZNF256	zinc finger protein 256
388335	3,02E-01	5,20E-01	2,64E-01	0,3017	1,1177825	0,33724455	32,63	TMEM220	transmembrane protein 220
51247	2,88E-16	1,55E+01	1,07E-16	0,0406	8,2965671	0,33723334	6499,68	PAIP2	poly(A) binding protein interacting protein 2
26511	1,24E-04	3,91E+00	7,55E-05	0,0852	3,9581057	0,33716316	892,08	CHIC2	cysteine rich hydrophobic domain 2
9541	2,95E-08	7,53E+00	1,47E-08	0,0594	5,6649446	0,33669466	1334,3	CIR1	corepressor interacting with RBPJ, CIR1
105373386	4,76E-01	3,22E-01	4,35E-01	0,431	0,7810696	0,3366237	16,39	LOC105373	uncharacterized LOC105373386
26135	3,09E-11	1,05E+01	1,36E-11	0,0498	6,7620885	0,33647993	24189,08	SERBP1	SERPINE1 mRNA binding protein 1
105376374	1,73E-02	1,76E+00	1,27E-02	0,1349	2,4931609	0,33629484	173,29	LOC105376	uncharacterized LOC105376374
9896	6,81E-09	8,17E+00	3,30E-09	0,0568	5,9160928	0,3362789	1400,5	FIG4	FIG4 phosphoinositide 5-phosphatase
22836	1,96E-15	1,47E+01	7,51E-16	0,0417	8,0619714	0,33598817	8708,58	RHOBTB3	Rho related BTB domain containing 3
10569	1,06E-09	8,97E+00	4,97E-10	0,054	6,2201107	0,33568272	4183,03	SLU7	SLU7 homolog, splicing factor
11266	6,29E-10	9,20E+00	2,91E-10	0,0532	6,3034102	0,33561757	1958,89	DUSP12	dual specificity phosphatase 12
4208	7,10E-05	4,15E+00	4,26E-05	0,082	4,0927129	0,33544493	584,1	MEF2C	myocyte enhancer factor 2C
100507530	2,97E-01	5,27E-01	2,59E-01	0,2972	1,1282118	0,33533671	34,02	MCPH1-AS1	MCPH1 antisense RNA 1
2551	9,39E-09	8,03E+00	4,57E-09	0,0572	5,8622974	0,33531692	1659,47	GABPA	GA binding protein transcription factor subunit alpha
6882	1,95E-07	6,71E+00	1,01E-07	0,063	5,3248323	0,33531105	2058,2	TAF11	TATA-box binding protein associated factor 11
257397	1,36E-08	7,87E+00	6,70E-09	0,0578	5,7982539	0,33526906	1941,64	TAB3	TGF-beta activated kinase 1 (MAP3K7) binding protein 3
7813	5,34E-11	1,03E+01	2,37E-11	0,0502	6,6813559	0,33507857	2420,84	EVI5	ecotropic viral integration site 5
100507178	6,54E-02	1,18E+00	5,15E-02	0,1718	1,9472568	0,33462136	104,71	SLFNL1-AS1	SLFNL1 antisense RNA 1
162963	3,74E-01	4,27E-01	3,33E-01	0,3456	0,9678749	0,33449208	25,1	ZNF610	zinc finger protein 610
55830	2,77E-12	1,16E+01	1,17E-12	0,047	7,1085427	0,33439524	2715,33	GLT8D1	glycosyltransferase 8 domain containing 1
105379393	3,40E-01	4,69E-01	3,00E-01	0,3223	1,0370937	0,33421226	28,8	KAT6A-AS1	KAT6A antisense RNA 1
56260	2,30E-01	6,38E-01	1,96E-01	0,2585	1,292147	0,33399928	47,58	C8orf44	chromosome 8 putative open reading frame 44
7428	1,45E-12	1,18E+01	6,08E-13	0,0464	7,1987066	0,33390204	3104,48	VHL	von Hippel-Lindau tumor suppressor
80179	1,92E-15	1,47E+01	7,34E-16	0,0414	8,0646942	0,33382253	5104,38	MYO19	myosin XIX
101928705	9,49E-02	1,02E+00	7,64E-02	0,1883	1,7721248	0,33372833	95,82	LOC101928	705
5504	4,89E-08	7,31E+00	2,46E-08	0,0598	5,5760289	0,33346314	2164,79	PPP1R2	protein phosphatase 1 regulatory inhibitor subunit 2
7643	1,70E-04	3,77E+00	1,05E-04	0,086	3,8787267	0,33345986	488,69	ZNF90	zinc finger protein 90
3787	4,22E-01	3,75E-01	3,80E-01	0,38	0,8770223	0,33329938	21,4	KCNS1	potassium voltage-gated channel modifier subfamily S member 1
27042	3,25E-12	1,15E+01	1,38E-12	0,047	7,0860865	0,33329481	2841,95	UTP25	UTP25 small subunit processome component
400713	3,19E-03	2,50E+00	2,18E-03	0,1087	3,0645621	0,33324809	277,47	ZNF880	zinc finger protein 880
25854	9,64E-02	1,02E+00	7,76E-02	0,1887	1,7646085	0,33302618	88,05	FAM149A	family with sequence similarity 149 member A
5217	5,53E-09	8,26E+00	2,67E-09	0,0559	5,9508766	0,33284895	2419,29	PFN2	profilin 2
23186	2,07E-13	1,27E+01	8,44E-14	0,0446	7,463264	0,33261871	3651,88	RCOR1	REST corepressor 1
84260	6,73E-10	9,17E+00	3,12E-10	0,0529	6,2927073	0,33259075	2274,81	TCHP	trichoplein keratin filament binding
79719	3,48E-11	1,05E+01	1,53E-11	0,0493	6,7448438	0,33256585	2266,44	AAGAB	alpha and gamma adaptin binding protein
81566	1,38E-06	5,86E+00	7,48E-07	0,0672	4,9484143	0,33256439	1020,46	CSRNP2	cysteine and serine rich nuclear protein 2
22990	9,87E-12	1,10E+01	4,25E-12	0,048	6,9284682	0,33256141	2880,76	PCNX1	pecanex 1
105372705	4,18E-01	3,79E-01	3,76E-01	0,3757	0,884912	0,33250283	21,75	LOC105372	uncharacterized LOC105372705
10219	5,87E-01	2,31E-01	5,47E-01	0,5524	0,6019439	0,33249608	10,09	KLRG1	killer cell lectin like receptor G1
201798	3,85E-01	4,15E-01	3,43E-01	0,3508	0,9474426	0,33232181	25,27	TIGD4	tigger transposable element derived 4
10924	1,03E-03	2,99E+00	6,75E-04	0,0977	3,3993648	0,33205801	366,85	SMPDL3A	sphingomyelin phosphodiesterase acid like 3A
114327	5,30E-04	3,28E+00	3,41E-04	0,0927	3,5823365	0,33198861	416,61	EFHC1	EF-hand domain containing 1
9685	1,37E-11	1,09E+01	5,94E-12	0,0482	6,8810959	0,33186606	6561,91	CLINT1	clathrin interactor 1
221960	5,79E-11	1,02E+01	2,57E-11	0,0498	6,6691089	0,33185819	2201,75	CCZ1B	CCZ1 homolog B, vacuolar protein trafficking and biogenesis associated
285381	2,06E-09	8,69E+00	9,78E-10	0,0543	6,112879	0,33169653	2215,88	DPH3	diphthamide biosynthesis 3

105371792	8,97E-03	2,05E+00	6,40E-03	0,1216	2,7263448	0,33162054	263,23	LOC105371	uncharacterized LOC105371792
51163	2,83E-06	5,55E+00	1,56E-06	0,069	4,8028575	0,33137267	861,99	DBR1	debranching RNA lariats 1
546	1,63E-11	1,08E+01	7,10E-12	0,0483	6,8557133	0,33133052	3608,67	ATRX	ATRX chromatin remodeler
253959	5,26E-08	7,28E+00	2,65E-08	0,0595	5,5631704	0,33127226	1426,02	RALGAPA1	Ral GTPase activating protein catalytic subunit alpha 1
25963	2,13E-11	1,07E+01	9,29E-12	0,0486	6,8170552	0,33122688	2633,35	TMEM87A	transmembrane protein 87A
64149	2,60E-07	6,59E+00	1,36E-07	0,0628	5,2712331	0,33122006	1178,62	C17orf75	chromosome 17 open reading frame 75
51773	1,17E-07	6,93E+00	5,98E-08	0,0611	5,4194173	0,33099751	3917,84	RSF1	remodeling and spacing factor 1
107986325	5,17E-01	2,87E-01	4,75E-01	0,463	0,7145722	0,33082793	15,01	LOC107986	uncharacterized LOC107986325
139324	1,56E-02	1,81E+00	1,14E-02	0,1307	2,5302903	0,3307866	204,81	HDX	highly divergent homeobox
5985	1,50E-11	1,08E+01	6,53E-12	0,0482	6,8676624	0,33073187	3868,49	RFC5	replication factor C subunit 5
28966	3,84E-10	9,42E+00	1,76E-10	0,0518	6,381035	0,33068498	2296,31	SNX24	sorting nexin 24
1452	3,24E-12	1,15E+01	1,37E-12	0,0466	7,0866314	0,33044411	9624,41	CSNK1A1	casein kinase 1 alpha 1
64772	2,48E-03	2,61E+00	1,68E-03	0,105	3,1420005	0,32976279	312,23	ENGASE	endo-beta-N-acetylglucosaminidase
2113	1,27E-18	1,79E+01	4,38E-19	0,0369	8,9268099	0,32976188	18184,29	ETS1	ETS proto-oncogene 1, transcription factor
113201	8,00E-10	9,10E+00	3,72E-10	0,0526	6,2654008	0,32959298	3073,18	GOLM2	golgi membrane protein 2
91574	4,65E-09	8,33E+00	2,23E-09	0,0551	5,9798358	0,32955039	2259,25	MTRFR	mitochondrial translation release factor in rescue
118924	1,07E-05	4,97E+00	6,11E-06	0,0729	4,5227155	0,32950735	722,74	FRA10AC1	FRA10A associated CGG repeat 1
79625	1,67E-02	1,78E+00	1,22E-02	0,1314	2,506161	0,32940733	190,54	NDNF	neuron derived neurotrophic factor
4001	7,54E-11	1,01E+01	3,36E-11	0,0496	6,6297338	0,32909352	8245,61	LMNB1	lamin B1
6416	2,48E-10	9,61E+00	1,13E-10	0,051	6,4486822	0,32896964	2251,39	MAP2K4	mitogen-activated protein kinase kinase 4
54039	2,63E-01	5,80E-01	2,27E-01	0,272	1,2091653	0,32886026	40,45	PCBP3	poly(rC) binding protein 3
2571	4,90E-03	2,31E+00	3,41E-03	0,1123	2,9280306	0,32871177	269,42	GAD1	glutamate decarboxylase 1
147804	2,72E-04	3,57E+00	1,71E-04	0,0874	3,7585077	0,32867213	490,69	TPM3P9	tropomyosin 3 pseudogene 9
10056	7,59E-10	9,12E+00	3,53E-10	0,0524	6,2735531	0,3285511	4234,11	FARSB	phenylalanyl-tRNA synthetase subunit beta
8801	7,72E-15	1,41E+01	3,01E-15	0,0416	7,8904429	0,32818409	4460,43	SUCLG2	succinate-CoA ligase GDP-forming subunit beta
27340	1,89E-13	1,27E+01	7,66E-14	0,0439	7,4759634	0,32796317	5003,22	UTP20	UTP20 small subunit processome component
51054	1,30E-01	8,86E-01	1,06E-01	0,2028	1,6145488	0,32749535	84,17	PLEKHA8P1	pleckstrin homology domain containing A8 pseudogene 1
23609	1,46E-11	1,08E+01	6,35E-12	0,0476	6,8716196	0,32719654	2642,12	MKRN2	makorin ring finger protein 2
9353	3,24E-13	1,25E+01	1,33E-13	0,0442	7,4033493	0,32715156	4423,05	SLIT2	slit guidance ligand 2
285521	1,39E-07	6,86E+00	7,16E-08	0,0607	5,387162	0,32701706	1240,49	COX18	cytochrome c oxidase assembly factor COX18
131544	1,53E-09	8,82E+00	7,23E-10	0,053	6,1608749	0,32679729	1812,67	CRYBG3	crystallin beta-gamma domain containing 3
115992	1,74E-05	4,76E+00	1,01E-05	0,074	4,4150363	0,32669852	721,46	RNF166	ring finger protein 166
9831	1,25E-08	7,90E+00	6,12E-09	0,0562	5,813531	0,32658261	1538,57	ZNF623	zinc finger protein 623
339524	5,68E-01	2,46E-01	5,28E-01	0,517	0,6315649	0,32654293	12,03	LINC01140	long intergenic non-protein coding RNA 1140
284309	3,01E-07	6,52E+00	1,58E-07	0,0622	5,2432236	0,32638874	1186,1	ZNF776	zinc finger protein 776
56900	3,46E-07	6,46E+00	1,82E-07	0,0626	5,2168885	0,32636733	1746,23	TMEM167B	transmembrane protein 167B
6787	7,67E-08	7,12E+00	3,90E-08	0,0594	5,4954553	0,32631153	1700,96	NEK4	NIMA related kinase 4
64376	1,04E-05	4,98E+00	5,91E-06	0,072	4,5295439	0,32627026	739,27	IKZF5	IKAROS family zinc finger 5
112268124	2,99E-02	1,52E+00	2,25E-02	0,143	2,2811621	0,32623117	179,54	BAZ1A-AS1	BAZ1A antisense RNA 1
118738	7,21E-03	2,14E+00	5,10E-03	0,1164	2,8007682	0,3260086	241,44	ZNF488	zinc finger protein 488
10393	2,95E-09	8,53E+00	1,41E-09	0,0538	6,0546572	0,32597118	1854,44	ANAPC10	anaphase promoting complex subunit 10
55334	5,70E-14	1,32E+01	2,28E-14	0,0427	7,633629	0,32594472	4255,7	SLC39A9	solute carrier family 39 member 9
29994	1,69E-05	4,77E+00	9,77E-06	0,0737	4,4221451	0,32590325	837,58	BAZ2B	bromodomain adjacent to zinc finger domain 2B
100302401	3,48E-01	4,58E-01	3,07E-01	0,3193	1,0207772	0,32588522	30,55	RASAL2-AS	RASAL2 antisense RNA 1
84547	1,56E-07	6,81E+00	8,04E-08	0,0607	5,3662325	0,32584775	1600,61	PGBD1	piggyBac transposable element derived 1
10884	6,85E-08	7,16E+00	3,47E-08	0,0591	5,5158595	0,32584523	1647,28	MRPS30	mitochondrial ribosomal protein S30
79841	4,52E-01	3,45E-01	4,10E-01	0,3955	0,8233488	0,32560045	21,11	AGBL2	AGBL carboxypeptidase 2
79730	3,45E-07	6,46E+00	1,81E-07	0,0624	5,2175797	0,32540054	1085,07	NSUN7	NOP2/Sun RNA methyltransferase family member 7
100873949	3,69E-03	2,43E+00	2,54E-03	0,1077	3,0184518	0,32520789	339,47	IPO9-AS1	IPO9 antisense RNA 1
100506746	5,00E-02	1,30E+00	3,87E-02	0,1573	2,0669282	0,32520185	152,48	AFF1-AS1	AFF1 antisense RNA 1
101060691	2,27E-02	1,64E+00	1,68E-02	0,1359	2,3902152	0,32492108	190,36	NUTM2B-AS	NUTM2B antisense RNA 1
375295	1,69E-05	4,77E+00	9,78E-06	0,0735	4,4220303	0,32486516	883,98	LINC01116	long intergenic non-protein coding RNA 1116
85476	2,34E-10	9,63E+00	1,06E-10	0,0503	6,4574837	0,32474796	2533,27	GFM1	G elongation factor mitochondrial 1
84733	7,56E-05	4,12E+00	4,55E-05	0,0796	4,0775737	0,32462649	632,79	CBX2	chromobox 2
10289	1,41E-09	8,85E+00	6,62E-10	0,0526	6,1748052	0,32448725	2543,37	EIF1B	eukaryotic translation initiation factor 1B
146909	1,40E-09	8,85E+00	6,59E-10	0,0525	6,175617	0,32444528	3691,79	KIF18B	kinesin family member 18B
4257	3,92E-11	1,04E+01	1,73E-11	0,0482	6,7272593	0,32432975	4435,27	MGST1	microsomal glutathione S-transferase 1
23101	6,80E-02	1,17E+00	5,36E-02	0,168	1,9300117	0,32422503	113,89	MCF2L2	MCF.2 cell line derived transforming sequence-like 2
341346	2,80E-01	5,53E-01	2,42E-01	0,2771	1,1688857	0,32388458	39,73	SMCO2	single-pass membrane protein with coiled-coil domains 2
54069	1,95E-06	5,71E+00	1,07E-06	0,0663	4,8786515	0,32369484	1008,38	MIS18A	MIS18 kinetochore protein A
79175	1,14E-05	4,94E+00	6,51E-06	0,0718	4,509069	0,32357875	839,77	ZNF343	zinc finger protein 343
23019	6,85E-18	1,72E+01	2,42E-18	0,037	8,7356351	0,32321024	12262,47	CNOT1	CCR4-NOT transcription complex subunit 1
54834	2,89E-06	5,54E+00	1,60E-06	0,0673	4,7989128	0,3228247	923,38	GDAP2	ganglioside induced differentiation associated protein 2
59348	1,12E-03	2,95E+00	7,37E-04	0,0956	3,3755302	0,32274256	371,84	ZNF350	zinc finger protein 350
3918	1,51E-19	1,88E+01	5,09E-20	0,0352	9,1621052	0,32271798	14477,34	LAMC2	laminin subunit gamma 2
79707	1,09E-07	6,96E+00	5,57E-08	0,0594	5,4319472	0,32263634	1240,32	NOL9	nucleolar protein 9
101927621	4,12E-01	3,85E-01	3,71E-01	0,3606	0,8943738	0,32248902	23,73	ZNF567-DT	ZNF567 divergent transcript
79088	7,73E-08	7,11E+00	3,93E-08	0,0587	5,4939969	0,32245128	1357,35	ZNF426	zinc finger protein 426
4300	8,44E-05	4,07E+00	5,10E-05	0,0796	4,0511803	0,32244123	782,18	MLLT3	MLLT3 super elongation complex subunit
55328	7,53E-03	2,12E+00	5,34E-03	0,1157	2,7860306	0,3223972	240,16	RNLS	renalase, FAD dependent amine oxidase
100422558	3,72E-02	1,43E+00	2,84E-02	0,147	2,1923792	0,32236032	145,04	SMG1P6	SMG1 pseudogene 6
79980	4,47E-10	9,35E+00	2,06E-10	0,0507	6,3568811	0,322351	2851,73	DSN1	DSN1 component of MIS12 kinetochore complex
116254	1,52E-06	5,82E+00	8,26E-07	0,0654	4,9291712	0,32234868	1860,85	GINM1	glycosylated integral membrane protein 1
2125	2,31E-07	6,64E+00	1,20E-07	0,0609	5,293325	0,32229308	1293,9	EVPL	envoplakin
220108	1,36E-01	8,66E-01	1,12E-01	0,2026	1,5900094	0,32218259	81,05	FAM124A	family with sequence similarity 124 member A
100505854	4,45E-03	2,35E+00	3,08E-03	0,1089	2,9592245	0,32215107	287,68	APTR	Alu-mediated CDKN1A/p21 transcriptional regulator
1657	8,45E-07	6,07E+00	4,53E-07	0,0638	5,0450292	0,3220993	1251,49	DMXL1	Dmx like 1
64216	2,30E-06	5,64E+00	1,27E-06	0,0665	4,8450682	0,32206509	1037,95	TFB2M	transcription factor B2, mitochondrial
80349	3,31E-07	6,48E+00	1,74E-07	0,0616	5,225351	0,32169873	1219,81	SKIC8	SKI8 subunit of superkiller complex
10802	2,33E-11	1,06E+01	1,02E-11	0,0473	6,8032912	0,32148184	2583,34	SEC24A	SEC24 homolog A, COPII coat complex component
80108	5,50E-01	2,60E-01	5,09E-01	0,4864	0,6606212	0,3213422	13,33	ZFP2	ZFP2 zinc finger protein
83959	5,05E-07	6,30E+00	2,68E-07	0,0625	5,1449483	0,32133454	1249,81	SLC4A11	solute carrier family 4 member 11
158228	3,51E-02	1,45E+00	2,67E-02	0,1449	2,2158489	0,32101315	156,93	FAM201A	family with sequence similarity 201 member A
22930	3,27E-12	1,15E+01	1,39E-12	0,0453	7,0849223	0,32087838	3567,51	RAB3GAP1	RAB3 GTPase activating protein catalytic subunit 1
107987245	1,02E-01	9,91E-01	8,23E-02	0,1847	1,7375548	0,3208773	91,55	LOC107987	uncharacterized LOC107987245
8624	5,17E-09	8,29E+00	2,49E-09	0,0538	5,9621174	0,32052912	3153,67	PSMG1	proteasome assembly chaperone 1
113174	1,72E-09	8,76E+00	8,13E-10	0,0522	6,1422769	0,32033121	2349,87	SAAL1	serum amyloid A like 1
79741	4,33E-02	1,36E+00	3,33E-02	0,1505	2,12853	0,32023953	175,63	CCDC7	coiled-coil domain containing 7
105371059	1,40E-01	8,54E-01	1,16E-01	0,2034	1,573469	0,3199764	73,07	LOC105371	uncharacterized LOC105371059
92345	1,36E-05	4,87E+00	7,80E-06	0,0715	4,4705779	0,31981135	1122,02	NAF1	nuclear assembly factor 1 ribonucleoprotein
107984344	4,31E-01	3,66E-01	3,89E-01	0,3712	0,8611584	0,31969927	22,28	LOC107984344	
107984063	5,82E-01	2,35E-01	5,42E-01	0,5234	0,6100466	0,31931379	11,87	LOC107984063	
64121	1,28E-07	6,89E+00	6,57E-08	0,0591	5,402556	0,3191249	2307,79	RRAGC	Ras related GTP binding C
1737	2,12E-13	1,27E+01	8,63E-14	0,0428	7,4603043	0,31906306	4922,57	DLAT	dihydrolipoamide S-acetyltransferase
2700	4,44E-03	2,35E+00	3,08E-03	0,1077	2,9595807	0,31863729	348,79	GJA3	gap junction protein alpha 3
9693	5,35E-10	9,27E+00	2,47E-10	0,0503	6,3288232	0,31841903	2501,73	RAPGEF2	Rap guanine nucleotide exchange factor 2
30061	2,40E-02	1,62E+00	1,78E-02	0,1344	2,3687557	0,31841748	173,08	SLC40A1	solute carrier family 40 member 1
51104	1,44E-05	4,84E+00	8,28E-06	0,0714	4,4579068	0,31836943	757,75	ABHD17B	abhydrolase domain containing 17B, depalmitoylase
3084	3,11E-13	1,25E+01	1,27E-13	0,0429	7,4088868	0,31807417	4797,84	NRG1	neuregulin 1
100313892	1,76E-01	7,54E-01	1,47E-01	0,2193	1,4493985	0,31784685	65,38	MIR761	microRNA 761
55904	6,88E-10	9,16E+00	3,19E-10	0,0505	6,289128	0,31784005	2557,38	KMT2E	lysine methyltransferase 2E (inactive)
8970	7,67E-02	1,12E+00	6,09E-02	0,1695	1,8744546	0,31763846	114,96	H2BC11	H2B clustered histone 11
387263	1,42E-07	6,85E+00	7,31E-08	0,059	5,3833771	0,31750913	1375,73	C6orf120	chromosome 6 open reading frame 120
124872	6,22E-01	2,06E-01	5,84E-01	0,5803	0,5471114	0,31748241	9,31	B4GALNT2	beta-1,4-N-acetyl-galactosaminyltransferase 2
5532	1,92E-10	9,72E+00	8,72E-11	0,0489	6,4875701	0,31742223	2665,62	PPP3CB	protein phosphatase 3 catalytic subunit beta
100505475	5,14E-01	2,89E-01	4,72E-01	0,4414	0,7189932	0,31739151	16,01	SYNE1-AS1	SYNE1 antisense RNA 1
11035	5,01E-01	3,00E-01	4,59E-01	0,4291	0,7397054	0,31737651	16,24	RIPK3	receptor interacting serine/threonine kinase 3
100134869	3,57E-01	4,47E-01	3,17E-01	0,3167	1,0013539	0,31712506	34,47	UBE2Q2P2	UBE2Q2 pseudogene 2
23643	2,22E-01	6,54E-01	1,89E-01	0,2413	1,3138375	0,31709173	54,51	LY96	lymphocyte antigen 96
51622	1,27E-08	7,90E+00	6,21E-09	0,0545	5,8109131	0,31692411	1735,1	CCZ1	CCZ1 homolog, vacuolar protein trafficking and biogenesis associated
729830	1,13E-03	2,95E+00	7,44E-04	0,094	3,3728987	0,31689972	404,37	FHIP1A	FHF complex subunit HOOK interacting protein 1A
7150	9,20E-11	1,00E+01	4,12E-11	0,048	6,5997528	0,3166666	8966,59	TOP1	DNA topoisomerase I
7403	1,51E-06	5,82E+00	8,22E-07	0,0642	4,9299606	0,31643233	1168,87	KDM6A	lysine demethylase 6A
5154	7,22E-03	2,14E+00	5,11E-03	0,113	2,8002794	0,31641744	270,06	PDGFA	platelet derived growth factor subunit A
56474	1,09E-05	4,96E+00	6,20E-06	0,07	4,5192967	0,31624399	836,96	CTPS2	CTP synthase 2
100506233	1,09E-02	1,96E+00	7,81E-03	0,1189	2,6599771	0,3162092	237,64	RAB30-DT	RAB30 divergent transcript
150590	2,08E-01	6,82E-01	1,76E-01	0,2335	1,3531692	0,31599838	62,94	C2orf15	chromosome 2 open reading frame 15
285540	3,03E-01	5,19E-01	2,65E-01	0,2833	1,1152821	0,31594541	41,27	SEPSECS-A	SEPSECS antisense RNA 1 (head to head)
83939	3,28E-14	1,35E+01	1,31E-14	0,0409	7,7053112	0,3152839	5335,42	EIF2A	eukaryotic translation initiation factor 2A
102724814	7,69E-05	4,11E+00	4,63E-05	0,0774	4,0734151	0,31526009	743,91	AP1G2-AS1	AP1G2 antisense RNA 1

101928099	3,61E-01	4,42E-01	3,20E-01	0,3169	0,9943126	0,31513214	30,66	PCAT7	prostate cancer associated transcript 7
6629	2,55E-12	1,16E+01	1,08E-12	0,0442	7,1202231	0,31504147	4701,83	SNRPB2	small nuclear ribonucleoprotein polypeptide B2
100533183	1,87E-02	1,73E+00	1,38E-02	0,1278	2,4630738	0,31486306	194,3	ZNF664-RFL	ZNF664-RFLNA readthrough
338755	5,73E-01	2,42E-01	5,33E-01	0,505	0,623139	0,31470211	12,45	OR2AG2	olfactory receptor family 2 subfamily AG member 2
100529215	5,91E-02	1,23E+00	4,63E-02	0,1578	1,9929074	0,31455643	134,24	ZNF559-ZNF	ZNF559-ZNF177 readthrough
60560	3,99E-12	1,14E+01	1,70E-12	0,0445	7,0570203	0,31423703	3762,14	NAA35	N-alpha-acetyltransferase 35, NatC auxiliary subunit
11188	1,05E-07	6,98E+00	5,36E-08	0,0577	5,4389099	0,31403013	1774,65	NISCH	nischarin
4691	5,51E-14	1,33E+01	2,21E-14	0,0411	7,6379803	0,31394911	69102,19	NCL	nucleolin
283596	3,37E-02	1,47E+00	2,56E-02	0,1405	2,2329282	0,31376908	157,36	SNHG10	small nucleolar RNA host gene 10
91404	1,48E-04	3,83E+00	9,11E-05	0,0802	3,9132182	0,31371721	639,59	SESTD1	SEC14 and spectrin domain containing 1
105371493	4,08E-01	3,89E-01	3,66E-01	0,3469	0,9033144	0,31338115	24,92	LOC105371	uncharacterized LOC105371493
200350	5,37E-01	2,70E-01	4,96E-01	0,4598	0,6813654	0,31326101	14,44	FOXD4L1	forkhead box D4 like 1
56911	8,67E-02	1,06E+00	6,93E-02	0,1724	1,8166589	0,31325607	116,52	MAP3K7CL	MAP3K7 C-terminal like
2549	3,25E-04	3,49E+00	2,05E-04	0,0844	3,7123243	0,31318325	600,31	GAB1	GRB2 associated binding protein 1
6607	9,09E-10	9,04E+00	4,24E-10	0,0501	6,2450589	0,31316747	2559,93	SMN2	survival of motor neuron 2, centromeric
1389	1,07E-08	7,97E+00	5,21E-09	0,0536	5,8401772	0,31308656	1937,52	CREBL2	cAMP responsive element binding protein like 2
1027	4,61E-06	5,34E+00	2,58E-06	0,0666	4,7019837	0,31305238	953,81	CDKN1B	cyclin dependent kinase inhibitor 1B
101927631	2,07E-01	6,84E-01	1,75E-01	0,2306	1,3551345	0,31252339	60,14	ADNP-AS1	ADNP antisense RNA 1
80013	4,30E-06	5,37E+00	2,40E-06	0,0662	4,7164823	0,3124584	1173,06	MINDY3	MINDY lysine 48 deubiquitinase 3
84196	1,21E-11	1,09E+01	5,25E-12	0,0453	6,8987744	0,31243947	3632,71	USP48	ubiquitin specific peptidase 48
597	6,71E-06	5,17E+00	3,78E-06	0,0676	4,6229335	0,31235368	946,76	BCL2A1	BCL2 related protein A1
5783	1,11E-05	4,95E+00	6,34E-06	0,0691	4,5147368	0,3120827	837,21	PTPN13	protein tyrosine phosphatase non-receptor type 13
3938	4,96E-01	3,05E-01	4,54E-01	0,4172	0,7479482	0,31208139	17,97	LCT	lactase
100505989	4,41E-02	1,36E+00	3,39E-02	0,1471	2,1214316	0,31203991	147,23	SMIM31	small integral membrane protein 31
101929780	7,11E-06	5,15E+00	4,02E-06	0,0677	4,6105757	0,31196129	875,82	NBPF25P	NBPF member 25, pseudogene
105370524	2,07E-02	1,68E+00	1,53E-02	0,1285	2,4262981	0,31184103	197,41	PCNX4-DT	PCNX4 divergent transcript
387751	3,38E-01	4,71E-01	2,98E-01	0,2996	1,039932	0,3115347	33,8	GVINP1	GTPase, very large interferon inducible pseudogene 1
105374249	3,66E-01	4,37E-01	3,25E-01	0,3161	0,9845376	0,31124118	30,84	EIF2B5-DT	EIF2B5 divergent transcript
10166	3,75E-06	5,43E+00	2,08E-06	0,0656	4,7450859	0,31123761	1064,74	SLC25A15	solute carrier family 25 member 15
102723409	6,05E-01	2,18E-01	5,67E-01	0,5429	0,5731735	0,31119321	10,19	LOC102723	uncharacterized LOC102723409
401509	9,62E-02	1,02E+00	7,75E-02	0,1761	1,7655467	0,31095644	100,98	ZNF658B	zinc finger protein 658B (pseudogene)
4660	3,31E-04	3,48E+00	2,09E-04	0,0838	3,7078556	0,31087749	549,51	PPP1R12B	protein phosphatase 1 regulatory subunit 12B
51382	1,24E-10	9,91E+00	5,60E-11	0,0474	6,5539765	0,31046991	4108,89	ATP6V1D	ATPase H+ transporting V1 subunit D
100129461	1,57E-04	3,80E+00	9,66E-05	0,0796	3,8989719	0,31041216	650,33	LYRM4-AS1	LYRM4 antisense RNA 1
64793	6,33E-10	9,20E+00	2,93E-10	0,0492	6,3022287	0,31023753	3033,25	CEP85	centrosomal protein 85
84859	1,07E-08	7,97E+00	5,22E-09	0,0531	5,8398458	0,31011517	2467,84	LRCH3	leucine rich repeats and calponin homology domain containing 3
55269	1,44E-07	6,84E+00	7,40E-08	0,0576	5,3810917	0,31009633	4715,43	PSPC1	paraspeckle component 1
55173	3,90E-12	1,14E+01	1,66E-12	0,0439	7,0604419	0,31006624	9205,41	MRPS10	mitochondrial ribosomal protein S10
23529	1,16E-05	4,94E+00	6,63E-06	0,0688	4,5051927	0,31003332	907,02	CLCF1	cardiotrophin like cytokine factor 1
254778	3,50E-02	1,46E+00	2,66E-02	0,1397	2,2177664	0,30979272	166,39	VXN	vexin
414778	3,49E-01	4,57E-01	3,09E-01	0,3046	1,0169843	0,30974157	34,92	HCG17	HLA complex group 17
654434	6,41E-02	1,19E+00	5,04E-02	0,1583	1,9564741	0,30963454	126,61	SNHG20	small nucleolar RNA host gene 20
7534	7,68E-14	1,31E+01	3,09E-14	0,0408	7,5946453	0,30958931	66280,52	YWHAZ	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein zeta
5049	1,50E-14	1,38E+01	5,92E-15	0,0397	7,8056417	0,30955333	7787,18	PAFAH1B2	platelet activating factor acetylhydrolase 1b catalytic subunit 2
84070	6,65E-01	1,77E-01	6,29E-01	0,6399	0,4826475	0,30886786	8,45	FAM186B	family with sequence similarity 186 member B
1432	3,22E-13	1,25E+01	1,32E-13	0,0417	7,4041656	0,30885277	8899,79	MAPK14	mitogen-activated protein kinase 14
2774	2,36E-01	6,27E-01	2,01E-01	0,2417	1,2773254	0,30874563	51,06	GNAL	G protein subunit alpha L
101928331	3,76E-01	4,25E-01	3,35E-01	0,3204	0,9636184	0,30869784	29,89	LOC101928	uncharacterized LOC101928331
5634	5,69E-07	6,24E+00	3,03E-07	0,0602	5,1217862	0,30852308	2138,25	PRPS2	phosphoribosyl pyrophosphate synthetase 2
11278	1,23E-06	5,91E+00	6,66E-07	0,0621	4,9709311	0,3084783	1223,02	KLF12	KLF transcription factor 12
51616	2,18E-08	7,66E+00	1,08E-08	0,0539	5,7176532	0,3081881	1720,8	TAF9B	TATA-box binding protein associated factor 9b
7884	3,79E-11	1,04E+01	1,67E-11	0,0458	6,7322173	0,30816728	4172,17	SLBP	stem-loop binding protein
728743	3,70E-01	4,32E-01	3,30E-01	0,3157	0,9750387	0,30783739	33,6	LOC728743	zinc finger domain-containing protein LOC728743
101927117	1,79E-06	5,75E+00	9,79E-07	0,0628	4,8958376	0,30768802	1074,92	PLCG1-AS1	PLCG1 antisense RNA 1
79882	8,17E-11	1,01E+01	3,65E-11	0,0465	6,6175852	0,30766716	6320,6	ZC3H14	zinc finger CCCH-type containing 14
22902	1,09E-06	5,96E+00	5,90E-07	0,0615	4,994501	0,30693713	1234,95	RUFY3	RUN and FYVE domain containing 3
149297	1,14E-01	9,43E-01	9,28E-02	0,1824	1,6807659	0,3065477	110,22	FAM78B	family with sequence similarity 78 member B
7691	2,57E-02	1,59E+00	1,92E-02	0,1307	2,3417882	0,3061626	192,27	ZNF132	zinc finger protein 132
105379362	5,01E-03	2,30E+00	3,49E-03	0,1048	2,921139	0,30605599	307,65	LOC105379	uncharacterized LOC105379362
100131691	3,58E-02	1,45E+00	2,72E-02	0,1385	2,2084659	0,30589915	164,42	MZF1-AS1	MZF1 antisense RNA 1
102725509	2,71E-01	5,67E-01	2,34E-01	0,2571	1,1896407	0,30587906	46,03	LINC01232	long intergenic non-protein coding RNA 1232
400644	2,70E-01	5,69E-01	2,33E-01	0,2565	1,1920245	0,30577977	45,63	LINC01443	long intergenic non-protein coding RNA 1443
56255	3,27E-08	7,49E+00	1,63E-08	0,0541	5,6469767	0,30563562	2170,8	TMX4	thioredoxin related transmembrane protein 4
79744	4,09E-03	2,39E+00	2,83E-03	0,1023	2,9857956	0,30547085	344,34	ZNF419	zinc finger protein 419
445815	1,30E-17	1,69E+01	4,64E-18	0,0352	8,6618498	0,30531125	23248,21	PALM2AKAF	PALM2 and AKAP2 fusion
256126	2,72E-01	5,65E-01	2,35E-01	0,2571	1,1871015	0,30518041	45,93	SYCE2	synaptonemal complex central element protein 2
107985044	1,89E-01	7,24E-01	1,59E-01	0,2166	1,4076822	0,30490929	66,69	LOC107985	uncharacterized LOC107985044
54414	4,56E-08	7,34E+00	2,29E-08	0,0545	5,5884012	0,30477427	1972,42	SIAE	sialic acid acetylesterase
104413891	5,55E-01	2,56E-01	5,15E-01	0,4677	0,651555	0,30476137	13,79	SAPCD1-AS	SAPCD1 antisense RNA 1
144577	2,33E-02	1,63E+00	1,73E-02	0,128	2,3802819	0,30461899	203,04	KICS2	KICSTOR subunit 2
100874259	2,56E-01	5,92E-01	2,21E-01	0,2481	1,2250426	0,30398442	48,64	SLC25A30-A	SLC25A30 antisense RNA 1
170712	8,91E-03	2,05E+00	6,36E-03	0,1114	2,7287859	0,30389078	335,13	COX7B2	cytochrome c oxidase subunit 7B2
5295	1,76E-06	5,75E+00	9,60E-07	0,062	4,8996287	0,30386649	1233,87	PIK3R1	phosphoinositide-3-kinase regulatory subunit 1
10951	2,15E-13	1,27E+01	8,75E-14	0,0407	7,4585691	0,30371993	6943,95	CBX1	chromobox 1
131034	4,27E-01	3,70E-01	3,86E-01	0,35	0,8675788	0,30364111	25,29	CPNE4	copine 4
387036	4,52E-01	3,45E-01	4,10E-01	0,3689	0,8230922	0,30362657	23,14	GUSBP2	GUSB pseudogene 2
84079	7,51E-10	9,12E+00	3,49E-10	0,0484	6,2754075	0,30354554	2516,42	ANKRD27	ankyrin repeat domain 27
3818	5,59E-01	2,53E-01	5,18E-01	0,4699	0,6457507	0,30346363	14,18	KLKB1	kallikrein B1
79618	2,65E-04	3,58E+00	1,66E-04	0,0806	3,7653479	0,3034263	614,44	HMBOX1	homeobox containing 1
9639	1,65E-08	7,78E+00	8,10E-09	0,0526	5,7663599	0,30328476	1801,06	ARHGEF10	Rho guanine nucleotide exchange factor 10
83695	1,37E-06	5,86E+00	7,45E-07	0,0613	4,9493337	0,30327234	2295,17	RHNO1	RAD9-HUS1-RAD1 interacting nuclear orphan 1
5507	4,96E-02	1,30E+00	3,84E-02	0,1464	2,070438	0,30317654	145,83	PPP1R3C	protein phosphatase 1 regulatory subunit 3C
100129842	2,92E-02	1,53E+00	2,19E-02	0,1322	2,2914643	0,30287483	186,34	ZNF737	zinc finger protein 737
282991	1,27E-07	6,90E+00	6,55E-08	0,056	5,4031673	0,30279566	1467,22	BLOC1S2	biogenesis of lysosomal organelles complex 1 subunit 2
28512	2,29E-07	6,64E+00	1,19E-07	0,0572	5,2948673	0,30271633	2140,49	NKIRAS1	NFKB inhibitor interacting Ras like 1
6768	1,97E-01	7,06E-01	1,66E-01	0,2186	1,3839683	0,30249228	63,74	ST14	ST14 transmembrane serine protease matriptase
3836	5,61E-11	1,03E+01	2,49E-11	0,0453	6,6739566	0,30242278	4498,74	KPNA1	karyopherin subunit alpha 1
3775	5,23E-04	3,28E+00	3,36E-04	0,0842	3,5858498	0,3020964	505,88	KCNK1	potassium two pore domain channel subfamily K member 1
2530	1,43E-15	1,48E+01	5,46E-16	0,0373	8,1009072	0,3020464	9330,25	FUT8	fucosyltransferase 8
107984311	6,63E-01	1,78E-01	6,27E-01	0,6206	0,4865145	0,30195293	7,83	LOC107984	uncharacterized LOC107984311
102724122	2,83E-01	5,48E-01	2,45E-01	0,2597	1,1619649	0,30181822	45,47	LOC102724	uncharacterized LOC102724122
10018	6,80E-04	3,17E+00	4,41E-04	0,0858	3,5144833	0,30160081	554,21	BCL2L11	BCL2 like 11
101929289	4,83E-01	3,16E-01	4,42E-01	0,3918	0,7694516	0,30150574	19,86	LOC101929	289
55171	7,43E-05	4,13E+00	4,47E-05	0,0738	4,0818443	0,30114882	712,53	TBCCD1	TBCC domain containing 1
105374118	5,20E-01	2,84E-01	4,78E-01	0,4248	0,7089573	0,30113811	17,41	LOC105374	uncharacterized LOC105374118
9747	2,60E-09	8,59E+00	1,24E-09	0,0495	6,0750937	0,3008166	2304,56	TCAF1	TRPM8 channel associated factor 1
643136	1,24E-02	1,91E+00	8,93E-03	0,115	2,6145625	0,30076583	272,49	ZC3H11B	zinc finger CCCH-type containing 11B
64146	7,95E-05	4,10E+00	4,79E-05	0,074	4,0656356	0,30073772	715,23	PDF	peptide deformylase, mitochondrial
23168	2,17E-09	8,66E+00	1,03E-09	0,0493	6,1044594	0,30069714	4612,98	RTF1	RTF1 homolog, Paf1/RNA polymerase II complex component
23033	1,27E-05	4,90E+00	7,27E-06	0,067	4,485691	0,30066754	950,6	DOP1A	DOP1 leucine zipper like protein A
9472	2,21E-02	1,66E+00	1,64E-02	0,1253	2,400115	0,30065585	208,8	AKAP6	A-kinase anchoring protein 6
105376026	5,19E-01	2,85E-01	4,77E-01	0,4228	0,7110771	0,30065199	16,96	LOC105376	uncharacterized LOC105376026
105375914	2,65E-01	5,77E-01	2,29E-01	0,2497	1,2038222	0,30059848	50,13	LOC105375	uncharacterized LOC105375914
59349	1,35E-08	7,87E+00	6,65E-09	0,0518	5,7996277	0,30059079	2034,82	KLHL12	kelch like family member 12
5144	8,81E-07	6,06E+00	4,73E-07	0,0597	5,0368424	0,30057866	1810,44	PDE4D	phosphodiesterase 4D
79788	1,81E-01	7,42E-01	1,52E-01	0,2098	1,4322289	0,30048012	81,85	ZNF665	zinc finger protein 665
105369725	5,90E-01	2,29E-01	5,51E-01	0,5035	0,5965546	0,30038304	12,45	LOC105369	uncharacterized LOC105369725
11198	2,66E-13	1,26E+01	1,09E-13	0,0404	7,4300294	0,30016282	23160,74	SUPT16H	SPT16 homolog, facilitates chromatin remodeling subunit
5393	1,67E-11	1,08E+01	7,25E-12	0,0438	6,8526694	0,3000155	4401,6	EXOSC9	exosome component 9
80864	5,36E-03	2,27E+00	3,75E-03	0,1035	2,8988619	0,29994523	303,87	EGFL8	EGF like domain multiple 8
57142	5,67E-09	8,25E+00	2,74E-09	0,0504	5,9465885	0,29974515	16726,75	RTN4	reticulon 4
55278	3,99E-05	4,40E+00	2,36E-05	0,0709	4,2279171	0,29965745	846,9	QRSL1	glutaminyl-tRNA amidotransferase subunit QRSL1
7699	3,53E-04	3,45E+00	2,23E-04	0,0812	3,6908889	0,29954274	554,21	ZNF140	zinc finger protein 140
105376748	6,36E-01	1,97E-01	5,99E-01	0,5689	0,5264603	0,29952412	9,61	NEMP2-DT	NEMP2 divergent transcript
400745	5,50E-03	2,26E+00	3,85E-03	0,1036	2,8902212	0,29939577	400,59	SH2D5	SH2 domain containing 5
102723741	3,72E-01	4,29E-01	3,32E-01	0,3084	0,9707915	0,29937657	32,72	LINC02863	long intergenic non-protein coding RNA 2863
107984139	3,24E-01	4,89E-01	2,85E-01	0,2799	1,0695343	0,29934241	40,79	LOC107984	replaced by ID 100289333
283547	2,40E-01	6,20E-01	2,06E-01	0,2364	1,2659066	0,29920562	58,37	LINC00639	long intergenic non-protein coding RNA 639
55030	1,08E-08	7,97E+00	5,25E-09	0,0512	5,8389447	0,29869652	2313,72	FBXO34	F-box protein 34
8939	5,59E-10	9,25E+00	2,58E-10	0,0472	6,3219306	0,29869405	5102,21	FUBP3	far upstream element binding protein 3

5256	3,78E-05	4,42E+00	2,23E-05	0,0704	4,2402229	0,29868503	812,63	PHKA2	phosphorylase kinase regulatory subunit alpha 2
9180	6,73E-12	1,12E+01	2,89E-12	0,0428	6,9831925	0,29854052	7791,94	OSMR	oncostatin M receptor
1111	3,97E-08	7,40E+00	1,99E-08	0,0532	5,6131526	0,29843564	4016,86	CHEK1	checkpoint kinase 1
5713	1,01E-12	1,20E+01	4,24E-13	0,0412	7,2478062	0,29842548	9359,94	PSMD7	proteasome 26S subunit, non-ATPase 7
29940	8,66E-07	6,06E+00	4,65E-07	0,0592	5,0402028	0,298299	1307,02	DSE	dermatan sulfate epimerase
259295	5,30E-01	2,76E-01	4,89E-01	0,4308	0,6919101	0,29807172	16,08	TAS2R20	taste 2 receptor member 20
83479	1,15E-06	5,94E+00	6,22E-07	0,0598	4,9843001	0,29806483	1207,59	DDX59	DEAD-box helicase 59
10475	5,65E-09	8,25E+00	2,72E-09	0,0501	5,9474005	0,29802489	2120,89	TRIM38	tripartite motif containing 38
51164	1,16E-10	9,94E+00	5,20E-11	0,0453	6,5650766	0,29771522	3934,07	DCTN4	dynactin subunit 4
23353	3,70E-12	1,14E+01	1,57E-12	0,0421	7,0678453	0,2975885	6297,13	SUN1	Sad1 and UNC84 domain containing 1
1490	2,17E-11	1,07E+01	9,50E-12	0,0437	6,8139089	0,29749973	10261,1	CCN2	cellular communication network factor 2
8560	5,83E-07	6,23E+00	3,10E-07	0,0581	5,1170246	0,29742645	6304,77	DEGS1	delta 4-desaturase, sphingolipid 1
8161	2,11E-06	5,68E+00	1,16E-06	0,0611	4,8628326	0,29734591	1570,19	COIL	coilin
2958	3,20E-06	5,49E+00	1,77E-06	0,0622	4,7782547	0,29732501	2098,4	GTF2A2	general transcription factor IIA subunit 2
9317	1,27E-05	4,90E+00	7,30E-06	0,0663	4,4848935	0,29719324	991,86	PTER	phosphotriesterase related
100133161	6,46E-02	1,19E+00	5,08E-02	0,1521	1,9530515	0,2969921	146,71	LINC01001	long intergenic non-protein coding RNA 1001
51752	5,26E-13	1,23E+01	2,17E-13	0,0405	7,3376631	0,2968939	6515,26	ERAP1	endoplasmic reticulum aminopeptidase 1
84750	7,23E-04	3,14E+00	4,69E-04	0,0848	3,4976186	0,29665613	498,82	FUT10	fucosyltransferase 10
55003	8,05E-10	9,09E+00	3,74E-10	0,0473	6,2643147	0,29638941	3085,78	PAK1IP1	PAK1 interacting protein 1
23165	5,44E-13	1,23E+01	2,25E-13	0,0404	7,3331049	0,29615755	7613,92	NUP205	nucleoporin 205
80863	3,63E-02	1,44E+00	2,77E-02	0,1344	2,2020639	0,29605834	175,67	PRRT1	proline rich transmembrane protein 1
25949	2,80E-06	5,55E+00	1,54E-06	0,0616	4,8056749	0,296044	2787,86	SYF2	SYF2 pre-mRNA splicing factor
7574	9,47E-04	3,02E+00	6,20E-04	0,0864	3,4227954	0,29577322	499,49	ZNF26	zinc finger protein 26
219749	1,09E-03	2,96E+00	7,17E-04	0,0874	3,3830858	0,29575381	534,74	ZNF25	zinc finger protein 25
55216	8,98E-10	9,05E+00	4,19E-10	0,0473	6,2468718	0,29570481	3526,4	NKAPD1	NKAP domain containing 1
101927151	1,14E-03	2,94E+00	7,49E-04	0,0877	3,3709398	0,29565252	475,94	LINC02987	long intergenic non-protein coding RNA 2987
501	3,52E-10	9,45E+00	1,61E-10	0,0462	6,3942244	0,295605	5760,63	ALDH7A1	aldehyde dehydrogenase 7 family member A1
55268	9,45E-06	5,02E+00	5,38E-06	0,0649	4,5494863	0,29512054	976,63	ECHDC2	enoyl-CoA hydratase domain containing 2
100506639	8,23E-03	2,08E+00	5,86E-03	0,1071	2,7557904	0,29501794	291,38	LOC100506(	uncharacterized LOC100506639
162517	6,40E-01	1,94E-01	6,03E-01	0,5664	0,5207738	0,29494033	9,53	FBXO39	F-box protein 39
26206	4,00E-01	3,98E-01	3,58E-01	0,3211	0,918493	0,29492084	29,67	SPAG8	sperm associated antigen 8
100526694	3,32E-06	5,48E+00	1,84E-06	0,0618	4,77022	0,29468873	1192,35	MSANTD3-T	MSANTD3-TMEFF1 readthrough
3416	9,12E-10	9,04E+00	4,26E-10	0,0472	6,2443542	0,29462606	2680,48	IDE	insulin degrading enzyme
6634	8,02E-12	1,11E+01	3,44E-12	0,0423	6,9582773	0,29452528	7725,58	SNRPD3	small nuclear ribonucleoprotein D3 polypeptide
387895	3,70E-01	4,32E-01	3,29E-01	0,3019	0,9755652	0,29448098	33,35	LINC00944	long intergenic non-protein coding RNA 944
6550	2,71E-03	2,57E+00	1,84E-03	0,0945	3,1148937	0,29444157	394,81	SLC9A3	solute carrier family 9 member A3
8932	3,87E-11	1,04E+01	1,71E-11	0,0437	6,7291699	0,29436051	3928,56	MBD2	methyl-CpG binding domain protein 2
100506084	2,87E-02	1,54E+00	2,15E-02	0,128	2,2984642	0,29418889	205,62	ARL17B	ADP ribosylation factor like GTPase 17B
25861	3,20E-02	1,49E+00	2,42E-02	0,1305	2,2543066	0,29407854	215,15	WHRN	whirlin
36	1,18E-05	4,93E+00	6,76E-06	0,0653	4,5011455	0,29402957	975,04	ACADSB	acyl-CoA dehydrogenase short/branched chain
100125288	3,70E-01	4,32E-01	3,29E-01	0,3014	0,9754145	0,29401431	32,93	ZGLP1	zinc finger GATA like protein 1
375056	5,16E-10	9,29E+00	2,38E-10	0,0464	6,3344783	0,29379439	4679,39	MIA3	MIA SH3 domain ER export factor 3
3553	2,79E-08	7,55E+00	1,39E-08	0,0517	5,6748954	0,29347662	2385,72	IL1B	interleukin 1 beta
9414	1,05E-12	1,20E+01	4,39E-13	0,0405	7,2430527	0,29343585	7629,17	TJP2	tight junction protein 2
110006322	4,12E-04	3,39E+00	2,62E-04	0,0803	3,6499147	0,29314115	648,62	PKD1P5-LO(	PKD1P5-LOC105376752 readthrough
57149	1,30E-04	3,89E+00	7,95E-05	0,0743	3,9459675	0,29302538	825,07	LYRM1	LYR motif containing 1
105370333	2,73E-02	1,56E+00	2,05E-02	0,1263	2,3176513	0,29277984	199,68	PCCA-DT	PCCA divergent transcript
115908	1,51E-01	8,21E-01	1,25E-01	0,191	1,5330489	0,29274539	85,43	CTHRC1	collagen triple helix repeat containing 1
90957	1,25E-06	5,90E+00	6,78E-07	0,0589	4,9674875	0,29268486	1416,3	DHX57	DExH-box helicase 57
100874002	2,05E-01	6,88E-01	1,73E-01	0,2148	1,362097	0,29263249	68,77	OXCT1-AS1	OXCT1 antisense RNA 1
57599	4,67E-10	9,33E+00	2,15E-10	0,0461	6,3502857	0,29255629	2943,09	WDR48	WD repeat domain 48
105373582	6,21E-01	2,07E-01	5,83E-01	0,5323	0,5492822	0,29237091	10,47	LOC105373(	uncharacterized LOC105373582
729156	5,27E-03	2,28E+00	3,68E-03	0,1006	2,9044505	0,29209172	339,58	GTF2IRD1P	GTF2I repeat domain containing 1 pseudogene 1
51244	5,17E-05	4,29E+00	3,08E-05	0,0701	4,1677686	0,29195602	977,02	CCDC174	coiled-coil domain containing 174
100189589	4,52E-01	3,45E-01	4,11E-01	0,3543	0,8229673	0,29155713	24,25	DCTN1-AS1	DCTN1 antisense RNA 1
127428	6,81E-05	4,17E+00	4,08E-05	0,0711	4,1027665	0,29153067	945,78	TCEANC2	transcription elongation factor A N-terminal and central domain containing 2
254827	3,54E-01	4,51E-01	3,14E-01	0,2895	1,0069801	0,29152329	40,86	NAALADL2	N-acetylated alpha-linked acidic dipeptidase like 2
107984837	8,10E-03	2,09E+00	5,75E-03	0,1056	2,7616119	0,29150013	319,96	LOC107984	837
56951	3,34E-06	5,48E+00	1,85E-06	0,0611	4,7691102	0,2913622	4606,53	C5orf15	chromosome 5 open reading frame 15
7553	9,93E-06	5,00E+00	5,67E-06	0,0642	4,5385209	0,29123853	1125,89	ZNF7	zinc finger protein 7
105372712	1,81E-02	1,74E+00	1,33E-02	0,1176	2,4749151	0,29096548	252,07	LINC02970	long intergenic non-protein coding RNA 2970
7270	2,12E-05	4,67E+00	1,23E-05	0,0666	4,371602	0,29094531	1195,01	TTF1	transcription termination factor 1
123207	5,77E-06	5,24E+00	3,24E-06	0,0625	4,6548036	0,29093146	1160,59	C15orf40	chromosome 15 open reading frame 40
113612	1,94E-05	4,71E+00	1,13E-05	0,0662	4,3915771	0,29092461	1058,58	CYP2U1	cytochrome P450 family 2 subfamily U member 1
340527	2,57E-01	5,90E-01	2,21E-01	0,2378	1,2231355	0,29090105	59,04	NHSL2	NHS like 2
55188	4,39E-07	6,36E+00	2,32E-07	0,0562	5,1715601	0,29087681	1758,48	RIC8B	RIC8 guanine nucleotide exchange factor B
81839	5,30E-10	9,28E+00	2,45E-10	0,0459	6,3303539	0,29080324	3484,62	VANGL1	VANGL planar cell polarity protein 1
57523	5,53E-01	2,57E-01	5,12E-01	0,4437	0,6549598	0,29058473	16,17	NYNRIN	NYN domain and retroviral integrase containing
51176	1,28E-03	2,89E+00	8,49E-04	0,0871	3,3361553	0,29054185	527,64	LEF1	lymphoid enhancer binding factor 1
79613	1,46E-05	4,84E+00	8,39E-06	0,0652	4,4549242	0,29041119	1050,3	TANGO6	transport and golgi organization 6 homolog
55331	2,84E-07	6,55E+00	1,48E-07	0,0553	5,2545286	0,29038342	1838,62	ACER3	alkaline ceramidase 3
55346	4,10E-06	5,39E+00	2,28E-06	0,0614	4,726615	0,29016971	1426,54	TCP11L1	t-complex 11 like 1
100873954	5,74E-03	2,24E+00	4,03E-03	0,1009	2,876192	0,29015519	340,7	SNRK-AS1	SNRK antisense RNA 1
90417	1,80E-08	7,74E+00	8,90E-09	0,0504	5,7504637	0,29009059	3932,78	KNSTRN	kinetochore localized astrin (SPAG5) binding protein
397	3,76E-07	6,42E+00	1,98E-07	0,0557	5,2014043	0,28962637	8967,01	ARHGDIB	Rho GDP dissociation inhibitor beta
440603	6,14E-01	2,12E-01	5,75E-01	0,5167	0,5601825	0,28944275	12,5	BCL2L15	BCL2 like 15
27184	5,68E-01	2,46E-01	5,27E-01	0,4579	0,6318851	0,28934411	14,19	DISC2	disrupted in schizophrenia 2
148423	6,43E-06	5,19E+00	3,62E-06	0,0624	4,631985	0,2891958	1114,38	C1orf52	chromosome 1 open reading frame 52
91683	2,10E-01	6,78E-01	1,78E-01	0,2146	1,3473422	0,28914309	65,88	SYT12	synaptotagmin 12
146059	1,75E-03	2,76E+00	1,17E-03	0,089	3,2453861	0,28883926	488,42	CDAN1	codanin 1
81689	1,62E-07	6,79E+00	8,39E-08	0,0539	5,3584869	0,28862358	2078,18	ISCA1	iron-sulfur cluster assembly 1
144108	6,47E-07	6,19E+00	3,45E-07	0,0566	5,0970393	0,28837659	2214,65	SPTY2D1	SPT2 chromatin protein domain containing 1
123263	2,30E-03	2,64E+00	1,56E-03	0,0911	3,1641996	0,28836697	471,3	MTFMT	mitochondrial methionyl-tRNA formyltransferase
9879	2,34E-08	7,63E+00	1,16E-08	0,0505	5,7051243	0,28835309	13340,44	DDX46	DEAD-box helicase 46
105371450	2,50E-01	6,02E-01	2,14E-01	0,2322	1,2413581	0,28824821	55,31	THBS3-AS1	THBS3 antisense RNA 1
146057	1,86E-05	4,73E+00	1,08E-05	0,0655	4,4008859	0,28815835	976,9	TTBK2	tau tubulin kinase 2
96610	5,62E-05	4,25E+00	3,35E-05	0,0695	4,1482685	0,28812576	830,69	BMS1P20	BMS1 pseudogene 20
901	1,90E-05	4,72E+00	1,10E-05	0,0655	4,3958534	0,28808219	1334,38	CCNG2	cyclin G2
26994	1,80E-06	5,74E+00	9,86E-07	0,0588	4,8944655	0,28802567	2895,65	RNF11	ring finger protein 11
4076	1,26E-14	1,39E+01	4,95E-15	0,0368	7,8281197	0,28783995	21860,46	CAPRIN1	cell cycle associated protein 1
95681	5,23E-05	4,28E+00	3,11E-05	0,0691	4,1649883	0,28774316	911,29	CEP41	centrosomal protein 41
79027	8,59E-07	6,07E+00	4,61E-07	0,0571	5,0419444	0,28767357	1550,97	ZNF655	zinc finger protein 655
283267	1,24E-02	1,91E+00	8,96E-03	0,11	2,6135975	0,28751934	273,95	LINC00294	long intergenic non-protein coding RNA 294
79822	9,62E-02	1,02E+00	7,75E-02	0,1628	1,7655721	0,28744984	119,92	ARHGAP28	Rho GTPase activating protein 28
8451	1,11E-09	8,95E+00	5,19E-10	0,0462	6,2133152	0,28734111	4654,58	CUL4A	cullin 4A
51611	5,55E-08	7,26E+00	2,80E-08	0,0517	5,5536181	0,28733432	2161,83	DPH5	diphthamide biosynthesis 5
107984858	1,58E-02	1,80E+00	1,15E-02	0,1137	2,5270303	0,28726803	263,94	CENPN-AS1	CENPN antisense RNA 1
375035	1,47E-05	4,83E+00	8,50E-06	0,0645	4,452304	0,2872218	1442,86	SFT2D2	SFT2 domain containing 2
7626	1,74E-03	2,76E+00	1,17E-03	0,0885	3,246994	0,28721509	482,01	ZNF75D	zinc finger protein 75D
1602	3,31E-01	4,80E-01	2,92E-01	0,2723	1,0544896	0,28710067	47,35	DACH1	dachshund family transcription factor 1
140460	2,22E-04	3,65E+00	1,38E-04	0,0752	3,8114493	0,28658809	682,39	ASB7	ankyrin repeat and SOCS box containing 7
64083	3,04E-10	9,52E+00	1,39E-10	0,0446	6,4169827	0,28624134	3915,53	GOLPH3	golgi phosphoprotein 3
102724105	2,40E-02	1,62E+00	1,78E-02	0,1208	2,3687343	0,28620799	223,85	ZNF528-AS1	ZNF528 antisense RNA 1
51668	5,16E-08	7,29E+00	2,60E-08	0,0514	5,5664793	0,28618754	2121,27	HSPB11	heat shock protein family B (small) member 11
93	1,25E-03	2,90E+00	8,28E-04	0,0856	3,3431431	0,28615685	520,98	ACVR2B	activin A receptor type 2B
26005	8,38E-07	6,08E+00	4,49E-07	0,0567	5,0468428	0,28605574	1865,52	C2CD3	C2 domain containing 3 centriole elongation regulator
101930105	3,77E-01	4,24E-01	3,36E-01	0,2975	0,961457	0,28602469	33,84	FAM239A	zinc finger protein 839 pseudogene
195827	1,81E-04	3,74E+00	1,12E-04	0,074	3,863193	0,28599417	788,73	PRXL2C	peroxiredoxin like 2C
10427	3,57E-09	8,45E+00	1,71E-09	0,0474	6,023455	0,28579794	3034,78	SEC24B	SEC24 homolog B, COPII coat complex component
22803	2,51E-13	1,26E+01	1,02E-13	0,0384	7,437719	0,28578176	11498,88	XRN2	5'-3' exoribonuclease 2
24138	2,49E-07	6,60E+00	1,30E-07	0,0541	5,2789224	0,2855041	1782,76	IFIT5	interferon induced protein with tetratricopeptide repeats 5
55212	3,55E-06	5,45E+00	1,97E-06	0,06	4,7561651	0,28537639	1284,91	BBS7	Bardet-Biedl syndrome 7
7111	6,14E-03	2,21E+00	4,32E-03	0,1	2,8540365	0,2852864	378,43	TMOD1	tropomodulin 1
144165	1,52E-04	3,82E+00	9,35E-05	0,073	3,9069871	0,2852667	764,65	PRICKLE1	prickle planar cell polarity protein 1
64288	2,95E-02	1,53E+00	2,22E-02	0,1247	2,2873779	0,2852349	211,06	ZSCAN31	zinc finger and SCAN domain containing 31
1291	1,40E-09	8,85E+00	6,61E-10	0,0461	6,175268	0,28449729	5202,3	COL6A1	collagen type VI alpha 1 chain
147837	2,10E-02	1,68E+00	1,55E-02	0,1175	2,4202796	0,28446967	308,68	ZNF563	zinc finger protein 563
10336	1,14E-07	6,94E+00	5,83E-08	0,0524	5,4240405	0,28446154	1950,14	PCGF3	polycomb group ring finger 3
55705	1,98E-13	1,27E+01	8,06E-14	0,0381	7,469393	0,28431503	9081,55	IPO9	importin 9
8420	1,27E-06	5,90E+00	6,91E-07	0,0573	4,9638561	0,28429506	2697,91	SNHG3	small nucleolar RNA host gene 3

7555	5,74E-12	1,12E+01	2,46E-12	0,0406	7,0057892	0,28426584	13037,74	CNBP	CCHC-type zinc finger nucleic acid binding protein
79966	1,39E-04	3,86E+00	8,50E-05	0,0723	3,9299265	0,28413264	724,42	SCD5	stearoyl-CoA desaturase 5
107986153	3,23E-01	4,91E-01	2,84E-01	0,2649	1,0723709	0,28407295	48,56	LOC107986153	
6080	3,79E-01	4,21E-01	3,38E-01	0,2965	0,9578481	0,2840221	33,79	SNORA73A	small nucleolar RNA, H/ACA box 73A
101927837	4,03E-01	3,95E-01	3,62E-01	0,3116	0,9112287	0,28395124	34,76	ATP6V0D1-D	ATP6V0D1 divergent transcript
25895	1,51E-02	1,82E+00	1,10E-02	0,1116	2,543157	0,28383534	277,83	EEF1AKMT3	EEF1A lysine methyltransferase 3
9453	1,36E-06	5,87E+00	7,36E-07	0,0573	4,9515568	0,28353624	1405,55	GGPS1	geranylgeranyl diphosphate synthase 1
100507600	2,01E-01	6,97E-01	1,70E-01	0,2064	1,3723507	0,28330955	78,87	LCT-AS1	LCT antisense RNA 1
105369632	2,68E-01	5,72E-01	2,31E-01	0,2366	1,1968825	0,2831603	57,26	LOC105369632	uncharacterized LOC105369632
1398	3,19E-11	1,05E+01	1,40E-11	0,0419	6,7577019	0,2829838	5858,61	CRK	CRK proto-oncogene, adaptor protein
100	8,68E-02	1,06E+00	6,94E-02	0,1557	1,815959	0,2827523	130,06	ADA	adenosine deaminase
93587	4,04E-03	2,39E+00	2,79E-03	0,0945	2,9902763	0,28254389	378,2	TRMT10A	tRNA methyltransferase 10A
107985360	4,09E-01	3,88E-01	3,68E-01	0,3136	0,8999968	0,28220656	30,99	LOC107985360	uncharacterized LOC107985360
79943	1,72E-03	2,76E+00	1,15E-03	0,0868	3,2505146	0,28219705	489,34	ZNF696	zinc finger protein 696
6733	2,24E-07	6,65E+00	1,16E-07	0,0532	5,2991366	0,2818902	1876,31	SRPK2	SRSF protein kinase 2
27005	5,84E-05	4,23E+00	3,48E-05	0,0681	4,1393756	0,28173627	1115,74	USP21	ubiquitin specific peptidase 21
11102	7,66E-06	5,12E+00	4,34E-06	0,0613	4,5945267	0,28170522	1105,83	RPP14	ribonuclease P/MRP subunit p14
400952	3,64E-01	4,39E-01	3,24E-01	0,2853	0,987254	0,2816532	37,43	LINC01121	long intergenic non-protein coding RNA 1121
29127	8,89E-12	1,11E+01	3,83E-12	0,0405	6,9433798	0,28127367	9436,41	RACGAP1	Rac GTPase activating protein 1
26872	6,54E-04	3,18E+00	4,23E-04	0,0798	3,5250711	0,28123161	746,66	STEAP1	STEAP family member 1
10294	1,58E-07	6,80E+00	8,17E-08	0,0524	5,3634288	0,28112591	4417,93	DNAJA2	DnaJ heat shock protein family (Hsp40) member A2
101929357	3,43E-04	3,46E+00	2,17E-04	0,076	3,6985948	0,28108134	839,33	HP09053	uncharacterized LOC101929357
1353	2,41E-06	5,62E+00	1,32E-06	0,0581	4,8364505	0,28100402	2041,33	COX11	cytochrome c oxidase copper chaperone COX11
50809	1,07E-07	6,97E+00	5,49E-08	0,0517	5,4347167	0,28097129	11870,33	HP1BP3	heterochromatin protein 1 binding protein 3
100289561	1,74E-01	7,59E-01	1,45E-01	0,1929	1,4568163	0,28095367	81,66	LOC100289561	uncharacterized LOC100289561
10112	8,62E-08	7,06E+00	4,39E-08	0,0513	5,4743581	0,2809198	11534,9	KIF20A	kinesin family member 20A
2055	3,11E-03	2,51E+00	2,12E-03	0,0914	3,0725853	0,28090675	507,15	CLN8	CLN8 transmembrane ER and ERGIC protein
25879	9,59E-08	7,02E+00	4,90E-08	0,0515	5,4550435	0,28078983	4813,93	DCAF13	DDB1 and CUL4 associated factor 13
101060195	1,08E-01	9,67E-01	8,72E-02	0,1641	1,7106089	0,28075565	114,94	FCF1P2	FCF1 pseudogene 2
641808	5,10E-01	2,92E-01	4,68E-01	0,3867	0,7259029	0,28067246	20,15	FAM185BP	family with sequence similarity 185, member A pseudogene
100506747	5,09E-01	2,93E-01	4,67E-01	0,3856	0,7269725	0,28034414	22,01	MGAT4FP	MGAT4 family member F, pseudogene
85463	7,35E-08	7,13E+00	3,73E-08	0,0509	5,5031746	0,28029742	3262,32	ZC3H12C	zinc finger CCCH-type containing 12C
107986114	2,01E-01	6,97E-01	1,70E-01	0,2036	1,3732809	0,27966367	73,44	NEPRO-AS1	NEPRO antisense RNA 1
5073	1,94E-07	6,71E+00	1,00E-07	0,0525	5,326031	0,27964421	1893,78	PARN	poly(A)-specific ribonuclease
9	1,29E-02	1,89E+00	9,33E-03	0,1075	2,599712	0,27939369	299,57	NAT1	N-acetyltransferase 1
55239	8,84E-09	8,05E+00	4,29E-09	0,0476	5,8724672	0,27929125	3032,77	OGFOD1	2-oxoglutarate and iron dependent oxygenase domain containing 1
55719	1,32E-07	6,88E+00	6,81E-08	0,0517	5,3962207	0,27913663	3301,39	SLF2	SMC5-SMC6 complex localization factor 2
100302736	1,58E-05	4,80E+00	9,14E-06	0,0629	4,4366759	0,2790779	1092,75	TMED7-TICA	TMED7-TICAM2 readthrough
54897	3,05E-02	1,52E+00	2,30E-02	0,1226	2,2733957	0,27872736	224,39	CASZ1	castor zinc finger 1
1965	9,42E-13	1,20E+01	3,93E-13	0,0384	7,2580447	0,27871534	11697,54	EIF2S1	eukaryotic translation initiation factor 2 subunit alpha
23174	3,10E-05	4,51E+00	1,82E-05	0,065	4,2857533	0,27851	1139,63	ZCCHC14	zinc finger CCHC-type containing 14
79838	6,13E-03	2,21E+00	4,31E-03	0,0975	2,8545964	0,27845256	363,49	TMC5	transmembrane channel like 5
100847026	5,88E-01	2,31E-01	5,49E-01	0,4641	0,5997404	0,27836622	14,22	MIR5006	microRNA 5006
6427	3,35E-12	1,15E+01	1,42E-12	0,0393	7,0818365	0,2783516	8292,41	SRSF2	serine and arginine rich splicing factor 2
441381	4,54E-02	1,34E+00	3,50E-02	0,132	2,1081847	0,27833768	186,68	LRRC24	leucine rich repeat containing 24
2107	6,60E-12	1,12E+01	2,83E-12	0,0398	6,985953	0,27833411	11831,23	ETF1	eukaryotic translation termination factor 1
5359	7,32E-05	4,14E+00	4,40E-05	0,0681	4,0855975	0,27827811	1080,63	PLSCR1	phospholipid scramblase 1
27236	3,96E-07	6,40E+00	2,09E-07	0,0536	5,1912433	0,2782688	2267,13	ARFIP1	ADP ribosylation factor interacting protein 1
23508	2,60E-03	2,59E+00	1,76E-03	0,0889	3,1275818	0,27789972	448,3	TTC9	tetratricopeptide repeat domain 9
79007	9,63E-03	2,02E+00	6,90E-03	0,1028	2,7016726	0,27775056	317,45	DBNDD1	dysbindin domain containing 1
84676	4,02E-01	3,96E-01	3,61E-01	0,3041	0,9130307	0,27762919	32,69	TRIM63	tripartite motif containing 63
10024	8,07E-06	5,09E+00	4,57E-06	0,0605	4,5833924	0,27735062	2546,77	TROAP	trophinin associated protein
57452	3,23E-01	4,91E-01	2,84E-01	0,2587	1,0718617	0,27728299	48,91	GALNT16	polypeptide N-acetylgalactosaminyltransferase 16
9684	9,03E-05	4,04E+00	5,46E-05	0,0687	4,0348828	0,27721147	1036,74	LRRC14	leucine rich repeat containing 14
100129940	3,12E-01	5,06E-01	2,73E-01	0,2527	1,09688	0,27718151	48,96	HMGA2-AS1	HMGA2 antisense RNA 1
10671	2,58E-05	4,59E+00	1,51E-05	0,064	4,3273413	0,27692579	1634,14	DCTN6	dynactin subunit 6
107985524	2,69E-01	5,70E-01	2,33E-01	0,2319	1,1937748	0,27686924	56,94	LOC107985524	uncharacterized LOC107985524
27316	1,52E-11	1,08E+01	6,58E-12	0,0403	6,8664402	0,27672944	15219,33	RBMX	RNA binding motif protein X-linked
10279	2,68E-01	5,72E-01	2,31E-01	0,2311	1,1972081	0,27669892	60,77	PRSS16	serine protease 16
3373	5,86E-01	2,32E-01	5,46E-01	0,4581	0,603817	0,2765789	14,87	HYAL1	hyaluronidase 1
105371084	2,39E-04	3,62E+00	1,50E-04	0,0729	3,7917758	0,27632934	1023,75	RSL1D1-DT	RSL1D1 divergent transcript
84561	7,63E-02	1,12E+00	6,06E-02	0,1471	1,876547	0,27595361	155,73	SLC12A8	solute carrier family 12 member 8
26140	6,65E-02	1,18E+00	5,24E-02	0,1422	1,9400258	0,27586905	160,42	TTLL3	tubulin tyrosine ligase like 3
5128	1,45E-06	5,84E+00	7,91E-07	0,0559	4,9375757	0,27585063	1996,18	CDK17	cyclin dependent kinase 17
54107	1,48E-09	8,83E+00	6,96E-10	0,0447	6,1669132	0,27581479	8571,31	POLE3	DNA polymerase epsilon 3, accessory subunit
5451	4,24E-05	4,37E+00	2,51E-05	0,0654	4,2142036	0,27570277	965,26	POU2F1	POU class 2 homeobox 1
25847	5,11E-06	5,29E+00	2,86E-06	0,0589	4,6802753	0,27561111	1564,55	ANAPC13	anaphase promoting complex subunit 13
26118	7,86E-08	7,10E+00	4,00E-08	0,0502	5,4910122	0,27557232	3142,26	WSB1	WD repeat and SOCS box containing 1
26747	1,36E-04	3,87E+00	8,30E-05	0,0699	3,9356074	0,27520646	815,5	NUFIP1	nuclear FMR1 interacting protein 1
81550	4,87E-05	4,31E+00	2,89E-05	0,0658	4,1817294	0,27518192	993,09	TDRD3	tudor domain containing 3
102724250	4,88E-08	7,31E+00	2,45E-08	0,0493	5,5765481	0,27514542	2328,54	LOC102724	neuroblastoma breakpoint family member 1-like
11276	1,08E-06	5,97E+00	5,82E-07	0,0551	4,9970918	0,2751427	1835,03	SYNRG	synergin gamma
93663	2,54E-08	7,60E+00	1,26E-08	0,0483	5,6909254	0,27503126	4235,4	ARHGAP18	Rho GTPase activating protein 18
91370	4,56E-02	1,34E+00	3,52E-02	0,1305	2,1064734	0,27495329	202,38	LIF-AS2	LIF antisense RNA 2
23759	1,20E-05	4,92E+00	6,89E-06	0,0611	4,4970453	0,27485188	1533,63	PPIL2	peptidylprolyl isomerase like 2
81786	3,23E-01	4,91E-01	2,84E-01	0,2564	1,0716054	0,27480573	47,41	TRIM7	tripartite motif containing 7
10228	1,47E-06	5,83E+00	8,00E-07	0,0557	4,9353994	0,27478266	1964,06	STX6	syntaxin 6
107984219	4,86E-04	3,31E+00	3,11E-04	0,076	3,6057784	0,2738776	746,31	LOC107984	uncharacterized LOC107984219
2309	2,55E-06	5,59E+00	1,40E-06	0,0568	4,8243928	0,27384996	1501,92	FOXO3	forkhead box O3
100885848	2,37E-01	6,25E-01	2,03E-01	0,2147	1,2740783	0,2735868	65,79	PTGES3L	prostaglandin E synthase 3 like
8725	1,05E-09	8,98E+00	4,93E-10	0,044	6,2213478	0,27348577	3684,73	URI1	URI1 prefoldin like chaperone
80307	4,70E-01	3,28E-01	4,29E-01	0,3456	0,7910344	0,27341271	25,04	FER1L4	fer-1 like family member 4 (pseudogene)
54545	2,18E-08	7,66E+00	1,08E-08	0,0478	5,7176296	0,27337328	2672,55	MTMR12	myotubularin related protein 12
128497	4,02E-01	3,96E-01	3,61E-01	0,2991	0,9134985	0,2732284	34,73	SPATA25	spermatogenesis associated 25
56128	1,76E-01	7,54E-01	1,47E-01	0,1881	1,4499024	0,27278721	87,63	PCDHB8	protocadherin beta 8
57148	5,17E-09	8,29E+00	2,49E-09	0,0457	5,9622236	0,27276789	5642,23	RALGAPB	Ral GTPase activating protein non-catalytic subunit beta
102725068	2,85E-01	5,45E-01	2,47E-01	0,2357	1,1569661	0,27274226	56,13	MICB-DT	MICB divergent transcript
101927574	4,98E-01	3,03E-01	4,56E-01	0,3659	0,7448793	0,27254898	22,7	LINC01186	long intergenic non-protein coding RNA 1186
139425	5,93E-01	2,27E-01	5,55E-01	0,4611	0,5909161	0,27244298	14,86	DCAF8L1	DDB1 and CUL4 associated factor 8 like 1
57585	3,52E-05	4,45E+00	2,08E-05	0,064	4,2565982	0,2724034	1088,82	CRAMP1	cramped chromatin regulator homolog 1
51631	2,57E-08	7,59E+00	1,28E-08	0,0478	5,6893145	0,27219199	3132,49	LUC7L2	LUC7 like 2, pre-mRNA splicing factor
54558	5,77E-01	2,39E-01	5,37E-01	0,4412	0,6168434	0,27214913	15,01	SPATA6	spermatogenesis associated 6
11340	1,33E-07	6,88E+00	6,84E-08	0,0504	5,3953044	0,2721445	2130,7	EXOSC8	exosome component 8
5791	1,28E-05	4,89E+00	7,38E-06	0,0607	4,4825681	0,27206741	1389,81	PTPRE	protein tyrosine phosphatase receptor type E
148304	1,14E-02	1,94E+00	8,25E-03	0,1029	2,6416701	0,27188702	319,61	C1orf74	chromosome 1 open reading frame 74
107986458	3,12E-01	5,06E-01	2,73E-01	0,2478	1,0963006	0,27166079	51,53	LOC107986	uncharacterized LOC107986458
54832	4,57E-05	4,34E+00	2,71E-05	0,0647	4,1966007	0,27156358	1075,1	VPS13C	vacuolar protein sorting 13 homolog C
55959	1,22E-02	1,91E+00	8,82E-03	0,1037	2,618887	0,27153365	316,34	SULF2	sulfatase 2
79954	5,82E-09	8,24E+00	2,81E-09	0,0457	5,9424557	0,27131921	3293,89	NOL10	nucleolar protein 10
2730	7,20E-07	6,14E+00	3,85E-07	0,0534	5,0762981	0,27128812	2298,34	GCLM	glutamate-cysteine ligase modifier subunit
100533182	5,85E-01	2,33E-01	5,45E-01	0,448	0,6051611	0,27110307	14,97	SEC24B-AS	SEC24B antisense RNA 1
102724865	3,89E-01	4,10E-01	3,47E-01	0,2883	0,9395205	0,27081804	39,14	LOC102724	replaced by ID 100420178
11339	1,07E-02	1,97E+00	7,69E-03	0,1016	2,6655643	0,27079236	428,08	OIP5	Opa interacting protein 5
100533195	2,53E-01	5,97E-01	2,17E-01	0,2193	1,2341288	0,2706359	65,8	FAM24B-CU	FAM24B-CUZD1 readthrough
10247	3,63E-03	2,44E+00	2,50E-03	0,0895	3,023444	0,27051815	482,43	RIDA	reactive intermediate imine deaminase A homolog
26136	1,17E-07	6,93E+00	6,01E-08	0,0499	5,4183668	0,27028766	2914,94	TES	testin LIM domain protein
5071	5,01E-01	3,00E-01	4,59E-01	0,3646	0,7410413	0,27014676	23,93	PRKN	parkin RBR E3 ubiquitin protein ligase
8906	1,09E-05	4,96E+00	6,23E-06	0,0597	4,5184465	0,26991634	1799,18	AP1G2	adaptor related protein complex 1 subunit gamma 2
51510	1,59E-06	5,80E+00	8,68E-07	0,0549	4,9195228	0,26991212	4770,55	CHMP5	charged multivesicular body protein 5
55790	2,39E-02	1,62E+00	1,78E-02	0,1139	2,3699315	0,26987622	252,21	CSGALNACT	chondroitin sulfate N-acetylgalactosaminyltransferase 1
388695	2,78E-02	1,56E+00	2,08E-02	0,1167	2,3112957	0,26980509	261,51	LYSMD1	LysM domain containing 1
100130827	3,93E-01	4,06E-01	3,52E-01	0,29	0,9303845	0,26977547	36,63	SBK3	SH3 domain binding kinase family member 3
79960	7,12E-07	6,15E+00	3,81E-07	0,0531	5,0784362	0,26971478	2161,52	JADE1	jade family PHD finger 1
145407	7,14E-03	2,15E+00	5,05E-03	0,0962	2,8039889	0,26960784	362,62	ARMH4	armadillo like helical domain containing 4
105373785	6,11E-01	2,14E-01	5,72E-01	0,477	0,5648384	0,26942936	13,89	LOC105373	uncharacterized LOC105373785
222658	2,35E-13	1,26E+01	9,56E-14	0,0362	7,4468226	0,26931526	15163,67	KCTD20	potassium channel tetramerization domain containing 20
105379566	6,89E-01	1,62E-01	6,54E-01	0,6007	0,4480679	0,2691635	8,19	LOC105379	endogenous retrovirus group K member 18 Pol protein-like
157697	1,29E-03	2,89E+00	8,56E-04	0,0807	3,333919	0,26914683	668,72	ERICH1	glutamate rich 1
158234	1,35E-04	3,87E+00	8,27E-05	0,0683	3,9363246	0,26865616	818,91	TRMT10B	tRNA methyltransferase 10B
10140	6,85E-05	4,16E+00	4,11E-05	0,0655	4,1012867	0,26847252	977,97	TOB1	transducer of ERBB2, 1

51118	8,97E-08	7,05E+00	4,57E-08	0,0491	5,4671994	0,26830222	4207,45	UTP11	UTP11 small subunit processome component
58492	7,85E-02	1,11E+00	6,24E-02	0,1438	1,8636955	0,26806985	158,61	ZNF77	zinc finger protein 77
54469	3,72E-06	5,43E+00	2,07E-06	0,0565	4,7465133	0,26800684	1997,24	ZFAND6	zinc finger AN1-type containing 6
100873985	3,93E-01	4,06E-01	3,51E-01	0,2876	0,9318074	0,26799461	38,26	MED14OS	MED14 opposite strand
4810	5,17E-04	3,29E+00	3,32E-04	0,0746	3,58928	0,26771315	691,72	NHS	NHS actin remodeling regulator
5728	2,33E-07	6,63E+00	1,21E-07	0,0505	5,2915315	0,26747558	2883,44	PTEN	phosphatase and tensin homolog
4162	3,39E-10	9,47E+00	1,55E-10	0,0418	6,4002784	0,26738152	7161,2	MCAM	melanoma cell adhesion molecule
645431	1,31E-01	8,83E-01	1,07E-01	0,1658	1,6095774	0,26693169	116,02	FUT8-AS1	FUT8 antisense RNA 1
26059	1,70E-01	7,70E-01	1,42E-01	0,1814	1,4682946	0,26638478	91,89	ERC2	ELKS/RAB6-interacting/CAST family member 2
8050	4,53E-07	6,34E+00	2,40E-07	0,0516	5,1654452	0,26631385	2452,37	PDHX	pyruvate dehydrogenase complex component X
401149	1,25E-01	9,03E-01	1,02E-01	0,163	1,6333197	0,26628499	134,26	LINC01061	long intergenic non-protein coding RNA 1061
51057	6,33E-02	1,20E+00	4,97E-02	0,1355	1,9624322	0,26590155	189,71	WDPCP	WD repeat containing planar cell polarity effector
710	3,24E-01	4,89E-01	2,85E-01	0,2485	1,0697474	0,26582298	49,94	SERPING1	serpin family G member 1
101928371	5,05E-02	1,30E+00	3,92E-02	0,1288	2,0623699	0,26557658	192,21	LOC101928	uncharacterized LOC101928371
27249	4,54E-02	1,34E+00	3,50E-02	0,1257	2,1082678	0,26504148	3893,01	MMADHC	metabolism of cobalamin associated D
102724474	7,13E-01	1,47E-01	6,80E-01	0,6433	0,411797	0,26489173	8,22	LOC102724	WAS/WASL-interacting protein family member 2-like
102723922	6,18E-01	2,09E-01	5,80E-01	0,4783	0,5538295	0,26487055	13,1	LOC102723	922
4734	4,08E-10	9,39E+00	1,88E-10	0,0415	6,3710883	0,26463631	4521,83	NEDD4	NEDD4 E3 ubiquitin protein ligase
107986265	1,02E-01	9,91E-01	8,20E-02	0,1521	1,7389979	0,26451154	156,08	LOC107986	265
55591	1,56E-09	8,81E+00	7,34E-10	0,0429	6,1585798	0,26415556	4852,77	VEZT	vezatin, adherens junctions transmembrane protein
3329	5,59E-10	9,25E+00	2,59E-10	0,0417	6,3218061	0,26389454	24285,62	HSPD1	heat shock protein family D (Hsp60) member 1
80380	7,83E-03	2,11E+00	5,55E-03	0,095	2,7729974	0,26353376	413,37	PDCD1LG2	programmed cell death 1 ligand 2
25977	1,02E-05	4,99E+00	5,85E-06	0,0581	4,5316623	0,26340647	1655,94	NECAP1	NECAP endocytosis associated 1
55227	6,77E-04	3,17E+00	4,38E-04	0,0749	3,5158406	0,26327066	713,35	LRRC1	leucine rich repeat containing 1
9924	3,72E-05	4,43E+00	2,19E-05	0,062	4,2442288	0,26325068	1102,42	PAN2	poly(A) specific ribonuclease subunit PAN2
339287	1,65E-09	8,78E+00	7,81E-10	0,0428	6,1488205	0,26318788	4127,04	MSL1	MSL complex subunit 1
1270	1,93E-01	7,14E-01	1,63E-01	0,1884	1,3956131	0,26297648	85,07	CNTF	ciliary neurotrophic factor
105369780	8,81E-02	1,06E+00	7,06E-02	0,1453	1,8082564	0,2628088	188,03	LOC105369	780
4116	4,01E-06	5,40E+00	2,23E-06	0,0555	4,7311058	0,26266606	3869,96	MAGOH	mago homolog, exon junction complex subunit
100131244	6,94E-01	1,59E-01	6,60E-01	0,5966	0,4402858	0,26265861	8,99	ANKRD63	ankyrin repeat domain 63
139322	7,89E-04	3,10E+00	5,14E-04	0,0755	3,4735511	0,26216369	869,56	APOOL	apolipoprotein O like
9909	1,27E-05	4,90E+00	7,27E-06	0,0584	4,4857412	0,26208669	1771,36	DENND4B	DENN domain containing 4B
9559	4,20E-08	7,38E+00	2,11E-08	0,0467	5,603092	0,2616887	4551,96	VPS26A	VPS26 retromer complex component A
4548	3,48E-06	5,46E+00	1,93E-06	0,055	4,7603951	0,26168707	2969,7	MTR	5-methyltetrahydrofolate-homocysteine methyltransferase
221718	2,71E-01	5,67E-01	2,34E-01	0,2196	1,1904943	0,26145356	66,04	LINC00518	long intergenic non-protein coding RNA 518
493869	1,51E-07	6,82E+00	7,79E-08	0,0487	5,3718423	0,2613515	3467,48	GPX8	glutathione peroxidase 8 (putative)
10576	1,17E-09	8,93E+00	5,50E-10	0,0421	6,2040291	0,26131021	14595,52	CCT2	chaperonin containing TCP1 subunit 2
105369557	2,01E-01	6,97E-01	1,70E-01	0,1905	1,3714712	0,26120433	104,71	TIRAP-AS1	TIRAP antisense RNA 1
4337	9,68E-08	7,01E+00	4,95E-08	0,0479	5,4532644	0,26097915	3451,02	MOCS1	molybdenum cofactor synthesis 1
54552	2,05E-07	6,69E+00	1,06E-07	0,0491	5,315396	0,2608341	2925,21	GNL3L	G protein nucleolar 3 like
25814	8,68E-10	9,06E+00	4,04E-10	0,0417	6,2524008	0,26078358	5473,45	ATXN10	ataxin 10
107984413	8,64E-02	1,06E+00	6,90E-02	0,1433	1,8182152	0,2604981	155,57	LOC107984	uncharacterized LOC107984413
3484	3,73E-06	5,43E+00	2,07E-06	0,0549	4,7463638	0,26041949	1762,79	IGFBP1	insulin like growth factor binding protein 1
101928649	5,60E-02	1,25E+00	4,37E-02	0,129	2,0171659	0,26014388	197,43	CTC-338M12	uncharacterized LOC101928649
4673	1,37E-10	9,86E+00	6,18E-11	0,0398	6,5393397	0,25995053	39949,02	NAP1L1	nucleosome assembly protein 1 like 1
4216	3,47E-06	5,46E+00	1,93E-06	0,0546	4,760852	0,25983136	1826,76	MAP3K4	mitogen-activated protein kinase kinase kinase 4
100131067	2,63E-02	1,58E+00	1,96E-02	0,1114	2,3330026	0,25980951	269,71	CKMT2-AS1	CKMT2 antisense RNA 1
57685	4,98E-03	2,30E+00	3,47E-03	0,0889	2,9226568	0,25974654	431,97	CACHD1	cache domain containing 1
5929	3,05E-06	5,52E+00	1,69E-06	0,0541	4,787788	0,25916928	1793,76	RBBP5	RB binding protein 5, histone lysine methyltransferase complex subunit
100506368	4,51E-01	3,46E-01	4,10E-01	0,3144	0,8236843	0,25898038	32,09	FZD4-DT	FZD4 divergent transcript
221527	4,79E-04	3,32E+00	3,06E-04	0,0717	3,6098821	0,25893881	893,12	ZBTB12	zinc finger and BTB domain containing 12
5395	1,41E-04	3,85E+00	8,65E-05	0,0659	3,9256553	0,2586053	1023,74	PMS2	PMS1 homolog 2, mismatch repair system component
105374715	4,21E-02	1,38E+00	3,23E-02	0,1208	2,1404184	0,25847	254,96	LOC105374	uncharacterized LOC105374715
55759	6,25E-08	7,20E+00	3,16E-08	0,0467	5,5321703	0,25845709	2755,51	WDR12	WD repeat domain 12
159013	1,93E-06	5,71E+00	1,06E-06	0,0529	4,8807788	0,25843078	1837,22	CXorf38	chromosome X open reading frame 38
79668	1,69E-05	4,77E+00	9,77E-06	0,0584	4,4222543	0,25837511	1432,26	PARP8	poly(ADP-ribose) polymerase family member 8
9892	1,90E-01	7,21E-01	1,60E-01	0,1838	1,4051589	0,25831446	89,52	SNAP91	synaptosome associated protein 91
5481	1,13E-06	5,95E+00	6,08E-07	0,0518	4,988581	0,25819824	2668,22	PPID	peptidylprolyl isomerase D
55255	4,51E-07	6,35E+00	2,39E-07	0,0499	5,1662129	0,25776011	2394,5	WDR41	WD repeat domain 41
105370062	3,83E-01	4,17E-01	3,42E-01	0,271	0,9510626	0,25775765	42,72	LOC105370	uncharacterized LOC105370062
360	2,78E-03	2,56E+00	1,89E-03	0,083	3,1065113	0,25774895	528,57	AQP3	aquaporin 3 (Gill blood group)
26354	4,12E-08	7,39E+00	2,06E-08	0,046	5,6066512	0,25768777	10930,14	GNL3	G protein nucleolar 3
113402	1,72E-01	7,64E-01	1,44E-01	0,1762	1,4619497	0,25754586	1534,45	SFT2D1	SFT2 domain containing 1
10714	2,72E-06	5,57E+00	1,50E-06	0,0535	4,8113645	0,25747578	2798,36	POLD3	DNA polymerase delta 3, accessory subunit
23076	2,40E-09	8,62E+00	1,14E-09	0,0422	6,0885801	0,25713013	4367,44	RRP1B	ribosomal RNA processing 1B
3097	3,91E-06	5,41E+00	2,18E-06	0,0542	4,7363564	0,25687162	2441,71	HIVEP2	HIVEP zinc finger 2
84105	2,94E-03	2,53E+00	2,00E-03	0,0831	3,0897182	0,25674975	522,14	PCBD2	pterin-4 alpha-carbinolamine dehydratase 2
84190	4,28E-02	1,37E+00	3,28E-02	0,1202	2,133968	0,25659362	239,97	METTL25	methyltransferase like 25
55064	6,62E-01	1,79E-01	6,25E-01	0,5255	0,4881167	0,25649407	10,83	SPATA6L	spermatogenesis associated 6 like
101927267	2,78E-01	5,56E-01	2,41E-01	0,2185	1,1733621	0,25633495	66,52	TROAP-AS1	TROAP and PRPH antisense RNA 1
107984986	9,03E-02	1,04E+00	7,24E-02	0,1426	1,7967121	0,25629155	153,3	LOC107984	986
80818	8,85E-05	4,05E+00	5,35E-05	0,0634	4,0396358	0,25607468	1001,67	ZNF436	zinc finger protein 436
109951030	2,37E-03	2,63E+00	1,60E-03	0,0811	3,1551319	0,25601025	666,59	PKD1P3-NPI	PKD1P3-NPIPA1 readthrough
8542	2,66E-04	3,58E+00	1,67E-04	0,068	3,7643322	0,25594281	888,32	APOL1	apolipoprotein L1
8634	8,13E-06	5,09E+00	4,61E-06	0,0559	4,5818555	0,25590572	2475,49	RTCA	RNA 3'-terminal phosphate cyclase
4907	6,71E-09	8,17E+00	3,25E-09	0,0432	5,9185448	0,25589323	28307,05	NT5E	5'-nucleotidase ecto
7566	8,76E-02	1,06E+00	7,01E-02	0,1413	1,8113236	0,25588359	167,29	ZNF18	zinc finger protein 18
10412	7,47E-08	7,13E+00	3,79E-08	0,0465	5,5003343	0,25587234	6506,61	NSA2	NSA2 ribosome biogenesis factor
84747	4,96E-06	5,30E+00	2,77E-06	0,0546	4,686905	0,25571954	2264,97	UNC119B	unc-119 lipid binding chaperone B
100505687	4,39E-04	3,36E+00	2,80E-04	0,0703	3,6330734	0,255512	795,16	LINC00888	long intergenic non-protein coding RNA 888
84953	1,91E-01	7,19E-01	1,61E-01	0,1822	1,40144	0,25535572	93,28	MICALCL	replaced by ID 9645
5090	6,01E-05	4,22E+00	3,59E-05	0,0618	4,1324667	0,25534153	1080,06	PBX3	PBX homeobox 3
55332	3,76E-06	5,42E+00	2,09E-06	0,0538	4,7447195	0,25530495	1899,01	DRAM1	DNA damage regulated autophagy modulator 1
1615	1,41E-08	7,85E+00	6,92E-09	0,0441	5,7928534	0,25518957	5760,66	DARS1	aspartyl-tRNA synthetase 1
8672	1,10E-07	6,96E+00	5,62E-08	0,047	5,430633	0,25500001	7807,36	EIF4G3	eukaryotic translation initiation factor 4 gamma 3
101929950	8,08E-02	1,09E+00	6,43E-02	0,1377	1,849929	0,2546905	166,19	LOC101929	puromycin-sensitive aminopeptidase-like protein
57096	1,58E-01	8,01E-01	1,31E-01	0,1686	1,508677	0,25436923	109,21	RPGRIP1	RPGR interacting protein 1
51535	2,54E-07	6,60E+00	1,32E-07	0,0482	5,2758957	0,25413884	2394,24	PPHLN1	periphilin 1
7905	8,11E-09	8,09E+00	3,94E-09	0,0431	5,8868808	0,2534956	6596,42	REEP5	receptor accessory protein 5
89781	2,86E-04	3,54E+00	1,80E-04	0,0677	3,7456211	0,25340093	1314,26	HPS4	HPS4 biogenesis of lysosomal organelles complex 3 subunit 2
123879	3,70E-03	2,43E+00	2,55E-03	0,0839	3,0176652	0,25309601	516,05	DCUN1D3	defective in cullin neddylation 1 domain containing 3
1781	8,91E-08	7,05E+00	4,54E-08	0,0463	5,4683611	0,25297374	6086,37	DYNC1I2	dynein cytoplasmic 1 intermediate chain 2
54328	6,63E-02	1,18E+00	5,22E-02	0,1302	1,9411757	0,25267687	207,81	GPR173	G protein-coupled receptor 173
9129	8,53E-07	6,07E+00	4,58E-07	0,0501	5,0432354	0,25243628	5181,51	PRPF3	pre-mRNA processing factor 3
4646	1,94E-06	5,71E+00	1,06E-06	0,0517	4,8795596	0,25211486	3801,5	MYO6	myosin VI
1112	7,06E-08	7,15E+00	3,58E-08	0,0457	5,5104706	0,25203501	3154,1	FOXN3	forkhead box N3
201161	1,67E-02	1,78E+00	1,22E-02	0,1004	2,5058933	0,25158303	409,39	CENPV	centromere protein V
54928	3,35E-07	6,47E+00	1,76E-07	0,0482	5,2233398	0,25157225	3976,72	BPNT2	3'(2'), 5'-bisphosphate nucleotidase 2
23064	2,59E-06	5,59E+00	1,42E-06	0,0522	4,8214844	0,25156203	3835,18	SETX	senataxin
1182	7,63E-08	7,12E+00	3,87E-08	0,0458	5,4965075	0,25155874	4756,29	CLCN3	chloride voltage-gated channel 3
6004	3,28E-01	4,84E-01	2,89E-01	0,237	1,0604189	0,25126931	56,06	RGS16	regulator of G protein signaling 16
342184	2,10E-06	5,68E+00	1,15E-06	0,0516	4,8641963	0,25112699	2428,42	FMN1	formin 1
204851	1,01E-07	7,00E+00	5,14E-08	0,0461	5,4464081	0,25105944	3565,99	HIPK1	homeodomain interacting protein kinase 1
55840	3,96E-01	4,02E-01	3,55E-01	0,2714	0,9247457	0,25099087	41,47	EAF2	ELL associated factor 2
359821	5,41E-01	2,67E-01	5,00E-01	0,3721	0,67411	0,25081557	21,5	MRPL42P5	mitochondrial ribosomal protein L42 pseudogene 5
83999	7,74E-02	1,11E+00	6,15E-02	0,134	1,86999	0,25052361	206,67	KREMEN1	kringle containing transmembrane protein 1
6905	1,64E-07	6,79E+00	8,48E-08	0,0468	5,3565565	0,25043478	2935,6	TBCE	tubulin folding cofactor E
6902	4,45E-05	4,35E+00	2,63E-05	0,0596	4,2029544	0,25043383	8580,16	TBCA	tubulin folding cofactor A
157	4,63E-02	1,33E+00	3,57E-02	0,1192	2,1001724	0,25032153	244,82	GRK3	G protein-coupled receptor kinase 3
401548	1,62E-05	4,79E+00	9,38E-06	0,0565	4,4309032	0,25020901	1568,51	SNX30	sorting nexin family member 30
617	1,22E-04	3,91E+00	7,46E-05	0,0631	3,9612029	0,25006271	1110,49	BCS1L	BCS1 homolog, ubiquinol-cytochrome c reductase complex chaperone
57654	4,18E-03	2,38E+00	2,89E-03	0,0839	2,9793932	0,25004943	531,09	UVSSA	UV stimulated scaffold protein A
5732	5,63E-01	2,49E-01	5,23E-01	0,3911	0,6391878	0,24997807	22,21	PTGER2	prostaglandin E receptor 2
197258	8,18E-02	1,09E+00	6,52E-02	0,1352	1,8437563	0,24930179	191,76	FCSK	fucose kinase
5917	4,77E-07	6,32E+00	2,53E-07	0,0483	5,1556238	0,24920238	6818,39	RARS1	arginyl-tRNA synthetase 1
105370795	2,06E-01	6,86E-01	1,74E-01	0,183	1,3585956	0,2485835	90,85	VPS39-DT	VPS39 divergent transcript
105375035	5,03E-01	2,98E-01	4,61E-01	0,3369	0,7376112	0,2485008	26,05	LOC105375	uncharacterized LOC105375035
51499	2,19E-04	3,66E+00	1,36E-04	0,0651	3,8149357	0,24846054	2032,81	TRIAP1	TP53 regulated inhibitor of apoptosis 1
8631	6,42E-01	1,92E-01	6,04E-01	0,4796	0,5179712	0,24843211	13,89	SKAP1	src kinase associated phosphoprotein 1
7528	2,11E-05	4,68E+00	1,22E-05	0,0567	4,3731612	0,24816905	5080,24	YY1	YY1 transcription factor

285500	6,99E-01	1,56E-01	6,65E-01	0,5731	0,4329475	0,24811467	9,37	AGA-DT	AGA divergent transcript
84520	2,04E-03	2,69E+00	1,37E-03	0,0775	3,1998775	0,24806972	620,32	GON7	GON7 subunit of KEOPS complex
101929397	3,89E-01	4,10E-01	3,48E-01	0,2638	0,9390072	0,24770732	43,09	LINC01518	long intergenic non-protein coding RNA 1518
10152	3,78E-08	7,42E+00	1,89E-08	0,0441	5,6215326	0,24768762	4600,01	ABI2	abl interactor 2
202374	5,30E-01	2,76E-01	4,89E-01	0,3578	0,6920355	0,24761556	24,19	STK32A	serine/threonine kinase 32A
388795	2,25E-01	6,48E-01	1,92E-01	0,1897	1,304424	0,24742767	96,14	EFCAB8	EF-hand calcium binding domain 8
7248	1,51E-05	4,82E+00	8,69E-06	0,0556	4,4475312	0,24738813	1987,46	TSC1	TSC complex subunit 1
5099	2,96E-02	1,53E+00	2,23E-02	0,1082	2,2858996	0,24731467	277,85	PCDH7	protocadherin 7
386607	2,40E-05	4,62E+00	1,40E-05	0,0569	4,3444069	0,24724678	2452,47	ZFP91-CNTF	ZFP91-CNTF readthrough (NMD candidate)
285643	3,72E-01	4,29E-01	3,31E-01	0,2543	0,9719758	0,2471404	47,45	KIF4B	kinesin family member 4B
84909	7,02E-07	6,15E+00	3,75E-07	0,0486	5,0813204	0,24711954	2378,9	AOPEP	aminopeptidase O (putative)
105374693	2,69E-01	5,70E-01	2,33E-01	0,207	1,1931162	0,24697859	81,25	LINC02211	long intergenic non-protein coding RNA 2211
101929191	4,12E-01	3,85E-01	3,71E-01	0,2759	0,8948285	0,24689338	43,38	LINC03022	long intergenic non-protein coding RNA 3022
79929	3,11E-02	1,51E+00	2,34E-02	0,1089	2,2662099	0,24681689	294,29	MAP6D1	MAP6 domain containing 1
90673	5,45E-03	2,26E+00	3,81E-03	0,0853	2,8935042	0,24680845	492	PPP1R3E	protein phosphatase 1 regulatory subunit 3E
5048	1,85E-09	8,73E+00	8,77E-10	0,0403	6,1303981	0,24676251	7688,6	PAFAH1B1	platelet activating factor acetylhydrolase 1b regulatory subunit 1
107986649	5,40E-01	2,68E-01	4,99E-01	0,3648	0,6762095	0,24671337	23,02	LOC107986649	
51320	1,30E-04	3,89E+00	7,97E-05	0,0625	3,945433	0,24666292	1489,37	MEX3C	mex-3 RNA binding family member C
151651	4,35E-02	1,36E+00	3,35E-02	0,1159	2,1264054	0,24646163	280,37	EFHB	EF-hand domain family member B
148641	2,25E-02	1,65E+00	1,67E-02	0,1029	2,3933837	0,24636088	330,9	SLC35F3	solute carrier family 35 member F3
10627	2,80E-10	9,55E+00	1,28E-10	0,0383	6,4299354	0,2462324	11312,6	MYL12A	myosin light chain 12A
4232	2,45E-03	2,61E+00	1,66E-03	0,0782	3,1457136	0,24614658	740,56	MEST	mesoderm specific transcript
10611	2,36E-07	6,63E+00	1,23E-07	0,0465	5,2895788	0,24589032	8968,29	PDLIM5	PDZ and LIM domain 5
10171	1,35E-02	1,87E+00	9,81E-03	0,0952	2,5823658	0,24587767	395,79	RCL1	RNA terminal phosphate cyclase like 1
659	7,84E-06	5,11E+00	4,44E-06	0,0536	4,5894777	0,24580324	2115,13	BMPR2	bone morphogenetic protein receptor type 2
105374306	6,05E-01	2,18E-01	5,67E-01	0,4289	0,573125	0,24578951	16,23	LOC105374306	uncharacterized LOC105374306
105369154	3,61E-02	1,44E+00	2,75E-02	0,1115	2,2039808	0,24577995	296,45	PKD1P6-NPI	PKD1P6-NPIPP1 readthrough
401431	3,64E-02	1,44E+00	2,78E-02	0,1117	2,200605	0,2457382	283,89	ATP6V0E2-A	ATP6V0E2 antisense RNA 1
129285	6,91E-04	3,16E+00	4,48E-04	0,07	3,5099741	0,24573123	844,67	PPP1R21	protein phosphatase 1 regulatory subunit 21
100874207	1,19E-01	9,24E-01	9,72E-02	0,1481	1,6585416	0,24564519	142,26	ST3GAL6-AS	ST3GAL6 antisense RNA 1
728747	7,03E-01	1,53E-01	6,69E-01	0,5748	0,4273129	0,24562975	8,94	ANKRD20A4	ankyrin repeat domain 20 family member A4, pseudogene
284339	7,32E-01	1,35E-01	7,00E-01	0,636	0,3854704	0,24514736	8,34	TMEM145	transmembrane protein 145
121260	1,98E-03	2,70E+00	1,33E-03	0,0763	3,2088598	0,24484329	919,42	SLC15A4	solute carrier family 15 member 4
10736	3,19E-02	1,50E+00	2,41E-02	0,1085	2,2548817	0,24476213	288,29	SIX2	SIX homeobox 2
128869	7,74E-04	3,11E+00	5,04E-04	0,0702	3,4784952	0,24427392	1989,57	PIGU	phosphatidylinositol glycan anchor biosynthesis class U
100534593	3,76E-04	3,42E+00	2,39E-04	0,0665	3,6740512	0,24425733	1041,18	STX16-NPEF	STX16-NPEPL1 readthrough (NMD candidate)
5684	1,05E-07	6,98E+00	5,35E-08	0,0449	5,4392599	0,24414052	5650,23	PSMA3	proteasome 20S subunit alpha 3
100272217	2,94E-01	5,32E-01	2,55E-01	0,2146	1,1371353	0,24404498	65,72	LOC100272217	uncharacterized LOC100272217
1902	1,38E-08	7,86E+00	6,77E-09	0,0421	5,7964965	0,2438393	4409,03	LPAR1	lysophosphatidic acid receptor 1
7151	4,74E-01	3,24E-01	4,32E-01	0,3102	0,7855302	0,2436325	31,44	TOP1P1	DNA topoisomerase I pseudogene 1
9218	5,20E-10	9,28E+00	2,40E-10	0,0385	6,3331414	0,24354665	9391,32	VAPA	VAMP associated protein A
23404	1,78E-07	6,75E+00	9,20E-08	0,0456	5,3418737	0,24347383	3158,02	EXOSC2	exosome component 2
7006	6,69E-03	2,17E+00	4,72E-03	0,0861	2,8256705	0,24328074	488,17	TEC	tec protein tyrosine kinase
7718	8,60E-02	1,07E+00	6,87E-02	0,1336	1,8203386	0,24326629	175,93	ZNF165	zinc finger protein 165
3437	2,93E-09	8,53E+00	1,40E-09	0,0401	6,0560308	0,24304883	6936,04	IFIT3	interferon induced protein with tetratricopeptide repeats 3
100101440	3,76E-01	4,25E-01	3,35E-01	0,2522	0,9634278	0,24293688	50,39	PMS2P7	PMS1 homolog 2, mismatch repair system component pseudogene 7
102724550	6,16E-01	2,10E-01	5,78E-01	0,4364	0,5558854	0,24258076	15,61	LINC02015	long intergenic non-protein coding RNA 2015
11222	2,50E-07	6,60E+00	1,30E-07	0,0459	5,2786188	0,24248182	4856,49	MRPL3	mitochondrial ribosomal protein L3
4539	4,36E-07	6,36E+00	2,30E-07	0,0469	5,1730927	0,24247168	40874,15	ND4L	NADH dehydrogenase subunit 4L
115825	8,49E-04	3,07E+00	5,54E-04	0,0701	3,4530628	0,24193925	994,78	WDFY2	WD repeat and FYVE domain containing 2
54148	1,94E-05	4,71E+00	1,13E-05	0,055	4,3908607	0,24168551	1938,38	MRPL39	mitochondrial ribosomal protein L39
100996928	2,58E-06	5,59E+00	1,42E-06	0,0501	4,8219277	0,2415605	3085,79	FMC1-LUC7	FMC1-LUC7L2 readthrough
64172	2,15E-02	1,67E+00	1,59E-02	0,1001	2,410573	0,24131218	372,29	OSGEPL1	O-sialoglycoprotein endopeptidase like 1
102723716	6,66E-01	1,77E-01	6,30E-01	0,4999	0,481297	0,24059116	12,08	LOC102723716	uncharacterized LOC102723716
80011	1,27E-07	6,90E+00	6,55E-08	0,0445	5,4032302	0,24044378	3878,08	PSME3IP1	proteasome activator subunit 3 interacting protein 1
9031	1,70E-07	6,77E+00	8,78E-08	0,0449	5,3502963	0,24039066	8533,51	BAZ1B	bromodomain adjacent to zinc finger domain 1B
146880	9,42E-02	1,03E+00	7,57E-02	0,1353	1,7761025	0,24032877	195,37	ARHGAP27F	Rho GTPase activating protein 27 pseudogene 1
4848	1,86E-06	5,73E+00	1,02E-06	0,0491	4,8884075	0,23994598	3167,08	CNOT2	CCR4-NOT transcription complex subunit 2
113219453	2,14E-01	6,70E-01	1,81E-01	0,1794	1,3365811	0,23977043	95,84	MIR12119	microRNA 12119
92106	3,39E-05	4,47E+00	1,99E-05	0,0562	4,2658052	0,23955374	1740,82	OXNAD1	oxidoreductase NAD binding domain containing 1
9141	1,15E-07	6,94E+00	5,89E-08	0,0442	5,4219774	0,2394963	5959,12	PDCD5	programmed cell death 5
104968399	1,25E-08	7,90E+00	6,13E-09	0,0412	5,8130425	0,23948922	7965,23	MYL12-AS1	MYL12A and MYL12B antisense RNA 1
9043	3,17E-08	7,50E+00	1,58E-08	0,0424	5,6522075	0,23946256	7849,68	SPAG9	sperm associated antigen 9
3843	2,00E-08	7,70E+00	9,88E-09	0,0418	5,7327141	0,23943776	21017,92	IPO5	importin 5
55791	3,72E-04	3,43E+00	2,36E-04	0,065	3,6769634	0,23915135	1176,68	LRIF1	ligand dependent nuclear receptor interacting factor 1
9373	1,07E-07	6,97E+00	5,46E-08	0,044	5,4357721	0,23913179	3813,95	PLAA	phospholipase A2 activating protein
171220	1,40E-01	8,54E-01	1,16E-01	0,1518	1,573458	0,23890194	151	DSTNP2	DSTN pseudogene 2
140711	1,93E-02	1,71E+00	1,42E-02	0,0974	2,4520696	0,23883552	372,04	TLDC2	TBC/LysM-associated domain containing 2
8833	7,66E-08	7,12E+00	3,89E-08	0,0435	5,4957227	0,23881388	6032,24	GMPS	guanine monophosphate synthase
478	5,68E-02	1,25E+00	4,43E-02	0,1188	2,0108766	0,23879406	263,68	ATP1A3	ATPase Na+/K+ transporting subunit alpha 3
374920	6,34E-04	3,20E+00	4,10E-04	0,0676	3,5335523	0,23878037	1210,79	ZSWIM9	zinc finger SWIM-type containing 9
6434	1,04E-08	7,98E+00	5,09E-09	0,0408	5,8443592	0,23871528	9235,43	TRA2B	transformer 2 beta homolog
168667	1,40E-02	1,85E+00	1,02E-02	0,0928	2,5700328	0,23843951	422,61	BMPER	BMP binding endothelial regulator
83700	5,66E-01	2,47E-01	5,26E-01	0,3759	0,6342066	0,23842614	21,13	JAM3	junctional adhesion molecule 3
83440	6,39E-06	5,19E+00	3,60E-06	0,0514	4,633184	0,23836674	2438,37	ADPGK	ADP dependent glucokinase
94027	6,48E-01	1,88E-01	6,11E-01	0,4682	0,5083887	0,23800635	13,51	CGB7	chorionic gonadotropin subunit beta 7
8528	2,33E-01	6,33E-01	1,99E-01	0,1854	1,2831131	0,23792334	88,76	DDO	D-aspartate oxidase
147081	1,53E-02	1,82E+00	1,11E-02	0,0936	2,5389563	0,23760718	421,85	LINC02210	long intergenic non-protein coding RNA 2210
57213	1,23E-03	2,91E+00	8,14E-04	0,0709	3,3480794	0,23744026	844,1	SPRYD7	SPRY domain containing 7
26019	3,96E-06	5,40E+00	2,20E-06	0,0501	4,7337859	0,23731678	2563,8	UPF2	UPF2 regulator of nonsense mediated mRNA decay
23172	1,56E-05	4,81E+00	9,00E-06	0,0534	4,4398813	0,23724576	1724,25	ABRAXAS2	abraxas 2, BRISC complex subunit
283104	1,58E-02	1,80E+00	1,15E-02	0,0939	2,5258122	0,23724084	435,66	SBF2-AS1	SBF2 antisense RNA 1
11191	4,51E-01	3,46E-01	4,09E-01	0,2871	0,8251223	0,23688169	37,81	PTENP1	phosphatase and tensin homolog pseudogene 1
253190	2,35E-01	6,29E-01	2,01E-01	0,1851	1,2795273	0,23681523	90,28	SERHL2	serine hydrolase like 2
4869	1,87E-08	7,73E+00	9,21E-09	0,0412	5,7446479	0,23671658	99478,54	NPM1	nucleophosmin 1
10885	8,47E-08	7,07E+00	4,32E-08	0,0432	5,4774384	0,23664184	5591,17	WDR3	WD repeat domain 3
1662	1,09E-06	5,96E+00	5,88E-07	0,0474	4,9949552	0,23652942	6427,94	DDX10	DEAD-box helicase 10
374786	1,73E-01	7,62E-01	1,45E-01	0,162	1,4587313	0,23631832	118,89	EFCAB5	EF-hand calcium binding domain 5
391712	1,96E-01	7,08E-01	1,65E-01	0,1703	1,386955	0,23618222	106,72	TRIM61	tripartite motif containing 61
100288162	4,14E-01	3,83E-01	3,72E-01	0,2647	0,8922315	0,23616775	42,12	LOC100288	uncharacterized LOC100288162
130752	4,30E-01	3,67E-01	3,88E-01	0,2734	0,8627976	0,23590885	41,92	MDH1B	malate dehydrogenase 1B
105377424	6,37E-01	1,96E-01	6,00E-01	0,4487	0,5250458	0,2355648	15,28	LINC02377	long intergenic non-protein coding RNA 2377
56681	6,01E-08	7,22E+00	3,04E-08	0,0425	5,539255	0,23542441	6968,57	SAR1A	secretion associated Ras related GTPase 1A
387032	2,58E-02	1,59E+00	1,92E-02	0,1005	2,3410062	0,23536762	434,39	ZKSCAN4	zinc finger with KRAB and SCAN domains 4
400945	6,67E-01	1,76E-01	6,31E-01	0,4888	0,4808583	0,23506598	12,86	LINC01376	long intergenic non-protein coding RNA 1376
10935	8,28E-08	7,08E+00	4,21E-08	0,0429	5,4816457	0,23495496	8434,99	PRDX3	peroxiredoxin 3
60491	1,12E-05	4,95E+00	6,41E-06	0,0521	4,5123518	0,23494893	1940,02	NIF3L1	NGG1 interacting factor 3 like 1
22944	5,66E-03	2,25E+00	3,96E-03	0,0814	2,8813432	0,23464655	599,67	KIN	Kin17 DNA and RNA binding protein
728695	1,95E-07	6,71E+00	1,01E-07	0,044	5,3250087	0,23435603	5627,79	SPANXB1	SPANX family member B1
8614	5,48E-01	2,61E-01	5,08E-01	0,3537	0,6624406	0,23432168	25,66	STC2	stanniocalcin 2
57110	2,44E-01	6,13E-01	2,10E-01	0,1865	1,2547817	0,23404931	94,32	PLAAT1	phospholipase A and acyltransferase 1
1826	2,15E-01	6,68E-01	1,82E-01	0,1749	1,3340637	0,23329631	107,44	DSCAM	DS cell adhesion molecule
23092	1,52E-04	3,82E+00	9,38E-05	0,0595	3,9059875	0,23236129	1517,53	ARHGAP26	Rho GTPase activating protein 26
9955	4,51E-01	3,46E-01	4,10E-01	0,2818	0,8244842	0,23236046	41,33	HS3ST3A1	heparan sulfate-glucosamine 3-sulfotransferase 3A1
353376	3,05E-02	1,52E+00	2,30E-02	0,1022	2,2729602	0,23223077	329,84	TICAM2	TIR domain containing adaptor molecule 2
23658	3,31E-04	3,48E+00	2,09E-04	0,0625	3,707708	0,23164865	1545,42	LSM5	LSM5 homolog, U6 small nuclear RNA and mRNA degradation associated
100996437	7,21E-01	1,42E-01	6,88E-01	0,5764	0,4016141	0,23147984	8,91	LOC100996	uncharacterized LOC100996437
11052	1,78E-07	6,75E+00	9,21E-08	0,0433	5,3416554	0,23145248	4339,7	CPSF6	cleavage and polyadenylation specific factor 6
25940	1,96E-07	6,71E+00	1,02E-07	0,0435	5,3233568	0,23139377	4065,35	FAM98A	family with sequence similarity 98 member A
382	2,60E-08	7,59E+00	1,29E-08	0,0407	5,6871564	0,23134831	9146,31	ARF6	ADP ribosylation factor 6
57704	6,01E-05	4,22E+00	3,59E-05	0,056	4,1325056	0,23123312	2017,95	GBA2	glucosylceramidase beta 2
8439	1,02E-05	4,99E+00	5,82E-06	0,051	4,5326625	0,23121238	2345,99	NSMAF	neutral sphingomyelinase activation associated factor
720	3,28E-01	4,84E-01	2,88E-01	0,2176	1,0619685	0,23109434	65,89	C4A	complement C4A (Rodgers blood group)
59343	5,71E-05	4,24E+00	3,41E-05	0,0557	4,1443747	0,23102398	3450,06	SENP2	SUMO specific peptidase 2
1130	5,79E-03	2,24E+00	4,06E-03	0,0803	2,873663	0,23089662	568,42	LYST	lysosomal trafficking regulator
63898	6,77E-05	4,17E+00	4,06E-05	0,0563	4,1042146	0,23088387	1542,04	SH2D4A	SH2 domain containing 4A
9692	2,53E-06	5,60E+00	1,39E-06	0,0478	4,8263004	0,23087515	2620,06	PRORP	protein only RNase P catalytic subunit
92421	7,56E-02	1,12E+00	6,00E-02	0,1226	1,8810119	0,23067362	211,27	CHMP4C	charged multivesicular body protein 4C
1503	1,96E-07	6,71E+00	1,02E-07	0,0433	5,3232026	0,23058818	7204,55	CTPS1	CTP synthase 1
54433	1,05E-03	2,98E+00	6,90E-04	0,0679	3,3934314	0,23048904	1601,39	GAR1	GAR1 ribonucleoprotein

51316	3,83E-05	4,42E+00	2,26E-05	0,0544	4,2374334	0,23041634	3150	PLAC8	placenta associated 8
102724927	3,93E-01	4,06E-01	3,51E-01	0,2471	0,9321276	0,2303267	52,2	LINC02861	long intergenic non-protein coding RNA 2861
26234	6,72E-05	4,17E+00	4,03E-05	0,056	4,1059971	0,23008382	3730,51	FBXL5	F-box and leucine rich repeat protein 5
401264	1,37E-02	1,86E+00	9,93E-03	0,0892	2,5782761	0,23005687	469,84	TRAM2-AS1	TRAM2 antisense RNA 1 (head to head)
9132	1,37E-01	8,63E-01	1,12E-01	0,1447	1,5870723	0,22972074	154,5	KCNQ4	potassium voltage-gated channel subfamily Q member 4
100506394	3,48E-02	1,46E+00	2,64E-02	0,1032	2,220003	0,22908112	362,48	GAS6-DT	GAS6 divergent transcript
1573	1,03E-01	9,87E-01	8,34E-02	0,1323	1,731178	0,2290743	191,97	CYP2J2	cytochrome P450 family 2 subfamily J member 2
9480	1,62E-02	1,79E+00	1,18E-02	0,0909	2,5178344	0,22896008	418,82	ONECUT2	one cut homeobox 2
51449	1,62E-07	6,79E+00	8,37E-08	0,0427	5,3589772	0,22883114	5685,01	PCYOX1	prenylcysteine oxidase 1
7159	1,88E-05	4,73E+00	1,09E-05	0,052	4,3981245	0,22878045	3753,26	TP53BP2	tumor protein p53 binding protein 2
23462	5,03E-01	2,98E-01	4,61E-01	0,3098	0,737452	0,22848877	31,76	HEY1	hes related family bHLH transcription factor with YRPW motif 1
107985897	5,84E-01	2,34E-01	5,44E-01	0,3761	0,6069729	0,22827847	22,09	LOC107985	uncharacterized LOC107985897
63910	1,80E-04	3,74E+00	1,12E-04	0,0591	3,8639855	0,22821444	2742,9	SLC17A9	solute carrier family 17 member 9
114826	4,02E-04	3,40E+00	2,56E-04	0,0624	3,6562503	0,22813367	1162,81	SMYD4	SET and MYND domain containing 4
728558	2,38E-01	6,23E-01	2,04E-01	0,1796	1,2700994	0,2280723	99,99	ENTPD1-AS	ENTPD1 antisense RNA 1
348751	3,57E-01	4,47E-01	3,16E-01	0,2275	1,0018579	0,22797252	61,1	FTCDNL1	formiminotransferase cyclodeaminase N-terminal like
103344928	7,29E-01	1,37E-01	6,97E-01	0,5847	0,3892791	0,227622	8,48	KIAA1614-AS	KIAA1614 antisense RNA 1
23218	3,77E-03	2,42E+00	2,60E-03	0,0755	3,0119516	0,22737859	1067,27	NBEAL2	neurobeachin like 2
105372884	5,52E-01	2,58E-01	5,12E-01	0,3461	0,6563932	0,22719895	25,41	LOC105372	uncharacterized LOC105372884
147949	7,75E-02	1,11E+00	6,16E-02	0,1215	1,8694652	0,22712755	236,41	ZNF583	zinc finger protein 583
130502	3,18E-02	1,50E+00	2,40E-02	0,1006	2,2564765	0,22706256	353,31	TTC32	tetratricopeptide repeat domain 32
83593	2,00E-03	2,70E+00	1,35E-03	0,0708	3,2056105	0,22691984	842,86	RASSF5	Ras association domain family member 5
80005	1,17E-05	4,93E+00	6,71E-06	0,0504	4,5028422	0,22678226	3869,66	DOCK5	dedicator of cytokinesis 5
105379152	6,13E-01	2,13E-01	5,74E-01	0,4037	0,5614922	0,22668501	18,27	PRDM6-AS1	PRDM6 antisense RNA 1
285148	5,73E-06	5,24E+00	3,22E-06	0,0487	4,6564103	0,22667944	2989,21	IAH1	isoamyl acetate hydrolyzing esterase 1 (putative)
153769	1,29E-04	3,89E+00	7,90E-05	0,0574	3,9473448	0,22653094	1502,13	SH3RF2	SH3 domain containing ring finger 2
374654	1,22E-02	1,91E+00	8,82E-03	0,0865	2,6189129	0,22645993	475,18	KIF7	kinesin family member 7
51319	3,67E-04	3,44E+00	2,33E-04	0,0614	3,680227	0,22607102	1804,35	RSRC1	arginine and serine rich coiled-coil 1
377677	4,13E-03	2,38E+00	2,85E-03	0,0757	2,9829925	0,22592907	638,85	CA13	carbonic anhydrase 13
2963	8,46E-06	5,07E+00	4,80E-06	0,0494	4,5731561	0,22581082	2879,59	GTF2F2	general transcription factor IIF subunit 2
7352	4,73E-01	3,25E-01	4,32E-01	0,2869	0,7865413	0,2256791	36,56	UCP3	uncoupling protein 3
102724907	3,78E-01	4,23E-01	3,37E-01	0,2347	0,9604911	0,22547184	55,3	CYLD-AS1	CYLD antisense RNA 1
101927759	6,51E-01	1,86E-01	6,14E-01	0,4472	0,504053	0,22541259	15,97	LOC101927	uncharacterized LOC101927759
101730217	2,29E-04	3,64E+00	1,43E-04	0,0593	3,8024692	0,225325	1393,63	SPECC1L-A	SPECC1L-ADORA2A readthrough (NMD candidate)
51065	7,68E-05	4,11E+00	4,62E-05	0,0553	4,07392	0,22522455	2037,33	RPS27L	ribosomal protein S27 like
51555	6,40E-01	1,94E-01	6,02E-01	0,4321	0,5210161	0,22511469	16,46	PEX5L	peroxisomal biogenesis factor 5 like
286	1,05E-02	1,98E+00	7,56E-03	0,0843	2,6711999	0,22507036	538,49	ANK1	ankyrin 1
196996	3,00E-01	5,23E-01	2,62E-01	0,2006	1,121952	0,22506296	75,94	GRAMD2A	GRAM domain containing 2A
267002	5,49E-02	1,26E+00	4,28E-02	0,1111	2,025907	0,22502194	272,03	PGBD2	piggyBac transposable element derived 2
8894	2,42E-08	7,62E+00	1,20E-08	0,0394	5,6996543	0,22480528	18171,85	EIF2S2	eukaryotic translation initiation factor 2 subunit beta
7763	4,86E-06	5,31E+00	2,72E-06	0,0479	4,6909689	0,22477116	6362,59	ZFAND5	zinc finger AN1-type containing 5
100874214	3,45E-01	4,62E-01	3,05E-01	0,2191	1,0252856	0,22462599	62,95	TM4SF19-AS	TM4SF19 antisense RNA 1
63931	1,40E-03	2,85E+00	9,30E-04	0,0678	3,3109288	0,22457056	924,03	MRPS14	mitochondrial ribosomal protein S14
101928059	4,65E-01	3,33E-01	4,23E-01	0,2805	0,8006009	0,22454876	38,52	LOC101928	uncharacterized LOC101928059
94234	3,13E-03	2,50E+00	2,14E-03	0,0731	3,0701434	0,22448394	1184,44	FOXQ1	forkhead box Q1
729291	2,94E-01	5,32E-01	2,56E-01	0,1977	1,1354848	0,22443717	77,2	LOC729291	uncharacterized LOC729291
64343	8,00E-05	4,10E+00	4,82E-05	0,0552	4,0641525	0,22438834	1778,05	AZI2	5-azacytidine induced 2
167555	4,11E-01	3,86E-01	3,69E-01	0,2495	0,8978495	0,2240249	51,51	FAM151B	family with sequence similarity 151 member B
285908	3,93E-01	4,06E-01	3,51E-01	0,2403	0,9317262	0,22387045	52,85	LINC00174	long intergenic non-protein coding RNA 174
105372795	7,36E-01	1,33E-01	7,04E-01	0,5891	0,3798012	0,22374189	9,29	LOC105372	replaced by ID 51227
552860	4,01E-01	3,97E-01	3,60E-01	0,2442	0,9161936	0,22370786	55,87	SAMD12-AS	SAMD12 antisense RNA 1
11212	1,24E-03	2,91E+00	8,19E-04	0,0668	3,3461459	0,22363224	992,02	PLPBP	pyridoxal phosphate binding protein
9650	9,13E-04	3,04E+00	5,97E-04	0,0651	3,4329674	0,22361417	1071,54	MTFR1	mitochondrial fission regulator 1
66008	1,01E-05	5,00E+00	5,77E-06	0,0493	4,5347725	0,2235504	2345,47	TRAK2	trafficking kinesin protein 2
2628	6,11E-01	2,14E-01	5,73E-01	0,3961	0,5641686	0,22346925	21,35	GATM	glycine amidinotransferase
84984	9,96E-03	2,00E+00	7,14E-03	0,083	2,6902905	0,22340269	511,92	CEP19	centrosomal protein 19
9516	5,90E-07	6,23E+00	3,14E-07	0,0437	5,1147688	0,22331025	4399,99	LITAF	lipopolysaccharide induced TNF factor
55813	4,22E-06	5,37E+00	2,35E-06	0,0473	4,7203162	0,22312085	4241,35	UTP6	UTP6 small subunit processome component
401612	2,77E-01	5,58E-01	2,39E-01	0,1896	1,1765629	0,22310965	103,95	SLC25A53	solute carrier family 25 member 53
51699	6,14E-07	6,21E+00	3,27E-07	0,0436	5,1071369	0,22286391	5192,19	VPS29	VPS29 retromer complex component
10159	1,76E-05	4,75E+00	1,02E-05	0,0504	4,4129256	0,22247604	3949,69	ATP6AP2	ATPase H+ transporting accessory protein 2
8546	1,33E-05	4,88E+00	7,62E-06	0,0497	4,4757126	0,22235188	5618,26	AP3B1	adaptor related protein complex 3 subunit beta 1
10694	5,22E-08	7,28E+00	2,63E-08	0,0399	5,5645635	0,22222774	21347,18	CCT8	chaperonin containing TCP1 subunit 8
79640	1,75E-03	2,76E+00	1,17E-03	0,0684	3,2449834	0,221908	2523,96	C22orf46P	CTA-216E10.6
440829	3,60E-02	1,44E+00	2,74E-02	0,1006	2,2054103	0,22184971	340,92	SHISA8	shisa family member 8
49854	1,22E-03	2,91E+00	8,03E-04	0,0662	3,3515884	0,22180381	980,09	ZBTB21	zinc finger and BTB domain containing 21
55862	8,49E-05	4,07E+00	5,13E-05	0,0547	4,049647	0,22167059	1840,31	ECHDC1	ethylmalonyl-CoA decarboxylase 1
7716	9,87E-07	6,01E+00	5,32E-07	0,0442	5,0143392	0,2216171	5759,18	VEZF1	vascular endothelial zinc finger 1
23291	1,13E-06	5,95E+00	6,13E-07	0,0444	4,9870925	0,22137677	3966,2	FBXW11	F-box and WD repeat domain containing 11
54737	2,29E-04	3,64E+00	1,43E-04	0,0582	3,8027717	0,22123322	2694,47	MPHOSPH8	M-phase phosphoprotein 8
2108	4,08E-06	5,39E+00	2,27E-06	0,0467	4,7275162	0,22099703	5597,34	ETFA	electron transfer flavoprotein subunit alpha
3676	7,11E-01	1,48E-01	6,77E-01	0,5312	0,416038	0,22098685	10,69	ITGA4	integrin subunit alpha 4
5874	5,02E-05	4,30E+00	2,98E-05	0,0529	4,1747658	0,22085584	2087,73	RAB27B	RAB27B, member RAS oncogene family
23181	1,04E-04	3,98E+00	6,32E-05	0,0552	4,0005432	0,22074663	1571,39	DIP2A	disco interacting protein 2 homolog A
65260	5,37E-06	5,27E+00	3,01E-06	0,0472	4,6699282	0,22053399	3121,27	COA7	cytochrome c oxidase assembly factor 7
26032	5,31E-04	3,27E+00	3,41E-04	0,0615	3,5819307	0,22040381	1244,75	SUSD5	sushi domain containing 5
101927655	1,10E-01	9,59E-01	8,93E-02	0,1292	1,6990197	0,21953185	194,02	ZASP	
56897	3,28E-07	6,48E+00	1,72E-07	0,042	5,2270186	0,21947046	4791,11	WRNIP1	WRN helicase interacting protein 1
114932	1,18E-05	4,93E+00	6,77E-06	0,0487	4,5006565	0,21926636	3290,99	MRFAP1L1	Morf4 family associated protein 1 like 1
5387	1,90E-01	7,21E-01	1,60E-01	0,1559	1,4060912	0,21920033	128,11	PMS2P3	PMS1 homolog 2, mismatch repair system component pseudogene 3
239	4,22E-01	3,75E-01	3,81E-01	0,2497	0,8769339	0,21900672	49,73	ALOX12	arachidonate 12-lipoxygenase, 12S type
23451	4,77E-09	8,32E+00	2,29E-09	0,0366	5,9756103	0,21875502	14596,8	SF3B1	splicing factor 3b subunit 1
161424	2,51E-04	3,60E+00	1,57E-04	0,0578	3,7798264	0,21864317	1312,84	NOP9	NOP9 nucleolar protein
100132815	4,59E-02	1,34E+00	3,54E-02	0,1039	2,1042872	0,21858346	310,23	IPO5P1	importin 5 pseudogene 1
7991	3,21E-04	3,49E+00	2,02E-04	0,0588	3,7158994	0,21857128	2486,87	TUSC3	tumor suppressor candidate 3
3223	3,41E-01	4,67E-01	3,01E-01	0,2111	1,0350412	0,21852187	72,49	HOXC6	homeobox C6
100506691	6,93E-01	1,59E-01	6,59E-01	0,4952	0,4411651	0,21848123	11,97	LINC02985	long intergenic non-protein coding RNA 2985
23568	7,61E-06	5,12E+00	4,31E-06	0,0475	4,5958718	0,21845806	2761,69	ARL2BP	ADP ribosylation factor like GTPase 2 binding protein
5682	2,58E-07	6,59E+00	1,35E-07	0,0414	5,2725726	0,21843189	11580,61	PSMA1	proteasome 20S subunit alpha 1
10794	3,62E-01	4,41E-01	3,21E-01	0,2202	0,9914939	0,21832217	90,21	ZNF460	zinc finger protein 460
23141	8,70E-06	5,06E+00	4,94E-06	0,0478	4,5671823	0,21818952	2495,53	ANKLE2	ankyrin repeat and LEM domain containing 2
57002	8,35E-03	2,08E+00	5,94E-03	0,0792	2,7511041	0,21790838	611,68	YAE1	YAE1 maturation factor of ABCE1
26152	1,34E-02	1,87E+00	9,74E-03	0,0842	2,5850495	0,21764738	558,93	ZNF337	zinc finger protein 337
3631	4,27E-04	3,37E+00	2,72E-04	0,0598	3,6401784	0,21761724	1275,71	INPP4A	inositol polyphosphate-4-phosphatase type I A
9334	1,20E-07	6,92E+00	6,14E-08	0,0402	5,4147972	0,21752566	5802,24	B4GALT5	beta-1,4-galactosyltransferase 5
23184	1,48E-05	4,83E+00	8,56E-06	0,0487	4,4507471	0,21695615	3570,25	MESD	mesoderm development LRP chaperone
63922	3,27E-03	2,49E+00	2,24E-03	0,0709	3,0564053	0,21677909	1118,98	CHTF18	chromosome transmission fidelity factor 18
102723701	3,13E-01	5,04E-01	2,74E-01	0,1983	1,0929909	0,21676933	81,79	LOC102723	uncharacterized LOC102723701
101929174	7,22E-01	1,41E-01	6,89E-01	0,542	0,3996756	0,21660476	10,27	LOC101929	uncharacterized LOC101929174
100533106	8,19E-03	2,09E+00	5,82E-03	0,0785	2,7576053	0,21660197	787,73	ZHX1-C8orf7	ZHX1-C8orf76 readthrough
219	4,72E-05	4,33E+00	2,80E-05	0,0517	4,189068	0,21655577	2341,41	ALDH1B1	aldehyde dehydrogenase 1 family member B1
163351	7,34E-01	1,34E-01	7,02E-01	0,566	0,3820225	0,21620637	9,35	GBP6	guanylate binding protein family member 6
125919	6,93E-02	1,16E+00	5,48E-02	0,1126	1,9207207	0,21619511	264,95	ZNF543	zinc finger protein 543
27148	4,55E-03	2,34E+00	3,16E-03	0,0732	2,9516233	0,21619352	727,01	STK36	serine/threonine kinase 36
100134868	1,87E-01	7,28E-01	1,57E-01	0,1528	1,413836	0,21608668	153,46	LOC100134	uncharacterized LOC100134868
441124	8,57E-02	1,07E+00	6,84E-02	0,1184	1,8221845	0,21575963	227,61	GTF2IP20	general transcription factor IIi pseudogene 20
80237	1,77E-01	7,52E-01	1,48E-01	0,149	1,4474906	0,21572794	139,37	ELL3	elongation factor for RNA polymerase II 3
5892	5,92E-03	2,23E+00	4,15E-03	0,0752	2,8664025	0,21567036	663,93	RAD51D	RAD51 paralog D
55672	6,02E-06	5,22E+00	3,39E-06	0,0464	4,6458939	0,2153381	2901,31	NBPF1	NBPF member 1
2222	1,26E-05	4,90E+00	7,22E-06	0,048	4,4869576	0,21524546	3890,29	FDFT1	farnesyl-diphosphate farnesyltransferase 1
105369547	5,48E-01	2,61E-01	5,07E-01	0,324	0,6634888	0,21494341	28,06	CCDC15-DT	CCDC15 divergent transcript
101927330	4,96E-01	3,05E-01	4,54E-01	0,2872	0,7484567	0,21492497	36,07	LOC101927	uncharacterized LOC101927330
6941	3,62E-07	6,44E+00	1,90E-07	0,0412	5,2084981	0,21480335	6519,33	TCF19	transcription factor 19
30849	3,60E-04	3,44E+00	2,28E-04	0,0583	3,6853886	0,21471388	1504,32	PIK3R4	phosphoinositide-3-kinase regulatory subunit 4
112268195	3,50E-01	4,56E-01	3,10E-01	0,2112	1,0159709	0,21458522	69,2	LOC112268	195
80279	1,94E-05	4,71E+00	1,13E-05	0,0488	4,3908968	0,2144794	3647,66	CDK5RAP3	CDK5 regulatory subunit associated protein 3
26289	1,73E-01	7,62E-01	1,45E-01	0,1467	1,4586078	0,21392053	170,42	AK5	adenylate kinase 5
729515	7,03E-02	1,15E+00	5,56E-02	0,1117	1,9141904	0,21383535	281,41	TMEM242	transmembrane protein 242
105373456	5,13E-01	2,90E-01	4,71E-01	0,2965	0,7208235	0,21374713	36,31	LOC105373	uncharacterized LOC105373456
84901	7,45E-05	4,13E+00	4,48E-05	0,0523	4,0813954	0,21359391	2066,23	NFATC2IP	nuclear factor of activated T cells 2 interacting protein

102466877	5,40E-01	2,68E-01	5,00E-01	0,3162	0,675181	0,21350715	29,3	MIR8072	microRNA 8072
4152	3,50E-05	4,46E+00	2,06E-05	0,05	4,2581925	0,21296379	2794,23	MBD1	methyl-CpG binding domain protein 1
2622	3,56E-03	2,45E+00	2,44E-03	0,0703	3,0301266	0,21296317	1004,31	GAS8	growth arrest specific 8
22871	5,11E-02	1,29E+00	3,96E-02	0,1035	2,0574845	0,21285234	383,07	NLGN1	neuroligin 1
55693	1,37E-01	8,63E-01	1,12E-01	0,1341	1,5871759	0,21284571	185,02	KDM4D	lysine demethylase 4D
5431	4,31E-08	7,37E+00	2,16E-08	0,038	5,5986227	0,21284209	12291,69	POLR2B	RNA polymerase II subunit B
339044	3,56E-03	2,45E+00	2,45E-03	0,0702	3,029755	0,21280171	892,78	PKD1P1	polycystin 1, transient receptor potential channel interacting pseudogene 1
10478	1,09E-03	2,96E+00	7,16E-04	0,0628	3,3834397	0,21245613	1040,27	SLC25A17	solute carrier family 25 member 17
653160	5,90E-01	2,29E-01	5,51E-01	0,3558	0,5969469	0,21236514	24,12	GPR199P	G protein-coupled receptor 199, pseudogene
11238	1,72E-01	7,64E-01	1,44E-01	0,1451	1,4623587	0,21212356	147,57	CA5B	carbonic anhydrase 5B
64965	9,94E-04	3,00E+00	6,52E-04	0,0621	3,4090744	0,21187041	1229,74	MRPS9	mitochondrial ribosomal protein S9
63892	5,40E-04	3,27E+00	3,47E-04	0,0591	3,5775752	0,21158727	1959,85	THADA	THADA armadillo repeat containing
84929	3,42E-01	4,66E-01	3,02E-01	0,2049	1,0317471	0,21136319	74,7	FIBCD1	fibrinogen C domain containing 1
130916	1,57E-03	2,80E+00	1,05E-03	0,0644	3,277202	0,21114591	1076,83	MTERF4	mitochondrial transcription termination factor 4
83461	1,10E-04	3,96E+00	6,70E-05	0,0529	3,9867805	0,21108801	2720,66	CDCA3	cell division cycle associated 3
1307	2,31E-01	6,36E-01	1,98E-01	0,1637	1,2885193	0,21098387	116,75	COL16A1	collagen type XVI alpha 1 chain
163059	1,38E-01	8,60E-01	1,14E-01	0,1333	1,5817584	0,21090931	179,4	ZNF433	zinc finger protein 433
389840	4,57E-02	1,34E+00	3,52E-02	0,0999	2,1057385	0,21030378	391,13	MAP3K15	mitogen-activated protein kinase kinase kinase 15
107984190	1,26E-01	9,00E-01	1,03E-01	0,1287	1,630851	0,20995684	192,84	LOC107984	uncharacterized LOC107984190
284402	6,40E-01	1,94E-01	6,02E-01	0,4028	0,5210098	0,20987446	20,18	SCGB2B2	secretoglobin family 2B member 2
55131	8,09E-04	3,09E+00	5,27E-04	0,0605	3,4664974	0,20955063	2380,41	RBM28	RNA binding motif protein 28
388531	6,56E-01	1,83E-01	6,20E-01	0,4224	0,4960908	0,20953538	20,07	RGS9BP	regulator of G protein signaling 9 binding protein
107984455	7,35E-01	1,34E-01	7,03E-01	0,5496	0,3812462	0,20952901	9,74	LOC107984	uncharacterized LOC107984455
4677	5,56E-07	6,25E+00	2,95E-07	0,0408	5,1263764	0,20933479	9941,68	NARS1	asparaginyl-tRNA synthetase 1
100507582	3,64E-01	4,39E-01	3,23E-01	0,2118	0,9883925	0,20929672	69,53	BHLHE40-AS	BHLHE40 antisense RNA 1
23111	5,72E-04	3,24E+00	3,68E-04	0,0587	3,5617291	0,20912366	3379,84	SPART	spartin
102723582	7,21E-01	1,42E-01	6,88E-01	0,521	0,4013739	0,20912014	11,14	WDR5B-DT	WDR5B divergent transcript
100422952	6,29E-01	2,01E-01	5,91E-01	0,3893	0,5371108	0,20908697	19,54	MIR4271	microRNA 4271
114827	6,68E-01	1,75E-01	6,33E-01	0,437	0,4781259	0,20896469	15,9	FHAD1	forkhead associated phosphopeptide binding domain 1
7024	7,04E-04	3,15E+00	4,57E-04	0,0596	3,5048152	0,20895201	1254,47	TFCP2	transcription factor CP2
144481	5,59E-01	2,53E-01	5,18E-01	0,3233	0,6462886	0,20895162	31,05	SOCS2-AS1	SOCS2 antisense RNA 1
80345	2,93E-02	1,53E+00	2,20E-02	0,0913	2,2896801	0,20894318	446,17	ZSCAN16	zinc finger and SCAN domain containing 16
646976	4,78E-01	3,21E-01	4,37E-01	0,2682	0,7780621	0,20870699	44,32	RALGPS2-A	RALGPS2 antisense RNA 1
11011	7,23E-06	5,14E+00	4,08E-06	0,0453	4,6070674	0,20856939	3505,38	TLK2	tousled like kinase 2
285343	2,14E-04	3,67E+00	1,34E-04	0,0545	3,819749	0,20816469	1726,5	TCAIM	T cell activation inhibitor, mitochondrial
400746	6,21E-01	2,07E-01	5,84E-01	0,3799	0,5479892	0,20816085	20,86	NCMAP	non-compact myelin associated protein
25917	2,14E-04	3,67E+00	1,33E-04	0,0545	3,8202814	0,20815396	1884,64	THUMPD3	THUMP domain containing 3
10537	3,16E-01	5,00E-01	2,77E-01	0,1914	1,0872263	0,20813853	91,38	UBD	ubiquitin D
4850	1,57E-03	2,80E+00	1,05E-03	0,0635	3,2779198	0,20811548	1038,8	CNOT4	CCR4-NOT transcription complex subunit 4
56478	3,59E-04	3,44E+00	2,28E-04	0,0565	3,6860331	0,20811087	1419,32	EIF4ENIF1	eukaryotic translation initiation factor 4E nuclear import factor 1
23198	2,04E-06	5,69E+00	1,12E-06	0,0427	4,8692375	0,20787466	7374,46	PSME4	proteasome activator subunit 4
6773	1,69E-04	3,77E+00	1,05E-04	0,0536	3,8796666	0,20783271	1887,32	STAT2	signal transducer and activator of transcription 2
60625	3,68E-04	3,43E+00	2,34E-04	0,0564	3,6796235	0,20755168	1672,16	DHX35	DEAH-box helicase 35
107985942	5,76E-01	2,40E-01	5,36E-01	0,3351	0,6191818	0,20751059	26,2	CLASP1-AS	CLASP1 antisense RNA 1
55388	1,91E-04	3,72E+00	1,19E-04	0,0538	3,8490801	0,20721613	3006,13	MCM10	minichromosome maintenance 10 replication initiation factor
5873	8,14E-04	3,09E+00	5,31E-04	0,0597	3,4646886	0,20699938	1496,09	RAB27A	RAB27A, member RAS oncogene family
9133	3,66E-05	4,44E+00	2,16E-05	0,0487	4,2478347	0,20686163	5079,54	CCNB2	cyclin B2
253724	6,73E-01	1,72E-01	6,37E-01	0,4377	0,4716394	0,2064462	16,43	TTC41P	tetratricopeptide repeat domain 41, pseudogene
192670	1,01E-02	2,00E+00	7,28E-03	0,0767	2,6836286	0,20574204	717,39	AGO4	argonaute RISC component 4
401397	1,09E-03	2,96E+00	7,16E-04	0,0608	3,3833599	0,20571664	1492,36	SMIM30	small integral membrane protein 30
64850	7,72E-01	1,12E-01	7,43E-01	0,627	0,3279792	0,20565228	8,34	ETNPPL	ethanolamine-phosphate phospho-lyase
55776	3,60E-03	2,44E+00	2,47E-03	0,0679	3,0264153	0,20557506	980,63	SAYSD1	SAYSVFN motif domain containing 1
126295	1,59E-01	7,99E-01	1,32E-01	0,1364	1,5064333	0,20554324	183,76	ZNF57	zinc finger protein 57
55198	1,48E-04	3,83E+00	9,11E-05	0,0525	3,9131844	0,20533896	2291,95	APPL2	adaptor protein, phosphotyrosine interacting with PH domain and leucine zipper 2
29089	7,01E-05	4,15E+00	4,21E-05	0,0501	4,0957145	0,20517457	2829,3	UBE2T	ubiquitin conjugating enzyme E2 T
23310	1,53E-06	5,82E+00	8,33E-07	0,0416	4,9274816	0,20504192	6653,09	NCAPD3	non-SMC condensin II complex subunit D3
222183	6,73E-01	1,72E-01	6,38E-01	0,4358	0,4704731	0,20501001	15,94	SRRM3	serine/arginine repetitive matrix 3
5289	7,09E-05	4,15E+00	4,26E-05	0,05	4,0931144	0,20481906	2835,18	PIK3C3	phosphatidylinositol 3-kinase catalytic subunit type 3
7107	2,71E-02	1,57E+00	2,03E-02	0,0882	2,3212009	0,20464481	536,67	GPR137B	G protein-coupled receptor 137B
27290	6,02E-01	2,20E-01	5,64E-01	0,3542	0,5776398	0,20458115	25,44	SPINK4	serine peptidase inhibitor Kazal type 4
85007	1,74E-04	3,76E+00	1,08E-04	0,0528	3,8723737	0,20439809	2677,73	PHYKPL	5-phosphohydroxy-L-lysine phospho-lyase
63929	8,48E-03	2,07E+00	6,04E-03	0,0744	2,7458169	0,20434708	685,72	XPNPEP3	X-prolyl aminopeptidase 3
375133	2,84E-02	1,55E+00	2,13E-02	0,0888	2,3022428	0,20433083	431,38	PI4KAP2	phosphatidylinositol 4-kinase alpha pseudogene 2
79023	3,25E-04	3,49E+00	2,05E-04	0,055	3,7124113	0,20422631	1942,28	NUP37	nucleoporin 37
29128	5,03E-05	4,30E+00	2,99E-05	0,0489	4,1741651	0,20419722	3975,91	UHRF1	ubiquitin like with PHD and ring finger domains 1
339929	4,38E-01	3,59E-01	3,96E-01	0,2406	0,848567	0,20415769	53,37	LPP-AS2	LPP antisense RNA 2
101927597	4,19E-01	3,78E-01	3,78E-01	0,2315	0,8816669	0,20413531	55,82	NCK1-DT	NCK1 divergent transcript
54625	5,09E-05	4,29E+00	3,02E-05	0,0489	4,1716279	0,20398755	2295,43	PARP14	poly(ADP-ribose) polymerase family member 14
341392	5,58E-01	2,53E-01	5,17E-01	0,3151	0,6472614	0,20396575	30,16	ACSM4	acyl-CoA synthetase medium chain family member 4
10928	3,72E-07	6,43E+00	1,96E-07	0,0392	5,2032998	0,20391146	6846,54	RALBP1	ralA binding protein 1
9063	1,04E-02	1,98E+00	7,47E-03	0,0762	2,6750535	0,20382262	642,2	PIAS2	protein inhibitor of activated STAT 2
80209	8,02E-05	4,10E+00	4,84E-05	0,0501	4,0634465	0,20366369	2181,68	PROSER1	proline and serine rich 1
51182	6,57E-05	4,18E+00	3,94E-05	0,0495	4,1112389	0,20364302	2981,78	HSPA14	heat shock protein family A (Hsp70) member 14
22948	1,82E-08	7,74E+00	8,97E-09	0,0354	5,7492305	0,20359009	39025,81	CCT5	chaperonin containing TCP1 subunit 5
549	2,25E-02	1,65E+00	1,67E-02	0,085	2,3939498	0,20352543	518,61	AUH	AU RNA binding methylglutaconyl-CoA hydratase
81617	2,19E-02	1,66E+00	1,62E-02	0,0846	2,4046606	0,20351396	493,22	CAB39L	calcium binding protein 39 like
100302138	1,85E-01	7,33E-01	1,55E-01	0,1431	1,4205251	0,20328176	174,55	MIR1292	microRNA 1292
102723696	7,61E-01	1,19E-01	7,31E-01	0,5911	0,3438236	0,2032404	8,85	LOC102723	uncharacterized LOC102723696
6573	7,93E-02	1,10E+00	6,31E-02	0,1093	1,858364	0,20314545	276,45	SLC19A1	solute carrier family 19 member 1
80196	1,85E-05	4,73E+00	1,07E-05	0,0461	4,4022714	0,20302244	3381,31	RNF34	ring finger protein 34
100505501	4,22E-01	3,75E-01	3,81E-01	0,2314	0,8769252	0,20295733	64,54	TOX-DT	TOX divergent transcript
868	2,69E-02	1,57E+00	2,02E-02	0,0872	2,3234535	0,2026816	481,77	CBLB	Cbl proto-oncogene B
8575	1,53E-03	2,82E+00	1,02E-03	0,0617	3,2844801	0,20264431	1266,36	PRKRA	protein activator of interferon induced protein kinase EIF2AK2
440498	5,61E-02	1,25E+00	4,38E-02	0,1005	2,0161851	0,20255204	353,68	HSBP1L1	heat shock factor binding protein 1 like 1
939	4,50E-01	3,47E-01	4,09E-01	0,2452	0,8261082	0,20252488	49,61	CD27	CD27 molecule
100820829	1,18E-01	9,28E-01	9,64E-02	0,1217	1,6627265	0,20241991	222,81	MYZAP	myocardial zonula adherens protein
3177	2,82E-02	1,55E+00	2,12E-02	0,0877	2,3048113	0,2021201	493,77	SLC29A2	solute carrier family 29 member 2
988	1,36E-05	4,87E+00	7,82E-06	0,0452	4,4699764	0,20207908	10481,38	CDC5L	cell division cycle 5 like
25758	7,30E-01	1,37E-01	6,98E-01	0,5207	0,3880099	0,20205272	11,13	KIAA1549L	KIAA1549 like
90293	7,02E-01	1,54E-01	6,68E-01	0,4718	0,4282399	0,20202698	16,04	KLHL13	kelch like family member 13
105371822	5,69E-01	2,45E-01	5,29E-01	0,3202	0,6301666	0,20180983	32,65	LOC105371	uncharacterized LOC105371822
100526794	2,68E-02	1,57E+00	2,01E-02	0,0868	2,3248501	0,20179134	495,32	NT5C1B-RD	NT5C1B-RDH14 readthrough
8082	3,01E-01	5,21E-01	2,63E-01	0,1802	1,1191644	0,20170474	108,5	SSPN	sarcospan
153743	4,07E-01	3,90E-01	3,66E-01	0,223	0,9039928	0,20158098	60,22	PPP1R2B	PPP1R2 family member B
112637020	3,37E-01	4,72E-01	2,97E-01	0,1934	1,0418317	0,20148334	82,38	SREBF2-AS	SREBF2 antisense RNA 1
11129	5,24E-03	2,28E+00	3,66E-03	0,0693	2,9064654	0,20145073	1192,74	CLASRP	CLK4 associating serine/arginine rich protein
4927	7,34E-06	5,13E+00	4,15E-06	0,0438	4,6035946	0,20142122	5349,58	NUP88	nucleoporin 88
57038	2,19E-03	2,66E+00	1,48E-03	0,0631	3,1785782	0,20052438	1215,51	RARS2	arginyl-tRNA synthetase 2, mitochondrial
5910	1,14E-03	2,94E+00	7,50E-04	0,0594	3,3706552	0,20020804	3876,87	RAP1GDS1	Rap1 GTPase-GDP dissociation stimulator 1
100131814	6,72E-01	1,73E-01	6,37E-01	0,4236	0,4725091	0,20013416	16,39	AHI1-DT	AHI1 divergent transcript
4034	1,49E-03	2,83E+00	9,91E-04	0,0607	3,2929607	0,19999953	1219,51	LRCH4	leucine rich repeats and calponin homology domain containing 4
387509	1,64E-02	1,79E+00	1,20E-02	0,0796	2,5126511	0,19990771	764,39	GPR153	G protein-coupled receptor 153
4651	2,90E-06	5,54E+00	1,60E-06	0,0416	4,7982358	0,19982459	6821,63	MYO10	myosin X
100533467	1,54E-03	2,81E+00	1,03E-03	0,0608	3,2826554	0,19956836	1230,45	BIVM-ERCC	BIVM-ERCC5 readthrough
220992	5,97E-02	1,22E+00	4,67E-02	0,1003	1,9887763	0,19951563	350,26	ZNF485	zinc finger protein 485
2965	6,10E-06	5,21E+00	3,43E-06	0,0429	4,6431741	0,19934537	4047,65	GTF2H1	general transcription factor IIH subunit 1
928	4,03E-04	3,39E+00	2,56E-04	0,0544	3,6560169	0,19883277	5402,71	CD9	CD9 molecule
101928578	4,39E-01	3,58E-01	3,97E-01	0,2348	0,8464823	0,19879089	57,37	RAP2C-AS1	RAP2C antisense RNA 1
29896	3,82E-04	3,42E+00	2,43E-04	0,0542	3,6698431	0,19877437	2474,99	TRA2A	transformer 2 alpha homolog
152100	9,55E-04	3,02E+00	6,25E-04	0,0581	3,4203098	0,19862202	1330,2	CMC1	C-X9-C motif containing 1
441194	5,73E-02	1,24E+00	4,48E-02	0,0989	2,006538	0,19852205	345,43	PMS2CL	PMS2 C-terminal like pseudogene
100302692	4,06E-01	3,91E-01	3,65E-01	0,2191	0,9055643	0,19839746	66,32	FTX	FTX transcript, XIST regulator
105379193	3,98E-03	2,40E+00	2,75E-03	0,0662	2,9945668	0,19822949	1102,89	LOC105379	uncharacterized LOC105379193
23008	1,93E-03	2,71E+00	1,30E-03	0,0616	3,2166548	0,19811406	1597,5	KLHDC10	kelch domain containing 10
100500820	2,92E-02	1,53E+00	2,20E-02	0,0865	2,2906214	0,19811232	676,24	MIR3655	microRNA 3655
729162	5,85E-01	2,33E-01	5,45E-01	0,3272	0,6048555	0,1979192	28,84	FAM239B	zinc finger protein 839 pseudogene
55760	9,48E-04	3,02E+00	6,20E-04	0,0578	3,4225337	0,19777728	2626,89	DHX32	DEAH-box helicase 32 (putative)
100131496	3,52E-01	4,53E-01	3,11E-01	0,1953	1,0126607	0,19774718	85,92	LOC100131	uncharacterized LOC100131496
7298	1,71E-05	4,77E+00	9,87E-06	0,0447	4,4200938	0,19769201	7459,1	TYMS	thymidylate synthetase
285193	2,67E-01	5,73E-01	2,31E-01	0,1648	1,1977306	0,1973865	117,74	DUSP28	dual specificity phosphatase 28

9960	2,78E-03	2,56E+00	1,89E-03	0,0635	3,1066849	0,1971588	1457,56	USP3	ubiquitin specific peptidase 3
57826	9,19E-03	2,04E+00	6,57E-03	0,0725	2,7178506	0,19712176	1635,68	RAP2C	RAP2C, member of RAS oncogene family
541471	7,63E-05	4,12E+00	4,59E-05	0,0483	4,0754499	0,19702847	3233,89	MIR4435-2H	MIR4435-2 host gene
57688	4,81E-04	3,32E+00	3,08E-04	0,0546	3,6085715	0,19697459	1770,99	ZSWIM6	zinc finger SWIM-type containing 6
107985414	7,90E-01	1,02E-01	7,62E-01	0,6511	0,3024556	0,19692617	8,12	LOC107985	uncharacterized LOC107985414
257169	5,67E-01	2,46E-01	5,27E-01	0,3108	0,633241	0,19681156	31,53	C9orf43	chromosome 9 open reading frame 43
92610	1,37E-02	1,86E+00	9,95E-03	0,0763	2,5774482	0,19675674	731,41	TIFA	TRAF interacting protein with forkhead associated domain
6791	6,14E-01	2,12E-01	5,76E-01	0,3513	0,5595611	0,19657238	24,76	AURKAP1	aurora kinase A pseudogene 1
253152	8,13E-02	1,09E+00	6,48E-02	0,1064	1,8467456	0,1964591	385,88	EPHX4	epoxide hydrolase 4
1859	2,19E-04	3,66E+00	1,36E-04	0,0515	3,8147703	0,19637834	2384,83	DYRK1A	dual specificity tyrosine phosphorylation regulated kinase 1A
9554	3,45E-05	4,46E+00	2,03E-05	0,0461	4,2617641	0,19637587	3972,16	SEC22B	SEC22 homolog B, vesicle trafficking protein
400506	3,91E-04	3,41E+00	2,49E-04	0,0536	3,6635648	0,19624186	1726,23	KNOP1	lysine rich nucleolar protein 1
388403	1,39E-01	8,57E-01	1,15E-01	0,1243	1,5780878	0,1962128	227,11	YPEL2	yippee like 2
90550	5,33E-04	3,27E+00	3,43E-04	0,0548	3,5807199	0,19611745	1692,06	MCU	mitochondrial calcium uniporter
5527	3,02E-05	4,52E+00	1,77E-05	0,0457	4,2918089	0,19611073	5657,61	PPP2R5C	protein phosphatase 2 regulatory subunit B'gamma
158160	5,27E-01	2,78E-01	4,86E-01	0,2812	0,6966311	0,19590018	39,71	HSD17B7P2	hydroxysteroid 17-beta dehydrogenase 7 pseudogene 2
26269	1,06E-02	1,97E+00	7,59E-03	0,0733	2,6696847	0,19578226	1008,58	FBXO8	F-box protein 8
7994	1,09E-04	3,96E+00	6,64E-05	0,0491	3,9887178	0,19569595	3423,4	KAT6A	lysine acetyltransferase 6A
79188	1,48E-06	5,83E+00	8,08E-07	0,0396	4,9334838	0,19554264	6802,74	TMEM43	transmembrane protein 43
9175	2,44E-03	2,61E+00	1,65E-03	0,0621	3,1470791	0,19551617	1261,47	MAP3K13	mitogen-activated protein kinase kinase kinase 13
84991	1,81E-05	4,74E+00	1,05E-05	0,0443	4,4068319	0,195353	4600,44	RBM17	RNA binding motif protein 17
7286	2,56E-03	2,59E+00	1,73E-03	0,0623	3,1323158	0,19523498	1210,84	TUFT1	tuftelin 1
83608	1,31E-02	1,88E+00	9,48E-03	0,0752	2,5942414	0,19498971	776,43	C18orf21	chromosome 18 open reading frame 21
56254	6,85E-04	3,16E+00	4,44E-04	0,0555	3,5125291	0,19498261	3486,3	RNF20	ring finger protein 20
3164	5,36E-01	2,71E-01	4,95E-01	0,2852	0,6830064	0,19481343	39,01	NR4A1	nuclear receptor subfamily 4 group A member 1
2491	1,05E-04	3,98E+00	6,37E-05	0,0486	3,9986508	0,19451525	2589,85	CENPI	centromere protein I
23109	4,90E-01	3,10E-01	4,48E-01	0,256	0,7591727	0,19435061	49,1	DDN	dendrin
7597	1,99E-03	2,70E+00	1,34E-03	0,0605	3,2082697	0,19422607	1177,89	ZBTB25	zinc finger and BTB domain containing 25
22856	4,71E-04	3,33E+00	3,01E-04	0,0537	3,6142662	0,19411172	2065,57	CHSY1	chondroitin sulfate synthase 1
23336	1,76E-03	2,75E+00	1,18E-03	0,0598	3,2437664	0,19401509	1353,78	SYNM	synemin
440894	1,05E-01	9,79E-01	8,50E-02	0,1126	1,7221805	0,19396983	260,85	LINC01123	long intergenic non-protein coding RNA 1123
80778	1,29E-01	8,89E-01	1,05E-01	0,1198	1,6188707	0,19395244	239,97	ZNF34	zinc finger protein 34
54906	9,21E-07	6,04E+00	4,95E-07	0,0385	5,0282888	0,19380039	6766,87	TASOR2	transcription activation suppressor family member 2
22920	3,23E-03	2,49E+00	2,21E-03	0,0633	3,0607435	0,19374927	1623,28	KIFAP3	kinesin associated protein 3
342371	9,34E-05	4,03E+00	5,66E-05	0,0481	4,0265276	0,19370431	2651,37	ATXN1L	ataxin 1 like
23256	1,19E-03	2,92E+00	7,84E-04	0,0576	3,3583026	0,19342412	2973,45	SCFD1	sec1 family domain containing 1
5062	3,22E-06	5,49E+00	1,78E-06	0,0405	4,7764677	0,19339805	11426,75	PAK2	p21 (RAC1) activated kinase 2
10615	3,42E-05	4,47E+00	2,01E-05	0,0454	4,2636643	0,1933818	7908,25	SPAG5	sperm associated antigen 5
51340	9,73E-05	4,01E+00	5,90E-05	0,0481	4,0168858	0,19330708	2436,41	CRNKL1	crooked neck pre-mRNA splicing factor 1
105370496	7,69E-01	1,14E-01	7,39E-01	0,5802	0,3330837	0,1932564	9,93	LINC02310	long intergenic non-protein coding RNA 2310
729603	7,50E-01	1,25E-01	7,19E-01	0,5367	0,3599432	0,19316922	11,59	CHP1P2	CHP1 pseudogene 2
2524	6,91E-01	1,61E-01	6,56E-01	0,4339	0,4451654	0,19314915	16,45	FUT2	fucosyltransferase 2
83452	4,36E-02	1,36E+00	3,35E-02	0,0907	2,1259794	0,19273246	425,31	RAB33B	RAB33B, member RAS oncogene family
126014	6,21E-01	2,07E-01	5,84E-01	0,3509	0,5481829	0,19234264	25,98	OSCAR	osteoclast associated Ig-like receptor
114793	1,08E-04	3,97E+00	6,56E-05	0,0481	3,9918113	0,19217681	3232,04	FMNL2	formin like 2
23560	6,02E-05	4,22E+00	3,60E-05	0,0465	4,1320149	0,19205991	8514,75	GTPBP4	GTP binding protein 4
10346	1,78E-01	7,50E-01	1,49E-01	0,1332	1,4418828	0,19202235	213,78	TRIM22	tripartite motif containing 22
2651	9,38E-06	5,03E+00	5,33E-06	0,042	4,5511927	0,19133807	5228,21	GCNT2	glucosaminyl (N-acetyl) transferase 2 (I blood group)
158219	1,94E-01	7,12E-01	1,63E-01	0,1371	1,3940542	0,19117425	169,4	TTC39B	tetratricopeptide repeat domain 39B
101928504	5,09E-01	2,93E-01	4,67E-01	0,2627	0,726996	0,19094649	45,15	GTF2A1-AS	GTF2A1 antisense RNA 1
3985	1,63E-02	1,79E+00	1,19E-02	0,0759	2,5142228	0,1908889	772,2	LIMK2	LIM domain kinase 2
4086	5,60E-02	1,25E+00	4,37E-02	0,0946	2,0170565	0,19074487	396,53	SMAD1	SMAD family member 1
9741	1,04E-03	2,98E+00	6,80E-04	0,0561	3,3974361	0,19073874	7955,57	LAPTM4A	lysosomal protein transmembrane 4 alpha
107987280	6,21E-01	2,07E-01	5,84E-01	0,3475	0,5480106	0,19042234	28,93	LOC107987	uncharacterized LOC107987280
9716	7,82E-05	4,11E+00	4,71E-05	0,0468	4,0695457	0,19037866	3440,2	AQR	aquarius intron-binding spliceosomal factor
282890	9,98E-02	1,00E+00	8,05E-02	0,1089	1,7476036	0,19031359	290,83	ZNF311	zinc finger protein 311
196294	9,58E-02	1,02E+00	7,71E-02	0,1077	1,7676407	0,19031021	282,74	IMMP1L	inner mitochondrial membrane peptidase subunit 1
285512	2,48E-01	6,06E-01	2,13E-01	0,1525	1,2463615	0,19001195	132,13	FAM13A-AS	FAM13A antisense RNA 1
23228	2,47E-02	1,61E+00	1,84E-02	0,0806	2,3565496	0,18995249	819,25	PLCL2	phospholipase C like 2
105369147	3,89E-01	4,10E-01	3,48E-01	0,202	0,9386426	0,18963779	75,75	LOC105369	uncharacterized LOC105369147
55002	5,42E-05	4,27E+00	3,23E-05	0,0456	4,1567296	0,18950031	3228,56	TMCO3	transmembrane and coiled-coil domains 3
3694	7,14E-01	1,46E-01	6,81E-01	0,4611	0,4109329	0,18948763	13,69	ITGB6	integrin subunit beta 6
6880	7,41E-05	4,13E+00	4,45E-05	0,0464	4,0825607	0,1893374	3876,94	TAF9	TATA-box binding protein associated factor 9
51060	8,47E-06	5,07E+00	4,81E-06	0,0414	4,5728939	0,18931776	4516,46	TXNDC12	thioredoxin domain containing 12
11123	4,41E-04	3,36E+00	2,81E-04	0,0521	3,6318128	0,18917684	1864,37	RCAN3	RCAN family member 3
90075	1,11E-01	9,55E-01	8,98E-02	0,1115	1,6963528	0,1890991	340,61	ZNF30	zinc finger protein 30
338596	5,90E-01	2,29E-01	5,50E-01	0,3162	0,5975728	0,1889442	29,58	ST8SIA6	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 6
84665	3,01E-01	5,21E-01	2,62E-01	0,1684	1,1207266	0,18874351	111,67	MYPN	myopalladin
51100	4,71E-06	5,33E+00	2,64E-06	0,0402	4,6973611	0,18864913	7533,94	SH3GLB1	SH3 domain containing GRB2 like, endophilin B1
57504	7,63E-04	3,12E+00	4,97E-04	0,0542	3,4826117	0,1885915	1715,69	MTA3	metastasis associated 1 family member 3
6046	1,08E-05	4,97E+00	6,16E-06	0,0417	4,5206819	0,18851845	16230,32	BRD2	bromodomain containing 2
110006323	5,54E-02	1,26E+00	4,32E-02	0,0931	2,0215941	0,18812809	437,37	PKD1P4-NPI	PKD1P4-NPIPA8 readthrough
140803	7,25E-01	1,40E-01	6,93E-01	0,4762	0,3949589	0,1880901	13,54	TRPM6	transient receptor potential cation channel subfamily M member 6
123775	2,65E-01	5,77E-01	2,29E-01	0,1564	1,2028639	0,18808905	127,7	C16orf46	chromosome 16 open reading frame 46
102724146	2,05E-02	1,69E+00	1,51E-02	0,0773	2,4299642	0,18791187	948,12	LOC102724	uncharacterized LOC102724146
7533	3,58E-06	5,45E+00	1,99E-06	0,0395	4,7548007	0,18782901	8094,62	YWHAH	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein eta
729852	9,79E-02	1,01E+00	7,90E-02	0,1068	1,75673	0,18756269	332,9	UMAD1	UBAP1-MVB12-associated (UMA) domain containing 1
80335	1,47E-05	4,83E+00	8,46E-06	0,0421	4,4532264	0,18748349	9870,16	WDR82	WD repeat domain 82
84992	9,48E-04	3,02E+00	6,21E-04	0,0548	3,4222894	0,18744433	1900,34	PIGY	phosphatidylinositol glycan anchor biosynthesis class Y
100996939	9,48E-04	3,02E+00	6,21E-04	0,0548	3,4222894	0,18744433	1900,34	PYURF	PIGY upstream open reading frame
129787	2,24E-04	3,65E+00	1,39E-04	0,0492	3,8091027	0,18743447	2195,39	TMEM18	transmembrane protein 18
9939	1,02E-05	4,99E+00	5,80E-06	0,0413	4,5334345	0,18738579	7022,71	RBM8A	RNA binding motif protein 8A
27258	6,89E-04	3,16E+00	4,46E-04	0,0533	3,5109845	0,18710649	3856,75	LSM3	LSM3 homolog, U6 small nuclear RNA and mRNA degradation associated
101928630	1,83E-01	7,38E-01	1,54E-01	0,1309	1,4262121	0,18662694	184,81	SMIM15-AS1	SMIM15 antisense RNA 1
2182	5,96E-05	4,22E+00	3,56E-05	0,0451	4,1345208	0,18662642	7016,68	ACSL4	acyl-CoA synthetase long chain family member 4
7079	4,66E-01	3,32E-01	4,24E-01	0,2333	0,7992867	0,18650739	59,36	TIMP4	TIMP metallopeptidase inhibitor 4
25890	7,20E-02	1,14E+00	5,69E-02	0,0978	1,9037363	0,18621622	364,4	ABI3BP	ABI family member 3 binding protein
102606465	3,11E-01	5,07E-01	2,72E-01	0,1694	1,0979731	0,18596716	108,75	DPH5-DT	DPH5 divergent transcript
118987	2,61E-05	4,58E+00	1,52E-05	0,043	4,3252803	0,18596306	3744,69	PDZD8	PDZ domain containing 8
100508120	2,35E-01	6,29E-01	2,01E-01	0,1453	1,2794053	0,18595347	155,14	GMDS-DT	GMDS divergent transcript
203430	6,17E-01	2,10E-01	5,79E-01	0,3346	0,5554804	0,18586395	27,95	RTL3	retrotransposon Gag like 3
51009	2,47E-03	2,61E+00	1,67E-03	0,0591	3,1426757	0,18577914	2239,2	DERL2	derlin 2
204801	6,79E-01	1,68E-01	6,44E-01	0,4012	0,4623253	0,18548424	19,29	NLRP11	NLR family pyrin domain containing 11
101927164	4,06E-01	3,91E-01	3,65E-01	0,2047	0,9056476	0,18534785	73,02	LOC101927	uncharacterized LOC101927164
84283	8,57E-02	1,07E+00	6,85E-02	0,1016	1,8219124	0,18514047	336,94	TMEM79	transmembrane protein 79
100302274	3,91E-01	4,08E-01	3,50E-01	0,1981	0,9347205	0,18512188	80,93	MIR1178	microRNA 1178
100049716	4,14E-01	3,83E-01	3,73E-01	0,2076	0,8911898	0,18498735	72,96	NINJ2-AS1	NINJ2 antisense RNA 1
1768	7,70E-01	1,14E-01	7,40E-01	0,5584	0,3312541	0,18496626	10,06	DNAH6	dynein axonemal heavy chain 6
4277	1,66E-04	3,78E+00	1,02E-04	0,0476	3,8851256	0,18493111	4445,07	MICB	MHC class I polypeptide-related sequence B
60313	3,60E-05	4,44E+00	2,12E-05	0,0434	4,2518897	0,18457571	5308,4	GPBP1L1	GC-rich promoter binding protein 1 like 1
2079	6,78E-05	4,17E+00	4,06E-05	0,0449	4,1038693	0,18444716	6212,56	ERH	ERH mRNA splicing and mitosis factor
27250	1,55E-03	2,81E+00	1,03E-03	0,0561	3,2812707	0,18419455	2582,66	PDCD4	programmed cell death 4
57498	5,63E-04	3,25E+00	3,62E-04	0,0516	3,5663078	0,18399488	3205,22	KIDINS220	kinase D interacting substrate 220
162514	7,92E-01	1,01E-01	7,64E-01	0,6116	0,3007193	0,18393273	8,39	TRPV3	transient receptor potential cation channel subfamily V member 3
80124	1,17E-02	1,93E+00	8,42E-03	0,0698	2,6348346	0,18389538	997,51	VCPIP1	valosin containing protein interacting protein 1
4898	5,42E-07	6,27E+00	2,88E-07	0,0358	5,1311245	0,18383009	13583,79	NRDC	nardilysin convertase
79048	1,25E-03	2,90E+00	8,23E-04	0,0549	3,3448004	0,18365436	1819,83	SECISBP2	SECIS binding protein 2
3382	3,18E-02	1,50E+00	2,41E-02	0,0814	2,2559653	0,18365009	541,9	ICA1	islet cell autoantigen 1
23197	7,05E-06	5,15E+00	3,98E-06	0,0398	4,6123081	0,18344371	5958,96	FAF2	Fas associated factor family member 2
101180901	2,96E-02	1,53E+00	2,23E-02	0,0802	2,2850749	0,18327239	596,6	IPO11-LRRC	IPO11-LRRC70 readthrough
151963	4,41E-02	1,36E+00	3,39E-02	0,0863	2,1210672	0,18314466	482,85	MB21D2	Mab-21 domain containing 2
283489	5,65E-04	3,25E+00	3,64E-04	0,0513	3,5649751	0,1829691	2505,49	CHAMP1	chromosome alignment maintaining phosphoprotein 1
25923	1,85E-05	4,73E+00	1,07E-05	0,0416	4,4019856	0,18295998	7648,33	ATL3	atlastin GTPase 3
23304	1,71E-05	4,77E+00	9,90E-06	0,0414	4,4193468	0,18280994	4698,89	UBR2	ubiquitin protein ligase E3 component n-recognin 2
6432	6,56E-06	5,18E+00	3,70E-06	0,0395	4,6276825	0,1826616	7367,72	SRSF7	serine and arginine rich splicing factor 7
100129858	6,79E-01	1,68E-01	6,44E-01	0,3943	0,4626016	0,18241063	19,78	SCOC-AS1	SCOC antisense RNA 1
10490	7,20E-05	4,14E+00	4,33E-05	0,0446	4,0892994	0,18227306	3919,62	VTI1B	vesicle transport through interaction with t-SNAREs 1B
125228	2,62E-03	2,58E+00	1,78E-03	0,0583	3,1250028	0,18203905	1419,12	FAM210A	family with sequence similarity 210 member A
375341	7,86E-02	1,10E+00	6,24E-02	0,0977	1,8631989	0,18196581	367,46	C3orf62	chromosome 3 open reading frame 62
26873	2,19E-01	6,60E-01	1,86E-01	0,1375	1,3226827	0,18182317	167,13	OPLAH	5-oxoprolinase, ATP-hydrolysing

5440	3,14E-04	3,50E+00	1,98E-04	0,0488	3,7216729	0,18167632	3404,19	POLR2K	RNA polymerase II, I and III subunit K
4528	7,95E-05	4,10E+00	4,79E-05	0,0446	4,0656546	0,18146742	4465,08	MTIF2	mitochondrial translational initiation factor 2
9867	1,29E-04	3,89E+00	7,88E-05	0,0459	3,9481003	0,18108049	6319,28	PJA2	praja ring finger ubiquitin ligase 2
10216	2,49E-01	6,04E-01	2,13E-01	0,1454	1,2440443	0,18088072	189,25	PRG4	proteoglycan 4
1039	3,07E-03	2,51E+00	2,10E-03	0,0588	3,0758686	0,18081181	1448,56	CDR2	cerebellar degeneration related protein 2
4430	1,15E-04	3,94E+00	7,03E-05	0,0455	3,9751896	0,18076003	5254,3	MYO1B	myosin IB
1063	2,90E-04	3,54E+00	1,83E-04	0,0483	3,7416443	0,18073857	19867,36	CENPF	centromere protein F
105371049	6,40E-01	1,94E-01	6,03E-01	0,3468	0,5203094	0,18043724	25,61	PKD1-AS1	PKD1 antisense RNA 1
7443	7,19E-05	4,14E+00	4,32E-05	0,0441	4,0896037	0,18021709	3708,21	VRK1	VRK serine/threonine kinase 1
8898	1,36E-04	3,87E+00	8,31E-05	0,0458	3,9353781	0,18015676	4132,08	MTMR2	myotubularin related protein 2
55367	5,03E-02	1,30E+00	3,90E-02	0,0872	2,0644953	0,18007762	588,83	PIDD1	p53-induced death domain protein 1
143879	6,18E-02	1,21E+00	4,85E-02	0,0912	1,9730306	0,18003278	417,04	KBTBD3	kelch repeat and BTB domain containing 3
112597	4,94E-04	3,31E+00	3,16E-04	0,05	3,6015209	0,17998939	4161,77	CYTOR	cytoskeleton regulator RNA
9221	1,01E-05	5,00E+00	5,75E-06	0,0397	4,535558	0,17998271	16426,33	NOLC1	nucleolar and coiled-body phosphoprotein 1
7529	1,13E-05	4,95E+00	6,44E-06	0,0399	4,5114847	0,17989258	27936,56	YWHAB	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein beta
2060	3,92E-04	3,41E+00	2,49E-04	0,0491	3,6632484	0,17968367	2791,65	EPS15	epidermal growth factor receptor pathway substrate 15
6662	4,72E-04	3,33E+00	3,02E-04	0,0496	3,6134458	0,17930163	2924,82	SOX9	SRY-box transcription factor 9
7391	9,48E-04	3,02E+00	6,21E-04	0,0524	3,422353	0,1792483	2072,39	USF1	upstream transcription factor 1
8611	1,49E-02	1,83E+00	1,08E-02	0,0703	2,5482836	0,17923675	936,47	PLPP1	phospholipid phosphatase 1
9816	2,18E-03	2,66E+00	1,47E-03	0,0563	3,1807551	0,17923356	1479,04	URB2	URB2 ribosome biogenesis homolog
79587	3,45E-03	2,46E+00	2,37E-03	0,0589	3,0398964	0,17913815	1351,95	CARS2	cysteinyl-tRNA synthetase 2, mitochondrial
30014	2,16E-01	6,66E-01	1,84E-01	0,1347	1,3299186	0,1790882	185,25	SPANXA1	sperm protein associated with the nucleus, X-linked, family member A1
6549	4,75E-01	3,23E-01	4,33E-01	0,2286	0,7832816	0,1790849	61,99	SLC9A2	solute carrier family 9 member A2
105372482	1,95E-01	7,10E-01	1,64E-01	0,1287	1,391092	0,17897127	196,49	ZNF8-DT	ZNF8 divergent transcript
92482	5,31E-02	1,27E+00	4,13E-02	0,0877	2,0402683	0,17885544	551,27	BBIP1	BBSome interacting protein 1
3980	9,22E-04	3,04E+00	6,03E-04	0,0521	3,4302462	0,17866356	2243,82	LIG3	DNA ligase 3
101929204	6,68E-01	1,75E-01	6,33E-01	0,3737	0,4780083	0,17865334	21,84	LOC101929	uncharacterized LOC101929204
25775	6,69E-01	1,75E-01	6,33E-01	0,3742	0,4770128	0,17847709	21,5	YWHAH-AS1	YWHAH antisense RNA 1
22916	2,72E-04	3,57E+00	1,71E-04	0,0474	3,7591203	0,1780285	4877,37	NCBP2	nuclear cap binding protein subunit 2
102724077	6,97E-01	1,57E-01	6,63E-01	0,4089	0,4352029	0,17796115	18,5	LINC01389	long intergenic non-protein coding RNA 1389
81577	2,08E-02	1,68E+00	1,54E-02	0,0734	2,4232217	0,17795775	839,15	GFOD2	glucose-fructose oxidoreductase domain containing 2
223	2,48E-05	4,61E+00	1,45E-05	0,041	4,3362761	0,17765403	5730,81	ALDH9A1	aldehyde dehydrogenase 9 family member A1
7504	8,58E-02	1,07E+00	6,86E-02	0,0975	1,8211928	0,17756399	385,57	XK	X-linked Kx blood group antigen, Kell and VPS13A binding protein
55006	5,31E-02	1,27E+00	4,13E-02	0,087	2,0401575	0,17748246	483,67	TRMT61B	tRNA methyltransferase 61B
5257	1,13E-03	2,95E+00	7,43E-04	0,0525	3,3732886	0,17723514	1915,47	PHKB	phosphorylase kinase regulatory subunit beta
54497	3,28E-03	2,48E+00	2,24E-03	0,0578	3,056019	0,1767807	1607,77	HEATR5B	HEAT repeat containing 5B
7728	9,40E-03	2,03E+00	6,73E-03	0,0652	2,7099122	0,17676818	1004,14	ZNF175	zinc finger protein 175
145864	2,97E-01	5,27E-01	2,59E-01	0,1567	1,1280719	0,17675444	158,29	HAPLN3	hyaluronan and proteoglycan link protein 3
106660612	1,49E-01	8,27E-01	1,23E-01	0,1146	1,5423738	0,17674149	263,06	LINC00680	long intergenic non-protein coding RNA 680
3920	1,63E-04	3,79E+00	1,01E-04	0,0454	3,8890199	0,17669365	8070,21	LAMP2	lysosomal associated membrane protein 2
4133	4,92E-01	3,08E-01	4,50E-01	0,2337	0,7556346	0,17657603	55,61	MAP2	microtubule associated protein 2
55622	9,24E-04	3,03E+00	6,04E-04	0,0514	3,4297255	0,17623049	2175,32	TTC27	tetratricopeptide repeat domain 27
25929	2,93E-04	3,53E+00	1,85E-04	0,0471	3,7389468	0,17599012	3949,94	GEMIN5	gem nuclear organelle associated protein 5
5861	2,12E-04	3,67E+00	1,32E-04	0,046	3,8224133	0,17598714	6313,23	RAB1A	RAB1A, member RAS oncogene family
2117	6,38E-03	2,20E+00	4,49E-03	0,0619	2,8413523	0,17597513	1295,39	ETV3	ETS variant transcription factor 3
23215	5,62E-04	3,25E+00	3,61E-04	0,0493	3,5667854	0,17595966	20421,24	PRRC2C	proline rich coiled-coil 2C
255082	6,34E-01	1,98E-01	5,96E-01	0,3322	0,5296373	0,17594238	31,36	CASC2	cancer susceptibility 2
8804	7,52E-04	3,12E+00	4,89E-04	0,0505	3,4865553	0,17593832	2496,41	CREG1	cellular repressor of E1A stimulated genes 1
29090	5,50E-03	2,26E+00	3,84E-03	0,0607	2,8906486	0,17551926	1276,44	TIMM21	translocase of inner mitochondrial membrane 21
55612	1,61E-03	2,79E+00	1,08E-03	0,0536	3,2695338	0,17532789	1634,9	FERMT1	FERM domain containing kindlin 1
79020	1,61E-02	1,79E+00	1,18E-02	0,0696	2,5182669	0,17532108	818,13	C7orf25	chromosome 7 open reading frame 25
171023	4,61E-06	5,34E+00	2,58E-06	0,0372	4,7019572	0,17507791	11773,7	ASXL1	ASXL transcriptional regulator 1
729178	6,03E-01	2,20E-01	5,65E-01	0,3041	0,5756463	0,17507125	34,84	STXBP5-AS	STXBP5 antisense RNA 1
10602	2,06E-05	4,69E+00	1,20E-05	0,0399	4,3776307	0,17455695	15079,56	CDC42EP3	CDC42 effector protein 3
79905	1,50E-01	8,24E-01	1,24E-01	0,1131	1,5393169	0,17407493	288,15	TMC7	transmembrane channel like 7
6790	7,16E-05	4,15E+00	4,30E-05	0,0425	4,0907464	0,17404957	13883,08	AURKA	aurora kinase A
5382	5,05E-01	2,97E-01	4,63E-01	0,2369	0,7343736	0,17399131	53,52	PMS2P4	PMS1 homolog 2, mismatch repair system component pseudogene 4
2959	7,99E-04	3,10E+00	5,20E-04	0,0501	3,4701005	0,17393299	2238,85	GTF2B	general transcription factor IIB
7324	6,66E-04	3,18E+00	4,31E-04	0,0493	3,5203668	0,17370647	3835,51	UBE2E1	ubiquitin conjugating enzyme E2 E1
55174	1,38E-03	2,86E+00	9,17E-04	0,0524	3,3149718	0,17368789	2237,76	INTS10	integrator complex subunit 10
3682	9,56E-03	2,02E+00	6,84E-03	0,0642	2,7043332	0,17367703	1054,38	ITGAE	integrin subunit alpha E
10285	3,25E-03	2,49E+00	2,22E-03	0,0567	3,0586153	0,17328911	2054,03	SMNDC1	survival motor neuron domain containing 1
201475	3,01E-03	2,52E+00	2,05E-03	0,0562	3,0826625	0,17327096	2232,63	RAB12	RAB12, member RAS oncogene family
51626	7,88E-02	1,10E+00	6,26E-02	0,0929	1,8617506	0,17301476	387,66	DYNC2LI1	dynein cytoplasmic 2 light intermediate chain 1
2983	2,88E-01	5,41E-01	2,51E-01	0,1505	1,1487898	0,17293459	159,8	GUCY1B1	guanylate cyclase 1 soluble subunit beta 1
340393	3,90E-01	4,09E-01	3,49E-01	0,1845	0,9363297	0,17275524	97,13	TMEM249	transmembrane protein 249
23588	1,13E-03	2,95E+00	7,45E-04	0,0512	3,3723054	0,17270764	2605,03	KLHDC2	kelch domain containing 2
8999	5,25E-01	2,80E-01	4,84E-01	0,2465	0,6999297	0,17255708	50,06	CDKL2	cyclin dependent kinase like 2
10768	6,05E-05	4,22E+00	3,62E-05	0,0418	4,1307576	0,17251249	6293,03	AHCYL1	adenosylhomocysteinase like 1
91283	2,21E-04	3,66E+00	1,38E-04	0,0452	3,8119242	0,17245802	3311,94	MSANTD3	Myb/SANT DNA binding domain containing 3
7754	2,59E-01	5,87E-01	2,24E-01	0,1415	1,2172642	0,17224009	155,94	ZNF204P	zinc finger protein 204, pseudogene
6712	5,96E-02	1,22E+00	4,67E-02	0,0865	1,989198	0,17213375	520,5	SPTBN2	spectrin beta, non-erythrocytic 2
38	4,00E-05	4,40E+00	2,37E-05	0,0406	4,2272947	0,17177083	5671,46	ACAT1	acetyl-CoA acetyltransferase 1
79961	2,90E-01	5,38E-01	2,52E-01	0,1499	1,1454703	0,17174072	139,75	DENND2D	DENN domain containing 2D
5238	5,42E-04	3,27E+00	3,49E-04	0,048	3,576236	0,17167887	2805,9	PGM3	phosphoglucomutase 3
84792	8,23E-02	1,08E+00	6,56E-02	0,0931	1,841056	0,17147649	731,43	FAM220A	family with sequence similarity 220 member A
131566	2,42E-05	4,62E+00	1,41E-05	0,0394	4,3419703	0,17128721	15614,6	DCBLD2	discoidin, CUB and LCCL domain containing 2
131474	2,90E-03	2,54E+00	1,98E-03	0,0553	3,093495	0,17121493	1799,06	CHCHD4	coiled-coil-helix-coiled-coil-helix domain containing 4
3306	4,48E-01	3,49E-01	4,06E-01	0,2062	0,8302116	0,17120956	79,93	HSPA2	heat shock protein family A (Hsp70) member 2
10424	2,11E-04	3,68E+00	1,32E-04	0,0448	3,8234228	0,17120268	3489,6	PGRMC2	progesterone receptor membrane component 2
57522	2,18E-03	2,66E+00	1,47E-03	0,0538	3,1804674	0,17113851	1907,61	SRGAP1	SLIT-ROBO Rho GTPase activating protein 1
23530	1,92E-04	3,72E+00	1,19E-04	0,0445	3,847858	0,1710915	3984,06	NNT	nicotinamide nucleotide transhydrogenase
4488	3,43E-01	4,65E-01	3,03E-01	0,1659	1,0309219	0,17106528	119,3	MSX2	msh homeobox 2
400960	3,68E-01	4,34E-01	3,27E-01	0,1745	0,9802127	0,17101325	102,56	PCBP1-AS1	PCBP1 antisense RNA 1
374383	4,20E-01	3,77E-01	3,79E-01	0,1943	0,8800245	0,17094926	91,38	NCR3LG1	natural killer cell cytotoxicity receptor 3 ligand 1
124817	3,30E-02	1,48E+00	2,50E-02	0,0762	2,2414296	0,17084626	689,34	CNTD1	cyclin N-terminal domain containing 1
11113	2,64E-04	3,58E+00	1,65E-04	0,0453	3,7667883	0,1707235	7275,42	CIT	citron rho-interacting serine/threonine kinase
84976	6,08E-02	1,22E+00	4,76E-02	0,0861	1,9806428	0,17060387	508,92	DISP1	dispatched RND transporter family member 1
5636	5,23E-03	2,28E+00	3,65E-03	0,0587	2,9072702	0,17058952	1477	PRPSAP2	phosphoribosyl pyrophosphate synthetase associated protein 2
4864	1,36E-04	3,87E+00	8,35E-05	0,0433	3,9340131	0,17051402	8801,65	NPC1	NPC intracellular cholesterol transporter 1
79631	1,90E-03	2,72E+00	1,27E-03	0,0529	3,2216262	0,1704999	2485,97	EFL1	elongation factor like GTPase 1
961	5,04E-04	3,30E+00	3,23E-04	0,0473	3,595962	0,1701896	4903,83	CD47	CD47 molecule
390928	5,08E-01	2,94E-01	4,66E-01	0,2335	0,7284496	0,17011122	55,43	ACP7	acid phosphatase 7, tartrate resistant (putative)
101927045	3,94E-01	4,05E-01	3,53E-01	0,183	0,9293141	0,17007962	97,85	LOC101927	uncharacterized LOC101927045
6874	6,33E-03	2,20E+00	4,46E-03	0,0597	2,8439256	0,16991496	1252,04	TAF4	TATA-box binding protein associated factor 4
51639	3,08E-04	3,51E+00	1,94E-04	0,0456	3,7266575	0,16983218	6117,17	SF3B6	splicing factor 3b subunit 6
259282	1,51E-03	2,82E+00	1,00E-03	0,0516	3,2895228	0,16973423	5293,01	BOD1L1	biorientation of chromosomes in cell division 1 like 1
80820	4,29E-01	3,68E-01	3,87E-01	0,1964	0,8644164	0,16973056	78,41	EEPD1	endonuclease/exonuclease/phosphatase family domain containing 1
23133	1,49E-03	2,83E+00	9,91E-04	0,0515	3,2930738	0,1696443	2058,1	PHF8	PHD finger protein 8
102724810	6,81E-01	1,67E-01	6,47E-01	0,3695	0,4585026	0,16941679	21,38	CHD1-DT	CHD1 divergent transcript
64761	4,14E-03	2,38E+00	2,86E-03	0,0568	2,9822037	0,16929027	1518,96	PARP12	poly(ADP-ribose) polymerase family member 12
9451	1,77E-02	1,75E+00	1,30E-02	0,0682	2,4834118	0,16928682	852,32	EIF2AK3	eukaryotic translation initiation factor 2 alpha kinase 3
220001	7,76E-01	1,10E-01	7,47E-01	0,5237	0,3225776	0,16892169	12,27	VWCE	von Willebrand factor C and EGF domains
256987	3,48E-02	1,46E+00	2,64E-02	0,076	2,2203196	0,16882331	627,84	SERINC5	serine incorporator 5
6400	1,04E-04	3,98E+00	6,34E-05	0,0422	3,9996775	0,16873125	5630,24	SEL1L	SEL1L adaptor subunit of ERAD E3 ubiquitin ligase
79739	4,98E-02	1,30E+00	3,86E-02	0,0816	2,0689214	0,16872426	612,48	TTLL7	tubulin tyrosine ligase like 7
10274	5,76E-04	3,24E+00	3,71E-04	0,0474	3,5597739	0,16871218	2972,56	STAG1	stromal antigen 1
126393	7,59E-01	1,20E-01	7,28E-01	0,4856	0,3471845	0,16860215	13	HSPB6	heat shock protein family B (small) member 6
1024	9,46E-03	2,02E+00	6,77E-03	0,0622	2,7078758	0,16845013	1061,34	CDK8	cyclin dependent kinase 8
2773	2,69E-04	3,57E+00	1,69E-04	0,0447	3,7616345	0,16832299	7840,88	GNAI3	G protein subunit alpha i3
23052	1,33E-03	2,88E+00	8,78E-04	0,0506	3,3269841	0,16823567	2293,53	ENDOD1	endonuclease domain containing 1
8518	1,05E-04	3,98E+00	6,39E-05	0,042	3,9979428	0,1680284	4451,44	ELP1	elongator acetyltransferase complex subunit 1
5422	6,79E-04	3,17E+00	4,40E-04	0,0477	3,5148972	0,1677468	2524,15	POLA1	DNA polymerase alpha 1, catalytic subunit
107984570	7,80E-01	1,08E-01	7,51E-01	0,5281	0,3175096	0,16766859	10,45	LINC00444	long intergenic non-protein coding RNA 444
129530	6,36E-01	1,97E-01	5,98E-01	0,3177	0,5266096	0,16732057	32,33	LYG1	lysozyme g1
11072	5,86E-04	3,23E+00	3,78E-04	0,047	3,5550114	0,16720035	2705,63	DUSP14	dual specificity phosphatase 14
100130027	2,15E-01	6,68E-01	1,82E-01	0,1252	1,3341877	0,16704936	210,67	LOC100130	uncharacterized LOC100130027
105378726	5,56E-01	2,55E-01	5,15E-01	0,2565	0,6510737	0,16700396	47,14	LOC105378	uncharacterized LOC105378726
55209	5,97E-04	3,22E+00	3,85E-04	0,0469	3,5501937	0,16651729	6964,88	SETD5	SET domain containing 5
3417	3,63E-03	2,44E+00	2,49E-03	0,055	3,023983	0,16632105	1965,82	IDH1	isocitrate dehydrogenase (NADP(+)) 1

7975	4,13E-02	1,38E+00	3,16E-02	0,0773	2,1488109	0,16615536	830,98	MAFK	MAF bZIP transcription factor K
23189	2,36E-02	1,63E+00	1,76E-02	0,0699	2,3747738	0,16592642	851,81	KANK1	KN motif and ankyrin repeat domains 1
8303	1,50E-01	8,24E-01	1,24E-01	0,1078	1,5391195	0,16591853	308,86	SNN	stannin
7874	4,01E-05	4,40E+00	2,37E-05	0,0393	4,2267696	0,16591055	6385,51	USP7	ubiquitin specific peptidase 7
523	2,71E-03	2,57E+00	1,84E-03	0,0531	3,1152617	0,16556775	2470,69	ATP6V1A	ATPase H+ transporting V1 subunit A
9889	3,08E-03	2,51E+00	2,10E-03	0,0538	3,0755757	0,16539609	1633,17	ZBED4	zinc finger BED-type containing 4
64745	1,45E-03	2,84E+00	9,67E-04	0,0501	3,2999741	0,16535143	2523,11	METTL17	methyltransferase like 17
64410	1,65E-01	7,83E-01	1,37E-01	0,1112	1,4869829	0,16534681	289,33	KLHL25	kelch like family member 25
107984913	8,16E-01	8,83E-02	7,90E-01	0,6206	0,2663756	0,16532054	8,56	LOC107984	uncharacterized LOC107984913
200035	1,87E-01	7,28E-01	1,58E-01	0,1169	1,4128409	0,16516416	233,19	NUDT17	nudix hydrolase 17
101927979	2,66E-01	5,75E-01	2,29E-01	0,1372	1,2025842	0,16495787	180,46	CAMTA2-AS	CAMTA2 antisense RNA 1
25845	1,46E-01	8,36E-01	1,21E-01	0,1061	1,5512576	0,16464677	288,5	PP7080	uncharacterized LOC25845
30837	1,42E-02	1,85E+00	1,03E-02	0,0642	2,5656332	0,16461227	1026,93	SOCS7	suppressor of cytokine signaling 7
441087	7,54E-01	1,23E-01	7,23E-01	0,465	0,3538401	0,16454083	14,76	LOC441087	uncharacterized LOC441087
388567	5,30E-02	1,28E+00	4,13E-02	0,0806	2,0408599	0,16443644	583,78	ZNF749	zinc finger protein 749
51177	7,45E-02	1,13E+00	5,90E-02	0,087	1,8879565	0,16427782	465,32	PLEKHO1	pleckstrin homology domain containing O1
25903	4,08E-01	3,89E-01	3,66E-01	0,1818	0,9032755	0,16419305	92,78	OLFML2B	olfactomedin like 2B
219738	2,69E-01	5,70E-01	2,32E-01	0,1373	1,1949009	0,16410666	168	FAM241B	family with sequence similarity 241 member B
64332	1,75E-03	2,76E+00	1,17E-03	0,0506	3,2458192	0,16409454	2687,82	NFKBIZ	NFKB inhibitor zeta
6419	9,18E-02	1,04E+00	7,37E-02	0,0916	1,7887402	0,16390175	418,25	SETMAR	SET domain and mariner transposase fusion gene
51023	1,34E-02	1,87E+00	9,68E-03	0,0633	2,5870941	0,16386822	1198,94	MRPS18C	mitochondrial ribosomal protein S18C
28970	4,46E-03	2,35E+00	3,10E-03	0,0554	2,9579906	0,16379697	1607,99	C11orf54	chromosome 11 open reading frame 54
644903	6,20E-01	2,08E-01	5,82E-01	0,2975	0,550121	0,16367734	34,29	GCC2-AS1	GCC2 antisense RNA 1
57606	6,44E-04	3,19E+00	4,16E-04	0,0464	3,5295082	0,16361626	4674,98	SLAIN2	SLAIN motif family member 2
1263	1,06E-01	9,75E-01	8,55E-02	0,0951	1,719798	0,16353111	488,74	PLK3	polo like kinase 3
106635539	7,13E-01	1,47E-01	6,80E-01	0,397	0,4117944	0,16349654	19,06	SNORA105A	small nucleolar RNA, H/ACA box 105A
6006	3,16E-03	2,50E+00	2,16E-03	0,0533	3,067516	0,16349405	1851,01	RHCE	Rh blood group CcEe antigens
10213	6,15E-05	4,21E+00	3,67E-05	0,0396	4,1271215	0,16341209	7427,76	PSMD14	proteasome 26S subunit, non-ATPase 14
55148	4,68E-04	3,33E+00	2,99E-04	0,0452	3,6158819	0,16336139	5104,82	UBR7	ubiquitin protein ligase E3 component n-recognin 7
11199	3,87E-01	4,12E-01	3,46E-01	0,1727	0,9422263	0,16272848	125,19	ANXA10	annexin A10
56910	4,61E-05	4,34E+00	2,73E-05	0,0388	4,1948037	0,16272128	8368,25	STARD7	StAR related lipid transfer domain containing 7
100302739	4,73E-03	2,33E+00	3,29E-03	0,0553	2,9393338	0,16265634	1635,59	PCNA-AS1	PCNA antisense RNA 1
150159	9,39E-02	1,03E+00	7,55E-02	0,0915	1,7774496	0,16261172	459,13	SLC9B1	solute carrier family 9 member B1
6621	4,33E-02	1,36E+00	3,32E-02	0,0763	2,1292602	0,16251332	890,22	SNAPC4	small nuclear RNA activating complex polypeptide 4
5426	8,74E-04	3,06E+00	5,71E-04	0,0471	3,4451941	0,1623152	3274,66	POLE	DNA polymerase epsilon, catalytic subunit
132001	3,32E-02	1,48E+00	2,52E-02	0,0724	2,2387055	0,16210893	817,59	TAMM41	TAM41 mitochondrial translocator assembly and maintenance homolog
641638	1,22E-01	9,14E-01	9,96E-02	0,0984	1,646765	0,1619767	767,83	SNHG6	small nucleolar RNA host gene 6
92014	4,07E-02	1,39E+00	3,12E-02	0,0751	2,154421	0,16189601	680,66	SLC25A51	solute carrier family 25 member 51
79833	2,50E-02	1,60E+00	1,86E-02	0,0687	2,3532119	0,16175039	1312,97	GEMIN6	gem nuclear organelle associated protein 6
109	1,44E-03	2,84E+00	9,57E-04	0,049	3,3030124	0,16172585	2756,26	ADCY3	adenylate cyclase 3
125488	6,96E-02	1,16E+00	5,50E-02	0,0843	1,9186584	0,16164721	555,56	TTC39C	tetratricopeptide repeat domain 39C
102723493	7,09E-01	1,49E-01	6,76E-01	0,3862	0,4181879	0,1614938	20,15	LOC102723	uncharacterized LOC102723493
51465	6,85E-04	3,16E+00	4,44E-04	0,0459	3,5125558	0,16114648	3248,55	UBE2J1	ubiquitin conjugating enzyme E2 J1
79139	5,23E-03	2,28E+00	3,65E-03	0,0554	2,9071901	0,16114605	4687,65	DERL1	derlin 1
348793	2,67E-02	1,57E+00	2,00E-02	0,0693	2,3263435	0,16110383	870,5	WDR53	WD repeat domain 53
10888	6,59E-01	1,81E-01	6,23E-01	0,3272	0,492128	0,16103811	31,19	GPR83	G protein-coupled receptor 83
27122	5,02E-01	2,99E-01	4,60E-01	0,2176	0,7391054	0,16081459	71,97	DKK3	dickkopf WNT signaling pathway inhibitor 3
347918	4,67E-01	3,31E-01	4,25E-01	0,2014	0,7976298	0,16066387	78,07	EP400P1	EP400 pseudogene 1
1982	4,65E-05	4,33E+00	2,76E-05	0,0383	4,19272	0,16055029	65324,01	EIF4G2	eukaryotic translation initiation factor 4 gamma 2
1962	1,35E-01	8,70E-01	1,11E-01	0,1006	1,5954889	0,16043207	410,28	EHHADH	enoyl-CoA hydratase and 3-hydroxyacyl CoA dehydrogenase
79660	6,86E-02	1,16E+00	5,42E-02	0,0833	1,9255463	0,16031687	545,4	PPP1R3B	protein phosphatase 1 regulatory subunit 3B
378	1,45E-04	3,84E+00	8,88E-05	0,0409	3,9193144	0,1602665	15860,33	ARF4	ADP ribosylation factor 4
102723859	1,50E-01	8,24E-01	1,24E-01	0,1041	1,5388153	0,16017271	321,89	TBC1D3E	TBC1 domain family member 3E
4854	7,91E-01	1,02E-01	7,63E-01	0,531	0,3010029	0,15983113	11,02	NOTCH3	notch receptor 3
151636	7,08E-03	2,15E+00	5,00E-03	0,0568	2,8067248	0,15941236	1685,81	DTX3L	deltex E3 ubiquitin ligase 3L
2649	2,97E-01	5,27E-01	2,59E-01	0,1411	1,1280786	0,15915811	164,29	NR6A1	nuclear receptor subfamily 6 group A member 1
107987266	7,64E-01	1,17E-01	7,34E-01	0,4677	0,3402776	0,15913684	13,52	LOC107987	uncharacterized LOC107987266
642843	3,63E-01	4,40E-01	3,22E-01	0,1608	0,9894584	0,15907083	117,71	CPSF4L	cleavage and polyadenylation specific factor 4 like
79659	4,31E-02	1,37E+00	3,31E-02	0,0746	2,1304624	0,15890779	805,9	DYNC2H1	dynein cytoplasmic 2 heavy chain 1
100507462	6,07E-01	2,17E-01	5,69E-01	0,2786	0,5699169	0,15879791	41	CCDC28A-A	CCDC28A antisense RNA 1
135112	5,00E-03	2,30E+00	3,48E-03	0,0543	2,921833	0,15878008	1936,29	NCOA7	nuclear receptor coactivator 7
105378519	4,93E-01	3,07E-01	4,51E-01	0,2106	0,7531659	0,15858591	71,03	LOC105378	uncharacterized LOC105378519
5594	1,65E-04	3,78E+00	1,02E-04	0,0408	3,886293	0,15847262	5408,33	MAPK1	mitogen-activated protein kinase 1
8934	2,74E-03	2,56E+00	1,86E-03	0,0509	3,110957	0,15819338	2008,66	RAB29	RAB29, member RAS oncogene family
492311	2,71E-01	5,67E-01	2,34E-01	0,133	1,1888489	0,1581052	183,81	IGIP	IgA inducing protein
3604	3,25E-01	4,88E-01	2,86E-01	0,1479	1,0674048	0,15787662	148,34	TNFRSF9	TNF receptor superfamily member 9
5176	5,23E-01	2,81E-01	4,81E-01	0,2241	0,7041393	0,15781063	60,17	SERPINF1	serpin family F member 1
7840	3,13E-03	2,50E+00	2,14E-03	0,0514	3,0702171	0,15776593	2701,51	ALMS1	ALMS1 centrosome and basal body associated protein
627	3,86E-02	1,41E+00	2,95E-02	0,0724	2,1763551	0,15752636	1271,93	BDNF	brain derived neurotrophic factor
80185	4,15E-02	1,38E+00	3,18E-02	0,0733	2,1464978	0,15742819	728,69	TTI2	TELO2 interacting protein 2
26027	7,83E-01	1,06E-01	7,54E-01	0,5024	0,3133482	0,15741266	12,61	ACOT11	acyl-CoA thioesterase 11
134265	2,88E-02	1,54E+00	2,17E-02	0,0684	2,296247	0,15714082	1192,45	AFAP1L1	actin filament associated protein 1 like 1
65010	2,66E-02	1,58E+00	1,99E-02	0,0673	2,3281078	0,15678732	1135,82	SLC26A6	solute carrier family 26 member 6
55703	7,54E-03	2,12E+00	5,34E-03	0,0562	2,7855764	0,15668111	1637,02	POLR3B	RNA polymerase III subunit B
23321	4,79E-02	1,32E+00	3,70E-02	0,0751	2,0853476	0,15656213	798,26	TRIM2	tripartite motif containing 2
721	5,36E-01	2,71E-01	4,95E-01	0,2292	0,682422	0,15638501	58,87	C4B	complement C4B (Chido blood group)
161253	7,46E-01	1,27E-01	7,14E-01	0,4274	0,3658475	0,15634954	16,13	REM2	RRAD and GEM like GTPase 2
81545	2,00E-03	2,70E+00	1,34E-03	0,0486	3,2067101	0,15582018	2631,22	FBXO38	F-box protein 38
7327	7,40E-04	3,13E+00	4,81E-04	0,0446	3,4913936	0,15564896	4460,71	UBE2G2	ubiquitin conjugating enzyme E2 G2
7789	3,68E-01	4,34E-01	3,27E-01	0,1585	0,9804039	0,15542398	131,8	ZXDA	zinc finger X-linked duplicated A
85302	1,54E-01	8,12E-01	1,28E-01	0,1018	1,5232078	0,15509039	328,51	FBF1	Fas binding factor 1
1519	9,38E-02	1,03E+00	7,54E-02	0,0872	1,7779501	0,15497907	474,39	CTSO	cathepsin O
63926	9,65E-02	1,02E+00	7,77E-02	0,0878	1,7641062	0,15491036	478,85	ANKEF1	ankyrin repeat and EF-hand domain containing 1
4534	5,30E-02	1,28E+00	4,12E-02	0,0757	2,0411458	0,1545528	684,01	MTM1	myotubularin 1
100506674	7,84E-01	1,06E-01	7,56E-01	0,4963	0,3113331	0,15451686	12,52	MRPS30-DT	MRPS30 divergent transcript
23048	4,30E-04	3,37E+00	2,74E-04	0,0425	3,638545	0,15446851	6071,87	FNBP1	formin binding protein 1
283635	1,38E-02	1,86E+00	1,00E-02	0,06	2,5746842	0,15445545	1851,29	FAM177A1	family with sequence similarity 177 member A1
57724	1,42E-03	2,85E+00	9,46E-04	0,0467	3,3061053	0,15443708	3386,93	EPG5	ectopic P-granules 5 autophagy tethering factor
7360	7,02E-04	3,15E+00	4,55E-04	0,044	3,5057658	0,15419697	5719,33	UGP2	UDP-glucose pyrophosphorylase 2
91775	4,62E-03	2,34E+00	3,21E-03	0,0523	2,947107	0,15406088	2032,47	NXPE3	neurexophilin and PC-esterase domain family member 3
57559	7,35E-03	2,13E+00	5,20E-03	0,0551	2,7940681	0,15399359	2086,15	STAMBPL1	STAM binding protein like 1
646603	2,25E-01	6,48E-01	1,92E-01	0,1178	1,305918	0,15389019	238,67	C4orf51	chromosome 4 open reading frame 51
100130557	2,57E-01	5,90E-01	2,22E-01	0,1258	1,2225307	0,15374828	218,2	NFYC-AS1	NFYC antisense RNA 1
100133941	2,20E-02	1,66E+00	1,63E-02	0,0639	2,4021047	0,15351836	1104,21	CD24	CD24 molecule
57763	9,52E-02	1,02E+00	7,66E-02	0,0866	1,770884	0,15336266	457,37	ANKRA2	ankyrin repeat family A member 2
387893	2,11E-03	2,68E+00	1,42E-03	0,0481	3,1900077	0,15332965	3477,71	KMT5A	lysine methyltransferase 5A
10584	7,32E-01	1,35E-01	7,00E-01	0,3967	0,3859166	0,15308697	19,64	COLEC10	collectin subfamily member 10
1775	6,94E-01	1,59E-01	6,60E-01	0,3476	0,4399375	0,15292072	24,37	DNASE1L2	deoxyribonuclease 1 like 2
51643	3,25E-02	1,49E+00	2,46E-02	0,068	2,2474885	0,15288223	1067,16	TMBIM4	transmembrane BAX inhibitor motif containing 4
105376806	4,43E-01	3,54E-01	4,02E-01	0,1821	0,8383206	0,15269727	93,32	LOC105376	uncharacterized LOC105376806
105376220	2,92E-01	5,35E-01	2,54E-01	0,1334	1,1410497	0,15222298	175,6	LINC02977	long intergenic non-protein coding RNA 2977
55628	4,87E-02	1,31E+00	3,77E-02	0,0732	2,0779837	0,15220239	685,48	ZNF407	zinc finger protein 407
23042	7,61E-04	3,12E+00	4,95E-04	0,0437	3,4834282	0,15217216	3782,94	PDXDC1	pyridoxal dependent decarboxylase domain containing 1
9780	5,66E-03	2,25E+00	3,96E-03	0,0528	2,8810522	0,15198653	5560,58	PIEZO1	piezo type mechanosensitive ion channel component 1
2009	4,55E-01	3,42E-01	4,14E-01	0,1857	0,8175614	0,15181348	95,19	EML1	EMAP like 1
10181	3,62E-03	2,44E+00	2,49E-03	0,0502	3,0244318	0,15180573	4101,56	RBM5	RNA binding motif protein 5
10846	2,14E-02	1,67E+00	1,58E-02	0,0629	2,412611	0,15167552	1077,71	PDE10A	phosphodiesterase 10A
284080	6,72E-01	1,73E-01	6,36E-01	0,3204	0,4730732	0,15158313	28,71	PICART1	p53 inducible cancer associated RNA transcript 1
57097	2,30E-01	6,38E-01	1,97E-01	0,1173	1,2915484	0,15145979	268,97	PARP11	poly(ADP-ribose) polymerase family member 11
256586	2,34E-01	6,31E-01	2,00E-01	0,1182	1,2805705	0,15142085	270,59	LYSMD2	LysM domain containing 2
100873945	4,54E-01	3,43E-01	4,13E-01	0,1848	0,8186331	0,15126786	88,2	HLTF-AS1	HLTF antisense RNA 1
57473	8,14E-03	2,09E+00	5,78E-03	0,0547	2,7599178	0,15106328	2175,09	ZNF512B	zinc finger protein 512B
6451	3,23E-02	1,49E+00	2,44E-02	0,0671	2,2506701	0,15099561	1634,65	SH3BGRL	SH3 domain binding glutamate rich protein like
841	3,08E-02	1,51E+00	2,32E-02	0,0662	2,2700749	0,15019152	1312,88	CASP8	caspase 8
25942	1,16E-03	2,94E+00	7,65E-04	0,0446	3,365281	0,15016479	4477,54	SIN3A	SIN3 transcription regulator family member A
80824	4,77E-02	1,32E+00	3,69E-02	0,0719	2,0872396	0,15002252	737,13	DUSP16	dual specificity phosphatase 16
8836	5,90E-03	2,23E+00	4,14E-03	0,0523	2,8674964	0,1498829	2127,9	GGH	gamma-glutamyl hydrolase
57404	2,44E-02	1,61E+00	1,82E-02	0,0634	2,361624	0,14965269	1309,11	CYP20A1	cytochrome P450 family 20 subfamily A member 1
1678	6,52E-02	1,19E+00	5,13E-02	0,0767	1,9492205	0,14956411	822,94	TIMM8A	translocase of inner mitochondrial membrane 8A
105274304	8,23E-01	8,46E-02	7,97E-01	0,5813	0,2569391	0,149369	9,18	LOC105274	uncharacterized LOC105274304

22879	1,26E-02	1,90E+00	9,08E-03	0,0572	2,6090181	0,14932444	1412,73	MON1B	MON1 homolog B, secretory trafficking associated
64783	5,76E-02	1,24E+00	4,50E-02	0,0744	2,0046562	0,14920348	720,72	RBM15	RNA binding motif protein 15
8559	1,78E-02	1,75E+00	1,31E-02	0,0601	2,4812545	0,14914229	1817,22	PRPF18	pre-mRNA processing factor 18
727936	1,43E-01	8,45E-01	1,18E-01	0,0953	1,5641408	0,14911644	388,63	GXYLT2	glucoside xylosyltransferase 2
102724438	6,30E-01	2,01E-01	5,92E-01	0,2781	0,5358523	0,14903229	39,13	LOC102724438	
23176	1,95E-03	2,71E+00	1,31E-03	0,0464	3,2130511	0,14901484	2847,65	SEPTIN8	septin 8
57665	1,05E-01	9,79E-01	8,50E-02	0,0864	1,7222452	0,14883302	505,89	RDH14	retinol dehydrogenase 14
4796	9,09E-03	2,04E+00	6,50E-03	0,0547	2,7214703	0,14878402	2542,31	TONSL	tonsoku like, DNA repair protein
100506083	2,93E-01	5,33E-01	2,55E-01	0,1304	1,1392938	0,14852596	201,64	DDX19A-DT	DDX19A divergent transcript
202781	3,08E-01	5,11E-01	2,69E-01	0,1342	1,1052955	0,14834457	198,34	PAXIP1-DT	PAXIP1 divergent transcript
105376369	4,56E-01	3,41E-01	4,15E-01	0,1817	0,8159953	0,14822991	103,72	LOC105376369	uncharacterized LOC105376369
100616400	5,94E-01	2,26E-01	5,55E-01	0,2501	0,5908324	0,14774156	48,91	MIR3198-2	microRNA 3198-2
10096	2,30E-04	3,64E+00	1,44E-04	0,0389	3,8016112	0,14772287	13272,86	ACTR3	actin related protein 3
56658	1,01E-02	2,00E+00	7,22E-03	0,0549	2,6865648	0,14760317	1528,68	TRIM39	tripartite motif containing 39
55069	1,01E-03	3,00E+00	6,65E-04	0,0434	3,4037714	0,14759357	4168,99	TMEM248	transmembrane protein 248
6871	2,02E-02	1,69E+00	1,49E-02	0,0606	2,4351743	0,14753331	1378,3	TADA2A	transcriptional adaptor 2A
56994	3,86E-02	1,41E+00	2,95E-02	0,0677	2,1762862	0,14728793	1410,54	CHPT1	choline phosphotransferase 1
692091	7,03E-01	1,53E-01	6,70E-01	0,3453	0,4264245	0,14725663	26,01	SNORD23	small nucleolar RNA, C/D box 23
729867	1,54E-01	8,12E-01	1,27E-01	0,0964	1,5246723	0,14705141	596,32	LOC729867	uncharacterized LOC729867
9957	6,01E-02	1,22E+00	4,70E-02	0,074	1,9858899	0,14697914	714,88	HS3ST1	heparan sulfate-glucosamine 3-sulfotransferase 1
55603	1,85E-01	7,33E-01	1,56E-01	0,1035	1,4200122	0,14697068	368,06	TENT5A	terminal nucleotidyltransferase 5A
3096	2,80E-02	1,55E+00	2,10E-02	0,0636	2,3071664	0,14680029	1282,85	HIVEP1	HIVEP zinc finger 1
6303	3,53E-03	2,45E+00	2,42E-03	0,0483	3,0325716	0,14661173	6891,4	SAT1	spermidine/spermine N1-acetyltransferase 1
51067	4,20E-02	1,38E+00	3,22E-02	0,0684	2,1418352	0,14660206	1096,86	YARS2	tyrosyl-tRNA synthetase 2
1306	5,25E-01	2,80E-01	4,83E-01	0,2089	0,700961	0,14643739	71,44	COL15A1	collagen type XV alpha 1 chain
254268	6,70E-01	1,74E-01	6,35E-01	0,308	0,4751761	0,146334	32,33	AKNAD1	AKNA domain containing 1
2969	1,35E-03	2,87E+00	8,98E-04	0,0441	3,3208019	0,14632543	3844,21	GTF2I	general transcription factor IIi
5089	4,53E-04	3,34E+00	2,89E-04	0,0403	3,6247565	0,14615389	5813,4	PBX2	PBX homeobox 2
5279	2,30E-02	1,64E+00	1,71E-02	0,0613	2,3850996	0,14612836	1238,06	PIGC	phosphatidylinositol glycan anchor biosynthesis class C
116224	4,21E-02	1,38E+00	3,23E-02	0,0683	2,1402068	0,14612019	822,97	PABIR1	PP2A Aalpha (PPP2R1A) and B55A (PPP2R2A) interacting phosphatase regulator 1
51512	2,16E-03	2,67E+00	1,45E-03	0,0459	3,1837766	0,14600368	4289,57	GTSE1	G2 and S-phase expressed 1
105372524	7,71E-01	1,13E-01	7,42E-01	0,4431	0,3292465	0,14590296	15,09	LOC105372524	uncharacterized LOC105372524
55809	4,83E-03	2,32E+00	3,36E-03	0,0497	2,9327904	0,14578872	4079,85	TRERF1	transcriptional regulating factor 1
8533	1,48E-03	2,83E+00	9,86E-04	0,0442	3,2944417	0,14567066	7507,49	COPS3	COP9 signalosome subunit 3
89978	3,01E-01	5,21E-01	2,62E-01	0,1298	1,1211393	0,14554791	198,51	DPH6	diphthamine biosynthesis 6
4185	6,64E-01	1,78E-01	6,28E-01	0,2999	0,4847652	0,14537971	38,9	ADAM11	ADAM metallopeptidase domain 11
56647	7,18E-04	3,14E+00	4,66E-04	0,0413	3,4993433	0,14455263	5528,29	BCCIP	BRCA2 and CDKN1A interacting protein
55308	3,31E-03	2,48E+00	2,27E-03	0,0473	3,052256	0,1442884	2796,21	DDX19A	DEAD-box helicase 19A
107985946	4,11E-01	3,86E-01	3,70E-01	0,1606	0,8969017	0,14406404	122,9	LOC107985946	uncharacterized LOC107985946
100996447	6,36E-01	1,97E-01	5,99E-01	0,2737	0,5258378	0,14393742	42,12	MLF1-DT	MLF1 divergent transcript
25853	2,58E-03	2,59E+00	1,75E-03	0,046	3,1298835	0,14392733	3790,29	DCAF12	DDB1 and CUL4 associated factor 12
92181	5,99E-03	2,22E+00	4,20E-03	0,0503	2,8623836	0,14386559	2238,8	UBTD2	ubiquitin domain containing 2
105379280	4,06E-01	3,91E-01	3,65E-01	0,1586	0,9059576	0,14369367	153,82	LOC105379280	uncharacterized LOC105379280
9117	5,79E-03	2,24E+00	4,06E-03	0,0498	2,87381	0,14324795	3620,52	SEC22C	SEC22 homolog C, vesicle trafficking protein
5889	3,29E-02	1,48E+00	2,49E-02	0,0639	2,2424165	0,14319695	1196,92	RAD51C	RAD51 paralog C
54901	1,67E-02	1,78E+00	1,22E-02	0,0571	2,5049944	0,14313962	1432,2	CDKAL1	CDK5 regulatory subunit associated protein 1 like 1
9858	2,57E-02	1,59E+00	1,92E-02	0,061	2,3423599	0,14295802	1324,19	PPP1R26	protein phosphatase 1 regulatory subunit 26
3776	5,16E-01	2,87E-01	4,74E-01	0,1993	0,7162671	0,14273517	84,84	KCNK2	potassium two pore domain channel subfamily K member 2
7011	4,43E-02	1,35E+00	3,41E-02	0,0673	2,1189542	0,14266617	872,37	TEP1	telomerase associated protein 1
107985878	8,25E-01	8,35E-02	8,00E-01	0,5626	0,2535152	0,1426375	9,46	LOC107985878	
121227	1,16E-01	9,36E-01	9,42E-02	0,085	1,6738212	0,14226021	485,38	LRIG3	leucine rich repeats and immunoglobulin like domains 3
3480	6,28E-03	2,20E+00	4,42E-03	0,05	2,8466669	0,1422179	2103,73	IGF1R	insulin like growth factor 1 receptor
92312	1,42E-01	8,48E-01	1,17E-01	0,0907	1,5678176	0,14221123	420,13	MEX3A	mex-3 RNA binding family member A
112268155	2,36E-02	1,63E+00	1,76E-02	0,0599	2,374516	0,1422036	1472,09	LOC112268155	
114991	2,88E-02	1,54E+00	2,16E-02	0,0618	2,2968409	0,14201029	1111,49	ZNF618	zinc finger protein 618
100652748	2,41E-01	6,18E-01	2,06E-01	0,1119	1,26392	0,14146819	268,98	TIMM23B	translocase of inner mitochondrial membrane 23 homolog B
23394	1,29E-03	2,89E+00	8,51E-04	0,0424	3,3356456	0,14140448	5088,3	ADNP	activity dependent neuroprotector homeobox
11154	2,02E-01	6,95E-01	1,71E-01	0,1032	1,3687308	0,14122184	336,8	AP4S1	adaptor related protein complex 4 subunit sigma 1
2752	8,63E-04	3,06E+00	5,64E-04	0,0409	3,4485057	0,1411991	5785,48	GLUL	glutamate-ammonia ligase
54910	3,24E-02	1,49E+00	2,45E-02	0,0627	2,2495063	0,14094878	1865,05	SEMA4C	semaphorin 4C
101927721	8,13E-01	8,99E-02	7,87E-01	0,5218	0,2699783	0,14087651	10,74	LNCPRESS1	lncRNA p53 regulated and ESC associated 1
105370902	4,76E-01	3,22E-01	4,35E-01	0,18	0,7809349	0,14059665	94,61	LOC105370902	uncharacterized LOC105370902
10342	8,47E-04	3,07E+00	5,53E-04	0,0406	3,4536019	0,14034005	8094,11	TFG	trafficking from ER to golgi regulator
9324	3,73E-02	1,43E+00	2,85E-02	0,064	2,1907057	0,14012559	1777,89	HMGN3	high mobility group nucleosomal binding domain 3
376267	2,44E-01	6,13E-01	2,10E-01	0,1117	1,2548077	0,14011879	266,58	RAB15	RAB15, member RAS oncogene family
102465448	8,22E-01	8,51E-02	7,97E-01	0,5431	0,257862	0,14003679	10	MIR6748	microRNA 6748
11173	5,42E-01	2,66E-01	5,01E-01	0,2082	0,6722282	0,13992633	69,75	ADAMTS7	ADAM metallopeptidase with thrombospondin type 1 motif 7
81579	5,03E-02	1,30E+00	3,90E-02	0,0676	2,063666	0,13960307	995,26	PLA2G12A	phospholipase A2 group XIIA
58478	9,59E-03	2,02E+00	6,87E-03	0,0516	2,7030826	0,13950834	3212,02	ENOPH1	enolase-phosphatase 1
81844	1,64E-02	1,79E+00	1,20E-02	0,0555	2,5127573	0,13933529	2223,44	TRIM56	tripartite motif containing 56
25925	3,75E-02	1,43E+00	2,86E-02	0,0637	2,1883735	0,1393224	1262,23	ZNF521	zinc finger protein 521
644714	1,44E-01	8,42E-01	1,19E-01	0,0894	1,5579648	0,13931739	423,6	LIMD1-AS1	LIMD1 antisense RNA 1
132321	2,11E-01	6,76E-01	1,79E-01	0,1036	1,3449693	0,13928963	350,47	C4orf33	chromosome 4 open reading frame 33
107986003	1,35E-01	8,70E-01	1,11E-01	0,0874	1,5931598	0,13918151	487,8	LOC107986003	uncharacterized LOC107986003
1955	5,38E-02	1,27E+00	4,19E-02	0,0684	2,0348535	0,1391638	1083,46	MEGF9	multiple EGF like domains 9
51020	3,51E-02	1,45E+00	2,67E-02	0,0627	2,2161496	0,13900748	1314,86	HDDC2	HD domain containing 2
10404	2,59E-01	5,87E-01	2,23E-01	0,1139	1,2194149	0,13890313	249,07	CPQ	carboxypeptidase Q
4247	1,92E-03	2,72E+00	1,29E-03	0,0432	3,2176993	0,1388724	4088,54	MGAT2	alpha-1,6-mannosyl-glycoprotein 2-beta-N-acetylglucosaminyltransferase
112268444	4,98E-01	3,03E-01	4,56E-01	0,1863	0,7452726	0,13883747	92,3	LOC112268444	
25888	5,06E-02	1,30E+00	3,93E-02	0,0673	2,0614076	0,13865158	1173,53	ZNF473	zinc finger protein 473
54902	1,40E-02	1,85E+00	1,01E-02	0,0539	2,5706954	0,13843438	2780,76	TTC19	tetratricopeptide repeat domain 19
107986008	8,16E-01	8,83E-02	7,90E-01	0,5189	0,2662335	0,13814986	11,5	LOC107986008	
29970	1,58E-01	8,01E-01	1,31E-01	0,0913	1,5109184	0,13800446	418,95	SCHIP1	schwannomin interacting protein 1
4249	5,50E-03	2,26E+00	3,84E-03	0,0477	2,8908528	0,13784087	2747,36	MGAT5	alpha-1,6-mannosylglycoprotein 6-beta-N-acetylglucosaminyltransferase
9813	2,39E-03	2,62E+00	1,62E-03	0,0437	3,1527715	0,13773552	4983,84	EFCAB14	EF-hand calcium binding domain 14
51335	2,14E-03	2,67E+00	1,44E-03	0,0432	3,1863706	0,13765722	5946,55	NGRN	neugrin, neurite outgrowth associated
54887	3,48E-03	2,46E+00	2,39E-03	0,0452	3,0367885	0,13725496	3088,09	BLTP3A	bridge-like lipid transfer protein family member 3A
25778	5,65E-02	1,25E+00	4,41E-02	0,0681	2,013237	0,13715134	1158,38	DSTYK	dual serine/threonine and tyrosine protein kinase
100093631	8,82E-03	2,05E+00	6,29E-03	0,0501	2,7323222	0,13698126	2483,69	GTF2IP4	general transcription factor IIi pseudogene 4
283579	3,20E-01	4,95E-01	2,81E-01	0,1269	1,0787187	0,13687096	202,18	C14orf178	chromosome 14 open reading frame 178
84895	7,64E-02	1,12E+00	6,07E-02	0,0729	1,8758749	0,13682316	828,35	MIGA2	mitoguardin 2
101929074	8,26E-01	8,30E-02	8,02E-01	0,5432	0,251256	0,13648812	10,35	PIK3CD-AS2	PIK3CD antisense RNA 2
9392	2,07E-02	1,68E+00	1,53E-02	0,0563	2,424981	0,13643968	1515,83	TGFBRAP1	transforming growth factor beta receptor associated protein 1
54944	2,37E-01	6,25E-01	2,02E-01	0,107	1,2751259	0,13641962	294,56	LINC01521	long intergenic non-protein coding RNA 1521
23491	7,24E-01	1,40E-01	6,91E-01	0,3431	0,3972229	0,13629538	27,74	CES3	carboxylesterase 3
3218	6,84E-01	1,65E-01	6,49E-01	0,299	0,4551365	0,13609345	35,97	HOXB8	homeobox B8
100506901	4,37E-01	3,60E-01	3,95E-01	0,1601	0,849824	0,13605023	122,19	LL0XNC01-2	uncharacterized LL0XNC01-250H12.3
1723	1,12E-01	9,51E-01	9,10E-02	0,0805	1,6901597	0,13601865	615,31	DHODH	dihydroorotate dehydrogenase (quinone)
154661	6,92E-01	1,60E-01	6,58E-01	0,3068	0,4433671	0,13601281	32,23	RUNDC3B	RUN domain containing 3B
284677	6,14E-01	2,12E-01	5,76E-01	0,2434	0,5587794	0,13599311	53,74	SNHG28	small nucleolar RNA host gene 28
79670	2,39E-02	1,62E+00	1,78E-02	0,0573	2,3695171	0,13581497	2385,38	TUT7	terminal uridylyl transferase 7
9223	1,84E-02	1,74E+00	1,35E-02	0,055	2,4695132	0,13579182	2121,54	MAGI1	membrane associated guanylate kinase, WW and PDZ domain containing 1
57465	1,02E-01	9,91E-01	8,22E-02	0,0781	1,7378068	0,13575034	676,27	TBC1D24	TBC1 domain family member 24
5717	5,73E-04	3,24E+00	3,69E-04	0,0381	3,5612686	0,13563914	11071,11	PSMD11	proteasome 26S subunit, non-ATPase 11
107984016	8,45E-01	7,31E-02	8,22E-01	0,6016	0,2244151	0,13501439	8,3	LOC107984016	uncharacterized LOC107984016
57185	1,70E-03	2,77E+00	1,13E-03	0,0414	3,2551235	0,13486654	4935,7	NIPAL3	NIPA like domain containing 3
404636	1,38E-02	1,86E+00	9,98E-03	0,0523	2,5764017	0,13473807	1925,42	DENND10	DENN domain containing 10
101060264	6,81E-01	1,67E-01	6,46E-01	0,2927	0,4596342	0,1345249	35,94	FOXP4-AS1	FOXP4 antisense RNA 1
100505385	1,69E-01	7,72E-01	1,41E-01	0,0913	1,4733478	0,1344661	419,71	IQCJ-SCHIP	IQCJ-SCHIP1 readthrough
84186	3,86E-02	1,41E+00	2,95E-02	0,0617	2,1771949	0,13432299	1158,66	ZCCHC7	zinc finger CCHC-type containing 7
1244	5,55E-01	2,56E-01	5,15E-01	0,2059	0,6517656	0,13417025	77,68	ABCC2	ATP binding cassette subfamily C member 2
8693	1,28E-01	8,93E-01	1,05E-01	0,0827	1,6209026	0,13398335	530,34	GALNT4	polypeptide N-acetylgalactosaminyltransferase 4
107987295	7,26E-01	1,39E-01	6,94E-01	0,34	0,3934045	0,13376596	28,93	LINC02246	long intergenic non-protein coding RNA 2246
107986085	8,23E-01	8,46E-02	7,97E-01	0,5202	0,256795	0,13357564	10,82	LINC02019	long intergenic non-protein coding RNA 2019
107987272	5,10E-01	2,92E-01	4,68E-01	0,184	0,7253847	0,1334864	99,3	LOC107987272	uncharacterized LOC107987272
84517	4,63E-01	3,34E-01	4,22E-01	0,1661	0,803407	0,13344355	111,6	ACTRT3	actin related protein T3
57541	8,75E-02	1,06E+00	7,00E-02	0,0736	1,8118004	0,13333714	740	ZNF398	zinc finger protein 398
57003	9,84E-04	3,01E+00	6,45E-04	0,0391	3,4120319	0,13331807	8740,74	CCDC47	coiled-coil domain containing 47
8773	2,72E-02	1,57E+00	2,04E-02	0,0575	2,3193198	0,13326458	1868,6	SNAP23	synaptosome associated protein 23
246329	8,47E-01	7,21E-02	8,25E-01	0,6014	0,2211946	0,13303353	8,71	STAC3	SH3 and cysteine rich domain 3

55244	6,55E-01	1,84E-01	6,18E-01	0,2668	0,4980829	0,13286895	44,05	SLC47A1	solute carrier family 47 member 1
100288428	8,08E-01	9,26E-02	7,82E-01	0,4788	0,2772217	0,13272024	12,89	LMCD1-AS1	LMCD1 antisense RNA 1
1874	2,27E-02	1,64E+00	1,69E-02	0,0555	2,3892546	0,13264039	3654,02	E2F4	E2F transcription factor 4
56922	6,73E-03	2,17E+00	4,75E-03	0,047	2,8237243	0,13259454	2668,38	MCCC1	methylcrotonyl-CoA carboxylase subunit 1
26750	2,20E-02	1,66E+00	1,63E-02	0,0552	2,4025921	0,1325857	1970,12	RPS6KC1	ribosomal protein S6 kinase C1
94239	3,38E-03	2,47E+00	2,32E-03	0,0435	3,0464459	0,13254756	10857,41	H2AZ2	H2A.Z variant histone 2
494514	9,45E-02	1,02E+00	7,60E-02	0,0746	1,7744024	0,13240907	690,53	TYMSOS	TYMS opposite strand RNA
9320	5,99E-04	3,22E+00	3,86E-04	0,0372	3,5493156	0,13219088	11508,18	TRIP12	thyroid hormone receptor interactor 12
4594	1,75E-02	1,76E+00	1,28E-02	0,0531	2,4893168	0,13218796	1895,36	MMUT	methylmalonyl-CoA mutase
100113380	7,79E-01	1,08E-01	7,50E-01	0,4144	0,3188319	0,13212348	18,58	SNORD125	small nucleolar RNA, C/D box 125
133015	7,30E-02	1,14E+00	5,78E-02	0,0696	1,8970528	0,13203812	872,2	PACRGL	parkin coregulated like
729799	6,11E-01	2,14E-01	5,72E-01	0,2336	0,564719	0,13192359	55,34	SEC14L1P1	SEC14 like 1 pseudogene 1
9415	2,87E-03	2,54E+00	1,95E-03	0,0426	3,0973623	0,13184738	6892,14	FADS2	fatty acid desaturase 2
286016	7,98E-01	9,80E-02	7,71E-01	0,4519	0,2916264	0,13179277	16,77	TPI1P2	triosephosphate isomerase 1 pseudogene 2
107985194	6,99E-01	1,56E-01	6,65E-01	0,3032	0,4325377	0,13116429	32,41	LINC02798	long intergenic non-protein coding RNA 2798
30000	4,71E-03	2,33E+00	3,27E-03	0,0446	2,9409539	0,13110424	12003,62	TNPO2	transportin 2
11311	1,70E-02	1,77E+00	1,25E-02	0,0524	2,4989357	0,13102782	1775,45	VPS45	vacuolar protein sorting 45 homolog
440104	2,96E-01	5,29E-01	2,58E-01	0,1158	1,1306422	0,13091841	237,55	TMEM198B	transmembrane protein 198B (pseudogene)
100422961	8,17E-01	8,78E-02	7,91E-01	0,4949	0,2644049	0,13084324	12,44	MIR4315-2	microRNA 4315-2
7372	6,52E-02	1,19E+00	5,13E-02	0,067	1,9488997	0,13062627	1482,5	UMPS	uridine monophosphate synthetase
200403	8,12E-01	9,04E-02	7,86E-01	0,4815	0,2710794	0,13053794	13,37	VWA3B	von Willebrand factor A domain containing 3B
105372582	7,38E-01	1,32E-01	7,06E-01	0,346	0,3769175	0,13039758	26,33	LOC105372	uncharacterized LOC105372582
150737	3,53E-01	4,52E-01	3,12E-01	0,1289	1,0106133	0,1302431	206,88	TTC30B	tetratricopeptide repeat domain 30B
692227	5,37E-01	2,70E-01	4,96E-01	0,1913	0,6802103	0,13015324	86,9	SNORD104	small nucleolar RNA, C/D box 104
83694	2,39E-01	6,22E-01	2,05E-01	0,1024	1,2675342	0,12973563	322,29	RPS6KL1	ribosomal protein S6 kinase like 1
55102	3,97E-02	1,40E+00	3,04E-02	0,0599	2,1649447	0,12967052	1314,42	ATG2B	autophagy related 2B
222223	7,22E-02	1,14E+00	5,71E-02	0,0681	1,9024397	0,12953286	855,21	ELAPOR2	endosome-lysosome associated apoptosis and autophagy regulator family member 2
106660610	8,02E-01	9,58E-02	7,75E-01	0,4522	0,2863135	0,12945783	14,65	MIR5689HG	MIR5689 host gene
23362	2,60E-02	1,59E+00	1,94E-02	0,0553	2,3377808	0,12926305	2027	PSD3	pleckstrin and Sec7 domain containing 3
102723508	5,99E-01	2,23E-01	5,60E-01	0,222	0,5821745	0,12924597	62,31	KANTR	KANTR integral membrane protein
83759	7,83E-02	1,11E+00	6,22E-02	0,0693	1,8646683	0,12920316	886,16	RBM4B	RNA binding motif protein 4B
83903	5,51E-02	1,26E+00	4,30E-02	0,0635	2,0239824	0,12858897	1427,26	HASPIN	histone H3 associated protein kinase
11069	8,10E-01	9,15E-02	7,84E-01	0,4694	0,2738939	0,12856781	14,16	RAPGEF4	Rap guanine nucleotide exchange factor 4
4575	3,92E-01	4,07E-01	3,51E-01	0,1375	0,9328919	0,12831197	218,58	TRNS2	tRNA-Ser
103752589	7,68E-01	1,15E-01	7,39E-01	0,3846	0,3333764	0,12820027	20,36	TMEM92-AS	TMEM92 antisense RNA 1
55145	1,62E-01	7,90E-01	1,35E-01	0,0855	1,4952134	0,1277896	502,61	THAP1	THAP domain containing 1
2188	2,59E-01	5,87E-01	2,24E-01	0,1047	1,2171626	0,1274973	309,02	FANCF	FA complementation group F
101927479	4,33E-01	3,64E-01	3,92E-01	0,1488	0,856455	0,12745241	144,26	EPHA2-AS1	EPHA2 antisense RNA 1
282997	6,44E-01	1,91E-01	6,07E-01	0,2476	0,5139629	0,12723958	53,38	PDCD4-AS1	PDCD4 antisense RNA 1
54877	1,46E-01	8,36E-01	1,20E-01	0,0819	1,5529453	0,12718101	587,3	ZCCHC2	zinc finger CCHC-type containing 2
100534612	2,60E-01	5,85E-01	2,24E-01	0,1045	1,2158085	0,12706998	315,56	C1QTNF3-A	C1QTNF3-AMACR readthrough (NMD candidate)
6339	3,41E-01	4,67E-01	3,01E-01	0,1227	1,0346392	0,1269224	255,96	SCNN1D	sodium channel epithelial 1 subunit delta
64747	6,07E-02	1,22E+00	4,76E-02	0,0639	1,9812849	0,12667674	2233,04	MFSD1	major facilitator superfamily domain containing 1
105378954	4,51E-01	3,46E-01	4,10E-01	0,1535	0,8247058	0,12658709	152,3	LOC105378	954
54882	8,50E-03	2,07E+00	6,05E-03	0,0461	2,7448646	0,12652003	3567,9	ANKHD1	ankyrin repeat and KH domain containing 1
100129794	6,33E-01	1,99E-01	5,95E-01	0,2379	0,5311699	0,12634228	53,87	SLC25A21-A	SLC25A21 antisense RNA 1
57478	1,28E-01	8,93E-01	1,05E-01	0,0778	1,6222482	0,12626326	713,85	USP31	ubiquitin specific peptidase 31
60684	2,40E-02	1,62E+00	1,78E-02	0,0533	2,3690188	0,12621322	1893,28	TRAPPC11	trafficking protein particle complex subunit 11
84804	2,00E-01	6,99E-01	1,69E-01	0,0917	1,3764299	0,12615118	413,81	MFSD9	major facilitator superfamily domain containing 9
4237	2,12E-01	6,74E-01	1,80E-01	0,0939	1,3418271	0,12593857	461,9	MFAP2	microfibril associated protein 2
4711	1,16E-02	1,94E+00	8,38E-03	0,0477	2,6364858	0,12580536	2837,2	NDUFB5	NADH:ubiquinone oxidoreductase subunit B5
100507065	8,29E-01	8,14E-02	8,05E-01	0,5104	0,2463276	0,12573402	11,53	MSRB3-AS1	MSRB3 antisense RNA 1
7292	5,51E-01	2,59E-01	5,11E-01	0,191	0,6580032	0,12570222	85,66	TNFSF4	TNF superfamily member 4
2247	4,15E-01	3,82E-01	3,73E-01	0,1412	0,8900129	0,12567493	158,15	FGF2	fibroblast growth factor 2
51375	1,59E-02	1,80E+00	1,16E-02	0,0498	2,5239534	0,12562717	2521,51	SNX7	sorting nexin 7
6240	1,03E-03	2,99E+00	6,74E-04	0,0369	3,3999702	0,12548242	14985,92	RRM1	ribonucleotide reductase catalytic subunit M1
642946	7,09E-01	1,49E-01	6,75E-01	0,2992	0,4190014	0,12535664	36,56	FLVCR1-DT	FLVCR1 divergent transcript
55093	6,77E-02	1,17E+00	5,34E-02	0,0648	1,931658	0,12510946	963,96	NTAQ1	N-terminal glutamine amidase 1
55149	4,63E-02	1,33E+00	3,57E-02	0,0594	2,100298	0,12484841	1226,07	MTPAP	mitochondrial poly(A) polymerase
79230	2,65E-01	5,77E-01	2,29E-01	0,1037	1,2033372	0,1247842	321,44	ZNF557	zinc finger protein 557
1477	1,65E-02	1,78E+00	1,21E-02	0,0497	2,5105837	0,12471505	3236,09	CSTF1	cleavage stimulation factor subunit 1
56928	1,38E-01	8,60E-01	1,14E-01	0,0788	1,5814907	0,12463204	690,69	SPPL2B	signal peptide peptidase like 2B
101927060	1,62E-01	7,90E-01	1,35E-01	0,0833	1,4956159	0,12458641	580,88	LOC101927(	uncharacterized LOC101927060
654	9,16E-02	1,04E+00	7,35E-02	0,0696	1,7895073	0,12457881	920,61	BMP6	bone morphogenetic protein 6
10668	1,16E-01	9,36E-01	9,41E-02	0,0744	1,6739631	0,12449222	762,5	CGRRF1	cell growth regulator with ring finger domain 1
3949	4,41E-03	2,36E+00	3,06E-03	0,042	2,9615999	0,12447025	16055,52	LDLR	low density lipoprotein receptor
91734	4,88E-01	3,12E-01	4,46E-01	0,1634	0,7617324	0,1244512	115,73	IDI2	isopentenyl-diphosphate delta isomerase 2
647087	4,89E-02	1,31E+00	3,79E-02	0,0598	2,0760217	0,12404396	1349,17	STMP1	short transmembrane mitochondrial protein 1
57690	1,20E-01	9,21E-01	9,76E-02	0,0748	1,6567269	0,12396361	691,97	TNRC6C	trinucleotide repeat containing adaptor 6C
107133515	3,36E-02	1,47E+00	2,55E-02	0,0554	2,2340378	0,12380939	1633,23	SMURF2P1-	SMURF2P1-LRRC37BP1 readthrough transcribed pseudogene
25831	4,45E-03	2,35E+00	3,09E-03	0,0418	2,9590291	0,12379892	8354,69	HECTD1	HECT domain E3 ubiquitin protein ligase 1
285613	3,20E-01	4,95E-01	2,80E-01	0,1144	1,0792141	0,12343613	253,27	RELL2	RELT like 2
203197	1,48E-01	8,30E-01	1,23E-01	0,0799	1,5438194	0,12338308	556,63	TMEM268	transmembrane protein 268
79823	2,63E-01	5,80E-01	2,27E-01	0,102	1,2079816	0,12320817	339,09	CAMKMT	calmodulin-lysine N-methyltransferase
105372483	8,16E-01	8,83E-02	7,90E-01	0,4629	0,2657146	0,12299386	15,32	ZNF497-AS1	ZNF497 antisense RNA 1
728392	6,93E-01	1,59E-01	6,59E-01	0,279	0,4408242	0,12298483	39,74	LOC728392	uncharacterized LOC728392
284802	1,36E-01	8,66E-01	1,12E-01	0,077	1,5909549	0,12257387	744,75	FRG1BP	FSHD region gene 1 family member B, pseudogene
22926	3,39E-03	2,47E+00	2,33E-03	0,0402	3,0449175	0,12253017	6198,97	ATF6	activating transcription factor 6
399671	6,91E-01	1,61E-01	6,57E-01	0,2755	0,4445196	0,12245537	38,75	HEATR4	HEAT repeat containing 4
11019	2,42E-01	6,16E-01	2,07E-01	0,0971	1,2612278	0,12243793	401,8	LIAS	lipoic acid synthetase
105416157	6,38E-01	1,95E-01	6,01E-01	0,2342	0,5227881	0,12242301	55,09	NKILA	NF-kappaB interacting lncRNA
100528030	1,43E-01	8,45E-01	1,18E-01	0,0784	1,5620417	0,12240736	591,29	POC1B-GAL	POC1B-GALNT4 readthrough
81565	2,63E-02	1,58E+00	1,97E-02	0,0524	2,3324326	0,12227113	3242,87	NDEL1	nudE neurodevelopment protein 1 like 1
7419	2,82E-02	1,55E+00	2,12E-02	0,053	2,3050452	0,12212747	6621,34	VDAC3	voltage dependent anion channel 3
55071	9,07E-02	1,04E+00	7,27E-02	0,0681	1,7945095	0,12212461	1437,76	C9orf40	chromosome 9 open reading frame 40
7730	6,28E-01	2,02E-01	5,91E-01	0,2269	0,5379294	0,12207521	61,11	ZNF177	zinc finger protein 177
100288778	1,83E-01	7,38E-01	1,53E-01	0,0855	1,4280897	0,12205466	535,66	WASH8P	WAS protein family homolog 8, pseudogene
400657	4,83E-01	3,16E-01	4,41E-01	0,1579	0,7704621	0,12169234	122,58	ZNF407-AS1	ZNF407 antisense RNA 1
54883	3,01E-02	1,52E+00	2,27E-02	0,0533	2,278568	0,12146707	1651,06	CWC25	CWC25 spliceosome associated protein homolog
54583	1,68E-02	1,77E+00	1,23E-02	0,0485	2,503567	0,1213136	2809,41	EGLN1	egl-9 family hypoxia inducible factor 1
867	8,21E-03	2,09E+00	5,84E-03	0,0439	2,7569031	0,12111328	4389,1	CBL	Cbl proto-oncogene
2483	5,35E-02	1,27E+00	4,16E-02	0,0593	2,0370366	0,12086265	2145,85	FRG1	FSHD region gene 1
51022	1,94E-01	7,12E-01	1,64E-01	0,0867	1,3931294	0,12079324	547,44	GLRX2	glutaredoxin 2
56133	2,91E-01	5,36E-01	2,53E-01	0,1054	1,1440892	0,12059401	314,47	PCDHB2	protocadherin beta 2
1992	5,02E-03	2,30E+00	3,50E-03	0,0412	2,9203659	0,12046341	6032,87	SERPINB1	serpin family B member 1
6891	4,60E-03	2,34E+00	3,19E-03	0,0408	2,9483963	0,12037938	10752,29	TAP2	transporter 2, ATP binding cassette subfamily B member
84864	1,93E-02	1,71E+00	1,42E-02	0,0491	2,4509808	0,12031245	2936,81	RIOX2	ribosomal oxygenase 2
100132911	3,92E-01	4,07E-01	3,51E-01	0,129	0,9325422	0,12027479	189,51	DPH3P1	diphthamide biosynthesis 3 pseudogene 1
3679	7,85E-01	1,05E-01	7,56E-01	0,3878	0,3100949	0,12026436	22,34	ITGA7	integrin subunit alpha 7
9857	2,95E-02	1,53E+00	2,22E-02	0,0525	2,2868867	0,12017521	3480,53	CEP350	centrosomal protein 350
10732	2,27E-02	1,64E+00	1,69E-02	0,0503	2,3892963	0,12013018	2471,1	TCFL5	transcription factor like 5
11083	1,06E-02	1,97E+00	7,62E-03	0,045	2,668679	0,12011229	4788,47	DIDO1	death inducer-obliterator 1
8826	4,26E-03	2,37E+00	2,95E-03	0,0404	2,9729494	0,12004423	23245,93	IQGAP1	IQ motif containing GTPase activating protein 1
1457	1,59E-03	2,80E+00	1,06E-03	0,0366	3,2734533	0,1198482	10406,26	CSNK2A1	casein kinase 2 alpha 1
388685	4,23E-01	3,74E-01	3,81E-01	0,1367	0,8757323	0,11975415	172,93	LINC01138	long intergenic non-protein coding RNA 1138
54621	9,22E-02	1,04E+00	7,40E-02	0,0669	1,7865698	0,11959816	935,74	VSIG10	V-set and immunoglobulin domain containing 10
101929559	7,77E-01	1,10E-01	7,48E-01	0,3711	0,3217653	0,11942122	23,63	PIRAT1	PU.1 (SP1) induced regulator of S100A8 and S100A9 alarmin transcription 1
80823	3,83E-01	4,17E-01	3,42E-01	0,1257	0,9498447	0,11938401	199,16	GPRASP3	G protein-coupled receptor associated sorting protein family member 3
100874113	5,88E-01	2,31E-01	5,49E-01	0,1992	0,5993156	0,11938147	76,6	YEATS2-AS1	YEATS2 antisense RNA 1
105372791	7,67E-01	1,15E-01	7,37E-01	0,354	0,3358046	0,118867	23,56	LOC105372	uncharacterized LOC105372791
150864	4,36E-01	3,61E-01	3,94E-01	0,1395	0,8514993	0,11881834	174,2	FAM117B	family with sequence similarity 117 member B
378708	1,56E-01	8,07E-01	1,29E-01	0,078	1,5172815	0,11832743	629,04	CENPS	centromere protein S
171483	7,57E-01	1,21E-01	7,27E-01	0,3388	0,3490679	0,11826396	27,62	FAM9B	family with sequence similarity 9 member B
286343	2,92E-01	5,35E-01	2,54E-01	0,1036	1,1399172	0,11811778	314,28	LURAP1L	leucine rich adaptor protein 1 like
400	1,60E-02	1,80E+00	1,17E-02	0,0468	2,5223564	0,11793536	5946,58	ARL1	ADP ribosylation factor like GTPase 1
100528062	1,06E-01	9,75E-01	8,59E-02	0,0684	1,7173954	0,11745062	867,89	ARMCX5-GF	ARMCX5-GPRASP2 readthrough
64648	7,91E-01	1,02E-01	7,63E-01	0,3887	0,3016035	0,11724561	20,06	SPANXD	SPANX family member D
11059	4,79E-02	1,32E+00	3,71E-02	0,0561	2,0848956	0,11703335	1529,66	WWP1	WW domain containing E3 ubiquitin protein ligase 1
54925	1,86E-01	7,30E-01	1,57E-01	0,0825	1,4163826	0,11690846	649,1	ZSCAN32	zinc finger and SCAN domain containing 32
128077	2,76E-02	1,56E+00	2,07E-02	0,0505	2,3136025	0,11686695	2810,95	LIX1L	limb and CNS expressed 1 like

10482	2,01E-02	1,70E+00	1,48E-02	0,0479	2,4360912	0,11677084	4335,09	NXF1	nuclear RNA export factor 1
55262	2,47E-01	6,07E-01	2,12E-01	0,0936	1,2480724	0,116761	383,59	TRAPPC14	trafficking protein particle complex subunit 14
6949	1,32E-02	1,88E+00	9,56E-03	0,045	2,5914756	0,11672392	6354,57	TCOF1	treacle ribosome biogenesis factor 1
64794	5,75E-02	1,24E+00	4,50E-02	0,0582	2,0050569	0,11670309	1417,18	DDX31	DEAD-box helicase 31
64087	9,70E-03	2,01E+00	6,95E-03	0,0431	2,6990039	0,11643048	3945,21	MCCC2	methylcrotonyl-CoA carboxylase subunit 2
6950	1,71E-03	2,77E+00	1,14E-03	0,0358	3,2526715	0,11634995	16004,6	TCP1	t-complex 1
693206	6,33E-01	1,99E-01	5,95E-01	0,219	0,5309757	0,11627398	63,21	MIR621	microRNA 621
51661	1,79E-01	7,47E-01	1,50E-01	0,0807	1,4380703	0,11602984	591,89	FKBP7	FKBP prolyl isomerase 7
3750	6,86E-01	1,64E-01	6,51E-01	0,2566	0,4522153	0,11602285	47,47	KCND1	potassium voltage-gated channel subfamily D member 1
3006	5,02E-02	1,30E+00	3,90E-02	0,0562	2,0646956	0,11597152	2215,24	H1-2	H1.2 linker histone, cluster member
5326	1,97E-02	1,71E+00	1,45E-02	0,0474	2,4437286	0,11588998	3047,05	PLAGL2	PLAG1 like zinc finger 2
107985481	2,49E-01	6,04E-01	2,14E-01	0,0932	1,2430917	0,11587888	481,75	LOC107985481	
649446	4,33E-01	3,64E-01	3,91E-01	0,1349	0,8574617	0,11564756	191,09	DLGAP1-AS	DLGAP1 antisense RNA 1
3005	2,31E-03	2,64E+00	1,56E-03	0,0364	3,1626302	0,11515247	11928,59	H1-0	H1.0 linker histone
11345	5,91E-02	1,23E+00	4,63E-02	0,0577	1,9929753	0,11492095	1411,85	GABARAPL2	GABA type A receptor associated protein like 2
54581	3,52E-01	4,53E-01	3,12E-01	0,1133	1,0115386	0,11459229	248,93	SCAND2P	SCAN domain containing 2 pseudogene
348801	6,29E-01	2,01E-01	5,91E-01	0,2131	0,5375636	0,11456564	67,95	LNP1	leukemia NUP98 fusion partner 1
25786	5,25E-01	2,80E-01	4,84E-01	0,1633	0,6999514	0,11428477	117,35	DGCR11	DiGeorge syndrome critical region gene 11
10849	4,67E-02	1,33E+00	3,61E-02	0,0544	2,0963053	0,11402815	1709,06	POLR1G	RNA polymerase I subunit G
100505865	7,91E-01	1,02E-01	7,63E-01	0,3788	0,3009353	0,1139931	22,42	LINC00920	long intergenic non-protein coding RNA 920
51566	8,19E-02	1,09E+00	6,53E-02	0,0618	1,8430917	0,11393136	1588,62	ARMCX3	armadillo repeat containing X-linked 3
79602	1,28E-02	1,89E+00	9,29E-03	0,0438	2,6013509	0,11391655	4219,25	ADIPOR2	adiponectin receptor 2
29919	5,94E-02	1,23E+00	4,65E-02	0,0572	1,9905821	0,11387497	1702,25	RMC1	regulator of MON1-CCZ1
139818	1,71E-01	7,67E-01	1,43E-01	0,0776	1,4648681	0,11371456	751,44	DOCK11	dedicator of cytokinesis 11
54842	1,02E-01	9,91E-01	8,25E-02	0,0654	1,7363962	0,11359465	1220,11	MFSD6	major facilitator superfamily domain containing 6
93973	2,39E-02	1,62E+00	1,78E-02	0,0479	2,3700849	0,11355774	3044,34	ACTR8	actin related protein 8
55837	4,37E-02	1,36E+00	3,36E-02	0,0534	2,1246307	0,11354182	1798,47	EAPP	E2F associated phosphoprotein
2932	2,08E-02	1,68E+00	1,53E-02	0,0468	2,4241858	0,11336874	3056,28	GSK3B	glycogen synthase kinase 3 beta
9887	1,54E-02	1,81E+00	1,12E-02	0,0447	2,5363278	0,11330785	5527,31	SMG7	SMG7 nonsense mediated mRNA decay factor
26819	7,78E-01	1,09E-01	7,49E-01	0,3531	0,3203028	0,11309817	23,97	SNORD32A	small nucleolar RNA, C/D box 32A
91869	8,31E-02	1,08E+00	6,63E-02	0,0615	1,8364087	0,11300061	1291,52	RFT1	RFT1 homolog
84059	3,66E-01	4,37E-01	3,25E-01	0,1148	0,9840973	0,11294715	255,29	ADGRV1	adhesion G protein-coupled receptor V1
11272	7,17E-01	1,44E-01	6,84E-01	0,2772	0,4072851	0,11289372	42,59	PRR4	proline rich 4
84933	1,79E-01	7,47E-01	1,50E-01	0,0784	1,4389238	0,11278212	776,93	C8orf76	chromosome 8 open reading frame 76
91452	2,00E-02	1,70E+00	1,48E-02	0,0462	2,4380859	0,11262028	2856,91	ACBD5	acyl-CoA binding domain containing 5
1806	2,24E-02	1,65E+00	1,66E-02	0,047	2,3955548	0,11255692	2960,19	DPYD	dihydropyrimidine dehydrogenase
114928	3,07E-01	5,13E-01	2,68E-01	0,1015	1,1072379	0,11234445	330,61	GPRASP2	G protein-coupled receptor associated sorting protein 2
91653	5,00E-01	3,01E-01	4,58E-01	0,1508	0,741996	0,11185903	142,17	BOC	BOC cell adhesion associated, oncogene regulated
8846	1,27E-01	8,96E-01	1,04E-01	0,0688	1,6244117	0,1118183	798,91	ALKBH1	alkB homolog 1, histone H2A dioxygenase
107986211	4,48E-01	3,49E-01	4,06E-01	0,1343	0,8306576	0,11158545	190,42	LOC107986	replaced by ID 100129917
7468	2,93E-03	2,53E+00	2,00E-03	0,036	3,0902177	0,11122272	15207,2	NSD2	nuclear receptor binding SET domain protein 2
101928163	8,56E-01	6,75E-02	8,35E-01	0,5322	0,208789	0,11112072	10,74	LOC101928	uncharacterized LOC101928163
23026	7,10E-01	1,49E-01	6,77E-01	0,2662	0,4170401	0,11102448	45,65	MYO16	myosin XVI
613126	8,35E-01	7,83E-02	8,11E-01	0,4651	0,2385258	0,11094992	14,1	CYP51A1-AS	CYP51A1 antisense RNA 1
6908	1,19E-01	9,24E-01	9,75E-02	0,0669	1,6571226	0,1109153	1046,33	TBP	TATA-box binding protein
105374879	7,66E-01	1,16E-01	7,37E-01	0,3295	0,3364665	0,11087236	28,65	LOC105374	uncharacterized LOC105374879
64746	7,31E-02	1,14E+00	5,79E-02	0,0584	1,8963701	0,11080203	2171,65	ACBD3	acyl-CoA binding domain containing 3
6500	7,00E-03	2,15E+00	4,95E-03	0,0394	2,8103112	0,11073389	17007,69	SKP1	S-phase kinase associated protein 1
25989	1,46E-01	8,36E-01	1,20E-01	0,0713	1,5536578	0,1107159	816,54	ULK3	unc-51 like kinase 3
7073	1,18E-02	1,93E+00	8,48E-03	0,042	2,6321748	0,110641	5548,5	TIAL1	TIA1 cytotoxic granule associated RNA binding protein like 1
347732	7,70E-01	1,14E-01	7,40E-01	0,333	0,331635	0,11044783	28,16	CATSPER3	cation channel sperm associated 3
27097	5,77E-02	1,24E+00	4,51E-02	0,055	2,0036509	0,11027997	1872,63	TAF5L	TATA-box binding protein associated factor 5 like
100507634	6,85E-01	1,64E-01	6,51E-01	0,2435	0,4528647	0,11026762	52,11	LOC100507	uncharacterized LOC100507634
107984910	8,60E-01	6,55E-02	8,39E-01	0,5419	0,2033659	0,11020299	9,88	LOC107984	910
83450	6,75E-01	1,71E-01	6,40E-01	0,2351	0,4682861	0,11007432	56,21	DRC3	dynein regulatory complex subunit 3
148189	3,63E-01	4,40E-01	3,22E-01	0,1111	0,990278	0,11000094	280,61	LINC00662	long intergenic non-protein coding RNA 662
7267	1,10E-02	1,96E+00	7,94E-03	0,0414	2,6545348	0,10987698	6587,32	TTC3	tetratricopeptide repeat domain 3
23514	8,23E-02	1,08E+00	6,56E-02	0,0597	1,8409769	0,1098509	1481,57	SPIDR	scaffold protein involved in DNA repair
23397	2,12E-02	1,67E+00	1,57E-02	0,0454	2,4160123	0,10969199	6375,15	NCAPH	non-SMC condensin I complex subunit H
54934	7,31E-02	1,14E+00	5,79E-02	0,0578	1,8967131	0,10957932	1373,53	KANSL2	KAT8 regulatory NSL complex subunit 2
56339	4,37E-02	1,36E+00	3,36E-02	0,0516	2,124902	0,1095653	2008,14	METTL3	methyltransferase 3, N6-adenosine-methyltransferase complex catalytic subunit
109617023	8,24E-01	8,41E-02	7,99E-01	0,4287	0,2549157	0,10928062	16,75	SNORA58B	small nucleolar RNA, H/ACA box 58B
105376383	8,02E-01	9,58E-02	7,75E-01	0,3816	0,2859234	0,10910397	21,38	LINC02678	long intergenic non-protein coding RNA 2678
29893	5,79E-02	1,24E+00	4,53E-02	0,0545	2,0018187	0,10904058	1869,43	PSMC3IP	PSMC3 interacting protein
9025	2,44E-02	1,61E+00	1,81E-02	0,0461	2,3628056	0,10898405	3404,3	RNF8	ring finger protein 8
55294	1,45E-01	8,39E-01	1,20E-01	0,07	1,5558258	0,10886305	786,05	FBXW7	F-box and WD repeat domain containing 7
1803	7,83E-01	1,06E-01	7,54E-01	0,3467	0,3128845	0,10848784	28,39	DPP4	dipeptidyl peptidase 4
55222	3,10E-02	1,51E+00	2,34E-02	0,0479	2,2668177	0,10846858	2552,66	LRRC20	leucine rich repeat containing 20
9690	5,48E-03	2,26E+00	3,83E-03	0,0374	2,8919868	0,10823036	9121,13	UBE3C	ubiquitin protein ligase E3C
54885	3,43E-01	4,65E-01	3,03E-01	0,1049	1,03096	0,10812851	347,87	TBC1D8B	TBC1 domain family member 8B
85437	4,98E-02	1,30E+00	3,86E-02	0,0521	2,0681962	0,10785259	1811,46	ZCRB1	zinc finger CCHC-type and RNA binding motif containing 1
84897	3,93E-02	1,41E+00	3,01E-02	0,0497	2,1690242	0,10779437	2536,21	TBRG1	transforming growth factor beta regulator 1
956	1,19E-01	9,24E-01	9,68E-02	0,0649	1,6606998	0,10769956	953,94	ENTPD3	ectonucleoside triphosphate diphosphohydrolase 3
404734	2,67E-02	1,57E+00	2,00E-02	0,0462	2,3272488	0,1076075	3599,47	ANKHD1-EIF	ANKHD1-EIF4EBP3 readthrough
118672	3,13E-01	5,04E-01	2,74E-01	0,0983	1,0940293	0,10755025	382,98	PSTK	phosphoseryl-tRNA kinase
604	1,46E-01	8,36E-01	1,21E-01	0,0693	1,5508977	0,10754997	967,37	BCL6	BCL6 transcription repressor
818	4,18E-02	1,38E+00	3,21E-02	0,0501	2,1435739	0,10745849	2219,21	CAMK2G	calcium/calmodulin dependent protein kinase II gamma
100286979	8,43E-01	7,42E-02	8,21E-01	0,4735	0,2268615	0,10742452	13,64	ANAPC1P1	ANAPC1 pseudogene 1
79958	8,45E-01	7,31E-02	8,22E-01	0,4777	0,2246338	0,10730181	13,61	DENND1C	DENN domain containing 1C
1184	2,75E-01	5,61E-01	2,38E-01	0,0905	1,1810668	0,10692327	416,51	CLCN5	chloride voltage-gated channel 5
1058	7,33E-02	1,13E+00	5,81E-02	0,0564	1,8950712	0,10686898	1632,07	CENPA	centromere protein A
54764	4,70E-02	1,33E+00	3,63E-02	0,0509	2,0933081	0,10656974	2045,97	ZRANB1	zinc finger RANBP2-type containing 1
197320	2,01E-01	6,97E-01	1,70E-01	0,0776	1,3732313	0,10656389	644,22	ZNF778	zinc finger protein 778
51074	7,42E-02	1,13E+00	5,88E-02	0,0564	1,889356	0,10646846	2125,14	APIP	APAF1 interacting protein
441172	7,57E-01	1,21E-01	7,26E-01	0,3043	0,3498062	0,10645567	32,02	NHSL1-AS1	NHSL1 antisense RNA 1
6659	2,31E-01	6,36E-01	1,97E-01	0,0823	1,2909501	0,10627904	689,15	SOX4	SRY-box transcription factor 4
79184	3,31E-02	1,48E+00	2,51E-02	0,0474	2,2396995	0,10617145	2566,74	BRCC3	BRCA1/BRCA2-containing complex subunit 3
2140	8,58E-02	1,07E+00	6,85E-02	0,0583	1,8216582	0,10615522	1441,08	EYA3	EYA transcriptional coactivator and phosphatase 3
123169	8,34E-02	1,08E+00	6,65E-02	0,0578	1,8349902	0,1060207	2638,82	LEO1	LEO1 homolog, Paf1/RNA polymerase II complex component
10006	5,70E-02	1,24E+00	4,45E-02	0,0527	2,0088857	0,10592952	2947,22	ABI1	abl interactor 1
64663	2,95E-01	5,30E-01	2,57E-01	0,0933	1,1346495	0,10583998	543,37	SPANXC	SPANX family member C
4054	2,24E-01	6,50E-01	1,91E-01	0,0804	1,3077604	0,10518439	603,69	LTBP3	latent transforming growth factor beta binding protein 3
51805	2,26E-01	6,46E-01	1,92E-01	0,0807	1,3040085	0,10516935	570,41	COQ3	coenzyme Q3, methyltransferase
55250	8,25E-02	1,08E+00	6,57E-02	0,0571	1,8401434	0,10505812	2534,93	ELP2	elongator acetyltransferase complex subunit 2
9125	2,44E-02	1,61E+00	1,81E-02	0,0443	2,362672	0,10478093	3479,07	CNOT9	CCR4-NOT transcription complex subunit 9
79009	2,74E-02	1,56E+00	2,06E-02	0,0452	2,3156108	0,10475249	4743,21	DDX50	DExD-box helicase 50
56888	2,49E-02	1,60E+00	1,85E-02	0,0444	2,3547728	0,10466352	3831,7	KCMF1	potassium channel modulatory factor 1
644794	6,77E-01	1,69E-01	6,42E-01	0,2253	0,4646157	0,10466098	75,85	LINC02604	long intergenic non-protein coding RNA 2604
100133091	3,97E-01	4,01E-01	3,56E-01	0,1132	0,9233602	0,1045331	253,93	LINC03009	long intergenic non-protein coding RNA 3009
57536	3,59E-01	4,45E-01	3,18E-01	0,1047	0,9978425	0,10449791	347,94	KIAA1328	KIAA1328
6613	2,61E-02	1,58E+00	1,95E-02	0,0447	2,3351734	0,10433827	16317,74	SUMO2	small ubiquitin like modifier 2
54521	5,42E-02	1,27E+00	4,22E-02	0,0512	2,0316832	0,10411456	2119,73	WDR44	WD repeat domain 44
91612	8,01E-02	1,10E+00	6,38E-02	0,0561	1,8536843	0,10403045	1479,32	CHURC1	churchill domain containing 1
4957	1,96E-02	1,71E+00	1,44E-02	0,0425	2,4469399	0,10402587	4664,09	ODF2	outer dense fiber of sperm tails 2
5770	9,78E-03	2,01E+00	7,01E-03	0,0385	2,6961612	0,10374278	8607,03	PTPN1	protein tyrosine phosphatase non-receptor type 1
148418	7,46E-01	1,27E-01	7,15E-01	0,2838	0,3651536	0,10362326	36,68	SAMD13	sterile alpha motif domain containing 13
169714	2,38E-02	1,62E+00	1,77E-02	0,0437	2,3712375	0,10361924	4582,76	QSOX2	quiescin sulfhydryl oxidase 2
57147	1,79E-01	7,47E-01	1,50E-01	0,0721	1,4379305	0,10361467	760,69	SCYL3	SCY1 like pseudokinase 3
861	2,22E-02	1,65E+00	1,65E-02	0,0432	2,3981656	0,10358135	4438,14	RUNX1	RUNX family transcription factor 1
55625	2,30E-02	1,64E+00	1,71E-02	0,0434	2,3845265	0,10356225	3846,16	ZDHHC7	zinc finger DHHC-type palmitoyltransferase 7
1191	2,26E-01	6,46E-01	1,93E-01	0,0794	1,3019821	0,10334069	631,76	CLU	clusterin
94015	7,79E-01	1,08E-01	7,51E-01	0,3245	0,3179667	0,10319303	29,21	TTYH2	tweety family member 2
9121	1,91E-01	7,19E-01	1,60E-01	0,0735	1,40361	0,10317245	767,68	SLC16A5	solute carrier family 16 member 5
404672	9,45E-02	1,02E+00	7,60E-02	0,0581	1,7742714	0,10315158	1515,19	GTF2H5	general transcription factor IIH subunit 5
6721	3,39E-02	1,47E+00	2,57E-02	0,0461	2,2302086	0,1029181	3191,5	SREBF2	sterol regulatory element binding transcription factor 2
286042	7,51E-01	1,24E-01	7,20E-01	0,2869	0,3585833	0,10288551	42,89	FAM86B3P	family with sequence similarity 86, member A pseudogene
107985152	8,30E-01	8,09E-02	8,06E-01	0,4183	0,2456138	0,10273532	17,43	LOC107985	uncharacterized LOC107985152
84725	1,62E-01	7,90E-01	1,35E-01	0,0686	1,495683	0,10259031	949,06	PLEKHA8	pleckstrin homology domain containing A8
317671	6,67E-01	1,76E-01	6,31E-01	0,2132	0,4806471	0,10247892	67,17	RFESD	Rieske Fe-S domain containing
26520	6,59E-02	1,18E+00	5,19E-02	0,0527	1,9442208	0,10236828	1930,3	TIMM9	translocase of inner mitochondrial membrane 9

101929704	8,51E-01	7,01E-02	8,30E-01	0,4754	0,2150743	0,10224556	13,2	TTC23L-AS1	TTC23L antisense RNA 1
107987063	7,59E-01	1,20E-01	7,28E-01	0,2942	0,3475402	0,10224422	36,75	LOC107987063	
6879	2,31E-02	1,64E+00	1,71E-02	0,0429	2,3839482	0,1021966	7350,54	TAF7	TATA-box binding protein associated factor 7
10940	1,47E-01	8,33E-01	1,22E-01	0,066	1,5483698	0,10213107	1036,03	POP1	POP1 homolog, ribonuclease P/MRP subunit
55729	5,05E-02	1,30E+00	3,92E-02	0,0493	2,0624086	0,10170013	3391,39	ATF7IP	activating transcription factor 7 interacting protein
146705	2,96E-01	5,29E-01	2,58E-01	0,0899	1,1310761	0,10165844	510,93	TEPSIN	TEPSIN adaptor related protein complex 4 accessory protein
55034	4,38E-02	1,36E+00	3,37E-02	0,0479	2,1234069	0,10165475	2436,22	MOCOS	molybdenum cofactor sulfurase
339487	1,20E-01	9,21E-01	9,79E-02	0,0613	1,6553514	0,10145272	1317,11	ZBTB8OS	zinc finger and BTB domain containing 8 opposite strand
5469	1,88E-02	1,73E+00	1,38E-02	0,0412	2,4612189	0,10143007	7699,78	MED1	mediator complex subunit 1
79888	3,14E-02	1,50E+00	2,38E-02	0,0446	2,2610747	0,10083609	4511,43	LPCAT1	lysophosphatidylcholine acyltransferase 1
106660613	6,65E-01	1,77E-01	6,29E-01	0,2088	0,482777	0,10080647	68,12	LINC00680-(	LINC00680-GUSBP4 readthrough
7358	5,52E-02	1,26E+00	4,31E-02	0,0496	2,0229156	0,10024615	2305,07	UGDH	UDP-glucose 6-dehydrogenase
9798	2,99E-02	1,52E+00	2,25E-02	0,0438	2,2819248	0,10005566	4815,62	IST1	IST1 factor associated with ESCRT-III
2729	1,10E-01	9,59E-01	8,94E-02	0,0588	1,6987257	0,09994322	1573,49	GCLC	glutamate-cysteine ligase catalytic subunit
54915	2,52E-02	1,60E+00	1,88E-02	0,0425	2,3493706	0,09985777	4617,2	YTHDF1	YTH N6-methyladenosine RNA binding protein 1
101954266	8,43E-01	7,42E-02	8,21E-01	0,4396	0,2266892	0,09965498	16,93	RNVU1-14	RNA, variant U1 small nuclear 14
1997	7,05E-02	1,15E+00	5,58E-02	0,0521	1,9128673	0,09961011	1874,99	ELF1	E74 like ETS transcription factor 1
23034	3,12E-02	1,51E+00	2,35E-02	0,0439	2,2648512	0,09949041	3554,76	SAMD4A	sterile alpha motif domain containing 4A
54535	6,07E-02	1,22E+00	4,76E-02	0,0501	1,9813351	0,09919438	2140,85	CCHCR1	coiled-coil alpha-helical rod protein 1
107986858	8,91E-01	5,01E-02	8,73E-01	0,6173	0,1598231	0,09866211	8,18	LOC107986(	uncharacterized LOC107986858
107984243	7,42E-01	1,30E-01	7,11E-01	0,2654	0,3705049	0,09834523	43,96	LOC107984(	uncharacterized LOC107984243
2775	3,96E-01	4,02E-01	3,54E-01	0,1061	0,9264418	0,09830953	330,59	GNAO1	G protein subunit alpha o1
25840	5,33E-01	2,73E-01	4,92E-01	0,143	0,6872207	0,09823974	158,65	METTL7A	methyltransferase like 7A
114880	3,25E-01	4,88E-01	2,86E-01	0,092	1,0674193	0,09819962	458,87	OSBPL6	oxysterol binding protein like 6
103908604	7,39E-01	1,31E-01	7,07E-01	0,2615	0,3753925	0,09815374	43,88	FAM88F	family with sequence similarity 88 member F
101928119	7,39E-01	1,31E-01	7,08E-01	0,2619	0,3744881	0,09808959	43,89	LOC101928(	uncharacterized LOC101928119
54617	5,10E-02	1,29E+00	3,96E-02	0,0476	2,0577547	0,09805131	2702,34	INO80	INO80 complex ATPase subunit
5292	1,69E-01	7,72E-01	1,41E-01	0,0664	1,4736147	0,09780591	1113,41	PIM1	Pim-1 proto-oncogene, serine/threonine kinase
9183	7,67E-02	1,12E+00	6,09E-02	0,0521	1,8744452	0,09768358	3260,62	ZW10	zw10 kinetochore protein
3672	5,18E-02	1,29E+00	4,03E-02	0,0476	2,0509961	0,09767622	2847,7	ITGA1	integrin subunit alpha 1
103625681	7,76E-01	1,10E-01	7,47E-01	0,3027	0,3225306	0,09763671	34,71	LLPH-DT	LLPH divergent transcript
107985023	6,30E-01	2,01E-01	5,93E-01	0,1824	0,5348362	0,09755868	95,97	LOC107985023	
81614	7,91E-02	1,10E+00	6,30E-02	0,0524	1,859499	0,0973726	2601,02	NIPA2	NIPA magnesium transporter 2
1373	3,80E-01	4,20E-01	3,39E-01	0,1017	0,9566014	0,09724965	322,13	CPS1	carbamoyl-phosphate synthase 1
29072	7,95E-02	1,10E+00	6,33E-02	0,0523	1,8574157	0,09720378	5047,63	SETD2	SET domain containing 2, histone lysine methyltransferase
52	3,79E-02	1,42E+00	2,89E-02	0,0445	2,1842825	0,09713682	4419,17	ACP1	acid phosphatase 1
10528	1,65E-02	1,78E+00	1,21E-02	0,0386	2,5089393	0,09693157	16374,6	NOP56	NOP56 ribonucleoprotein
9663	3,25E-02	1,49E+00	2,46E-02	0,043	2,2475137	0,09669905	4092,7	LPIN2	lipin 2
100532746	1,26E-01	9,00E-01	1,04E-01	0,0592	1,627746	0,09642458	1241,3	PPT2-EGFL8	PPT2-EGFL8 readthrough (NMD candidate)
105374807	8,62E-01	6,45E-02	8,41E-01	0,4806	0,2003584	0,09630174	13,95	LOC105374(	uncharacterized LOC105374807
80146	1,12E-01	9,51E-01	9,11E-02	0,0569	1,6895003	0,09607273	1978,64	UXS1	UDP-glucuronate decarboxylase 1
101927454	8,23E-01	8,46E-02	7,98E-01	0,3757	0,2556662	0,09606598	20,88	LOC101927(	uncharacterized LOC101927454
51659	1,38E-01	8,60E-01	1,13E-01	0,0603	1,5829624	0,09552445	1217,91	GINS2	GINS complex subunit 2
9341	2,59E-02	1,59E+00	1,94E-02	0,0407	2,3384165	0,09528972	6656,97	VAMP3	vesicle associated membrane protein 3
23450	1,93E-02	1,71E+00	1,42E-02	0,0387	2,4524903	0,09502906	15490,88	SF3B3	splicing factor 3b subunit 3
11132	4,59E-01	3,38E-01	4,18E-01	0,1171	0,8106757	0,09489235	284,74	CAPN10	calpain 10
79762	4,99E-01	3,02E-01	4,57E-01	0,1275	0,7436885	0,09485508	204,51	C1orf115	chromosome 1 open reading frame 115
64927	3,47E-01	4,60E-01	3,07E-01	0,0927	1,0218153	0,09476197	462,17	TTC23	tetratricopeptide repeat domain 23
340371	1,92E-01	7,17E-01	1,62E-01	0,0677	1,3986143	0,09472215	1002,03	NRBP2	nuclear receptor binding protein 2
2200	1,01E-01	9,96E-01	8,17E-02	0,0544	1,7407543	0,09468845	3079,03	FBN1	fibrillin 1
105373150	8,79E-01	5,60E-02	8,60E-01	0,5327	0,176729	0,09414554	10,75	LOC105373(	uncharacterized LOC105373150
3087	4,00E-01	3,98E-01	3,58E-01	0,1024	0,9186966	0,09409437	316,89	HHEX	hematopoietically expressed homeobox
79753	1,33E-01	8,76E-01	1,09E-01	0,0587	1,6019378	0,09407172	1272,25	SNIP1	Smad nuclear interacting protein 1
105374309	7,40E-01	1,31E-01	7,09E-01	0,2517	0,37367	0,09404001	51,59	LOC105374(	uncharacterized LOC105374309
2970	6,53E-02	1,19E+00	5,14E-02	0,0482	1,9483161	0,09388907	2679,22	GTF2IP1	general transcription factor IIi pseudogene 1
388969	1,27E-01	8,96E-01	1,04E-01	0,0577	1,6253243	0,09379045	1431,61	C2orf68	chromosome 2 open reading frame 68
8780	3,70E-02	1,43E+00	2,82E-02	0,0427	2,1946531	0,09369612	4603,44	RIOK3	RIO kinase 3
136051	4,49E-01	3,48E-01	4,07E-01	0,1131	0,8283673	0,09365653	268,37	ZNF786	zinc finger protein 786
27342	5,84E-02	1,23E+00	4,57E-02	0,0468	1,9983242	0,09354543	2834,47	RABGEF1	RAB guanine nucleotide exchange factor 1
101929295	7,89E-01	1,03E-01	7,61E-01	0,3067	0,3046729	0,09342828	32,25	LNCRNA-IU(	lncRNA imatinib upregulated
105374841	6,74E-01	1,71E-01	6,39E-01	0,1988	0,4697005	0,09337206	640,68	LOC105374(	uncharacterized LOC105374841
2926	4,95E-02	1,31E+00	3,84E-02	0,045	2,0710089	0,09319901	6650,2	GRSF1	G-rich RNA sequence binding factor 1
51187	9,31E-02	1,03E+00	7,48E-02	0,0523	1,7817394	0,09317552	2928,95	RSL24D1	ribosomal L24 domain containing 1
23093	6,98E-02	1,16E+00	5,51E-02	0,0486	1,9179373	0,09315936	2525,2	TTLL5	tubulin tyrosine ligase like 5
10069	1,84E-01	7,35E-01	1,55E-01	0,0654	1,4235264	0,09310493	958,88	RWDD2B	RWD domain containing 2B
54487	1,01E-01	9,96E-01	8,17E-02	0,0534	1,7406264	0,0929829	1834,92	DGCR8	DGCR8 microprocessor complex subunit
3213	6,55E-01	1,84E-01	6,18E-01	0,1861	0,4986964	0,09281763	97,28	HOXB3	homeobox B3
124245	6,05E-02	1,22E+00	4,74E-02	0,0468	1,9828167	0,09276593	3193,45	ZC3H18	zinc finger CCCH-type containing 18
3140	3,84E-01	4,16E-01	3,43E-01	0,0977	0,949024	0,09274031	356,34	MR1	major histocompatibility complex, class I-related
10944	8,51E-02	1,07E+00	6,80E-02	0,0508	1,8251588	0,09272854	9860,29	C11orf58	chromosome 11 open reading frame 58
55975	1,84E-01	7,35E-01	1,54E-01	0,0651	1,4244505	0,09270847	986,35	KLHL7	kelch like family member 7
727677	2,08E-01	6,82E-01	1,76E-01	0,0685	1,3531077	0,09269426	905,88	CASC8	cancer susceptibility 8
3192	3,26E-02	1,49E+00	2,47E-02	0,0412	2,2457407	0,09258892	36903,38	HNRNPU	heterogeneous nuclear ribonucleoprotein U
170591	8,53E-01	6,91E-02	8,31E-01	0,4342	0,2131317	0,09253451	15,72	S100Z	S100 calcium binding protein Z
114876	1,74E-01	7,59E-01	1,45E-01	0,0632	1,4572431	0,09208228	1211,35	OSBPL1A	oxysterol binding protein like 1A
57336	5,61E-01	2,51E-01	5,21E-01	0,1432	0,6424217	0,09198762	176,27	ZNF287	zinc finger protein 287
7633	4,19E-01	3,78E-01	3,78E-01	0,1043	0,8818998	0,09194355	300,9	ZNF79	zinc finger protein 79
643719	6,73E-01	1,72E-01	6,37E-01	0,1947	0,4715009	0,09182202	86,02	SCGB1B2P	secretoglobin family 1B member 2, pseudogene
51390	1,71E-01	7,67E-01	1,43E-01	0,0626	1,4649766	0,09165537	1288,85	AIG1	androgen induced 1
100288123	7,81E-01	1,07E-01	7,52E-01	0,2903	0,3156	0,09162119	37	LOC100288(	uncharacterized LOC100288123
4486	3,34E-01	4,76E-01	2,94E-01	0,0873	1,0486545	0,09158684	499,29	MST1R	macrophage stimulating 1 receptor
104472848	8,07E-01	9,31E-02	7,81E-01	0,3284	0,27847	0,09145129	27,18	IRAIN	IGF1R antisense imprinted non-protein coding RNA
83468	8,17E-01	8,78E-02	7,91E-01	0,3458	0,2644211	0,09144439	25,43	GLT8D2	glycosyltransferase 8 domain containing 2
107986578	6,71E-01	1,73E-01	6,36E-01	0,1928	0,4739352	0,09139526	82,31	LOC107986(	uncharacterized LOC107986578
998	1,80E-02	1,74E+00	1,32E-02	0,0368	2,477326	0,09116796	20312,57	CDC42	cell division cycle 42
100287944	7,83E-01	1,06E-01	7,54E-01	0,2912	0,3128766	0,09111365	35,65	LOC100287(	uncharacterized LOC100287944
3688	2,58E-02	1,59E+00	1,93E-02	0,0389	2,3405984	0,0909681	69573,73	ITGB1	integrin subunit beta 1
9910	2,52E-01	5,99E-01	2,17E-01	0,0736	1,2348533	0,09090386	859,72	RABGAP1L	RAB GTPase activating protein 1 like
5793	4,60E-02	1,34E+00	3,55E-02	0,0431	2,1025443	0,09059578	4016,12	PTPRG	protein tyrosine phosphatase receptor type G
138649	8,64E-01	6,35E-02	8,44E-01	0,4598	0,1970457	0,09059475	14,13	ANKRD19P	ankyrin repeat domain 19, pseudogene
10252	1,77E-01	7,52E-01	1,48E-01	0,0625	1,4466643	0,09036183	1081,82	SPRY1	sprouty RTK signaling antagonist 1
79017	1,11E-01	9,55E-01	9,05E-02	0,0533	1,6928142	0,09026649	1922,59	GGCT	gamma-glutamylcyclotransferase
221143	5,41E-01	2,67E-01	5,01E-01	0,134	0,673552	0,09026395	193,72	EEF1AKMT1	EEF1A lysine methyltransferase 1
84461	1,62E-01	7,90E-01	1,35E-01	0,0603	1,4957652	0,09026073	1467,06	NEURL4	neuralized E3 ubiquitin protein ligase 4
2071	7,94E-02	1,10E+00	6,32E-02	0,0484	1,8579494	0,0899349	3129,97	ERCC3	ERCC excision repair 3, TFIIH core complex helicase subunit
7456	1,70E-01	7,70E-01	1,42E-01	0,0612	1,4685086	0,08993165	1307,58	WIPF1	WAS/WASL interacting protein family member 1
5817	2,20E-02	1,66E+00	1,63E-02	0,0374	2,4027907	0,08988867	8246,51	PVR	PVR cell adhesion molecule
8914	6,75E-02	1,17E+00	5,32E-02	0,0464	1,9330111	0,0896811	3054,94	TIMELESS	timeless circadian regulator
219833	5,59E-01	2,53E-01	5,18E-01	0,1386	0,6460494	0,08951104	161,98	KCNJ5-AS1	KCNJ5 antisense RNA 1
100289388	5,62E-01	2,50E-01	5,21E-01	0,1396	0,6414223	0,08951053	164,78	KCTD21-AS	KCTD21 antisense RNA 1
10135	4,22E-02	1,37E+00	3,24E-02	0,0418	2,1396548	0,08949087	25092,88	NAMPT	nicotinamide phosphoribosyltransferase
23368	2,72E-01	5,65E-01	2,35E-01	0,0749	1,1874003	0,08899408	767,35	PPP1R13B	protein phosphatase 1 regulatory subunit 13B
3313	3,53E-02	1,45E+00	2,69E-02	0,0402	2,213139	0,08897874	27954,9	HSPA9	heat shock protein family A (Hsp70) member 9
91304	1,72E-01	7,64E-01	1,44E-01	0,0608	1,46183	0,08889695	2627,41	TMEM259	transmembrane protein 259
8148	8,42E-02	1,07E+00	6,72E-02	0,0484	1,8305668	0,08852221	15436,91	TAF15	TATA-box binding protein associated factor 15
107985246	6,80E-01	1,67E-01	6,45E-01	0,1919	0,4610126	0,08845196	81,47	CSRP1-AS1	CSRP1 antisense RNA 1
83640	2,38E-01	6,23E-01	2,03E-01	0,0694	1,2724216	0,08826736	798,63	RAMAC	RNA guanine-7 methyltransferase activating subunit
4891	1,72E-01	7,64E-01	1,44E-01	0,0603	1,4607885	0,08806478	1944,21	SLC11A2	solute carrier family 11 member 2
160518	1,63E-01	7,88E-01	1,35E-01	0,0588	1,493589	0,08789264	1376,89	DENND5B	DENN domain containing 5B
8609	3,51E-01	4,55E-01	3,11E-01	0,0866	1,0134716	0,08775138	470,59	KLF7	KLF transcription factor 7
100505696	5,06E-01	2,96E-01	4,64E-01	0,1197	0,7318747	0,08759714	231,64	SH3BP5-AS	SH3BP5 antisense RNA 1
64425	8,13E-02	1,09E+00	6,48E-02	0,0474	1,846839	0,0875528	2903,64	POLR1E	RNA polymerase I subunit E
64769	1,11E-01	9,55E-01	8,97E-02	0,0516	1,6970389	0,08751978	2352,6	MEAF6	MYST/Esa1 associated factor 6
23358	3,86E-02	1,41E+00	2,95E-02	0,0402	2,1765167	0,08750165	5694,14	USP24	ubiquitin specific peptidase 24
101927699	8,34E-01	7,88E-02	8,10E-01	0,3637	0,2403571	0,08741646	23,41	SYT15-AS1	SYT15 antisense RNA 1
100507086	6,95E-01	1,58E-01	6,61E-01	0,1986	0,4389242	0,08717637	77,58	DLG1-AS1	DLG1 antisense RNA 1
64429	1,06E-01	9,75E-01	8,56E-02	0,0506	1,7192118	0,08694848	2903,02	ZDHHC6	zinc finger DHHC-type palmitoyltransferase 6
5498	3,23E-01	4,91E-01	2,84E-01	0,081	1,0722445	0,08683737	607,78	PPOX	protoporphyrinogen oxidase
79778	5,10E-01	2,92E-01	4,68E-01	0,1197	0,7255705	0,0868187	288,84	MICALL2	MICAL like 2
950	4,34E-02	1,36E+00	3,33E-02	0,0407	2,1278556	0,08658615	5923,08	SCARB2	scavenger receptor class B member 2

9697	2,33E-02	1,63E+00	1,73E-02	0,0364	2,3797045	0,08655801	13678,84	TRAM2	translocation associated membrane protein 2
51108	6,12E-02	1,21E+00	4,80E-02	0,0437	1,9774318	0,08648548	4234,06	METTL9	methyltransferase like 9
26810	8,93E-01	4,91E-02	8,76E-01	0,5535	0,1561012	0,08640836	10,29	SNORD41	small nucleolar RNA, C/D box 41
23126	6,91E-02	1,16E+00	5,46E-02	0,0449	1,9220724	0,08636334	3360,86	POGZ	pogo transposable element derived with ZNF domain
9329	6,34E-02	1,20E+00	4,98E-02	0,044	1,9615148	0,08634094	3863,9	GTF3C4	general transcription factor IIIC subunit 4
105377623	8,69E-01	6,10E-02	8,49E-01	0,4524	0,1907523	0,08630132	14,82	LOC105377(	uncharacterized LOC105377623
131118	2,04E-01	6,90E-01	1,73E-01	0,0633	1,3630482	0,08628564	1222,29	DNAJC19	DnaJ heat shock protein family (Hsp40) member C19
51003	3,12E-01	5,06E-01	2,74E-01	0,0786	1,0947952	0,08607118	579,93	MED31	mediator complex subunit 31
677814	8,29E-01	8,14E-02	8,05E-01	0,3483	0,2469561	0,08602384	25,21	SNORA31	small nucleolar RNA, H/ACA box 31
957	1,25E-01	9,03E-01	1,02E-01	0,0526	1,6353872	0,08597454	1755,96	ENTPD5	ectonucleoside triphosphate diphosphohydrolase 5 (inactive)
55204	1,84E-01	7,35E-01	1,54E-01	0,0602	1,4247224	0,08582396	1264,55	GOLPH3L	golgi phosphoprotein 3 like
64708	2,48E-01	6,06E-01	2,13E-01	0,0689	1,2454233	0,08579711	1454,2	COPS7B	COP9 signalosome subunit 7B
10827	2,76E-01	5,59E-01	2,39E-01	0,0728	1,1774522	0,08566261	893,46	FAM114A2	family with sequence similarity 114 member A2
8916	1,84E-01	7,35E-01	1,55E-01	0,0599	1,4235603	0,08532138	1402,44	HERC3	HECT and RLD domain containing E3 ubiquitin protein ligase 3
84552	6,75E-01	1,71E-01	6,40E-01	0,1815	0,4678057	0,08489431	90,7	PARD6G	par-6 family cell polarity regulator gamma
388730	7,37E-01	1,33E-01	7,06E-01	0,2247	0,3776015	0,08486348	62,78	TMEM81	transmembrane protein 81
347273	6,77E-01	1,69E-01	6,42E-01	0,1819	0,4650184	0,08459902	91,21	CAVIN4	caveolae associated protein 4
55827	1,15E-01	9,39E-01	9,33E-02	0,0504	1,6784571	0,08454468	3576,81	DCAF6	DDB1 and CUL4 associated factor 6
64326	2,23E-01	6,52E-01	1,89E-01	0,0641	1,3123746	0,08417331	1634,31	COP1	COP1 E3 ubiquitin ligase
7798	5,11E-02	1,29E+00	3,96E-02	0,0408	2,057491	0,08402373	5719,33	LUZP1	leucine zipper protein 1
283337	1,66E-01	7,80E-01	1,38E-01	0,0564	1,482904	0,08364267	1558,87	ZNF740	zinc finger protein 740
54065	3,82E-01	4,18E-01	3,41E-01	0,0877	0,9530617	0,08354756	479,4	SMIM11	small integral membrane protein 11
102724200	3,36E-01	4,74E-01	2,96E-01	0,0799	1,0450968	0,08350598	564,52	LOC102724;	trafficking protein particle complex subunit 10-like
286059	8,84E-01	5,35E-02	8,65E-01	0,4907	0,1696861	0,08326382	12,3	LOC286059	TNF receptor superfamily member 10d pseudogene
55333	2,38E-01	6,23E-01	2,04E-01	0,0655	1,2708106	0,08326036	1231,87	SYNJ2BP	synaptojanin 2 binding protein
51170	1,18E-01	9,28E-01	9,61E-02	0,05	1,6642068	0,08322957	3408,17	HSD17B11	hydroxysteroid 17-beta dehydrogenase 11
2521	6,93E-02	1,16E+00	5,47E-02	0,0433	1,9209959	0,08318052	20941,19	FUS	FUS RNA binding protein
5784	8,45E-02	1,07E+00	6,74E-02	0,0455	1,8287757	0,08316236	8247,79	PTPN14	protein tyrosine phosphatase non-receptor type 14
115196	6,35E-01	1,97E-01	5,98E-01	0,1561	0,52763	0,08234699	137,84	ZNF554	zinc finger protein 554
123036	5,59E-01	2,53E-01	5,18E-01	0,1275	0,6459337	0,08234375	217,08	TC2N	tandem C2 domains, nuclear
9672	8,58E-02	1,07E+00	6,85E-02	0,0452	1,8214989	0,08225287	3901,87	SDC3	syndecan 3
646471	5,40E-01	2,68E-01	4,99E-01	0,1213	0,6764666	0,08206422	241,06	LOC646471	uncharacterized LOC646471
7621	5,81E-01	2,36E-01	5,41E-01	0,1341	0,6110996	0,08193163	202,56	ZNF70	zinc finger protein 70
107984126	8,61E-01	6,50E-02	8,40E-01	0,4054	0,2019758	0,08188423	17,81	LOC107984	zinc finger protein 658B-like
116028	4,00E-01	3,98E-01	3,58E-01	0,089	0,9184585	0,08178672	520,67	RMI2	RecQ mediated genome instability 2
9266	1,10E-01	9,59E-01	8,91E-02	0,0481	1,7003865	0,08177322	3298,46	CYTH2	cytohesin 2
1968	5,16E-02	1,29E+00	4,00E-02	0,0398	2,0532887	0,08165198	6865,26	EIF2S3	eukaryotic translation initiation factor 2 subunit gamma
10541	9,75E-02	1,01E+00	7,85E-02	0,0464	1,7591762	0,08161404	17102,34	ANP32B	acidic nuclear phosphoprotein 32 family member B
995	1,94E-01	7,12E-01	1,64E-01	0,0586	1,3920599	0,08160924	1458,37	CDC25C	cell division cycle 25C
112268051	9,05E-01	4,34E-02	8,89E-01	0,5831	0,1398972	0,08157383	9,01	LOC112268051	
23660	2,71E-01	5,67E-01	2,35E-01	0,0686	1,1884816	0,08148196	946,1	ZKSCAN5	zinc finger with KRAB and SCAN domains 5
94081	7,37E-02	1,13E+00	5,84E-02	0,043	1,8927593	0,08143471	4035,48	SFXN1	sideroflexin 1
54749	1,02E-01	9,91E-01	8,26E-02	0,0467	1,7359643	0,0810469	3540,06	EPDR1	ependymin related 1
93349	2,66E-01	5,75E-01	2,30E-01	0,0673	1,2007685	0,08082806	910,78	SP140L	SP140 nuclear body protein like
221785	3,58E-01	4,46E-01	3,18E-01	0,0805	0,9995958	0,08042641	614,42	ZSCAN25	zinc finger and SCAN domain containing 25
161394	8,26E-01	8,30E-02	8,01E-01	0,3181	0,2519799	0,08015956	31,95	SAMD15	sterile alpha motif domain containing 15
80213	4,37E-01	3,60E-01	3,95E-01	0,0943	0,849919	0,08013766	450,94	TM2D3	TM2 domain containing 3
5780	1,55E-01	8,10E-01	1,29E-01	0,0528	1,5181163	0,08013678	2237,6	PTPN9	protein tyrosine phosphatase non-receptor type 9
100526739	3,48E-01	4,58E-01	3,08E-01	0,0784	1,0201308	0,080026	615,27	CENPS-COF	CENPS-CORT readthrough
4610	8,08E-01	9,26E-02	7,81E-01	0,2879	0,2773758	0,07984815	36,57	MYCL	MYCL proto-oncogene, bHLH transcription factor
7753	2,46E-01	6,09E-01	2,11E-01	0,0636	1,2517392	0,07962718	1107,55	ZNF202	zinc finger protein 202
6795	8,64E-01	6,35E-02	8,43E-01	0,4017	0,197876	0,07948311	19,55	AURKC	aurora kinase C
10797	1,75E-01	7,57E-01	1,46E-01	0,0543	1,4535401	0,07895728	2424,84	MTHFD2	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 2, methenyltetrahydrofolate cyclohydrolase
693199	6,62E-01	1,79E-01	6,26E-01	0,1617	0,4880404	0,0789053	124,31	MIR614	microRNA 614
348110	1,97E-01	7,06E-01	1,66E-01	0,0568	1,3856896	0,07877284	1600,92	ARPIN	actin related protein 2/3 complex inhibitor
147727	2,83E-01	5,48E-01	2,45E-01	0,0677	1,1620595	0,07869106	925,72	ILF3-DT	ILF3 divergent transcript
114044	4,02E-01	3,96E-01	3,61E-01	0,086	0,9143012	0,07867557	477,63	MCM3AP-AS	MCM3AP antisense RNA 1
100130197	5,88E-01	2,31E-01	5,49E-01	0,1303	0,5999656	0,07818606	200,99	EFCAB14-AS	EFCAB14 antisense RNA 1
1838	4,52E-01	3,45E-01	4,11E-01	0,0951	0,8217623	0,07817984	362,93	DTNB	dystrobrevin beta
79969	3,03E-01	5,19E-01	2,65E-01	0,0701	1,1157045	0,07816187	841,55	ATAT1	alpha tubulin acetyltransferase 1
5336	5,25E-01	2,80E-01	4,84E-01	0,1116	0,7002811	0,07813066	263,24	PLCG2	phospholipase C gamma 2
100189393	8,70E-01	6,05E-02	8,50E-01	0,4125	0,1887413	0,07786187	17,27	TRI-AAT4-1	tRNA-Ile (anticodon AAT) 4-1
112268048	6,46E-01	1,90E-01	6,09E-01	0,1521	0,5115882	0,07779042	155,22	LOC112268(	uncharacterized LOC112268048
102723553	3,91E-01	4,08E-01	3,50E-01	0,0832	0,9345273	0,07772538	530,31	LOC102723(	small integral membrane protein 11B
5931	5,28E-02	1,28E+00	4,11E-02	0,0379	2,0425145	0,07736616	10944,03	RBBP7	RB binding protein 7, chromatin remodeling factor
221443	9,65E-02	1,02E+00	7,77E-02	0,0438	1,7640446	0,07733462	4326,32	OARD1	O-acyl-ADP-ribose deacylase 1
105375350	6,68E-01	1,75E-01	6,33E-01	0,1616	0,4782023	0,07729924	115,77	LOC105375(	uncharacterized LOC105375350
51759	1,72E-01	7,64E-01	1,44E-01	0,0529	1,4619472	0,07728654	3739,19	C9orf78	chromosome 9 open reading frame 78
2170	8,36E-01	7,78E-02	8,13E-01	0,3262	0,2367983	0,07724507	28,32	FABP3	fatty acid binding protein 3
100507032	7,50E-01	1,25E-01	7,20E-01	0,2151	0,3590558	0,07724033	67,95	TMCC1-DT	TMCC1 divergent transcript
84766	3,12E-01	5,06E-01	2,74E-01	0,0706	1,0946867	0,07723718	755,02	CRACR2A	calcium release activated channel regulator 2A
100129550	7,04E-01	1,52E-01	6,71E-01	0,1812	0,4252648	0,07706282	92,02	LINC02035	long intergenic non-protein coding RNA 2035
22979	6,99E-01	1,56E-01	6,66E-01	0,178	0,4319309	0,07689266	104,94	EFR3B	EFR3 homolog B
90861	7,15E-02	1,15E+00	5,66E-02	0,0403	1,906477	0,07686224	6979,4	JPT2	Jupiter microtubule associated homolog 2
286053	4,70E-01	3,28E-01	4,28E-01	0,0965	0,7919164	0,07638378	372,78	NSMCE2	NSE2 (MMS21) homolog, SMC5-SMC6 complex SUMO ligase
403150	9,14E-01	3,91E-02	8,98E-01	0,598	0,1275747	0,07628727	9,31	FOSL2-AS1	FOSL2 antisense RNA 1
65998	3,24E-01	4,89E-01	2,85E-01	0,0712	1,0699218	0,07622916	789,73	ZFTA	zinc finger translocation associated
8928	6,07E-01	2,17E-01	5,68E-01	0,1333	0,5705291	0,0760506	175	FOXH1	forkhead box H1
57514	1,83E-01	7,38E-01	1,54E-01	0,0532	1,4271185	0,07597351	1750,44	ARHGAP31	Rho GTPase activating protein 31
1653	8,95E-02	1,05E+00	7,18E-02	0,0422	1,8006324	0,07593911	9862,74	DDX1	DEAD-box helicase 1
6612	1,45E-01	8,39E-01	1,20E-01	0,0488	1,5540452	0,07584029	8469,61	SUMO3	small ubiquitin like modifier 3
22974	1,63E-01	7,88E-01	1,35E-01	0,0508	1,4934748	0,07581816	27834,71	TPX2	TPX2 microtubule nucleation factor
59283	8,67E-01	6,20E-02	8,47E-01	0,3928	0,1929077	0,07577692	20,25	CACNG8	calcium voltage-gated channel auxiliary subunit gamma 8
55508	3,00E-01	5,23E-01	2,62E-01	0,0672	1,1218682	0,0754233	865,41	SLC35E3	solute carrier family 35 member E3
84632	3,13E-01	5,04E-01	2,74E-01	0,0688	1,0944306	0,07526321	907,59	AFAP1L2	actin filament associated protein 1 like 2
2631	2,31E-01	6,36E-01	1,97E-01	0,0584	1,2888005	0,07526033	2517,17	NIPSNAP2	nipsnap homolog 2
1660	4,80E-02	1,32E+00	3,72E-02	0,0361	2,0838478	0,07513116	19975,2	DHX9	DExH-box helicase 9
316	1,16E-01	9,36E-01	9,49E-02	0,045	1,6701687	0,07510059	5798,19	AOX1	aldehyde oxidase 1
5915	3,67E-01	4,35E-01	3,26E-01	0,0764	0,9814613	0,07493848	623,71	RARB	retinoic acid receptor beta
57126	7,57E-01	1,21E-01	7,27E-01	0,2145	0,3494201	0,07493845	64,65	CD177	CD177 molecule
6672	1,37E-01	8,63E-01	1,13E-01	0,0472	1,5863755	0,07486478	3472,86	SP100	SP100 nuclear antigen
286336	7,06E-01	1,51E-01	6,73E-01	0,1771	0,4224381	0,07483308	96,53	FAM78A	family with sequence similarity 78 member A
10617	1,10E-01	9,59E-01	8,88E-02	0,0438	1,7017547	0,07446731	4307,15	STAMBP	STAM binding protein
101926918	7,63E-01	1,17E-01	7,33E-01	0,2176	0,3417031	0,07434922	64,45	GTF2IP12	general transcription factor IIi pseudogene 12
79892	8,80E-02	1,06E+00	7,05E-02	0,041	1,8088584	0,07409829	7009,14	MCMBP	minichromosome maintenance complex binding protein
493856	2,11E-01	6,76E-01	1,79E-01	0,055	1,3427929	0,07386609	1567,28	CISD2	CDGSH iron sulfur domain 2
3976	1,70E-01	7,70E-01	1,42E-01	0,0502	1,4695711	0,07382389	2745,82	LIF	LIF interleukin 6 family cytokine
113655	4,36E-01	3,61E-01	3,95E-01	0,0859	0,8510706	0,07313667	655,93	MFSD3	major facilitator superfamily domain containing 3
133522	5,11E-01	2,92E-01	4,69E-01	0,1009	0,7233372	0,07298227	321,05	PPARGC1B	PPARG coactivator 1 beta
51559	2,86E-01	5,44E-01	2,48E-01	0,0632	1,1554889	0,07297801	1118,26	NT5DC3	5'-nucleotidase domain containing 3
55164	2,96E-01	5,29E-01	2,58E-01	0,0645	1,1317107	0,07293902	1164,73	SHQ1	SHQ1, H/ACA ribonucleoprotein assembly factor
112268060	8,97E-01	4,72E-02	8,80E-01	0,4814	0,1513794	0,07286777	12,68	LOC112268(	uncharacterized LOC112268060
110006327	8,97E-01	4,72E-02	8,80E-01	0,4814	0,1513106	0,07283433	12,66	ANKRD20A4	ANKRD20A4-ANKRD20A20P readthrough
10015	9,40E-02	1,03E+00	7,56E-02	0,041	1,7770554	0,07282981	10937,37	PDCD6IP	programmed cell death 6 interacting protein
100128361	7,38E-01	1,32E-01	7,06E-01	0,1924	0,377146	0,0725755	81	LOC100128(	uncharacterized LOC100128361
94056	2,68E-01	5,72E-01	2,31E-01	0,0605	1,1974331	0,07249301	2496,13	SYAP1	synapse associated protein 1
56902	1,72E-01	7,64E-01	1,43E-01	0,0494	1,4634246	0,07231356	3134,37	PNO1	partner of NOB1 homolog
101927322	7,75E-01	1,11E-01	7,46E-01	0,2216	0,3242745	0,07184815	63,1	MALT1-AS1	MALT1 antisense RNA 1
100529063	1,68E-01	7,75E-01	1,40E-01	0,0486	1,4742572	0,07159061	2786,52	BCL2L2-PAB	BCL2L2-PABPN1 readthrough
2956	1,02E-01	9,91E-01	8,21E-02	0,0412	1,7385027	0,0715456	9901,94	MSH6	mutS homolog 6
84669	1,10E-01	9,59E-01	8,93E-02	0,0421	1,6991082	0,07152817	5606,59	USP32	ubiquitin specific peptidase 32
7549	4,57E-01	3,40E-01	4,16E-01	0,0874	0,8142095	0,07120115	446,95	ZNF2	zinc finger protein 2
9311	6,94E-01	1,59E-01	6,59E-01	0,1615	0,4406131	0,07117492	141,8	ASIC3	acid sensing ion channel subunit 3
81556	2,50E-01	6,02E-01	2,15E-01	0,0573	1,2412585	0,07115502	1574,89	INTS14	integrator complex subunit 14
56995	4,06E-01	3,91E-01	3,64E-01	0,0782	0,9071543	0,07098355	660,62	TULP4	TUB like protein 4
64756	2,75E-01	5,61E-01	2,38E-01	0,06	1,1811706	0,07085092	1596,18	ATPAF1	ATP synthase mitochondrial F1 complex assembly factor 1
130814	3,72E-01	4,29E-01	3,32E-01	0,073	0,9706632	0,07084546	746,07	SLC66A3	solute carrier family 66 member 3
100616668	7,34E-01	1,34E-01	7,02E-01	0,1848	0,3828865	0,0707718	91,61	TPTE2P5	TPTE2 pseudogene 5
56984	2,43E-01	6,14E-01	2,08E-01	0,0562	1,2582031	0,07066423	2628,3	PSMG2	proteasome assembly chaperone 2
338811	9,14E-01	3,91E-02	8,99E-01	0,554	0,1272025	0,07047443	10,01	TAFA2	TAFA chemokine like family member 2

375484	3,27E-01	4,85E-01	2,88E-01	0,0662	1,0627521	0,07036606	925,86	SIMC1	SUMO interacting motifs containing 1
57129	1,99E-01	7,01E-01	1,68E-01	0,0509	1,3783423	0,07019592	3142,85	MRPL47	mitochondrial ribosomal protein L47
3823	7,92E-01	1,01E-01	7,64E-01	0,2324	0,2997542	0,06965811	66,59	KLRC3	killer cell lectin like receptor C3
57519	4,05E-01	3,93E-01	3,63E-01	0,0766	0,9090828	0,06963794	634,82	STARD9	StAR related lipid transfer domain containing 9
55007	4,19E-01	3,78E-01	3,77E-01	0,0779	0,8827833	0,06872726	635,55	FAM118A	family with sequence similarity 118 member A
57619	2,66E-01	5,75E-01	2,30E-01	0,0572	1,2008982	0,06865737	1667,82	SHROOM3	shroom family member 3
7227	4,01E-01	3,97E-01	3,60E-01	0,0749	0,9160969	0,06862887	691,67	TRPS1	transcriptional repressor GATA binding 1
23478	1,45E-01	8,39E-01	1,20E-01	0,0441	1,5543704	0,06856179	4567,67	SEC11A	SEC11 homolog A, signal peptidase complex subunit
83933	5,16E-01	2,87E-01	4,74E-01	0,0955	0,7155919	0,0683401	450,22	HDAC10	histone deacetylase 10
105376736	5,50E-01	2,60E-01	5,09E-01	0,1035	0,6599718	0,06829913	347,58	EXOSC10-A	EXOSC10 antisense RNA 1
84960	8,05E-01	9,42E-02	7,78E-01	0,2411	0,2825569	0,06813272	51,45	CCDC183	coiled-coil domain containing 183
112268240	8,97E-01	4,72E-02	8,80E-01	0,4507	0,1510664	0,06807812	14,75	CCDST	cervical cancer associated DHX9 suppressive transcript
3112	8,14E-01	8,94E-02	7,88E-01	0,253	0,2690416	0,0680738	49,16	HLA-DOB	major histocompatibility complex, class II, DO beta
200162	6,21E-01	2,07E-01	5,83E-01	0,124	0,5486333	0,06802629	220,33	SPAG17	sperm associated antigen 17
9836	4,39E-01	3,58E-01	3,97E-01	0,0802	0,8468884	0,06788303	623	LCMT2	leucine carboxyl methyltransferase 2
64764	1,33E-01	8,76E-01	1,09E-01	0,0423	1,6013467	0,06779437	4323,88	CREB3L2	cAMP responsive element binding protein 3 like 2
51560	8,28E-01	8,20E-02	8,03E-01	0,2717	0,2490617	0,06768239	39,94	RAB6B	RAB6B, member RAS oncogene family
10229	4,89E-01	3,11E-01	4,47E-01	0,0889	0,7605367	0,06758565	509,57	COQ7	coenzyme Q7, hydroxylase
8110	3,87E-01	4,12E-01	3,46E-01	0,0716	0,9421486	0,06745276	793,13	DPF3	double PHD fingers 3
10564	1,38E-01	8,60E-01	1,13E-01	0,0425	1,583492	0,06723499	6017,08	ARFGEF2	ADP ribosylation factor guanine nucleotide exchange factor 2
51637	2,08E-01	6,82E-01	1,76E-01	0,0496	1,3526723	0,06708187	9786,75	RTRAF	RNA transcription, translation and transport factor
653082	8,68E-01	6,15E-02	8,47E-01	0,3485	0,1923346	0,06702657	24,01	ZDHHC11B	zinc finger DHHC-type containing 11B
100422860	8,05E-01	9,42E-02	7,77E-01	0,2371	0,2826042	0,06700828	53,26	MIR4292	microRNA 4292
64110	2,50E-01	6,02E-01	2,15E-01	0,054	1,2401308	0,06692406	1701,62	MAGEF1	MAGE family member F1
80174	2,62E-01	5,82E-01	2,25E-01	0,0552	1,21238	0,06691539	1670,4	DBF4B	DBF4 zinc finger B
8837	2,01E-01	6,97E-01	1,70E-01	0,0486	1,3727471	0,06664767	2738,85	CFLAR	CASP8 and FADD like apoptosis regulator
3556	3,12E-01	5,06E-01	2,73E-01	0,0605	1,0960819	0,0663506	1212,59	IL1RAP	interleukin 1 receptor accessory protein
102724965	8,89E-01	5,11E-02	8,71E-01	0,4069	0,1626642	0,06619116	17,66	LOC102724	uncharacterized LOC102724965
107985320	8,70E-01	6,05E-02	8,50E-01	0,3487	0,1894069	0,06604401	24,57	LOC107985	uncharacterized LOC107985320
1876	3,65E-01	4,38E-01	3,24E-01	0,0669	0,9862135	0,06597825	1008,54	E2F6	E2F transcription factor 6
493860	4,01E-01	3,97E-01	3,60E-01	0,0721	0,9154013	0,06597466	1501,32	CCDC73	coiled-coil domain containing 73
57001	4,34E-01	3,63E-01	3,92E-01	0,0769	0,8552289	0,06580922	659,06	SDHAF3	succinate dehydrogenase complex assembly factor 3
9730	1,77E-01	7,52E-01	1,48E-01	0,0455	1,446501	0,06580826	5031,3	DCAF1	DDB1 and CUL4 associated factor 1
100750246	5,27E-01	2,78E-01	4,86E-01	0,0942	0,697373	0,06570465	429,92	HIF1A-AS1	HIF1A antisense RNA 1
9052	1,23E-01	9,10E-01	1,01E-01	0,0399	1,6410125	0,0655578	11814,11	GPRC5A	G protein-coupled receptor class C group 5 member A
114548	4,56E-01	3,41E-01	4,14E-01	0,0803	0,8160376	0,06555283	625,95	NLRP3	NLR family pyrin domain containing 3
23463	1,11E-01	9,55E-01	9,04E-02	0,0386	1,6933519	0,06539733	10103,37	ICMT	isoprenylcysteine carboxyl methyltransferase
11166	7,51E-01	1,24E-01	7,21E-01	0,1826	0,3575747	0,06530728	101,23	SOX21	SRY-box transcription factor 21
22828	1,98E-01	7,03E-01	1,67E-01	0,0472	1,3814801	0,06525796	2943,22	SCAF8	SR-related CTD associated factor 8
101929709	7,97E-01	9,85E-02	7,70E-01	0,2219	0,2925956	0,0649236	65,76	RIPK2-DT	RIPK2 divergent transcript
10715	8,22E-01	8,51E-02	7,96E-01	0,2512	0,2582505	0,06487339	47,65	CERS1	ceramide synthase 1
286467	8,77E-01	5,70E-02	8,58E-01	0,3618	0,1792447	0,06485668	22,65	FIRRE	firre intergenic repeating RNA element
10943	2,70E-01	5,69E-01	2,33E-01	0,0544	1,1914625	0,06484926	1750,27	MSL3	MSL complex subunit 3
100287015	7,84E-01	1,06E-01	7,56E-01	0,2088	0,3105219	0,06483459	76,95	MCPH1-DT	MCPH1 divergent transcript
10036	2,34E-01	6,31E-01	2,00E-01	0,0505	1,2805612	0,06470624	2667,59	CHAF1A	chromatin assembly factor 1 subunit A
80314	3,48E-01	4,58E-01	3,07E-01	0,0633	1,0207945	0,06458783	1133,77	EPC1	enhancer of polycomb homolog 1
84458	2,47E-01	6,07E-01	2,12E-01	0,0517	1,2485906	0,06454324	2461,42	LCOR	ligand dependent nuclear receptor corepressor
84619	4,82E-01	3,17E-01	4,40E-01	0,0835	0,7723779	0,06447576	772,65	ZGPAT	zinc finger CCCH-type and G-patch domain containing
79041	3,43E-01	4,65E-01	3,03E-01	0,0626	1,0295176	0,06442362	1118,31	TMEM38A	transmembrane protein 38A
201158	5,16E-01	2,87E-01	4,74E-01	0,0899	0,7157044	0,06430889	442,26	TVP23C	trans-golgi network vesicle protein 23 homolog C
135152	4,06E-01	3,91E-01	3,65E-01	0,071	0,9054009	0,06423981	757,23	B3GAT2	beta-1,3-glucuronyltransferase 2
100526767	1,78E-01	7,50E-01	1,49E-01	0,0445	1,441998	0,06419347	5241,29	RNF103-CH	RNF103-CHMP3 readthrough
51278	3,11E-01	5,07E-01	2,72E-01	0,0584	1,0981561	0,06415341	2638,32	IER5	immediate early response 5
5805	3,55E-01	4,50E-01	3,15E-01	0,0636	1,0057954	0,06401574	1216,23	PTS	6-pyruvoyltetrahydropterin synthase
10421	2,06E-01	6,86E-01	1,74E-01	0,0471	1,3580087	0,06396529	2920,27	CD2BP2	CD2 cytoplasmic tail binding protein 2
84705	3,09E-01	5,10E-01	2,71E-01	0,058	1,1014221	0,0638564	1634,02	GTPBP3	GTP binding protein 3, mitochondrial
285456	8,90E-01	5,06E-02	8,72E-01	0,3961	0,1608732	0,06372928	19,8	RPL34-DT	RPL34 divergent transcript
51755	1,66E-01	7,80E-01	1,38E-01	0,0429	1,4837794	0,06360155	6064,24	CDK12	cyclin dependent kinase 12
105376335	8,48E-01	7,16E-02	8,26E-01	0,29	0,219216	0,06357458	35,45	LOC105376	serine/arginine repetitive matrix protein 1-like
284058	2,65E-01	5,77E-01	2,28E-01	0,0527	1,2049265	0,06345281	1877,71	KANSL1	KAT8 regulatory NSL complex subunit 1
9372	3,33E-01	4,78E-01	2,94E-01	0,06	1,0500522	0,06304051	1662,35	ZFYVE9	zinc finger FYVE-type containing 9
483	2,20E-01	6,58E-01	1,87E-01	0,0478	1,3185053	0,06298611	5069,21	ATP1B3	ATPase Na+/K+ transporting subunit beta 3
100506012	8,97E-01	4,72E-02	8,80E-01	0,4179	0,1506769	0,06296835	16,84	PPP5D1P	PPP5 tetratricopeptide repeat domain containing 1, pseudogene
104169670	7,62E-01	1,18E-01	7,32E-01	0,1835	0,3426127	0,06287749	90,45	RXYLT1-AS1	RXYLT1 antisense RNA 1
79133	4,58E-01	3,39E-01	4,17E-01	0,0766	0,8122235	0,06219396	638,44	NDUFAF5	NADH:ubiquinone oxidoreductase complex assembly factor 5
7551	3,73E-01	4,28E-01	3,33E-01	0,0636	0,9688752	0,06159667	1217,97	ZNF3	zinc finger protein 3
157869	9,25E-01	3,39E-02	9,11E-01	0,5536	0,1112024	0,06156412	10,12	SBSPON	somatomedin B and thrombospondin type 1 domain containing
302	1,67E-01	7,77E-01	1,40E-01	0,0417	1,4775092	0,06156314	114343,78	ANXA2	annexin A2
90990	4,88E-01	3,12E-01	4,46E-01	0,0806	0,761581	0,06138113	642,49	KIFC2	kinesin family member C2
101927599	6,94E-01	1,59E-01	6,60E-01	0,1394	0,4396188	0,06127461	174,61	ZNF529-AS1	ZNF529 antisense RNA 1
64135	5,32E-01	2,74E-01	4,91E-01	0,0889	0,688691	0,06125675	595,4	IFIH1	interferon induced with helicase C domain 1
29941	4,01E-01	3,97E-01	3,60E-01	0,0669	0,9150812	0,06120005	1386,35	PKN3	protein kinase N3
728039	8,84E-01	5,35E-02	8,65E-01	0,3587	0,1701035	0,06101238	24,55	SSR4P1	signal sequence receptor subunit 4 pseudogene 1
25962	2,03E-01	6,93E-01	1,72E-01	0,0446	1,3669743	0,060905	3456,45	VIRMA	vir like m6A methyltransferase associated
151195	4,30E-01	3,67E-01	3,89E-01	0,0706	0,8616906	0,06082093	968,39	CCNYL1	cyclin Y like 1
8701	2,94E-01	5,32E-01	2,56E-01	0,0535	1,136701	0,06080063	1674,28	DNAH11	dynein axonemal heavy chain 11
3183	1,45E-01	8,39E-01	1,20E-01	0,0389	1,556508	0,06055649	53414,45	HNRNPC	heterogeneous nuclear ribonucleoprotein C
285527	2,09E-01	6,80E-01	1,77E-01	0,0448	1,3503868	0,06055224	3409,81	FRYL	FRY like transcription coactivator
87769	8,34E-01	7,88E-02	8,10E-01	0,2518	0,2403949	0,06053186	49,48	GGACT	gamma-glutamylamine cyclotransferase
105375443	9,02E-01	4,48E-02	8,85E-01	0,4185	0,1443274	0,06039781	17,18	LOC105375443	
388753	5,24E-01	2,81E-01	4,82E-01	0,0859	0,7029386	0,06035815	519,45	COA6	cytochrome c oxidase assembly factor 6
7375	2,46E-01	6,09E-01	2,11E-01	0,0482	1,2515824	0,06031521	3317,35	USP4	ubiquitin specific peptidase 4
284459	4,01E-01	3,97E-01	3,60E-01	0,0658	0,9161462	0,06030416	1102,78	ZNF875	zinc finger protein 875
9946	3,87E-01	4,12E-01	3,45E-01	0,0638	0,9436653	0,06017561	1090,38	CRYZL1	crystallin zeta like 1
10982	2,79E-01	5,54E-01	2,42E-01	0,0514	1,1701644	0,06009233	2116,22	MAPRE2	microtubule associated protein RP/EB family member 2
84083	5,67E-01	2,46E-01	5,27E-01	0,0949	0,6329453	0,06005429	405,29	ZRANB3	zinc finger RANBP2-type containing 3
11043	5,44E-01	2,64E-01	5,03E-01	0,0897	0,6690255	0,06004184	438,32	MID2	midline 2
134285	3,79E-01	4,21E-01	3,38E-01	0,0626	0,958767	0,06002675	1117,01	TMEM171	transmembrane protein 171
427	2,32E-01	6,35E-01	1,98E-01	0,0466	1,2877078	0,05996813	3165,4	ASAH1	N-acylsphingosine amidohydrolase 1
23516	1,94E-01	7,12E-01	1,64E-01	0,043	1,392873	0,05993275	5690,06	SLC39A14	solute carrier family 39 member 14
11325	1,85E-01	7,33E-01	1,56E-01	0,0422	1,4191564	0,05991852	7719,72	DDX42	DEAD-box helicase 42
5997	6,67E-01	1,76E-01	6,31E-01	0,1246	0,4807629	0,05989561	277,9	RGS2	regulator of G protein signaling 2
81631	2,01E-01	6,97E-01	1,70E-01	0,0435	1,3722041	0,05971615	3947,48	MAP1LC3B	microtubule associated protein 1 light chain 3 beta
27257	4,09E-01	3,88E-01	3,68E-01	0,0662	0,9011283	0,05966932	1207,3	LSM1	LSM1 homolog, mRNA degradation associated
11189	6,14E-01	2,12E-01	5,76E-01	0,1066	0,5587528	0,05958122	288,48	CELF3	CUGBP Elav-like family member 3
107986644	9,21E-01	3,57E-02	9,07E-01	0,507	0,1174206	0,0595376	13,99	LOC107986	uncharacterized LOC107986644
100130015	6,92E-01	1,60E-01	6,58E-01	0,1338	0,4431646	0,0592748	190,76	URAHP	urate (hydroxyiso-) hydrolase, pseudogene
51434	1,95E-01	7,10E-01	1,65E-01	0,0426	1,3894269	0,05922988	4353,58	ANAPC7	anaphase promoting complex subunit 7
339201	6,45E-01	1,90E-01	6,08E-01	0,1145	0,5135199	0,05877461	254,74	ASB16-AS1	ASB16 antisense RNA 1
60674	1,97E-01	7,06E-01	1,67E-01	0,0423	1,3832312	0,05856147	4571,26	GAS5	growth arrest specific 5
100874362	9,22E-01	3,53E-02	9,08E-01	0,5059	0,1154472	0,05840672	12,87	HOXB-AS1	HOXB cluster antisense RNA 1
387597	5,41E-01	2,67E-01	5,01E-01	0,0865	0,6736497	0,05826745	473,85	ILDR2	immunoglobulin like domain containing receptor 2
105369149	8,10E-01	9,15E-02	7,83E-01	0,2116	0,2750709	0,05820825	67,25	LOC105369	uncharacterized LOC105369149
1033	3,06E-01	5,14E-01	2,67E-01	0,0522	1,1089745	0,05791754	3477,16	CDKN3	cyclin dependent kinase inhibitor 3
100874001	5,88E-01	2,31E-01	5,48E-01	0,0961	0,6001657	0,0576928	429,44	NCBP2-AS1	NCBP2 antisense RNA 1
440300	7,33E-01	1,35E-01	7,02E-01	0,1503	0,3831128	0,05758906	136,24	LOC440300	chondroitin sulfate proteoglycan 4 pseudogene
3837	1,52E-01	8,18E-01	1,26E-01	0,0376	1,5297916	0,05753868	43244,2	KPNB1	karyopherin subunit beta 1
105372401	3,80E-01	4,20E-01	3,39E-01	0,0602	0,9555393	0,0574839	1370,44	LOC105372	uncharacterized LOC105372401
8318	3,21E-01	4,93E-01	2,82E-01	0,0534	1,0756286	0,05746085	2116,92	CDC45	cell division cycle 45
2034	2,47E-01	6,07E-01	2,12E-01	0,0461	1,24726	0,05744894	3412,93	EPAS1	endothelial PAS domain protein 1
128061	5,85E-01	2,33E-01	5,45E-01	0,0949	0,6048221	0,05739408	405,37	C1orf131	chromosome 1 open reading frame 131
107985714	9,28E-01	3,25E-02	9,16E-01	0,5422	0,1058304	0,0573829	10,73	LOC107985	uncharacterized LOC107985714
22992	2,13E-01	6,72E-01	1,81E-01	0,0428	1,338851	0,05731797	7239,39	KDM2A	lysine demethylase 2A
331	3,66E-01	4,37E-01	3,25E-01	0,0581	0,9833789	0,05714922	2290,7	XIAP	X-linked inhibitor of apoptosis
6489	9,01E-01	4,53E-02	8,84E-01	0,3919	0,1457402	0,05711385	19,87	ST8SIA1	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 1
105374114	5,82E-01	2,35E-01	5,43E-01	0,0934	0,6088803	0,0568855	452,2	LOC105374	uncharacterized LOC105374114
163259	6,44E-01	1,91E-01	6,07E-01	0,1105	0,5148335	0,05687864	279,23	DENND2C	DENN domain containing 2C
7980	3,67E-01	4,35E-01	3,26E-01	0,0575	0,9821196	0,05642693	3138,58	TFPI2	tissue factor pathway inhibitor 2
10302	4,54E-01	3,43E-01	4,12E-01	0,0681	0,8199573	0,0558768	971,29	SNAPC5	small nuclear RNA activating complex polypeptide 5
51645	2,63E-01	5,80E-01	2,26E-01	0,0461	1,209887	0,0557487	6988,41	PPIL1	peptidylprolyl isomerase like 1

90411	1,42E-01	8,48E-01	1,17E-01	0,0355	1,5684773	0,05568328	18741,99	MCFD2	multiple coagulation factor deficiency 2, ER cargo receptor complex subunit
6729	2,37E-01	6,25E-01	2,03E-01	0,0432	1,2737051	0,05507632	4495,46	SRP54	signal recognition particle 54
81573	3,18E-01	4,98E-01	2,78E-01	0,0504	1,0836966	0,05463675	2973,94	ANKRD13C	ankyrin repeat domain 13C
10950	4,26E-01	3,71E-01	3,85E-01	0,0628	0,8693158	0,05462471	1253,12	BTG3	BTG anti-proliferation factor 3
9022	8,04E-01	9,47E-02	7,77E-01	0,1927	0,2833926	0,05460693	94,82	CLIC3	chloride intracellular channel 3
101928152	8,25E-01	8,35E-02	8,00E-01	0,2151	0,2537522	0,05458235	69,02	LOC101928	replaced by ID 101928173
51324	3,24E-01	4,89E-01	2,85E-01	0,0508	1,0701867	0,05438428	4689,37	SPG21	SPG21 abhydrolase domain containing, maspardin
2281	5,71E-01	2,43E-01	5,31E-01	0,0867	0,6265341	0,05431715	842,75	FKBP1B	FKBP prolyl isomerase 1B
92806	6,02E-01	2,20E-01	5,64E-01	0,0941	0,5774426	0,05431512	438,9	CENPBD1P	CENPB DNA-binding domain containing 1, pseudogene
8027	2,78E-01	5,56E-01	2,41E-01	0,0463	1,1725759	0,05424934	2972,29	STAM	signal transducing adaptor molecule
801	1,97E-01	7,06E-01	1,66E-01	0,0392	1,3840788	0,05422927	16188,82	CALM1	calmodulin 1
27239	8,84E-01	5,35E-02	8,65E-01	0,3188	0,169894	0,05416826	33	GPR162	G protein-coupled receptor 162
101928243	6,07E-01	2,17E-01	5,68E-01	0,0949	0,570372	0,05410661	421,34	DARS1-AS1	DARS1 antisense RNA 1
27346	3,57E-01	4,47E-01	3,16E-01	0,0539	1,0026353	0,05399449	1811	TMEM97	transmembrane protein 97
11104	4,51E-01	3,46E-01	4,09E-01	0,0653	0,8248313	0,05384605	971,05	KATNA1	katanin catalytic subunit A1
51652	2,63E-01	5,80E-01	2,26E-01	0,0445	1,2095347	0,05381389	5196,3	CHMP3	charged multivesicular body protein 3
84464	4,89E-01	3,11E-01	4,47E-01	0,0707	0,759681	0,05374518	866,81	SLX4	SLX4 structure-specific endonuclease subunit
8034	5,39E-01	2,68E-01	4,98E-01	0,0791	0,6781187	0,05366991	571,32	SLC25A16	solute carrier family 25 member 16
57089	4,19E-01	3,78E-01	3,78E-01	0,0608	0,8824511	0,05363117	1140,62	ENTPD7	ectonucleoside triphosphate diphosphohydrolase 7
55313	4,01E-01	3,97E-01	3,59E-01	0,0585	0,9164975	0,05362702	1623,94	CPPED1	calcineurin like phosphoesterase domain containing 1
55687	5,36E-01	2,71E-01	4,95E-01	0,0785	0,6822932	0,05355558	716,2	TRMU	tRNA mitochondrial 2-thiouridylase
107984552	9,28E-01	3,25E-02	9,16E-01	0,5053	0,1053849	0,05325168	12,22	LOC107984	uncharacterized LOC107984552
9326	3,27E-01	4,85E-01	2,87E-01	0,05	1,0643725	0,05322193	2246,88	ZNHIT3	zinc finger HIT-type containing 3
5888	3,99E-01	3,99E-01	3,57E-01	0,0578	0,9204879	0,05318407	1366,03	RAD51	RAD51 recombinase
6399	6,75E-01	1,71E-01	6,40E-01	0,1123	0,4679344	0,05253022	335,84	TRAPPC2	trafficking protein particle complex subunit 2
22927	4,74E-01	3,24E-01	4,32E-01	0,0669	0,7850094	0,05249806	974,32	HABP4	hyaluronan binding protein 4
55252	2,86E-01	5,44E-01	2,48E-01	0,0454	1,1552253	0,05244355	4360,04	ASXL2	ASXL transcriptional regulator 2
23600	6,46E-01	1,90E-01	6,09E-01	0,1025	0,5111967	0,05238494	325,86	AMACR	alpha-methylacyl-CoA racemase
107985154	6,75E-01	1,71E-01	6,39E-01	0,1117	0,4684343	0,05230694	254,95	LOC107985	uncharacterized LOC107985154
84942	4,80E-01	3,19E-01	4,39E-01	0,0674	0,7746983	0,05221986	868,88	WDR73	WD repeat domain 73
10144	4,60E-01	3,37E-01	4,19E-01	0,064	0,8085723	0,05171709	1106,2	FAM13A	family with sequence similarity 13 member A
6667	2,87E-01	5,42E-01	2,49E-01	0,0446	1,1530167	0,05145126	4868,08	SP1	Sp1 transcription factor
5316	4,95E-01	3,05E-01	4,53E-01	0,0684	0,7502047	0,05128428	873,42	PKNOX1	PBX/knotted 1 homeobox 1
101928820	7,85E-01	1,05E-01	7,56E-01	0,165	0,3101667	0,05117226	116,55	LINC02535	long intergenic non-protein coding RNA 2535
105371520	9,06E-01	4,29E-02	8,90E-01	0,3699	0,1378592	0,05099213	22,58	LOC105371	uncharacterized LOC105371520
11098	2,00E-01	6,99E-01	1,69E-01	0,0371	1,3742985	0,0509203	13638,15	PRSS23	serine protease 23
114004397	6,85E-01	1,64E-01	6,50E-01	0,1106	0,4540076	0,05020422	264,39	CA5BP1-CA	CA5BP1-CA5B readthrough
107986696	6,91E-01	1,61E-01	6,56E-01	0,1124	0,4452241	0,05003235	258,74	LOC107986696	
255762	6,43E-01	1,92E-01	6,06E-01	0,0968	0,5160023	0,049939	351,61	PDZD9	PDZ domain containing 9
5511	3,09E-01	5,10E-01	2,71E-01	0,0453	1,1013122	0,04989953	3556,64	PPP1R8	protein phosphatase 1 regulatory subunit 8
54807	6,72E-01	1,73E-01	6,36E-01	0,1055	0,4728737	0,04989841	336,76	ZNF586	zinc finger protein 586
220963	9,21E-01	3,57E-02	9,06E-01	0,4243	0,117599	0,0498976	16,43	SLC16A9	solute carrier family 16 member 9
80854	2,39E-01	6,22E-01	2,05E-01	0,0391	1,2686943	0,04966397	7968,74	SETD7	SET domain containing 7, histone lysine methyltransferase
105376257	9,37E-01	2,83E-02	9,26E-01	0,5304	0,0925958	0,04911409	11	LOC105376	uncharacterized LOC105376257
145438	9,00E-01	4,58E-02	8,83E-01	0,3335	0,1472247	0,04910089	29,63	FRMD6-AS1	FRMD6 antisense RNA 1
8824	4,07E-01	3,90E-01	3,66E-01	0,0542	0,9034556	0,04895469	1683,42	CES2	carboxylesterase 2
11160	3,74E-01	4,27E-01	3,33E-01	0,0503	0,9684444	0,04871573	2475,07	ERLIN2	ER lipid raft associated 2
54954	5,14E-01	2,89E-01	4,73E-01	0,0674	0,7182836	0,04843812	1008,18	FAM120C	family with sequence similarity 120C
5270	4,88E-01	3,12E-01	4,46E-01	0,0635	0,7615404	0,04839466	1595,22	SERPINE2	serpin family E member 2
9649	7,64E-01	1,17E-01	7,34E-01	0,1421	0,3404125	0,04837276	153,17	RALGPS1	Ral GEF with PH domain and SH3 binding motif 1
79068	4,03E-01	3,95E-01	3,62E-01	0,053	0,9122042	0,04830445	1781,12	FTO	FTO alpha-ketoglutarate dependent dioxygenase
91433	4,73E-01	3,25E-01	4,31E-01	0,061	0,7873265	0,04806402	1172,76	RCCD1	RCC1 domain containing 1
107985478	9,42E-01	2,59E-02	9,31E-01	0,5561	0,0863778	0,04803489	11,02	LOC107985	uncharacterized LOC107985478
163590	3,16E-01	5,00E-01	2,77E-01	0,044	1,0862081	0,04778717	4107,72	TOR1AIP2	torsin 1A interacting protein 2
84275	5,94E-01	2,26E-01	5,56E-01	0,0811	0,5895265	0,04778431	682,2	SLC25A33	solute carrier family 25 member 33
339488	7,57E-01	1,21E-01	7,27E-01	0,1358	0,3493326	0,04742844	166,54	TFAP2E	transcription factor AP-2 epsilon
101929054	9,29E-01	3,20E-02	9,17E-01	0,4527	0,1047444	0,04741326	16,78	TWF2-DT	TWF2 divergent transcript
102724351	8,97E-01	4,72E-02	8,80E-01	0,3127	0,1511304	0,04726111	30,53	LOC102724	uncharacterized LOC102724351
9943	2,55E-01	5,93E-01	2,19E-01	0,0383	1,2283949	0,04699353	10331,47	OXSR1	oxidative stress responsive kinase 1
56882	2,99E-01	5,24E-01	2,61E-01	0,0418	1,125105	0,04698359	5019,31	CDC42SE1	CDC42 small effector 1
56171	9,29E-01	3,20E-02	9,17E-01	0,452	0,1038839	0,04695243	15,16	DNAH7	dynein axonemal heavy chain 7
5460	8,84E-01	5,35E-02	8,66E-01	0,2774	0,1691595	0,04693116	38,6	POU5F1	POU class 5 homeobox 1
116936	8,79E-01	5,60E-02	8,61E-01	0,2663	0,1757361	0,04679833	42,73	SNORD139	small nucleolar RNA, C/D box 139
202243	6,05E-01	2,18E-01	5,67E-01	0,0816	0,5725621	0,04673096	536,49	CCDC125	coiled-coil domain containing 125
7156	3,49E-01	4,57E-01	3,09E-01	0,0459	1,0180302	0,04669973	3560,48	TOP3A	DNA topoisomerase III alpha
7127	3,58E-01	4,46E-01	3,17E-01	0,0466	0,9999052	0,04663807	3958,91	TNFAIP2	TNF alpha induced protein 2
84197	7,63E-01	1,17E-01	7,33E-01	0,1364	0,3414014	0,04656053	225,22	POMK	protein O-mannose kinase
10785	6,98E-01	1,56E-01	6,64E-01	0,107	0,4341398	0,04645251	325,67	WDR4	WD repeat domain 4
145200	9,05E-01	4,34E-02	8,89E-01	0,3323	0,1395147	0,04636188	27,11	LINC00239	long intergenic non-protein coding RNA 239
3363	5,73E-01	2,42E-01	5,32E-01	0,0741	0,6244939	0,04627419	721,4	HTR7	5-hydroxytryptamine receptor 7
254065	4,86E-01	3,13E-01	4,44E-01	0,0604	0,7652538	0,04624289	1431,6	BRWD3	bromodomain and WD repeat domain containing 3
10124	5,80E-01	2,37E-01	5,40E-01	0,0744	0,6128113	0,04558791	1276,85	ARL4A	ADP ribosylation factor like GTPase 4A
23531	5,21E-01	2,83E-01	4,80E-01	0,0643	0,7069203	0,04542119	1334,86	MMD	monocyte to macrophage differentiation associated
79695	7,13E-01	1,47E-01	6,80E-01	0,11	0,4119529	0,04529583	263,67	GALNT12	polypeptide N-acetylgalactosaminyltransferase 12
60493	4,50E-01	3,47E-01	4,09E-01	0,0547	0,8256322	0,04519358	1540,77	FASTKD5	FAST kinase domains 5
1107	3,37E-01	4,72E-01	2,97E-01	0,0432	1,0431497	0,04503261	6502,29	CHD3	chromodomain helicase DNA binding protein 3
585	6,69E-01	1,75E-01	6,33E-01	0,094	0,4778929	0,04494017	440,63	BBS4	Bardet-Biedl syndrome 4
100009676	7,25E-01	1,40E-01	6,92E-01	0,1131	0,3958068	0,0447809	256,96	ZBTB11-AS1	ZBTB11 antisense RNA 1
339942	8,23E-01	8,46E-02	7,98E-01	0,1741	0,2561075	0,04458549	113,18	H1-10-AS1	H1-10 antisense RNA 1
9770	7,85E-01	1,05E-01	7,56E-01	0,1434	0,3102311	0,04448345	163,32	RASSF2	Ras association domain family member 2
8292	9,39E-01	2,73E-02	9,28E-01	0,4918	0,0904269	0,04447274	12,93	COLQ	collagen like tail subunit of asymmetric acetylcholinesterase
10409	3,65E-01	4,38E-01	3,25E-01	0,0451	0,9846332	0,04444295	4140,09	BASP1	brain abundant membrane attached signal protein 1
27291	5,89E-01	2,30E-01	5,50E-01	0,0743	0,5981685	0,04443675	858,71	R3HCC1L	R3H domain and coiled-coil containing 1 like
105370910	9,22E-01	3,53E-02	9,08E-01	0,3821	0,115803	0,04425322	20,38	LOC105370	uncharacterized LOC105370910
85440	4,12E-01	3,85E-01	3,71E-01	0,0492	0,8943109	0,04396476	4128,93	DOCK7	dedicator of cytokinesis 7
85364	5,64E-01	2,49E-01	5,23E-01	0,0689	0,6383725	0,04395425	1048,15	ZCCHC3	zinc finger CCHC-type containing 3
107984665	7,98E-01	9,80E-02	7,70E-01	0,1502	0,292319	0,04390826	159,22	LOC107984665	
23365	3,24E-01	4,89E-01	2,85E-01	0,041	1,069949	0,04382687	11894,76	ARHGEF12	Rho guanine nucleotide exchange factor 12
136895	7,41E-01	1,30E-01	7,10E-01	0,1177	0,3722822	0,04381343	250,15	C7orf31	chromosome 7 open reading frame 31
92259	6,41E-01	1,93E-01	6,04E-01	0,0844	0,5183774	0,04373378	947,35	MRPS36	mitochondrial ribosomal protein S36
58985	9,37E-01	2,83E-02	9,25E-01	0,4646	0,0939473	0,04365015	14,29	IL22RA1	interleukin 22 receptor subunit alpha 1
8454	3,31E-01	4,80E-01	2,92E-01	0,0414	1,0543832	0,04362299	5133,78	CUL1	cullin 1
9611	4,21E-01	3,76E-01	3,80E-01	0,0497	0,8779927	0,04362233	6618,58	NCOR1	nuclear receptor corepressor 1
51072	4,81E-01	3,18E-01	4,39E-01	0,0563	0,7739006	0,04358122	1697,88	MEMO1	mediator of cell motility 1
105374003	5,14E-01	2,89E-01	4,72E-01	0,0605	0,7194222	0,04353943	1369,92	LOC105374	uncharacterized LOC105374003
54733	3,57E-01	4,47E-01	3,17E-01	0,0431	1,0015086	0,04314194	4750,93	SLC35F2	solute carrier family 35 member F2
3176	5,75E-01	2,40E-01	5,34E-01	0,0691	0,621545	0,04294868	860,99	HNMT	histamine N-methyltransferase
57630	4,28E-01	3,69E-01	3,86E-01	0,0495	0,8664547	0,0429205	2256,45	SH3RF1	SH3 domain containing ring finger 1
91942	5,09E-01	2,93E-01	4,67E-01	0,059	0,7267149	0,04287677	2990,74	NDUFAF2	NADH:ubiquinone oxidoreductase complex assembly factor 2
84448	8,52E-01	6,96E-02	8,30E-01	0,1994	0,214847	0,04283902	78,71	ABLIM2	actin binding LIM protein family member 2
65244	5,77E-01	2,39E-01	5,37E-01	0,0693	0,6180318	0,04281571	922,34	SPATS2	spermatogenesis associated serine rich 2
283171	9,40E-01	2,69E-02	9,29E-01	0,4798	0,0889025	0,04265809	14,83	LINC02873	long intergenic non-protein coding RNA 2873
1459	5,23E-01	2,81E-01	4,81E-01	0,06	0,7039813	0,04225866	1773,29	CSNK2A2	casein kinase 2 alpha 2
23673	5,33E-01	2,73E-01	4,92E-01	0,0615	0,6872768	0,04225219	1123,92	STX12	syntaxin 12
79018	5,56E-01	2,55E-01	5,15E-01	0,0649	0,6503998	0,04222096	999,95	GID4	GID complex subunit 4 homolog
57107	6,20E-01	2,08E-01	5,82E-01	0,0764	0,550429	0,04206294	643,31	PDSS2	decaprenyl diphosphate synthase subunit 2
55179	6,04E-01	2,19E-01	5,66E-01	0,0732	0,574542	0,04205441	822,79	FAIM	Fas apoptotic inhibitory molecule
4719	3,56E-01	4,49E-01	3,16E-01	0,0417	1,0027714	0,04182535	7212,21	NDUFS1	NADH:ubiquinone oxidoreductase core subunit S1
84817	6,04E-01	2,19E-01	5,66E-01	0,0727	0,5742521	0,04177226	2877,07	TXNDC17	thioredoxin domain containing 17
6627	4,55E-01	3,42E-01	4,14E-01	0,051	0,8165572	0,04167686	2491,61	SNRPA1	small nuclear ribonucleoprotein polypeptide A'
84937	5,85E-01	2,33E-01	5,45E-01	0,0687	0,6055447	0,04160984	1054,21	ZNRF1	zinc and ring finger 1
100507554	7,60E-01	1,19E-01	7,30E-01	0,1204	0,3454069	0,04158799	226,81	RPL37A-DT	RPL37A divergent transcript
51660	6,09E-01	2,15E-01	5,71E-01	0,0733	0,5672365	0,04156081	865,6	MPC1	mitochondrial pyruvate carrier 1
51741	7,11E-01	1,48E-01	6,78E-01	0,1002	0,4148475	0,04155566	349,12	WWOX	WW domain containing oxidoreductase
10325	5,71E-01	2,43E-01	5,31E-01	0,0658	0,6266836	0,04121133	927,31	RRAGB	Ras related GTP binding B
5757	3,86E-01	4,13E-01	3,45E-01	0,0435	0,9444182	0,04105216	60314,08	PTMA	prothymosin alpha
11254	9,04E-01	4,38E-02	8,88E-01	0,2916	0,1404414	0,04094786	38,45	SLC6A14	solute carrier family 6 member 14
84722	4,90E-01	3,10E-01	4,49E-01	0,0539	0,75756	0,04080741	2163,42	PSRC1	proline and serine rich coiled-coil 1
79891	7,95E-01	9,96E-02	7,67E-01	0,1366	0,2965606	0,04051841	202,56	ZNF671	zinc finger protein 671
100507346	8,77E-01	5,70E-02	8,58E-01	0,2262	0,1790486	0,04050892	59,14	LOC100507	uncharacterized LOC100507346

3431	5,90E-01	2,29E-01	5,51E-01	0,0676	0,5965014	0,04033854	971,39	SP110	SP110 nuclear body protein
84516	3,90E-01	4,09E-01	3,48E-01	0,0429	0,9380118	0,04025398	5125,01	DCTN5	dynactin subunit 5
65980	4,27E-01	3,70E-01	3,85E-01	0,0463	0,8681177	0,0402364	2916,63	BRD9	bromodomain containing 9
51729	3,99E-01	3,99E-01	3,58E-01	0,0437	0,9198417	0,04020418	6306,82	WBP11	WW domain binding protein 11
23438	4,99E-01	3,02E-01	4,57E-01	0,0538	0,7443072	0,04005274	1723,18	HARS2	histidyl-tRNA synthetase 2, mitochondrial
26130	4,38E-01	3,59E-01	3,97E-01	0,0468	0,8470371	0,03960821	3852,32	GAPVD1	GTPase activating protein and VPS9 domains 1
29954	5,20E-01	2,84E-01	4,78E-01	0,0558	0,7087666	0,03956724	1623,63	POMT2	protein O-mannosyltransferase 2
100847046	9,18E-01	3,72E-02	9,04E-01	0,3253	0,1209908	0,03935502	29,44	MIR5010	microRNA 5010
23522	6,28E-01	2,02E-01	5,91E-01	0,073	0,5378063	0,03926781	1408,22	KAT6B	lysine acetyltransferase 6B
79690	9,14E-01	3,91E-02	8,99E-01	0,3079	0,1272306	0,03917483	35,91	GAL3ST4	galactose-3-O-sulfotransferase 4
115207	5,59E-01	2,53E-01	5,18E-01	0,0604	0,646221	0,03903229	1626,63	KCTD12	potassium channel tetramerization domain containing 12
26268	5,25E-01	2,80E-01	4,84E-01	0,0557	0,7002719	0,03901014	1686,5	FBXO9	F-box protein 9
143384	4,72E-01	3,26E-01	4,30E-01	0,0494	0,7888521	0,03895965	2629,4	CACUL1	CDK2 associated cullin domain 1
107985353	7,64E-01	1,17E-01	7,34E-01	0,1136	0,3394761	0,03857047	251,2	ACBD3-AS1	ACBD3 antisense RNA 1
348327	7,22E-01	1,41E-01	6,89E-01	0,0962	0,3995662	0,03845053	375,77	ZNF530	zinc finger protein 530
112268144	8,81E-01	5,50E-02	8,62E-01	0,2209	0,1736274	0,03834798	61,01	LOC112268	144
54927	4,52E-01	3,45E-01	4,11E-01	0,0465	0,822553	0,03823494	3779,73	CHCHD3	coiled-coil-helix-coiled-coil-helix domain containing 3
3660	5,46E-01	2,63E-01	5,06E-01	0,0573	0,665854	0,03817702	1388,84	IRF2	interferon regulatory factor 2
301	4,44E-01	3,53E-01	4,03E-01	0,0456	0,8368219	0,03817532	34202,42	ANXA1	annexin A1
122525	8,28E-01	8,20E-02	8,04E-01	0,1532	0,2484097	0,03806653	135,22	C14orf28	chromosome 14 open reading frame 28
9325	5,58E-01	2,53E-01	5,17E-01	0,0583	0,6476825	0,03779104	1358,21	TRIP4	thyroid hormone receptor interactor 4
51138	5,39E-01	2,68E-01	4,98E-01	0,0554	0,6781338	0,03755399	2970,86	COPS4	COP9 signalosome subunit 4
10202	8,49E-01	7,11E-02	8,27E-01	0,1718	0,21852	0,0375332	120,47	DHRS2	dehydrogenase/reductase 2
26151	6,50E-01	1,87E-01	6,13E-01	0,0741	0,5059976	0,03751158	835,86	NAT9	N-acetyltransferase 9 (putative)
9743	5,34E-01	2,72E-01	4,93E-01	0,0542	0,6852047	0,03710646	1866,08	ARHGAP32	Rho GTPase activating protein 32
80025	4,70E-01	3,28E-01	4,28E-01	0,0467	0,7920889	0,03700787	3793,07	PANK2	pantothenate kinase 2
89932	8,94E-01	4,87E-02	8,77E-01	0,2373	0,1552529	0,036848	53,97	PAPLN	papilin, proteoglycan like sulfated glycoprotein
2131	3,42E-01	4,66E-01	3,02E-01	0,0357	1,0316347	0,03678711	19259,42	EXT1	exostosin glycosyltransferase 1
338069	9,41E-01	2,64E-02	9,31E-01	0,4228	0,0869813	0,03677546	16,27	ST7-OT4	ST7 overlapping transcript 4
6942	5,19E-01	2,85E-01	4,78E-01	0,0518	0,7099276	0,03676771	2554,69	TCF20	transcription factor 20
10162	6,39E-01	1,94E-01	6,02E-01	0,0704	0,5216456	0,03673204	848,43	LPCAT3	lysophosphatidylcholine acyltransferase 3
5433	5,12E-01	2,91E-01	4,70E-01	0,0507	0,7227489	0,03667768	2465,28	POLR2D	RNA polymerase II subunit D
84650	6,94E-01	1,59E-01	6,60E-01	0,0835	0,439259	0,03667143	598,46	EBPL	EBP like
27300	4,93E-01	3,07E-01	4,51E-01	0,0485	0,7535827	0,03652379	2662,02	ZNF544	zinc finger protein 544
3170	5,78E-01	2,38E-01	5,38E-01	0,0588	0,6158533	0,036225	1535,2	FOXA2	forkhead box A2
605	6,77E-01	1,69E-01	6,42E-01	0,0776	0,4652622	0,03608271	625,11	BCL7A	BAF chromatin remodeling complex subunit BCL7A
60492	5,92E-01	2,28E-01	5,53E-01	0,0606	0,5933865	0,03597314	2354,74	CCDC90B	coiled-coil domain containing 90B
27439	9,36E-01	2,87E-02	9,25E-01	0,3808	0,0943783	0,03593561	20,82	TMEM121B	transmembrane protein 121B
164237	9,59E-01	1,82E-02	9,50E-01	0,5736	0,0622263	0,03569022	9,47	WFDC13	WAP four-disulfide core domain 13
171546	5,82E-01	2,35E-01	5,42E-01	0,0585	0,6102138	0,03567765	1594,06	SPTSSA	serine palmitoyltransferase small subunit A
55507	9,27E-01	3,29E-02	9,14E-01	0,3294	0,1082576	0,03565752	29,81	GPRC5D	G protein-coupled receptor class C group 5 member D
400618	9,53E-01	2,09E-02	9,45E-01	0,5111	0,0696018	0,03557692	11,7	SOX9-AS1	SOX9 antisense RNA 1
6272	4,41E-01	3,56E-01	3,99E-01	0,0421	0,8425695	0,03544384	7400,92	SORT1	sortilin 1
5362	5,93E-01	2,27E-01	5,54E-01	0,0596	0,5911948	0,0352194	1478,62	PLXNA2	plexin A2
91544	7,50E-01	1,25E-01	7,20E-01	0,0972	0,3590321	0,03491585	397,59	UBXN11	UBX domain protein 11
8440	6,61E-01	1,80E-01	6,25E-01	0,0709	0,4889531	0,03468704	761,26	NCK2	NCK adaptor protein 2
27072	5,49E-01	2,60E-01	5,09E-01	0,0522	0,6609248	0,0345103	1937,08	VPS41	VPS41 subunit of HOPS complex
23432	6,22E-01	2,06E-01	5,84E-01	0,063	0,5468755	0,03443467	1218,1	GPR161	G protein-coupled receptor 161
22950	5,39E-01	2,68E-01	4,98E-01	0,0502	0,6784114	0,03403212	3596,61	SLC4A1AP	solute carrier family 4 member 1 adaptor protein
84807	7,92E-01	1,01E-01	7,64E-01	0,1132	0,2997699	0,03393464	255,55	NFKBID	NFKB inhibitor delta
5700	5,71E-01	2,43E-01	5,30E-01	0,054	0,6275325	0,03389024	11213,1	PSMC1	proteasome 26S subunit, ATPase 1
55143	5,38E-01	2,69E-01	4,97E-01	0,0497	0,6794044	0,03374465	8214,08	CDCA8	cell division cycle associated 8
91369	5,01E-01	3,00E-01	4,59E-01	0,0455	0,7407327	0,033728	3120,18	ANKRD40	ankyrin repeat domain 40
112268267	7,59E-01	1,20E-01	7,29E-01	0,0974	0,3462602	0,03371091	362,39	LOC112268	uncharacterized LOC112268267
7171	4,20E-01	3,77E-01	3,79E-01	0,0379	0,8796683	0,03338117	78340,67	TPM4	tropomyosin 4
101928868	8,57E-01	6,70E-02	8,35E-01	0,1601	0,2078737	0,03328136	131,92	LOC101928	uncharacterized LOC101928868
10401	6,24E-01	2,05E-01	5,87E-01	0,0608	0,5438331	0,03304133	1616,93	PIAS3	protein inhibitor of activated STAT 3
80852	5,88E-01	2,31E-01	5,49E-01	0,0544	0,5992369	0,03260734	2192,19	GRIP2	glutamate receptor interacting protein 2
100506235	9,44E-01	2,50E-02	9,34E-01	0,3929	0,0823162	0,0323386	19,58	LOC100506	uncharacterized LOC100506235
84787	8,44E-01	7,37E-02	8,21E-01	0,1422	0,2260451	0,03213291	179,99	KMT5C	lysine methyltransferase 5C
84133	7,58E-01	1,20E-01	7,27E-01	0,0919	0,348774	0,03204889	405,27	ZNRF3	zinc and ring finger 3
79628	6,67E-01	1,76E-01	6,31E-01	0,0666	0,4807022	0,03203417	970,24	SH3TC2	SH3 domain and tetratricopeptide repeats 2
152048	8,46E-01	7,26E-02	8,24E-01	0,1431	0,2221369	0,0317849	157,33	GOLGA4-AS	GOLGA4 antisense RNA 1
1022	6,01E-01	2,21E-01	5,63E-01	0,0548	0,5786912	0,03173701	1982,43	CDK7	cyclin dependent kinase 7
9586	7,32E-01	1,35E-01	7,00E-01	0,0822	0,3853963	0,03168692	519,24	CREB5	cAMP responsive element binding protein 5
414761	8,46E-01	7,26E-02	8,24E-01	0,1425	0,2221754	0,03164952	155,04	HCG15	HLA complex group 15
386758	9,55E-01	2,00E-02	9,47E-01	0,4698	0,0668483	0,03140628	13,4	ZNF582-DT	ZNF582 divergent transcript
110006325	8,02E-01	9,58E-02	7,75E-01	0,1096	0,285806	0,03131992	269,97	PPIP5K1P1-	PPIP5K1P1-CATSPER2 readthrough
89884	8,03E-01	9,53E-02	7,76E-01	0,1091	0,2850679	0,03111318	269,33	LHX4	LIM homeobox 4
8658	6,49E-01	1,88E-01	6,13E-01	0,0611	0,5064542	0,03095754	1282,9	TNKS	tankyrase
203286	6,14E-01	2,12E-01	5,75E-01	0,0549	0,5602526	0,03077652	1651,55	ANKS6	ankyrin repeat and sterile alpha motif domain containing 6
51513	9,32E-01	3,06E-02	9,20E-01	0,306	0,1000341	0,0306098	34,4	ETV7	ETS variant transcription factor 7
102724827	9,34E-01	2,97E-02	9,22E-01	0,3106	0,0977963	0,03037563	31,17	MIATNB	MIAT neighbor
337873	9,48E-01	2,32E-02	9,39E-01	0,3932	0,0770577	0,03030079	19,24	H2BC20P	H2B clustered histone 20, pseudogene
7482	8,68E-01	6,15E-02	8,48E-01	0,1576	0,1919757	0,03024677	133,28	WNT2B	Wnt family member 2B
84856	9,09E-01	4,14E-02	8,93E-01	0,225	0,1340451	0,03015433	61,34	LINC00839	long intergenic non-protein coding RNA 839
102723665	9,27E-01	3,29E-02	9,14E-01	0,2789	0,1078628	0,03007865	38,16	LOC102723	uncharacterized LOC102723665
51071	6,72E-01	1,73E-01	6,36E-01	0,0635	0,4733106	0,03006356	1410,32	DERA	deoxyribose-phosphate aldolase
102465501	9,45E-01	2,46E-02	9,35E-01	0,366	0,0820004	0,03001082	22,39	MIR6834	microRNA 6834
339803	8,24E-01	8,41E-02	7,99E-01	0,1176	0,2546181	0,02994812	228,85	C2orf74-DT	C2orf74 divergent transcript
105370526	8,63E-01	6,40E-02	8,42E-01	0,15	0,1995034	0,0299275	143,98	HIF1A-AS3	HIF1A antisense RNA 3
10230	8,65E-01	6,30E-02	8,44E-01	0,1514	0,1968642	0,02980411	149,48	NBR2	neighbor of BRCA1 lncRNA 2
644215	9,48E-01	2,32E-02	9,38E-01	0,3845	0,077253	0,02970437	20,25	LOC644215	uncharacterized LOC644215
55847	6,46E-01	1,90E-01	6,09E-01	0,0581	0,5109903	0,02967274	1788,86	CISD1	CDGSH iron sulfur domain 1
10392	8,22E-01	8,51E-02	7,97E-01	0,115	0,2578211	0,02963695	270,91	NOD1	nucleotide binding oligomerization domain containing 1
106660606	9,64E-01	1,59E-02	9,57E-01	0,5496	0,0538806	0,0296117	9,97	MIR3677HG	MIR3677 and MIR940 host gene
3625	7,96E-01	9,91E-02	7,69E-01	0,1	0,2942776	0,02943817	369,43	INHBB	inhibin subunit beta B
55739	6,78E-01	1,69E-01	6,43E-01	0,063	0,4630726	0,02915909	1064,8	NAXD	NAD(P)HX dehydratase
51421	5,72E-01	2,43E-01	5,32E-01	0,0465	0,6256136	0,02911843	6254,12	AMOTL2	angiomotin like 2
101928569	9,64E-01	1,59E-02	9,57E-01	0,5389	0,0534315	0,02879275	11,65	LINC02101	long intergenic non-protein coding RNA 2101
8443	5,97E-01	2,24E-01	5,59E-01	0,049	0,5846822	0,02864099	2427,42	GNPAT	glyceronephosphate O-acyltransferase
9712	6,62E-01	1,79E-01	6,26E-01	0,0587	0,4879457	0,02862229	1334,82	USP6NL	USP6 N-terminal like
11099	6,28E-01	2,02E-01	5,90E-01	0,0531	0,5388066	0,02861855	1739,37	PTPN21	protein tyrosine phosphatase non-receptor type 21
642987	9,60E-01	1,77E-02	9,52E-01	0,4732	0,0600834	0,02842924	13,8	TMEM232	transmembrane protein 232
55718	6,89E-01	1,62E-01	6,55E-01	0,0631	0,4471556	0,0282325	1316,57	POLR3E	RNA polymerase III subunit E
641518	9,31E-01	3,11E-02	9,19E-01	0,2782	0,1012748	0,02817247	42,56	LEF1-AS1	LEF1 antisense RNA 1
11112	6,27E-01	2,03E-01	5,89E-01	0,0518	0,5399144	0,02796407	2032,08	HIBADH	3-hydroxyisobutyrate dehydrogenase
55170	6,73E-01	1,72E-01	6,37E-01	0,0593	0,4714767	0,02795881	1320,54	PRMT6	protein arginine methyltransferase 6
653645	8,25E-01	8,35E-02	8,00E-01	0,1102	0,2533468	0,02790621	271,39	TBC1D3P1-E	TBC1D3P1-DHX40P1 readthrough, transcribed pseudogene
7405	6,77E-01	1,69E-01	6,42E-01	0,0598	0,4650742	0,02782926	1320,62	UVRAG	UV radiation resistance associated
101928212	9,27E-01	3,29E-02	9,14E-01	0,2555	0,1083506	0,02768257	48,76	LOC101928	uncharacterized LOC101928212
142684	9,51E-01	2,18E-02	9,42E-01	0,3783	0,0727184	0,02751072	20,77	RAB40A	RAB40A, member RAS oncogene family
390916	6,74E-01	1,71E-01	6,39E-01	0,058	0,4689152	0,02718759	1331,98	NUDT19	nudix hydrolase 19
10499	7,52E-01	1,24E-01	7,22E-01	0,076	0,3563906	0,02707096	779,97	NCOA2	nuclear receptor coactivator 2
114659	8,39E-01	7,62E-02	8,16E-01	0,1143	0,2323568	0,02655376	253,99	LRRC37B	leucine rich repeat containing 37B
101929718	7,80E-01	1,08E-01	7,51E-01	0,0827	0,3172676	0,02623222	545,85	LOC101929	uncharacterized LOC101929718
5334	9,51E-01	2,18E-02	9,43E-01	0,3631	0,0718473	0,02608721	22,84	PLCL1	phospholipase C like 1 (inactive)
102723849	9,63E-01	1,64E-02	9,56E-01	0,4695	0,0551848	0,02591001	13,28	SPDYE17	speedy/RINGO cell cycle regulator family member E17
645967	9,59E-01	1,82E-02	9,51E-01	0,4201	0,0616275	0,02589063	16,63	LOC645967	uncharacterized LOC645967
161742	6,64E-01	1,78E-01	6,28E-01	0,0534	0,4841867	0,02584126	3091,68	SPRED1	sprouty related EVH1 domain containing 1
100130275	9,15E-01	3,86E-02	9,00E-01	0,2041	0,1262231	0,0257572	74,92	TFAP2A-AS1	TFAP2A antisense RNA 1
128239	5,86E-01	2,32E-01	5,46E-01	0,0424	0,6033879	0,02561191	7392,18	IQGAP3	IQ motif containing GTPase activating protein 3
101926987	9,44E-01	2,50E-02	9,34E-01	0,3089	0,0827692	0,02557062	31,55	DLGAP4-AS	DLGAP4 antisense RNA 1
4644	6,45E-01	1,90E-01	6,08E-01	0,0496	0,5127724	0,02544135	2903,38	MYO5A	myosin VA
55661	5,90E-01	2,29E-01	5,51E-01	0,0421	0,5965758	0,0250967	7279,92	DDX27	DEAD-box helicase 27
107986694	8,47E-01	7,21E-02	8,24E-01	0,113	0,2217696	0,02505811	253,81	LOC107986694	
22919	5,48E-01	2,61E-01	5,08E-01	0,0376	0,6626826	0,02492152	18167,63	MAPRE1	microtubule associated protein RP/EB family member 1
105371423	9,63E-01	1,64E-02	9,56E-01	0,4529	0,0548028	0,02482086	14,14	LINC02193	long intergenic non-protein coding RNA 2193
138429	9,37E-01	2,83E-02	9,26E-01	0,265	0,0934235	0,02476044	46,61	PIP5KL1	phosphatidylinositol-4-phosphate 5-kinase like 1
142	5,78E-01	2,38E-01	5,38E-01	0,0401	0,6161464	0,02469559	15265,68	PARP1	poly(ADP-ribose) polymerase 1

23239	7,33E-01	1,35E-01	7,01E-01	0,0642	0,3834658	0,024636	1030,4	PHLPP1	PH domain and leucine rich repeat protein phosphatase 1
65999	8,23E-01	8,46E-02	7,98E-01	0,096	0,2562572	0,02459777	788,7	LRRC61	leucine rich repeat containing 61
6453	6,47E-01	1,89E-01	6,10E-01	0,0482	0,5093735	0,02457082	2950,25	ITSN1	intersectin 1
101928570	9,47E-01	2,37E-02	9,38E-01	0,3125	0,0782897	0,02446162	31,48	LOC101928	uncharacterized LOC101928570
284751	9,29E-01	3,20E-02	9,17E-01	0,2334	0,1039264	0,02425992	62,19	LINC01270	long intergenic non-protein coding RNA 1270
26577	8,84E-01	5,35E-02	8,66E-01	0,1428	0,1692021	0,02415879	160,23	PCOLCE2	procollagen C-endopeptidase enhancer 2
5608	8,87E-01	5,21E-02	8,69E-01	0,1452	0,1654483	0,02402156	145,95	MAP2K6	mitogen-activated protein kinase kinase 6
171017	7,11E-01	1,48E-01	6,78E-01	0,0577	0,4149581	0,02394648	2036,69	ZNF384	zinc finger protein 384
2150	5,85E-01	2,33E-01	5,45E-01	0,0394	0,6049948	0,02385583	18234,03	F2RL1	F2R like trypsin receptor 1
105378721	7,93E-01	1,01E-01	7,65E-01	0,0787	0,2992569	0,02356008	594,2	LOC105378721	
55765	8,01E-01	9,64E-02	7,74E-01	0,082	0,2870019	0,02353225	645,67	INAVA	innate immunity activator
84661	6,92E-01	1,60E-01	6,58E-01	0,0529	0,443107	0,02345574	1942,37	DPY30	dpy-30 histone methyltransferase complex regulatory subunit
107984034	9,71E-01	1,28E-02	9,66E-01	0,5422	0,0430849	0,02336175	10,3	LOC107984	uncharacterized LOC107984034
7109	6,53E-01	1,85E-01	6,16E-01	0,0465	0,5014739	0,02333638	2693,62	TRAPPC10	trafficking protein particle complex subunit 10
84958	9,05E-01	4,34E-02	8,89E-01	0,1663	0,139946	0,02327109	120,86	SYTL1	synaptotagmin like 1
8226	7,72E-01	1,12E-01	7,43E-01	0,0706	0,3284565	0,02318529	880,94	PUDP	pseudouridine 5'-phosphatase
7855	7,90E-01	1,02E-01	7,62E-01	0,0762	0,3026638	0,02307118	663,48	FZD5	frizzled class receptor 5
158572	9,51E-01	2,18E-02	9,42E-01	0,3167	0,0727597	0,02304316	30,23	USP27X-DT	USP27X divergent transcript
54995	8,18E-01	8,72E-02	7,93E-01	0,0873	0,2628893	0,02295943	536,64	OXSM	3-oxoacyl-ACP synthase, mitochondrial
100128890	9,47E-01	2,37E-02	9,37E-01	0,2904	0,0786719	0,02284504	35,51	FAM66B	family with sequence similarity 66 member B
118491	9,42E-01	2,59E-02	9,31E-01	0,2624	0,0863385	0,02265377	44,91	CFAP70	cilia and flagella associated protein 70
102724330	9,36E-01	2,87E-02	9,24E-01	0,2369	0,0951934	0,02255488	53,83	PCMTD1-DT	PCMTD1 divergent transcript
9367	7,42E-01	1,30E-01	7,11E-01	0,0606	0,370406	0,02243807	1353,24	RAB9A	RAB9A, member RAS oncogene family
105378353	9,66E-01	1,50E-02	9,59E-01	0,438	0,0511969	0,02242382	15,92	LOC105378	uncharacterized LOC105378353
5104	9,73E-01	1,19E-02	9,68E-01	0,555	0,040074	0,02224196	10,8	SERPINA5	serpin family A member 5
4756	6,86E-01	1,64E-01	6,51E-01	0,0489	0,4518056	0,02207078	3044,99	NEO1	neogenin 1
57224	8,76E-01	5,75E-02	8,56E-01	0,1208	0,1813585	0,02190754	223,91	NHSL1	NHS like 1
100507437	9,20E-01	3,62E-02	9,06E-01	0,1846	0,1183023	0,02183912	98,07	MTA1-DT	MTA1 divergent transcript
23187	7,29E-01	1,37E-01	6,97E-01	0,0559	0,3892602	0,02176078	2036,34	PHLDB1	pleckstrin homology like domain family B member 1
84069	8,33E-01	7,94E-02	8,09E-01	0,0896	0,2419785	0,02169318	478,58	PLEKHN1	pleckstrin homology domain containing N1
29995	8,46E-01	7,26E-02	8,23E-01	0,0967	0,223139	0,02157889	377,44	LMCD1	LIM and cysteine rich domains 1
107984128	9,53E-01	2,09E-02	9,44E-01	0,3063	0,0699787	0,02143449	33,41	LOC107984	uncharacterized LOC107984128
6594	6,42E-01	1,92E-01	6,05E-01	0,0413	0,517022	0,02133301	7978,37	SMARCA1	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 1
26134	9,33E-01	3,01E-02	9,21E-01	0,2158	0,0985788	0,02127238	63,35	RALGAPA1P	RALGAPA1 pseudogene 1
2237	6,56E-01	1,83E-01	6,19E-01	0,0425	0,4972269	0,021127	8424,39	FEN1	flap structure-specific endonuclease 1
10207	8,30E-01	8,09E-02	8,06E-01	0,0855	0,2461017	0,02104937	525,52	PATJ	PATJ crumbs cell polarity complex component
107986408	9,67E-01	1,46E-02	9,60E-01	0,4247	0,0495272	0,02103458	16,5	LINC02100	long intergenic non-protein coding RNA 2100
100874097	8,35E-01	7,83E-02	8,11E-01	0,0878	0,2385652	0,0209552	504,24	UBE2Q1-AS	UBE2Q1 antisense RNA 1
6146	6,65E-01	1,77E-01	6,29E-01	0,0433	0,4829942	0,0209178	22786,53	RPL22	ribosomal protein L22
5204	7,00E-01	1,55E-01	6,67E-01	0,0481	0,4307288	0,02073085	5726,76	PFDN5	prefoldin subunit 5
80762	7,32E-01	1,35E-01	7,00E-01	0,0533	0,3851763	0,02051072	3346,79	NDFIP1	Nedd4 family interacting protein 1
60677	9,64E-01	1,59E-02	9,57E-01	0,3754	0,0543305	0,02039725	21,49	CELF6	CUGBP Elav-like family member 6
54660	9,76E-01	1,06E-02	9,72E-01	0,57	0,0354911	0,02023072	9,14	PCDHB18P	protocadherin beta 18 pseudogene
729085	9,64E-01	1,59E-02	9,57E-01	0,3742	0,0533543	0,01996457	21,25	GASK1A	golgi associated kinase 1A
55617	8,77E-01	5,70E-02	8,58E-01	0,1116	0,1786578	0,01994509	284,7	TASP1	taspase 1
120892	9,30E-01	3,15E-02	9,18E-01	0,1921	0,1033892	0,01986139	81,73	LRRK2	leucine rich repeat kinase 2
9793	6,90E-01	1,61E-01	6,56E-01	0,0445	0,445907	0,01984112	21911,81	CKAP5	cytoskeleton associated protein 5
285855	5,96E-01	2,25E-01	5,57E-01	0,0335	0,5875695	0,01967702	39898,94	RPL7L1	ribosomal protein L7 like 1
6648	6,85E-01	1,64E-01	6,50E-01	0,0428	0,4531076	0,01938954	7370,29	SOD2	superoxide dismutase 2
63877	7,67E-01	1,15E-01	7,38E-01	0,0579	0,3348092	0,01937401	1587,72	FAM204A	family with sequence similarity 204 member A
93010	8,12E-01	9,04E-02	7,85E-01	0,0709	0,2723795	0,01930029	768,75	B3GNT7	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 7
100630923	8,56E-01	6,75E-02	8,34E-01	0,0916	0,2093029	0,01917256	414,14	LOC100630	LOC100289561-PRKRIP1 readthrough
8863	8,20E-01	8,62E-02	7,95E-01	0,0724	0,2600951	0,0188423	852	PER3	period circadian regulator 3
107985733	9,74E-01	1,14E-02	9,69E-01	0,482	0,0390626	0,018829	59,54	LOC107985	733
8632	9,47E-01	2,37E-02	9,38E-01	0,2356	0,0784021	0,01847461	58,1	DNAH17	dynein axonemal heavy chain 17
23408	8,28E-01	8,20E-02	8,03E-01	0,0742	0,2488399	0,01846008	684,2	SIRT5	sirtuin 5
51186	8,88E-01	5,16E-02	8,70E-01	0,112	0,1637557	0,01834678	5073,63	TCEAL9	transcription elongation factor A like 9
105372489	9,48E-01	2,32E-02	9,39E-01	0,2373	0,0768969	0,0182452	57,89	SERTAD3-AS	SERTAD3 antisense RNA 1
56062	8,08E-01	9,26E-02	7,81E-01	0,0647	0,2774749	0,017949	990,59	KLHL4	kelch like family member 4
105369779	9,23E-01	3,48E-02	9,09E-01	0,1548	0,1145448	0,0177348	134,03	CD63-AS1	CD63 antisense RNA 1
3190	7,03E-01	1,53E-01	6,69E-01	0,0412	0,426919	0,0176094	45242,84	HNRNPK	heterogeneous nuclear ribonucleoprotein K
8935	8,05E-01	9,42E-02	7,78E-01	0,0612	0,2825153	0,01728559	1375,54	SKAP2	src kinase associated phosphoprotein 2
54108	7,77E-01	1,10E-01	7,48E-01	0,0527	0,321328	0,01692416	3223,66	CHRAC1	chromatin accessibility complex subunit 1
9217	7,20E-01	1,43E-01	6,87E-01	0,042	0,4025552	0,01689872	4259,17	VAPB	VAMP associated protein B and C
5582	9,59E-01	1,82E-02	9,51E-01	0,2765	0,0608326	0,01681735	42,4	PRKCG	protein kinase C gamma
158427	8,06E-01	9,37E-02	7,79E-01	0,0596	0,2803222	0,01671673	1356,28	TSTD2	thiosulfate sulfurtransferase like domain containing 2
104355295	9,70E-01	1,32E-02	9,64E-01	0,3619	0,0454423	0,01644701	22,73	SGMS1-AS1	SGMS1 antisense RNA 1
5082	8,12E-01	9,04E-02	7,86E-01	0,0604	0,2721115	0,01643343	1280,1	PDCL	phosducin like
23179	8,28E-01	8,20E-02	8,03E-01	0,0659	0,2492308	0,01642309	989,17	RGL1	ral guanine nucleotide dissociation stimulator like 1
4157	9,19E-01	3,67E-02	9,04E-01	0,136	0,1204009	0,01637454	170,21	MC1R	melanocortin 1 receptor
4792	7,42E-01	1,30E-01	7,11E-01	0,0438	0,3711476	0,01627038	6728,06	NFKBIA	NFKB inhibitor alpha
107986363	9,33E-01	3,01E-02	9,21E-01	0,1631	0,0993242	0,01620297	123,58	LOC107986	uncharacterized LOC107986363
105377700	9,24E-01	3,43E-02	9,11E-01	0,1439	0,1123737	0,01616759	164,3	LOC105377	uncharacterized LOC105377700
23341	8,00E-01	9,69E-02	7,72E-01	0,0555	0,2895761	0,01607502	1471,2	DNAJC16	DnaJ heat shock protein family (Hsp40) member C16
130888	9,32E-01	3,06E-02	9,20E-01	0,1593	0,1002033	0,01596727	126,3	FBXO36	F-box protein 36
55341	7,73E-01	1,12E-01	7,44E-01	0,0474	0,3263599	0,01548484	3663,58	LSG1	large 60S subunit nuclear export GTPase 1
9550	7,66E-01	1,16E-01	7,36E-01	0,0457	0,3375443	0,01543226	3766,38	ATP6V1G1	ATPase H+ transporting V1 subunit G1
124783	9,75E-01	1,10E-02	9,71E-01	0,4072	0,0368309	0,0149975	18,1	SPATA32	spermatogenesis associated 32
23335	8,57E-01	6,70E-02	8,36E-01	0,0712	0,2076105	0,01478957	771,91	WDR7	WD repeat domain 7
23649	8,38E-01	7,68E-02	8,15E-01	0,063	0,2344077	0,01475659	1472,77	POLA2	DNA polymerase alpha 2, accessory subunit
55727	7,92E-01	1,01E-01	7,64E-01	0,0488	0,3000905	0,01464935	2297,04	BTBD7	BTB domain containing 7
56063	9,21E-01	3,57E-02	9,07E-01	0,1251	0,117015	0,01463992	215,45	TMEM234	transmembrane protein 234
29062	9,03E-01	4,43E-02	8,87E-01	0,1022	0,1426091	0,01456838	338,26	WDR91	WD repeat domain 91
101928415	9,72E-01	1,23E-02	9,67E-01	0,3518	0,0414028	0,01456379	24,89	LOC101928	uncharacterized LOC101928415
23670	7,79E-01	1,08E-01	7,50E-01	0,0453	0,3186332	0,01444905	4545,69	CEMIP2	cell migration inducing hyaluronidase 2
285195	9,76E-01	1,06E-02	9,71E-01	0,3896	0,0361953	0,01410072	20,41	SLC9A9	solute carrier family 9 member A9
25807	8,99E-01	4,62E-02	8,83E-01	0,0926	0,1477775	0,01369036	469,91	RHBDD3	rhomboid domain containing 3
102724563	9,66E-01	1,50E-02	9,60E-01	0,2706	0,0503708	0,01362866	41,45	LOC102724	transcription factor E2F6-like
3633	9,00E-01	4,58E-02	8,83E-01	0,092	0,1466458	0,01348683	442,93	INPP5B	inositol polyphosphate-5-phosphatase B
338657	8,74E-01	5,85E-02	8,54E-01	0,0722	0,1838069	0,01326681	867,05	CENATAC	centrosomal AT-AC splicing factor
441250	9,52E-01	2,14E-02	9,44E-01	0,1783	0,0703592	0,01254346	93,76	TYW1B	tRNA-yW synthesizing protein 1 homolog B
121274	8,90E-01	5,06E-02	8,73E-01	0,0783	0,1601449	0,01253469	587,92	ZNF641	zinc finger protein 641
10766	8,42E-01	7,47E-02	8,19E-01	0,0548	0,2287156	0,01253449	1924,25	TOB2	transducer of ERBB2, 2
285074	8,79E-01	5,60E-02	8,60E-01	0,0695	0,1758526	0,01222968	859,16	ANAPC1P2	ANAPC1 pseudogene 2
100847012	9,81E-01	8,33E-03	9,78E-01	0,4313	0,0281986	0,01216205	16,09	MIR5004	microRNA 5004
8831	8,99E-01	4,62E-02	8,83E-01	0,082	0,1477301	0,01211865	717,79	SYNGAP1	synaptic Ras GTPase activating protein 1
8013	9,70E-01	1,32E-02	9,64E-01	0,2709	0,0445562	0,01206988	40,51	NR4A3	nuclear receptor subfamily 4 group A member 3
6605	8,08E-01	9,26E-02	7,81E-01	0,0433	0,2782669	0,01205709	7475,67	SMARCE1	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily e, member 1
100507500	9,27E-01	3,29E-02	9,14E-01	0,1101	0,1080922	0,01189575	263,36	EGFR-AS1	EGFR antisense RNA 1
79864	9,13E-01	3,95E-02	8,98E-01	0,0925	0,1281778	0,01185555	465,79	JHY	junctional cadherin complex regulator
100129148	9,04E-01	4,38E-02	8,87E-01	0,0835	0,1416054	0,01182916	512,99	LOC100129	uncharacterized LOC100129148
84833	8,61E-01	6,50E-02	8,40E-01	0,0584	0,2016321	0,01178015	3640,45	ATP5MK	ATP synthase membrane subunit k
9950	8,31E-01	8,04E-02	8,07E-01	0,0466	0,2442102	0,0113723	2987,01	GOLGA5	golgin A5
114787	9,07E-01	4,24E-02	8,92E-01	0,0832	0,1361073	0,01132196	537,04	GPRIN1	G protein regulated inducer of neurite outgrowth 1
55248	8,77E-01	5,70E-02	8,58E-01	0,062	0,1791116	0,01110359	1152,02	PACC1	proton activated chloride channel 1
57653	9,36E-01	2,87E-02	9,24E-01	0,1159	0,0949225	0,0109976	240,36	SUGT1P4-S	SUGT1P4-STRA6LP-CCDC180 readthrough
102723356	9,23E-01	3,48E-02	9,10E-01	0,096	0,1135507	0,01089909	361,97	ZFPM2-AS1	ZFPM2 antisense RNA 1
6575	8,80E-01	5,55E-02	8,61E-01	0,0623	0,1746574	0,01087657	1264,37	SLC20A2	solute carrier family 20 member 2
5781	8,38E-01	7,68E-02	8,15E-01	0,046	0,2341634	0,01078305	17105,98	PTPN11	protein tyrosine phosphatase non-receptor type 11
109729146	9,80E-01	8,77E-03	9,76E-01	0,3295	0,0298973	0,00985262	26,77	POC1B-AS1	POC1B antisense RNA 1
5894	8,32E-01	7,99E-02	8,08E-01	0,0404	0,2433065	0,00983652	6868,66	RAF1	Raf-1 proto-oncogene, serine/threonine kinase
4595	9,19E-01	3,67E-02	9,05E-01	0,0799	0,1195726	0,00955057	666,05	MUTYH	mutY DNA glycosylase
347252	8,82E-01	5,45E-02	8,64E-01	0,0551	0,1718532	0,00947131	1586,34	IGFBPL1	insulin like growth factor binding protein like 1
9748	8,66E-01	6,25E-02	8,45E-01	0,0474	0,1955431	0,00926438	5861,52	SLK	STE20 like kinase
79134	8,76E-01	5,75E-02	8,56E-01	0,0505	0,1812771	0,00914891	2086,94	TMEM185B	transmembrane protein 185B
23384	8,75E-01	5,80E-02	8,56E-01	0,0495	0,1816105	0,00898142	2216,7	SPECC1L	sperm antigen with calponin homology and coiled-coil domains 1 like
90557	9,73E-01	1,19E-02	9,67E-01	0,2167	0,0411556	0,00892043	63,15	CCDC74A	coiled-coil domain containing 74A
79029	9,28E-01	3,25E-02	9,16E-01	0,0843	0,1057174	0,00891468	523,35	SPATA5L1	spermatogenesis associated 5 like 1
106479524	9,85E-01	6,56E-03	9,83E-01	0,4027	0,0219151	0,00882588	20,83	RN7SL832P	RNA, 7SL, cytoplasmic 832, pseudogene
23644	8,77E-01	5,70E-02	8,58E-01	0,049	0,1791392	0,00877763	3079,21	EDC4	enhancer of mRNA decapping 4

105378649	9,66E-01	1,50E-02	9,59E-01	0,1695	0,0508781	0,00862278	108,86	LOC105378(	uncharacterized LOC105378649
10964	9,78E-01	9,66E-03	9,74E-01	0,2611	0,0324187	0,00846461	42,91	IFI44L	interferon induced protein 44 like
100302132	9,81E-01	8,33E-03	9,77E-01	0,2861	0,028955	0,00828526	35,92	MIR1182	microRNA 1182
100847090	9,87E-01	5,68E-03	9,85E-01	0,4351	0,0188831	0,0082151	17,07	MIR5187	microRNA 5187
5191	9,61E-01	1,73E-02	9,53E-01	0,1377	0,0583626	0,00803796	182,59	PEX7	peroxisomal biogenesis factor 7
84908	8,67E-01	6,20E-02	8,46E-01	0,041	0,1940461	0,00795749	6489,12	FAM136A	family with sequence similarity 136 member A
29968	8,84E-01	5,35E-02	8,65E-01	0,0457	0,1701802	0,00778499	4847	PSAT1	phosphoserine aminotransferase 1
401505	8,91E-01	5,01E-02	8,74E-01	0,048	0,1590339	0,0076269	4289,58	TOMM5	translocase of outer mitochondrial membrane 5
57609	8,96E-01	4,77E-02	8,79E-01	0,0498	0,1528623	0,00761062	2415,39	DIP2B	disco interacting protein 2 homolog B
6767	8,82E-01	5,45E-02	8,64E-01	0,044	0,1716773	0,00754651	9430,04	ST13	ST13 Hsp70 interacting protein
10817	9,50E-01	2,23E-02	9,41E-01	0,0983	0,074544	0,0073291	365,41	FRS3	fibroblast growth factor receptor substrate 3
54971	9,37E-01	2,83E-02	9,26E-01	0,0772	0,0929673	0,00718102	673,43	BANP	BTG3 associated nuclear protein
645513	9,65E-01	1,55E-02	9,58E-01	0,1341	0,0523356	0,00701644	190,64	SEPTIN7P14	septin 7 pseudogene 14
133957	9,20E-01	3,62E-02	9,06E-01	0,0586	0,1180468	0,00691209	1431,92	CCDC127	coiled-coil domain containing 127
64061	9,22E-01	3,53E-02	9,08E-01	0,058	0,1155891	0,00670286	1796,76	TSPYL2	TSPY like 2
7100	9,73E-01	1,19E-02	9,68E-01	0,1648	0,0399767	0,00658806	115,43	TLR5	toll like receptor 5
9654	9,23E-01	3,48E-02	9,10E-01	0,0579	0,1134765	0,00657303	1285,35	TTLL4	tubulin tyrosine ligase like 4
23590	9,40E-01	2,69E-02	9,29E-01	0,074	0,0885313	0,00654925	874,4	PDSS1	decaprenyl diphosphate synthase subunit 1
202333	9,91E-01	3,93E-03	9,89E-01	0,4713	0,0136106	0,00641455	13,59	CMYA5	cardiomyopathy associated 5
339448	9,31E-01	3,11E-02	9,19E-01	0,0613	0,1017424	0,00623947	1170,62	C1orf174	chromosome 1 open reading frame 174
2633	9,25E-01	3,39E-02	9,12E-01	0,0552	0,1102514	0,00608259	2843,08	GBP1	guanylate binding protein 1
50939	9,93E-01	3,05E-03	9,91E-01	0,5597	0,0106809	0,00597789	11,27	IMPG2	interphotoreceptor matrix proteoglycan 2
109729137	9,85E-01	6,56E-03	9,82E-01	0,2493	0,022881	0,00570535	47,05	MEF2C-AS2	MEF2C antisense RNA 2
51283	9,23E-01	3,48E-02	9,09E-01	0,047	0,1143554	0,00537566	2965,43	BFAR	bifunctional apoptosis regulator
400927	9,90E-01	4,36E-03	9,89E-01	0,3655	0,0143873	0,005258	21,83	TPTEP2	TPTE pseudogene 2
25939	9,26E-01	3,34E-02	9,13E-01	0,0471	0,1097565	0,00517415	4662,03	SAMHD1	SAM and HD domain containing deoxynucleoside triphosphate triphosphohydrolase 1
65065	9,43E-01	2,55E-02	9,33E-01	0,0607	0,0841027	0,00510255	1329,94	NBEAL1	neurobeachin like 1
114898	9,92E-01	3,49E-03	9,91E-01	0,432	0,0117411	0,00507242	15,67	C1QTNF2	C1q and TNF related 2
107986593	9,94E-01	2,61E-03	9,93E-01	0,5646	0,0085131	0,00480657	9,37	ZFAND3-DT	ZFAND3 divergent transcript
402573	9,95E-01	2,18E-03	9,94E-01	0,5802	0,0079257	0,00459854	9,12	SPACDR	sperm acrosome developmental regulator
55005	9,63E-01	1,64E-02	9,56E-01	0,0839	0,0546636	0,00458786	562,78	RMND1	required for meiotic nuclear division 1 homolog
79696	9,80E-01	8,77E-03	9,76E-01	0,1538	0,029782	0,00458068	142,71	ZC2HC1C	zinc finger C2HC-type containing 1C
107984658	9,71E-01	1,28E-02	9,65E-01	0,1022	0,0438214	0,00447845	336,93	LOC107984(	uncharacterized LOC107984658
5095	9,77E-01	1,01E-02	9,73E-01	0,1255	0,0339666	0,00426117	218,78	PCCA	propionyl-CoA carboxylase subunit alpha
84141	9,51E-01	2,18E-02	9,42E-01	0,0577	0,0723347	0,00417726	1600,87	EVA1A	eva-1 homolog A, regulator of programmed cell death
646074	9,90E-01	4,36E-03	9,88E-01	0,2667	0,0151848	0,00404937	41,14	POM121L10	POM121 transmembrane nucleoporin like 10, pseudogene
145447	9,93E-01	3,05E-03	9,91E-01	0,357	0,0112831	0,00402793	23,36	ABHD12B	abhydrolase domain containing 12B
84172	9,45E-01	2,46E-02	9,35E-01	0,049	0,0818937	0,00401019	2574,26	POLR1B	RNA polymerase I subunit B
93487	9,43E-01	2,55E-02	9,32E-01	0,0465	0,0847228	0,00393691	7812,64	MAPK1IP1L	mitogen-activated protein kinase 1 interacting protein 1 like
100049076	9,90E-01	4,36E-03	9,88E-01	0,2669	0,0146873	0,00392069	41,1	GUSBP17	GUSB pseudogene 17
7812	9,25E-01	3,39E-02	9,12E-01	0,0353	0,1107377	0,00391125	39752,56	CSDE1	cold shock domain containing E1
440695	9,96E-01	1,74E-03	9,95E-01	0,584	0,0064058	0,00374127	8,58	ETV3L	ETS variant transcription factor 3 like
8165	9,42E-01	2,59E-02	9,32E-01	0,0427	0,0852386	0,00363938	4285,55	AKAP1	A-kinase anchoring protein 1
100505478	9,95E-01	2,18E-03	9,94E-01	0,4814	0,0074751	0,00359852	13,52	TEX48	testis expressed 48
55775	9,49E-01	2,27E-02	9,40E-01	0,0449	0,074964	0,00336719	4207,39	TDP1	tyrosyl-DNA phosphodiesterase 1
84268	9,51E-01	2,18E-02	9,43E-01	0,0465	0,0716709	0,00333606	3911,94	RPAIN	RPA interacting protein
100506804	9,90E-01	4,36E-03	9,88E-01	0,2267	0,014661	0,00332293	63,09	TMEM30A-D	TMEM30A divergent transcript
3021	9,59E-01	1,82E-02	9,52E-01	0,052	0,0608072	0,00316135	20696,33	H3-3B	H3.3 histone B
388796	9,75E-01	1,10E-02	9,70E-01	0,0835	0,0370924	0,00309735	669,06	SNHG17	small nucleolar RNA host gene 17
23080	9,62E-01	1,68E-02	9,54E-01	0,0531	0,0572073	0,0030399	1851,99	AVL9	AVL9 cell migration associated
107986083	9,91E-01	3,93E-03	9,89E-01	0,2122	0,0134813	0,00286042	66,48	LOC107986083	
31	9,59E-01	1,82E-02	9,51E-01	0,0427	0,0616176	0,00263398	4854,81	ACACA	acetyl-CoA carboxylase alpha
130074	9,62E-01	1,68E-02	9,55E-01	0,0442	0,0567409	0,00250552	4400,79	FAM168B	family with sequence similarity 168 member B
81608	9,65E-01	1,55E-02	9,58E-01	0,0455	0,052603	0,00239286	4160,2	FIP1L1	factor interacting with PAPOLA and CPSF1
8682	9,63E-01	1,64E-02	9,56E-01	0,043	0,0547514	0,00235486	17931,04	PEA15	proliferation and apoptosis adaptor protein 15
105369968	9,95E-01	2,18E-03	9,94E-01	0,3089	0,0073771	0,00227901	31,31	LOC105369(	uncharacterized LOC105369968
107181291	9,97E-01	1,30E-03	9,97E-01	0,5546	0,0038255	0,00212169	9,49	PYDC5	pyrin domain containing 5
111082993	9,98E-01	8,69E-04	9,97E-01	0,5767	0,0033848	0,00195213	9,44	LINC02569	long intergenic non-protein coding RNA 2569
101928728	9,96E-01	1,74E-03	9,95E-01	0,2897	0,005834	0,00168999	37,31	LOC101928(	uncharacterized LOC101928728
1302	9,97E-01	1,30E-03	9,97E-01	0,4104	0,0038862	0,00159474	17,99	COL11A2	collagen type XI alpha 2 chain
92104	9,91E-01	3,93E-03	9,90E-01	0,1227	0,0129109	0,00158403	209,72	TTC30A	tetratricopeptide repeat domain 30A
110806272	9,93E-01	3,05E-03	9,92E-01	0,1505	0,0100284	0,00150973	158,66	BTG3-AS1	BTG3 antisense RNA 1
5877	9,83E-01	7,45E-03	9,80E-01	0,0597	0,025143	0,00149988	1619,97	RABIF	RAB interacting factor
2120	9,84E-01	7,00E-03	9,81E-01	0,059	0,0238161	0,00140632	1797,64	ETV6	ETS variant transcription factor 6
728323	9,94E-01	2,61E-03	9,92E-01	0,1417	0,0094666	0,00134179	158,77	LINC01881	long intergenic non-protein coding RNA 1881
51524	9,85E-01	6,56E-03	9,81E-01	0,0568	0,0232477	0,00132153	1930,33	TMEM138	transmembrane protein 138
2800	9,87E-01	5,68E-03	9,84E-01	0,0556	0,0195779	0,00108874	1816,45	GOLGA1	golgin A1
10385	9,89E-01	4,80E-03	9,87E-01	0,0558	0,0162575	0,00090689	1602,6	BTN2A2	butyrophilin subfamily 2 member A2
654466	9,98E-01	8,69E-04	9,97E-01	0,1628	0,0033936	0,00055251	116,37	FGF7P3	fibroblast growth factor 7 pseudogene 3
4919	9,93E-01	3,05E-03	9,92E-01	0,0488	0,0104684	0,00051097	2264,52	ROR1	receptor tyrosine kinase like orphan receptor 1
5253	9,94E-01	2,61E-03	9,93E-01	0,0523	0,0083774	0,00043773	1787,08	PHF2	PHD finger protein 2
65108	9,96E-01	1,74E-03	9,95E-01	0,0458	0,0056435	0,0002585	2974,76	MARCKSL1	MARCKS like 1
50862	9,99E-01	4,35E-04	9,99E-01	0,0728	0,0011421	0,00008312	855,2	RNF141	ring finger protein 141
678655	1	0,00E+00	1	0,1315	0,0000682	0,00000897	185,75	CD27-AS1	CD27 antisense RNA 1
6429	9,98E-01	8,69E-04	9,98E-01	0,0466	-0,0029181	-0,00013594	5904,49	SRSF4	serine and arginine rich splicing factor 4
493753	9,98E-01	8,69E-04	9,98E-01	0,0922	-0,0027212	-0,00025088	701,76	COA5	cytochrome c oxidase assembly factor 5
100527960	9,96E-01	1,74E-03	9,95E-01	0,0561	-0,006097	-0,00034223	1504,54	MROH7-TTC	MROH7-TTC4 readthrough (NMD candidate)
3955	9,97E-01	1,30E-03	9,96E-01	0,0837	-0,0045086	-0,00037731	595,99	LFNG	LFNG O-fucosylpeptide 3-beta-N-acetylglucosaminyltransferase
27154	9,90E-01	4,36E-03	9,88E-01	0,0456	-0,0153923	-0,00070186	5643,07	BRPF3	bromodomain and PHD finger containing 3
37	9,89E-01	4,80E-03	9,86E-01	0,0428	-0,0174231	-0,00074521	15293,31	ACADVL	acyl-CoA dehydrogenase very long chain
79680	9,91E-01	3,93E-03	9,89E-01	0,0695	-0,0132986	-0,00092463	875,87	RTL10	retrotransposon Gag like 10
105373077	9,98E-01	8,69E-04	9,98E-01	0,4748	-0,0020362	-0,00096676	13,12	LOC105373(	uncharacterized LOC105373077
9128	9,83E-01	7,45E-03	9,80E-01	0,0443	-0,0247941	-0,00109823	5791,66	PRPF4	pre-mRNA processing factor 4
100131454	9,97E-01	1,30E-03	9,96E-01	0,2682	-0,0048547	-0,00130217	41,25	DBIL5P	diazepam binding inhibitor-like 5, pseudogene
8459	9,87E-01	5,68E-03	9,84E-01	0,0678	-0,0194927	-0,00132158	870,56	TPST2	tyrosylprotein sulfotransferase 2
55234	9,76E-01	1,06E-02	9,72E-01	0,0399	-0,0350207	-0,00139647	5737,08	SMU1	SMU1 DNA replication regulator and spliceosomal factor
5026	9,90E-01	4,36E-03	9,87E-01	0,099	-0,0157904	-0,00156337	383,02	P2RX5	purinergic receptor P2X 5
2734	9,73E-01	1,19E-02	9,68E-01	0,0393	-0,040026	-0,0015723	8907,03	GLG1	golgi glycoprotein 1
201134	9,90E-01	4,36E-03	9,88E-01	0,1125	-0,014676	-0,00165089	286,95	CEP112	centrosomal protein 112
50846	9,97E-01	1,30E-03	9,96E-01	0,37	-0,0047725	-0,00176583	22,2	DHH	desert hedgehog signaling molecule
254428	9,74E-01	1,14E-02	9,70E-01	0,0469	-0,0381583	-0,00178877	3595,46	SLC41A1	solute carrier family 41 member 1
64785	9,81E-01	8,33E-03	9,78E-01	0,0643	-0,0281714	-0,00181065	1148,25	GINS3	GINS complex subunit 3
51281	9,85E-01	6,56E-03	9,82E-01	0,0883	-0,022175	-0,00195813	458,33	ANKMY1	ankyrin repeat and MYND domain containing 1
54453	9,73E-01	1,19E-02	9,68E-01	0,0489	-0,0406773	-0,00198838	3013,49	RIN2	Ras and Rab interactor 2
84708	9,81E-01	8,33E-03	9,78E-01	0,0718	-0,0280398	-0,00201399	780,52	LNX1	ligand of numb-protein X 1
283232	9,87E-01	5,68E-03	9,85E-01	0,1073	-0,0190345	-0,00204209	289,25	TMEM80	transmembrane protein 80
55054	9,75E-01	1,10E-02	9,70E-01	0,0562	-0,0372302	-0,00209286	1466,28	ATG16L1	autophagy related 16 like 1
10477	9,70E-01	1,32E-02	9,64E-01	0,0467	-0,0453795	-0,00211863	4162,81	UBE2E3	ubiquitin conjugating enzyme E2 E3
23299	9,69E-01	1,37E-02	9,63E-01	0,0477	-0,0467236	-0,00222656	3213,68	BICD2	BICD cargo adaptor 2
58497	9,76E-01	1,06E-02	9,72E-01	0,0631	-0,0353438	-0,00222975	1251,65	PRUNE1	prune exopolyphosphatase 1
100130111	9,83E-01	7,45E-03	9,80E-01	0,1022	-0,02528	-0,00258398	342,2	LCIIAR	lung cancer immune cell infiltration associated lncRNA
63971	9,63E-01	1,64E-02	9,55E-01	0,048	-0,0560168	-0,00269049	3000,62	KIF13A	kinesin family member 13A
105369304	9,97E-01	1,30E-03	9,96E-01	0,5388	-0,0050869	-0,00274099	10,27	LOC105369(	uncharacterized LOC105369304
199746	9,79E-01	9,22E-03	9,75E-01	0,0924	-0,0311629	-0,00287927	463,26	U2AF1L4	U2 small nuclear RNA auxiliary factor 1 like 4
23585	9,59E-01	1,82E-02	9,51E-01	0,0473	-0,0617156	-0,00291778	3639,24	TMEM50A	transmembrane protein 50A
80765	9,94E-01	2,61E-03	9,93E-01	0,3548	-0,0086059	-0,00305374	23,7	STARD5	StAR related lipid transfer domain containing 5
84939	9,71E-01	1,28E-02	9,65E-01	0,0715	-0,044175	-0,00315713	811,18	PWWP3A	PWWP domain containing 3A, DNA repair factor
64718	9,74E-01	1,14E-02	9,69E-01	0,082	-0,0386497	-0,00316908	593	UNKL	unk like zinc finger
90141	9,68E-01	1,41E-02	9,62E-01	0,0703	-0,0480593	-0,00337652	769,53	EFCAB11	EF-hand calcium binding domain 11
7268	9,58E-01	1,86E-02	9,49E-01	0,0552	-0,063472	-0,0035008	1538,02	TTC4	tetratricopeptide repeat domain 4
9646	9,50E-01	2,23E-02	9,41E-01	0,0491	-0,0741437	-0,00364168	4822,97	CTR9	CTR9 homolog, Paf1/RNA polymerase II complex component
25966	9,61E-01	1,73E-02	9,54E-01	0,0631	-0,0582459	-0,00367531	1023,28	C2CD2	C2 calcium dependent domain containing 2
11200	9,70E-01	1,32E-02	9,65E-01	0,0883	-0,0443482	-0,0039139	448,52	CHEK2	checkpoint kinase 2
3184	9,39E-01	2,73E-02	9,29E-01	0,044	-0,0897136	-0,00394586	23305,11	HNRNPD	heterogeneous nuclear ribonucleoprotein D
728537	9,85E-01	6,56E-03	9,82E-01	0,1817	-0,0225959	-0,0041066	98,08	C2orf92	chromosome 2 open reading frame 92
92140	9,51E-01	2,18E-02	9,42E-01	0,0566	-0,0729394	-0,00412896	8516,44	MTDH	metadherin
2673	9,39E-01	2,73E-02	9,28E-01	0,0481	-0,0907165	-0,00436026	5209,05	GFPT1	glutamine--fructose-6-phosphate transaminase 1
100288142	9,47E-01	2,37E-02	9,37E-01	0,0559	-0,0790587	-0,00441922	1693,97	NBPF20	NBPF member 20
4175	9,30E-01	3,15E-02	9,18E-01	0,0439	-0,1025965	-0,00449886	4583,9	MCM6	minichromosome maintenance complex component 6
101929595	9,90E-01	4,36E-03	9,88E-01	0,2954	-0,0156265	-0,00461544	33,8	CYP2U1-AS	CYP2U1 and SGMS2 antisense RNA 1

84311	9,27E-01	3,29E-02	9,14E-01	0,0432	-0,1078452	-0,00465933	3915,15	MRPL45	mitochondrial ribosomal protein L45
5707	9,16E-01	3,81E-02	9,01E-01	0,038	-0,1245123	-0,00473699	12864,07	PSMD1	proteasome 26S subunit, non-ATPase 1
101927221	9,94E-01	2,61E-03	9,93E-01	0,5306	-0,0089754	-0,00476221	10,24	UBR5-DT	UBR5 divergent transcript
23613	9,27E-01	3,29E-02	9,14E-01	0,0473	-0,1080295	-0,0051142	7485,34	ZMYND8	zinc finger MYND-type containing 8
9853	9,39E-01	2,73E-02	9,28E-01	0,0574	-0,0901825	-0,00517743	2943,54	RUSC2	RUN and SH3 domain containing 2
9232	9,34E-01	2,97E-02	9,22E-01	0,0584	-0,0978358	-0,00571769	11220,24	PTTG1	PTTG1 regulator of sister chromatid separation, securin
440585	9,91E-01	3,93E-03	9,89E-01	0,4252	-0,0137324	-0,00583925	16,77	FAM183A	family with sequence similarity 183 member A
23107	8,95E-01	4,82E-02	8,77E-01	0,0385	-0,1543847	-0,00593834	6699,86	MRPS27	mitochondrial ribosomal protein S27
643837	9,38E-01	2,78E-02	9,27E-01	0,0657	-0,0916847	-0,00602584	1024,49	LINC01128	long intergenic non-protein coding RNA 1128
4236	9,26E-01	3,34E-02	9,14E-01	0,0592	-0,108581	-0,00642274	2601,83	MFAP1	microfibril associated protein 1
83851	9,76E-01	1,06E-02	9,72E-01	0,1945	-0,0355416	-0,00691126	82,05	SYT16	synaptotagmin 16
80208	9,15E-01	3,86E-02	9,00E-01	0,0552	-0,125897	-0,00694692	2173,21	SPG11	SPG11 vesicle trafficking associated, spatacsin
89941	9,28E-01	3,25E-02	9,16E-01	0,0672	-0,1054708	-0,00709018	1691,97	RHOT2	ras homolog family member T2
9404	8,88E-01	5,16E-02	8,71E-01	0,0439	-0,162899	-0,00714617	4978,03	LPXN	leupaxin
100507547	9,66E-01	1,50E-02	9,60E-01	0,1418	-0,0507132	-0,00718969	164,94	LOC100507	uncharacterized LOC100507547
51447	9,00E-01	4,58E-02	8,83E-01	0,0504	-0,1467787	-0,00740209	2223,62	IP6K2	inositol hexakisphosphate kinase 2
7014	9,05E-01	4,34E-02	8,90E-01	0,0541	-0,138835	-0,00751045	1631,23	TERF2	telomeric repeat binding factor 2
64397	8,94E-01	4,87E-02	8,77E-01	0,0501	-0,155007	-0,00777076	3812,08	ZNF106	zinc finger protein 106
441295	9,78E-01	9,66E-03	9,74E-01	0,2395	-0,0325139	-0,00778672	51,65	OR2A9P	olfactory receptor family 2 subfamily A member 9 pseudogene
90187	9,78E-01	9,66E-03	9,74E-01	0,2487	-0,0320555	-0,00797208	49,69	EMILIN3	elastin microfibril interfacer 3
10457	9,90E-01	4,36E-03	9,88E-01	0,5219	-0,015372	-0,00802231	11,67	GPNMB	glycoprotein nmb
728730	9,51E-01	2,18E-02	9,43E-01	0,1124	-0,0718874	-0,00808293	343,97	MAP4K3-DT	MAP4K3 divergent transcript
349075	9,59E-01	1,82E-02	9,51E-01	0,1318	-0,0613969	-0,0080897	196,3	ZNF713	zinc finger protein 713
11196	8,74E-01	5,85E-02	8,54E-01	0,0442	-0,1841396	-0,0081378	3511,35	SEC23IP	SEC23 interacting protein
2230	9,15E-01	3,86E-02	9,00E-01	0,0659	-0,1252681	-0,00825841	1165,7	FDX1	ferredoxin 1
112268238	9,71E-01	1,28E-02	9,65E-01	0,1881	-0,0440539	-0,0082851	87,67	LOC112268	replaced by ID 554313
51303	9,64E-01	1,59E-02	9,57E-01	0,1561	-0,0536605	-0,00837376	125,82	FKBP11	FKBP prolyl isomerase 11
128209	9,60E-01	1,77E-02	9,53E-01	0,1422	-0,0593877	-0,00844568	183,34	KLF17	KLF transcription factor 17
28985	8,93E-01	4,91E-02	8,76E-01	0,0577	-0,1565151	-0,0090338	2923,16	MCTS1	MCTS1 re-initiation and release factor
113218481	9,63E-01	1,64E-02	9,56E-01	0,1622	-0,0557094	-0,00903554	123,89	MIR9718	microRNA 9718
203054	9,42E-01	2,59E-02	9,31E-01	0,1052	-0,0861458	-0,00905941	353,18	ADCK5	aarF domain containing kinase 5
4867	9,58E-01	1,86E-02	9,50E-01	0,1468	-0,0628193	-0,00922168	147,81	NPHP1	nephrocystin 1
100216001	8,94E-01	4,87E-02	8,76E-01	0,0593	-0,1559855	-0,00925053	1468,39	MANCR	mitotically associated long non coding RNA
3017	9,11E-01	4,05E-02	8,95E-01	0,0707	-0,1316027	-0,00929788	806,15	H2BC5	H2B clustered histone 5
107987009	9,81E-01	8,33E-03	9,77E-01	0,3304	-0,0288146	-0,00951984	27,02	LOC107987	uncharacterized LOC107987009
100506314	9,67E-01	1,46E-02	9,61E-01	0,1967	-0,048919	-0,00962028	93,69	GPRC5D-AS	GPRC5D and HEBP1 antisense RNA 1
254102	8,45E-01	7,31E-02	8,23E-01	0,0431	-0,2241977	-0,00966788	5954,07	EHBP1L1	EH domain binding protein 1 like 1
27130	9,18E-01	3,72E-02	9,03E-01	0,0799	-0,1212417	-0,00969027	609,44	INVS	inversin
254225	8,84E-01	5,35E-02	8,65E-01	0,0588	-0,1698611	-0,00998253	1605,94	RNF169	ring finger protein 169
119392	9,16E-01	3,81E-02	9,02E-01	0,0818	-0,123701	-0,01011736	565,39	SFR1	SWI5 dependent homologous recombination repair protein 1
3995	8,70E-01	6,05E-02	8,50E-01	0,0535	-0,1892616	-0,01012526	2282,9	FADS3	fatty acid desaturase 3
148137	8,85E-01	5,31E-02	8,67E-01	0,0612	-0,1674121	-0,01023782	1279,19	PROSER3	proline and serine rich 3
84319	8,46E-01	7,26E-02	8,23E-01	0,0469	-0,2232245	-0,01047779	3554,47	CMSS1	cms1 ribosomal small subunit homolog
105377342	9,82E-01	7,89E-03	9,78E-01	0,389	-0,0270202	-0,01051026	21,13	TSPAN5-DT	TSPAN5 divergent transcript
79667	9,77E-01	1,01E-02	9,73E-01	0,3164	-0,0338018	-0,01069605	29,54	KLF3-AS1	KLF3 antisense RNA 1
10038	8,72E-01	5,95E-02	8,51E-01	0,0585	-0,1873031	-0,01095731	3112,84	PARP2	poly(ADP-ribose) polymerase 2
1893	8,68E-01	6,15E-02	8,47E-01	0,057	-0,1926546	-0,01097232	1775,75	ECM1	extracellular matrix protein 1
84656	8,57E-01	6,70E-02	8,35E-01	0,0528	-0,2077564	-0,01097301	2690,3	GLYR1	glyoxylate reductase 1 homolog
202	8,56E-01	6,75E-02	8,34E-01	0,0533	-0,2093583	-0,0111499	2352,36	CRYBG1	crystallin beta-gamma domain containing 1
152206	9,87E-01	5,68E-03	9,85E-01	0,6037	-0,0189076	-0,01141421	8,51	CCDC13	coiled-coil domain containing 13
102723834	9,85E-01	6,56E-03	9,82E-01	0,5184	-0,0221323	-0,0114725	11,08	LOC102723	uncharacterized LOC102723834
105376223	9,83E-01	7,45E-03	9,79E-01	0,4485	-0,0259227	-0,01162762	14,77	LOC105376	uncharacterized LOC105376223
107987284	9,78E-01	9,66E-03	9,74E-01	0,3639	-0,0322225	-0,01172553	22,47	LOC107987	uncharacterized LOC107987284
4929	9,46E-01	2,41E-02	9,37E-01	0,1479	-0,0795149	-0,01175901	144,85	NR4A2	nuclear receptor subfamily 4 group A member 2
147841	8,51E-01	7,01E-02	8,29E-01	0,0544	-0,216174	-0,01176395	1677,55	SPC24	SPC24 component of NDC80 kinetochore complex
51058	9,21E-01	3,57E-02	9,07E-01	0,1022	-0,1167874	-0,01193079	374,74	ZNF691	zinc finger protein 691
984	8,24E-01	8,41E-02	7,99E-01	0,0477	-0,254832	-0,01215225	3850,93	CDK11B	cyclin dependent kinase 11B
22932	9,22E-01	3,53E-02	9,08E-01	0,1061	-0,1152568	-0,01223088	284,7	POMZP3	POM121 and ZP3 fusion
64420	8,54E-01	6,85E-02	8,32E-01	0,0582	-0,2115994	-0,01231056	1335,45	SUSD1	sushi domain containing 1
7015	9,41E-01	2,64E-02	9,30E-01	0,1405	-0,0877184	-0,01232498	170,63	TERT	telomerase reverse transcriptase
11284	8,60E-01	6,55E-02	8,38E-01	0,061	-0,2038519	-0,01243239	1195,45	PNKP	polynucleotide kinase 3'-phosphatase
440952	9,82E-01	7,89E-03	9,79E-01	0,4758	-0,0263142	-0,01252138	12,7	EIF1B-AS1	EIF1B antisense RNA 1
4026	8,12E-01	9,04E-02	7,86E-01	0,0469	-0,2719369	-0,01274211	3373,41	LPP	LIM domain containing preferred translocation partner in lipoma
51768	8,05E-01	9,42E-02	7,78E-01	0,0458	-0,2818863	-0,01290619	2944,5	TM7SF3	transmembrane 7 superfamily member 3
166379	9,24E-01	3,43E-02	9,11E-01	0,1159	-0,1119884	-0,01298263	280,63	BBS12	Bardet-Biedl syndrome 12
57636	7,91E-01	1,02E-01	7,63E-01	0,0431	-0,3019078	-0,01301194	4555	ARHGAP23	Rho GTPase activating protein 23
1717	8,46E-01	7,26E-02	8,24E-01	0,059	-0,2223996	-0,01312552	2092,18	DHCR7	7-dehydrocholesterol reductase
84324	8,34E-01	7,88E-02	8,11E-01	0,056	-0,2393534	-0,013412	2662,72	SARNP	SAP domain containing ribonucleoprotein
29097	8,36E-01	7,78E-02	8,12E-01	0,057	-0,2372074	-0,01351219	3006,43	CNIH4	cornichon family AMPA receptor auxiliary protein 4
2657	9,75E-01	1,10E-02	9,70E-01	0,3665	-0,0369984	-0,0135603	22,11	GDF1	growth differentiation factor 1
100287808	9,78E-01	9,66E-03	9,75E-01	0,4287	-0,0319257	-0,01368649	18,28	LOC100287	uncharacterized LOC100287808
58527	8,55E-01	6,80E-02	8,33E-01	0,0651	-0,2104334	-0,01369561	1410,69	ABRACL	ABRA C-terminal like
1355	8,28E-01	8,20E-02	8,04E-01	0,0556	-0,2486996	-0,01383575	1540,23	COX15	cytochrome c oxidase assembly homolog COX15
152195	9,03E-01	4,43E-02	8,87E-01	0,0985	-0,1420873	-0,01399666	371,94	NUDT16L2P	nudix hydrolase 16 like 2, pseudogene
57520	9,24E-01	3,43E-02	9,11E-01	0,126	-0,112336	-0,01415502	196,22	HECW2	HECT, C2 and WW domain containing E3 ubiquitin protein ligase 2
54937	9,75E-01	1,10E-02	9,71E-01	0,3886	-0,0365509	-0,01420203	19,21	SOHLH2	spermatogenesis and oogenesis specific basic helix-loop-helix 2
101929882	9,74E-01	1,14E-02	9,70E-01	0,3738	-0,0382065	-0,01428153	22,26	KLF11-DT	KLF11 divergent transcript
55812	9,14E-01	3,91E-02	8,99E-01	0,1136	-0,1270729	-0,01443987	271,02	SPATA7	spermatogenesis associated 7
132864	8,59E-01	6,60E-02	8,38E-01	0,0709	-0,2045218	-0,01450271	826,28	CPEB2	cytoplasmic polyadenylation element binding protein 2
105373975	9,61E-01	1,73E-02	9,54E-01	0,2552	-0,0577729	-0,01474301	46,92	LOC105373	975
84816	8,75E-01	5,80E-02	8,55E-01	0,0811	-0,1823009	-0,01478988	530,43	RTN4IP1	reticulon 4 interacting protein 1
80759	8,76E-01	5,75E-02	8,56E-01	0,0832	-0,1808538	-0,01504317	531,13	KHDC1	KH domain containing 1
284757	9,38E-01	2,78E-02	9,27E-01	0,1672	-0,0911202	-0,01523264	118,59	MIR646HG	MIR646 host gene
23236	9,25E-01	3,39E-02	9,12E-01	0,1398	-0,1107166	-0,0154777	170,57	PLCB1	phospholipase C beta 1
55755	7,72E-01	1,12E-01	7,43E-01	0,0475	-0,3284741	-0,01561363	4378,75	CDK5RAP2	CDK5 regulatory subunit associated protein 2
25938	8,24E-01	8,41E-02	7,99E-01	0,0613	-0,2547406	-0,01561918	1728,35	HEATR5A	HEAT repeat containing 5A
94031	9,48E-01	2,32E-02	9,39E-01	0,2056	-0,0762172	-0,01567305	80,08	HTRA3	HtrA serine peptidase 3
100874211	9,71E-01	1,28E-02	9,65E-01	0,3678	-0,0432928	-0,01592493	21,61	MID1IP1-AS	MID1IP1 antisense RNA 1
3627	9,48E-01	2,32E-02	9,38E-01	0,2051	-0,0777736	-0,01595297	73,19	CXCL10	C-X-C motif chemokine ligand 10
648791	9,73E-01	1,19E-02	9,68E-01	0,3997	-0,0399372	-0,01596399	18,51	PPP1R3G	protein phosphatase 1 regulatory subunit 3G
6430	7,72E-01	1,12E-01	7,43E-01	0,0496	-0,3280576	-0,01626685	7681,36	SRSF5	serine and arginine rich splicing factor 5
130535	8,73E-01	5,90E-02	8,53E-01	0,0884	-0,1848799	-0,01633906	455,35	KCTD18	potassium channel tetramerization domain containing 18
8853	7,44E-01	1,28E-01	7,13E-01	0,0444	-0,3679906	-0,01634621	4596,3	ASAP2	ArfGAP with SH3 domain, ankyrin repeat and PH domain 2
3312	6,69E-01	1,75E-01	6,33E-01	0,0343	-0,4775435	-0,01638365	164218,95	HSPA8	heat shock protein family A (Hsp70) member 8
105376486	9,48E-01	2,32E-02	9,39E-01	0,2168	-0,077106	-0,01671683	66,01	LOC105376	486
27075	9,00E-01	4,58E-02	8,84E-01	0,1145	-0,1462371	-0,01674323	277,69	TSPAN13	tetraspanin 13
4146	9,78E-01	9,66E-03	9,73E-01	0,5052	-0,0332215	-0,01678324	12	MATN1	matrilin 1
88455	7,38E-01	1,32E-01	7,07E-01	0,045	-0,3762123	-0,0169129	4426,84	ANKRD13A	ankyrin repeat domain 13A
4074	7,27E-01	1,38E-01	6,95E-01	0,0433	-0,3921625	-0,01696322	4048,38	M6PR	mannose-6-phosphate receptor, cation dependent
83872	9,28E-01	3,25E-02	9,16E-01	0,1605	-0,105989	-0,01701477	130,05	HMCN1	hemicentin 1
100652758	8,65E-01	6,30E-02	8,44E-01	0,0874	-0,1967907	-0,01720925	514,97	LOC100652	uncharacterized LOC100652758
353116	8,54E-01	6,85E-02	8,33E-01	0,0823	-0,2109531	-0,01737123	642,52	RILPL1	Rab interacting lysosomal protein like 1
6711	6,81E-01	1,67E-01	6,46E-01	0,0378	-0,4594732	-0,01737397	33644,34	SPTBN1	spectrin beta, non-erythrocytic 1
9498	9,25E-01	3,39E-02	9,12E-01	0,1575	-0,1104555	-0,0173919	122,91	SLC4A8	solute carrier family 4 member 8
100506411	8,60E-01	6,55E-02	8,39E-01	0,0861	-0,2033843	-0,01750213	481,58	MAP3K9-DT	MAP3K9 divergent transcript
81849	9,30E-01	3,15E-02	9,17E-01	0,1721	-0,1036399	-0,01783295	120,64	ST6GALNAC	ST6 N-acetylgalactosaminide alpha-2,6-sialyltransferase 5
283459	7,10E-01	1,49E-01	6,77E-01	0,043	-0,4167474	-0,01793915	5522,67	GATC	glutamyl-tRNA amidotransferase subunit C
11138	7,75E-01	1,11E-01	7,46E-01	0,0555	-0,3239515	-0,01798758	1557,14	TBC1D8	TBC1 domain family member 8
6792	8,63E-01	6,40E-02	8,42E-01	0,0907	-0,1990171	-0,01805838	468,19	CDKL5	cyclin dependent kinase like 5
55768	7,59E-01	1,20E-01	7,29E-01	0,0522	-0,3466999	-0,01810258	1924,86	NGLY1	N-glycanase 1
23071	7,59E-01	1,20E-01	7,28E-01	0,0522	-0,3474663	-0,01812469	3533,99	ERP44	endoplasmic reticulum protein 44
22826	7,12E-01	1,48E-01	6,79E-01	0,0438	-0,4139795	-0,01814059	7735,67	DNAJC8	DnaJ heat shock protein family (Hsp40) member C8
79706	8,72E-01	5,95E-02	8,52E-01	0,0976	-0,1869972	-0,01824203	370,79	PRKRIP1	PRKR interacting protein 1
283237	7,64E-01	1,17E-01	7,34E-01	0,0541	-0,3395374	-0,01838328	1600,38	TTC9C	tetratricopeptide repeat domain 9C
105376512	9,74E-01	1,14E-02	9,69E-01	0,481	-0,038287	-0,01841606	13,66	LOC105376	replaced by ID 54472
23780	8,05E-01	9,42E-02	7,78E-01	0,0658	-0,2825735	-0,01858613	1002,4	APOL2	apolipoprotein L2
23334	7,41E-01	1,30E-01	7,09E-01	0,0503	-0,3728526	-0,01876197	2543,82	SZT2	SZT2 subunit of KICSTOR complex
645676	9,48E-01	2,32E-02	9,38E-01	0,2439	-0,0777979	-0,01897303	51,84	ASH1L-AS1	ASH1L antisense RNA 1
340719	8,89E-01	5,11E-02	8,72E-01	0,1174	-0,1616319	-0,01898343	228,89	NANOS1	nanos C2HC-type zinc finger 1
84002	7,84E-01	1,06E-01	7,56E-01	0,0616	-0,3109366	-0,01915536	1224,52	B3GNT5	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 5

6311	7,33E-01	1,35E-01	7,01E-01	0,0499	-0,3843857	-0,01918897	3313,35	ATXN2	ataxin 2
114960	9,31E-01	3,11E-02	9,19E-01	0,1907	-0,1020437	-0,01946287	91,5	TSGA13	testis specific 13
9338	7,82E-01	1,07E-01	7,54E-01	0,0622	-0,3135475	-0,01949618	1173,3	TCEAL1	transcription elongation factor A like 1
200734	6,97E-01	1,57E-01	6,63E-01	0,0448	-0,4354117	-0,01951677	3347,84	SPRED2	sprouty related EVH1 domain containing 2
51667	6,90E-01	1,61E-01	6,55E-01	0,044	-0,4464898	-0,01966245	5240,57	NUB1	negative regulator of ubiquitin like proteins 1
84233	8,36E-01	7,78E-02	8,12E-01	0,0837	-0,2374761	-0,01987012	697,38	TMEM126A	transmembrane protein 126A
7004	7,83E-01	1,06E-01	7,54E-01	0,0634	-0,3133898	-0,01988036	1205,48	TEAD4	TEA domain transcription factor 4
60436	7,45E-01	1,28E-01	7,14E-01	0,055	-0,3662514	-0,02014267	2128,54	TGIF2	TGFB induced factor homeobox 2
2650	7,65E-01	1,16E-01	7,35E-01	0,0597	-0,3378191	-0,02015831	1557,37	GCNT1	glucosaminyl (N-acetyl) transferase 1
80742	7,67E-01	1,15E-01	7,37E-01	0,0605	-0,3359331	-0,02031861	1363,31	PRR3	proline rich 3
84844	7,31E-01	1,36E-01	6,99E-01	0,0526	-0,3871448	-0,0203758	1939,31	PHF5A	PHD finger protein 5A
4359	9,70E-01	1,32E-02	9,64E-01	0,4563	-0,0450361	-0,02055065	14,8	MPZ	myelin protein zero
27246	7,06E-01	1,51E-01	6,73E-01	0,0488	-0,4224021	-0,02062077	2309,33	RNF115	ring finger protein 115
84132	8,04E-01	9,47E-02	7,77E-01	0,0732	-0,2837976	-0,02077675	750,31	USP42	ubiquitin specific peptidase 42
101927612	9,67E-01	1,46E-02	9,60E-01	0,4192	-0,049733	-0,02085035	17,78	RNF139-DT	RNF139 divergent transcript
83890	8,39E-01	7,62E-02	8,16E-01	0,0907	-0,2328665	-0,02112581	469,59	SPATA9	spermatogenesis associated 9
54802	7,54E-01	1,23E-01	7,23E-01	0,0597	-0,353917	-0,02113118	1249,97	TRIT1	tRNA isopentenyltransferase 1
55253	7,68E-01	1,15E-01	7,38E-01	0,065	-0,3339845	-0,02170998	1030,46	TYW1	tRNA-yW synthesizing protein 1 homolog
84811	7,26E-01	1,39E-01	6,93E-01	0,0556	-0,3945876	-0,02194669	3059,01	BUD13	BUD13 homolog
105371730	9,48E-01	2,32E-02	9,39E-01	0,2898	-0,0763022	-0,02211574	35,03	LOC1053717	uncharacterized LOC105371730
11141	8,46E-01	7,26E-02	8,23E-01	0,0991	-0,2232423	-0,02212424	386,37	IL1RAPL1	interleukin 1 receptor accessory protein like 1
4070	7,01E-01	1,54E-01	6,67E-01	0,052	-0,4302079	-0,02236512	2127,29	TACSTD2	tumor associated calcium signal transducer 2
100506686	8,75E-01	5,80E-02	8,55E-01	0,1232	-0,1822716	-0,0224555	231,18	IQCH-AS1	IQCH antisense RNA 1
3822	9,22E-01	3,53E-02	9,09E-01	0,1961	-0,1148672	-0,02252007	77,48	KLRC2	killer cell lectin like receptor C2
9980	7,44E-01	1,28E-01	7,13E-01	0,0622	-0,3683227	-0,02290334	1233,07	DOP1B	DOP1 leucine zipper like protein B
642361	9,48E-01	2,32E-02	9,39E-01	0,3004	-0,0765263	-0,02298494	34,05	LOC642361	uncharacterized LOC642361
27247	6,95E-01	1,58E-01	6,61E-01	0,0524	-0,4386704	-0,02300063	1804,09	NFU1	NFU1 iron-sulfur cluster scaffold
8030	6,59E-01	1,81E-01	6,23E-01	0,0471	-0,491965	-0,02314758	2826,18	CCDC6	coiled-coil domain containing 6
56674	7,28E-01	1,38E-01	6,96E-01	0,0592	-0,391064	-0,02314779	1441,81	TMEM9B	TMEM9 domain family member B
55884	6,15E-01	2,11E-01	5,77E-01	0,0418	-0,5578638	-0,02334425	5021,74	WSB2	WD repeat and SOCS box containing 2
143	5,93E-01	2,27E-01	5,53E-01	0,0396	-0,5925415	-0,02344529	11309,15	PARP4	poly(ADP-ribose) polymerase family member 4
1793	6,54E-01	1,84E-01	6,17E-01	0,047	-0,4994703	-0,02348121	3851,61	DOCK1	dedicator of cytokinesis 1
9681	8,15E-01	8,88E-02	7,89E-01	0,0887	-0,2670307	-0,02368434	479,03	DEPDC5	DEP domain containing 5, GATOR1 subcomplex subunit
84193	6,56E-01	1,83E-01	6,20E-01	0,0478	-0,4964315	-0,02373885	4069,3	SETD3	SET domain containing 3, actin histidine methyltransferase
386627	9,36E-01	2,87E-02	9,24E-01	0,2504	-0,0948526	-0,02374666	49,1	SAP30L-AS1	SAP30L antisense RNA 1 (head to head)
100996485	7,20E-01	1,43E-01	6,87E-01	0,0593	-0,402737	-0,02386561	1215,59	PITX1-AS1	PITX1 antisense RNA 1
400073	8,64E-01	6,35E-02	8,43E-01	0,1217	-0,1974836	-0,02402945	213,11	C12orf76	chromosome 12 open reading frame 76
89894	7,29E-01	1,37E-01	6,97E-01	0,062	-0,3894843	-0,02413177	1158,93	TMEM116	transmembrane protein 116
9270	5,96E-01	2,25E-01	5,57E-01	0,0411	-0,5874981	-0,02413384	5478,19	ITGB1BP1	integrin subunit beta 1 binding protein 1
105374002	9,24E-01	3,43E-02	9,11E-01	0,2191	-0,1120468	-0,02454857	75,28	LOC105374(	uncharacterized LOC105374002
5271	6,64E-01	1,78E-01	6,28E-01	0,0513	-0,4847435	-0,0248874	2260,45	SERPINB8	serpin family B member 8
56833	9,26E-01	3,34E-02	9,13E-01	0,2271	-0,10961	-0,0248912	61,82	SLAMF8	SLAM family member 8
112268317	9,55E-01	2,00E-02	9,47E-01	0,3758	-0,0662622	-0,02489855	21,47	LOC112268(	extensin-like
23177	8,21E-01	8,57E-02	7,95E-01	0,0965	-0,2592707	-0,02502933	416,11	CEP68	centrosomal protein 68
10256	9,48E-01	2,32E-02	9,39E-01	0,3252	-0,0770803	-0,02506924	28,14	CNKSR1	connector enhancer of kinase suppressor of Ras 1
3889	9,65E-01	1,55E-02	9,59E-01	0,4901	-0,0515352	-0,02525528	12,67	KRT83	keratin 83
9374	6,44E-01	1,91E-01	6,07E-01	0,0492	-0,5139596	-0,02529762	2453,67	PPT2	palmitoyl-protein thioesterase 2
55770	5,78E-01	2,38E-01	5,38E-01	0,0413	-0,6160094	-0,02547177	5254,4	EXOC2	exocyst complex component 2
51692	5,90E-01	2,29E-01	5,50E-01	0,0431	-0,5975123	-0,02577909	4208,83	CPSF3	cleavage and polyadenylation specific factor 3
199870	8,20E-01	8,62E-02	7,94E-01	0,0997	-0,2608404	-0,02600419	391,78	FAM76A	family with sequence similarity 76 member A
50717	5,71E-01	2,43E-01	5,30E-01	0,0415	-0,6275237	-0,02604894	5719,59	DCAF8	DDB1 and CUL4 associated factor 8
102723989	9,53E-01	2,09E-02	9,45E-01	0,376	-0,0693893	-0,0260898	20,42	FRMD3-AS1	FRMD3 antisense RNA 1
6117	5,44E-01	2,64E-01	5,03E-01	0,039	-0,6694209	-0,02612284	10749,33	RPA1	replication protein A1
7322	7,00E-01	1,55E-01	6,66E-01	0,0609	-0,4314056	-0,02625568	4739,7	UBE2D2	ubiquitin conjugating enzyme E2 D2
10575	4,95E-01	3,05E-01	4,53E-01	0,0352	-0,7509366	-0,02639955	19277,54	CCT4	chaperonin containing TCP1 subunit 4
55041	5,61E-01	2,51E-01	5,20E-01	0,0412	-0,6431988	-0,02650465	9059,89	PLEKHB2	pleckstrin homology domain containing B2
338699	7,49E-01	1,26E-01	7,18E-01	0,074	-0,361334	-0,02674807	751,85	ANKRD42	ankyrin repeat domain 42
10857	6,14E-01	2,12E-01	5,76E-01	0,0479	-0,5594635	-0,0267755	3451,39	PGRMC1	progesterone receptor membrane component 1
55634	7,64E-01	1,17E-01	7,35E-01	0,0797	-0,339087	-0,02701541	576,38	KRBOX4	KRAB box domain containing 4
25943	6,98E-01	1,56E-01	6,65E-01	0,0635	-0,4334267	-0,02752045	1044,54	DNAAF9	dynein axonemal assembly factor 9
100500827	8,35E-01	7,83E-02	8,12E-01	0,1167	-0,2380567	-0,02778453	243,33	MIR3614	microRNA 3614
112268189	9,18E-01	3,72E-02	9,04E-01	0,2304	-0,1210263	-0,02788643	58,01	LOC112268189	
102723904	9,18E-01	3,72E-02	9,03E-01	0,2298	-0,1219404	-0,02802464	62,44	LOC102723(	uncharacterized LOC102723904
79665	5,76E-01	2,40E-01	5,36E-01	0,0454	-0,618497	-0,02805751	3258,36	DHX40	DEAH-box helicase 40
101927441	9,22E-01	3,53E-02	9,08E-01	0,244	-0,1152721	-0,02812338	52,38	EFHD2-AS1	EFHD2 antisense RNA 1
57719	7,05E-01	1,52E-01	6,72E-01	0,0668	-0,4233702	-0,02826653	1005,69	ANO8	anoctamin 8
5170	6,06E-01	2,18E-01	5,68E-01	0,05	-0,5711888	-0,0285642	2101,79	PDPK1	3-phosphoinositide dependent protein kinase 1
23534	5,67E-01	2,46E-01	5,27E-01	0,0455	-0,6331486	-0,02879361	4256,84	TNPO3	transportin 3
90933	6,27E-01	2,03E-01	5,90E-01	0,0535	-0,5392947	-0,02883988	2079,28	TRIM41	tripartite motif containing 41
59339	6,47E-01	1,89E-01	6,10E-01	0,0568	-0,5097771	-0,02895004	1609,79	PLEKHA2	pleckstrin homology domain containing A2
79673	7,48E-01	1,26E-01	7,17E-01	0,0811	-0,3625404	-0,02941154	573,68	ZNF329	zinc finger protein 329
100532731	5,78E-01	2,38E-01	5,38E-01	0,0478	-0,6154129	-0,02943155	3046,64	COMMD3-BI	COMMD3-BMI1 readthrough
10240	6,88E-01	1,62E-01	6,53E-01	0,0662	-0,4490237	-0,02971034	1193,55	MRPS31	mitochondrial ribosomal protein S31
2176	6,65E-01	1,77E-01	6,28E-01	0,0616	-0,4838428	-0,02979817	1097,99	FANCC	FA complementation group C
92935	7,49E-01	1,26E-01	7,18E-01	0,0828	-0,3614816	-0,02993265	573,22	MARS2	methionyl-tRNA synthetase 2, mitochondrial
100128908	9,64E-01	1,59E-02	9,57E-01	0,5579	-0,0538207	-0,03002712	9,9	CIROP	ciliated left-right organizer metallopeptidase
23028	4,75E-01	3,23E-01	4,34E-01	0,0386	-0,7831583	-0,03023809	7493,35	KDM1A	lysine demethylase 1A
101059954	9,18E-01	3,72E-02	9,03E-01	0,2537	-0,1216872	-0,03086934	48,52	LOC1010599	replaced by ID 105371773
100499483	8,24E-01	8,41E-02	7,99E-01	0,1223	-0,2544977	-0,03113133	209,42	CCDC180	coiled-coil domain containing 180
105376177	8,36E-01	7,78E-02	8,13E-01	0,1317	-0,2370415	-0,03120979	190,13	LOC105376(	uncharacterized LOC105376177
2618	4,63E-01	3,34E-01	4,22E-01	0,0389	-0,8035361	-0,03125756	10435,09	GART	phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide synthetase, phosphoribosylaminoimidazole synthetase
9826	5,66E-01	2,47E-01	5,26E-01	0,0493	-0,6346611	-0,03130666	2560,34	ARHGEF11	Rho guanine nucleotide exchange factor 11
141	8,98E-01	4,67E-02	8,81E-01	0,2091	-0,1498789	-0,0313456	75,71	ADPRH	ADP-ribosylarginine hydrolase
4616	6,74E-01	1,71E-01	6,39E-01	0,0671	-0,4696234	-0,03153481	1044,85	GADD45B	growth arrest and DNA damage inducible beta
105373311	7,98E-01	9,80E-02	7,70E-01	0,1083	-0,292122	-0,0316364	278,82	LOC105373(	uncharacterized LOC105373311
891	4,54E-01	3,43E-01	4,12E-01	0,0386	-0,8198445	-0,03165331	15720,12	CCNB1	cyclin B1
102723575	9,59E-01	1,82E-02	9,51E-01	0,522	-0,0609354	-0,03180589	11,27	LOC102723(	uncharacterized LOC102723575
619562	9,21E-01	3,57E-02	9,07E-01	0,2733	-0,1168647	-0,03193624	39,39	SNORA3A	small nucleolar RNA, H/ACA box 3A
25799	6,97E-01	1,57E-01	6,63E-01	0,0733	-0,4355713	-0,03194846	676,61	ZNF324	zinc finger protein 324
105369844	9,05E-01	4,34E-02	8,89E-01	0,2293	-0,1393303	-0,03195235	56,26	LOC105369(	uncharacterized LOC105369844
107986486	7,97E-01	9,85E-02	7,69E-01	0,109	-0,2933498	-0,03197198	315	LOC107986486	
27161	4,82E-01	3,17E-01	4,40E-01	0,0414	-0,7724069	-0,03200581	5503,33	AGO2	argonaute RISC catalytic component 2
10165	5,79E-01	2,37E-01	5,39E-01	0,0522	-0,6137923	-0,0320227	2138,56	SLC25A13	solute carrier family 25 member 13
51526	5,29E-01	2,77E-01	4,88E-01	0,0466	-0,693317	-0,03230986	3543,17	OSER1	oxidative stress responsive serine rich 1
2145	6,14E-01	2,12E-01	5,75E-01	0,0579	-0,5602013	-0,03241751	1754,74	EZH1	enhancer of zeste 1 polycomb repressive complex 2 subunit
8527	5,89E-01	2,30E-01	5,49E-01	0,0546	-0,5985207	-0,03266381	1770,53	DGKD	diacylglycerol kinase delta
10309	7,97E-01	9,85E-02	7,70E-01	0,1118	-0,2929043	-0,0327601	376,28	CCNO	cyclin O
102724723	8,95E-01	4,82E-02	8,77E-01	0,2125	-0,1544585	-0,03282458	68,36	LOC102724(	uncharacterized LOC102724723
26057	4,30E-01	3,67E-01	3,89E-01	0,0382	-0,8617318	-0,0329454	10072,08	ANKRD17	ankyrin repeat domain 17
3735	4,06E-01	3,91E-01	3,64E-01	0,0366	-0,9073189	-0,0331755	11365,46	KARS1	lysyl-tRNA synthetase 1
64940	7,48E-01	1,26E-01	7,17E-01	0,092	-0,3620066	-0,03328999	422,46	STAG3L4	stromal antigen 3-like 4 (pseudogene)
220906	5,54E-01	2,56E-01	5,14E-01	0,0511	-0,6531952	-0,03335356	2878,15	WAC-AS1	WAC antisense RNA 1 (head to head)
54800	7,11E-01	1,48E-01	6,78E-01	0,0804	-0,4151923	-0,03337348	612,86	KLHL24	kelch like family member 24
107986465	8,50E-01	7,06E-02	8,28E-01	0,1554	-0,2169736	-0,033725	126,75	LOC107986(	uncharacterized LOC107986465
103910	4,55E-01	3,42E-01	4,13E-01	0,0416	-0,8180887	-0,03403324	20393,85	MYL12B	myosin light chain 12B
105373159	8,60E-01	6,55E-02	8,39E-01	0,1681	-0,2035159	-0,03420769	110,33	RAB4A-AS1	RAB4A antisense RNA 1
220929	6,92E-01	1,60E-01	6,58E-01	0,0776	-0,4425173	-0,03432805	709,36	ZNF438	zinc finger protein 438
57610	6,52E-01	1,86E-01	6,16E-01	0,0686	-0,5021418	-0,03445288	916,42	RANBP10	RAN binding protein 10
23729	7,23E-01	1,41E-01	6,90E-01	0,0866	-0,3982549	-0,03447775	510,09	SHPK	sedoheptulokinase
84061	4,70E-01	3,28E-01	4,29E-01	0,0437	-0,7913679	-0,03457727	4737,28	MAGT1	magnesium transporter 1
100874278	9,59E-01	1,82E-02	9,51E-01	0,5614	-0,0616517	-0,03461338	10,13	ERI3-IT1	ERI3 intronic transcript 1
93058	7,19E-01	1,43E-01	6,86E-01	0,0859	-0,4038575	-0,03468485	514,71	COQ10A	coenzyme Q10A
8551	9,46E-01	2,41E-02	9,36E-01	0,4386	-0,0799155	-0,03505437	15	INE2	inactivation escape 2
1382	8,28E-01	8,20E-02	8,04E-01	0,1414	-0,2483815	-0,03512543	165,48	CRABP2	cellular retinoic acid binding protein 2
93655	8,48E-01	7,16E-02	8,26E-01	0,1598	-0,2200779	-0,03517203	120,58	ST7-OT3	ST7 overlapping transcript 3
9931	5,40E-01	2,68E-01	4,99E-01	0,0523	-0,6757125	-0,03532365	2364,33	HELZ	helicase with zinc finger
65258	8,35E-01	7,83E-02	8,11E-01	0,1481	-0,2388681	-0,03537866	144,37	MPPE1	metallophosphoesterase 1
3730	5,56E-01	2,55E-01	5,16E-01	0,0548	-0,6500746	-0,03564947	1707,24	ANOS1	anosmin 1
100500842	8,28E-01	8,20E-02	8,04E-01	0,1447	-0,2483428	-0,03593309	3674,78	MIR3652	microRNA 3652
284266	8,85E-01	5,31E-02	8,67E-01	0,2148	-0,1673671	-0,03594943	68,01	SIGLEC15	sialic acid binding Ig like lectin 15

84285	5,15E-01	2,88E-01	4,74E-01	0,0509	-0,7167642	-0,0364638	1977,88	EIF1AD	eukaryotic translation initiation factor 1A domain containing
387338	5,69E-01	2,45E-01	5,28E-01	0,0579	-0,6303915	-0,03652235	1430,65	NSUN4	NOP2/Sun RNA methyltransferase 4
112267877	8,76E-01	5,75E-02	8,56E-01	0,2025	-0,1814136	-0,0367387	73,84	PPP1CB-DT	PPP1CB divergent transcript
54870	4,62E-01	3,35E-01	4,20E-01	0,0457	-0,8058329	-0,03686125	6586,86	QRICH1	glutamine rich 1
100130298	9,51E-01	2,18E-02	9,43E-01	0,5133	-0,0720816	-0,03699686	12,15	LOC1001302	hCG1816373-like
23345	6,11E-01	2,14E-01	5,73E-01	0,0662	-0,5643603	-0,03736587	1058,59	SYNE1	spectrin repeat containing nuclear envelope protein 1
79172	4,33E-01	3,64E-01	3,91E-01	0,0438	-0,8570919	-0,03750938	3705,33	CENPO	centromere protein O
6642	4,81E-01	3,18E-01	4,39E-01	0,0485	-0,7733771	-0,03751076	4082,24	SNX1	sorting nexin 1
112268419	7,42E-01	1,30E-01	7,11E-01	0,1022	-0,3711362	-0,03794804	311,31	LOC112268	uncharacterized LOC112268419
101927102	7,81E-01	1,07E-01	7,53E-01	0,1204	-0,3151926	-0,03795095	221,75	ITFG1-AS1	ITFG1 antisense RNA 1
1655	3,41E-01	4,67E-01	3,01E-01	0,0368	-1,033393	-0,03805136	42664,77	DDX5	DEAD-box helicase 5
23357	7,38E-01	1,32E-01	7,07E-01	0,1012	-0,3761571	-0,03807218	360,05	ANGEL1	angel homolog 1
619207	9,43E-01	2,55E-02	9,33E-01	0,4552	-0,0837669	-0,03813164	14,21	SCART1	scavenger receptor family member expressed on T cells 1
56134	9,42E-01	2,59E-02	9,31E-01	0,4435	-0,0864604	-0,03834795	16,44	PCDHAC2	protocadherin alpha subfamily C, 2
27297	4,86E-01	3,13E-01	4,44E-01	0,0503	-0,764824	-0,03845405	2200,07	CRCP	CGRP receptor component
92399	5,16E-01	2,87E-01	4,74E-01	0,0539	-0,715872	-0,0385625	2351,46	MRRF	mitochondrial ribosome recycling factor
51366	3,78E-01	4,23E-01	3,37E-01	0,0402	-0,9603457	-0,03860885	6857,36	UBR5	ubiquitin protein ligase E3 component n-recognin 5
10874	7,81E-01	1,07E-01	7,52E-01	0,1224	-0,3156233	-0,03861863	219,93	NMU	neuromedin U
79729	6,86E-01	1,64E-01	6,51E-01	0,086	-0,4516992	-0,03886145	639,08	SH3D21	SH3 domain containing 21
105371082	9,37E-01	2,83E-02	9,26E-01	0,418	-0,0930984	-0,03891758	18,82	LOC105371(	uncharacterized LOC105371082
54492	6,82E-01	1,66E-01	6,47E-01	0,0851	-0,4573142	-0,0389325	516,27	NEURL1B	neuralized E3 ubiquitin protein ligase 1B
23550	7,25E-01	1,40E-01	6,92E-01	0,0985	-0,3954926	-0,03896063	354,67	PSD4	pleckstrin and Sec7 domain containing 4
100128782	8,25E-01	8,35E-02	8,00E-01	0,1541	-0,2534636	-0,03906437	144,1	ERCC6L2-A	ERCC6L2 antisense RNA 1
83439	8,78E-01	5,65E-02	8,59E-01	0,2212	-0,1772469	-0,03920386	69,54	TCF7L1	transcription factor 7 like 1
112268089	5,87E-01	2,31E-01	5,47E-01	0,0652	-0,6024729	-0,03927601	1270,43	GAPDH-DT	GAPDH divergent transcript
219988	3,37E-01	4,72E-01	2,97E-01	0,0381	-1,0422277	-0,03970374	8315,78	PATL1	PAT1 homolog 1, processing body mRNA decay factor
100144748	9,04E-01	4,38E-02	8,88E-01	0,285	-0,1406941	-0,04009143	37,75	KLLN	killin, p53 regulated DNA replication inhibitor
644873	5,75E-01	2,40E-01	5,35E-01	0,0647	-0,6204452	-0,04016221	979,27	SLC12A2-DT	SLC12A2 divergent transcript
79837	5,12E-01	2,91E-01	4,70E-01	0,0557	-0,7217384	-0,04016514	1630,29	PIP4K2C	phosphatidylinositol-5-phosphate 4-kinase type 2 gamma
112574	6,39E-01	1,94E-01	6,02E-01	0,0771	-0,5220726	-0,04026194	761,92	SNX18	sorting nexin 18
85365	4,83E-01	3,16E-01	4,41E-01	0,0524	-0,7701049	-0,04034632	2155,07	ALG2	ALG2 alpha-1,3/1,6-mannosyltransferase
28574	9,41E-01	2,64E-02	9,30E-01	0,4618	-0,0879713	-0,04062574	15,2	TRBV13	T cell receptor beta variable 13
102724224	8,86E-01	5,26E-02	8,68E-01	0,2467	-0,1659536	-0,04093972	54,91	LINC01117	long intergenic non-protein coding RNA 1117
11130	3,48E-01	4,58E-01	3,08E-01	0,0404	-1,0194513	-0,04120414	6393,97	ZWINT	ZW10 interacting kinetochore protein
197135	8,84E-01	5,35E-02	8,66E-01	0,2456	-0,1691595	-0,04154397	50,91	PATL2	PAT1 homolog 2
83752	4,23E-01	3,74E-01	3,81E-01	0,0475	-0,8753196	-0,04156768	2723,81	LONP2	lon peptidase 2, peroxisomal
10657	3,32E-01	4,79E-01	2,93E-01	0,0395	-1,0520346	-0,04158214	9447,62	KHDRBS1	KH RNA binding domain containing, signal transduction associated 1
3141	4,71E-01	3,27E-01	4,30E-01	0,053	-0,7895644	-0,04184076	1765,33	HLCS	holocarboxylase synthetase
23059	6,31E-01	2,00E-01	5,94E-01	0,0785	-0,5334262	-0,04186724	790,83	CLUAP1	clusterin associated protein 1
130576	6,79E-01	1,68E-01	6,44E-01	0,0915	-0,4626974	-0,04233408	489,31	LYPD6B	LY6/PLAUR domain containing 6B
51302	8,59E-01	6,60E-02	8,38E-01	0,2077	-0,2045751	-0,04248741	71,54	CYP39A1	cytochrome P450 family 39 subfamily A member 1
27175	5,37E-01	2,70E-01	4,96E-01	0,0624	-0,6815322	-0,04254885	1751,36	TUBG2	tubulin gamma 2
4815	8,29E-01	8,14E-02	8,05E-01	0,1724	-0,2470002	-0,04257375	109,91	NINJ2	ninjurin 2
105370489	8,75E-01	5,80E-02	8,55E-01	0,2333	-0,1828733	-0,04265923	53,9	LOC1053704	uncharacterized LOC105370489
203076	9,50E-01	2,23E-02	9,41E-01	0,5801	-0,0738216	-0,04282597	9,6	C8orf74	chromosome 8 open reading frame 74
51400	4,13E-01	3,84E-01	3,72E-01	0,0483	-0,8924275	-0,04306339	4203,13	PPME1	protein phosphatase methylesterase 1
27309	4,93E-01	3,07E-01	4,51E-01	0,0572	-0,7532166	-0,04307583	2055,08	ZNF330	zinc finger protein 330
7586	4,65E-01	3,33E-01	4,23E-01	0,0538	-0,8009909	-0,043116	1910,54	ZKSCAN1	zinc finger with KRAB and SCAN domains 1
8195	3,84E-01	4,16E-01	3,43E-01	0,0455	-0,9478909	-0,04313202	4515,03	MKKS	MKKS centrosomal shuttling protein
100128191	5,60E-01	2,52E-01	5,20E-01	0,0674	-0,6438267	-0,0433651	1142,54	TMPO-AS1	TMPO antisense RNA 1
101930085	6,84E-01	1,65E-01	6,49E-01	0,0954	-0,4554101	-0,04346601	381,51	HERPUD2-A	HERPUD2 antisense RNA 1
4117	8,21E-01	8,57E-02	7,96E-01	0,1686	-0,2586658	-0,04362236	110,69	MAK	male germ cell associated kinase
375775	9,16E-01	3,81E-02	9,01E-01	0,3552	-0,1239514	-0,0440288	25,12	PNPLA7	patatin like phospholipase domain containing 7
26524	4,84E-01	3,15E-01	4,42E-01	0,0573	-0,7691218	-0,04407393	1513,81	LATS2	large tumor suppressor kinase 2
10479	5,16E-01	2,87E-01	4,74E-01	0,0616	-0,7162071	-0,04413027	1296,95	SLC9A6	solute carrier family 9 member A6
9620	5,77E-01	2,39E-01	5,37E-01	0,0714	-0,6180007	-0,04414648	783,42	CELSR1	cadherin EGF LAG seven-pass G-type receptor 1
85021	4,49E-01	3,48E-01	4,07E-01	0,0535	-0,8288663	-0,04431432	2157,58	REPS1	RALBP1 associated Eps domain containing 1
55437	5,94E-01	2,26E-01	5,55E-01	0,0751	-0,5906734	-0,0443483	995,92	STRADB	STE20 related adaptor beta
8125	3,15E-01	5,02E-01	2,76E-01	0,0408	-1,0894117	-0,04440435	7764,55	ANP32A	acidic nuclear phosphoprotein 32 family member A
100287467	9,03E-01	4,43E-02	8,87E-01	0,3131	-0,1424156	-0,04458393	31,72	LOC100287	uncharacterized LOC100287467
23233	4,49E-01	3,48E-01	4,07E-01	0,0538	-0,8287491	-0,04460784	1741,39	EXOC6B	exocyst complex component 6B
63826	4,11E-01	3,86E-01	3,70E-01	0,05	-0,8962393	-0,04480666	2155,2	SRR	serine racemase
374819	8,43E-01	7,42E-02	8,20E-01	0,1973	-0,2275618	-0,04489416	78,33	LRRC37A3	leucine rich repeat containing 37 member A3
10001	4,24E-01	3,73E-01	3,82E-01	0,0516	-0,8733431	-0,04504566	1897,12	MED6	mediator complex subunit 6
93323	4,09E-01	3,88E-01	3,68E-01	0,0501	-0,9010472	-0,0451013	2205,06	HAUS8	HAUS augmin like complex subunit 8
28232	5,78E-01	2,38E-01	5,38E-01	0,0733	-0,6155709	-0,04514918	707,73	SLCO3A1	solute carrier organic anion transporter family member 3A1
124801	4,34E-01	3,63E-01	3,93E-01	0,0528	-0,8550739	-0,04516514	3010,99	LSM12	LSM12 homolog
10184	4,89E-01	3,11E-01	4,47E-01	0,0598	-0,760151	-0,04546427	1763,96	LHFPL2	LHFPL tetraspan subfamily member 2
80154	6,14E-01	2,12E-01	5,76E-01	0,082	-0,5597864	-0,04587798	553,84	GOLGA2P1(	GOLGA2 pseudogene 10
5569	5,51E-01	2,59E-01	5,10E-01	0,0698	-0,6589991	-0,04602786	830,64	PKIA	cAMP-dependent protein kinase inhibitor alpha
79568	6,03E-01	2,20E-01	5,64E-01	0,0801	-0,5767118	-0,04618331	579,1	MAIP1	matrix AAA peptidase interacting protein 1
10953	3,53E-01	4,52E-01	3,12E-01	0,0464	-1,010005	-0,04681971	11045,03	TOMM34	translocase of outer mitochondrial membrane 34
119369	9,14E-01	3,91E-02	8,99E-01	0,368	-0,1272875	-0,04684119	22,25	NUDT9P1	nudix hydrolase 9 pseudogene 1
8736	9,41E-01	2,64E-02	9,30E-01	0,5347	-0,0877465	-0,04691533	10,08	MYOM1	myomesin 1
51479	3,45E-01	4,62E-01	3,05E-01	0,0457	-1,0264561	-0,04691623	3118,34	ANKFY1	ankyrin repeat and FYVE domain containing 1
100996720	8,29E-01	8,14E-02	8,05E-01	0,1902	-0,246688	-0,04691666	87,7	LOC100996	uncharacterized LOC100996720
109729173	7,73E-01	1,12E-01	7,44E-01	0,1438	-0,3266937	-0,04699245	149,12	TFAP2A-AS2	TFAP2A antisense RNA 2
79716	7,13E-01	1,47E-01	6,80E-01	0,1141	-0,4123732	-0,04703739	259,36	NPEPL1	aminopeptidase like 1
55720	3,16E-01	5,00E-01	2,77E-01	0,0433	-1,0874072	-0,04708407	8943,28	TSR1	TSR1 ribosome maturation factor
256691	5,76E-01	2,40E-01	5,36E-01	0,0766	-0,6187652	-0,04740443	630,08	MAMDC2	MAM domain containing 2
148413	5,78E-01	2,38E-01	5,38E-01	0,0773	-0,6158338	-0,04761229	668,48	MRPL20-AS	MRPL20 antisense RNA 1
23380	3,38E-01	4,71E-01	2,98E-01	0,0459	-1,0403756	-0,04777144	3131,19	SRGAP2	SLIT-ROBO Rho GTPase activating protein 2
56	9,20E-01	3,62E-02	9,06E-01	0,4065	-0,1179998	-0,04796804	17,73	ACRV1	acrosomal vesicle protein 1
65095	3,04E-01	5,17E-01	2,66E-01	0,0432	-1,1130166	-0,04806943	5605,04	KRI1	KRI1 homolog
6651	2,29E-01	6,40E-01	1,96E-01	0,0372	-1,2940444	-0,04810277	16934,52	SON	SON DNA and RNA binding protein
11165	2,89E-01	5,39E-01	2,51E-01	0,0419	-1,1473071	-0,04811347	6058,47	NUDT3	nudix hydrolase 3
90529	5,14E-01	2,89E-01	4,73E-01	0,0675	-0,7181732	-0,04845626	877,86	STPG1	sperm tail PG-rich repeat containing 1
56886	2,87E-01	5,42E-01	2,49E-01	0,0421	-1,1515874	-0,04852636	5612,33	UGGT1	UDP-glucose glycoprotein glucosyltransferase 1
1104	2,51E-01	6,00E-01	2,16E-01	0,0393	-1,2374157	-0,04865511	6283,81	RCC1	regulator of chromosome condensation 1
10180	4,22E-01	3,75E-01	3,80E-01	0,0557	-0,8771469	-0,04887361	4742,6	RBM6	RNA binding motif protein 6
23014	4,02E-01	3,96E-01	3,61E-01	0,0536	-0,914333	-0,04896971	2449,61	FBXO21	F-box protein 21
5364	7,61E-01	1,19E-01	7,31E-01	0,1436	-0,3434565	-0,04931589	157,74	PLXNB1	plexin B1
728190	5,28E-01	2,77E-01	4,87E-01	0,071	-0,6950258	-0,04935857	826,42	NUTM2A-AS	NUTM2A antisense RNA 1
57198	4,60E-01	3,37E-01	4,19E-01	0,061	-0,8089712	-0,04938162	1179,69	ATP8B2	ATPase phospholipid transporting 8B2
118433	6,55E-01	1,84E-01	6,18E-01	0,099	-0,4986141	-0,04938561	398,91	RPL23AP7	ribosomal protein L23a pseudogene 7
5394	2,61E-01	5,83E-01	2,25E-01	0,0408	-1,2143115	-0,04954836	7631,19	EXOSC10	exosome component 10
79153	9,13E-01	3,95E-02	8,98E-01	0,3869	-0,1281878	-0,04959736	21,97	GDPD3	glycerophosphodiester phosphodiesterase domain containing 3
27348	3,46E-01	4,61E-01	3,06E-01	0,0488	-1,0233468	-0,04993221	2757,95	TOR1B	torsin family 1 member B
653479	7,27E-01	1,38E-01	6,94E-01	0,1275	-0,3930402	-0,05009769	190,91	MRPL45P2	mitochondrial ribosomal protein L45 pseudogene 2
105374694	8,59E-01	6,60E-02	8,38E-01	0,2452	-0,2042856	-0,05010088	52,4	LINC02228	long intergenic non-protein coding RNA 2228
64787	3,01E-01	5,21E-01	2,62E-01	0,0448	-1,120508	-0,0501517	4193,05	EPS8L2	EPS8 like 2
9731	4,06E-01	3,91E-01	3,65E-01	0,0554	-0,9055159	-0,05019133	1797,29	CEP104	centrosomal protein 104
6769	4,96E-01	3,05E-01	4,54E-01	0,0672	-0,7487026	-0,05027964	968,26	STAC	SH3 and cysteine rich domain
153768	6,08E-01	2,16E-01	5,69E-01	0,0891	-0,5689861	-0,05071988	505,64	PRELID2	PRELI domain containing 2
102465504	9,19E-01	3,67E-02	9,04E-01	0,4237	-0,1203696	-0,05100556	16,11	MIR6838	microRNA 6838
56061	3,52E-01	4,53E-01	3,12E-01	0,0507	-1,0117055	-0,05132028	2175,94	UBFD1	ubiquitin family domain containing 1
283349	3,79E-01	4,21E-01	3,38E-01	0,0537	-0,958241	-0,05142645	2588,58	RASSF3	Ras association domain family member 3
966	1,75E-01	7,57E-01	1,46E-01	0,0354	-1,4527311	-0,05144796	24870,25	CD59	CD59 molecule (CD59 blood group)
285962	9,06E-01	4,29E-02	8,90E-01	0,3731	-0,1382196	-0,05157644	21,72	WEE2-AS1	WEE2 antisense RNA 1
55177	4,30E-01	3,67E-01	3,89E-01	0,06	-0,8621764	-0,05172764	1335,8	RMDN3	regulator of microtubule dynamics 3
255308	6,89E-01	1,62E-01	6,54E-01	0,1156	-0,4483063	-0,05183634	282,03	EIF2S3B	eukaryotic translation initiation factor 2 subunit gamma B
9897	4,35E-01	3,62E-01	3,93E-01	0,0609	-0,8537524	-0,0519752	1408,69	WASHC5	WASH complex subunit 5
345757	6,05E-01	2,18E-01	5,67E-01	0,0909	-0,5729464	-0,05205269	474,1	FAM174A	family with sequence similarity 174 member A
22934	4,16E-01	3,81E-01	3,74E-01	0,0586	-0,8883785	-0,05207428	1448,84	RPIA	ribose 5-phosphate isomerase A
55857	5,64E-01	2,49E-01	5,24E-01	0,0818	-0,6376294	-0,05213371	532,63	KIZ	kizuna centrosomal protein
29889	3,16E-01	5,00E-01	2,77E-01	0,048	-1,0872161	-0,05216961	6368,87	GNL2	G protein nucleolar 2
2710	6,90E-01	1,61E-01	6,55E-01	0,117	-0,4463556	-0,05223846	272,33	GK	glycerol kinase
124045	5,83E-01	2,34E-01	5,43E-01	0,0862	-0,6082704	-0,05241199	463,25	SPATA33	spermatogenesis associated 33
8208	3,43E-01	4,65E-01	3,03E-01	0,051	-1,0295738	-0,05249791	2409,64	CHAF1B	chromatin assembly factor 1 subunit B
220359	9,02E-01	4,48E-02	8,86E-01	0,3666	-0,1435305	-0,05262003	23,64	TIGD3	tigger transposable element derived 3

54899	3,69E-01	4,33E-01	3,29E-01	0,054	-0,9768066	-0,0527341	2263,59	PXK	PX domain containing serine/threonine kinase like
56977	7,55E-01	1,22E-01	7,24E-01	0,1495	-0,3530529	-0,0527945	139,47	STOX2	storkhead box 2
1748	8,73E-01	5,90E-02	8,53E-01	0,2877	-0,184817	-0,05316446	38,14	DLX4	distal-less homeobox 4
347735	4,33E-01	3,64E-01	3,92E-01	0,0624	-0,8568921	-0,0534706	2279,81	SERINC2	serine incorporator 2
55230	2,99E-01	5,24E-01	2,60E-01	0,0477	-1,1253029	-0,05363937	2661,08	USP40	ubiquitin specific peptidase 40
23354	4,56E-01	3,41E-01	4,14E-01	0,0658	-0,8163834	-0,05370077	1188,07	HAUS5	HAUS augmin like complex subunit 5
26505	4,20E-01	3,77E-01	3,79E-01	0,0611	-0,8796251	-0,05370147	1271,99	CNNM3	cyclin and CBS domain divalent metal cation transport mediator 3
51280	2,11E-01	6,76E-01	1,79E-01	0,0402	-1,3453431	-0,05402932	9143,15	GOLM1	golgi membrane protein 1
91695	6,14E-01	2,12E-01	5,75E-01	0,0966	-0,5601049	-0,05409837	418,66	RRP7BP	ribosomal RNA processing 7 homolog B, pseudogene
10380	3,27E-01	4,85E-01	2,87E-01	0,051	-1,0642835	-0,05426122	2785,9	BPNT1	3'(2'), 5'-bisphosphate nucleotidase 1
105369347	8,18E-01	8,72E-02	7,92E-01	0,2064	-0,2633967	-0,05436247	72,14	RELA-DT	RELA divergent transcript
55780	4,43E-01	3,54E-01	4,01E-01	0,0651	-0,8390912	-0,05458707	1252,78	ERMARD	ER membrane associated RNA degradation
9070	2,66E-01	5,75E-01	2,30E-01	0,0458	-1,2010948	-0,05500188	3003,9	ASH2L	ASH2 like, histone lysine methyltransferase complex subunit
9391	2,23E-01	6,52E-01	1,89E-01	0,0421	-1,3126038	-0,05520338	4333,03	CIAO1	cytosolic iron-sulfur assembly component 1
9640	2,80E-01	5,53E-01	2,42E-01	0,0474	-1,1689685	-0,05540877	3018,41	ZNF592	zinc finger protein 592
107986554	6,33E-01	1,99E-01	5,96E-01	0,1045	-0,5307518	-0,05543966	319,32	LOC107986554	
221692	6,31E-01	2,00E-01	5,93E-01	0,1039	-0,5342819	-0,05549635	309,58	PHACTR1	phosphatase and actin regulator 1
100129060	6,02E-01	2,20E-01	5,63E-01	0,0961	-0,5782735	-0,05559893	356,61	SEMA3F-AS	SEMA3F antisense RNA 1
105373510	9,06E-01	4,29E-02	8,90E-01	0,4037	-0,1377717	-0,05561539	19,38	LOC105373	uncharacterized LOC105373510
84162	2,86E-01	5,44E-01	2,48E-01	0,0482	-1,1542422	-0,05569051	2919,96	BLTP1	bridge-like lipid transfer protein family member 1
1140	3,32E-01	4,79E-01	2,93E-01	0,053	-1,0522894	-0,05575803	2322,2	CHRNB1	cholinergic receptor nicotinic beta 1 subunit
253143	4,00E-01	3,98E-01	3,59E-01	0,061	-0,9172629	-0,05593161	1230,36	PRR14L	proline rich 14 like
9054	3,25E-01	4,88E-01	2,86E-01	0,0524	-1,067045	-0,05595163	1906,18	NFS1	NFS1 cysteine desulfurase
51259	4,13E-01	3,84E-01	3,72E-01	0,0627	-0,8935949	-0,05601793	1051,08	TMEM216	transmembrane protein 216
11057	2,81E-01	5,51E-01	2,44E-01	0,0482	-1,1657958	-0,05613696	2536,34	ABHD2	abhydrolase domain containing 2, acylglycerol lipase
10060	8,87E-01	5,21E-02	8,69E-01	0,3418	-0,1644284	-0,05620757	32,55	ABCC9	ATP binding cassette subfamily C member 9
105371056	9,15E-01	3,86E-02	9,00E-01	0,4476	-0,125695	-0,05626546	14,48	LOC105371056	
93953	8,95E-01	4,82E-02	8,77E-01	0,3667	-0,1544369	-0,0566356	22,32	GCNA	germ cell nuclear acidic peptidase
80781	2,92E-01	5,35E-01	2,54E-01	0,0501	-1,1417277	-0,05724772	2563,92	COL18A1	collagen type XVIII alpha 1 chain
129685	2,33E-01	6,33E-01	1,99E-01	0,0446	-1,2845585	-0,05733021	4564,9	TAF8	TATA-box binding protein associated factor 8
114789	4,81E-01	3,18E-01	4,39E-01	0,0741	-0,773997	-0,05733465	958,69	SLC25A25	solute carrier family 25 member 25
654433	3,86E-01	4,13E-01	3,45E-01	0,0607	-0,9446207	-0,05736494	1268,21	PAX8-AS1	PAX8 antisense RNA 1
101926943	5,15E-01	2,88E-01	4,73E-01	0,08	-0,7173029	-0,05738335	573,52	GTF2I-AS1	GTF2I antisense RNA 1
134549	5,26E-01	2,79E-01	4,85E-01	0,0823	-0,698658	-0,05749145	724,06	SHROOM1	shroom family member 1
56943	2,37E-01	6,25E-01	2,02E-01	0,0453	-1,2751022	-0,0577233	4498,54	ENY2	ENY2 transcription and export complex 2 subunit
8994	3,12E-01	5,06E-01	2,73E-01	0,0527	-1,0956603	-0,05774729	1771,24	LIMD1	LIM domain containing 1
372	1,73E-01	7,62E-01	1,45E-01	0,0397	-1,4578828	-0,05783642	18941,34	ARCN1	archain 1
805	1,70E-01	7,70E-01	1,42E-01	0,0394	-1,4701477	-0,05794381	28934,29	CALM2	calmodulin 2
80021	4,98E-01	3,03E-01	4,56E-01	0,0778	-0,7451053	-0,05794875	720,51	TMEM62	transmembrane protein 62
57505	4,07E-01	3,90E-01	3,66E-01	0,0643	-0,9043872	-0,05817311	1119,7	AARS2	alanyl-tRNA synthetase 2, mitochondrial
619565	9,37E-01	2,83E-02	9,25E-01	0,6229	-0,0935282	-0,05826095	8,84	SNORA52	small nucleolar RNA, H/ACA box 52
126432	9,05E-01	4,34E-02	8,89E-01	0,419	-0,1390818	-0,05828056	18,2	RINL	Ras and Rab interactor like
100129405	4,28E-01	3,69E-01	3,87E-01	0,0674	-0,8650972	-0,05828222	903,67	MSTO2P	misato family member 2, pseudogene
51128	3,51E-01	4,55E-01	3,11E-01	0,0576	-1,0132081	-0,05831066	1583,36	SAR1B	secretion associated Ras related GTPase 1B
57449	6,76E-01	1,70E-01	6,41E-01	0,1256	-0,4661571	-0,05856937	217,56	PLEKHG5	pleckstrin homology and RhoGEF domain containing G5
55905	2,15E-01	6,68E-01	1,82E-01	0,044	-1,3335397	-0,05862815	3914,14	RNF114	ring finger protein 114
375449	4,05E-01	3,93E-01	3,64E-01	0,0646	-0,9080797	-0,05863123	1005,58	MAST4	microtubule associated serine/threonine kinase family member 4
10713	1,56E-01	8,07E-01	1,30E-01	0,0387	-1,5158822	-0,05865727	6927,43	USP39	ubiquitin specific peptidase 39
9906	4,16E-01	3,81E-01	3,74E-01	0,0664	-0,8885906	-0,05898336	1052,91	SLC35E2A	solute carrier family 35 member E2A
5464	1,70E-01	7,70E-01	1,41E-01	0,0404	-1,4704388	-0,05935544	6739,86	PPA1	inorganic pyrophosphatase 1
3833	1,67E-01	7,77E-01	1,39E-01	0,0403	-1,4795107	-0,05955113	9225,34	KIFC1	kinesin family member C1
100129075	7,76E-01	1,10E-01	7,47E-01	0,1847	-0,3230398	-0,05966849	113,73	KTN1-AS1	KTN1 antisense RNA 1
7786	4,18E-01	3,79E-01	3,76E-01	0,0677	-0,8844861	-0,0598746	935,58	MAP3K12	mitogen-activated protein kinase kinase kinase 12
8243	2,67E-01	5,73E-01	2,30E-01	0,0501	-1,1992221	-0,0601271	14085,72	SMC1A	structural maintenance of chromosomes 1A
51131	6,44E-01	1,91E-01	6,07E-01	0,1172	-0,5136993	-0,06021813	242,95	PHF11	PHD finger protein 11
115123	4,76E-01	3,22E-01	4,34E-01	0,0772	-0,7817589	-0,06037979	592,74	MARCHF3	membrane associated ring-CH-type finger 3
23091	3,93E-01	4,06E-01	3,51E-01	0,065	-0,9320644	-0,06060456	5303,42	ZC3H13	zinc finger CCCH-type containing 13
100505728	7,67E-01	1,15E-01	7,38E-01	0,181	-0,3349317	-0,06060953	92,84	LOC100505	uncharacterized LOC100505728
55094	3,89E-01	4,10E-01	3,47E-01	0,0647	-0,9395635	-0,06077695	1058,79	GPATCH1	G-patch domain containing 1
100507404	9,24E-01	3,43E-02	9,11E-01	0,546	-0,1117127	-0,06100038	9,67	TMLHE-AS1	TMLHE antisense RNA 1
2261	8,58E-01	6,65E-02	8,37E-01	0,2964	-0,2061676	-0,06111634	36,47	FGFR3	fibroblast growth factor receptor 3
23051	1,87E-01	7,28E-01	1,58E-01	0,0434	-1,4133243	-0,06140713	4059,5	ZHX3	zinc fingers and homeoboxes 3
3700	8,24E-01	8,41E-02	7,98E-01	0,2409	-0,255296	-0,06149451	52,02	ITIH4	inter-alpha-trypsin inhibitor heavy chain 4
101928492	8,41E-01	7,52E-02	8,19E-01	0,2714	-0,2293852	-0,06224525	41,67	OR2A1-AS1	OR2A1 antisense RNA 1
3221	8,85E-01	5,31E-02	8,67E-01	0,3723	-0,167289	-0,06228826	20,94	HOXC4	homeobox C4
650	7,51E-01	1,24E-01	7,21E-01	0,1746	-0,3577181	-0,06246702	100,05	BMP2	bone morphogenetic protein 2
3576	2,73E-01	5,64E-01	2,36E-01	0,0529	-1,185438	-0,06267571	15970,34	CXCL8	C-X-C motif chemokine ligand 8
55636	3,57E-01	4,47E-01	3,17E-01	0,063	-1,0009003	-0,06301723	1056,59	CHD7	chromodomain helicase DNA binding protein 7
8797	2,52E-01	5,99E-01	2,16E-01	0,051	-1,2366094	-0,06305486	2134,89	TNFRSF10A	TNF receptor superfamily member 10a
6637	2,21E-01	6,56E-01	1,88E-01	0,0479	-1,3157785	-0,06307067	6575,22	SNRPG	small nuclear ribonucleoprotein polypeptide G
4676	1,43E-01	8,45E-01	1,18E-01	0,0405	-1,5617845	-0,06322358	7755,57	NAP1L4	nucleosome assembly protein 1 like 4
23158	3,25E-01	4,88E-01	2,86E-01	0,0593	-1,0675844	-0,06332406	1827,21	TBC1D9	TBC1 domain family member 9
1911	2,78E-01	5,56E-01	2,41E-01	0,054	-1,172543	-0,06335846	1764,22	PHC1	polyhomeotic homolog 1
27086	1,83E-01	7,38E-01	1,53E-01	0,0444	-1,4276689	-0,06337763	3368,5	FOXP1	forkhead box P1
112268114	9,26E-01	3,34E-02	9,13E-01	0,5827	-0,1089638	-0,06348916	8,91	LOC112268	uncharacterized LOC112268114
107985363	9,11E-01	4,05E-02	8,95E-01	0,4807	-0,1321038	-0,06350413	13,76	LOC107985	uncharacterized LOC107985363
137682	4,16E-01	3,81E-01	3,75E-01	0,0715	-0,8880406	-0,06351772	745,6	NDUFAF6	NADH:ubiquinone oxidoreductase complex assembly factor 6
6945	1,44E-01	8,42E-01	1,19E-01	0,0407	-1,5607318	-0,0635357	5044,63	MLX	MAX dimerization protein MLX
107986935	9,11E-01	4,05E-02	8,96E-01	0,4847	-0,1310922	-0,06354119	13,25	LOC107986	uncharacterized LOC107986935
8795	1,14E-01	9,43E-01	9,29E-02	0,038	-1,6805149	-0,06384754	8445,49	TNFRSF10B	TNF receptor superfamily member 10b
10962	5,77E-01	2,39E-01	5,37E-01	0,1034	-0,6178028	-0,06389161	325,56	MLLT11	MLLT11 transcription factor 7 cofactor
101927974	8,05E-01	9,42E-02	7,78E-01	0,2274	-0,2812911	-0,06395225	64,23	CBLL1-AS1	CBLL1 antisense RNA 1
1164	1,85E-01	7,33E-01	1,55E-01	0,045	-1,4207251	-0,06398336	4747,72	CKS2	CDC28 protein kinase regulatory subunit 2
284403	2,30E-01	6,38E-01	1,96E-01	0,0497	-1,2929635	-0,06421988	3310	WDR62	WD repeat domain 62
101927275	8,84E-01	5,35E-02	8,66E-01	0,3806	-0,1690979	-0,06435067	20,98	NDUFV2-AS	NDUFV2 antisense RNA 1
10807	1,97E-01	7,06E-01	1,67E-01	0,0465	-1,3834681	-0,06436256	4113,22	ENTR1	endosome associated trafficking regulator 1
146956	4,20E-01	3,77E-01	3,79E-01	0,0734	-0,8795904	-0,06453535	1417,03	EME1	essential meiotic structure-specific endonuclease 1
8945	2,59E-01	5,87E-01	2,23E-01	0,0531	-1,2172861	-0,06457763	1929,41	BTRC	beta-transducin repeat containing E3 ubiquitin protein ligase
51720	2,51E-01	6,00E-01	2,16E-01	0,0522	-1,2378596	-0,06459184	2044,18	UIMC1	ubiquitin interaction motif containing 1
407050	8,41E-01	7,52E-02	8,18E-01	0,282	-0,2296585	-0,06476489	50,2	MIR93	microRNA 93
57644	8,10E-01	9,15E-02	7,83E-01	0,2369	-0,2749254	-0,06513381	53,79	MYH7B	myosin heavy chain 7B
8315	2,27E-01	6,44E-01	1,94E-01	0,0501	-1,3002127	-0,06518121	2030,53	BRAP	BRCA1 associated protein
389906	5,91E-01	2,28E-01	5,52E-01	0,1107	-0,5951898	-0,06587779	265,33	LOC389906	zinc finger protein 839 pseudogene
126626	5,13E-01	2,90E-01	4,71E-01	0,0913	-0,7211864	-0,0658787	414,14	GABPB2	GA binding protein transcription factor subunit beta 2
2271	1,59E-01	7,99E-01	1,32E-01	0,0438	-1,5057951	-0,06596896	6321,5	FH	fumarate hydratase
10677	7,99E-01	9,75E-02	7,72E-01	0,2277	-0,2899286	-0,06601002	56,77	AVIL	advillin
55520	7,26E-01	1,39E-01	6,94E-01	0,1683	-0,3933655	-0,06619655	107,53	ELAC1	elaC ribonuclease Z 1
1163	1,55E-01	8,10E-01	1,28E-01	0,0436	-1,5212576	-0,06636829	7066,7	CKS1B	CDC28 protein kinase regulatory subunit 1B
57568	5,46E-01	2,63E-01	5,05E-01	0,0997	-0,666095	-0,06643351	398,52	SIPA1L2	signal induced proliferation associated 1 like 2
100289511	3,74E-01	4,27E-01	3,33E-01	0,0686	-0,9684478	-0,06643898	1192,5	LOC100289	uncharacterized LOC100289511
102723672	8,10E-01	9,15E-02	7,84E-01	0,2427	-0,274189	-0,06654298	51,89	LINC03015	long intergenic non-protein coding RNA 3015
10312	2,80E-01	5,53E-01	2,43E-01	0,0571	-1,1672338	-0,06669448	2814,34	TCIRG1	T cell immune regulator 1, ATPase H+ transporting V0 subunit a3
11248	9,12E-01	4,00E-02	8,96E-01	0,5108	-0,1306172	-0,06672363	11,35	NXPH3	neurexophilin 3
669	4,30E-01	3,67E-01	3,88E-01	0,0777	-0,8630959	-0,06706476	752,28	BPGM	bisphosphoglycerate mutase
83854	6,66E-01	1,77E-01	6,30E-01	0,1393	-0,4819993	-0,0671408	166,12	ANGPTL6	angiopoietin like 6
90390	3,71E-01	4,31E-01	3,30E-01	0,0691	-0,9734878	-0,0672726	992,43	MED30	mediator complex subunit 30
284306	5,87E-01	2,31E-01	5,48E-01	0,1121	-0,6010381	-0,06734843	290,17	ZNF547	zinc finger protein 547
653113	8,36E-01	7,78E-02	8,13E-01	0,2851	-0,2370843	-0,06758299	36,12	FAM86FP	family with sequence similarity 86, member A pseudogene
5166	5,94E-01	2,26E-01	5,55E-01	0,115	-0,5907964	-0,06795652	318,89	PDK4	pyruvate dehydrogenase kinase 4
55683	1,44E-01	8,42E-01	1,19E-01	0,0436	-1,5580711	-0,06797006	3954,66	KANSL3	KAT8 regulatory NSL complex subunit 3
26286	2,25E-01	6,48E-01	1,92E-01	0,0521	-1,3051282	-0,06797772	2176,38	ARFGAP3	ADP ribosylation factor GTPase activating protein 3
55734	3,79E-01	4,21E-01	3,38E-01	0,0711	-0,9576674	-0,06807358	871,17	ZFP64	ZFP64 zinc finger protein
100506504	7,53E-01	1,23E-01	7,22E-01	0,1917	-0,3554039	-0,0681276	84,16	PRKCZ-AS1	PRKCZ antisense RNA 1
7328	1,59E-01	7,99E-01	1,32E-01	0,0453	-1,5068754	-0,06826694	4452,5	UBE2H	ubiquitin conjugating enzyme E2 H
22978	1,52E-01	8,18E-01	1,26E-01	0,0446	-1,5318332	-0,06828143	3901,78	NT5C2	5'-nucleotidase, cytosolic II
102724542	7,22E-01	1,41E-01	6,89E-01	0,1713	-0,3996036	-0,06846719	116,81	LOC102724	uncharacterized LOC102724542
1399	1,28E-01	8,93E-01	1,05E-01	0,0425	-1,6209748	-0,06884039	4593,14	CRKL	CRK like proto-oncogene, adaptor protein
54956	5,72E-01	2,43E-01	5,32E-01	0,1106	-0,6254724	-0,06920693	262,85	PARP16	poly(ADP-ribose) polymerase family member 16
9861	1,84E-01	7,35E-01	1,55E-01	0,0487	-1,422614	-0,06924199	5712,57	PSMD6	proteasome 26S subunit, non-ATPase 6
685	8,11E-01	9,10E-02	7,84E-01	0,2534	-0,2736794	-0,06933679	58,43	BTC	betacellulin

6533	1,42E-01	8,48E-01	1,17E-01	0,0443	-1,5673544	-0,06943827	3917,78	SLC6A6	solute carrier family 6 member 6
133619	1,78E-01	7,50E-01	1,49E-01	0,0487	-1,4419074	-0,07024487	3913,88	PRRC1	proline rich coiled-coil 1
139716	8,37E-01	7,73E-02	8,14E-01	0,2984	-0,2355405	-0,07028781	35,17	GAB3	GRB2 associated binding protein 3
5125	5,57E-01	2,54E-01	5,17E-01	0,1086	-0,6485438	-0,07040572	294,65	PCSK5	proprotein convertase subtilisin/kexin type 5
22880	2,21E-01	6,56E-01	1,88E-01	0,0536	-1,3169973	-0,07061062	2640,02	MORC2	MORC family CW-type zinc finger 2
1464	4,88E-01	3,12E-01	4,46E-01	0,093	-0,7613851	-0,07079547	442,26	CSPG4	chondroitin sulfate proteoglycan 4
105378410	8,97E-01	4,72E-02	8,80E-01	0,4705	-0,1506357	-0,07087883	14,14	LOC105378	uncharacterized LOC105378410
10137	9,31E-02	1,03E+00	7,48E-02	0,0398	-1,7814891	-0,07089729	5972,84	RBM12	RNA binding motif protein 12
64782	3,33E-01	4,78E-01	2,93E-01	0,0677	-1,0512539	-0,07121727	1549,23	AEN	apoptosis enhancing nuclease
677808	9,12E-01	4,00E-02	8,96E-01	0,5465	-0,1303466	-0,07122908	9,96	SNORA23	small nucleolar RNA, H/ACA box 23
84837	6,19E-01	2,08E-01	5,81E-01	0,129	-0,5522832	-0,07124643	186,04	ARHGAP5-A	ARHGAP5 antisense RNA 1 (head to head)
7520	6,35E-02	1,20E+00	4,99E-02	0,0364	-1,9608695	-0,07129851	26781,82	XRCC5	X-ray repair cross complementing 5
94121	4,09E-01	3,88E-01	3,68E-01	0,0793	-0,9001292	-0,07137063	692,84	SYTL4	synaptotagmin like 4
85406	1,75E-01	7,57E-01	1,47E-01	0,0492	-1,4515469	-0,07138934	2303,82	DNAJC14	DnaJ heat shock protein family (Hsp40) member C14
101927586	8,25E-01	8,35E-02	8,00E-01	0,2825	-0,2533555	-0,07157521	37,04	LINC01271	long intergenic non-protein coding RNA 1271
64857	2,98E-01	5,26E-01	2,60E-01	0,0636	-1,1269434	-0,07163422	1195,66	PLEKHG2	pleckstrin homology and RhoGEF domain containing G2
5899	1,68E-01	7,75E-01	1,40E-01	0,0486	-1,474252	-0,07165478	2310,36	RALB	RAS like proto-oncogene B
56945	1,75E-01	7,57E-01	1,47E-01	0,0495	-1,4515206	-0,07179393	2701,91	MRPS22	mitochondrial ribosomal protein S22
6604	5,89E-01	2,30E-01	5,49E-01	0,1199	-0,5991576	-0,0718653	235,49	SMARCD3	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 3
54856	1,78E-01	7,50E-01	1,49E-01	0,05	-1,4413592	-0,07200466	3137,64	GON4L	gon-4 like
55325	2,67E-01	5,73E-01	2,31E-01	0,0602	-1,1978446	-0,07207439	1582,84	UFSP2	UFM1 specific peptidase 2
105369355	8,94E-01	4,87E-02	8,77E-01	0,4647	-0,1552876	-0,07215853	13,27	LOC105369355	
100128881	5,48E-01	2,61E-01	5,07E-01	0,1088	-0,6639584	-0,07221752	368,76	VPS9D1-AS	VPS9D1 antisense RNA 1
55129	1,71E-01	7,67E-01	1,43E-01	0,0495	-1,4652228	-0,0724608	3148,23	ANO10	anoctamin 10
64375	5,22E-01	2,82E-01	4,80E-01	0,1027	-0,7057984	-0,07250436	359,98	IKZF4	IKAROS family zinc finger 4
728806	3,90E-01	4,09E-01	3,49E-01	0,0774	-0,9372696	-0,07252421	604,25	NSFP1	N-ethylmaleimide-sensitive factor pseudogene 1
85026	5,01E-01	3,00E-01	4,59E-01	0,0981	-0,7406573	-0,07267861	388,02	ARRDC1-AS	ARRDC1 antisense RNA 1
57693	1,39E-01	8,57E-01	1,15E-01	0,0461	-1,5773794	-0,07268575	2836,2	ZNF317	zinc finger protein 317
55689	1,50E-01	8,24E-01	1,24E-01	0,0474	-1,537518	-0,07281259	3142,8	YEATS2	YEATS domain containing 2
22906	1,20E-01	9,21E-01	9,76E-02	0,044	-1,656633	-0,07294578	3483,21	TRAK1	trafficking kinesin protein 1
3778	9,03E-01	4,43E-02	8,87E-01	0,5135	-0,1422087	-0,07302171	11,53	KCNMA1	potassium calcium-activated channel subfamily M alpha 1
4155	9,28E-02	1,03E+00	7,46E-02	0,041	-1,783026	-0,07302928	5511,35	MBP	myelin basic protein
23005	2,74E-01	5,62E-01	2,37E-01	0,0618	-1,1827006	-0,07309273	1298,34	MAPKBP1	mitogen-activated protein kinase binding protein 1
146923	2,25E-01	6,48E-01	1,92E-01	0,0561	-1,3043757	-0,07315124	1764,44	RUNDC1	RUN domain containing 1
105371480	8,08E-01	9,26E-02	7,81E-01	0,2634	-0,2777043	-0,0731582	43,94	LOC105371	uncharacterized LOC105371480
5110	1,23E-01	9,10E-01	1,00E-01	0,0447	-1,6440949	-0,07344693	4046,75	PCMT1	protein-L-isoaspartate (D-aspartate) O-methyltransferase
2305	1,51E-01	8,21E-01	1,25E-01	0,048	-1,5348934	-0,07365811	8222,09	FOXM1	forkhead box M1
1647	1,99E-01	7,01E-01	1,68E-01	0,0536	-1,3792541	-0,07394217	2010,79	GADD45A	growth arrest and DNA damage inducible alpha
9792	1,04E-01	9,83E-01	8,39E-02	0,0428	-1,7285217	-0,07394416	4864,19	SERTAD2	SERTA domain containing 2
57608	5,37E-01	2,70E-01	4,96E-01	0,1086	-0,6811836	-0,07397836	278,32	JCAD	junctional cadherin 5 associated
387103	3,22E-01	4,92E-01	2,83E-01	0,0689	-1,07363	-0,07402381	958,36	CENPW	centromere protein W
53340	3,75E-01	4,26E-01	3,34E-01	0,0766	-0,9665716	-0,07407452	840,09	SPA17	sperm autoantigenic protein 17
114034	2,24E-01	6,50E-01	1,90E-01	0,0566	-1,3099009	-0,07409863	1374,42	TOE1	target of EGR1, exonuclease
100507458	7,30E-01	1,37E-01	6,98E-01	0,1917	-0,3882632	-0,07441705	81,99	ZNF213-AS1	ZNF213 antisense RNA 1 (head to head)
93550	4,85E-01	3,14E-01	4,43E-01	0,0973	-0,7670127	-0,07461058	348,77	ZFAND4	zinc finger AN1-type containing 4
3551	2,16E-01	6,66E-01	1,83E-01	0,0561	-1,3309934	-0,07464785	1476,28	IKBKB	inhibitor of nuclear factor kappa B kinase subunit beta
140680	3,93E-01	4,06E-01	3,52E-01	0,0802	-0,9311058	-0,07469272	597,39	C20orf96	chromosome 20 open reading frame 96
101927886	7,76E-01	1,10E-01	7,47E-01	0,2322	-0,3219551	-0,07476918	57,28	RFX5-AS1	RFX5 antisense RNA 1
100505555	8,75E-01	5,80E-02	8,55E-01	0,4101	-0,1827699	-0,07495129	18,63	LOC100505	uncharacterized LOC100505555
102465834	7,57E-01	1,21E-01	7,27E-01	0,2144	-0,349649	-0,07495397	71,31	MIR7844	microRNA 7844
143689	8,29E-01	8,14E-02	8,05E-01	0,3029	-0,2475253	-0,07498379	38,38	PIWIL4	piwi like RNA-mediated gene silencing 4
170622	4,14E-01	3,83E-01	3,73E-01	0,0842	-0,8913692	-0,07504025	905,36	COMMD6	COMM domain containing 6
80833	4,52E-01	3,45E-01	4,10E-01	0,0912	-0,8232314	-0,0750696	413,94	APOL3	apolipoprotein L3
285600	8,79E-01	5,60E-02	8,60E-01	0,426	-0,1763052	-0,07509935	16,74	KIAA0825	KIAA0825
26128	1,22E-01	9,14E-01	9,94E-02	0,0456	-1,6478177	-0,07521089	3324,5	KIFBP	kinesin family binding protein
10898	2,53E-01	5,97E-01	2,18E-01	0,0611	-1,2321423	-0,07527515	1246,41	CPSF4	cleavage and polyadenylation specific factor 4
493754	3,44E-01	4,63E-01	3,04E-01	0,0733	-1,0287729	-0,07542961	784,99	RABGEF1P1	RABGEF1 pseudogene 1
140710	1,13E-01	9,47E-01	9,20E-02	0,0448	-1,6850927	-0,07544212	6814,44	SOGA1	suppressor of glucose, autophagy associated 1
112268219	6,59E-01	1,81E-01	6,22E-01	0,1531	-0,4930239	-0,0754831	134,88	LOC112268	uncharacterized LOC112268219
54808	2,84E-01	5,47E-01	2,46E-01	0,0651	-1,1598397	-0,07550988	1316,72	DYM	dymeclin
4515	6,29E-01	2,01E-01	5,92E-01	0,1409	-0,5361939	-0,07553568	165,23	MTCP1	mature T cell proliferation 1
349408	7,29E-01	1,37E-01	6,96E-01	0,1939	-0,3902866	-0,07568588	89,58	TLR8-AS1	TLR8 antisense RNA 1
112268278	8,31E-01	8,04E-02	8,07E-01	0,3098	-0,2444523	-0,07573346	33,77	LOC112268278	
4839	1,50E-01	8,24E-01	1,24E-01	0,0493	-1,5383369	-0,07583313	4095,49	NOP2	NOP2 nucleolar protein
55686	4,47E-01	3,50E-01	4,05E-01	0,0913	-0,8325338	-0,07598333	498,02	MREG	melanoregulin
7532	8,80E-02	1,06E+00	7,05E-02	0,042	-1,8088333	-0,07599851	9240,94	YWHAG	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein gamma
7277	2,19E-01	6,60E-01	1,86E-01	0,0576	-1,3234698	-0,07620295	3178,24	TUBA4A	tubulin alpha 4a
29058	1,19E-01	9,24E-01	9,67E-02	0,0459	-1,6612733	-0,0762627	5425,83	TMEM230	transmembrane protein 230
7421	3,45E-01	4,62E-01	3,05E-01	0,0743	-1,0263807	-0,07630369	691,41	VDR	vitamin D receptor
10188	2,68E-01	5,72E-01	2,31E-01	0,0638	-1,1975773	-0,07640758	1602,71	TNK2	tyrosine kinase non receptor 2
10103	2,92E-01	5,35E-01	2,54E-01	0,067	-1,1411726	-0,07650983	950,56	TSPAN1	tetraspanin 1
9517	8,98E-02	1,05E+00	7,20E-02	0,0425	-1,7991138	-0,07654482	4855,42	SPTLC2	serine palmitoyltransferase long chain base subunit 2
24149	2,12E-01	6,74E-01	1,79E-01	0,057	-1,3427066	-0,07654632	3712,85	ZNF318	zinc finger protein 318
100507373	5,84E-01	2,34E-01	5,44E-01	0,127	-0,606748	-0,07703988	200,85	ADGRL1-AS	ADGRL1 antisense RNA 1
11321	1,11E-01	9,55E-01	8,98E-02	0,0455	-1,6965506	-0,07714982	4079,52	GPN1	GPN-loop GTPase 1
9732	1,11E-01	9,55E-01	9,01E-02	0,0455	-1,6946943	-0,07717538	3083,66	DOCK4	dedicator of cytokinesis 4
90102	1,43E-01	8,45E-01	1,18E-01	0,0495	-1,5619076	-0,07724977	3233,96	PHLDB2	pleckstrin homology like domain family B member 2
55217	6,13E-01	2,13E-01	5,75E-01	0,1378	-0,5612475	-0,07736459	186,59	TMLHE	trimethyllysine hydroxylase, epsilon
28987	1,10E-01	9,59E-01	8,91E-02	0,0456	-1,7002006	-0,07749596	3443,64	NOB1	NIN1 (RPN12) binding protein 1 homolog
26061	2,89E-01	5,39E-01	2,51E-01	0,0676	-1,1471227	-0,07752834	865,16	HACL1	2-hydroxyacyl-CoA lyase 1
5538	6,81E-02	1,17E+00	5,37E-02	0,0403	-1,9289934	-0,07775071	16968,16	PPT1	palmitoyl-protein thioesterase 1
65125	1,07E-01	9,71E-01	8,65E-02	0,0454	-1,7139063	-0,0778018	9254,83	WNK1	WNK lysine deficient protein kinase 1
80198	2,96E-01	5,29E-01	2,58E-01	0,0688	-1,1320836	-0,07788206	1136,56	MUS81	MUS81 structure-specific endonuclease subunit
100271874	8,97E-01	4,72E-02	8,80E-01	0,5184	-0,1503941	-0,07796595	10,81	ZNRF2P2	zinc and ring finger 2 pseudogene 2
84245	2,72E-01	5,65E-01	2,35E-01	0,0657	-1,1873966	-0,07806175	1084,58	MRI1	methylthioribose-1-phosphate isomerase 1
252884	7,76E-01	1,10E-01	7,47E-01	0,2424	-0,3220965	-0,07806958	52,82	ZNF396	zinc finger protein 396
729970	7,11E-01	1,48E-01	6,78E-01	0,1883	-0,414743	-0,07811529	88,05	CNN3-DT	CNN3 divergent transcript
83930	9,56E-02	1,02E+00	7,69E-02	0,0442	-1,7690247	-0,07823602	3446,52	STARD3NL	STARD3 N-terminal like
56965	1,87E-01	7,28E-01	1,57E-01	0,0554	-1,4151981	-0,07837419	2097,94	PARP6	poly(ADP-ribose) polymerase family member 6
8728	1,09E-01	9,63E-01	8,83E-02	0,046	-1,7041743	-0,07838566	3590,8	ADAM19	ADAM metallopeptidase domain 19
112616	1,67E-01	7,77E-01	1,39E-01	0,0532	-1,4778343	-0,07863836	2335,17	CMTM7	CKLF like MARVEL transmembrane domain containing 7
128637	1,49E-01	8,27E-01	1,23E-01	0,051	-1,5425239	-0,0786994	2375,42	TBC1D20	TBC1 domain family member 20
1730	3,05E-01	5,16E-01	2,66E-01	0,0709	-1,1121539	-0,07886548	1134,05	DIAPH2	diaphanous related formin 2
80851	2,48E-01	6,06E-01	2,13E-01	0,0634	-1,2454701	-0,07900031	1965,4	SH3BP5L	SH3 binding domain protein 5 like
7374	8,08E-02	1,09E+00	6,43E-02	0,0428	-1,8498866	-0,07912461	5319,33	UNG	uracil DNA glycosylase
9785	1,04E-01	9,83E-01	8,39E-02	0,0458	-1,7285363	-0,0791321	3130,14	DHX38	DEAH-box helicase 38
105378853	7,16E-01	1,45E-01	6,83E-01	0,1951	-0,4079829	-0,07959395	78,9	LINC02609	long intergenic non-protein coding RNA 2609
65979	1,83E-01	7,38E-01	1,54E-01	0,0558	-1,4260882	-0,07961558	3500,92	PHACTR4	phosphatase and actin regulator 4
91754	1,01E-01	9,96E-01	8,17E-02	0,0458	-1,7410193	-0,07971478	3344,76	NEK9	NIMA related kinase 9
23526	1,73E-01	7,62E-01	1,44E-01	0,0547	-1,4596838	-0,07983651	1641,49	ARHGAP45	Rho GTPase activating protein 45
535	1,27E-01	8,96E-01	1,04E-01	0,0491	-1,625599	-0,07988698	2664,33	ATP6V0A1	ATPase H+ transporting V0 subunit a1
57707	9,91E-02	1,00E+00	8,00E-02	0,0457	-1,7508588	-0,08002575	2912,97	MEAK7	MTOR associated protein, eak-7 homolog
8293	3,80E-01	4,20E-01	3,39E-01	0,0838	-0,9554256	-0,08003402	540,6	SERF1A	small EDRK-rich factor 1A
105369301	7,39E-01	1,31E-01	7,08E-01	0,2144	-0,3748217	-0,08036321	72,14	CLDN14-AS	CLDN14 antisense RNA 1
107986100	7,84E-01	1,06E-01	7,55E-01	0,2586	-0,3117443	-0,08061674	45,84	LINC02018	long intergenic non-protein coding RNA 2018
84852	5,73E-02	1,24E+00	4,48E-02	0,0402	-2,0068758	-0,08068846	9269,06	ATP1A1-AS1	ATP1A1 antisense RNA 1
101927278	8,86E-01	5,26E-02	8,67E-01	0,4838	-0,1668414	-0,08072259	13,41	HPS1-AS1	HPS1 antisense RNA 1
5129	8,44E-01	7,37E-02	8,22E-01	0,3586	-0,2251235	-0,08072721	23,98	CDK18	cyclin dependent kinase 18
153090	1,14E-01	9,43E-01	9,25E-02	0,0482	-1,6824502	-0,08109198	2569,61	DAB2IP	DAB2 interacting protein
101929125	8,88E-01	5,16E-02	8,70E-01	0,4969	-0,1636091	-0,08129285	12,5	LINC01730	long intergenic non-protein coding RNA 1730
4163	4,49E-01	3,48E-01	4,08E-01	0,0984	-0,8273547	-0,0814177	346,54	MCC	MCC regulator of WNT signaling pathway
728492	3,60E-01	4,44E-01	3,19E-01	0,0817	-0,9964096	-0,081425	561,26	SERF1B	small EDRK-rich factor 1B
55450	2,37E-01	6,25E-01	2,02E-01	0,0641	-1,2747706	-0,08173573	1075,63	CAMK2N1	calcium/calmodulin dependent protein kinase II inhibitor 1
94241	5,60E-01	2,52E-01	5,19E-01	0,1268	-0,6446695	-0,08174136	211,45	TP53INP1	tumor protein p53 inducible nuclear protein 1
25821	1,48E-01	8,30E-01	1,22E-01	0,0531	-1,5448944	-0,08199117	1901,07	MTO1	mitochondrial tRNA translation optimization 1
4140	7,52E-02	1,12E+00	5,97E-02	0,0436	-1,8831094	-0,08207354	4224,23	MARK3	microtubule affinity regulating kinase 3
100507297	6,44E-01	1,91E-01	6,07E-01	0,1608	-0,5141306	-0,08267444	129,26	TMEM44-AS	TMEM44 antisense RNA 1
6932	5,76E-01	2,40E-01	5,36E-01	0,1336	-0,6190606	-0,08267667	176,94	TCF7	transcription factor 7
6091	1,68E-01	7,75E-01	1,40E-01	0,0561	-1,4749387	-0,08278672	2603,31	ROBO1	roundabout guidance receptor 1
105372906	8,40E-01	7,57E-02	8,17E-01	0,3576	-0,231717	-0,08285698	23,89	LOC105372	uncharacterized LOC105372906

1540	1,18E-01	9,28E-01	9,64E-02	0,0498	-1,6625559	-0,08287052	2988,29	CYLD	CYLD lysine 63 deubiquitinase
90843	2,70E-01	5,69E-01	2,33E-01	0,0697	-1,1918267	-0,08304514	1719,84	TCEAL8	transcription elongation factor A like 8
2672	8,73E-01	5,90E-02	8,52E-01	0,4467	-0,1859339	-0,08306493	15,29	GFI1	growth factor independent 1 transcriptional repressor
105375674	8,80E-01	5,55E-02	8,61E-01	0,4743	-0,1752329	-0,08311729	13,82	LINC03044	long intergenic non-protein coding RNA 3044
649395	7,45E-01	1,28E-01	7,13E-01	0,2268	-0,3673	-0,0832873	61,57	YWHAEP1	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein epsilon pseudogene 1
22850	1,73E-01	7,62E-01	1,44E-01	0,0571	-1,4593404	-0,08335731	1691,95	ADNP2	ADNP homeobox 2
105373302	5,08E-01	2,94E-01	4,66E-01	0,1144	-0,729162	-0,08340707	240,62	LOC105373302	
102724720	8,82E-01	5,45E-02	8,64E-01	0,4864	-0,171518	-0,0834349	12,41	LOC102724720	uncharacterized LOC102724720
6016	1,87E-01	7,28E-01	1,57E-01	0,0591	-1,4155068	-0,08367642	1486,7	RIT1	Ras like without CAAX 1
55633	1,08E-01	9,67E-01	8,74E-02	0,0491	-1,7095052	-0,08389597	2249,68	TBC1D22B	TBC1 domain family member 22B
9489	3,07E-01	5,13E-01	2,68E-01	0,0758	-1,1068406	-0,08393913	752,53	PGS1	phosphatidylglycerophosphate synthase 1
85371	7,11E-01	1,48E-01	6,78E-01	0,2025	-0,4156946	-0,08417432	73,07	KIAA1656	KIAA1656 protein
154064	8,01E-01	9,64E-02	7,73E-01	0,2926	-0,2880668	-0,08429039	35,1	RAET1L	retinoic acid early transcript 1L
11319	1,11E-01	9,55E-01	9,01E-02	0,0501	-1,6949792	-0,08487266	2387,83	ECD	ecdysoneless cell cycle regulator
151009	6,09E-01	2,15E-01	5,70E-01	0,1495	-0,5677149	-0,0848897	137,85	LINC01106	long intergenic non-protein coding RNA 1106
136647	2,43E-01	6,14E-01	2,08E-01	0,0679	-1,2594565	-0,08548347	1223,65	MPLKIP	M-phase specific PLK1 interacting protein
9354	8,03E-02	1,10E+00	6,39E-02	0,0462	-1,8526622	-0,08559674	4844,32	UBE4A	ubiquitination factor E4A
84328	8,66E-02	1,06E+00	6,92E-02	0,0471	-1,8169616	-0,08564773	2587,8	LZIC	leucine zipper and CTNNBIP1 domain containing
2186	1,29E-01	8,89E-01	1,06E-01	0,0529	-1,6179752	-0,08567002	5106,44	BPTF	bromodomain PHD finger transcription factor
100506243	4,34E-01	3,63E-01	3,92E-01	0,1001	-0,8557133	-0,08567551	367,49	KRBOX1	KRAB box domain containing 1
51227	4,97E-01	3,04E-01	4,55E-01	0,1147	-0,7469865	-0,08568393	405,54	PIGP	phosphatidylinositol glycan anchor biosynthesis class P
84441	8,88E-02	1,05E+00	7,12E-02	0,0475	-1,804491	-0,08573762	3289,1	MAML2	mastermind like transcriptional coactivator 2
137392	3,31E-01	4,80E-01	2,92E-01	0,0816	-1,0545337	-0,08602625	606,17	CIBAR1	CBY1 interacting BAR domain containing 1
246184	1,90E-01	7,21E-01	1,60E-01	0,0612	-1,4060568	-0,08607822	1786,99	CDC26	cell division cycle 26
6899	6,36E-01	1,97E-01	5,98E-01	0,1634	-0,5267893	-0,08609436	121,48	TBX1	T-box transcription factor 1
23057	1,15E-01	9,39E-01	9,38E-02	0,0514	-1,6757744	-0,08610601	1976,72	NMNAT2	nicotinamide nucleotide adenylyltransferase 2
64422	1,80E-01	7,45E-01	1,51E-01	0,0601	-1,4364028	-0,08630615	3301,97	ATG3	autophagy related 3
79000	2,11E-01	6,76E-01	1,79E-01	0,0645	-1,343157	-0,08669803	1063,7	AUNIP	aurora kinase A and ninein interacting protein
5901	2,89E-02	1,54E+00	2,17E-02	0,0378	-2,2951697	-0,08675941	22876,32	RAN	RAN, member RAS oncogene family
112268148	6,25E-01	2,04E-01	5,87E-01	0,1611	-0,5425401	-0,08737776	135,79	LOC112268	uncharacterized LOC112268148
64097	3,14E-01	5,03E-01	2,75E-01	0,0801	-1,0914331	-0,08740946	612,91	EPB41L4A	erythrocyte membrane protein band 4.1 like 4A
51121	1,21E-01	9,17E-01	9,85E-02	0,0529	-1,6520739	-0,08743048	2012,84	RPL26L1	ribosomal protein L26 like 1
440275	4,65E-02	1,33E+00	3,59E-02	0,0417	-2,0985771	-0,0874769	4931,76	EIF2AK4	eukaryotic translation initiation factor 2 alpha kinase 4
150684	9,66E-02	1,02E+00	7,78E-02	0,0496	-1,7638085	-0,0875636	3148,3	COMMD1	copper metabolism domain containing 1
100526836	1,93E-02	1,71E+00	1,42E-02	0,0357	-2,4521782	-0,08756805	14692,32	BLOC1S5-T	BLOC1S5-TXNDC5 readthrough (NMD candidate)
64780	2,67E-01	5,73E-01	2,30E-01	0,0734	-1,1992242	-0,08803242	846,47	MICAL1	microtubule associated monooxygenase, calponin and LIM domain containing 1
5383	7,01E-01	1,54E-01	6,68E-01	0,2053	-0,4291432	-0,0880919	78,91	PMS2P5	PMS1 homolog 2, mismatch repair system component pseudogene 5
9722	6,21E-01	2,07E-01	5,83E-01	0,1607	-0,5485013	-0,08812565	123,31	NOS1AP	nitric oxide synthase 1 adaptor protein
606495	4,07E-01	3,90E-01	3,66E-01	0,0977	-0,9037105	-0,08827521	353,5	CYB5RL	cytochrome b5 reductase like
9659	9,60E-02	1,02E+00	7,73E-02	0,05	-1,7666337	-0,08840815	2228,5	PDE4DIP	phosphodiesterase 4D interacting protein
438	6,14E-01	2,12E-01	5,75E-01	0,158	-0,5600784	-0,08847262	130,44	ASMT	acetylserotonin O-methyltransferase
91875	2,95E-01	5,30E-01	2,57E-01	0,0784	-1,132835	-0,08877932	720,13	TTC5	tetratricopeptide repeat domain 5
101928605	7,64E-01	1,17E-01	7,34E-01	0,2617	-0,3398083	-0,08891265	42,82	ARHGEF35-A	ARHGEF35 antisense RNA 1
27345	6,34E-01	1,98E-01	5,97E-01	0,1688	-0,5287613	-0,08925048	109,53	KCNMB4	potassium calcium-activated channel subfamily M regulatory beta subunit 4
201292	8,66E-02	1,06E+00	6,92E-02	0,0491	-1,8171429	-0,08928034	2511,83	TRIM65	tripartite motif containing 65
22996	8,07E-01	9,31E-02	7,80E-01	0,3214	-0,2791901	-0,08972389	30,46	TTC39A	tetratricopeptide repeat domain 39A
108903150	1,14E-01	9,43E-01	9,31E-02	0,0534	-1,6794853	-0,08975934	1801,99	ZNF8-ERVK3	ZNF8-ERVK3-1 readthrough
57050	6,84E-02	1,16E+00	5,40E-02	0,0468	-1,9265598	-0,09011067	2949,4	UTP3	UTP3 small subunit processome component
253461	6,80E-02	1,17E+00	5,36E-02	0,0467	-1,9298271	-0,09020524	4783,78	ZBTB38	zinc finger and BTB domain containing 38
101929977	7,53E-01	1,23E-01	7,22E-01	0,2541	-0,3552404	-0,09028067	46,61	MARCHF6-D	MARCHF6 divergent transcript
57180	3,21E-01	4,93E-01	2,82E-01	0,084	-1,0764918	-0,0903999	528,87	ACTR3B	actin related protein 3B
112942	1,28E-01	8,93E-01	1,05E-01	0,0559	-1,6221224	-0,09064839	1887,59	CFAP36	cilia and flagella associated protein 36
55798	1,66E-01	7,80E-01	1,38E-01	0,0611	-1,4834669	-0,09066891	1634,77	METTL2B	methyltransferase 2B, methylcytidine
23395	7,87E-02	1,10E+00	6,25E-02	0,0487	-1,8624084	-0,09076632	2255,26	LARS2	leucyl-tRNA synthetase 2, mitochondrial
100506753	8,51E-01	7,01E-02	8,29E-01	0,4208	-0,2158632	-0,09082597	18,02	MAILR	macrophage interferon regulatory lncRNA
3608	2,25E-02	1,65E+00	1,67E-02	0,038	-2,392771	-0,09095883	19319,79	ILF2	interleukin enhancer binding factor 2
101928527	4,95E-01	3,05E-01	4,53E-01	0,1214	-0,7506285	-0,09108993	227,76	PIGBOS1	PIGB opposite strand 1
1736	2,61E-02	1,58E+00	1,95E-02	0,039	-2,336022	-0,09117227	9946,38	DKC1	dyskerin pseudouridine synthase 1
57558	3,29E-01	4,83E-01	2,90E-01	0,0862	-1,0584113	-0,09118521	469,75	USP35	ubiquitin specific peptidase 35
8405	8,39E-02	1,08E+00	6,69E-02	0,0498	-1,832029	-0,09119291	2745	SPOP	speckle type BTB/POZ protein
116236	2,54E-01	5,95E-01	2,19E-01	0,0744	-1,2296471	-0,09149297	712,83	ABHD15	abhydrolase domain containing 15
1472	6,63E-02	1,18E+00	5,23E-02	0,0474	-1,9410551	-0,09190911	3476,15	CST4	cystatin S
152098	5,66E-01	2,47E-01	5,25E-01	0,1449	-0,6354078	-0,09210164	153,78	ZCWPW2	zinc finger CW-type and PWWP domain containing 2
101928421	8,07E-01	9,31E-02	7,80E-01	0,3305	-0,2790726	-0,09223691	26,64	LOC101928	uncharacterized LOC101928421
27295	4,16E-01	3,81E-01	3,74E-01	0,104	-0,8887142	-0,0924432	317,99	PDLIM3	PDZ and LIM domain 3
7508	1,73E-01	7,62E-01	1,44E-01	0,0634	-1,4604526	-0,09253897	1275,1	XPC	XPC complex subunit, DNA damage recognition and repair factor
631	3,28E-01	4,84E-01	2,88E-01	0,0872	-1,0620913	-0,09261443	461,58	BFSP1	beaded filament structural protein 1
105374952	3,98E-01	4,00E-01	3,57E-01	0,1006	-0,9212949	-0,09266731	337,94	NUP153-AS1	NUP153 antisense RNA 1
29092	2,48E-01	6,06E-01	2,13E-01	0,0745	-1,2460792	-0,09285813	761,51	LINC00339	long intergenic non-protein coding RNA 339
9212	7,59E-02	1,12E+00	6,02E-02	0,0495	-1,8792656	-0,09296213	4831,44	AURKB	aurora kinase B
7903	3,52E-01	4,53E-01	3,12E-01	0,092	-1,0110106	-0,0929938	424,21	ST8SIA4	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 4
79840	2,19E-01	6,60E-01	1,86E-01	0,0704	-1,3217098	-0,09305293	826,98	NHEJ1	non-homologous end joining factor 1
100996732	7,97E-01	9,85E-02	7,69E-01	0,3171	-0,2937539	-0,0931436	40,05	LINC02802	long intergenic non-protein coding RNA 2802
201501	6,92E-01	1,60E-01	6,58E-01	0,2104	-0,4429422	-0,09320278	68,68	ZBTB7C	zinc finger and BTB domain containing 7C
105372942	8,75E-01	5,80E-02	8,55E-01	0,511	-0,1824889	-0,09324798	11,1	FAM247D	family with sequence similarity 247 member D
8661	4,71E-02	1,33E+00	3,64E-02	0,0446	-2,0921354	-0,09326583	28382,15	EIF3A	eukaryotic translation initiation factor 3 subunit A
1967	6,36E-02	1,20E+00	5,00E-02	0,0476	-1,9599121	-0,09338664	4666,11	EIF2B1	eukaryotic translation initiation factor 2B subunit alpha
26058	7,38E-02	1,13E+00	5,84E-02	0,0494	-1,8923792	-0,09348168	3688,42	GIGYF2	GRB10 interacting GYF protein 2
140700	3,47E-01	4,60E-01	3,07E-01	0,0916	-1,0224188	-0,09369659	557,15	SAMD10	sterile alpha motif domain containing 10
25806	7,19E-01	1,43E-01	6,86E-01	0,2328	-0,4044401	-0,09414224	57,85	VAX2	ventral anterior homeobox 2
8462	1,81E-01	7,42E-01	1,52E-01	0,0657	-1,433728	-0,09414238	965,21	KLF11	KLF transcription factor 11
171423	9,35E-02	1,03E+00	7,51E-02	0,0529	-1,7798961	-0,09423179	1771,25	PDIA3P1	protein disulfide isomerase family A member 3 pseudogene 1
9898	3,87E-02	1,41E+00	2,96E-02	0,0434	-2,1759655	-0,09439584	18412,89	UBAP2L	ubiquitin associated protein 2 like
8073	2,89E-02	1,54E+00	2,17E-02	0,0412	-2,2953857	-0,09455956	17225,7	PTP4A2	protein tyrosine phosphatase 4A2
100289580	5,87E-01	2,31E-01	5,47E-01	0,157	-0,6023728	-0,09456262	137,98	LOC100289	uncharacterized LOC100289580
105371925	5,24E-01	2,81E-01	4,82E-01	0,1348	-0,703036	-0,09480137	178,08	LOC105371	uncharacterized LOC105371925
129293	2,79E-01	5,54E-01	2,42E-01	0,0811	-1,1704759	-0,09496361	600,38	TRABD2A	TraB domain containing 2A
2058	3,50E-02	1,46E+00	2,66E-02	0,0428	-2,2176961	-0,09501035	14723,58	EPRS1	glutamyl-prolyl-tRNA synthetase 1
84163	5,52E-01	2,58E-01	5,12E-01	0,1454	-0,6560347	-0,09539871	145,19	GTF2IRD2	GTF2I repeat domain containing 2
440456	4,32E-01	3,65E-01	3,91E-01	0,1116	-0,8580124	-0,09578086	386,3	PLEKHM1P1	pleckstrin homology and RUN domain containing M1 pseudogene 1
55061	5,73E-01	2,42E-01	5,33E-01	0,1536	-0,6239304	-0,09580533	132,51	SUSD4	sushi domain containing 4
3428	3,48E-02	1,46E+00	2,64E-02	0,0433	-2,2195971	-0,09612151	7099	IFI16	interferon gamma inducible protein 16
4998	8,27E-02	1,08E+00	6,59E-02	0,0523	-1,8388362	-0,09617289	1923,61	ORC1	origin recognition complex subunit 1
100532732	3,39E-01	4,70E-01	2,99E-01	0,0927	-1,0382429	-0,09628251	405,19	MSH5-SAPC	MSH5-SAPCD1 readthrough (NMD candidate)
643827	5,95E-01	2,25E-01	5,56E-01	0,1639	-0,5882664	-0,096438	115,78	CNTNAP3P2	CNTNAP3 pseudogene 2
643072	8,11E-01	9,10E-02	7,85E-01	0,3529	-0,2733782	-0,09647605	23,81	BAZ2B-AS1	BAZ2B antisense RNA 1
85464	1,33E-01	8,76E-01	1,09E-01	0,0603	-1,6021025	-0,09653811	1573,49	SSH2	slingshot protein phosphatase 2
51304	3,46E-02	1,46E+00	2,63E-02	0,0434	-2,2223381	-0,09655992	4600,55	ZDHHC3	zinc finger DHHC-type palmitoyltransferase 3
56121	8,46E-01	7,26E-02	8,23E-01	0,4323	-0,2234633	-0,09661379	16,8	PCDHB15	protocadherin beta 15
728673	4,18E-01	3,79E-01	3,77E-01	0,1095	-0,8836895	-0,0967954	280,46	FAM88B	family with sequence similarity 88 member B
1469	4,70E-02	1,33E+00	3,63E-02	0,0462	-2,0935639	-0,09680498	18103,42	CST1	cystatin SN
100507291	8,01E-01	9,64E-02	7,73E-01	0,3368	-0,2882055	-0,09707621	26,79	COPB2-DT	COPB2 divergent transcript
83723	8,67E-01	6,20E-02	8,47E-01	0,5022	-0,193586	-0,09721483	12,09	TLCD3B	TLC domain containing 3B
10810	2,37E-01	6,25E-01	2,03E-01	0,0764	-1,274376	-0,09735457	835,23	WASF3	WASP family member 3
255187	8,33E-01	7,94E-02	8,10E-01	0,4045	-0,2407667	-0,09739985	19,06	SH3TC2-DT	SH3TC2 divergent transcript
5252	1,01E-01	9,96E-01	8,17E-02	0,056	-1,7407429	-0,09741434	3314,29	PHF1	PHD finger protein 1
7087	3,65E-01	4,38E-01	3,25E-01	0,099	-0,9850872	-0,09752457	356,75	ICAM5	intercellular adhesion molecule 5
90342	8,74E-01	5,85E-02	8,54E-01	0,5292	-0,1843293	-0,0975496	10,34	FER1L5	fer-1 like family member 5
79149	5,43E-01	2,65E-01	5,02E-01	0,1454	-0,6711688	-0,09757671	155,93	ZSCAN5A	zinc finger and SCAN domain containing 5A
8915	1,21E-01	9,17E-01	9,85E-02	0,0591	-1,6521046	-0,09762866	1515,9	BCL10	BCL10 immune signaling adaptor
79583	2,40E-01	6,20E-01	2,05E-01	0,0771	-1,2664517	-0,09765114	775,49	TMEM231	transmembrane protein 231
10343	8,28E-01	8,20E-02	8,03E-01	0,3925	-0,2490441	-0,0977462	20,7	PKDREJ	polycystin family receptor for egg jelly
54974	1,36E-01	8,66E-01	1,12E-01	0,0615	-1,5904344	-0,097879	1092,39	THG1L	tRNA-histidine guanylyltransferase 1 like
1106	7,45E-02	1,13E+00	5,90E-02	0,0519	-1,8880468	-0,09790635	4283,34	CHD2	chromodomain helicase DNA binding protein 2
2595	1,83E-01	7,38E-01	1,53E-01	0,0687	-1,4279357	-0,09808157	841,96	GANC	glucosidase alpha, neutral C
23382	1,84E-01	7,35E-01	1,55E-01	0,0689	-1,4234757	-0,0980847	875,03	AHCYL2	adenosylhomocysteinase like 2
79611	2,27E-01	6,44E-01	1,93E-01	0,0755	-1,3005701	-0,09816047	730,65	ACSS3	acyl-CoA synthetase short chain family member 3
57646	7,89E-02	1,10E+00	6,27E-02	0,0528	-1,8610797	-0,09817391	1999,73	USP28	ubiquitin specific peptidase 28
100132111	8,00E-01	9,69E-02	7,72E-01	0,3407	-0,2897148	-0,09871799	27,23	C2CD4D-AS	C2CD4D and THEM5 antisense RNA 1
81567	8,30E-03	2,08E+00	5,91E-03	0,0359	-2,7528367	-0,09873384	14525,97	TXNDC5	thioredoxin domain containing 5

1500	2,97E-02	1,53E+00	2,24E-02	0,0433	-2,2837228	-0,09880869	5510,55	CTNND1	catenin delta 1
4649	8,37E-02	1,08E+00	6,68E-02	0,054	-1,8329904	-0,09896402	1780,94	MYO9A	myosin IXA
79658	1,22E-01	9,14E-01	9,97E-02	0,0602	-1,6464559	-0,09905225	1232,32	ARHGAP10	Rho GTPase activating protein 10
100506963	3,22E-01	4,92E-01	2,83E-01	0,0925	-1,0734652	-0,09928752	401,94	ELOA-AS1	ELOA antisense RNA 1
29103	4,70E-02	1,33E+00	3,63E-02	0,0475	-2,0931049	-0,09938082	2457,56	DNAJC15	DnaJ heat shock protein family (Hsp40) member C15
7029	7,27E-02	1,14E+00	5,76E-02	0,0524	-1,899041	-0,09959793	1839,23	TFDP2	transcription factor Dp-2
22822	1,46E-02	1,84E+00	1,07E-02	0,039	-2,5537283	-0,09961093	20016,89	PHLDA1	pleckstrin homology like domain family A member 1
55846	1,33E-01	8,76E-01	1,09E-01	0,0623	-1,6014061	-0,09977281	1151,05	ITFG2	integrin alpha FG-GAP repeat containing 2
112268243	8,65E-01	6,30E-02	8,45E-01	0,5093	-0,1959196	-0,0997827	11,2	ZSCAN5A-A	ZSCAN5A antisense RNA 1
285266	5,15E-01	2,88E-01	4,73E-01	0,1391	-0,7173738	-0,09979366	168,06	ENTPD3-AS	ENTPD3 antisense RNA 1
105373853	8,14E-01	8,94E-02	7,88E-01	0,3714	-0,2688692	-0,09984879	22,37	MYOSLID	myocardin-induced smooth muscle lncRNA, inducer of differentiation
79038	1,70E-01	7,70E-01	1,42E-01	0,0681	-1,4672043	-0,09997301	900,17	ZFYVE21	zinc finger FYVE-type containing 21
1525	1,70E-01	7,70E-01	1,42E-01	0,0682	-1,4695298	-0,10026004	904,17	CXADR	CXADR Ig-like cell adhesion molecule
7170	6,76E-03	2,17E+00	4,77E-03	0,0355	-2,8222315	-0,10028627	32733,88	TPM3	tropomyosin 3
10395	3,62E-02	1,44E+00	2,76E-02	0,0455	-2,2029867	-0,10032769	3173,82	DLC1	DLC1 Rho GTPase activating protein
81606	3,58E-01	4,46E-01	3,17E-01	0,1004	-1,0002656	-0,10042112	360,41	LBH	LBH regulator of WNT signaling pathway
4985	8,77E-01	5,70E-02	8,58E-01	0,5598	-0,1793821	-0,10042591	9,59	OPRD1	opioid receptor delta 1
55614	2,28E-01	6,42E-01	1,94E-01	0,0779	-1,2989182	-0,10116661	740,78	KIF16B	kinesin family member 16B
84904	1,49E-01	8,27E-01	1,23E-01	0,0659	-1,5403516	-0,10144313	933,76	ARHGEF39	Rho guanine nucleotide exchange factor 39
153527	5,11E-02	1,29E+00	3,97E-02	0,0494	-2,0567431	-0,10152757	4977,57	ZMAT2	zinc finger matrin-type 2
105370756	8,35E-01	7,83E-02	8,11E-01	0,4259	-0,2386075	-0,10161691	16,26	LOC105370	uncharacterized LOC105370756
359948	5,27E-02	1,28E+00	4,09E-02	0,0498	-2,0440559	-0,10169597	2552,29	IRF2BP2	interferon regulatory factor 2 binding protein 2
729338	8,38E-01	7,68E-02	8,15E-01	0,4348	-0,2339839	-0,10174709	16,35	CETN4P	centrin 4, pseudogene
55717	4,91E-02	1,31E+00	3,80E-02	0,0491	-2,0745507	-0,10180156	2588,06	WDR11	WD repeat domain 11
22938	8,57E-02	1,07E+00	6,85E-02	0,0559	-1,8218085	-0,10184057	6251,49	SNW1	SNW domain containing 1
84504	4,74E-01	3,24E-01	4,33E-01	0,1299	-0,784509	-0,101912	185,36	NKX6-2	NK6 homeobox 2
23216	4,49E-02	1,35E+00	3,46E-02	0,0482	-2,1130726	-0,10192934	2908,22	TBC1D1	TBC1 domain family member 1
101929145	5,00E-01	3,01E-01	4,58E-01	0,1373	-0,7422683	-0,10193668	166,52	PPP3CB-AS	PPP3CB antisense RNA 1 (head to head)
2166	8,03E-01	9,53E-02	7,76E-01	0,3583	-0,2848637	-0,10206004	22,71	FAAH	fatty acid amide hydrolase
64784	1,61E-01	7,93E-01	1,33E-01	0,068	-1,5007048	-0,10206109	925,84	CRTC3	CREB regulated transcription coactivator 3
340385	4,14E-01	3,83E-01	3,72E-01	0,1145	-0,8919223	-0,1021509	256,8	ZNF517	zinc finger protein 517
113218500	8,89E-02	1,05E+00	7,13E-02	0,0566	-1,8038007	-0,10217289	3984,46	MIR10393	microRNA 10393
100652999	3,80E-01	4,20E-01	3,39E-01	0,1069	-0,956888	-0,1022982	313,16	LOC100652	uncharacterized LOC100652999
23066	7,85E-01	1,05E-01	7,57E-01	0,3308	-0,3092828	-0,10231246	28,2	CAND2	cullin associated and neddylation dissociated 2 (putative)
3632	1,61E-01	7,93E-01	1,34E-01	0,0683	-1,4996222	-0,10248496	1091,45	INPP5A	inositol polyphosphate-5-phosphatase A
3835	3,48E-02	1,46E+00	2,64E-02	0,0463	-2,2203505	-0,10279165	4044,1	KIF22	kinesin family member 22
26589	1,40E-01	8,54E-01	1,16E-01	0,0654	-1,5732014	-0,10281039	1140,79	MRPL46	mitochondrial ribosomal protein L46
284618	6,03E-02	1,22E+00	4,73E-02	0,052	-1,9838224	-0,10309506	2010,52	RUSC1-AS1	RUSC1 antisense RNA 1
5836	2,18E-02	1,66E+00	1,61E-02	0,0429	-2,4056174	-0,10319701	7257,39	PYGL	glycogen phosphorylase L
11274	6,17E-01	2,10E-01	5,79E-01	0,1859	-0,5551092	-0,10322196	93,3	USP18	ubiquitin specific peptidase 18
10146	3,18E-02	1,50E+00	2,40E-02	0,0458	-2,256979	-0,1033348	15019,1	G3BP1	G3BP stress granule assembly factor 1
2961	9,78E-02	1,01E+00	7,88E-02	0,0588	-1,7575406	-0,10342627	1628,25	GTF2E2	general transcription factor IIE subunit 2
5162	2,09E-02	1,68E+00	1,54E-02	0,0427	-2,4221344	-0,10347764	5821,14	PDHB	pyruvate dehydrogenase E1 subunit beta
101927765	5,11E-01	2,92E-01	4,69E-01	0,143	-0,724017	-0,10352752	153,4	COA6-AS1	COA6 antisense RNA 1
441208	8,16E-01	8,83E-02	7,90E-01	0,39	-0,2657265	-0,10363368	20,92	ZNRF2P1	zinc and ring finger 2 pseudogene 1
55073	1,44E-01	8,42E-01	1,19E-01	0,0666	-1,5587171	-0,10377385	929,76	LRRC37A4P	leucine rich repeat containing 37 member A4, pseudogene
7251	1,93E-02	1,71E+00	1,42E-02	0,0423	-2,4529435	-0,10377414	4828,62	TSG101	tumor susceptibility 101
105379154	8,79E-01	5,60E-02	8,59E-01	0,586	-0,1770942	-0,10378223	8,65	LOC105379	uncharacterized LOC105379154
105372296	8,28E-01	8,20E-02	8,04E-01	0,4176	-0,2485822	-0,10380665	17,09	LOC105372	uncharacterized LOC105372296
107984654	7,43E-01	1,29E-01	7,12E-01	0,281	-0,3694001	-0,10381315	38,89	LOC107984	uncharacterized LOC107984654
56548	3,77E-01	4,24E-01	3,36E-01	0,1082	-0,9614854	-0,10403578	277,48	CHST7	carbohydrate sulfotransferase 7
8463	2,20E-01	6,58E-01	1,87E-01	0,079	-1,3182244	-0,10415315	674,12	TEAD2	TEA domain transcription factor 2
100132832	7,29E-01	1,37E-01	6,97E-01	0,2677	-0,3890965	-0,10417895	42,8	PMS2P9	PMS1 homolog 2, mismatch repair system component pseudogene 9
55339	2,83E-02	1,55E+00	2,13E-02	0,0453	-2,3031706	-0,10423799	3504,39	WDR33	WD repeat domain 33
64222	7,19E-02	1,14E+00	5,69E-02	0,0548	-1,9042174	-0,10432029	1971,88	TOR3A	torsin family 3 member A
6601	3,50E-02	1,46E+00	2,66E-02	0,0471	-2,2170002	-0,10445936	3610,95	SMARCC2	SWI/SNF related, matrix associated, actin dependent regulator of chromatin subfamily c member 2
27069	3,36E-02	1,47E+00	2,55E-02	0,0468	-2,234501	-0,10459427	10537,7	GHITM	growth hormone inducible transmembrane protein
51646	1,26E-01	9,00E-01	1,03E-01	0,0643	-1,6293415	-0,1047723	2208,86	YPEL5	yippee like 5
4803	4,43E-01	3,54E-01	4,02E-01	0,1251	-0,8386489	-0,10492282	230,48	NGF	nerve growth factor
7474	5,28E-01	2,77E-01	4,87E-01	0,151	-0,6950161	-0,10497625	141,85	WNT5A	Wnt family member 5A
23332	4,90E-02	1,31E+00	3,79E-02	0,0506	-2,0756053	-0,10500401	2382,81	CLASP1	cytoplasmic linker associated protein 1
105378230	2,90E-01	5,38E-01	2,52E-01	0,0917	-1,1454629	-0,1050372	416,42	LOC105378	uncharacterized LOC105378230
64221	2,14E-01	6,70E-01	1,81E-01	0,0786	-1,3371147	-0,10515977	928,6	ROBO3	roundabout guidance receptor 3
112268213	8,51E-01	7,01E-02	8,29E-01	0,4867	-0,2161175	-0,10518054	12,31	LOC112268	213
389856	3,93E-01	4,06E-01	3,51E-01	0,1132	-0,9317196	-0,10542794	312,14	USP27X	ubiquitin specific peptidase 27 X-linked
8460	1,94E-01	7,12E-01	1,63E-01	0,0757	-1,3939467	-0,10554998	771,39	TPST1	tyrosylprotein sulfotransferase 1
111240474	5,96E-01	2,25E-01	5,57E-01	0,1801	-0,5871278	-0,10572641	94,05	CRYZL2P-S	CRYZL2P-SEC16B readthrough
100507436	5,21E-02	1,28E+00	4,05E-02	0,0518	-2,0483528	-0,10604985	2649,42	MICA	MHC class I polypeptide-related sequence A
440600	5,91E-01	2,28E-01	5,51E-01	0,1781	-0,5956317	-0,10607458	94,49	RBM15-AS1	RBM15 antisense RNA 1
339263	6,82E-02	1,17E+00	5,38E-02	0,0551	-1,9285017	-0,10625871	1659,75	LINC02693	long intergenic non-protein coding RNA 2693
29880	1,33E-01	8,76E-01	1,09E-01	0,0664	-1,6008769	-0,10627228	1354	ALG5	ALG5 dolichyl-phosphate beta-glucosyltransferase
84159	2,66E-01	5,75E-01	2,29E-01	0,0884	-1,2022596	-0,1063126	582,11	ARID5B	AT-rich interaction domain 5B
5533	1,98E-01	7,03E-01	1,67E-01	0,077	-1,3815312	-0,10633944	631,49	PPP3CC	protein phosphatase 3 catalytic subunit gamma
56683	8,12E-02	1,09E+00	6,47E-02	0,0577	-1,8472458	-0,10650852	1354,46	CFAP298	cilia and flagella associated protein 298
9794	4,13E-02	1,38E+00	3,17E-02	0,0496	-2,1484037	-0,1066573	3007,2	MAML1	mastermind like transcriptional coactivator 1
100506922	7,34E-01	1,34E-01	7,03E-01	0,2801	-0,3817238	-0,10691048	39,43	MAP3K2-DT	MAP3K2 divergent transcript
55742	8,29E-03	2,08E+00	5,90E-03	0,0389	-2,7533329	-0,10698895	6946,43	PARVA	parvin alpha
440193	6,70E-02	1,17E+00	5,28E-02	0,0553	-1,9362018	-0,1070038	1875,74	CCDC88C	coiled-coil domain containing 88C
387628	5,96E-01	2,25E-01	5,57E-01	0,1825	-0,5869725	-0,10713305	89,57	FGF7P6	fibroblast growth factor 7 pseudogene 6
103611081	5,34E-01	2,72E-01	4,93E-01	0,1568	-0,6850965	-0,10741189	126,91	LOC103611	replaced by ID 399979
10788	7,68E-01	1,15E-01	7,38E-01	0,3217	-0,3339943	-0,10743908	33,88	IQGAP2	IQ motif containing GTPase activating protein 2
22905	8,80E-02	1,06E+00	7,05E-02	0,0594	-1,8089202	-0,10749992	1500,29	EPN2	epsin 2
206358	1,03E-01	9,87E-01	8,36E-02	0,0622	-1,7304427	-0,10756807	1203,56	SLC36A1	solute carrier family 36 member 1
84226	6,94E-01	1,59E-01	6,60E-01	0,2448	-0,4394927	-0,10757351	51,44	C2orf16	chromosome 2 open reading frame 16
9733	2,78E-02	1,56E+00	2,09E-02	0,0467	-2,3102325	-0,10792964	4807,16	SART3	spliceosome associated factor 3, U4/U6 recycling protein
64969	3,72E-02	1,43E+00	2,84E-02	0,0494	-2,1916189	-0,10836131	3960,09	MRPS5	mitochondrial ribosomal protein S5
7531	4,86E-03	2,31E+00	3,38E-03	0,037	-2,9305259	-0,10837572	42494,69	YWHAE	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein epsilon
728586	7,15E-01	1,46E-01	6,82E-01	0,2651	-0,4090819	-0,10845639	41,61	CCDC192	coiled-coil domain containing 192
116039	6,38E-01	1,95E-01	6,01E-01	0,2079	-0,5232558	-0,10879613	70,47	OSR2	odd-skipped related transciption factor 2
55785	6,53E-02	1,19E+00	5,14E-02	0,0559	-1,947955	-0,10881425	1639,41	FGD6	FYVE, RhoGEF and PH domain containing 6
112268421	6,73E-01	1,72E-01	6,38E-01	0,2317	-0,4707425	-0,10909394	56,41	LOC112268	421
284408	6,20E-01	2,08E-01	5,82E-01	0,1989	-0,5498242	-0,10934611	75,6	ZNF790-AS1	ZNF790 antisense RNA 1
9191	1,03E-01	9,87E-01	8,33E-02	0,0631	-1,7320313	-0,10936303	1328,91	DEDD	death effector domain containing
9688	1,40E-02	1,85E+00	1,02E-02	0,0426	-2,5689468	-0,10947132	4077,91	NUP93	nucleoporin 93
9110	2,81E-02	1,55E+00	2,11E-02	0,0475	-2,3061153	-0,1095776	2581,89	MTMR4	myotubularin related protein 4
1368	3,98E-01	4,00E-01	3,56E-01	0,1189	-0,9221821	-0,10960275	232,03	CPM	carboxypeptidase M
100287722	3,56E-01	4,49E-01	3,15E-01	0,1093	-1,0038316	-0,10975231	274,51	AP4B1-AS1	AP4B1 antisense RNA 1
5727	2,26E-01	6,46E-01	1,92E-01	0,0842	-1,3040465	-0,10978864	505,8	PTCH1	patched 1
101928464	3,16E-01	5,00E-01	2,77E-01	0,1011	-1,0862868	-0,10984148	345,27	ZNF433-AS1	ZNF433 and ZNF878 antisense RNA 1
9467	3,64E-01	4,39E-01	3,23E-01	0,1114	-0,9878157	-0,11004788	278,36	SH3BP5	SH3 domain binding protein 5
57459	4,49E-02	1,35E+00	3,45E-02	0,0521	-2,1137143	-0,11013553	2590,24	GATAD2B	GATA zinc finger domain containing 2B
2632	1,18E-02	1,93E+00	8,49E-03	0,0419	-2,6318915	-0,1103964	6193,11	GBE1	1,4-alpha-glucan branching enzyme 1
23060	2,46E-02	1,61E+00	1,83E-02	0,0468	-2,3590846	-0,11040212	3396,38	ZNF609	zinc finger protein 609
10539	4,52E-02	1,34E+00	3,48E-02	0,0523	-2,1108152	-0,11049719	3999,56	GLRX3	glutaredoxin 3
100128569	4,74E-01	3,24E-01	4,32E-01	0,1408	-0,7849382	-0,11051344	160,2	TEKTIP1	tektin bundle interacting protein 1
105369344	7,04E-01	1,52E-01	6,70E-01	0,2596	-0,4258862	-0,11057386	48,69	LOC105369	uncharacterized LOC105369344
4217	1,43E-01	8,45E-01	1,18E-01	0,0707	-1,5640044	-0,1106493	872,72	MAP3K5	mitogen-activated protein kinase kinase kinase 5
112724	1,67E-01	7,77E-01	1,39E-01	0,0748	-1,4802062	-0,11075679	662,38	RDH13	retinol dehydrogenase 13
840	4,78E-02	1,32E+00	3,70E-02	0,0533	-2,0858032	-0,11113383	1760,67	CASP7	caspase 7
23307	3,30E-02	1,48E+00	2,50E-02	0,0496	-2,241284	-0,11121881	2476,17	FKBP15	FKBP prolyl isomerase family member 15
7074	2,87E-01	5,42E-01	2,50E-01	0,0967	-1,1509407	-0,11123865	463,72	TIAM1	TIAM Rac1 associated GEF 1
224	3,39E-02	1,47E+00	2,57E-02	0,05	-2,2301438	-0,11151972	2356,54	ALDH3A2	aldehyde dehydrogenase 3 family member A2
26523	4,84E-02	1,32E+00	3,74E-02	0,0538	-2,0808394	-0,11194964	1655,29	AGO1	argonaute RISC component 1
64108	6,90E-01	1,61E-01	6,55E-01	0,2507	-0,4468464	-0,11204041	48,5	RTP4	receptor transporter protein 4
5906	3,89E-02	1,41E+00	2,97E-02	0,0516	-2,1739842	-0,11208647	1921,75	RAP1A	RAP1A, member of RAS oncogene family
727910	4,49E-01	3,48E-01	4,08E-01	0,1354	-0,828184	-0,11214083	176,75	TLCD2	TLC domain containing 2
5432	1,49E-02	1,83E+00	1,08E-02	0,0441	-2,5480727	-0,11243819	3609,98	POLR2C	RNA polymerase II subunit C
110091775	1,25E-01	9,03E-01	1,02E-01	0,0688	-1,6340686	-0,11244206	1013,24	CFAP298-TC	CFAP298-TCP10L readthrough
9093	2,29E-02	1,64E+00	1,70E-02	0,0472	-2,3858806	-0,1125612	2908,14	DNAJA3	DnaJ heat shock protein family (Hsp40) member A3
7335	2,03E-02	1,69E+00	1,49E-02	0,0463	-2,4336498	-0,11261686	7307,39	UBE2V1	ubiquitin conjugating enzyme E2 V1

22834	1,40E-01	8,54E-01	1,15E-01	0,0716	-1,5747084	-0,11279039	868,5	ZNF652	zinc finger protein 652
1827	2,43E-02	1,61E+00	1,81E-02	0,0478	-2,364104	-0,11289323	3193,98	RCAN1	regulator of calcineurin 1
79091	2,87E-01	5,42E-01	2,49E-01	0,0985	-1,1518471	-0,11343356	350,85	METTL22	methyltransferase 22, Kin17 lysine
5663	1,33E-02	1,88E+00	9,62E-03	0,0439	-2,589155	-0,11355632	4182,78	PSEN1	presenilin 1
5478	5,19E-03	2,28E+00	3,62E-03	0,0391	-2,909779	-0,11378134	87939,91	PPIA	peptidylprolyl isomerase A
9677	1,57E-01	8,04E-01	1,30E-01	0,0753	-1,5125952	-0,11396574	635,02	PPIP5K1	diphosphoinositol pentakisphosphate kinase 1
64145	3,27E-02	1,49E+00	2,48E-02	0,0509	-2,2447865	-0,11433381	1959,19	RBSN	rabenosyn, RAB effector
27158	1,05E-01	9,79E-01	8,53E-02	0,0665	-1,7205312	-0,11440639	1650,83	NDOR1	NADPH dependent diflavin oxidoreductase 1
126248	7,06E-01	1,51E-01	6,73E-01	0,2711	-0,4224043	-0,11450031	39,58	WDR88	WD repeat domain 88
3171	6,47E-01	1,89E-01	6,10E-01	0,2251	-0,5100355	-0,11482529	60,42	FOXA3	forkhead box A3
2073	1,17E-01	9,32E-01	9,52E-02	0,0688	-1,6685381	-0,11485839	879,11	ERCC5	ERCC excision repair 5, endonuclease
84793	5,55E-01	2,56E-01	5,15E-01	0,1763	-0,6515097	-0,11489074	104,29	FOXD2-AS1	FOXD2 adjacent opposite strand RNA 1
245973	3,12E-02	1,51E+00	2,35E-02	0,0508	-2,2649369	-0,11513501	2871,08	ATP6V1C2	ATPase H+ transporting V1 subunit C2
10186	8,62E-02	1,06E+00	6,89E-02	0,0634	-1,8193717	-0,11528058	1201,06	LHFPL6	LHFPL tetraspan subfamily member 6
440584	7,75E-01	1,11E-01	7,46E-01	0,3563	-0,3241228	-0,1154847	22,92	SLC2A1-DT	SLC2A1 divergent transcript
102724238	4,99E-01	3,02E-01	4,57E-01	0,1556	-0,7437099	-0,11573273	126,19	FAM88C	family with sequence similarity 88 member C
6616	8,51E-01	7,01E-02	8,29E-01	0,5383	-0,215988	-0,1162688	10,58	SNAP25	synaptosome associated protein 25
80731	8,37E-01	7,73E-02	8,14E-01	0,4956	-0,2347955	-0,11636712	12,85	THSD7B	thrombospondin type 1 domain containing 7B
5379	2,62E-01	5,82E-01	2,26E-01	0,0962	-1,2113117	-0,1164924	362,21	PMS2P1	PMS1 homolog 2, mismatch repair system component pseudogene 1
84678	1,46E-02	1,84E+00	1,06E-02	0,0456	-2,5543246	-0,11653179	3001,23	KDM2B	lysine demethylase 2B
221481	7,33E-01	1,35E-01	7,01E-01	0,3038	-0,3842759	-0,11676208	31,67	ARMC12	armadillo repeat containing 12
284086	3,83E-01	4,17E-01	3,42E-01	0,123	-0,9501505	-0,11690008	222,19	NEK8	NIMA related kinase 8
105378616	7,54E-01	1,23E-01	7,24E-01	0,3312	-0,3533934	-0,11703628	27,81	TAF12-DT	TAF12 divergent transcript
7485	2,48E-01	6,06E-01	2,13E-01	0,0942	-1,2461533	-0,11735078	451,24	GET1	guided entry of tail-anchored proteins factor 1
192668	7,73E-01	1,12E-01	7,44E-01	0,3606	-0,3265091	-0,11774406	22,46	CYS1	cystin 1
124637	1,96E-01	7,08E-01	1,66E-01	0,0855	-1,3865982	-0,11851524	497,07	CYB5D1	cytochrome b5 domain containing 1
51275	1,12E-01	9,51E-01	9,09E-02	0,0705	-1,6904521	-0,1192176	784,2	MAPKAPK5-	MAPKAPK5 antisense RNA 1
64427	7,26E-02	1,14E+00	5,75E-02	0,0628	-1,8997609	-0,11932074	1194,34	TTC31	tetratricopeptide repeat domain 31
22848	2,23E-02	1,65E+00	1,66E-02	0,0498	-2,3965157	-0,11944816	2669,99	AAK1	AP2 associated kinase 1
23163	4,29E-02	1,37E+00	3,30E-02	0,056	-2,1324533	-0,11945825	2501,32	GGA3	golgi associated, gamma adaptin ear containing, ARF binding protein 3
49856	8,75E-02	1,06E+00	7,00E-02	0,0659	-1,8120267	-0,11949801	1182,65	WRAP73	WD repeat containing, antisense to TP73
10614	4,72E-03	2,33E+00	3,28E-03	0,0408	-2,9400838	-0,11987164	5550,6	HEXIM1	HEXIM P-TEFb complex subunit 1
105373354	5,33E-01	2,73E-01	4,91E-01	0,1742	-0,6881665	-0,11989238	102,92	TMEM18-DT	TMEM18 divergent transcript
2648	4,40E-02	1,36E+00	3,39E-02	0,0565	-2,1217071	-0,11994917	3889,25	KAT2A	lysine acetyltransferase 2A
27068	6,19E-02	1,21E+00	4,86E-02	0,061	-1,9724404	-0,12035713	2281,31	PPA2	inorganic pyrophosphatase 2
3020	2,42E-03	2,62E+00	1,64E-03	0,0382	-3,1492767	-0,12038345	8093,9	H3-3A	H3.3 histone A
64760	8,70E-02	1,06E+00	6,96E-02	0,0665	-1,8146945	-0,12067355	959,9	FHIP2B	FHF complex subunit HOOK interacting protein 2B
100506380	2,73E-01	5,64E-01	2,36E-01	0,1019	-1,1845924	-0,12068683	319,95	RNF32-DT	RNF32 divergent transcript
899	1,83E-02	1,74E+00	1,34E-02	0,0488	-2,4720641	-0,12069013	2540,49	CCNF	cyclin F
51123	1,57E-02	1,80E+00	1,15E-02	0,0477	-2,5279228	-0,12069894	3616,96	ZNF706	zinc finger protein 706
255758	5,64E-01	2,49E-01	5,24E-01	0,1895	-0,6370235	-0,12073663	91,46	DYNLT2B	dynein light chain Tctex-type 2B
84808	5,93E-01	2,27E-01	5,54E-01	0,2042	-0,5920603	-0,12089588	71,03	PERM1	PPARGC1 and ESRR induced regulator, muscle 1
6602	2,25E-02	1,65E+00	1,67E-02	0,0506	-2,3936177	-0,12115233	3760,69	SMARCD1	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 1
5058	6,37E-02	1,20E+00	5,01E-02	0,0619	-1,9591486	-0,12134149	1388,58	PAK1	p21 (RAC1) activated kinase 1
3139	8,37E-01	7,73E-02	8,14E-01	0,5154	-0,2356339	-0,12143409	128,69	HLA-L	major histocompatibility complex, class I, L (pseudogene)
55344	3,01E-01	5,21E-01	2,63E-01	0,1084	-1,1203287	-0,12144055	344,72	PLCXD1	phosphatidylinositol specific phospholipase C X domain containing 1
2898	3,70E-01	4,32E-01	3,29E-01	0,1247	-0,9752462	-0,12164484	210,82	GRIK2	glutamate ionotropic receptor kainate type subunit 2
152503	1,55E-02	1,81E+00	1,13E-02	0,0481	-2,5337955	-0,12197954	2535,37	SH3D19	SH3 domain containing 19
8720	3,62E-03	2,44E+00	2,49E-03	0,0404	-3,024807	-0,12210445	7713,21	MBTPS1	membrane bound transcription factor peptidase, site 1
2842	4,62E-01	3,35E-01	4,21E-01	0,1517	-0,8053975	-0,12214669	137,08	GPR19	G protein-coupled receptor 19
1031	1,54E-02	1,81E+00	1,12E-02	0,0482	-2,536073	-0,12216723	3137,85	CDKN2C	cyclin dependent kinase inhibitor 2C
3423	1,97E-03	2,71E+00	1,33E-03	0,0381	-3,2102938	-0,12223624	9787,95	IDS	iduronate 2-sulfatase
107985236	2,24E-01	6,50E-01	1,91E-01	0,0935	-1,3081596	-0,12225229	376,78	LOC107985	uncharacterized LOC107985236
58505	1,61E-02	1,79E+00	1,18E-02	0,0486	-2,5195378	-0,12248105	4527,24	OSTC	oligosaccharyltransferase complex non-catalytic subunit
80895	1,18E-01	9,28E-01	9,64E-02	0,0737	-1,6626576	-0,12249401	943,28	ILKAP	ILK associated serine/threonine phosphatase
9989	1,81E-03	2,74E+00	1,21E-03	0,0379	-3,2353633	-0,12260099	8911,77	PPP4R1	protein phosphatase 4 regulatory subunit 1
222068	8,31E-03	2,08E+00	5,92E-03	0,0446	-2,7523437	-0,12263619	4435,94	TMED4	transmembrane p24 trafficking protein 4
112268058	6,67E-01	1,76E-01	6,31E-01	0,255	-0,481015	-0,12264973	45,98	LOC112268058	
23269	2,27E-02	1,64E+00	1,68E-02	0,0513	-2,3902979	-0,12265608	2820,25	MGA	MAX dimerization protein MGA
8000	8,36E-01	7,78E-02	8,13E-01	0,5181	-0,2372004	-0,12289083	11,72	PSCA	prostate stem cell antigen
114926	2,28E-01	6,42E-01	1,94E-01	0,0947	-1,2985154	-0,1230008	386,64	SMIM19	small integral membrane protein 19
107984826	8,27E-01	8,25E-02	8,02E-01	0,4935	-0,2503321	-0,12354203	11,83	LOC107984826	
389072	1,65E-01	7,83E-01	1,37E-01	0,0833	-1,486372	-0,12375741	515,58	PLEKHM3	pleckstrin homology domain containing M3
55108	2,92E-02	1,53E+00	2,19E-02	0,0541	-2,2915936	-0,1239038	2459,08	BSDC1	BSD domain containing 1
100505894	5,79E-01	2,37E-01	5,39E-01	0,2018	-0,6140455	-0,12393379	72,53	TMEM161B-	TMEM161B divergent transcript
199223	5,92E-01	2,28E-01	5,53E-01	0,2087	-0,5939452	-0,12396528	68,65	TTC21A	tetratricopeptide repeat domain 21A
100506451	6,02E-01	2,20E-01	5,63E-01	0,2143	-0,5786321	-0,12400075	72,85	RASSF8-AS	RASSF8 antisense RNA 1
10946	3,29E-03	2,48E+00	2,26E-03	0,0406	-3,054353	-0,12406576	10974,07	SF3A3	splicing factor 3a subunit 3
401428	6,17E-01	2,10E-01	5,79E-01	0,2237	-0,5546513	-0,12408923	60,67	OR2A20P	olfactory receptor family 2 subfamily A member 20 pseudogene
23185	8,51E-03	2,07E+00	6,06E-03	0,0452	-2,7444251	-0,12415295	4787,5	LARP4B	La ribonucleoprotein 4B
9658	2,12E-01	6,74E-01	1,79E-01	0,0926	-1,3425247	-0,12429059	397,81	ZNF516	zinc finger protein 516
55081	3,21E-02	1,49E+00	2,43E-02	0,0552	-2,2528141	-0,12434828	1497,39	IFT57	intraflagellar transport 57
9265	1,93E-02	1,71E+00	1,42E-02	0,0507	-2,4522102	-0,1243757	2540,38	CYTH3	cytohesin 3
100506737	8,25E-01	8,35E-02	8,00E-01	0,4926	-0,2531766	-0,12471947	14,63	LINC01589	long intergenic non-protein coding RNA 1589
619563	6,07E-01	2,17E-01	5,69E-01	0,2188	-0,5700091	-0,12473816	64,49	SNORA7A	small nucleolar RNA, H/ACA box 7A
285958	7,45E-02	1,13E+00	5,91E-02	0,0662	-1,8874905	-0,12491657	1175,03	SNHG15	small nucleolar RNA host gene 15
10160	1,36E-02	1,87E+00	9,88E-03	0,0484	-2,5799459	-0,12495478	2789,82	FARP1	FERM, ARH/RhoGEF and pleckstrin domain protein 1
110806300	3,60E-01	4,44E-01	3,19E-01	0,1258	-0,9955295	-0,12525792	198,75	FLNC-AS1	FLNC antisense RNA 1
29774	8,33E-01	7,94E-02	8,10E-01	0,5202	-0,2408652	-0,12529425	11	POM121L9P	POM121 transmembrane nucleoporin like 9, pseudogene
100506325	5,77E-01	2,39E-01	5,37E-01	0,203	-0,6175062	-0,12535315	71,93	SP2-AS1	SP2 antisense RNA 1
118426	3,01E-01	5,21E-01	2,63E-01	0,1122	-1,1200393	-0,12566098	295,57	BORCS5	BLOC-1 related complex subunit 5
3915	2,22E-03	2,65E+00	1,49E-03	0,0396	-3,1757921	-0,12571516	21218,6	LAMC1	laminin subunit gamma 1
50854	3,05E-03	2,52E+00	2,08E-03	0,0408	-3,0784658	-0,1257463	7306,18	SNHG32	small nucleolar RNA host gene 32
79567	1,13E-02	1,95E+00	8,15E-03	0,0475	-2,6456457	-0,12578889	5095,95	RIPOR1	RHO family interacting cell polarization regulator 1
441376	4,33E-01	3,64E-01	3,91E-01	0,1469	-0,8570179	-0,12587291	145,05	AARD	alanine and arginine rich domain containing protein
2760	7,18E-03	2,14E+00	5,08E-03	0,0449	-2,8022121	-0,12592612	3984,93	GM2A	ganglioside GM2 activator
85019	1,23E-01	9,10E-01	1,01E-01	0,0768	-1,6412577	-0,12610346	707,07	TMEM241	transmembrane protein 241
100419583	2,50E-01	6,02E-01	2,15E-01	0,1018	-1,2407427	-0,12636735	320,02	LOC100419	ring finger protein 4 pseudogene
540	2,80E-01	5,53E-01	2,43E-01	0,1084	-1,1681998	-0,12663074	289,61	ATP7B	ATPase copper transporting beta
79070	3,10E-01	5,09E-01	2,71E-01	0,1152	-1,1007245	-0,1268202	256,68	POGLUT2	protein O-glucosyltransferase 2
10598	2,07E-03	2,68E+00	1,39E-03	0,0397	-3,19642	-0,1269048	8283,93	AHSA1	activator of HSP90 ATPase activity 1
107984875	6,45E-01	1,90E-01	6,08E-01	0,2477	-0,5125528	-0,12696481	48,34	ZNF747-DT	ZNF747 divergent transcript
23509	1,45E-03	2,84E+00	9,63E-04	0,0385	-3,3012316	-0,12702738	11518,73	POFUT1	protein O-fucosyltransferase 1
645958	7,02E-01	1,54E-01	6,69E-01	0,2968	-0,4280807	-0,12705213	34,38	RPS18P9	ribosomal protein S18 pseudogene 9
1870	2,21E-01	6,56E-01	1,87E-01	0,0965	-1,3180142	-0,12712499	382,07	E2F2	E2F transcription factor 2
100270746	6,00E-01	2,22E-01	5,61E-01	0,219	-0,5808406	-0,12720584	67,19	LOC100270	uncharacterized LOC100270746
98	1,78E-01	7,50E-01	1,49E-01	0,0883	-1,441535	-0,1273233	529,62	ACYP2	acylphosphatase 2
84693	4,35E-01	3,62E-01	3,94E-01	0,1496	-0,8523231	-0,12753128	150,37	MCEE	methylmalonyl-CoA epimerase
7857	4,66E-01	3,32E-01	4,25E-01	0,1597	-0,7986191	-0,12756625	121,16	SCG2	secretogranin II
105372497	8,22E-01	8,51E-02	7,97E-01	0,496	-0,2574305	-0,12769588	11,85	LOC105372	uncharacterized LOC105372497
463	5,64E-02	1,25E+00	4,40E-02	0,0634	-2,0140582	-0,12771478	1288,99	ZFHX3	zinc finger homeobox 3
6929	1,69E-02	1,77E+00	1,23E-02	0,0511	-2,5019901	-0,12791723	2549,24	TCF3	transcription factor 3
10972	4,05E-03	2,39E+00	2,80E-03	0,0428	-2,9889684	-0,12807337	11655,83	TMED10	transmembrane p24 trafficking protein 10
57466	1,57E-02	1,80E+00	1,14E-02	0,0506	-2,5293866	-0,12809533	3371,34	SCAF4	SR-related CTD associated factor 4
3209	7,35E-01	1,34E-01	7,03E-01	0,3368	-0,3813246	-0,12842745	25,7	HOXA13	homeobox A13
105378756	6,97E-01	1,57E-01	6,63E-01	0,2952	-0,435398	-0,12852346	33,93	FGGY-DT	FGGY divergent transcript
25901	1,53E-01	8,15E-01	1,27E-01	0,0843	-1,5277345	-0,1287646	528,62	CCDC28A	coiled-coil domain containing 28A
344558	1,30E-01	8,86E-01	1,06E-01	0,0798	-1,6142315	-0,12878498	595,47	SH3RF3	SH3 domain containing ring finger 3
9962	2,14E-02	1,67E+00	1,58E-02	0,0535	-2,4127416	-0,12899646	1864,79	SLC23A2	solute carrier family 23 member 2
4281	1,77E-02	1,75E+00	1,30E-02	0,052	-2,4831574	-0,12905575	2125,25	MID1	midline 1
400793	2,21E-01	6,56E-01	1,88E-01	0,098	-1,3178911	-0,12909683	342,38	C1orf226	chromosome 1 open reading frame 226
2547	4,14E-04	3,38E+00	2,64E-04	0,0354	-3,6485315	-0,12926581	32749,15	XRCC6	X-ray repair cross complementing 6
9698	6,80E-03	2,17E+00	4,80E-03	0,0459	-2,8202892	-0,12949236	4990,19	PUM1	pumilio RNA binding family member 1
140825	7,97E-01	9,85E-02	7,69E-01	0,4408	-0,2939724	-0,12957663	16,29	NEURL2	neuralized E3 ubiquitin protein ligase 2
144811	5,56E-02	1,25E+00	4,34E-02	0,0642	-2,0198916	-0,12959902	988,09	LACC1	laccase domain containing 1
26781	5,36E-01	2,71E-01	4,94E-01	0,1899	-0,6832344	-0,12971575	90,27	SNORA67	small nucleolar RNA, H/ACA box 67
51373	4,53E-02	1,34E+00	3,49E-02	0,0616	-2,1092594	-0,13003152	2226,66	MRPS17	mitochondrial ribosomal protein S17
105373957	5,35E-01	2,72E-01	4,94E-01	0,1905	-0,6844686	-0,13037153	86,41	LOC105373	uncharacterized LOC105373957
9533	7,92E-03	2,10E+00	5,62E-03	0,0471	-2,7693085	-0,13041153	2849,94	POLR1C	RNA polymerase I and III subunit C
641776	8,17E-01	8,78E-02	7,91E-01	0,492	-0,2652456	-0,13051092	12,22	SPDYE14	speedy/RINGO cell cycle regulator family member E14

23132	5,23E-02	1,28E+00	4,07E-02	0,0638	-2,0466838	-0,1306068	1313,51	RAD54L2	RAD54 like 2
2020	5,76E-01	2,40E-01	5,36E-01	0,2118	-0,6190977	-0,13109787	67,52	EN2	engrailed homeobox 2
79600	1,11E-01	9,55E-01	9,02E-02	0,0774	-1,6940963	-0,13118964	611,46	TCTN1	tectonic family member 1
126298	3,03E-02	1,52E+00	2,28E-02	0,0577	-2,2764235	-0,13128425	1359,6	IRGQ	immunity related GTPase Q
1767	1,61E-01	7,93E-01	1,34E-01	0,0876	-1,5000756	-0,13141987	505,93	DNAH5	dynein axonemal heavy chain 5
3891	7,85E-01	1,05E-01	7,56E-01	0,4241	-0,3102264	-0,13157956	16,52	KRT85	keratin 85
100131755	3,31E-01	4,80E-01	2,92E-01	0,1247	-1,054822	-0,13158131	205,04	ARMCX4	armadillo repeat containing X-linked 4
9706	4,36E-01	3,61E-01	3,95E-01	0,155	-0,8511345	-0,13195853	143,7	ULK2	unc-51 like autophagy activating kinase 2
24145	9,41E-03	2,03E+00	6,74E-03	0,0487	-2,709491	-0,13201986	3660,08	PANX1	pannexin 1
7332	8,13E-03	2,09E+00	5,78E-03	0,0479	-2,7600157	-0,13227875	8094,4	UBE2L3	ubiquitin conjugating enzyme E2 L3
9344	2,65E-02	1,58E+00	1,98E-02	0,0568	-2,3303376	-0,13244449	2083,83	TAOK2	TAO kinase 2
2846	8,08E-01	9,26E-02	7,81E-01	0,4767	-0,2780595	-0,13254792	14,23	LPAR4	lysophosphatidic acid receptor 4
27134	8,10E-01	9,15E-02	7,84E-01	0,4845	-0,2739244	-0,13270998	13,47	TJP3	tight junction protein 3
401232	4,96E-01	3,05E-01	4,54E-01	0,1772	-0,7488844	-0,13272908	99,2	LINC01011	long intergenic non-protein coding RNA 1011
10461	5,80E-02	1,24E+00	4,53E-02	0,0664	-2,0014007	-0,13289862	989,41	MERTK	MER proto-oncogene, tyrosine kinase
8604	3,44E-02	1,46E+00	2,61E-02	0,0598	-2,2246193	-0,13292856	1234,47	SLC25A12	solute carrier family 25 member 12
93611	3,53E-01	4,52E-01	3,13E-01	0,1317	-1,0095266	-0,13298331	203,6	FBXO44	F-box protein 44
26817	8,31E-01	8,04E-02	8,07E-01	0,5455	-0,2438876	-0,13304401	10,66	SNORD34	small nucleolar RNA, C/D box 34
3705	1,88E-02	1,73E+00	1,39E-02	0,0542	-2,4609032	-0,13337826	4583,97	ITPK1	inositol-tetrakisphosphate 1-kinase
102465665	7,91E-01	1,02E-01	7,63E-01	0,4433	-0,3010046	-0,13342932	15,19	MIR7107	microRNA 7107
101927741	6,06E-02	1,22E+00	4,75E-02	0,0675	-1,9818862	-0,13368636	903,43	LOC101927	uncharacterized LOC101927741
57578	8,30E-01	8,09E-02	8,06E-01	0,5454	-0,2451392	-0,13369822	10,73	UNC79	unc-79 homolog, NALCN channel complex subunit
1154	6,21E-01	2,07E-01	5,83E-01	0,2442	-0,5495739	-0,13418503	52,49	CISH	cytokine inducible SH2 containing protein
5701	7,39E-03	2,13E+00	5,23E-03	0,0481	-2,7923594	-0,13440582	7051,16	PSMC2	proteasome 26S subunit, ATPase 2
119032	2,78E-01	5,56E-01	2,41E-01	0,1148	-1,1730319	-0,13469524	315,03	BORCS7	BLOC-1 related complex subunit 7
100133991	4,93E-01	3,07E-01	4,51E-01	0,1791	-0,7534131	-0,13494623	98,24	MAP3K14-A	MAP3K14 antisense RNA 1
84259	2,14E-02	1,67E+00	1,58E-02	0,0561	-2,4128708	-0,13531083	3308,59	DCUN1D5	defective in cullin neddylation 1 domain containing 5
1488	4,59E-03	2,34E+00	3,19E-03	0,0459	-2,9486506	-0,13543601	3955,38	CTBP2	C-terminal binding protein 2
101929664	6,49E-01	1,88E-01	6,12E-01	0,2671	-0,5071948	-0,1354513	41,34	HORMAD2-A	HORMAD2 and MTMR3 antisense RNA 1
5201	1,40E-03	2,85E+00	9,27E-04	0,0409	-3,311788	-0,13546009	5917,44	PFDN1	prefoldin subunit 1
100144603	8,16E-01	8,83E-02	7,91E-01	0,5106	-0,2654919	-0,13556416	11	CHKB-DT	CHKB divergent transcript
5611	5,93E-03	2,23E+00	4,16E-03	0,0473	-2,8654815	-0,13556824	3162,27	DNAJC3	DnaJ heat shock protein family (Hsp40) member C3
4439	1,84E-01	7,35E-01	1,55E-01	0,0954	-1,4223635	-0,13563674	371,61	MSH5	mutS homolog 5
56950	8,55E-03	2,07E+00	6,09E-03	0,0495	-2,7429974	-0,13567589	2558,55	SMYD2	SET and MYND domain containing 2
3037	8,82E-03	2,05E+00	6,29E-03	0,0497	-2,7322564	-0,13577803	2132,67	HAS2	hyaluronan synthase 2
375791	5,25E-01	2,80E-01	4,83E-01	0,1939	-0,7012363	-0,13593893	96,88	CYSRT1	cysteine rich tail 1
286223	8,09E-01	9,21E-02	7,83E-01	0,4937	-0,2754452	-0,13599497	12,66	C9orf47	replaced by ID 1903
10730	9,28E-04	3,03E+00	6,07E-04	0,0397	-3,4283886	-0,13612453	10989	YME1L1	YME1 like 1 ATPase
51478	2,30E-01	6,38E-01	1,96E-01	0,1053	-1,2932167	-0,13615321	338,57	HSD17B7	hydroxysteroid 17-beta dehydrogenase 7
5036	2,64E-04	3,58E+00	1,66E-04	0,0362	-3,7660824	-0,13617263	18845,22	PA2G4	proliferation-associated 2G4
285972	6,32E-01	1,99E-01	5,95E-01	0,2566	-0,5318159	-0,13644729	44,33	LINC00996	long intergenic non-protein coding RNA 996
7105	3,28E-02	1,48E+00	2,48E-02	0,0608	-2,2438038	-0,13653462	1703,18	TSPAN6	tetraspanin 6
554203	2,25E-01	6,48E-01	1,91E-01	0,1046	-1,3066044	-0,13667089	329,5	JPX	JPX transcript, XIST activator
112495	2,60E-02	1,59E+00	1,94E-02	0,0587	-2,3373948	-0,13709044	1619,82	GTF3C6	general transcription factor IIIC subunit 6
10290	2,81E-01	5,51E-01	2,44E-01	0,118	-1,1648577	-0,13741986	223,99	SPEG	striated muscle enriched protein kinase
284018	1,76E-01	7,54E-01	1,48E-01	0,095	-1,44791	-0,13749062	436,62	C17orf58	chromosome 17 open reading frame 58
55920	4,75E-04	3,32E+00	3,04E-04	0,0381	-3,6121339	-0,13749084	7881,02	RCC2	regulator of chromosome condensation 2
119391	3,93E-01	4,06E-01	3,52E-01	0,1477	-0,9309262	-0,13752312	151,67	GSTO2	glutathione S-transferase omega 2
90	5,55E-02	1,26E+00	4,33E-02	0,0681	-2,0210899	-0,13754504	992,56	ACVR1	activin A receptor type 1
93233	6,46E-01	1,90E-01	6,09E-01	0,2689	-0,5115861	-0,13754949	42,92	ODAD1	outer dynein arm docking complex subunit 1
55238	5,16E-02	1,29E+00	4,01E-02	0,0671	-2,0530693	-0,13768679	971,13	SLC38A7	solute carrier family 38 member 7
100131626	3,08E-01	5,11E-01	2,69E-01	0,1247	-1,1046445	-0,13774092	202,93	LOC100131	uncharacterized LOC100131626
105374493	8,43E-01	7,42E-02	8,20E-01	0,606	-0,2276805	-0,13798566	8,19	LOC105374	uncharacterized LOC105374493
8482	1,57E-02	1,80E+00	1,15E-02	0,0546	-2,5279107	-0,13806022	3126,47	SEMA7A	semaphorin 7A (John Milton Hagen blood group)
107987276	6,22E-01	2,06E-01	5,84E-01	0,2524	-0,5478569	-0,13830447	47,88	LOC107987276	
8193	2,14E-01	6,70E-01	1,82E-01	0,1036	-1,3357029	-0,13833996	315,92	DPF1	double PHD fingers 1
84902	2,74E-02	1,56E+00	2,05E-02	0,0599	-2,3165775	-0,13865755	1272,16	CEP89	centrosomal protein 89
22853	3,87E-02	1,41E+00	2,96E-02	0,0638	-2,1758392	-0,1387193	1485,64	LMTK2	lemur tyrosine kinase 2
105372481	1,64E-02	1,79E+00	1,20E-02	0,0553	-2,5117899	-0,13888312	1607,38	ERVK3-1	endogenous retrovirus group K3 member 1
9700	8,52E-03	2,07E+00	6,07E-03	0,0507	-2,7440386	-0,13908209	2471,21	ESPL1	extra spindle pole bodies like 1, separase
79683	1,73E-01	7,62E-01	1,45E-01	0,0955	-1,4587114	-0,13932138	400,19	ZDHHC14	zinc finger DHHC-type palmitoyltransferase 14
57545	5,68E-02	1,25E+00	4,44E-02	0,0694	-2,0103071	-0,139492	801,5	CC2D2A	coiled-coil and C2 domain containing 2A
10313	3,56E-04	3,45E+00	2,25E-04	0,0378	-3,6887817	-0,13955134	9479,61	RTN3	reticulon 3
6271	6,38E-01	1,95E-01	6,01E-01	0,2667	-0,5232106	-0,13956274	45,88	S100A1	S100 calcium binding protein A1
5356	1,53E-03	2,82E+00	1,02E-03	0,0425	-2,3843831	-0,13972313	5455,09	PLRG1	pleiotropic regulator 1
723788	2,89E-01	5,39E-01	2,51E-01	0,1219	-1,1479848	-0,13992012	212,05	MIG7	replaced by ID 8412
6832	8,62E-03	2,06E+00	6,14E-03	0,0511	-2,7400025	-0,14003504	2100,95	SUPV3L1	Suv3 like RNA helicase
105372282	2,21E-01	6,56E-01	1,87E-01	0,1064	-1,3180231	-0,14018183	295,62	LOC105372	uncharacterized LOC105372282
4860	1,70E-03	2,77E+00	1,14E-03	0,0431	-3,2537442	-0,14039621	6976,33	PNP	purine nucleoside phosphorylase
79157	2,99E-02	1,52E+00	2,26E-02	0,0617	-2,2807406	-0,14068371	1377,44	MFSD11	major facilitator superfamily domain containing 11
64858	2,04E-02	1,69E+00	1,51E-02	0,058	-2,4302942	-0,14085828	1739,53	DCLRE1B	DNA cross-link repair 1B
51062	2,03E-01	6,93E-01	1,71E-01	0,1035	-1,3674951	-0,14149451	311,45	ATL1	atlastin GTPase 1
2395	6,36E-02	1,20E+00	5,00E-02	0,0722	-1,9603287	-0,14158235	895,57	FXN	frataxin
78996	6,93E-03	2,16E+00	4,90E-03	0,0504	-2,8137827	-0,14173601	2362,89	CYREN	cell cycle regulator of NHEJ
515	1,92E-04	3,72E+00	1,19E-04	0,0369	-3,8478575	-0,14180113	10250,89	ATP5PB	ATP synthase peripheral stalk-membrane subunit b
100306951	3,04E-01	5,17E-01	2,65E-01	0,1275	-1,1138703	-0,14206499	194,77	PITPNA-AS1	PITPNA antisense RNA 1
100303755	1,64E-01	7,85E-01	1,37E-01	0,0955	-1,4888108	-0,1421521	377,85	PET117	PET117 cytochrome c oxidase chaperone
5987	1,05E-03	2,98E+00	6,89E-04	0,0419	-3,3938563	-0,1421673	5369,57	TRIM27	tripartite motif containing 27
80312	5,35E-01	2,72E-01	4,94E-01	0,2079	-0,6837235	-0,14217783	86,69	TET1	tet methylcytosine dioxygenase 1
112268098	5,33E-01	2,73E-01	4,92E-01	0,2069	-0,687812	-0,14229034	70,61	CNPY2-AS1	CNPY2 antisense RNA 1
387522	3,15E-03	2,50E+00	2,15E-03	0,0464	-3,0680944	-0,14234717	7741,25	PEDS1-UBE	PEDS1-UBE2V1 readthrough
84418	6,86E-02	1,16E+00	5,42E-02	0,074	-1,9253446	-0,14240702	903,21	CYSTM1	cysteine rich transmembrane module containing 1
192683	6,01E-02	1,22E+00	4,70E-02	0,0718	-1,9858918	-0,1425011	930,04	SCAMP5	secretory carrier membrane protein 5
25875	4,39E-02	1,36E+00	3,38E-02	0,0672	-2,1229563	-0,14255935	1130,38	LETMD1	LETM1 domain containing 1
4087	4,09E-03	2,39E+00	2,83E-03	0,0478	-2,985887	-0,14269509	3261,07	SMAD2	SMAD family member 2
317649	3,31E-01	4,80E-01	2,91E-01	0,1353	-1,055162	-0,14273434	168,97	EIF4E3	eukaryotic translation initiation factor 4E family member 3
340277	3,30E-01	4,81E-01	2,90E-01	0,1349	-1,0579226	-0,14274001	180,85	FAM221A	family with sequence similarity 221 member A
140901	1,15E-02	1,94E+00	8,28E-03	0,0541	-2,6404847	-0,14278649	1624,61	STK35	serine/threonine kinase 35
347240	2,50E-02	1,60E+00	1,86E-02	0,0608	-2,3531334	-0,14300094	1326,95	KIF24	kinesin family member 24
8667	4,61E-04	3,34E+00	2,95E-04	0,0396	-3,6198349	-0,14322286	14772,01	EIF3H	eukaryotic translation initiation factor 3 subunit H
23276	1,19E-02	1,92E+00	8,56E-03	0,0545	-2,62897	-0,14327054	1829,68	KLHL18	kelch like family member 18
11269	1,31E-02	1,88E+00	9,51E-03	0,0553	-2,5933313	-0,14349463	1678,21	DDX19B	DEAD-box helicase 19B
9394	2,66E-02	1,58E+00	1,99E-02	0,0616	-2,3285734	-0,14353078	1144,95	HS6ST1	heparan sulfate 6-O-sulfotransferase 1
147700	8,60E-02	1,07E+00	6,87E-02	0,0789	-1,820308	-0,1436544	634,56	KLC3	kinesin light chain 3
7727	1,22E-01	9,14E-01	9,98E-02	0,0873	-1,6456856	-0,14368599	460,92	ZNF174	zinc finger protein 174
100505738	2,15E-01	6,68E-01	1,83E-01	0,1082	-1,3318705	-0,14410729	323,34	MIR4458HG	MIR4458 host gene
79078	1,21E-01	9,17E-01	9,89E-02	0,0873	-1,6501199	-0,14413411	487,41	C1orf50	chromosome 1 open reading frame 50
152485	4,77E-02	1,32E+00	3,69E-02	0,0691	-2,0874197	-0,14421673	899,35	ZNF827	zinc finger protein 827
7265	5,86E-03	2,23E+00	4,11E-03	0,0503	-2,8698452	-0,14426164	4903,66	TTC1	tetratricopeptide repeat domain 1
54948	8,23E-03	2,08E+00	5,86E-03	0,0524	-2,7556822	-0,14435229	2617,79	MRPL16	mitochondrial ribosomal protein L16
326624	5,41E-01	2,67E-01	5,00E-01	0,2145	-0,6742229	-0,14461587	64,42	RAB37	RAB37, member RAS oncogene family
10550	1,28E-03	2,89E+00	8,48E-04	0,0435	-3,3367468	-0,1452755	4166,47	ARL6IP5	ADP ribosylation factor like GTPase 6 interacting protein 5
29982	1,42E-02	1,85E+00	1,03E-02	0,0567	-2,5644035	-0,14531464	1797,92	NRBF2	nuclear receptor binding factor 2
63917	1,31E-02	1,88E+00	9,50E-03	0,056	-2,5933966	-0,14534067	1724,26	GALNT11	polypeptide N-acetylgalactosaminyltransferase 11
117583	8,43E-02	1,07E+00	6,73E-02	0,0796	-1,8299556	-0,14561872	581,62	PARD3B	par-3 family cell polarity regulator beta
107984889	7,78E-01	1,09E-01	7,49E-01	0,4551	-0,3204219	-0,14581745	14,58	LOC107984	uncharacterized LOC107984889
5116	1,29E-03	2,89E+00	8,54E-04	0,0438	-3,33471	-0,14591375	4645,18	PCNT	pericentrin
3707	2,63E-01	5,80E-01	2,27E-01	0,1211	-1,2094183	-0,14646007	224,04	ITPKB	inositol-trisphosphate 3-kinase B
83478	3,87E-02	1,41E+00	2,95E-02	0,0673	-2,1761012	-0,14647486	1185,43	ARHGAP24	Rho GTPase activating protein 24
5927	7,04E-03	2,15E+00	4,98E-03	0,0522	-2,8085664	-0,14654512	1935,75	KDM5A	lysine demethylase 5A
117157	7,23E-01	1,41E-01	6,91E-01	0,3683	-0,3979691	-0,14658831	22,38	SH2D1B	SH2 domain containing 1B
7818	1,63E-03	2,79E+00	1,09E-03	0,0449	-3,2671007	-0,14667882	6759,86	DAP3	death associated protein 3
821	3,07E-04	3,51E+00	1,94E-04	0,0394	-3,7271451	-0,14677251	76899,74	CANX	calnexin
83641	7,35E-04	3,13E+00	4,77E-04	0,042	-3,4931415	-0,14678438	8609,46	FAM107B	family with sequence similarity 107 member B
81572	1,46E-02	1,84E+00	1,07E-02	0,0575	-2,5536292	-0,14684264	1333,84	PDRG1	p53 and DNA damage regulated 1
150094	1,21E-01	9,17E-01	9,91E-02	0,0891	-1,6491002	-0,1469769	489,95	SIK1	salt inducible kinase 1
22949	1,54E-02	1,81E+00	1,12E-02	0,0581	-2,5357763	-0,14721387	1804,1	PTGR1	prostaglandin reductase 1
54206	7,17E-04	3,14E+00	4,65E-04	0,0421	-3,4999081	-0,14730877	23139,1	ERRFI1	ERBB receptor feedback inhibitor 1
8844	1,06E-01	9,75E-01	8,55E-02	0,0858	-1,7194231	-0,14758787	565,21	KSR1	kinase suppressor of ras 1
57572	3,52E-02	1,45E+00	2,67E-02	0,0666	-2,2152515	-0,14763804	1074,63	DOCK6	dedicator of cytokinesis 6

25819	8,73E-02	1,06E+00	6,99E-02	0,0815	-1,8126796	-0,14766749	599,34	NOCT	nocturnin
100506157	6,65E-01	1,77E-01	6,29E-01	0,3055	-0,4834104	-0,14770091	33,03	SRP54-AS1	SRP54 antisense RNA 1
5621	4,41E-04	3,36E+00	2,81E-04	0,0407	-3,6319725	-0,14780247	13188,85	PRNP	prion protein
112611	1,38E-01	8,60E-01	1,14E-01	0,0935	-1,5815715	-0,14790554	380,38	RWDD2A	RWD domain containing 2A
3912	9,46E-03	2,02E+00	6,77E-03	0,0547	-2,7078153	-0,14801246	1726,94	LAMB1	laminin subunit beta 1
100528016	5,38E-04	3,27E+00	3,45E-04	0,0414	-3,5785706	-0,14818439	6526,54	TMX2-CTNN	TMX2-CTNND1 readthrough (NMD candidate)
83860	6,45E-02	1,19E+00	5,07E-02	0,076	-1,954006	-0,14857201	1380,56	TAF3	TATA-box binding protein associated factor 3
97	1,16E-01	9,36E-01	9,49E-02	0,0892	-1,6701866	-0,14905133	515,33	ACYP1	acylphosphatase 1
10436	3,71E-03	2,43E+00	2,55E-03	0,0495	-3,0168154	-0,14941298	2394,04	EMG1	EMG1 N1-specific pseudouridine methyltransferase
102723897	1,26E-01	9,00E-01	1,03E-01	0,0918	-1,6290054	-0,14954845	583,67	WASH9P	WAS protein family homolog 9, pseudogene
9695	9,82E-04	3,01E+00	6,43E-04	0,0438	-3,41262	-0,14961428	3750,1	EDEM1	ER degradation enhancing alpha-mannosidase like protein 1
283106	5,57E-02	1,25E+00	4,34E-02	0,0741	-2,019621	-0,14962167	765,4	CSNK2A3	casein kinase 2 alpha 3
414328	2,33E-01	6,33E-01	1,99E-01	0,1167	-1,2830365	-0,14966936	236,28	IDNK	IDNK gluconokinase
10201	1,27E-02	1,90E+00	9,18E-03	0,0575	-2,6052274	-0,14969871	1652,48	NME6	NME/NM23 nucleoside diphosphate kinase 6
100533952	6,06E-01	2,18E-01	5,68E-01	0,262	-0,5717065	-0,14979395	45,17	RBAK-RBAK	RBAK-RBAKDN readthrough
100500860	6,46E-01	1,90E-01	6,09E-01	0,2929	-0,5115159	-0,14982329	33,98	MIR3618	microRNA 3618
323	2,28E-03	2,64E+00	1,54E-03	0,0473	-3,167583	-0,14982771	4093,08	APBB2	amyloid beta precursor protein binding family B member 2
9687	7,21E-01	1,42E-01	6,88E-01	0,3737	-0,4011909	-0,14992654	21,82	GREB1	growth regulating estrogen receptor binding 1
55585	8,69E-04	3,06E+00	5,68E-04	0,0436	-3,4466412	-0,15027789	4374,18	UBE2Q1	ubiquitin conjugating enzyme E2 Q1
107987102	5,31E-01	2,75E-01	4,90E-01	0,2178	-0,6903417	-0,15035382	62,29	LOC107987	uncharacterized LOC107987102
64224	2,26E-02	1,65E+00	1,68E-02	0,0629	-2,3912721	-0,15041935	1271,91	HERPUD2	HERPUD family member 2
115509	5,65E-02	1,25E+00	4,41E-02	0,0747	-2,0127596	-0,15044075	687	ZNF689	zinc finger protein 689
11137	3,45E-04	3,46E+00	2,18E-04	0,0407	-3,6969464	-0,1504699	6407,51	PWP1	PWP1 homolog, endonuclein
10428	9,31E-03	2,03E+00	6,66E-03	0,0555	-2,7134999	-0,15052927	3978,01	CFDP1	craniofacial development protein 1
751071	2,99E-01	5,24E-01	2,61E-01	0,134	-1,1244072	-0,15065379	200,75	CSKMT	citrate synthase lysine methyltransferase
100500905	6,62E-02	1,18E+00	5,21E-02	0,0776	-1,9419591	-0,15070854	749,87	MIR3661	microRNA 3661
137835	1,19E-02	1,92E+00	8,61E-03	0,0576	-2,6270649	-0,15136425	1358,47	TMEM71	transmembrane protein 71
411	1,41E-02	1,85E+00	1,02E-02	0,059	-2,5676365	-0,15136788	1441,62	ARSB	arylsulfatase B
56123	2,34E-01	6,31E-01	2,00E-01	0,1184	-1,2804314	-0,15156586	229,62	PCDHB13	protocadherin beta 13
5588	6,27E-01	2,03E-01	5,89E-01	0,2806	-0,5402156	-0,15156696	37,9	PRKCQ	protein kinase C theta
2903	5,91E-01	2,28E-01	5,52E-01	0,2552	-0,5953575	-0,15192808	49,11	GRIN2A	glutamate ionotropic receptor NMDA type subunit 2A
10483	6,64E-04	3,18E+00	4,30E-04	0,0432	-3,5211703	-0,15223136	6463,98	SEC23B	SEC23 homolog B, COPII coat complex component
26003	8,22E-04	3,09E+00	5,36E-04	0,044	-3,4619554	-0,15226345	5946,63	GORASP2	golgi reassembly stacking protein 2
1415	7,81E-01	1,07E-01	7,52E-01	0,4819	-0,3161131	-0,15233411	12,51	CRYBB2	crystallin beta B2
100133205	5,26E-01	2,79E-01	4,85E-01	0,2181	-0,6986691	-0,152352	62,39	LINC00240	long intergenic non-protein coding RNA 240
55860	2,48E-03	2,61E+00	1,68E-03	0,0486	-3,1414623	-0,15257255	3294,43	ACTR10	actin related protein 10
9815	6,22E-04	3,21E+00	4,02E-04	0,0432	-3,5388789	-0,1527756	4498,38	GIT2	GIT ArfGAP 2
1376	3,05E-02	1,52E+00	2,30E-02	0,0673	-2,2735732	-0,15310441	1051,22	CPT2	carnitine palmitoyltransferase 2
105370687	9,73E-02	1,01E+00	7,84E-02	0,087	-1,7602132	-0,1531064	452,74	LOC105370	uncharacterized LOC105370687
2280	3,32E-04	3,48E+00	2,10E-04	0,0414	-3,7067791	-0,15344712	17326,43	FKBP1A	FKBP prolyl isomerase 1A
55964	7,47E-01	1,27E-01	7,16E-01	0,4223	-0,3639612	-0,15371091	16,41	SEPTIN3	septin 3
7979	2,60E-03	2,59E+00	1,76E-03	0,0492	-3,1275529	-0,15394447	3402,93	SEM1	SEM1 26S proteasome subunit
26960	1,12E-01	9,51E-01	9,09E-02	0,0911	-1,6907107	-0,15404309	410,24	NBEA	neurobeachin
442075	8,87E-02	1,05E+00	7,10E-02	0,0854	-1,8052764	-0,15425962	472,07	EMC3-AS1	EMC3 antisense RNA 1
29071	1,70E-02	1,77E+00	1,25E-02	0,0617	-2,4991239	-0,15427587	1590,47	C1GALT1C1	C1GALT1 specific chaperone 1
4129	6,52E-01	1,86E-01	6,15E-01	0,3068	-0,5030227	-0,15432749	31,96	MAOB	monoamine oxidase B
6897	2,23E-05	4,65E+00	1,30E-05	0,0354	-4,3602678	-0,15433813	21765,31	TARS1	threonyl-tRNA synthetase 1
340348	4,00E-01	3,98E-01	3,59E-01	0,1683	-0,917538	-0,15445261	110,14	TSPAN33	tetraspanin 33
79084	8,90E-04	3,05E+00	5,81E-04	0,045	-3,440124	-0,15464994	3294,94	WDR77	WD repeat domain 77
2519	7,02E-04	3,15E+00	4,55E-04	0,0441	-3,5058301	-0,1547148	5063,15	FUCA2	alpha-L-fucosidase 2
90025	2,24E-01	6,50E-01	1,91E-01	0,1184	-1,3075722	-0,15483944	250,87	UBE3D	ubiquitin protein ligase E3D
5867	3,52E-02	1,45E+00	2,68E-02	0,0701	-2,2150575	-0,15518377	856,1	RAB4A	RAB4A, member RAS oncogene family
23062	1,38E-03	2,86E+00	9,18E-04	0,0469	-3,3146645	-0,15530815	2846,74	GGA2	golgi associated, gamma adaptin ear containing, ARF binding protein 2
100528021	2,08E-01	6,82E-01	1,76E-01	0,115	-1,3518682	-0,15542606	239,8	ST20-MTHF	ST20-MTHFS readthrough
7158	2,13E-03	2,67E+00	1,43E-03	0,0488	-3,187726	-0,15564759	3321,75	TP53BP1	tumor protein p53 binding protein 1
100527963	2,13E-02	1,67E+00	1,58E-02	0,0645	-2,4145746	-0,15581011	976,27	PMF1-BGLA	PMF1-BGLAP readthrough
151525	1,96E-01	7,08E-01	1,65E-01	0,1123	-1,3882315	-0,1559387	303,73	WDSUB1	WD repeat, sterile alpha motif and U-box domain containing 1
64897	6,84E-03	2,16E+00	4,83E-03	0,0553	-2,8183349	-0,15596323	1731,61	C12orf43	chromosome 12 open reading frame 43
105372507	6,61E-01	1,80E-01	6,24E-01	0,3189	-0,4894846	-0,15610676	29,45	LOC105372	uncharacterized LOC105372507
819	1,56E-02	1,81E+00	1,14E-02	0,0619	-2,5310691	-0,15659728	1325,19	CAMLG	calcium modulating ligand
79726	4,77E-02	1,32E+00	3,69E-02	0,0752	-2,0871153	-0,15685052	740,85	WDR59	WD repeat domain 59
101926907	6,29E-01	2,01E-01	5,92E-01	0,2929	-0,53617	-0,15704478	33,87	LOC101926	uncharacterized LOC101926907
11162	1,58E-01	8,01E-01	1,32E-01	0,1043	-1,5079104	-0,15727076	306,19	NUDT6	nudix hydrolase 6
7869	8,86E-02	1,05E+00	7,10E-02	0,0871	-1,8054672	-0,15730276	515,5	SEMA3B	semaphorin 3B
689	1,17E-05	4,93E+00	6,73E-06	0,035	-4,50215	-0,15735398	33744,44	BTF3	basic transcription factor 3
101927492	2,58E-01	5,88E-01	2,22E-01	0,1288	-1,2219692	-0,15738547	205,12	MRPS9-AS1	MRPS9 antisense RNA 1
488	3,57E-05	4,45E+00	2,10E-05	0,037	-4,2538846	-0,15739248	20280,07	ATP2A2	ATPase sarcoplasmic/endoplasmic reticulum Ca2+ transporting 2
8492	8,28E-03	2,08E+00	5,89E-03	0,0572	-2,7539638	-0,157435	1725,56	PRSS12	serine protease 12
91	3,98E-02	1,40E+00	3,04E-02	0,0727	-2,1646094	-0,15745538	736,71	ACVR1B	activin A receptor type 1B
4190	2,52E-04	3,60E+00	1,58E-04	0,0417	-3,7779906	-0,15745871	7771,24	MDH1	malate dehydrogenase 1
221477	5,44E-05	4,26E+00	3,24E-05	0,038	-4,1560766	-0,157741	7601,21	C6orf89	chromosome 6 open reading frame 89
7297	2,77E-03	2,56E+00	1,88E-03	0,0508	-3,1079886	-0,15779248	4657,63	TYK2	tyrosine kinase 2
5891	2,04E-02	1,69E+00	1,51E-02	0,065	-2,430156	-0,15800354	1035,73	MOK	MOK protein kinase
56127	3,98E-01	4,00E-01	3,57E-01	0,1717	-0,9211045	-0,15818795	102,09	PCDHB9	protocadherin beta 9
100507266	5,68E-01	2,46E-01	5,28E-01	0,2508	-0,6311794	-0,15830001	48,76	STX18-AS1	STX18 antisense RNA 1 (head to head)
646278	4,63E-01	3,34E-01	4,22E-01	0,1971	-0,8033744	-0,15832144	79,45	PDCD6IPP2	PDCD6IP pseudogene 2
100302197	5,22E-01	2,82E-01	4,80E-01	0,2242	-0,7063642	-0,15836276	58,43	MIR1306	microRNA 1306
107985403	1,64E-01	7,85E-01	1,36E-01	0,1063	-1,4897509	-0,15837326	325,83	LOC107985	403
106144532	6,92E-01	1,60E-01	6,57E-01	0,357	-0,443679	-0,15838899	26,52	ARF4-AS1	ARF4 antisense RNA 1
26468	3,62E-01	4,41E-01	3,22E-01	0,1603	-0,9910801	-0,15883346	117,79	LHX6	LIM homeobox 6
51533	6,82E-02	1,17E+00	5,38E-02	0,0824	-1,9283711	-0,15891392	509,28	PHF7	PHD finger protein 7
2329	4,90E-01	3,10E-01	4,49E-01	0,2098	-0,7577632	-0,15901208	69,97	FMO4	flavin containing dimethylaniline monoxygenase 4
100996660	4,69E-01	3,29E-01	4,27E-01	0,2003	-0,794167	-0,15905789	73,82	LOC100996	uncharacterized LOC100996660
7301	7,22E-02	1,14E+00	5,72E-02	0,0836	-1,902138	-0,15909616	574,41	TYRO3	TYRO3 protein tyrosine kinase
105378828	6,78E-01	1,69E-01	6,43E-01	0,3433	-0,4639733	-0,15925901	24,53	CLCA4-AS1	CLCA4 antisense RNA 1
81875	2,77E-03	2,56E+00	1,89E-03	0,0513	-3,1074391	-0,15941508	2695,36	ISG20L2	interferon stimulated exonuclease gene 20 like 2
100505761	3,22E-01	4,92E-01	2,83E-01	0,1485	-1,0734781	-0,15946125	139,43	C10orf95-AS	C10orf95 antisense RNA 1
286527	2,89E-01	5,39E-01	2,51E-01	0,1391	-1,1467732	-0,15950647	158,94	TMSB15B	thymosin beta 15B
26986	2,46E-05	4,61E+00	1,43E-05	0,0368	-4,3385825	-0,15956035	71717,07	PABPC1	poly(A) binding protein cytoplasmic 1
7388	2,41E-04	3,62E+00	1,51E-04	0,0421	-3,7893703	-0,15958118	6340,6	UQCRH	ubiquinol-cytochrome c reductase hinge protein
92521	5,45E-03	2,26E+00	3,81E-03	0,0552	-2,8935572	-0,15967231	2005,66	SPECC1	sperm antigen with calponin homology and coiled-coil domains 1
100533975	1,95E-04	3,71E+00	1,21E-04	0,0416	-3,8435569	-0,15992025	6521,87	SLMO2-ATP	SLMO2-ATP5E readthrough
56957	5,36E-03	2,27E+00	3,74E-03	0,0552	-2,8991125	-0,16000256	1942,87	OTUD7B	OTU deubiquitinase 7B
57492	1,11E-02	1,95E+00	8,00E-03	0,0604	-2,6519545	-0,16008966	1173,59	ARID1B	AT-rich interaction domain 1B
27022	7,23E-01	1,41E-01	6,90E-01	0,4023	-0,3982518	-0,16019825	18,27	FOXD3	forkhead box D3
79031	2,89E-03	2,54E+00	1,97E-03	0,0518	-3,0951073	-0,16026516	4151,21	PDCL3	phosducin like 3
91893	8,70E-02	1,06E+00	6,96E-02	0,0884	-1,8144129	-0,16031372	448,91	FDXACB1	ferredoxin-fold anticodon binding domain containing 1
57332	5,62E-02	1,25E+00	4,39E-02	0,0796	-2,01523	-0,16031728	625,71	CBX8	chromobox 8
23196	2,56E-05	4,59E+00	1,49E-05	0,037	-4,3298484	-0,16038344	9199,13	FAM120A	family with sequence similarity 120A
389084	6,30E-01	2,01E-01	5,93E-01	0,2999	-0,534984	-0,16042884	34,04	SNORC	secondary ossification center associated regulator of chondrocyte maturation
105374333	7,31E-01	1,36E-01	6,99E-01	0,4147	-0,3868868	-0,16045107	18,13	LOC105374	uncharacterized LOC105374333
23248	1,46E-03	2,84E+00	9,67E-04	0,0486	-3,2998554	-0,16045446	3236,26	RPRD2	regulation of nuclear pre-mRNA domain containing 2
6819	6,08E-01	2,16E-01	5,69E-01	0,2821	-0,5691328	-0,16052954	40,23	SULT1C2	sulfotransferase family 1C member 2
12	5,93E-01	2,27E-01	5,55E-01	0,2717	-0,5909848	-0,16054155	40,65	SERPINA3	serpin family A member 3
84181	8,62E-04	3,06E+00	5,63E-04	0,0465	-3,4489819	-0,16054862	3335,78	CHD6	chromodomain helicase DNA binding protein 6
100630918	5,43E-01	2,65E-01	5,02E-01	0,2391	-0,6717365	-0,1606153	52,9	PARTICL	promoter of MAT2A antisense radiation-induced circulating long non-coding RNA
102723663	7,60E-02	1,12E+00	6,03E-02	0,0855	-1,8783828	-0,16062271	473,05	LOC102723	uncharacterized LOC102723663
285359	7,44E-01	1,28E-01	7,13E-01	0,4367	-0,3683323	-0,16083728	16,66	PDCL3P4	PDCL3 pseudogene 4
105374723	7,76E-01	1,10E-01	7,47E-01	0,4987	-0,3227031	-0,16092703	13,87	RAI14-DT	RAI14 divergent transcript
4291	2,52E-02	1,60E+00	1,88E-02	0,0686	-2,3495004	-0,16106512	998,31	MLF1	myeloid leukemia factor 1
55112	1,98E-02	1,70E+00	1,46E-02	0,0659	-2,4431367	-0,16106922	1063,06	DYNC2I1	dynein 2 intermediate chain 1
2941	1,92E-01	7,17E-01	1,62E-01	0,1153	-1,3986935	-0,16125003	295,08	GSTA4	glutathione S-transferase alpha 4
84823	1,71E-04	3,77E+00	1,05E-04	0,0416	-3,8778256	-0,16135873	11280,5	LMNB2	lamin B2
100873979	4,53E-01	3,44E-01	4,11E-01	0,1965	-0,8215393	-0,1614445	81,96	RBMS3-AS3	RBMS3 antisense RNA 3
26993	2,74E-03	2,56E+00	1,86E-03	0,0519	-3,1113737	-0,16155684	3800,48	AKAP8L	A-kinase anchoring protein 8 like
105371818	8,05E-01	9,42E-02	7,78E-01	0,5732	-0,2820561	-0,16168188	10,03	LOC105371	uncharacterized LOC105371818
135250	3,00E-01	5,23E-01	2,61E-01	0,144	-1,1228972	-0,16168808	151,69	RAET1E	retinoic acid early transcript 1E
529	2,19E-04	3,66E+00	1,37E-04	0,0425	-3,8141328	-0,16193623	4578,44	ATP6V1E1	ATPase H+ transporting V1 subunit E1
445329	3,89E-01	4,10E-01	3,48E-01	0,1725	-0,9393306	-0,1619931	100,19	SULT1A4	sulfotransferase family 1A member 4
50649	6,86E-04	3,16E+00	4,45E-04	0,0462	-3,5120571	-0,16210016	3151,44	ARHGEF4	Rho guanine nucleotide exchange factor 4

9675	6,17E-04	3,21E+00	3,98E-04	0,0458	-3,5411479	-0,16211495	3363,54	TTI1	TELO2 interacting protein 1
5786	6,10E-04	3,21E+00	3,94E-04	0,0457	-3,5441987	-0,16211897	5629,64	PTPRA	protein tyrosine phosphatase receptor type A
116443	7,63E-01	1,17E-01	7,33E-01	0,4755	-0,3409651	-0,16213157	12,88	GRIN3A	glutamate ionotropic receptor NMDA type subunit 3A
22882	2,87E-02	1,54E+00	2,16E-02	0,0706	-2,2980536	-0,162278	835,55	ZHX2	zinc fingers and homeoboxes 2
50937	1,61E-02	1,79E+00	1,17E-02	0,0644	-2,5201969	-0,16240743	1137,82	CDON	cell adhesion associated, oncogene regulated
7837	4,46E-05	4,35E+00	2,64E-05	0,0387	-4,2024	-0,16253423	25173,81	PXDN	peroxidasin
10588	2,07E-01	6,84E-01	1,75E-01	0,12	-1,3548729	-0,1626001	219,4	MTHFS	methenyltetrahydrofolate synthetase
8639	6,48E-01	1,88E-01	6,11E-01	0,3205	-0,5083226	-0,16289878	30,17	AOC3	amine oxidase copper containing 3
85369	2,83E-03	2,55E+00	1,93E-03	0,0526	-3,1010582	-0,16308494	1768,63	STRIP1	striatin interacting protein 1
113278	3,97E-01	4,01E-01	3,56E-01	0,1767	-0,9231015	-0,16313644	102,12	SLC52A3	solute carrier family 52 member 3
84936	1,59E-02	1,80E+00	1,16E-02	0,0647	-2,5243784	-0,16323241	1113,22	ZFYVE19	zinc finger FYVE-type containing 19
101927476	5,88E-01	2,31E-01	5,49E-01	0,2725	-0,5994287	-0,16333647	42,37	LOC101927	uncharacterized LOC101927476
56829	5,98E-04	3,22E+00	3,86E-04	0,046	-3,5496526	-0,16340352	3577,17	ZC3HAV1	zinc finger CCCH-type containing, antiviral 1
9885	2,07E-03	2,68E+00	1,39E-03	0,0512	-3,1959904	-0,16348298	2294,51	OSBPL2	oxysterol binding protein like 2
219402	1,14E-02	1,94E+00	8,25E-03	0,0619	-2,6418122	-0,16357132	1190,32	MTIF3	mitochondrial translational initiation factor 3
6002	2,05E-02	1,69E+00	1,51E-02	0,0675	-2,4291251	-0,16384929	1104,38	RGS12	regulator of G protein signaling 12
284	3,42E-01	4,66E-01	3,02E-01	0,159	-1,0323334	-0,16409035	123,89	ANGPT1	angiopoietin 1
203427	7,10E-03	2,15E+00	5,02E-03	0,0586	-2,8056683	-0,16451555	1329,64	SLC25A43	solute carrier family 25 member 43
25858	5,40E-01	2,68E-01	4,99E-01	0,2437	-0,6767272	-0,16492483	51,37	CATSPERZ	catsper channel auxiliary subunit zeta
4172	1,74E-05	4,76E+00	1,01E-05	0,0374	-4,4154994	-0,16502919	18405,32	MCM3	minichromosome maintenance complex component 3
8313	1,50E-01	8,24E-01	1,24E-01	0,1074	-1,5373312	-0,16506313	290,04	AXIN2	axin 2
101928909	5,40E-01	2,68E-01	4,99E-01	0,2445	-0,6755868	-0,16520659	51,98	TTC7B-AS1	TTC7B antisense RNA 1
100506033	1,18E-01	9,28E-01	9,64E-02	0,0994	-1,6625976	-0,16529105	340,11	PTOV1-AS1	PTOV1 antisense RNA 1
106780802	5,35E-01	2,72E-01	4,94E-01	0,2419	-0,6836467	-0,16535545	52,54	KCNK4-TEX	KCNK4-TEX40 readthrough
1499	8,75E-06	5,06E+00	4,98E-06	0,0362	-4,5658284	-0,16543172	19818,39	CTNNB1	catenin beta 1
340554	5,29E-01	2,77E-01	4,88E-01	0,2386	-0,6938169	-0,1655669	53,94	ZC3H12B	zinc finger CCCH-type containing 12B
3636	8,71E-04	3,06E+00	5,69E-04	0,0481	-3,4461038	-0,16564548	6201,38	INPPL1	inositol polyphosphate phosphatase like 1
125476	3,24E-02	1,49E+00	2,45E-02	0,0737	-2,2492134	-0,16575793	829,92	INO80C	INO80 complex subunit C
5554	3,57E-01	4,47E-01	3,17E-01	0,1656	-1,0014924	-0,16587296	111,56	PRH1	proline rich protein HaeIII subfamily 1
79842	2,55E-01	5,93E-01	2,19E-01	0,1352	-1,228222	-0,16603659	176,87	ZBTB3	zinc finger and BTB domain containing 3
5202	1,16E-03	2,94E+00	7,69E-04	0,0494	-3,3637882	-0,16603966	3355,01	PFDN2	prefoldin subunit 2
4670	1,69E-03	2,77E+00	1,13E-03	0,051	-3,2563584	-0,16605873	19018,75	HNRNPM	heterogeneous nuclear ribonucleoprotein M
105372817	6,14E-01	2,12E-01	5,76E-01	0,2972	-0,5588113	-0,16607824	33,42	LOC105372	uncharacterized LOC105372817
7371	1,09E-04	3,96E+00	6,63E-05	0,0417	-3,9892687	-0,16622195	4320,29	UCK2	uridine-cytidine kinase 2
101929479	1,32E-01	8,79E-01	1,08E-01	0,1035	-1,606876	-0,1662821	307,91	LOC101929	golgin A2 pseudogene
7775	8,02E-02	1,10E+00	6,39E-02	0,0898	-1,8529129	-0,16629923	441,72	ZNF232	zinc finger protein 232
150726	2,51E-02	1,60E+00	1,88E-02	0,0708	-2,3503729	-0,16634046	904,65	FBXO41	F-box protein 41
23113	4,60E-03	2,34E+00	3,20E-03	0,0565	-2,9482085	-0,16650777	2017,67	CUL9	cullin 9
54825	7,05E-01	1,52E-01	6,72E-01	0,3931	-0,4235534	-0,1665078	19,16	CDHR2	cadherin related family member 2
29123	4,97E-04	3,30E+00	3,19E-04	0,0464	-3,5996003	-0,16686339	6987,93	ANKRD11	ankyrin repeat domain containing 11
57154	6,39E-04	3,19E+00	4,13E-04	0,0473	-3,5317489	-0,16697892	2752,69	SMURF1	SMAD specific E3 ubiquitin protein ligase 1
79868	1,48E-02	1,83E+00	1,08E-02	0,0656	-2,5488355	-0,1671898	1308,26	ALG13	ALG13 UDP-N-acetylglucosaminyltransferase subunit
3182	3,98E-05	4,40E+00	2,35E-05	0,0395	-4,228962	-0,16719328	10424,46	HNRNPAB	heterogeneous nuclear ribonucleoprotein A/B
22985	2,43E-04	3,61E+00	1,52E-04	0,0443	-3,7878953	-0,16769283	11670,17	ACIN1	apoptotic chromatin condensation inducer 1
268	4,28E-01	3,69E-01	3,87E-01	0,1941	-0,8658867	-0,16808554	81,84	AMH	anti-Mullerian hormone
3508	7,97E-03	2,10E+00	5,66E-03	0,0608	-2,767077	-0,16820496	1240,99	IGHMBP2	immunoglobulin mu DNA binding protein 2
6934	3,01E-02	1,52E+00	2,27E-02	0,0739	-2,2783638	-0,16827296	825,15	TCF7L2	transcription factor 7 like 2
123096	6,39E-03	2,19E+00	4,50E-03	0,0592	-2,8410671	-0,16830351	1358,79	SLC25A29	solute carrier family 25 member 29
84273	3,98E-03	2,40E+00	2,75E-03	0,0563	-2,9948847	-0,16847059	1573,51	NOA1	nitric oxide associated 1
81602	1,19E-01	9,24E-01	9,67E-02	0,1015	-1,6612406	-0,16863109	316,11	CDADC1	cytidine and dCMP deaminase domain containing 1
105372859	4,38E-01	3,59E-01	3,97E-01	0,1989	-0,8478463	-0,1686526	87,67	LOC105372	uncharacterized LOC105372859
201514	3,15E-03	2,50E+00	2,15E-03	0,055	-3,0686196	-0,16881659	1706,61	ZNF584	zinc finger protein 584
91368	2,74E-03	2,56E+00	1,86E-03	0,0543	-3,1118391	-0,168871	1585,28	CDKN2AIPN	CDKN2A interacting protein N-terminal like
9870	1,37E-04	3,86E+00	8,41E-05	0,043	-3,9325208	-0,16914142	3959,52	AREL1	apoptosis resistant E3 ubiquitin protein ligase 1
57153	1,09E-04	3,96E+00	6,61E-05	0,0424	-3,9898837	-0,16936242	6206,25	SLC44A2	solute carrier family 44 member 2
55128	2,66E-02	1,58E+00	1,99E-02	0,0728	-2,3281881	-0,16944341	808,56	TRIM68	tripartite motif containing 68
6818	3,61E-01	4,42E-01	3,21E-01	0,1706	-0,993307	-0,16947136	103,05	SULT1A3	sulfotransferase family 1A member 3
4928	2,68E-05	4,57E+00	1,57E-05	0,0392	-4,3189793	-0,16949508	11712,34	NUP98	nucleoporin 98 and 96 precursor
9215	7,49E-01	1,26E-01	7,19E-01	0,4704	-0,3604517	-0,16956303	14,78	LARGE1	LARGE xylosyl- and glucuronyltransferase 1
2040	1,18E-02	1,93E+00	8,48E-03	0,0646	-2,6322001	-0,17003307	1058,95	STOM	stomatin
8464	1,85E-02	1,73E+00	1,36E-02	0,069	-2,4672927	-0,17024309	1024,96	SUPT3H	SPT3 homolog, SAGA and STAGA complex component
100130958	6,91E-01	1,61E-01	6,56E-01	0,3827	-0,4450765	-0,17030908	20,64	SYCE1L	synaptonemal complex central element protein 1 like
925	3,68E-01	4,34E-01	3,27E-01	0,1739	-0,9792774	-0,17031673	108,07	CD8A	CD8a molecule
2900	5,16E-01	2,87E-01	4,74E-01	0,238	-0,7157368	-0,17033252	52,44	GRIK4	glutamate ionotropic receptor kainate type subunit 4
105374366	5,62E-01	2,50E-01	5,22E-01	0,2658	-0,6409183	-0,17034733	41,99	LINC02482	long intergenic non-protein coding RNA 2482
100533464	2,81E-01	5,51E-01	2,43E-01	0,146	-1,1668554	-0,17037648	151,37	PRH1-PRR4	PRH1-PRR4 readthrough
257160	5,21E-03	2,28E+00	3,63E-03	0,0587	-2,9082816	-0,1705856	2283,16	RNF214	ring finger protein 214
56261	3,01E-02	1,52E+00	2,27E-02	0,0749	-2,278444	-0,17064923	795,36	GPCPD1	glycerophosphocholine phosphodiesterase 1
374739	6,44E-01	1,91E-01	6,07E-01	0,3321	-0,5148236	-0,17095742	28,5	TEPP	testis, prostate and placenta expressed
116211	4,02E-01	3,96E-01	3,60E-01	0,1869	-0,914805	-0,17098178	86,46	TM4SF19	transmembrane 4 L six family member 19
100500914	7,10E-01	1,49E-01	6,77E-01	0,4117	-0,4165961	-0,17150992	18,61	MIR3610	microRNA 3610
64778	7,21E-04	3,14E+00	4,68E-04	0,049	-3,4982193	-0,1715659	9010,99	FNDC3B	fibronectin type III domain containing 3B
847	8,06E-04	3,09E+00	5,25E-04	0,0497	-3,4676372	-0,17217286	3406,92	CAT	catalase
196513	1,13E-01	9,47E-01	9,15E-02	0,1021	-1,6876815	-0,17226846	344,93	DCP1B	decapping mRNA 1B
152189	4,25E-01	3,72E-01	3,84E-01	0,1978	-0,87138	-0,1723174	83,88	CMTM8	CKLF like MARVEL transmembrane domain containing 8
105374085	5,28E-01	2,77E-01	4,86E-01	0,2476	-0,6962304	-0,17241226	51	LOC105374	uncharacterized LOC105374085
8496	2,81E-03	2,55E+00	1,91E-03	0,0557	-3,1038024	-0,17273957	3985,06	PPFIBP1	PPFIA binding protein 1
29074	7,65E-04	3,12E+00	4,98E-04	0,0497	-3,4818749	-0,17298823	2271,4	MRPL18	mitochondrial ribosomal protein L18
51669	2,37E-04	3,63E+00	1,48E-04	0,0456	-3,7941684	-0,17309012	4781,19	SARAF	store-operated calcium entry associated regulatory factor
256364	4,76E-03	2,32E+00	3,31E-03	0,059	-2,9370715	-0,17314825	1426,35	EML3	EMAP like 3
114884	2,56E-04	3,59E+00	1,61E-04	0,0459	-3,7739406	-0,17316062	4281,57	OSBPL10	oxysterol binding protein like 10
105371743	1,13E-01	9,47E-01	9,18E-02	0,1027	-1,685779	-0,17316273	333,79	SNHG30	small nucleolar RNA host gene 30
23234	4,81E-04	3,32E+00	3,08E-04	0,048	-3,6083528	-0,17332534	3733,18	DNAJC9	DnaJ heat shock protein family (Hsp40) member C9
128486	4,18E-03	2,38E+00	2,89E-03	0,0582	-2,9789072	-0,17342192	1445,33	FITM2	fat storage inducing transmembrane protein 2
23403	3,35E-02	1,47E+00	2,54E-02	0,0777	-2,2349908	-0,17366446	593,44	FBXO46	F-box protein 46
839	1,39E-02	1,86E+00	1,01E-02	0,0676	-2,5713417	-0,17389468	1042,69	CASP6	caspase 6
29803	1,72E-04	3,76E+00	1,06E-04	0,0449	-3,8754398	-0,17398648	3406,43	REPIN1	replication initiator 1
8480	4,28E-05	4,37E+00	2,53E-05	0,0413	-4,2120428	-0,17409737	5682,59	RAE1	ribonucleic acid export 1
107986086	7,16E-01	1,45E-01	6,83E-01	0,4262	-0,4087247	-0,17418259	16,34	LOC107986	uncharacterized LOC107986086
59274	2,93E-02	1,53E+00	2,21E-02	0,0761	-2,289393	-0,17426858	648,34	TLNRD1	talin rod domain containing 1
11157	9,05E-03	2,04E+00	6,47E-03	0,064	-2,7229592	-0,17437761	1482,26	LSM6	LSM6 homolog, U6 small nuclear RNA and mRNA degradation associated
57019	1,20E-04	3,92E+00	7,33E-05	0,044	-3,9654125	-0,17442081	3338,65	CIAPIN1	cytokine induced apoptosis inhibitor 1
54682	4,91E-02	1,31E+00	3,80E-02	0,0842	-2,0749104	-0,1746582	536,22	MANSC1	MANSC domain containing 1
105373106	6,82E-01	1,66E-01	6,47E-01	0,3814	-0,4581304	-0,17471557	20,17	CNIH3-AS1	CNIH3 antisense RNA 1
440434	3,13E-02	1,50E+00	2,36E-02	0,0772	-2,2634492	-0,17479946	630,96	NPEPPSP1	NPEPPS pseudogene 1
100310756	6,06E-02	1,22E+00	4,75E-02	0,0882	-1,9816848	-0,17486489	510,23	LOC100310	uncharacterized LOC100310756
53358	4,58E-03	2,34E+00	3,18E-03	0,0593	-2,9496826	-0,17488214	1568,59	SHC3	SHC adaptor protein 3
3305	3,69E-01	4,33E-01	3,28E-01	0,1789	-0,9780058	-0,17494321	94,5	HSPA1L	heat shock protein family A (Hsp70) member 1 like
4638	3,44E-03	2,46E+00	2,36E-03	0,0576	-3,0407439	-0,17505092	1305,02	MYLK	myosin light chain kinase
55870	2,26E-04	3,65E+00	1,41E-04	0,046	-3,806232	-0,17510655	3482,61	ASH1L	ASH1 like histone lysine methyltransferase
199800	4,34E-01	3,63E-01	3,93E-01	0,205	-0,8544833	-0,17514879	75,3	ADM5	adrenomedullin 5 (putative)
55922	4,38E-03	2,36E+00	3,04E-03	0,0592	-2,9640127	-0,17540579	1526,68	NKRF	NFKB repressing factor
23283	6,14E-04	3,21E+00	3,97E-04	0,0495	-3,5423619	-0,17548255	2220,28	CSTF2T	cleavage stimulation factor subunit 2 tau variant
10613	2,14E-05	4,67E+00	1,25E-05	0,0402	-4,3695318	-0,17561685	6143,49	ERLIN1	ER lipid raft associated 1
56947	6,49E-04	3,19E+00	4,19E-04	0,0498	-3,5275478	-0,17563054	2435,81	MFF	mitochondrial fission factor
107984895	7,20E-01	1,43E-01	6,88E-01	0,4367	-0,4022228	-0,17563636	15,4	LOC107984	895
10904	3,37E-03	2,47E+00	2,31E-03	0,0577	-3,0467321	-0,17583518	2534,33	BLCAP	BLCAP apoptosis inducing factor
107984035	2,58E-01	5,88E-01	2,22E-01	0,1439	-1,2217366	-0,17583786	157,77	LOC107984	uncharacterized LOC107984035
9905	1,14E-03	2,94E+00	7,53E-04	0,0522	-3,3694145	-0,17585394	2218,77	SGSM2	small G protein signaling modulator 2
219347	3,69E-01	4,33E-01	3,29E-01	0,1801	-0,9766738	-0,17592636	93,16	TMEM254-A	TMEM254 antisense RNA 1
51096	7,02E-04	3,15E+00	4,55E-04	0,0502	-3,5057594	-0,17614496	4113,9	UTP18	UTP18 small subunit processome component
150967	1,34E-01	8,73E-01	1,10E-01	0,1103	-1,5970347	-0,17614559	262,65	LINC01963	long intergenic non-protein coding RNA 1963
115948	7,39E-02	1,13E+00	5,86E-02	0,0932	-1,8913141	-0,1762648	784,11	ODAD3	outer dynein arm docking complex subunit 3
9686	1,29E-03	2,89E+00	8,52E-04	0,0529	-3,3353203	-0,1763393	1789,04	VGLL4	vestigial like family member 4
102724428	3,09E-02	1,51E+00	2,33E-02	0,0782	-2,268458	-0,17741361	707,01	LOC102724	salt inducible kinase 1B (putative)
60682	4,51E-03	2,35E+00	3,13E-03	0,0601	-2,954915	-0,1775122	1491,67	SMAP1	small ArfGAP 1
197358	7,16E-01	1,45E-01	6,83E-01	0,4353	-0,4077941	-0,17751424	16,21	NLRC3	NLR family CARD domain containing 3
105371393	3,95E-01	4,03E-01	3,54E-01	0,1914	-0,9277322	-0,17752416	82,07	LOC105371	393
151473	5,81E-01	2,36E-01	5,41E-01	0,2905	-0,6115469	-0,17763759	36,62	SLC16A14	solute carrier family 16 member 14
22955	1,85E-03	2,73E+00	1,24E-03	0,055	-3,2285651	-0,17766189	1738,81	SCMH1	Scm polycomb group protein homolog 1

5547	2,91E-05	4,54E+00	1,71E-05	0,0413	-4,2999407	-0,17769565	5313,33	PRCP	prolylcarboxypeptidase
284942	4,42E-02	1,35E+00	3,40E-02	0,0841	-2,1200863	-0,17834066	579,97	RPL23AP82	ribosomal protein L23a pseudogene 82
57493	3,07E-05	4,51E+00	1,80E-05	0,0416	-4,2879487	-0,1783569	15547,16	HEG1	heart development protein with EGF like domains 1
84203	6,79E-01	1,68E-01	6,44E-01	0,3865	-0,4615474	-0,17839085	20,47	TXNDC2	thioredoxin domain containing 2
107985471	3,90E-01	4,09E-01	3,48E-01	0,1903	-0,93775	-0,17843618	84,46	PEF1-AS1	PEF1 and COL16A1 antisense RNA 1
105369438	3,78E-01	4,23E-01	3,37E-01	0,1859	-0,9605358	-0,17852962	86,13	PIWIL4-AS1	PIWIL4 antisense RNA 1
283932	2,28E-01	6,42E-01	1,94E-01	0,1377	-1,2981751	-0,17875123	164,19	FBXL19-AS1	FBXL19 antisense RNA 1
200424	3,19E-03	2,50E+00	2,18E-03	0,0584	-3,0640347	-0,17880502	1382,08	TET3	tet methylcytosine dioxygenase 3
286499	1,15E-02	1,94E+00	8,30E-03	0,0678	-2,6397288	-0,17887739	1060,87	FAM133A	family with sequence similarity 133 member A
79776	3,41E-02	1,47E+00	2,59E-02	0,0804	-2,22753	-0,17899764	653,38	ZFHX4	zinc finger homeobox 4
57194	5,60E-02	1,25E+00	4,37E-02	0,0887	-2,0170102	-0,1790025	458,72	ATP10A	ATPase phospholipid transporting 10A (putative)
54790	1,64E-02	1,79E+00	1,20E-02	0,0713	-2,5125793	-0,17903454	1234,44	TET2	tet methylcytosine dioxygenase 2
10579	2,05E-03	2,69E+00	1,38E-03	0,056	-3,1984175	-0,17912629	2500,59	TACC2	transforming acidic coiled-coil containing protein 2
80131	3,72E-02	1,43E+00	2,84E-02	0,0817	-2,1923598	-0,1791587	623,72	LRRC8E	leucine rich repeat containing 8 VRAC subunit E
55621	1,13E-02	1,95E+00	8,14E-03	0,0677	-2,6463648	-0,17918598	2933,33	TRMT1	tRNA methyltransferase 1
143187	4,48E-03	2,35E+00	3,11E-03	0,0606	-2,9566828	-0,1792141	1196,4	VTI1A	vesicle transport through interaction with t-SNAREs 1A
599	1,89E-03	2,72E+00	1,27E-03	0,0556	-3,2228064	-0,17925772	2259,04	BCL2L2	BCL2 like 2
101929586	5,02E-01	2,99E-01	4,60E-01	0,2428	-0,7383101	-0,17928137	52,42	LOC101929	uncharacterized LOC101929586
29964	1,24E-01	9,07E-01	1,02E-01	0,1096	-1,6374382	-0,1794005	291,07	PRICKLE4	prickle planar cell polarity protein 4
4709	3,51E-03	2,45E+00	2,41E-03	0,0592	-3,0344613	-0,17962913	1445,14	NDUFB3	NADH:ubiquinone oxidoreductase subunit B3
9095	5,04E-01	2,98E-01	4,62E-01	0,2445	-0,7349014	-0,17967159	51,6	TBX19	T-box transcription factor 19
6727	2,58E-04	3,59E+00	1,62E-04	0,0477	-3,7723137	-0,1797632	8852,85	SRP14	signal recognition particle 14
3376	1,12E-06	5,95E+00	6,07E-07	0,0361	-4,9889307	-0,18010872	20028,24	IARS1	isoleucyl-tRNA synthetase 1
107986700	7,66E-01	1,16E-01	7,36E-01	0,535	-0,3366818	-0,18012931	10,12	PRR15-DT	PRR15 divergent transcript
7126	2,83E-04	3,55E+00	1,78E-04	0,0481	-3,7478883	-0,18035219	4691,14	TNFAIP1	TNF alpha induced protein 1
51250	2,16E-02	1,67E+00	1,60E-02	0,075	-2,4094892	-0,1806063	779,23	MTRES1	mitochondrial transcription rescue factor 1
441272	2,47E-01	6,07E-01	2,12E-01	0,1446	-1,2491631	-0,18063738	151,79	SPDYE3	speedy/RINGO cell cycle regulator family member E3
101929066	6,36E-01	1,97E-01	5,99E-01	0,3433	-0,5265094	-0,18075907	24,78	ASAH1-AS1	ASAH1 antisense RNA 1
7381	3,80E-04	3,42E+00	2,42E-04	0,0492	-3,671085	-0,18079971	8241,26	UQCRB	ubiquinol-cytochrome c reductase binding protein
100422914	3,38E-01	4,71E-01	2,98E-01	0,174	-1,0408628	-0,18109757	119,74	MIR4253	microRNA 4253
157680	1,03E-03	2,99E+00	6,78E-04	0,0533	-3,3981649	-0,18112622	2018,43	VPS13B	vacuolar protein sorting 13 homolog B
6749	6,13E-06	5,21E+00	3,45E-06	0,0391	-4,6421159	-0,18132837	23031,36	SSRP1	structure specific recognition protein 1
400961	1,24E-01	9,07E-01	1,02E-01	0,1109	-1,6359444	-0,1814051	259,41	PAIP2B	poly(A) binding protein interacting protein 2B
105376392	4,87E-01	3,12E-01	4,46E-01	0,2381	-0,7628088	-0,18162205	494,39	LOC105376	uncharacterized LOC105376392
11091	1,80E-05	4,74E+00	1,04E-05	0,0412	-4,4077061	-0,18164709	4644,03	WDR5	WD repeat domain 5
23761	7,99E-03	2,10E+00	5,68E-03	0,0657	-2,7659617	-0,1817148	1171,74	PISD	phosphatidylserine decarboxylase
23639	2,72E-01	5,65E-01	2,35E-01	0,1531	-1,1880922	-0,18187198	137,66	DNAAF11	dynein axonemal assembly factor 11
83877	2,09E-03	2,68E+00	1,41E-03	0,057	-3,1927957	-0,18190131	1847,61	TM2D2	TM2 domain containing 2
131870	2,63E-03	2,58E+00	1,79E-03	0,0583	-3,1236564	-0,18213548	1471,27	NUDT16	nudix hydrolase 16
100132163	5,07E-01	2,95E-01	4,65E-01	0,2499	-0,7299631	-0,18245234	48,2	PHKA2-AS1	PHKA2 antisense RNA 1
9866	6,04E-04	3,22E+00	3,90E-04	0,0515	-3,5467991	-0,18269836	8029,81	TRIM66	tripartite motif containing 66
10425	3,41E-05	4,47E+00	2,00E-05	0,0429	-4,26453	-0,18278903	5887,6	ARIH2	ariadne RBR E3 ubiquitin protein ligase 2
23250	4,15E-03	2,38E+00	2,87E-03	0,0614	-2,9813849	-0,18298135	1339,72	ATP11A	ATPase phospholipid transporting 11A
653635	7,83E-02	1,11E+00	6,22E-02	0,0981	-1,8648	-0,18300926	473,79	WASH7P	WASP family homolog 7, pseudogene
56125	3,30E-01	4,81E-01	2,90E-01	0,1731	-1,0577523	-0,1831014	106,49	PCDHB11	protocadherin beta 11
29088	1,93E-04	3,71E+00	1,20E-04	0,0477	-3,8460403	-0,18339777	2590,56	MRPL15	mitochondrial ribosomal protein L15
9267	1,44E-03	2,84E+00	9,57E-04	0,0556	-3,3029485	-0,183748	1463,63	CYTH1	cytohesin 1
105370208	7,16E-01	1,45E-01	6,83E-01	0,4504	-0,4079482	-0,18375909	14,4	LINC00345	long intergenic non-protein coding RNA 345
64860	5,43E-03	2,27E+00	3,79E-03	0,0635	-2,894922	-0,18377846	1028,66	ARMCX5	armadillo repeat containing X-linked 5
729678	1,63E-02	1,79E+00	1,19E-02	0,0731	-2,5154386	-0,18395033	685,17	LINC00847	long intergenic non-protein coding RNA 847
8874	3,89E-04	3,41E+00	2,47E-04	0,0502	-3,6650867	-0,18406927	2201,03	ARHGEF7	Rho guanine nucleotide exchange factor 7
5198	4,02E-04	3,40E+00	2,56E-04	0,0504	-3,6565337	-0,18430923	2865,47	PFAS	phosphoribosylformylglycinamidine synthase
100499405	3,62E-01	4,41E-01	3,21E-01	0,1857	-0,9926902	-0,18437163	90,25	LINC00987	long intergenic non-protein coding RNA 987
100534611	2,55E-01	5,93E-01	2,19E-01	0,15	-1,229193	-0,18437959	139,1	TM4SF19-D	TM4SF19-DYNLT2B readthrough (NMD candidate)
126917	9,96E-05	4,00E+00	6,04E-05	0,046	-4,0110973	-0,18438067	3203,62	IFFO2	intermediate filament family orphan 2
100873932	3,73E-01	4,28E-01	3,32E-01	0,1903	-0,9695727	-0,18455318	83,2	DPYD-AS1	DPYD antisense RNA 1
22954	2,97E-03	2,53E+00	2,02E-03	0,0598	-3,0869583	-0,1847363	1366,16	TRIM32	tripartite motif containing 32
64091	6,71E-01	1,73E-01	6,36E-01	0,3902	-0,4737668	-0,18485595	19,42	POPDC2	popeye domain containing 2
112268064	7,46E-01	1,27E-01	7,15E-01	0,5059	-0,3655319	-0,18492411	11,59	LOC112268	uncharacterized LOC112268064
399821	5,51E-01	2,59E-01	5,10E-01	0,2811	-0,658338	-0,1850791	38,34	EDRF1-DT	EDRF1 divergent transcript
79364	6,35E-03	2,20E+00	4,47E-03	0,0651	-2,8428283	-0,1851005	956	ZXDC	ZXD family zinc finger C
2861	3,53E-01	4,52E-01	3,13E-01	0,1837	-1,0088066	-0,18528207	94,27	GPR37	G protein-coupled receptor 37
400673	5,65E-01	2,48E-01	5,24E-01	0,2911	-0,6366428	-0,18533358	37,1	VMAC	vimentin type intermediate filament associated coiled-coil protein
8800	1,67E-01	7,77E-01	1,40E-01	0,1255	-1,477283	-0,1853494	209,1	PEX11A	peroxisomal biogenesis factor 11 alpha
65080	2,42E-03	2,62E+00	1,63E-03	0,0589	-3,1496457	-0,18543089	1383,26	MRPL44	mitochondrial ribosomal protein L44
51406	4,66E-05	4,33E+00	2,76E-05	0,0443	-4,1922898	-0,18555945	6183,11	NOL7	nucleolar protein 7
7862	1,46E-03	2,84E+00	9,69E-04	0,0563	-3,2992368	-0,1858011	1791,48	BRPF1	bromodomain and PHD finger containing 1
9922	1,55E-03	2,81E+00	1,03E-03	0,0566	-3,2817177	-0,18586418	1462,07	IQSEC1	IQ motif and Sec7 domain ArfGEF 1
10058	4,08E-02	1,39E+00	3,12E-02	0,0864	-2,1540301	-0,18602124	450,04	ABCB6	ATP binding cassette subfamily B member 6 (Langereis blood group)
308	4,26E-07	6,37E+00	2,25E-07	0,0359	-5,1775588	-0,18608987	40618,97	ANXA5	annexin A5
105371175	7,13E-01	1,47E-01	6,80E-01	0,4514	-0,4131006	-0,18649264	14,35	LOC105371	uncharacterized LOC105371175
284021	6,24E-03	2,20E+00	4,39E-03	0,0655	-2,8489023	-0,18663065	925,42	MILR1	mast cell immunoglobulin like receptor 1
105373883	6,98E-01	1,56E-01	6,64E-01	0,4304	-0,4337552	-0,18669564	15,95	LOC105373	uncharacterized LOC105373883
114609	1,07E-01	9,71E-01	8,66E-02	0,109	-1,7137367	-0,18683221	296,18	TIRAP	TIR domain containing adaptor protein
116938	6,63E-01	1,78E-01	6,27E-01	0,3841	-0,4863704	-0,18683286	20,18	SNORD83B	small nucleolar RNA, C/D box 83B
84333	5,63E-04	3,25E+00	3,63E-04	0,0524	-3,5659228	-0,18693835	2781,86	PCGF5	polycomb group ring finger 5
10127	8,23E-03	2,08E+00	5,85E-03	0,0679	-2,7559747	-0,18713311	1022,92	ZNF263	zinc finger protein 263
23367	4,75E-06	5,32E+00	2,65E-06	0,0399	-4,6958647	-0,18722472	19442,96	LARP1	La ribonucleoprotein 1, translational regulator
113130	2,33E-05	4,63E+00	1,36E-05	0,043	-4,3505293	-0,18725296	5394,51	CDCA5	cell division cycle associated 5
101929162	1,52E-01	8,18E-01	1,26E-01	0,1224	-1,5304102	-0,18726333	217,19	PRDM4-AS1	PRDM4 antisense RNA 1
471	3,68E-06	5,43E+00	2,04E-06	0,0394	-4,7491367	-0,18726629	7116,78	ATIC	5-aminoimidazole-4-carboxamide ribonucleotide formyltransferase/IMP cyclohydrolase
55139	3,30E-03	2,48E+00	2,26E-03	0,0614	-3,0537934	-0,18740109	1248,25	ANKZF1	ankyrin repeat and zinc finger peptidyl tRNA hydrolase 1
7351	5,65E-04	3,25E+00	3,64E-04	0,0526	-3,5648909	-0,18741213	1880,6	UCP2	uncoupling protein 2
55764	2,66E-02	1,58E+00	1,99E-02	0,0807	-2,3277296	-0,18789807	562,25	IFT122	intraflagellar transport 122
153020	6,82E-01	1,66E-01	6,47E-01	0,4109	-0,4583595	-0,18834995	16,99	RASGEF1B	RasGEF domain family member 1B
100134229	4,24E-01	3,73E-01	3,82E-01	0,2161	-0,8735108	-0,18873811	65,1	KDM7A-DT	KDM7A divergent transcript
81889	1,34E-02	1,87E+00	9,74E-03	0,0731	-2,584814	-0,1888487	742,45	FAHD1	fumarylacetoacetate hydrolase domain containing 1
153478	2,55E-01	5,93E-01	2,19E-01	0,1538	-1,2289867	-0,18904694	127,2	PLEKHG4B	pleckstrin homology and RhoGEF domain containing G4B
9240	3,31E-04	3,48E+00	2,09E-04	0,051	-3,7074753	-0,18908791	4323,52	PNMA1	PNMA family member 1
54926	6,09E-06	5,22E+00	3,42E-06	0,0408	-4,6436311	-0,18946053	4802,7	UBE2R2	ubiquitin conjugating enzyme E2 R2
4799	4,66E-05	4,33E+00	2,77E-05	0,0452	-4,1920006	-0,18958064	3061,14	NFX1	nuclear transcription factor, X-box binding 1
6391	2,54E-05	4,60E+00	1,48E-05	0,0438	-4,3312284	-0,1898951	4920,23	SDHC	succinate dehydrogenase complex subunit C
9673	9,02E-05	4,04E+00	5,46E-05	0,0471	-4,034977	-0,18995871	2776,14	SLC25A44	solute carrier family 25 member 44
29914	6,08E-04	3,22E+00	3,93E-04	0,0536	-3,5450262	-0,19000578	1978,68	UBIAD1	UbiA prenyltransferase domain containing 1
100286925	1,31E-01	8,83E-01	1,08E-01	0,1181	-1,6092404	-0,19004252	239,76	PPM1F-AS1	PPM1F antisense RNA 1
105374938	4,50E-01	3,47E-01	4,09E-01	0,2303	-0,825515	-0,19014504	58,14	LOC105374	uncharacterized LOC105374938
11016	3,08E-03	2,51E+00	2,10E-03	0,0618	-3,0754276	-0,19016621	1282,57	ATF7	activating transcription factor 7
32	7,86E-02	1,10E+00	6,25E-02	0,1021	-1,8628935	-0,19020301	357,08	ACACB	acetyl-CoA carboxylase beta
9570	2,62E-04	3,58E+00	1,64E-04	0,0505	-3,7683558	-0,19021897	2153,66	GOSR2	golgi SNAP receptor complex member 2
3142	1,77E-01	7,52E-01	1,48E-01	0,1318	-1,4450004	-0,19048494	184,5	HLX	H2.0 like homeobox
112268296	4,49E-01	3,48E-01	4,08E-01	0,2302	-0,8278848	-0,19059027	56,83	LOC112268	296
6541	1,05E-06	5,98E+00	5,68E-07	0,0382	-5,0018943	-0,19094497	9427,64	SLC7A1	solute carrier family 7 member 1
57510	2,63E-07	6,58E+00	1,37E-07	0,0362	-5,2690565	-0,19097783	10815,28	XPO5	exportin 5
389337	4,63E-01	3,34E-01	4,21E-01	0,2376	-0,8041024	-0,19101838	56,79	ARHGEF37	Rho guanine nucleotide exchange factor 37
5380	4,66E-01	3,32E-01	4,24E-01	0,2392	-0,7988661	-0,19105996	52,71	PMS2P2	PMS1 homolog 2, mismatch repair system component pseudogene 2
10957	1,38E-02	1,86E+00	1,00E-02	0,0743	-2,5756276	-0,19125285	878,9	PNRC1	proline rich nuclear receptor coactivator 1
5631	8,35E-05	4,08E+00	5,04E-05	0,0472	-4,0537697	-0,19129963	3962,55	PRPS1	phosphoribosyl pyrophosphate synthetase 1
51651	2,94E-03	2,53E+00	2,00E-03	0,062	-3,0899208	-0,19158862	2137,34	PTRH2	peptidyl-tRNA hydrolase 2
6595	8,84E-05	4,05E+00	5,34E-05	0,0474	-4,0400746	-0,1916456	3470,65	SMARCA2	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2
54980	5,42E-02	1,27E+00	4,22E-02	0,0944	-2,031601	-0,1916906	420,33	C2orf42	chromosome 2 open reading frame 42
105376411	5,30E-01	2,76E-01	4,89E-01	0,2771	-0,6918713	-0,1917493	37,81	LOC105376	uncharacterized LOC105376411
692158	7,03E-01	1,53E-01	6,70E-01	0,4501	-0,4261304	-0,19181152	15,09	SNORA57	small nucleolar RNA, H/ACA box 57
57406	2,86E-02	1,54E+00	2,15E-02	0,0835	-2,2995074	-0,19203101	515,33	ABHD6	abhydrolase domain containing 6, acylglycerol lipase
143570	1,11E-02	1,95E+00	7,95E-03	0,0724	-2,6540586	-0,19210146	742,45	XRRA1	X-ray radiation resistance associated 1
55856	1,11E-03	2,95E+00	7,29E-04	0,0569	-3,3782636	-0,1922244	1523,5	ACOT13	acyl-CoA thioesterase 13
340562	4,12E-01	3,85E-01	3,71E-01	0,2153	-0,8941489	-0,19247376	68,7	SATL1	spermidine/spermine N1-acetyl transferase like 1
100506144	5,47E-02	1,26E+00	4,26E-02	0,095	-2,0273408	-0,19253931	434,31	TMEM35B	transmembrane protein 35B
1909	2,27E-01	6,44E-01	1,93E-01	0,1483	-1,3003481	-0,19287188	140,76	EDNRA	endothelin receptor type A
54981	1,21E-01	9,17E-01	9,88E-02	0,1169	-1,6506528	-0,1929523	235,99	NMRK1	nicotinamide riboside kinase 1
57488	7,30E-06	5,14E+00	4,13E-06	0,0419	-4,6049802	-0,19310163	8528,12	ESYT2	extended synaptotagmin 2

22796	6,47E-04	3,19E+00	4,18E-04	0,0548	-3,5282006	-0,19322593	1658,41	COG2	component of oligomeric golgi complex 2
1729	5,79E-07	6,24E+00	3,08E-07	0,0378	-5,1184552	-0,19323629	14797,95	DIAPH1	diaphanous related formin 1
8553	3,18E-04	3,50E+00	2,01E-04	0,052	-3,7183616	-0,19329064	2050,66	BHLHE40	basic helix-loop-helix family member e40
441024	2,06E-02	1,69E+00	1,52E-02	0,0797	-2,4267642	-0,19336044	559,61	MTHFD2L	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 2 like
3178	1,11E-05	4,95E+00	6,32E-06	0,0428	-4,5152817	-0,19336324	49410,08	HNRNPA1	heterogeneous nuclear ribonucleoprotein A1
105369952	3,84E-01	4,16E-01	3,43E-01	0,2039	-0,9486126	-0,19339767	75,96	LOC105369	uncharacterized LOC105369952
84667	7,52E-01	1,24E-01	7,21E-01	0,5424	-0,3569541	-0,1936095	10,39	HES7	hes family bHLH transcription factor 7
1025	1,18E-03	2,93E+00	7,78E-04	0,0576	-3,3604559	-0,19370205	2716,5	CDK9	cyclin dependent kinase 9
126282	1,06E-02	1,97E+00	7,63E-03	0,0726	-2,667961	-0,19377171	701,66	TNFAIP8L1	TNF alpha induced protein 8 like 1
8289	5,12E-05	4,29E+00	3,05E-05	0,0465	-4,1699573	-0,1938588	5456,6	ARID1A	AT-rich interaction domain 1A
7629	3,50E-04	3,46E+00	2,21E-04	0,0526	-3,6933304	-0,19414154	2922,85	ZNF76	zinc finger protein 76
3716	6,33E-06	5,20E+00	3,56E-06	0,042	-4,635301	-0,19456959	7493,01	JAK1	Janus kinase 1
55017	9,06E-05	4,04E+00	5,48E-05	0,0482	-4,0340277	-0,19461487	3854,13	C14orf119	chromosome 14 open reading frame 119
79783	5,78E-01	2,38E-01	5,38E-01	0,3165	-0,6151306	-0,19470369	31,46	SUGCT	succinyl-CoA:glutarate-CoA transferase
144406	1,69E-02	1,77E+00	1,23E-02	0,078	-2,5021503	-0,19517081	606,83	CFAP251	cilia and flagella associated protein 251
6522	1,82E-04	3,74E+00	1,13E-04	0,0506	-3,8612591	-0,19524689	5474,73	SLC4A2	solute carrier family 4 member 2
55337	1,51E-02	1,82E+00	1,10E-02	0,0768	-2,5437367	-0,19533042	731,86	SHFL	shiftless antiviral inhibitor of ribosomal frameshifting
5999	8,10E-02	1,09E+00	6,45E-02	0,1057	-1,8484674	-0,1954104	330,78	RGS4	regulator of G protein signaling 4
2330	1,81E-01	7,42E-01	1,51E-01	0,1366	-1,4347368	-0,19593479	170,87	FMO5	flavin containing dimethylaniline monoxygenase 5
3628	1,39E-03	2,86E+00	9,22E-04	0,0591	-3,313356	-0,19593604	1488,77	INPP1	inositol polyphosphate-1-phosphatase
9918	1,72E-05	4,76E+00	9,96E-06	0,0444	-4,4180305	-0,19635009	12145,95	NCAPD2	non-SMC condensin I complex subunit D2
105372717	5,78E-01	2,38E-01	5,38E-01	0,3193	-0,6155162	-0,1965382	28,55	LOC105372	uncharacterized LOC105372717
100616361	6,52E-01	1,86E-01	6,15E-01	0,3914	-0,5023213	-0,19662389	19,4	MIR4775	microRNA 4775
27034	2,12E-04	3,67E+00	1,32E-04	0,0515	-3,8224149	-0,19683627	2084,74	ACAD8	acyl-CoA dehydrogenase family member 8
105377134	6,98E-01	1,56E-01	6,65E-01	0,4546	-0,4333828	-0,19700286	15,6	LOC105377	uncharacterized LOC105377134
6294	3,14E-05	4,50E+00	1,84E-05	0,046	-4,2830306	-0,19709346	6938,76	SAFB	scaffold attachment factor B
4509	1,93E-04	3,71E+00	1,20E-04	0,0512	-3,8463602	-0,19711182	60622,77	ATP8	ATP synthase F0 subunit 8
84077	5,03E-01	2,98E-01	4,61E-01	0,2681	-0,7365163	-0,19749238	40,79	C3orf20	chromosome 3 open reading frame 20
399979	2,69E-06	5,57E+00	1,48E-06	0,041	-4,8134383	-0,19751571	5315,71	SNX19	sorting nexin 19
94134	3,02E-04	3,52E+00	1,90E-04	0,0529	-3,731703	-0,19758923	2088,88	ARHGAP12	Rho GTPase activating protein 12
6993	4,53E-05	4,34E+00	2,69E-05	0,0471	-4,1984823	-0,19768269	2756,77	DYNLT1	dynein light chain Tctex-type 1
54567	7,14E-01	1,46E-01	6,81E-01	0,4809	-0,4112184	-0,19776493	12,96	DLL4	delta like canonical Notch ligand 4
166785	1,18E-01	9,28E-01	9,63E-02	0,1193	-1,6628843	-0,1984037	244,2	MMAA	metabolism of cobalamin associated A
10939	1,49E-05	4,83E+00	8,57E-06	0,0446	-4,4505427	-0,1984638	4611,03	AFG3L2	AFG3 like matrix AAA peptidase subunit 2
25794	4,86E-01	3,13E-01	4,45E-01	0,2596	-0,7645821	-0,19847062	48,13	FSCN2	fascin actin-bundling protein 2, retinal
26017	5,75E-07	6,24E+00	3,06E-07	0,0388	-5,119869	-0,19847822	9287,05	FAM32A	family with sequence similarity 32 member A
101927126	4,51E-01	3,46E-01	4,09E-01	0,241	-0,8253262	-0,19890859	57,7	GTF2IP7	general transcription factor IIi pseudogene 7
102724805	6,52E-01	1,86E-01	6,16E-01	0,3968	-0,5022267	-0,19929278	18,55	LOC102724	uncharacterized LOC102724805
57820	5,46E-05	4,26E+00	3,25E-05	0,048	-4,1549836	-0,19939241	2844,02	CCNB1IP1	cyclin B1 interacting protein 1
200197	7,41E-01	1,30E-01	7,10E-01	0,5361	-0,3721967	-0,19954737	10,3	TMEM51-AS	TMEM51 antisense RNA 1
7319	4,43E-06	5,35E+00	2,47E-06	0,0424	-4,7102452	-0,19979696	5627,27	UBE2A	ubiquitin conjugating enzyme E2 A
57673	1,49E-04	3,83E+00	9,13E-05	0,0511	-3,9125803	-0,19990618	1927,08	BEND3	BEN domain containing 3
2098	9,37E-05	4,03E+00	5,68E-05	0,0497	-4,0259272	-0,19997571	3205,76	ESD	esterase D
10328	6,73E-04	3,17E+00	4,36E-04	0,0569	-3,5174434	-0,19998206	1489,06	EMC8	ER membrane protein complex subunit 8
89845	4,96E-03	2,30E+00	3,46E-03	0,0684	-2,9240317	-0,19998956	1468,53	ABCC10	ATP binding cassette subfamily C member 10
57602	1,39E-04	3,86E+00	8,52E-05	0,051	-3,9293675	-0,20047566	2985,09	USP36	ubiquitin specific peptidase 36
1797	1,67E-02	1,78E+00	1,22E-02	0,08	-2,5060151	-0,20054315	883,22	DXO	decapping exoribonuclease
6780	2,80E-06	5,55E+00	1,55E-06	0,0417	-4,8051659	-0,20054379	11352,42	STAU1	staufen double-stranded RNA binding protein 1
728661	3,77E-05	4,42E+00	2,22E-05	0,0474	-4,2410659	-0,20083414	3826,35	SLC35E2B	solute carrier family 35 member E2B
553103	3,47E-01	4,60E-01	3,07E-01	0,1966	-1,0222534	-0,20100565	78,99	MIR3936HG	MIR3936 host gene
57117	3,86E-04	3,41E+00	2,46E-04	0,0549	-3,6668623	-0,20144485	1567,34	INTS12	integrator complex subunit 12
23065	1,28E-06	5,89E+00	6,95E-07	0,0406	-4,9628077	-0,20147084	6248,29	EMC1	ER membrane protein complex subunit 1
6710	2,94E-01	5,32E-01	2,56E-01	0,1775	-1,1361662	-0,20164406	96,65	SPTB	spectrin beta, erythrocytic
23786	2,35E-04	3,63E+00	1,47E-04	0,0531	-3,7968562	-0,2016452	1718,49	BCL2L13	BCL2 like 13
100616329	3,38E-01	4,71E-01	2,98E-01	0,1937	-1,0415067	-0,20172003	84,6	MIR4700	microRNA 4700
79869	1,72E-06	5,76E+00	9,41E-07	0,0412	-4,9035603	-0,20187403	8002,99	CPSF7	cleavage and polyadenylation specific factor 7
94240	2,66E-01	5,75E-01	2,29E-01	0,1679	-1,2027218	-0,20190055	107,58	EPSTI1	epithelial stromal interaction 1
317662	1,55E-04	3,81E+00	9,52E-05	0,0518	-3,9024944	-0,20200764	2048,42	FAM149B1	family with sequence similarity 149 member B1
493900	5,42E-01	2,66E-01	5,01E-01	0,3002	-0,6733784	-0,20212436	32,94	TMEM9B-AS	TMEM9B antisense RNA 1
1656	2,62E-07	6,58E+00	1,37E-07	0,0384	-5,269323	-0,20222718	9004,23	DDX6	DEAD-box helicase 6
50807	5,87E-06	5,23E+00	3,30E-06	0,0435	-4,6511178	-0,20236206	7105,22	ASAP1	ArfGAP with SH3 domain, ankyrin repeat and PH domain 1
388436	7,70E-01	1,14E-01	7,41E-01	0,6128	-0,3305546	-0,20255669	8,16	LOC388436	uncharacterized protein ENSP00000382042
57584	5,56E-06	5,25E+00	3,12E-06	0,0435	-4,6625458	-0,20261383	7255,64	ARHGAP21	Rho GTPase activating protein 21
3619	1,57E-06	5,80E+00	8,57E-07	0,0413	-4,9218111	-0,20310511	4664,86	INCENP	inner centromere protein
374868	7,53E-03	2,12E+00	5,34E-03	0,0729	-2,7859231	-0,20311311	845,67	ATP9B	ATPase phospholipid transporting 9B (putative)
105372411	4,06E-01	3,91E-01	3,65E-01	0,2243	-0,9064064	-0,20326989	63,24	LOC105372	uncharacterized LOC105372411
23633	4,73E-06	5,33E+00	2,65E-06	0,0433	-4,6964515	-0,20340996	6200,69	KPNA6	karyopherin subunit alpha 6
123355	4,79E-02	1,32E+00	3,70E-02	0,0977	-2,0855257	-0,20375688	370,07	LRRC28	leucine rich repeat containing 28
105376046	5,66E-01	2,47E-01	5,26E-01	0,3215	-0,6347466	-0,20404199	28,37	LOC105376046	
147007	8,86E-04	3,05E+00	5,79E-04	0,0593	-3,4412317	-0,20407093	1440,17	TMEM199	transmembrane protein 199
1786	1,48E-07	6,83E+00	7,62E-08	0,038	-5,3758031	-0,20426908	24218,92	DNMT1	DNA methyltransferase 1
105371050	1,31E-01	8,83E-01	1,08E-01	0,1271	-1,607546	-0,20432377	193,49	LOC105371	uncharacterized LOC105371050
84084	6,88E-01	1,62E-01	6,53E-01	0,455	-0,4493776	-0,20446397	15,05	RAB6C	RAB6C, member RAS oncogene family
8550	1,59E-04	3,80E+00	9,82E-05	0,0525	-3,8950147	-0,20451884	2051,37	MAPKAPK5	MAPK activated protein kinase 5
9854	9,94E-04	3,00E+00	6,51E-04	0,0601	-3,4093241	-0,20483574	2216,47	C2CD2L	C2CD2 like
2077	9,49E-05	4,02E+00	5,75E-05	0,0509	-4,0228374	-0,204846	2754,09	ERF	ETS2 repressor factor
101928062	3,64E-01	4,39E-01	3,23E-01	0,2073	-0,9885339	-0,20491278	69,67	PRANCR	progenitor renewal associated non-coding RNA
159686	3,27E-01	4,85E-01	2,88E-01	0,1928	-1,0629067	-0,20494419	97,25	CFAP58	cilia and flagella associated protein 58
5902	1,26E-04	3,90E+00	7,72E-05	0,0519	-3,9527891	-0,20505782	6000,54	RANBP1	RAN binding protein 1
4790	3,96E-06	5,40E+00	2,20E-06	0,0433	-4,7336788	-0,20509922	4346,32	NFKB1	nuclear factor kappa B subunit 1
7701	1,96E-04	3,71E+00	1,22E-04	0,0534	-3,8427917	-0,20539317	1773,66	ZNF142	zinc finger protein 142
83734	1,51E-01	8,21E-01	1,25E-01	0,1342	-1,5327201	-0,20570204	184,49	ATG10	autophagy related 10
338707	2,25E-01	6,48E-01	1,91E-01	0,1575	-1,3066723	-0,2058617	144,28	B4GALNT4	beta-1,4-N-acetyl-galactosaminyltransferase 4
8760	6,06E-05	4,22E+00	3,62E-05	0,0498	-4,1304805	-0,20589683	3617,07	CDS2	CDP-diacylglycerol synthase 2
101929272	6,72E-01	1,73E-01	6,37E-01	0,4364	-0,4720034	-0,20596217	16,11	DTNB-AS1	DTNB antisense RNA 1
7546	5,44E-02	1,26E+00	4,24E-02	0,1018	-2,0294852	-0,20657804	347,97	ZIC2	Zic family member 2
107986195	5,81E-01	2,36E-01	5,41E-01	0,3379	-0,6115586	-0,20664352	25,74	LOC107986	uncharacterized LOC107986195
100616483	2,49E-01	6,04E-01	2,14E-01	0,1663	-1,2426615	-0,20669403	110,93	MIR4751	microRNA 4751
283687	2,44E-01	6,13E-01	2,09E-01	0,1646	-1,2562134	-0,20676108	114,82	ST20-AS1	ST20 antisense RNA 1
374666	6,53E-02	1,19E+00	5,14E-02	0,1062	-1,9483428	-0,20683143	386,5	WASH3P	WASP family homolog 3, pseudogene
171391	3,65E-01	4,38E-01	3,24E-01	0,2098	-0,9858363	-0,206854	70,01	GATD1-DT	GATD1 divergent transcript
101928545	5,58E-01	2,53E-01	5,17E-01	0,3196	-0,6474273	-0,20690963	29,34	SEPTIN7-DT	SEPTIN7 divergent transcript
100128055	7,99E-02	1,10E+00	6,36E-02	0,1117	-1,8547936	-0,20715189	254,28	SMARCA5-A	SMARCA5 antisense RNA 1
1849	5,60E-05	4,25E+00	3,34E-05	0,05	-4,1491069	-0,20736934	3338,42	DUSP7	dual specificity phosphatase 7
65072	1,89E-01	7,24E-01	1,59E-01	0,1472	-1,4086144	-0,20740686	146,19	CFLAR-AS1	CFLAR antisense RNA 1
1821	4,00E-01	3,98E-01	3,59E-01	0,2261	-0,9173396	-0,20742523	58,32	DRP2	dystrophin related protein 2
55068	6,83E-02	1,17E+00	5,39E-02	0,1076	-1,9276616	-0,2074916	284,61	ENOX1	ecto-NOX disulfide-thiol exchanger 1
8884	1,61E-04	3,79E+00	9,93E-05	0,0534	-3,8922713	-0,20778622	2770,47	SLC5A6	solute carrier family 5 member 6
2534	8,66E-05	4,06E+00	5,24E-05	0,0514	-4,0448136	-0,20789831	2105,75	FYN	FYN proto-oncogene, Src family tyrosine kinase
222166	1,54E-02	1,81E+00	1,12E-02	0,082	-2,5359714	-0,20790359	547,21	MTURN	maturin, neural progenitor differentiation regulator homolog
9333	5,93E-01	2,27E-01	5,54E-01	0,3513	-0,5918647	-0,20794226	23,77	TGM5	transglutaminase 5
10623	2,60E-05	4,59E+00	1,52E-05	0,0481	-4,3260851	-0,20796015	2674,33	POLR3C	RNA polymerase III subunit C
79925	4,61E-01	3,36E-01	4,19E-01	0,2581	-0,8074929	-0,20838283	44,81	SPEF2	sperm flagellar 2
729967	2,03E-02	1,69E+00	1,50E-02	0,0856	-2,4331388	-0,20839549	492,15	MORN2	MORN repeat containing 2
102724135	6,40E-02	1,19E+00	5,03E-02	0,1065	-1,9573266	-0,20850594	298,51	LOC102724	uncharacterized LOC102724135
8573	3,41E-05	4,47E+00	2,00E-05	0,0491	-4,264417	-0,20918439	3597,57	CASK	calcium/calmodulin dependent serine protein kinase
55565	1,65E-01	7,83E-01	1,37E-01	0,141	-1,4865707	-0,20958677	155,73	ZNF821	zinc finger protein 821
6304	2,73E-03	2,56E+00	1,85E-03	0,0673	-3,1126791	-0,2096151	922,12	SATB1	SATB homeobox 1
91833	7,33E-04	3,13E+00	4,76E-04	0,06	-3,4940115	-0,20962444	1555,32	WDR20	WD repeat domain 20
28951	7,45E-04	3,13E+00	4,84E-04	0,0601	-3,4893724	-0,20965231	2120,7	TRIB2	tribbles pseudokinase 2
79850	2,34E-04	3,63E+00	1,46E-04	0,0552	-3,7974252	-0,20973018	1585,26	TLCD3A	TLC domain containing 3A
112268437	3,27E-02	1,49E+00	2,48E-02	0,0935	-2,245057	-0,20991285	400,61	LOC112268	uncharacterized protein FLJ45252
100287482	6,27E-01	2,03E-01	5,89E-01	0,3888	-0,5401199	-0,20999459	20,8	SMKR1	small lysine rich protein 1
10232	7,99E-03	2,10E+00	5,67E-03	0,0759	-2,7660777	-0,21004878	1144,58	MSLN	mesothelin
109729127	4,86E-03	2,31E+00	3,38E-03	0,0717	-2,9307506	-0,21008349	854,59	KRT7-AS	KRT7 antisense RNA 1
389524	1,49E-01	8,27E-01	1,23E-01	0,1363	-1,5416685	-0,21013277	190,26	GTF2IRD2B	GTF2I repeat domain containing 2B
3078	6,02E-01	2,20E-01	5,63E-01	0,3636	-0,5781977	-0,21023104	22,36	CFHR1	complement factor H related 1
283377	1,75E-02	1,76E+00	1,29E-02	0,0845	-2,4876434	-0,21030019	507,69	SPRYD4	SPRY domain containing 4
4678	2,01E-05	4,70E+00	1,17E-05	0,048	-4,3838808	-0,21035298	15676,31	NASP	nuclear autoantigenic sperm protein
7050	1,59E-04	3,80E+00	9,77E-05	0,054	-3,8962284	-0,21036141	2619,85	TGIF1	TGFB induced factor homeobox 1

23095	3,44E-05	4,46E+00	2,03E-05	0,0494	-4,2620654	-0,21041028	3840,13	KIF1B	kinesin family member 1B
92565	3,16E-01	5,00E-01	2,77E-01	0,1939	-1,0866358	-0,21069453	85,69	FANK1	fibronectin type III and ankyrin repeat domains 1
9528	9,15E-05	4,04E+00	5,54E-05	0,0523	-4,0314897	-0,2107053	5495,33	TMEM59	transmembrane protein 59
404220	7,56E-04	3,12E+00	4,92E-04	0,0605	-3,4851155	-0,21074938	2185,1	TEX56P	testis expressed 56, pseudogene
8563	5,87E-05	4,23E+00	3,50E-05	0,0509	-4,1379475	-0,21077851	1891,3	THOC5	THO complex subunit 5
339210	2,08E-01	6,82E-01	1,77E-01	0,156	-1,3512624	-0,21082015	125,22	C17orf67	chromosome 17 open reading frame 67
100101478	5,49E-01	2,60E-01	5,08E-01	0,3185	-0,6619129	-0,21083389	29,52	H2BW3P	H2B.W histone 3, pseudogene
64768	5,72E-03	2,24E+00	4,01E-03	0,0733	-2,8773735	-0,21084454	726,91	IPPK	inositol-pentakisphosphate 2-kinase
284004	1,25E-02	1,90E+00	9,06E-03	0,0809	-2,6097319	-0,2110004	548,83	HEXD	hexosaminidase D
105377275	5,27E-01	2,78E-01	4,86E-01	0,3027	-0,6971654	-0,21102608	33,04	LOC10537772	uncharacterized LOC105377275
85358	1,00E-01	1,00E+00	8,08E-02	0,121	-1,7460205	-0,21135083	229,01	SHANK3	SH3 and multiple ankyrin repeat domains 3
8543	4,67E-04	3,33E+00	2,99E-04	0,0584	-3,6162683	-0,21135575	1833,68	LMO4	LIM domain only 4
1497	9,81E-04	3,01E+00	6,42E-04	0,0619	-3,4130229	-0,2113714	1182,74	CTNS	cystinosin, lysosomal cystine transporter
9294	1,59E-01	7,99E-01	1,32E-01	0,1406	-1,5044012	-0,21152869	160,16	S1PR2	sphingosine-1-phosphate receptor 2
64129	1,44E-05	4,84E+00	8,31E-06	0,0475	-4,4569307	-0,21154431	3879,09	TINAGL1	tubulointerstitial nephritis antigen like 1
101927963	3,64E-01	4,39E-01	3,24E-01	0,2144	-0,9867061	-0,21159818	65	DENND3-AS	DENND3 antisense RNA 1
100874006	1,81E-01	7,42E-01	1,52E-01	0,1477	-1,4338884	-0,21177859	143,44	TTC3-AS1	TTC3 antisense RNA 1
140739	8,90E-03	2,05E+00	6,35E-03	0,0777	-2,7289217	-0,21191304	771,9	UBE2F	ubiquitin conjugating enzyme E2 F (putative)
9927	2,80E-07	6,55E+00	1,46E-07	0,0403	-5,2570941	-0,21198854	9092,32	MFN2	mitofusin 2
1594	4,73E-01	3,25E-01	4,31E-01	0,2695	-0,786792	-0,21207386	43,92	CYP27B1	cytochrome P450 family 27 subfamily B member 1
402055	3,24E-04	3,49E+00	2,05E-04	0,0571	-3,7129236	-0,2121897	1430,8	SRRD	SRR1 domain containing
57099	8,63E-03	2,06E+00	6,15E-03	0,0775	-2,739724	-0,21231709	611,59	AVEN	apoptosis and caspase activation inhibitor
10691	4,60E-03	2,34E+00	3,20E-03	0,0721	-2,9481397	-0,21242548	1218,77	GMEB1	glucocorticoid modulatory element binding protein 1
5635	1,01E-04	4,00E+00	6,16E-05	0,053	-4,0065328	-0,21246887	1939	PRPSAP1	phosphoribosyl pyrophosphate synthetase associated protein 1
6678	5,96E-01	2,25E-01	5,58E-01	0,3624	-0,5864148	-0,21248892	23,28	SPARC	secreted protein acidic and cysteine rich
84879	5,50E-03	2,26E+00	3,85E-03	0,0736	-2,8902836	-0,21261355	725,45	MFSD2A	MFSD2 lysolipid transporter A, lysophospholipid
2298	6,01E-01	2,21E-01	5,62E-01	0,3668	-0,5796761	-0,21264437	23,42	FOXD4	forkhead box D4
283335	2,98E-01	5,26E-01	2,59E-01	0,1887	-1,1278811	-0,2127927	86,87	TNS2-AS1	TNS2 antisense RNA 1
83595	5,83E-01	2,34E-01	5,43E-01	0,3501	-0,6081199	-0,21292288	24,15	SOX7	SRY-box transcription factor 7
8888	2,28E-06	5,64E+00	1,25E-06	0,0439	-4,8470133	-0,21299381	3908,1	MCM3AP	minichromosome maintenance complex component 3 associated protein
7385	4,02E-06	5,40E+00	2,24E-06	0,045	-4,7309063	-0,21305266	4685,93	UQCRC2	ubiquinol-cytochrome c reductase core protein 2
105372602	3,66E-01	4,37E-01	3,26E-01	0,2169	-0,9827014	-0,21317251	63,7	LOC10537260	uncharacterized LOC105372602
105372621	6,22E-02	1,21E+00	4,88E-02	0,1082	-1,9703334	-0,21319363	317,84	LOC10537262	uncharacterized LOC105372621
9737	5,13E-01	2,90E-01	4,71E-01	0,2962	-0,7203219	-0,21335203	33,68	GPRASP1	G protein-coupled receptor associated sorting protein 1
1141	1,51E-04	3,82E+00	9,32E-05	0,0546	-3,9077196	-0,21338299	2049,99	CHRNB2	cholinergic receptor nicotinic beta 2 subunit
10270	9,80E-06	5,01E+00	5,59E-06	0,047	-4,5414279	-0,2134891	2847,8	AKAP8	A-kinase anchoring protein 8
2968	2,26E-03	2,65E+00	1,53E-03	0,0674	-3,1692891	-0,21351646	2299,68	GTF2H4	general transcription factor IIH subunit 4
100529257	4,84E-03	2,32E+00	3,37E-03	0,0728	-2,932247	-0,21354129	832,2	SYNJ2BP-C(	SYNJ2BP-COX16 readthrough
90271	5,22E-01	2,82E-01	4,81E-01	0,3034	-0,7054757	-0,21404894	34,51	OLMALINC	oligodendrocyte maturation-associated long intergenic non-coding RNA
106707243	2,47E-01	6,07E-01	2,12E-01	0,1714	-1,2491885	-0,21405337	103,4	PRH1-TAS2I	PRH1-TAS2R14 readthrough
2627	1,67E-03	2,78E+00	1,11E-03	0,0657	-3,2600023	-0,21407267	973,07	GATA6	GATA binding protein 6
101927541	5,52E-01	2,58E-01	5,11E-01	0,3258	-0,6571294	-0,2140731	30,56	LINC01273	long intergenic non-protein coding RNA 1273
11346	1,26E-03	2,90E+00	8,30E-04	0,0642	-3,3425396	-0,21446227	1179,89	SYNPO	synaptopodin
27102	1,54E-07	6,81E+00	7,97E-08	0,04	-5,3677571	-0,21457462	6683,31	EIF2AK1	eukaryotic translation initiation factor 2 alpha kinase 1
105377945	3,23E-02	1,49E+00	2,45E-02	0,0954	-2,2497537	-0,21467509	368,92	LOC10537794	uncharacterized LOC105377945
10929	4,90E-05	4,31E+00	2,91E-05	0,0514	-4,1801832	-0,21503201	2050,5	SRSF8	serine and arginine rich splicing factor 8
101927100	7,09E-01	1,49E-01	6,75E-01	0,5136	-0,4188245	-0,2150943	12,07	TICAM2-AS1	TICAM2 antisense RNA 1
155054	1,50E-01	8,24E-01	1,24E-01	0,1401	-1,5361566	-0,21517855	170,31	ZNF425	zinc finger protein 425
51083	5,31E-01	2,75E-01	4,90E-01	0,3115	-0,6909038	-0,2152019	30,27	GAL	galanin and GMAP prepropeptide
105370409	5,62E-01	2,50E-01	5,21E-01	0,3355	-0,6414846	-0,21520377	27,77	LOC10537040	uncharacterized LOC105370409
23070	8,20E-07	6,09E+00	4,39E-07	0,0426	-5,0511314	-0,21526399	5724,51	CMTR1	cap methyltransferase 1
622	1,51E-04	3,82E+00	9,29E-05	0,0552	-3,9083157	-0,2155647	1683,62	BDH1	3-hydroxybutyrate dehydrogenase 1
611	2,94E-01	5,32E-01	2,56E-01	0,1898	-1,1360799	-0,21560467	83,69	OPN1SW	opsin 1, short wave sensitive
23067	4,52E-04	3,34E+00	2,89E-04	0,0595	-3,6252826	-0,21577704	1603,16	SETD1B	SET domain containing 1B, histone lysine methyltransferase
127002	3,99E-02	1,40E+00	3,06E-02	0,0998	-2,1627824	-0,21587418	366,11	ATXN7L2	ataxin 7 like 2
64112	2,72E-04	3,57E+00	1,71E-04	0,0575	-3,7590847	-0,21602596	1553,4	MOAP1	modulator of apoptosis 1
85366	4,82E-01	3,17E-01	4,40E-01	0,2808	-0,7715176	-0,21666027	38,37	MYLK2	myosin light chain kinase 2
9026	5,48E-04	3,26E+00	3,52E-04	0,0606	-3,5736222	-0,21670751	2066,31	HIP1R	huntingtin interacting protein 1 related
100271722	4,49E-01	3,48E-01	4,07E-01	0,2616	-0,8287416	-0,21681461	42,56	LINC00899	long intergenic non-protein coding RNA 899
2274	4,03E-05	4,39E+00	2,38E-05	0,0513	-4,2256392	-0,21685631	2256,68	FHL2	four and a half LIM domains 2
105378891	7,07E-01	1,51E-01	6,74E-01	0,5154	-0,4207685	-0,21686585	11,08	LOC10537882	uncharacterized LOC105378891
9811	2,58E-03	2,59E+00	1,75E-03	0,0693	-3,1293439	-0,21691787	861,84	CTIF	cap binding complex dependent translation initiation factor
10681	1,31E-04	3,88E+00	7,99E-05	0,055	-3,9445923	-0,21713301	1546,86	GNB5	G protein subunit beta 5
79813	1,73E-05	4,76E+00	1,00E-05	0,0492	-4,4163598	-0,21731938	2637,42	EHMT1	euchromatic histone lysine methyltransferase 1
116843	1,64E-02	1,79E+00	1,20E-02	0,0866	-2,511927	-0,21758264	608,7	SLC18B1	solute carrier family 18 member B1
728568	4,31E-03	2,37E+00	2,99E-03	0,0735	-2,9692475	-0,21837683	672,07	UQCC6	ubiquinol-cytochrome c reductase complex assembly factor 6
388574	5,48E-01	2,61E-01	5,07E-01	0,329	-0,6640401	-0,21846617	26,87	RPL23AP87	ribosomal protein L23a pseudogene 87
26260	1,75E-02	1,76E+00	1,28E-02	0,0879	-2,4886832	-0,21872779	576,7	FBXO25	F-box protein 25
101930420	2,99E-01	5,24E-01	2,61E-01	0,1946	-1,1241438	-0,21879881	79,73	LOC10193040	DNA primase large subunit-like
23378	1,98E-03	2,70E+00	1,33E-03	0,0683	-3,2089938	-0,21912735	1172,96	RRP8	ribosomal RNA processing 8
100302183	3,59E-02	1,44E+00	2,73E-02	0,0994	-2,2071642	-0,21930478	337,58	MIR1825	microRNA 1825
107987181	3,50E-01	4,56E-01	3,10E-01	0,2162	-1,0154051	-0,21950964	65,93	LOC107987181	
23479	1,28E-04	3,89E+00	7,85E-05	0,0557	-3,9490035	-0,22013972	2400,77	ISCU	iron-sulfur cluster assembly enzyme
150290	1,88E-01	7,26E-01	1,58E-01	0,1559	-1,4121911	-0,22014436	137,98	DUSP18	dual specificity phosphatase 18
65082	2,88E-06	5,54E+00	1,59E-06	0,0459	-4,7993687	-0,22037364	3418,68	VPS33A	VPS33A core subunit of CORVET and HOPS complexes
105372919	6,20E-01	2,08E-01	5,82E-01	0,4009	-0,5498964	-0,22045867	18,48	LOC10537295	replaced by ID 124904599
101927809	5,78E-01	2,38E-01	5,39E-01	0,3585	-0,6150495	-0,22052104	23,37	COSMOC	cell fate and sterol metabolism associated divergent transcript of MOCOS
100128081	5,96E-01	2,25E-01	5,57E-01	0,376	-0,586659	-0,22058211	20,94	JAZF1-AS1	JAZF1 antisense RNA 1
729975	6,55E-01	1,84E-01	6,18E-01	0,4429	-0,4985736	-0,22080213	15,25	LINC01530	long intergenic non-protein coding RNA 1530
257	2,01E-01	6,97E-01	1,70E-01	0,161	-1,3712953	-0,22083202	118,56	ALX3	ALX homeobox 3
105369850	5,64E-01	2,49E-01	5,23E-01	0,3461	-0,6382292	-0,2209118	26,52	LOC10536982	uncharacterized LOC105369850
105377540	8,69E-02	1,06E+00	6,95E-02	0,1217	-1,8152007	-0,22092472	218,23	SAP30-DT	SAP30 divergent transcript
53343	1,58E-03	2,80E+00	1,05E-03	0,0674	-3,2761817	-0,22092796	957,7	NUDT9	nudix hydrolase 9
4292	4,15E-06	5,38E+00	2,31E-06	0,0468	-4,723942	-0,22105345	3586,51	MLH1	mutL homolog 1
824	6,97E-10	9,16E+00	3,23E-10	0,0352	-6,2871028	-0,22114825	39498,79	CAPN2	calpain 2
401472	9,92E-02	1,00E+00	8,00E-02	0,1263	-1,7506438	-0,22119097	196,24	GASAL1	growth arrest associated lncRNA 1
5716	1,49E-04	3,83E+00	9,18E-05	0,0566	-3,9114244	-0,22131407	1893,33	PSMD10	proteasome 26S subunit, non-ATPase 10
490	5,90E-08	7,23E+00	2,98E-08	0,0399	-5,5425798	-0,22140572	10828,59	ATP2B1	ATPase plasma membrane Ca2+ transporting 1
114108587	3,90E-02	1,41E+00	2,98E-02	0,102	-2,1722305	-0,22151458	329,79	ATF7-NPFF	ATF7-NPFF readthrough
7204	5,92E-09	8,23E+00	2,86E-09	0,0373	-5,9395462	-0,22164022	10423,68	TRIO	trio Rho guanine nucleotide exchange factor
199857	2,99E-02	1,52E+00	2,25E-02	0,0972	-2,2809763	-0,22165172	399,92	ALG14	ALG14 UDP-N-acetylglucosaminyltransferase subunit
441191	2,23E-03	2,65E+00	1,51E-03	0,0699	-3,1731445	-0,22166562	782,35	RNF216P1	ring finger protein 216 pseudogene 1
23648	4,04E-04	3,39E+00	2,57E-04	0,0607	-3,6548197	-0,22167572	1361,05	SSBP3	single stranded DNA binding protein 3
161176	1,67E-03	2,78E+00	1,11E-03	0,068	-3,2603094	-0,22179649	858,94	SYNE3	spectrin repeat containing nuclear envelope family member 3
92370	2,96E-02	1,53E+00	2,23E-02	0,0971	-2,2856511	-0,22195369	446,08	PXYLP1	2-phosphoxylose phosphatase 1
84498	4,44E-05	4,35E+00	2,63E-05	0,0528	-4,2033473	-0,22200949	1899,65	FAM120B	family with sequence similarity 120B
4952	5,64E-07	6,25E+00	3,00E-07	0,0433	-5,1234831	-0,22202778	3992,65	OCRL	OCRL inositol polyphosphate-5-phosphatase
10194	1,69E-02	1,77E+00	1,24E-02	0,089	-2,500261	-0,22258458	439,61	TSHZ1	teashirt zinc finger homeobox 1
84327	9,17E-05	4,04E+00	5,55E-05	0,0553	-4,0311461	-0,22282268	1525,55	ZBED3	zinc finger BED-type containing 3
374286	4,77E-01	3,21E-01	4,35E-01	0,2857	-0,7799143	-0,22285207	37,13	FBXW10B	F-box and WD repeat domain containing 10B
283038	5,19E-01	2,85E-01	4,77E-01	0,3136	-0,7106931	-0,22287594	29,8	LOC283038	uncharacterized LOC283038
3945	2,29E-07	6,64E+00	1,19E-07	0,0421	-5,2945359	-0,22290001	26754,93	LDHB	lactate dehydrogenase B
81873	9,97E-06	5,00E+00	5,69E-06	0,0491	-4,537587	-0,22299918	2731,51	ARPC5L	actin related protein 2/3 complex subunit 5 like
2030	2,93E-06	5,53E+00	1,62E-06	0,0465	-4,7960715	-0,22302999	13188,21	SLC29A1	solute carrier family 29 member 1 (Augustine blood group)
79145	9,03E-03	2,04E+00	6,45E-03	0,0819	-2,7238173	-0,22305192	719,05	CHCHD7	coiled-coil-helix-coiled-coil-helix domain containing 7
221504	2,39E-04	3,62E+00	1,50E-04	0,0588	-3,7914553	-0,22308849	1536,46	ZBTB9	zinc finger and BTB domain containing 9
3550	1,85E-05	4,73E+00	1,07E-05	0,0507	-4,4024689	-0,22323654	9323,05	IK	IK cytokine
51230	6,90E-05	4,16E+00	4,14E-05	0,0545	-4,0994515	-0,22323935	4153,53	PHF20	PHD finger protein 20
4899	1,54E-03	2,81E+00	1,03E-03	0,068	-3,2829201	-0,22333509	927,19	NRF1	nuclear respiratory factor 1
4520	9,73E-05	4,01E+00	5,90E-05	0,0556	-4,0168206	-0,22343073	1429,77	MTF1	metal regulatory transcription factor 1
151176	1,31E-01	8,83E-01	1,07E-01	0,1388	-1,6101154	-0,22355285	163,75	ERFE	erythroferrone
79796	2,23E-05	4,65E+00	1,30E-05	0,0513	-4,3605071	-0,22358933	2358,94	ALG9	ALG9 alpha-1,2-mannosyltransferase
55039	1,22E-01	9,14E-01	1,00E-01	0,1362	-1,6443407	-0,22396979	176,52	TRMT12	tRNA methyltransferase 12 homolog
4724	1,51E-05	4,82E+00	8,70E-06	0,0504	-4,4470703	-0,22403418	2597,52	NDUFS4	NADH:ubiquinone oxidoreductase subunit S4
145165	3,01E-01	5,21E-01	2,62E-01	0,2001	-1,120521	-0,2242191	76,3	ST13P4	ST13, Hsp70 interacting protein pseudogene 4
5982	4,42E-07	6,35E+00	2,34E-07	0,0434	-5,1703791	-0,22440204	3586,47	RFC2	replication factor C subunit 2
106635533	2,74E-03	2,56E+00	1,86E-03	0,0722	-3,1113161	-0,22459886	765,34	SNORA103	small nucleolar RNA, H/ACA box 103
1646	4,46E-01	3,51E-01	4,05E-01	0,2698	-0,8328417	-0,22470734	40,52	AKR1C2	aldo-keto reductase family 1 member C2
5337	2,08E-03	2,68E+00	1,40E-03	0,0704	-3,1950723	-0,22485581	845,7	PLD1	phospholipase D1
80339	2,35E-01	6,29E-01	2,01E-01	0,1759	-1,2791768	-0,22494889	101,87	PNPLA3	patatin like phospholipase domain containing 3

84034	1,08E-02	1,97E+00	7,80E-03	0,0846	-2,6607811	-0,2250007	548,07	EMILIN2	elastin microfibril interfacer 2
5824	5,90E-08	7,23E+00	2,98E-08	0,0406	-5,5424173	-0,22504312	5086,83	PEX19	peroxisomal biogenesis factor 19
6129	4,71E-09	8,33E+00	2,27E-09	0,0377	-5,9775418	-0,22522253	23833,92	RPL7	ribosomal protein L7
54476	9,59E-06	5,02E+00	5,46E-06	0,0496	-4,5462119	-0,22527834	2244,5	RNF216	ring finger protein 216
84342	5,61E-04	3,25E+00	3,61E-04	0,0632	-3,5670517	-0,22537979	1191,63	COG8	component of oligomeric golgi complex 8
538	4,58E-03	2,34E+00	3,18E-03	0,0764	-2,9498393	-0,22541994	634,12	ATP7A	ATPase copper transporting alpha
4947	6,47E-06	5,19E+00	3,64E-06	0,0488	-4,6307107	-0,22579781	3840,87	OAZ2	ornithine decarboxylase antizyme 2
51258	3,06E-06	5,51E+00	1,69E-06	0,0472	-4,7872868	-0,22612496	5033,52	MRPL51	mitochondrial ribosomal protein L51
25983	4,16E-05	4,38E+00	2,46E-05	0,0536	-4,2180514	-0,22619313	2073,29	NGDN	neuroguidin
102465252	4,35E-01	3,62E-01	3,94E-01	0,2654	-0,8525255	-0,22624427	43,51	MIR6506	microRNA 6506
91782	3,93E-06	5,41E+00	2,19E-06	0,0478	-4,7352293	-0,22642365	3256,08	CHMP7	charged multivesicular body protein 7
23016	1,86E-04	3,73E+00	1,15E-04	0,0588	-3,8557353	-0,22677049	1637,74	EXOSC7	exosome component 7
6611	2,76E-07	6,56E+00	1,45E-07	0,0431	-5,2594302	-0,22686448	12285,59	SMS	spermine synthase
373863	1,61E-02	1,79E+00	1,18E-02	0,0901	-2,51943	-0,22693087	419,63	DND1	DND microRNA-mediated repression inhibitor 1
2992	6,53E-04	3,19E+00	4,22E-04	0,0644	-3,5258186	-0,22698108	1247,95	GYG1	glycogenin 1
102466719	4,24E-01	3,73E-01	3,83E-01	0,2601	-0,8726819	-0,22701149	45,14	MIR6716	microRNA 6716
100131089	6,85E-01	1,64E-01	6,50E-01	0,5005	-0,4539485	-0,22719162	12,31	SRP14-DT	SRP14 divergent transcript
148479	1,09E-04	3,96E+00	6,61E-05	0,0569	-3,9898804	-0,22721009	1463,29	PHF13	PHD finger protein 13
107986571	2,68E-01	5,72E-01	2,32E-01	0,1899	-1,1964181	-0,22721239	84,51	LOC107986571	uncharacterized LOC107986571
8776	1,22E-06	5,91E+00	6,63E-07	0,0458	-4,9720409	-0,22750633	3176,22	MTMR1	myotubularin related protein 1
9219	5,48E-09	8,26E+00	2,64E-09	0,0382	-5,9524503	-0,22755516	9806,84	MTA2	metastasis associated 1 family member 2
116225	3,33E-03	2,48E+00	2,28E-03	0,0746	-3,0511138	-0,22769143	1201	ZMYND19	zinc finger MYND-type containing 19
51441	2,13E-07	6,67E+00	1,11E-07	0,0429	-5,3079492	-0,22770225	5889,4	YTHDF2	YTH N6-methyladenosine RNA binding protein 2
55670	1,64E-04	3,79E+00	1,01E-04	0,0587	-3,8879776	-0,22810398	1425,5	PEX26	peroxisomal biogenesis factor 26
112268150	3,45E-01	4,62E-01	3,05E-01	0,2227	-1,0251146	-0,22827622	62,69	LOC112268	uncharacterized LOC112268150
29801	1,89E-03	2,72E+00	1,27E-03	0,0709	-3,2234877	-0,22839485	1103,65	ZDHHC8	zinc finger DHHC-type palmitoyltransferase 8
57215	1,38E-03	2,86E+00	9,13E-04	0,0689	-3,3159498	-0,22853808	1192,98	THAP11	THAP domain containing 11
100131017	2,62E-03	2,58E+00	1,78E-03	0,0731	-3,1249153	-0,22854192	736,04	ZNF316	zinc finger protein 316
123803	1,79E-05	4,75E+00	1,03E-05	0,0519	-4,4097865	-0,22871904	1859,81	NTAN1	N-terminal asparagine amidase
10480	7,24E-09	8,14E+00	3,51E-09	0,0387	-5,9059054	-0,2287668	10613,73	EIF3M	eukaryotic translation initiation factor 3 subunit M
9855	1,12E-02	1,95E+00	8,04E-03	0,0864	-2,6503987	-0,22893907	499,44	FARP2	FERM, ARH/RhoGEF and pleckstrin domain protein 2
107986411	5,83E-01	2,34E-01	5,43E-01	0,3763	-0,6085726	-0,22897754	21,79	TARS1-DT	TARS1 divergent transcript
55909	7,70E-03	2,11E+00	5,46E-03	0,0824	-2,7784359	-0,22905049	559,3	BIN3	bridging integrator 3
101929231	2,36E-02	1,63E+00	1,75E-02	0,0967	-2,3751026	-0,22955636	389,88	MMADHC-D	MMADHC divergent transcript
23131	4,73E-07	6,33E+00	2,50E-07	0,0445	-5,1573298	-0,22962088	6464,87	GPATCH8	G-patch domain containing 8
2130	5,06E-08	7,30E+00	2,55E-08	0,0413	-5,5701528	-0,22993823	15178,3	EWSR1	EWS RNA binding protein 1
84176	3,45E-01	4,62E-01	3,05E-01	0,2244	-1,0251991	-0,23003193	57,93	MYH16	myosin heavy chain 16 pseudogene
26958	5,18E-06	5,29E+00	2,91E-06	0,0492	-4,6773852	-0,23005948	2845,93	COPG2	COPI coat complex subunit gamma 2
51530	1,52E-03	2,82E+00	1,01E-03	0,07	-3,2878673	-0,23010098	888,01	ZC3HC1	zinc finger C3HC-type containing 1
105377290	5,99E-01	2,23E-01	5,61E-01	0,3956	-0,5818791	-0,23018111	18,98	LOC105377	uncharacterized LOC105377290
728577	1,82E-01	7,40E-01	1,53E-01	0,1612	-1,429467	-0,23040695	118,83	CNTNAP3B	contactin associated protein family member 3B
1854	2,92E-04	3,53E+00	1,84E-04	0,0616	-3,7397968	-0,23045436	2031,76	DUT	deoxyuridine triphosphatase
146712	5,27E-03	2,28E+00	3,68E-03	0,0794	-2,9043649	-0,23049248	620,65	B3GNTL1	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase like 1
57205	9,66E-05	4,02E+00	5,86E-05	0,0574	-4,0185319	-0,23062797	2070,92	ATP10D	ATPase phospholipid transporting 10D (putative)
51103	1,93E-02	1,71E+00	1,42E-02	0,0941	-2,4525335	-0,23073888	558,49	NDUFAF1	NADH:ubiquinone oxidoreductase complex assembly factor 1
8643	6,33E-01	1,99E-01	5,96E-01	0,4347	-0,5308327	-0,23074447	15,19	PTCH2	patched 2
90410	4,38E-03	2,36E+00	3,04E-03	0,0779	-2,9639846	-0,23075585	656,8	IFT20	intraflagellar transport 20
22980	3,54E-06	5,45E+00	1,96E-06	0,0485	-4,7572063	-0,23075756	3446,3	TCF25	transcription factor 25
126433	6,46E-05	4,19E+00	3,87E-05	0,0561	-4,1152773	-0,23094479	1666,12	FBXO27	F-box protein 27
127943	4,39E-01	3,58E-01	3,98E-01	0,2732	-0,8454674	-0,23095762	39,33	FCRLB	Fc receptor like B
112268140	2,00E-01	6,99E-01	1,69E-01	0,1678	-1,3767965	-0,23095869	109,71	LOC112268	loricrin-like
158293	8,67E-06	5,06E+00	4,92E-06	0,0506	-4,5679944	-0,23098995	2093,54	FAM120AOS	family with sequence similarity 120A opposite strand
8239	8,59E-07	6,07E+00	4,61E-07	0,0459	-5,0419403	-0,23120633	8630,21	USP9X	ubiquitin specific peptidase 9 X-linked
51094	1,05E-07	6,98E+00	5,36E-08	0,0426	-5,4390051	-0,23174488	6169,28	ADIPOR1	adiponectin receptor 1
80324	4,56E-03	2,34E+00	3,16E-03	0,0787	-2,9512525	-0,23236387	782,96	PUS1	pseudouridine synthase 1
114049	9,23E-04	3,03E+00	6,04E-04	0,0678	-3,4300117	-0,23252067	1664,1	BUD23	BUD23 rRNA methyltransferase and ribosome maturation factor
56941	5,63E-06	5,25E+00	3,16E-06	0,0499	-4,6598663	-0,23265336	2588,47	HMCES	5-hydroxymethylcytosine binding, ES cell specific
100505715	5,19E-01	2,85E-01	4,77E-01	0,3273	-0,7108558	-0,23266441	28,67	LOC100505	uncharacterized LOC100505715
158801	3,50E-01	4,56E-01	3,09E-01	0,2289	-1,0167241	-0,23269004	57,92	NKAPP1	NFKB activating protein pseudogene 1
55122	2,75E-04	3,56E+00	1,73E-04	0,062	-3,7559441	-0,23271949	1369,9	AKIRIN2	akirin 2
84278	2,63E-02	1,58E+00	1,97E-02	0,0998	-2,3323625	-0,23287793	343,44	MFSD14CP	major facilitator superfamily domain containing 14C, pseudogene
55051	2,15E-06	5,67E+00	1,18E-06	0,0479	-4,859298	-0,23291546	5365,48	NRDE2	NRDE-2, necessary for RNA interference, domain containing
51284	5,90E-01	2,29E-01	5,50E-01	0,3904	-0,5971827	-0,23316938	19,11	TLR7	toll like receptor 7
100506826	2,44E-01	6,13E-01	2,09E-01	0,1857	-1,2555856	-0,23321789	91,2	MYLK-AS1	MYLK antisense RNA 1
7329	4,01E-07	6,40E+00	2,11E-07	0,045	-5,1889979	-0,23330409	7018,28	UBE2I	ubiquitin conjugating enzyme E2 I
219670	6,14E-01	2,12E-01	5,76E-01	0,4172	-0,5597856	-0,23352129	18,32	ENKUR	enkurin, TRPC channel interacting protein
105371502	6,43E-01	1,92E-01	6,06E-01	0,4531	-0,5154658	-0,23354208	14,03	LOC105371	502
23582	8,25E-05	4,08E+00	4,98E-05	0,0576	-4,0566454	-0,23357431	1681,63	CCNDBP1	cyclin D1 binding protein 1
79770	3,32E-06	5,48E+00	1,84E-06	0,049	-4,7700997	-0,23362433	2480,52	TXNDC15	thioredoxin domain containing 15
1416	3,61E-03	2,44E+00	2,48E-03	0,0772	-3,0259757	-0,2336582	747,88	CRYBB2P1	crystallin beta B2 pseudogene 1
116983	9,24E-04	3,03E+00	6,04E-04	0,0681	-3,4296909	-0,23369706	1122,88	ACAP3	ArfGAP with coiled-coil, ankyrin repeat and PH domains 3
5959	4,46E-01	3,51E-01	4,04E-01	0,2803	-0,8340392	-0,23376082	36,92	RDH5	retinol dehydrogenase 5
3925	5,41E-07	6,27E+00	2,87E-07	0,0456	-5,1314882	-0,23385831	30224,64	STMN1	stathmin 1
163	1,26E-10	9,90E+00	5,66E-11	0,0357	-6,5525129	-0,23391464	43227,14	AP2B1	adaptor related protein complex 2 subunit beta 1
161291	5,40E-01	2,68E-01	4,99E-01	0,3457	-0,6766122	-0,2339333	26,54	TMEM30B	transmembrane protein 30B
79844	2,25E-01	6,48E-01	1,91E-01	0,1791	-1,306694	-0,23408784	106,34	ZDHHC11	zinc finger DHHC-type containing 11
51726	2,38E-05	4,62E+00	1,39E-05	0,0539	-4,3459321	-0,23427157	5769,79	DNAJB11	DnaJ heat shock protein family (Hsp40) member B11
3561	6,50E-01	1,87E-01	6,13E-01	0,4636	-0,5054238	-0,23433203	13,68	IL2RG	interleukin 2 receptor subunit gamma
90204	1,38E-03	2,86E+00	9,13E-04	0,0707	-3,3161433	-0,23434292	886,1	ZSWIM1	zinc finger SWIM-type containing 1
5335	1,06E-08	7,97E+00	5,15E-09	0,0401	-5,8422525	-0,23446283	6404,21	PLCG1	phospholipase C gamma 1
80195	3,38E-03	2,47E+00	2,32E-03	0,077	-3,0461312	-0,23456486	698,11	TMEM254	transmembrane protein 254
5869	1,71E-06	5,77E+00	9,33E-07	0,0479	-4,9053218	-0,23491775	2862,1	RAB5B	RAB5B, member RAS oncogene family
51241	7,77E-04	3,11E+00	5,06E-04	0,0676	-3,4774522	-0,23507675	943,39	COX16	cytochrome c oxidase assembly factor COX16
51429	4,42E-06	5,35E+00	2,47E-06	0,0499	-4,7108388	-0,2350821	2780,05	SNX9	sorting nexin 9
55063	5,60E-03	2,25E+00	3,92E-03	0,0815	-2,8844161	-0,2352053	644,19	ZCWPW1	zinc finger CW-type and PWWP domain containing 1
10049	3,88E-08	7,41E+00	1,94E-08	0,0419	-5,6172596	-0,23552251	14772,92	DNAJB6	DnaJ heat shock protein family (Hsp40) member B6
642	2,84E-07	6,55E+00	1,49E-07	0,0449	-5,2540331	-0,23582269	3694,42	BLMH	bleomycin hydrolase
4301	6,97E-07	6,16E+00	3,72E-07	0,0464	-5,0826021	-0,23586586	4596,76	AFDN	afadin, adherens junction formation factor
58160	4,92E-01	3,08E-01	4,50E-01	0,3123	-0,7557653	-0,23600767	29,69	NFE4	nuclear factor, erythroid 4
10204	2,04E-06	5,69E+00	1,12E-06	0,0485	-4,8694511	-0,23628562	5737,28	NUTF2	nuclear transport factor 2
138050	9,02E-07	6,04E+00	4,85E-07	0,047	-5,0322212	-0,23641909	2600,01	HGSNAT	heparan-alpha-glucosaminide N-acetyltransferase
105371729	2,19E-03	2,66E+00	1,47E-03	0,0744	-3,1796156	-0,23650606	1058,06	LOC105371	uncharacterized LOC105371729
83987	2,38E-03	2,62E+00	1,61E-03	0,075	-3,1536379	-0,23650883	666,86	CCDC8	coiled-coil domain containing 8
27183	1,42E-08	7,85E+00	6,98E-09	0,0409	-5,7913916	-0,23659398	4855,38	VPS4A	vacuolar protein sorting 4 homolog A
54993	7,50E-02	1,12E+00	5,95E-02	0,1257	-1,8845173	-0,23695539	200,2	ZSCAN2	zinc finger and SCAN domain containing 2
100126321	4,00E-01	3,98E-01	3,59E-01	0,2584	-0,9170626	-0,23697991	44,09	MIR922	microRNA 922
23214	4,84E-07	6,32E+00	2,57E-07	0,046	-5,1528406	-0,23699295	5621,55	XPO6	exportin 6
1845	1,17E-07	6,93E+00	6,00E-08	0,0438	-5,4188856	-0,23707847	4295,8	DUSP3	dual specificity phosphatase 3
84532	4,35E-02	1,36E+00	3,35E-02	0,1116	-2,1264368	-0,23722631	287,36	ACSS1	acyl-CoA synthetase short chain family member 1
140894	3,50E-01	4,56E-01	3,10E-01	0,234	-1,0149825	-0,23745518	53,96	CNBD2	cyclic nucleotide binding domain containing 2
54849	4,39E-04	3,36E+00	2,80E-04	0,0654	-3,6329947	-0,23753017	1370,87	DEF8	differentially expressed in FDCP 8 homolog
8202	2,86E-06	5,54E+00	1,58E-06	0,0495	-4,8010227	-0,23760624	2781,77	NCOA3	nuclear receptor coactivator 3
107984396	2,67E-01	5,73E-01	2,31E-01	0,1984	-1,1978343	-0,23766957	79,61	CENATAC-D	CENATAC divergent transcript
107985720	6,97E-01	1,57E-01	6,63E-01	0,5459	-0,435367	-0,23768412	9,89	LOC107985	uncharacterized LOC107985720
304	1,59E-04	3,80E+00	9,80E-05	0,061	-3,8954658	-0,23774238	2619,5	ANXA2P2	annexin A2 pseudogene 2
50848	9,41E-06	5,03E+00	5,36E-06	0,0524	-4,550301	-0,2382226	1827,58	F11R	F11 receptor
57037	1,36E-03	2,87E+00	9,02E-04	0,0718	-3,3195198	-0,23827742	786,73	ANKMY2	ankyrin repeat and MYND domain containing 2
654342	4,82E-02	1,32E+00	3,73E-02	0,1145	-2,0823477	-0,23835922	243,39	LSP1P4	LSP1 pseudogene 4
23192	1,74E-05	4,76E+00	1,01E-05	0,054	-4,4160799	-0,23841395	1849,27	ATG4B	autophagy related 4B cysteine peptidase
56477	1,55E-02	1,81E+00	1,13E-02	0,0941	-2,5331863	-0,23847929	373,91	CCL28	C-C motif chemokine ligand 28
10040	3,90E-04	3,41E+00	2,48E-04	0,0651	-3,6644107	-0,2385545	1326,81	TOM1L1	target of myb1 like 1 membrane trafficking protein
745	1,40E-03	2,85E+00	9,30E-04	0,0722	-3,310983	-0,2390051	759,83	MYRF	myelin regulatory factor
84433	1,48E-03	2,83E+00	9,82E-04	0,0726	-3,2956217	-0,23912499	839,38	CARD11	caspase recruitment domain family member 11
107985395	5,37E-01	2,70E-01	4,96E-01	0,352	-0,6801813	-0,23943186	23,53	PANK2-AS1	PANK2 antisense RNA 1
106478991	5,75E-01	2,40E-01	5,35E-01	0,3859	-0,6208671	-0,239596	19,81	LINC00449	long intergenic non-protein coding RNA 449
51490	6,36E-05	4,20E+00	3,81E-05	0,0582	-4,1189979	-0,23959839	1460,59	SPOUT1	SPOUT domain containing methyltransferase 1
79774	1,87E-02	1,73E+00	1,37E-02	0,0972	-2,4642171	-0,23960285	352,36	GRTP1	growth hormone regulated TBC protein 1
7458	8,33E-10	9,08E+00	3,88E-10	0,0383	-6,2589356	-0,23983834	18857,05	EIF4H	eukaryotic translation initiation factor 4H
79169	1,80E-03	2,74E+00	1,21E-03	0,0741	-3,2374962	-0,23996148	749,85	C1orf35	chromosome 1 open reading frame 35
4131	7,45E-06	5,13E+00	4,21E-06	0,0522	-4,6005456	-0,24002661	15054,23	MAP1B	microtubule associated protein 1B

80328	1,69E-04	3,77E+00	1,04E-04	0,0619	-3,8799129	-0,24013476	1159,16	ULBP2	UL16 binding protein 2
105180390	6,66E-01	1,77E-01	6,30E-01	0,4983	-0,4820051	-0,240183	11,81	SPDYE13	speedy/RINGO cell cycle regulator family member E13
317762	1,45E-06	5,84E+00	7,88E-07	0,0487	-4,9382729	-0,24028646	4324,26	CCDC85C	coiled-coil domain containing 85C
100188893	2,44E-09	8,61E+00	1,16E-09	0,0395	-6,0856246	-0,24047149	12486,3	TOMM6	translocase of outer mitochondrial membrane 6
54853	6,96E-06	5,16E+00	3,93E-06	0,0521	-4,6150512	-0,24049986	2382,84	WDR55	WD repeat domain 55
6118	1,22E-08	7,91E+00	5,95E-09	0,0413	-5,818064	-0,24054693	5085,9	RPA2	replication protein A2
26773	5,20E-01	2,84E-01	4,78E-01	0,3398	-0,7087842	-0,24084519	25,43	SNORD4A	small nucleolar RNA, C/D box 4A
100129516	3,39E-01	4,70E-01	2,99E-01	0,2319	-1,0389001	-0,24093571	55,54	LINC02012	long intergenic non-protein coding RNA 2012
84989	5,46E-01	2,63E-01	5,05E-01	0,3623	-0,666108	-0,24131649	23,03	JMJD1C-AS1	JMJD1C antisense RNA 1
83636	5,68E-04	3,25E+00	3,65E-04	0,0677	-3,56385	-0,24142528	937,86	C19orf12	chromosome 19 open reading frame 12
80217	5,99E-01	2,23E-01	5,61E-01	0,4153	-0,5818974	-0,24165619	16,72	CFAP43	cilia and flagella associated protein 43
5130	1,82E-08	7,74E+00	8,96E-09	0,042	-5,749418	-0,24174653	4253,98	PCYT1A	phosphate cytidylyltransferase 1A, choline
388962	2,33E-05	4,63E+00	1,36E-05	0,0556	-4,3505061	-0,24178433	1577,94	BOLA3	bolA family member 3
29923	5,37E-03	2,27E+00	3,75E-03	0,0834	-2,8984122	-0,24184235	506,33	HILPDA	hypoxia inducible lipid droplet associated
6478	2,51E-03	2,60E+00	1,70E-03	0,0771	-3,1383	-0,2420117	843,3	SIAH2	siah E3 ubiquitin protein ligase 2
105375259	5,30E-01	2,76E-01	4,89E-01	0,3497	-0,6923999	-0,24210131	28,81	LOC105375259	uncharacterized LOC105375259
3149	4,09E-06	5,39E+00	2,28E-06	0,0512	-4,7272638	-0,24221728	9191,63	HMGB3	high mobility group box 3
58499	2,12E-04	3,67E+00	1,32E-04	0,0634	-3,8226542	-0,24225284	1185,98	ZNF462	zinc finger protein 462
387849	4,83E-01	3,16E-01	4,41E-01	0,3143	-0,770788	-0,24227208	29,98	REP15	RAB15 effector protein
6185	1,50E-10	9,82E+00	6,76E-11	0,0372	-6,525904	-0,24247899	27127,48	RPN2	ribophorin II
23315	5,68E-04	3,25E+00	3,65E-04	0,0681	-3,5638244	-0,24261637	1256,59	SLC9A8	solute carrier family 9 member A8
11181	9,42E-02	1,03E+00	7,57E-02	0,1367	-1,7759655	-0,24279367	168,84	TREH	trehalase
128229	1,64E-01	7,85E-01	1,36E-01	0,163	-1,4900455	-0,24283377	114,28	TSACC	TSSK6 activating cochaperone
51603	7,27E-07	6,14E+00	3,89E-07	0,0479	-5,074397	-0,24284084	2871,79	METTL13	methyltransferase 13, eEF1A lysine and N-terminal methyltransferase
5439	1,46E-04	3,84E+00	8,95E-05	0,062	-3,9174283	-0,24286332	2886,52	POLR2J	RNA polymerase II subunit J
105374721	6,15E-01	2,11E-01	5,77E-01	0,4354	-0,5578011	-0,24286935	16,26	LOC105374721	uncharacterized LOC105374721
10983	3,53E-08	7,45E+00	1,76E-08	0,0431	-5,6337739	-0,24301178	10253,55	CCNI	cyclin I
148103	3,53E-01	4,52E-01	3,13E-01	0,241	-1,0089199	-0,24314723	51,86	ZNF599	zinc finger protein 599
27163	1,42E-03	2,85E+00	9,43E-04	0,0736	-3,3071436	-0,24345583	735,79	NAAA	N-acylethanolamine acid amidase
105378859	3,35E-01	4,75E-01	2,95E-01	0,2326	-1,0466988	-0,24346698	56,81	LOC105378859	
79717	1,29E-03	2,89E+00	8,53E-04	0,0731	-3,3348594	-0,24371286	1331,31	PPCS	phosphopantothenoylcysteine synthetase
4325	3,72E-01	4,29E-01	3,31E-01	0,2508	-0,971577	-0,24371826	47,51	MMP16	matrix metallopeptidase 16
349565	4,12E-01	3,85E-01	3,71E-01	0,2725	-0,8944657	-0,24372623	41,31	NMNAT3	nicotinamide nucleotide adenylyltransferase 3
157638	1,08E-06	5,97E+00	5,83E-07	0,0489	-4,9968908	-0,24417804	2558,83	LRATD2	LRAT domain containing 2
101928725	6,92E-01	1,60E-01	6,58E-01	0,5519	-0,4425907	-0,24425429	10,26	MINDY2-DT	MINDY2 divergent transcript
10197	1,34E-10	9,87E+00	6,05E-11	0,0373	-6,5425769	-0,24426858	14209,11	PSME3	proteasome activator subunit 3
107985767	6,21E-01	2,07E-01	5,83E-01	0,4457	-0,5482932	-0,24435036	14,82	LOC107985767	uncharacterized LOC107985767
105375683	2,86E-01	5,44E-01	2,49E-01	0,2119	-1,1538466	-0,24453856	66,71	LOC105375683	uncharacterized LOC105375683
100506007	5,97E-01	2,24E-01	5,58E-01	0,4179	-0,5852298	-0,24459385	16,7	RTCA-AS1	RTCA antisense RNA 1
23164	3,96E-10	9,40E+00	1,82E-10	0,0384	-6,3760623	-0,24494525	14619,25	MPRIP	myosin phosphatase Rho interacting protein
200014	4,23E-06	5,37E+00	2,36E-06	0,0519	-4,7202862	-0,24515901	2741,87	CC2D1B	coiled-coil and C2 domain containing 1B
200081	5,56E-09	8,25E+00	2,68E-09	0,0413	-5,9500932	-0,24545235	7165,01	TXLNA	taxilin alpha
100528007	9,35E-02	1,03E+00	7,52E-02	0,1379	-1,7794589	-0,24546054	172,05	BORCS7-AS1	BORCS7-ASMT readthrough (NMD candidate)
414765	4,01E-03	2,40E+00	2,77E-03	0,082	-2,9925786	-0,24546102	607,46	HCG25	HLA complex group 25
23235	1,47E-06	5,83E+00	8,00E-07	0,0497	-4,9352838	-0,24549406	2381,4	SIK2	salt inducible kinase 2
92715	3,28E-05	4,48E+00	1,93E-05	0,0574	-4,2732284	-0,24549621	1367,94	DPH7	diphthamide biosynthesis 7
147525	2,81E-01	5,51E-01	2,44E-01	0,2105	-1,1660702	-0,24551044	75,58	LINC00526	long intergenic non-protein coding RNA 526
686	1,22E-06	5,91E+00	6,60E-07	0,0494	-4,9726816	-0,24565328	2179,89	BTD	biotinidase
9734	7,51E-06	5,12E+00	4,25E-06	0,0534	-4,5986722	-0,24566188	2544,5	HDAC9	histone deacetylase 9
204	7,75E-09	8,11E+00	3,76E-09	0,0417	-5,8944858	-0,24589286	11745,8	AK2	adenylate kinase 2
51520	1,82E-10	9,74E+00	8,24E-11	0,0379	-6,4961107	-0,24600739	13552,52	LARS1	leucyl-tRNA synthetase 1
100506713	3,83E-01	4,17E-01	3,41E-01	0,2586	-0,9514311	-0,24603332	44,9	ALOX12-AS1	ALOX12 antisense RNA 1
79089	1,47E-05	4,83E+00	8,49E-06	0,0553	-4,4524655	-0,24605404	2037,1	TMUB2	transmembrane and ubiquitin like domain containing 2
3589	1,76E-07	6,75E+00	9,10E-08	0,046	-5,3438198	-0,24606909	4588,6	IL11	interleukin 11
401577	1,74E-01	7,59E-01	1,45E-01	0,1691	-1,4561499	-0,24620928	118,58	CD99P1	CD99 molecule pseudogene 1
5708	5,23E-13	1,23E+01	2,16E-13	0,0336	-7,3384526	-0,24625447	55832,91	PSMD2	proteasome 26S subunit ubiquitin receptor, non-ATPase 2
112937	5,97E-01	2,24E-01	5,59E-01	0,4216	-0,584589	-0,24643673	17,05	GLB1L3	galactosidase beta 1 like 3
4285	1,74E-03	2,76E+00	1,16E-03	0,076	-3,2477805	-0,24669886	648	MIPEP	mitochondrial intermediate peptidase
51061	1,58E-04	3,80E+00	9,74E-05	0,0634	-3,8969628	-0,24694084	1105,98	TXNDC11	thioredoxin domain containing 11
112268432	6,70E-01	1,74E-01	6,34E-01	0,5195	-0,4757183	-0,24713779	10,59	LOC112268432	uncharacterized LOC112268432
10449	1,11E-07	6,95E+00	5,67E-08	0,0455	-5,428786	-0,2471705	2952,26	ACAA2	acetyl-CoA acyltransferase 2
100533179	1,12E-03	2,95E+00	7,41E-04	0,0733	-3,3741265	-0,24733263	859,91	UBE2F-SCLY	UBE2F-SCLY readthrough (NMD candidate)
2224	1,45E-07	6,84E+00	7,48E-08	0,046	-5,3792904	-0,24737729	4592,93	FDPS	farnesyl diphosphate synthase
10129	1,35E-01	8,70E-01	1,11E-01	0,1555	-1,5942543	-0,24787713	140,1	FRY	FRY microtubule binding protein
7187	2,69E-07	6,57E+00	1,40E-07	0,0471	-5,264681	-0,24787923	2501,15	TRAF3	TNF receptor associated factor 3
84449	7,72E-03	2,11E+00	5,48E-03	0,0893	-2,7775061	-0,24799482	540,43	ZNF333	zinc finger protein 333
10063	1,42E-04	3,85E+00	8,69E-05	0,0633	-3,9245516	-0,24827603	1054,11	COX17	cytochrome c oxidase copper chaperone COX17
124401	3,33E-02	1,48E+00	2,52E-02	0,111	-2,2378157	-0,24828707	275,31	ANKS3	ankyrin repeat and sterile alpha motif domain containing 3
9805	2,07E-10	9,68E+00	9,39E-11	0,0384	-6,4763857	-0,24838867	11580,34	SCRN1	secernin 1
9828	1,18E-04	3,93E+00	7,17E-05	0,0626	-3,9706326	-0,24847272	1754,63	ARHGEF17	Rho guanine nucleotide exchange factor 17
2886	1,27E-01	8,96E-01	1,04E-01	0,1528	-1,6272438	-0,24858616	134,14	GRB7	growth factor receptor bound protein 7
128387	3,13E-02	1,50E+00	2,37E-02	0,1099	-2,2627611	-0,24860128	278,24	TATDN3	TatD DNase domain containing 3
404550	1,05E-01	9,79E-01	8,50E-02	0,1443	-1,7224528	-0,24861582	213,45	C16orf74	chromosome 16 open reading frame 74
93109	1,11E-03	2,95E+00	7,31E-04	0,0737	-3,3776153	-0,24876978	726,38	TMEM44	transmembrane protein 44
7023	1,77E-03	2,75E+00	1,18E-03	0,0767	-3,2424762	-0,24882245	786,12	TFAP4	transcription factor AP-4
79867	1,17E-03	2,93E+00	7,72E-04	0,074	-3,3626	-0,24897325	712,44	TCTN2	tectonic family member 2
1687	7,93E-06	5,10E+00	4,49E-06	0,0543	-4,5871489	-0,24910051	2160,18	GSDME	gasdermin E
64130	2,84E-01	5,47E-01	2,46E-01	0,2148	-1,1598035	-0,24911348	68,55	LIN7B	lin-7 homolog B, crumbs cell polarity complex component
4905	9,05E-08	7,04E+00	4,61E-08	0,0456	-5,465589	-0,249232	4186,78	NSF	N-ethylmaleimide sensitive factor, vesicle fusing ATPase
3643	1,51E-04	3,82E+00	9,29E-05	0,0638	-3,9084292	-0,24926949	1164,71	INSR	insulin receptor
51031	2,12E-08	7,67E+00	1,05E-08	0,0436	-5,7227037	-0,24930436	3655,26	GLOD4	glyoxalase domain containing 4
29785	1,28E-01	8,93E-01	1,05E-01	0,1538	-1,6226208	-0,24957774	129,49	CYP2S1	cytochrome P450 family 2 subfamily S member 1
148645	3,21E-01	4,93E-01	2,81E-01	0,2317	-1,0771033	-0,24959351	56,84	ICMT-DT	ICMT divergent transcript
23417	4,36E-02	1,36E+00	3,35E-02	0,1176	-2,1255482	-0,25004389	238,24	MLYCD	malonyl-CoA decarboxylase
1616	1,98E-08	7,70E+00	9,79E-09	0,0436	-5,7342542	-0,25020027	6330,64	DAXX	death domain associated protein
728554	5,03E-06	5,30E+00	2,82E-06	0,0534	-4,6837054	-0,25027264	1833,7	LOC728554	THO complex 3 pseudogene
4126	1,09E-02	1,96E+00	7,84E-03	0,0942	-2,6588961	-0,25035887	407,37	MANBA	mannosidase beta
11322	1,04E-03	2,98E+00	6,84E-04	0,0738	-3,3958811	-0,25046531	1128,88	TMC6	transmembrane channel like 6
7564	6,03E-03	2,22E+00	4,24E-03	0,0876	-2,8599676	-0,25051869	493,9	ZNF16	zinc finger protein 16
56851	6,92E-06	5,16E+00	3,91E-06	0,0543	-4,6163081	-0,25056079	2233,6	EMC7	ER membrane protein complex subunit 7
4077	4,07E-09	8,39E+00	1,95E-09	0,0418	-6,0019348	-0,25064939	8673,89	NBR1	NBR1 autophagy cargo receptor
54102	1,38E-04	3,86E+00	8,43E-05	0,0638	-3,9318301	-0,25092409	1081,21	CLIC6	chloride intracellular channel 6
3052	7,30E-07	6,14E+00	3,91E-07	0,0495	-5,0735145	-0,25108305	2202,09	HCCS	holocytochrome c synthase
78988	1,53E-05	4,82E+00	8,82E-06	0,0565	-4,4441698	-0,25110112	1414,24	MRPL57	mitochondrial ribosomal protein L57
30813	6,90E-01	1,61E-01	6,56E-01	0,5641	-0,4457632	-0,25144402	9,48	VSX1	visual system homeobox 1
55715	7,16E-02	1,15E+00	5,66E-02	0,1319	-1,9060466	-0,2514463	176,93	DOK4	docking protein 4
6331	9,66E-06	5,02E+00	5,51E-06	0,0554	-4,544552	-0,25159968	2252,24	SCN5A	sodium voltage-gated channel alpha subunit 5
10987	5,97E-07	6,22E+00	3,18E-07	0,0492	-5,1124693	-0,25165181	2410,32	COPS5	COP9 signalosome subunit 5
10465	6,17E-07	6,21E+00	3,29E-07	0,0493	-5,1060971	-0,25176683	2818,7	PPIH	peptidylprolyl isomerase H
107985944	5,97E-01	2,24E-01	5,58E-01	0,4297	-0,5860518	-0,25181962	15,96	LOC107985944	uncharacterized LOC107985944
10494	4,50E-05	4,35E+00	2,67E-05	0,06	-4,1999973	-0,25182337	2801,81	STK25	serine/threonine kinase 25
219931	4,54E-03	2,34E+00	3,15E-03	0,0854	-2,9523888	-0,25219234	532,54	TPCN2	two pore segment channel 2
1760	2,01E-03	2,70E+00	1,35E-03	0,0787	-3,2047389	-0,25222764	605,14	DMPK	DM1 protein kinase
284252	6,54E-04	3,18E+00	4,23E-04	0,0716	-3,5254187	-0,25224479	845,63	KCTD1	potassium channel tetramerization domain containing 1
10073	3,61E-04	3,44E+00	2,29E-04	0,0686	-3,6847263	-0,25259164	914,55	SNUPN	snurportin 1
80176	2,16E-04	3,67E+00	1,34E-04	0,0662	-3,8182226	-0,25272488	1239,41	SPSB1	splA/ryanodine receptor domain and SOCS box containing 1
138715	5,90E-01	2,29E-01	5,50E-01	0,4234	-0,5971455	-0,25284509	17,65	ARID3C	AT-rich interaction domain 3C
101928085	6,43E-01	1,92E-01	6,06E-01	0,49	-0,5161821	-0,25293401	12,19	ERICH6-AS1	ERICH6 antisense RNA 1
6636	2,84E-05	4,55E+00	1,66E-05	0,0588	-4,305787	-0,25299981	5157,97	SNRPF	small nuclear ribonucleoprotein polypeptide F
9938	3,08E-01	5,11E-01	2,69E-01	0,2292	-1,1043223	-0,25308329	58,07	ARHGAP25	Rho GTPase activating protein 25
64285	6,50E-04	3,19E+00	4,21E-04	0,0718	-3,5267526	-0,25322303	886,97	RHBDF1	rhomboid 5 homolog 1
121053	5,63E-03	2,25E+00	3,94E-03	0,088	-2,8829805	-0,25356476	467,49	NOPCHAP1	NOP protein chaperone 1
105369699	1,13E-01	9,47E-01	9,15E-02	0,1503	-1,6874069	-0,25363732	142,63	LOC105369699	uncharacterized LOC105369699
8816	8,74E-07	6,06E+00	4,69E-07	0,0504	-5,0385087	-0,25372418	3642,59	DCAF5	DDB1 and CUL4 associated factor 5
89795	7,99E-07	6,10E+00	4,28E-07	0,0502	-5,0561006	-0,25374917	2312,82	NAV3	neuron navigator 3
11004	6,21E-09	8,21E+00	3,00E-09	0,0428	-5,9315833	-0,25387466	11819,21	KIF2C	kinesin family member 2C
80714	1,16E-01	9,36E-01	9,49E-02	0,1521	-1,6701584	-0,25401225	145,87	PBX4	PBX homeobox 4
6652	3,68E-08	7,43E+00	1,84E-08	0,0452	-5,6264461	-0,2541961	3095,64	SORD	sorbitol dehydrogenase
100128262	4,33E-01	3,64E-01	3,92E-01	0,2968	-0,8564955	-0,25424014	33,37	TNK2-AS1	TNK2 antisense RNA 1
401106	5,63E-01	2,49E-01	5,23E-01	0,398	-0,638871	-0,25424355	18,5	ATP13A3-DT	ATP13A3 divergent transcript

57720	2,19E-09	8,66E+00	1,04E-09	0,0417	-6,103073	-0,25424801	6258,73	GPR107	G protein-coupled receptor 107
550112	1,94E-03	2,71E+00	1,30E-03	0,0791	-3,215041	-0,25428713	566,22	UBA6-DT	UBA6 divergent transcript
619189	4,67E-02	1,33E+00	3,61E-02	0,1214	-2,0960805	-0,25450838	215,47	SERINC4	serine incorporator 4
5790	6,61E-01	1,80E-01	6,25E-01	0,5206	-0,4889074	-0,25452444	11,41	PTPRCAP	protein tyrosine phosphatase receptor type C associated protein
101927506	4,16E-01	3,81E-01	3,74E-01	0,2871	-0,8886171	-0,25515715	36,65	LOC101927	uncharacterized LOC101927506
55627	1,87E-07	6,73E+00	9,69E-08	0,0479	-5,3323544	-0,25548279	4713,92	SMPD4	sphingomyelin phosphodiesterase 4
103091866	3,91E-02	1,41E+00	2,99E-02	0,1177	-2,1712784	-0,25563739	235,65	LINC01145	long intergenic non-protein coding RNA 1145
51149	1,08E-02	1,97E+00	7,77E-03	0,096	-2,6617933	-0,25564567	393,12	MRNIP	MRN complex interacting protein
25921	8,56E-11	1,01E+01	3,83E-11	0,0387	-6,6106043	-0,25569692	8769,69	ZDHHC5	zinc finger DHHC-type palmitoyltransferase 5
105369339	6,62E-01	1,79E-01	6,26E-01	0,5247	-0,4877788	-0,25592707	10,67	LOC105369	uncharacterized LOC105369339
8348	3,04E-01	5,17E-01	2,66E-01	0,23	-1,1131345	-0,2560125	59,3	H2BC17	H2B clustered histone 17
7184	1,29E-12	1,19E+01	5,42E-13	0,0355	-7,2143431	-0,25614114	76518,77	HSP90B1	heat shock protein 90 beta family member 1
10220	3,75E-04	3,43E+00	2,38E-04	0,0697	-3,6746963	-0,25615198	915,92	GDF11	growth differentiation factor 11
2806	1,58E-10	9,80E+00	7,15E-11	0,0393	-6,5174592	-0,25616634	7838,5	GOT2	glutamic-oxaloacetic transaminase 2
55692	2,76E-07	6,56E+00	1,44E-07	0,0487	-5,259614	-0,2563185	2458,93	LUC7L	LUC7 like
51780	1,29E-07	6,89E+00	6,64E-08	0,0475	-5,4007255	-0,25656104	5409,28	KDM3B	lysine demethylase 3B
107985017	1,74E-02	1,76E+00	1,27E-02	0,103	-2,4914195	-0,25657439	336,89	LOC107985	uncharacterized LOC107985017
1857	8,17E-07	6,09E+00	4,38E-07	0,0508	-5,0518554	-0,25664732	4227,17	DVL3	dishevelled segment polarity protein 3
55038	9,40E-08	7,03E+00	4,80E-08	0,047	-5,4584963	-0,25664987	2826,57	CDCA4	cell division cycle associated 4
84720	4,22E-07	6,37E+00	2,23E-07	0,0496	-5,1790493	-0,2566995	2267,55	PIGO	phosphatidylinositol glycan anchor biosynthesis class O
107987097	5,76E-01	2,40E-01	5,36E-01	0,4149	-0,6187598	-0,25674553	18,77	LOC107987	uncharacterized LOC107987097
100128079	5,11E-01	2,92E-01	4,69E-01	0,3551	-0,7235256	-0,2569595	23,42	LOC100128	uncharacterized LOC100128079
113219470	1,97E-01	7,06E-01	1,66E-01	0,1857	-1,3839974	-0,25698599	91,24	MIR12127	microRNA 12127
157489	3,25E-01	4,88E-01	2,86E-01	0,2409	-1,0672378	-0,2571316	52,01	SDAD1P1	SDA1 domain containing 1 pseudogene 1
6041	2,82E-02	1,55E+00	2,11E-02	0,1116	-2,3056119	-0,25722008	275,56	RNASEL	ribonuclease L
100302650	1,35E-01	8,70E-01	1,11E-01	0,1616	-1,5920697	-0,25734983	123,59	BABAM2-AS	BABAM2 antisense RNA 1
8819	2,66E-05	4,58E+00	1,56E-05	0,0596	-4,320402	-0,25748526	1438,48	SAP30	Sin3A associated protein 30
23511	1,16E-10	9,94E+00	5,23E-11	0,0392	-6,564335	-0,25756011	10962,67	NUP188	nucleoporin 188
9665	6,01E-07	6,22E+00	3,20E-07	0,0504	-5,1112905	-0,25761387	2170,64	MARF1	meiosis regulator and mRNA stability factor 1
54494	7,28E-02	1,14E+00	5,76E-02	0,1358	-1,898821	-0,25794645	230,49	C11orf71	chromosome 11 open reading frame 71
51606	5,48E-04	3,26E+00	3,52E-04	0,0722	-3,5736841	-0,25800003	1854,13	ATP6V1H	ATPase H+ transporting V1 subunit H
28972	3,61E-02	1,44E+00	2,75E-02	0,1172	-2,2037766	-0,25830875	3661,04	SPCS1	signal peptidase complex subunit 1
9276	1,23E-11	1,09E+01	5,32E-12	0,0375	-6,8968215	-0,25831108	10269,95	COPB2	COPI coat complex subunit beta 2
121268	1,03E-01	9,87E-01	8,32E-02	0,1491	-1,7326405	-0,25832234	141,51	RHEBL1	RHEB like 1
5430	1,17E-08	7,93E+00	5,73E-09	0,0444	-5,8245921	-0,25834268	12815,74	POLR2A	RNA polymerase II subunit A
286075	4,87E-03	2,31E+00	3,39E-03	0,0882	-2,9299523	-0,25849864	566,13	ZNF707	zinc finger protein 707
7295	1,40E-10	9,85E+00	6,30E-11	0,0396	-6,5363704	-0,25861091	19563,63	TXN	thioredoxin
101927550	3,47E-02	1,46E+00	2,63E-02	0,1165	-2,2210259	-0,25879351	237,11	LOC101927	uncharacterized LOC101927550
11257	4,34E-01	3,63E-01	3,92E-01	0,3025	-0,8558434	-0,25885823	33,82	TP53TG1	TP53 target 1
509	5,00E-11	1,03E+01	2,22E-11	0,0387	-6,690852	-0,25899636	10613,79	ATP5F1C	ATP synthase F1 subunit gamma
107985911	2,51E-04	3,60E+00	1,57E-04	0,0686	-3,7796396	-0,2593528	817,26	LOC107985	lymphocyte specific protein 1 pseudogene
81563	2,26E-05	4,65E+00	1,32E-05	0,0596	-4,3572633	-0,25949747	1568,05	C1orf21	chromosome 1 open reading frame 21
56893	3,81E-08	7,42E+00	1,91E-08	0,0462	-5,6204053	-0,25980781	3564,28	UBQLN4	ubiquilin 4
9580	1,31E-04	3,88E+00	8,04E-05	0,066	-3,9432641	-0,26006094	1753,83	SOX13	SRY-box transcription factor 13
10699	6,70E-01	1,74E-01	6,34E-01	0,5477	-0,4755451	-0,26046917	9,74	CORIN	corin, serine peptidase
79998	5,93E-05	4,23E+00	3,54E-05	0,063	-4,1357551	-0,26049387	1039,8	ANKRD53	ankyrin repeat domain 53
84254	3,49E-02	1,46E+00	2,65E-02	0,1174	-2,2190276	-0,26052977	257,82	CAMKK1	calcium/calmodulin dependent protein kinase kinase 1
7343	2,11E-09	8,68E+00	1,00E-09	0,0426	-6,1094657	-0,26053234	6107,98	UBTF	upstream binding transcription factor
54466	1,41E-01	8,51E-01	1,16E-01	0,1659	-1,5714817	-0,2607632	109,43	SPIN2A	spindlin family member 2A
56616	2,07E-07	6,68E+00	1,07E-07	0,0491	-5,3138622	-0,26080752	2738,08	DIABLO	diablo IAP-binding mitochondrial protein
337867	1,70E-06	5,77E+00	9,31E-07	0,0532	-4,9057372	-0,26082421	2025,47	UBAC2	UBA domain containing 2
267	1,22E-08	7,91E+00	5,97E-09	0,0449	-5,8177355	-0,2610662	3268,37	AMFR	autocrine motility factor receptor
100506660	6,22E-01	2,06E-01	5,84E-01	0,4768	-0,5476453	-0,26110918	15,02	DDX11-AS1	DDX11 antisense RNA 1
2990	1,42E-08	7,85E+00	6,98E-09	0,0451	-5,7914974	-0,26116879	3183,35	GUSB	glucuronidase beta
10013	4,32E-07	6,36E+00	2,28E-07	0,0505	-5,1748465	-0,26119268	2955,98	HDAC6	histone deacetylase 6
9746	9,56E-04	3,02E+00	6,26E-04	0,0764	-3,4201492	-0,26128746	761,02	CLSTN3	calsyntenin 3
7517	1,07E-04	3,97E+00	6,47E-05	0,0654	-3,9948343	-0,26134347	1180,5	XRCC3	X-ray repair cross complementing 3
80896	1,75E-01	7,57E-01	1,46E-01	0,1802	-1,4520158	-0,26159383	94,28	NPL	N-acetylneuraminate pyruvate lyase
728752	1,62E-01	7,90E-01	1,35E-01	0,1749	-1,4962695	-0,26169119	102,91	ZNF566-AS1	ZNF566 antisense RNA 1
84321	1,71E-07	6,77E+00	8,86E-08	0,049	-5,3486161	-0,26193978	2277,49	THOC3	THO complex subunit 3
149986	1,09E-07	6,96E+00	5,56E-08	0,0482	-5,4325134	-0,26202834	3254,81	LSM14B	LSM family member 14B
57461	4,22E-05	4,37E+00	2,50E-05	0,0622	-4,2151344	-0,26218213	1086,88	ISY1	ISY1 splicing factor homolog
2580	3,40E-06	5,47E+00	1,89E-06	0,055	-4,765347	-0,26229551	1620,11	GAK	cyclin G associated kinase
441951	6,81E-10	9,17E+00	3,16E-10	0,0417	-6,29075	-0,26235122	5470,81	ZFAS1	ZNFX1 antisense RNA 1
374969	3,28E-03	2,48E+00	2,24E-03	0,0859	-3,0558532	-0,2625265	533,76	SVBP	small vasohibin binding protein
401474	4,10E-06	5,39E+00	2,28E-06	0,0556	-4,7265028	-0,26268066	1975,43	SAMD12	sterile alpha motif domain containing 12
105377805	6,74E-01	1,71E-01	6,38E-01	0,559	-0,4700774	-0,2627732	9,89	LOC105377	basic salivary proline-rich protein 4-like
8396	1,96E-09	8,71E+00	9,29E-10	0,043	-6,1210913	-0,26295208	4168,03	PIP4K2B	phosphatidylinositol-5-phosphate 4-kinase type 2 beta
54840	4,48E-07	6,35E+00	2,37E-07	0,0509	-5,1676066	-0,26297011	2070,91	APTX	aprataxin
3609	1,75E-12	1,18E+01	7,36E-13	0,0367	-7,1725694	-0,26325671	30877,02	ILF3	interleukin enhancer binding factor 3
3251	9,54E-07	6,02E+00	5,13E-07	0,0524	-5,0212371	-0,26335165	2484,47	HPRT1	hypoxanthine phosphoribosyltransferase 1
79863	4,01E-05	4,40E+00	2,37E-05	0,0623	-4,2269574	-0,26336148	1122,23	RBFA	ribosome binding factor A
348	5,24E-01	2,81E-01	4,82E-01	0,3751	-0,7024478	-0,26347168	22,44	APOE	apolipoprotein E
3838	2,94E-13	1,25E+01	1,20E-13	0,0355	-7,4165512	-0,2634852	29763,06	KPNA2	karyopherin subunit alpha 2
84795	2,86E-04	3,54E+00	1,80E-04	0,0704	-3,7460085	-0,2635928	767,05	PYROXD2	pyridine nucleotide-disulphide oxidoreductase domain 2
6599	7,24E-10	9,14E+00	3,36E-10	0,042	-6,2811228	-0,26362986	8488,14	SMARCC1	SWI/SNF related, matrix associated, actin dependent regulator of chromatin subfamily c member 1
6100	5,18E-04	3,29E+00	3,33E-04	0,0735	-3,5884359	-0,26373657	886,91	RP9	RP9 pre-mRNA splicing factor
100151684	5,29E-01	2,77E-01	4,88E-01	0,3808	-0,6936615	-0,26415126	21,94	RNU6ATAC	RNA, U6atac small nuclear
2318	8,22E-08	7,09E+00	4,18E-08	0,0482	-5,4828661	-0,26420943	7439,2	FLNC	filamin C
7145	1,11E-01	9,55E-01	8,99E-02	0,1561	-1,6956708	-0,26461202	130,96	TNS1	tensin 1
11180	1,67E-07	6,78E+00	8,66E-08	0,0494	-5,3528122	-0,26464428	8613,99	WDR6	WD repeat domain 6
10109	1,47E-12	1,18E+01	6,16E-13	0,0368	-7,1969796	-0,26470789	13712,91	ARPC2	actin related protein 2/3 complex subunit 2
101928140	2,59E-02	1,59E+00	1,94E-02	0,1132	-2,3382481	-0,26480208	266,53	PTPRK-AS1	PTPRK antisense RNA 1
2119	2,51E-09	8,60E+00	1,19E-09	0,0436	-6,0810852	-0,26492252	4484,01	ETV5	ETS variant transcription factor 5
6433	5,13E-07	6,29E+00	2,72E-07	0,0515	-5,1419686	-0,26495727	2501,02	SFSWAP	splicing factor SWAP
9846	6,43E-05	4,19E+00	3,85E-05	0,0644	-4,1161966	-0,26509197	1379,64	GAB2	GRB2 associated binding protein 2
64779	1,95E-03	2,71E+00	1,31E-03	0,0826	-3,213926	-0,26551422	657,43	MTHFSD	methenyltetrahydrofolate synthetase domain containing
8896	5,41E-06	5,27E+00	3,04E-06	0,0569	-4,6682723	-0,26555026	2075,44	BUD31	BUD31 homolog
4571	8,59E-06	5,07E+00	4,88E-06	0,0581	-4,5699898	-0,26561983	5558,87	TRNP	tRNA-Pro
728723	4,18E-01	3,79E-01	3,77E-01	0,3005	-0,8840829	-0,26564542	32,36	ZBED3-AS1	ZBED3 antisense RNA 1
101929523	6,64E-01	1,78E-01	6,27E-01	0,5471	-0,4855592	-0,26566012	9,8	THBS2-AS1	THBS2 antisense RNA 1
79794	3,23E-07	6,49E+00	1,69E-07	0,0508	-5,2303673	-0,26584126	3104,69	SPRING1	SREBF pathway regulator in golgi 1
57128	9,63E-07	6,02E+00	5,19E-07	0,053	-5,0192038	-0,26587047	1858,66	LYRM4	LYR motif containing 4
10447	2,57E-05	4,59E+00	1,50E-05	0,0615	-4,3284273	-0,26616085	4696,09	FAM3C	FAM3 metabolism regulating signaling molecule C
165829	1,87E-01	7,28E-01	1,57E-01	0,1882	-1,4145854	-0,26616655	84,78	GPR156	G protein-coupled receptor 156
9555	2,53E-11	1,06E+01	1,11E-11	0,0392	-6,7915702	-0,26639465	10458,17	MACROH2A	macroH2A.1 histone
51665	8,83E-07	6,05E+00	4,74E-07	0,0529	-5,0365022	-0,26648629	2649,35	ASB1	ankyrin repeat and SOCS box containing 1
10293	2,92E-04	3,53E+00	1,84E-04	0,0714	-3,7405782	-0,2671174	861,36	TRAIP	TRAF interacting protein
55315	1,85E-02	1,73E+00	1,36E-02	0,1083	-2,4674632	-0,26713487	339,9	SLC29A3	solute carrier family 29 member 3
9308	2,88E-05	4,54E+00	1,69E-05	0,0621	-4,3027421	-0,26724119	1106,98	CD83	CD83 molecule
51011	2,93E-05	4,53E+00	1,72E-05	0,0622	-4,298499	-0,26724308	1115,17	FAHD2A	fumarylacetoacetate hydrolase domain containing 2A
9812	5,25E-07	6,28E+00	2,78E-07	0,0521	-5,1375588	-0,26749948	2098,83	DELE1	DAP3 binding cell death enhancer 1
9200	2,92E-05	4,53E+00	1,71E-05	0,0622	-4,2996638	-0,2675126	1173,26	HACD1	3-hydroxyacyl-CoA dehydratase 1
10963	3,04E-09	8,52E+00	1,45E-09	0,0442	-6,0495202	-0,2675691	19568,02	STIP1	stress induced phosphoprotein 1
648809	5,92E-01	2,28E-01	5,53E-01	0,4509	-0,593518	-0,26759662	14,95	EFL1P1	elongation factor like GTPase 1 pseudogene 1
400410	1,76E-01	7,54E-01	1,47E-01	0,1847	-1,4506976	-0,26789679	92,3	ST20	suppressor of tumorigenicity 20
2936	4,78E-07	6,32E+00	2,53E-07	0,052	-5,1554918	-0,26799029	2047,01	GSR	glutathione-disulfide reductase
105374352	3,66E-01	4,37E-01	3,26E-01	0,2727	-0,9826589	-0,26799371	39,1	LOC105374	uncharacterized LOC105374352
11031	3,96E-10	9,40E+00	1,82E-10	0,042	-6,3759971	-0,26806947	4875,87	RAB31	RAB31, member RAS oncogene family
80222	5,99E-07	6,22E+00	3,19E-07	0,0524	-5,1119599	-0,26807059	1909,67	TARS2	threonyl-tRNA synthetase 2, mitochondrial
55219	4,59E-06	5,34E+00	2,56E-06	0,057	-4,7031741	-0,26809126	1532,63	MACO1	macoilin 1
51503	7,52E-07	6,12E+00	4,02E-07	0,053	-5,0678248	-0,26844261	3455,81	CWC15	CWC15 spliceosome associated protein homolog
2827	3,95E-03	2,40E+00	2,73E-03	0,0896	-2,9969363	-0,26854166	582,17	GPR3	G protein-coupled receptor 3
100129250	1,49E-01	8,27E-01	1,23E-01	0,1741	-1,5423836	-0,26855835	118,86	SMIM27	small integral membrane protein 27
11213	4,36E-06	5,36E+00	2,43E-06	0,057	-4,7137504	-0,26864444	1367,09	IRAK3	interleukin 1 receptor associated kinase 3
132158	2,94E-02	1,53E+00	2,21E-02	0,1174	-2,2888457	-0,2687469	270,87	GLYCTK	glycerate kinase
112268241	4,26E-01	3,71E-01	3,84E-01	0,3092	-0,8698182	-0,26898051	33,69	ZNF470-DT	ZNF470 divergent transcript
25900	2,97E-01	5,27E-01	2,58E-01	0,2381	-1,1300033	-0,26900282	54,23	IFFO1	intermediate filament family orphan 1
124454	3,26E-06	5,49E+00	1,81E-06	0,0564	-4,7739835	-0,26901638	1480,76	EARS2	glutamyl-tRNA synthetase 2, mitochondrial
105369574	5,40E-01	2,68E-01	4,99E-01	0,3979	-0,6763255	-0,2690976	18,75	LOC105369	uncharacterized LOC105369574

5820	5,84E-04	3,23E+00	3,77E-04	0,0758	-3,5559022	-0,26947153	636,04	PVT1	Pvt1 oncogene
23552	1,47E-01	8,33E-01	1,21E-01	0,1739	-1,549994	-0,2695489	107,24	CDK20	cyclin dependent kinase 20
158055	3,20E-01	4,95E-01	2,80E-01	0,2499	-1,0794789	-0,26978152	49,07	C9orf163	chromosome 9 putative open reading frame 163
101929188	2,78E-01	5,56E-01	2,41E-01	0,2301	-1,173021	-0,26990868	59,67	ITPR3-AS1	ITPR3 antisense RNA 1
25996	4,31E-08	7,37E+00	2,16E-08	0,0482	-5,5986369	-0,26996468	6208,72	REXO2	RNA exonuclease 2
51	8,31E-07	6,08E+00	4,45E-07	0,0535	-5,0484656	-0,27004439	1948,43	ACOX1	acyl-CoA oxidase 1
7589	1,04E-02	1,98E+00	7,46E-03	0,101	-2,6754413	-0,27010752	325,86	ZSCAN21	zinc finger and SCAN domain containing 21
1861	7,47E-09	8,13E+00	3,62E-09	0,0458	-5,900817	-0,27013257	3175,47	TOR1A	torsin family 1 member A
55092	1,03E-03	2,99E+00	6,73E-04	0,0795	-3,4001855	-0,27015396	682,4	TMEM51	transmembrane protein 51
100533789	4,70E-01	3,28E-01	4,29E-01	0,3415	-0,791029	-0,27017231	25,21	LRRC37A8P	leucine rich repeat containing 37 member A8, pseudogene
5993	1,31E-09	8,88E+00	6,16E-10	0,0437	-6,1862372	-0,27026736	3982,76	RFX5	regulatory factor X5
85450	5,95E-08	7,23E+00	3,01E-08	0,0488	-5,5410646	-0,27027973	3145,94	ITPRIP	inositol 1,4,5-trisphosphate receptor interacting protein
27235	1,95E-06	5,71E+00	1,07E-06	0,0554	-4,8786323	-0,27036503	1643,65	COQ2	coenzyme Q2, polyprenyltransferase
79191	7,15E-03	2,15E+00	5,06E-03	0,0965	-2,8034417	-0,27048918	378,05	IRX3	iroquois homeobox 3
51517	2,56E-05	4,59E+00	1,50E-05	0,0625	-4,3291309	-0,27056966	1772,08	NCKIPSD	NCK interacting protein with SH3 domain
9789	3,63E-09	8,44E+00	1,74E-09	0,0449	-6,0204674	-0,27058513	3931,21	SPCS2	signal peptidase complex subunit 2
101927688	6,40E-01	1,94E-01	6,03E-01	0,5204	-0,5203449	-0,27079621	11,36	SEPTIN4-AS	SEPTIN4 antisense RNA 1
10761	2,43E-01	6,14E-01	2,08E-01	0,2155	-1,259124	-0,27132845	65,64	PLAC1	placenta enriched 1
3295	3,04E-10	9,52E+00	1,39E-10	0,0423	-6,4172038	-0,27135978	5841,03	HSD17B4	hydroxysteroid 17-beta dehydrogenase 4
102191832	3,46E-01	4,61E-01	3,06E-01	0,2649	-1,0246809	-0,27141911	42,43	FBXW7-AS1	FBXW7 antisense RNA 1
23129	7,47E-06	5,13E+00	4,22E-06	0,059	-4,6000043	-0,27156424	1788,58	PLXND1	plexin D1
102724334	3,11E-01	5,07E-01	2,72E-01	0,2472	-1,0987919	-0,27165948	47,79	LOC102724	histone H2B type F-S-like
9869	3,08E-07	6,51E+00	1,61E-07	0,0519	-5,2389885	-0,27200667	1878,63	SETDB1	SET domain bifurcated histone lysine methyltransferase 1
6293	2,77E-10	9,56E+00	1,27E-10	0,0423	-6,4312336	-0,27226729	4121,71	VPS52	VPS52 subunit of GARP complex
57710	5,61E-01	2,51E-01	5,21E-01	0,4242	-0,6424317	-0,27253865	16,79	KIAA1614	KIAA1614
402096	5,21E-01	2,83E-01	4,79E-01	0,3852	-0,7078001	-0,272618	20,27	ANAPC1P6	ANAPC1 pseudogene 6
152816	2,98E-01	5,26E-01	2,60E-01	0,242	-1,1267867	-0,27273437	55,64	ODAPH	odontogenesis associated phosphoprotein
57649	4,80E-07	6,32E+00	2,54E-07	0,053	-5,1544702	-0,27320061	2640,71	PHF12	PHD finger protein 12
196913	3,82E-01	4,18E-01	3,41E-01	0,2872	-0,9519056	-0,27342376	35,36	LINC01599	long intergenic non-protein coding RNA 1599
23049	1,28E-10	9,89E+00	5,76E-11	0,0418	-6,5499086	-0,27349489	4524,82	SMG1	SMG1 nonsense mediated mRNA decay associated PI3K related kinase
9726	1,53E-05	4,82E+00	8,81E-06	0,0616	-4,4444182	-0,27363263	1102,05	ZNF646	zinc finger protein 646
375346	8,29E-06	5,08E+00	4,71E-06	0,0598	-4,5775046	-0,27369703	1208,17	STIMATE	STIM activating enhancer
10989	3,35E-12	1,15E+01	1,43E-12	0,0387	-7,0815833	-0,27382685	11699,48	IMMT	inner membrane mitochondrial protein
401331	4,39E-01	3,58E-01	3,98E-01	0,3242	-0,845189	-0,27401813	28,18	RASA4CP	RAS p21 protein activator 4C, pseudogene
661	8,28E-07	6,08E+00	4,44E-07	0,0543	-5,0491564	-0,27420795	1655,62	POLR3D	RNA polymerase III subunit D
55652	2,40E-03	2,62E+00	1,62E-03	0,0871	-3,151612	-0,27440032	500,16	SLC48A1	solute carrier family 48 member 1
22849	2,90E-02	1,54E+00	2,18E-02	0,1198	-2,2944102	-0,27479387	222,01	CPEB3	cytoplasmic polyadenylation element binding protein 3
11022	9,14E-05	4,04E+00	5,54E-05	0,0682	-4,0317941	-0,2748219	914,1	TDRKH	tudor and KH domain containing
55249	2,18E-06	5,66E+00	1,20E-06	0,0566	-4,8561037	-0,27485652	4169,19	YY1AP1	YY1 associated protein 1
161725	6,26E-01	2,03E-01	5,88E-01	0,5079	-0,5412094	-0,27489912	11,31	OTUD7A	OTU deubiquitinase 7A
157922	1,30E-08	7,89E+00	6,38E-09	0,0473	-5,8065086	-0,27492521	3006,37	CAMSAP1	calmodulin regulated spectrin associated protein 1
25999	3,15E-01	5,02E-01	2,76E-01	0,2526	-1,0886611	-0,27494507	50,69	CLIP3	CAP-Gly domain containing linker protein 3
55114	7,02E-08	7,15E+00	3,56E-08	0,0499	-5,5114856	-0,27495105	2507,16	ARHGAP17	Rho GTPase activating protein 17
4718	2,69E-06	5,57E+00	1,48E-06	0,0572	-4,8136931	-0,27516551	1837,21	NDUFC2	NADH:ubiquinone oxidoreductase subunit C2
1506	5,14E-01	2,89E-01	4,73E-01	0,3832	-0,7181516	-0,2752226	22,64	CTRL	chymotrypsin like
440957	1,71E-03	2,77E+00	1,14E-03	0,0847	-3,2531667	-0,27538661	478,89	UQCC5	ubiquinol-cytochrome c reductase complex assembly factor 5
10417	5,16E-01	2,87E-01	4,74E-01	0,3846	-0,716149	-0,27540475	21,4	SPON2	spondin 2
51205	1,64E-05	4,79E+00	9,45E-06	0,0622	-4,4293622	-0,2754135	1097,04	ACP6	acid phosphatase 6, lysophosphatidic
51540	3,15E-03	2,50E+00	2,15E-03	0,0898	-3,0687606	-0,27544091	472,75	SCLY	selenocysteine lyase
646626	6,52E-02	1,19E+00	5,13E-02	0,1414	-1,9491032	-0,27558784	166,3	BCL10-AS1	BCL10 antisense RNA 1
9797	5,33E-09	8,27E+00	2,57E-09	0,0463	-5,9570624	-0,27563177	3540,96	TATDN2	TatD DNase domain containing 2
83480	3,03E-04	3,52E+00	1,91E-04	0,0739	-3,7305198	-0,27564245	727,98	PUS3	pseudouridine synthase 3
101060341	5,88E-01	2,31E-01	5,48E-01	0,4597	-0,6001612	-0,27588829	14,4	LOC101060	putative uncharacterized protein FLJ44672
2799	7,05E-13	1,22E+01	2,93E-13	0,0378	-7,2976598	-0,27594509	10085,69	GNS	glucosamine (N-acetyl)-6-sulfatase
112267961	5,42E-01	2,66E-01	5,01E-01	0,4102	-0,6731422	-0,27613592	17,24	LOC112267961	
51506	2,46E-09	8,61E+00	1,17E-09	0,0454	-6,0845947	-0,27628819	3737,77	UFC1	ubiquitin-fold modifier conjugating enzyme 1
51523	6,62E-04	3,18E+00	4,28E-04	0,0785	-3,5220231	-0,27634093	569,09	CXXC5	CXXC finger protein 5
85451	5,80E-06	5,24E+00	3,26E-06	0,0594	-4,6538347	-0,2763963	1411,54	UNK	unk zinc finger
159091	2,99E-02	1,52E+00	2,25E-02	0,1212	-2,2816058	-0,2764195	240,63	PABIR3	PABIR family member 3
4522	1,24E-10	9,91E+00	5,56E-11	0,0422	-6,5551752	-0,27647179	12328,3	MTHFD1	methylenetetrahydrofolate dehydrogenase, cyclohydrolase and formyltetrahydrofolate synthetase 1
115353	1,43E-08	7,84E+00	7,01E-09	0,0478	-5,7906117	-0,27651333	2621,52	LRRC42	leucine rich repeat containing 42
102723099	5,91E-01	2,28E-01	5,52E-01	0,4654	-0,5943012	-0,27660256	14,15	GHET1	gastric carcinoma proliferation enhancing transcript 1
140735	1,19E-08	7,92E+00	5,83E-09	0,0475	-5,8214226	-0,27663648	4757,66	DYNLL2	dynein light chain LC8-type 2
102724159	3,09E-06	5,51E+00	1,71E-06	0,0578	-4,7852644	-0,27673669	1957,61	LOC102724	periodic tryptophan protein 2 homolog
201283	4,07E-02	1,39E+00	3,12E-02	0,1285	-2,1543216	-0,27692445	197,32	AMZ2P1	AMZ2 pseudogene 1
291	1,21E-07	6,92E+00	6,21E-08	0,0513	-5,4125166	-0,27742008	2023,62	SLC25A4	solute carrier family 25 member 4
7307	1,89E-08	7,72E+00	9,34E-09	0,0483	-5,7422789	-0,27758497	2850,62	U2AF1	U2 small nuclear RNA auxiliary factor 1
8799	4,58E-03	2,34E+00	3,18E-03	0,0942	-2,9499291	-0,27794759	436,74	PEX11B	peroxisomal biogenesis factor 11 beta
64359	9,75E-06	5,01E+00	5,56E-06	0,0612	-4,5424419	-0,27804813	1622,53	NXN	nucleoredoxin
80216	4,21E-02	1,38E+00	3,23E-02	0,1299	-2,1408719	-0,27807014	200,51	ALPK1	alpha kinase 1
55536	4,93E-09	8,31E+00	2,37E-09	0,0466	-5,9702011	-0,27835716	8199,56	CDCA7L	cell division cycle associated 7 like
554249	1,22E-01	9,14E-01	9,96E-02	0,1691	-1,6466626	-0,27846243	108,61	FAM88D	family with sequence similarity 88 member D
84838	6,45E-08	7,19E+00	3,26E-08	0,0505	-5,5266236	-0,27887287	2500,44	ZNF496	zinc finger protein 496
101929746	5,05E-01	2,97E-01	4,63E-01	0,3799	-0,7341359	-0,27890897	20,63	ZNF341-AS1	ZNF341 antisense RNA 1
338557	4,22E-01	3,75E-01	3,80E-01	0,3179	-0,877384	-0,27893228	30,74	FFAR4	free fatty acid receptor 4
26164	1,81E-05	4,74E+00	1,05E-05	0,0633	-4,4063191	-0,2790289	1734,27	MTG2	mitochondrial ribosome associated GTPase 2
102724646	2,25E-01	6,48E-01	1,92E-01	0,2139	-1,3048729	-0,27905858	67,68	LOC102724	uncharacterized LOC102724646
203068	3,22E-14	1,35E+01	1,28E-14	0,0362	-7,7081125	-0,27916277	195505,1	TUBB	tubulin beta class I
100506469	4,56E-03	2,34E+00	3,16E-03	0,0947	-2,9513221	-0,27947863	476,5	TMEM147-A	TMEM147 antisense RNA 1
54676	9,09E-09	8,04E+00	4,42E-09	0,0476	-5,867731	-0,27957232	4827,36	GTPBP2	GTP binding protein 2
29894	6,86E-07	6,16E+00	3,66E-07	0,055	-5,0857869	-0,27977569	4083,38	CPSF1	cleavage and polyadenylation specific factor 1
64798	1,80E-01	7,45E-01	1,51E-01	0,1949	-1,4354828	-0,27978998	85,29	DEPTOR	DEP domain containing MTOR interacting protein
26012	2,94E-08	7,53E+00	1,46E-08	0,0494	-5,6657525	-0,27980431	2917,52	NSMF	NMDA receptor synaptonuclear signaling and neuronal migration factor
10284	4,99E-10	9,30E+00	2,30E-10	0,0442	-6,3396871	-0,28010128	5509,62	SAP18	Sin3A associated protein 18
200931	3,95E-01	4,03E-01	3,54E-01	0,3021	-0,9275829	-0,2801883	35,16	SLC51A	solute carrier family 51 subunit alpha
834	6,48E-03	2,19E+00	4,56E-03	0,0988	-2,8364645	-0,2802354	352,56	CASP1	caspase 1
1325	4,96E-01	3,05E-01	4,55E-01	0,3749	-0,747672	-0,28027478	20,65	CORT	cortistatin
79921	1,93E-02	1,71E+00	1,42E-02	0,1144	-2,4523468	-0,28048143	5170,84	TCEAL4	transcription elongation factor A like 4
9139	2,27E-06	5,64E+00	1,24E-06	0,0579	-4,8484126	-0,28048677	1355,98	CBFA2T2	CBFA2/RUNX1 partner transcriptional co-repressor 2
9112	8,67E-08	7,06E+00	4,42E-08	0,0514	-5,4731911	-0,28109308	2160,25	MTA1	metastasis associated 1
8703	1,34E-07	6,87E+00	6,90E-08	0,0521	-5,3937406	-0,28118554	2610,8	B4GALT3	beta-1,4-galactosyltransferase 3
7410	2,03E-08	7,69E+00	1,01E-08	0,0491	-5,7298773	-0,2815063	2382,3	VAV2	vav guanine nucleotide exchange factor 2
105378512	4,01E-02	1,40E+00	3,07E-02	0,1303	-2,1612628	-0,28154176	207,49	LOC105378	uncharacterized LOC105378512
10102	3,58E-05	4,45E+00	2,11E-05	0,0662	-4,25303	-0,28159596	922,55	TSFM	Ts translation elongation factor, mitochondrial
26276	1,55E-04	3,81E+00	9,55E-05	0,0723	-3,9017527	-0,28206899	735,91	VPS33B	VPS33B late endosome and lysosome associated
105370854	3,05E-01	5,16E-01	2,67E-01	0,2542	-1,1100771	-0,28215428	46,33	LOC105370	uncharacterized LOC105370854
10907	1,04E-06	5,98E+00	5,61E-07	0,0564	-5,0042519	-0,28220046	2628,43	TXNL4A	thioredoxin like 4A
4149	4,47E-08	7,35E+00	2,24E-08	0,0505	-5,5922561	-0,28243189	2604,11	MAX	MYC associated factor X
9159	5,11E-06	5,29E+00	2,86E-06	0,0604	-4,6805695	-0,28247303	1382,05	PCSK7	proprotein convertase subtilisin/kexin type 7
474343	6,19E-03	2,21E+00	4,35E-03	0,0991	-2,8512794	-0,2825725	353,36	SPIN2B	spindlin family member 2B
27289	3,17E-01	4,99E-01	2,78E-01	0,2606	-1,0851216	-0,28279447	45,81	RND1	Rho family GTPase 1
360200	4,42E-01	3,55E-01	4,01E-01	0,3365	-0,840402	-0,28281299	27,44	TMPRSS9	transmembrane serine protease 9
114625	3,35E-04	3,47E+00	2,12E-04	0,0764	-3,7044335	-0,28307135	636,01	ERMAP	erythroblast membrane associated protein (Scianna blood group)
54145	2,74E-01	5,62E-01	2,37E-01	0,2394	-1,18238	-0,28308726	53,37	H2BC12L	H2B clustered histone 12 like
105369563	5,25E-01	2,80E-01	4,84E-01	0,4045	-0,6998741	-0,28310776	18,33	LINC02725	long intergenic non-protein coding RNA 2725
107986162	4,32E-01	3,65E-01	3,90E-01	0,3296	-0,8595465	-0,28327558	28,5	LOC107986	uncharacterized LOC107986162
55924	5,37E-02	1,27E+00	4,18E-02	0,1392	-2,0355825	-0,28328558	160,39	INKA2	inka box actin regulator 2
4599	1,46E-04	3,84E+00	8,99E-05	0,0724	-3,916255	-0,28336205	825,75	MX1	MX dynamin like GTPase 1
6483	3,45E-06	5,46E+00	1,92E-06	0,0595	-4,7621064	-0,28338283	1425,73	ST3GAL2	ST3 beta-galactoside alpha-2,3-sialyltransferase 2
65265	1,90E-08	7,72E+00	9,39E-09	0,0494	-5,7414808	-0,28357596	4117,1	C8orf33	chromosome 8 open reading frame 33
5607	2,51E-04	3,60E+00	1,57E-04	0,0751	-3,7795883	-0,28387254	726,5	MAP2K5	mitogen-activated protein kinase kinase 5
4016	6,85E-05	4,16E+00	4,11E-05	0,0692	-4,1013883	-0,28390196	832,72	LOXL1	lysyl oxidase like 1
152877	4,83E-02	1,32E+00	3,74E-02	0,1364	-2,0817972	-0,28394896	172,17	FAM53A	family with sequence similarity 53 member A
23708	3,54E-04	3,45E+00	2,24E-04	0,0771	-3,6898575	-0,28433483	675,19	GSPT2	G1 to S phase transition 2
140775	1,86E-09	8,73E+00	8,82E-10	0,0464	-6,1294135	-0,2843682	2884,27	SMCR8	SMCR8-C9orf72 complex subunit
148113	4,40E-01	3,57E-01	3,99E-01	0,337	-0,8439032	-0,28439278	25,89	CILP2	cartilage intermediate layer protein 2
9425	2,52E-08	7,60E+00	1,25E-08	0,05	-5,6924251	-0,28439605	2593,43	CDYL	chromodomain Y like
7416	3,56E-13	1,24E+01	1,46E-13	0,0385	-7,3904515	-0,28454725	22408,99	VDAC1	voltage dependent anion channel 1
641700	5,97E-01	2,24E-01	5,58E-01	0,4861	-0,5854228	-0,28454748	12,98	ECSCR	endothelial cell surface expressed chemotaxis and apoptosis regulator
105374407	6,11E-01	2,14E-01	5,73E-01	0,5052	-0,5636262	-0,28472242	12,49	LOC105374407	

101929057	1,10E-01	9,59E-01	8,89E-02	0,1674	-1,7012862	-0,28477519	111,68	MDN1-AS1	MDN1 antisense RNA 1
9441	1,06E-04	3,97E+00	6,43E-05	0,0713	-3,9962979	-0,28493499	855,32	MED26	mediator complex subunit 26
23480	3,48E-08	7,46E+00	1,74E-08	0,0506	-5,6361736	-0,28495837	2377,85	SEC61G	SEC61 translocon subunit gamma
64118	2,22E-07	6,65E+00	1,16E-07	0,0538	-5,3002248	-0,285055	1890,37	DUS1L	dihydrouridine synthase 1 like
6574	1,76E-11	1,08E+01	7,66E-12	0,0416	-6,8447406	-0,28505617	14771,52	SLC20A1	solute carrier family 20 member 1
348013	2,88E-04	3,54E+00	1,81E-04	0,0762	-3,7434886	-0,28526593	909,19	TMEM255B	transmembrane protein 255B
124997	1,78E-03	2,75E+00	1,19E-03	0,088	-3,2409106	-0,28528482	500,3	WDR81	WD repeat domain 81
7692	1,48E-03	2,83E+00	9,87E-04	0,0866	-3,2943012	-0,28534769	560,41	ZNF133	zinc finger protein 133
57474	6,86E-03	2,16E+00	4,84E-03	0,1013	-2,817454	-0,28536136	348,33	ZNF490	zinc finger protein 490
2588	1,42E-04	3,85E+00	8,69E-05	0,0727	-3,9246473	-0,28544599	843,73	GALNS	galactosamine (N-acetyl)-6-sulfatase
4067	3,18E-06	5,50E+00	1,76E-06	0,0598	-4,7795409	-0,28579855	1375,98	LYN	LYN proto-oncogene, Src family tyrosine kinase
351	4,22E-16	1,54E+01	1,58E-16	0,0346	-8,2504928	-0,28580417	37659,51	APP	amyloid beta precursor protein
10376	7,99E-13	1,21E+01	3,32E-13	0,0393	-7,280562	-0,28593418	109487,86	TUBA1B	tubulin alpha 1b
55915	5,65E-07	6,25E+00	3,00E-07	0,0559	-5,1231381	-0,2862993	1951,18	LANCL2	LanC like glutathione S-transferase 2
7185	2,19E-07	6,66E+00	1,14E-07	0,054	-5,3034759	-0,28634237	1975,52	TRAF1	TNF receptor associated factor 1
283651	2,32E-01	6,35E-01	1,98E-01	0,2227	-1,2867378	-0,28658394	67,18	HMGN2P46	high mobility group nucleosomal binding domain 2 pseudogene 46
201895	2,10E-04	3,68E+00	1,31E-04	0,075	-3,8250675	-0,28683569	808,2	SMIM14	small integral membrane protein 14
399726	7,04E-02	1,15E+00	5,57E-02	0,1499	-1,9134747	-0,28689524	154,44	MIR1915HG	MIR1915 host gene
80003	2,60E-05	4,59E+00	1,52E-05	0,0663	-4,325746	-0,28700032	917,4	PCNX2	pecanex 2
9416	1,79E-09	8,75E+00	8,46E-10	0,0468	-6,1361257	-0,28700553	4547,41	DDX23	DEAD-box helicase 23
3831	4,76E-11	1,03E+01	2,11E-11	0,0429	-6,6984139	-0,28704469	6682,85	KLC1	kinesin light chain 1
8365	2,92E-01	5,35E-01	2,54E-01	0,2519	-1,1396965	-0,28705109	53,66	H4C8	H4 clustered histone 8
10769	1,41E-10	9,85E+00	6,36E-11	0,044	-6,5349504	-0,28756757	20194,57	PLK2	polo like kinase 2
102724057	2,25E-01	6,48E-01	1,92E-01	0,2203	-1,3057073	-0,28760379	65,87	LOC102724(	replaced by ID 23287
84276	2,14E-04	3,67E+00	1,34E-04	0,0753	-3,8198594	-0,28760748	633,25	NICN1	nicolin 1, tubulin polyglutamylase complex subunit
112268460	5,97E-05	4,22E+00	3,57E-05	0,0696	-4,1340004	-0,2877559	1022,05	LOC112268(	uncharacterized LOC112268460
10311	1,14E-09	8,94E+00	5,36E-10	0,0464	-6,208114	-0,28784889	3264,13	VPS26C	VPS26 endosomal protein sorting factor C
729440	2,05E-02	1,69E+00	1,52E-02	0,1186	-2,4286309	-0,28791969	222	CCDC61	coiled-coil domain containing 61
487	2,05E-01	6,88E-01	1,74E-01	0,2117	-1,3600384	-0,28794214	67,79	ATP2A1	ATPase sarcoplasmic/endoplasmic reticulum Ca2+ transporting 1
60686	9,26E-03	2,03E+00	6,62E-03	0,1061	-2,7152112	-0,28797073	297	C14orf93	chromosome 14 open reading frame 93
79946	3,72E-01	4,29E-01	3,31E-01	0,2965	-0,97111	-0,28797112	32,95	C10orf95	chromosome 10 open reading frame 95
51126	3,18E-06	5,50E+00	1,76E-06	0,0603	-4,7793622	-0,2879854	3721,75	NAA20	N-alpha-acetyltransferase 20, NatB catalytic subunit
9777	2,24E-10	9,65E+00	1,02E-10	0,0446	-6,4644294	-0,28827879	6274,26	TM9SF4	transmembrane 9 superfamily member 4
55140	5,97E-09	8,22E+00	2,88E-09	0,0486	-5,9380292	-0,28845461	2295,87	ELP3	elongator acetyltransferase complex subunit 3
10542	4,58E-09	8,34E+00	2,20E-09	0,0482	-5,9822123	-0,28851392	2431,11	LAMTOR5	late endosomal/lysosomal adaptor, MAPK and MTOR activator 5
2630	3,33E-06	5,48E+00	1,85E-06	0,0605	-4,7695795	-0,28867908	1403,5	GBAP1	glucosylceramidase beta pseudogene 1
27010	3,68E-03	2,43E+00	2,54E-03	0,0956	-3,0191207	-0,28875097	370,89	TPK1	thiamin pyrophosphokinase 1
84881	1,93E-06	5,71E+00	1,06E-06	0,0592	-4,8810017	-0,28913085	1459,09	RPUSD4	RNA pseudouridine synthase D4
5066	3,51E-11	1,05E+01	1,55E-11	0,0429	-6,7435975	-0,28916289	9266,17	PAM	peptidylglycine alpha-amidating monooxygenase
7020	8,37E-04	3,08E+00	5,46E-04	0,0837	-3,4571732	-0,2892265	501,43	TFAP2A	transcription factor AP-2 alpha
100499466	4,16E-08	7,38E+00	2,09E-08	0,0516	-5,6046427	-0,28935942	2091,5	LINC00674	long intergenic non-protein coding RNA 674
56898	8,35E-05	4,08E+00	5,04E-05	0,0714	-4,0537603	-0,28948528	829,68	BDH2	3-hydroxybutyrate dehydrogenase 2
7259	8,32E-09	8,08E+00	4,04E-09	0,0492	-5,8826086	-0,28952938	2983,77	TSPYL1	TSPY like 1
211	1,04E-10	9,98E+00	4,67E-11	0,044	-6,5811281	-0,28970255	4455,25	ALAS1	5'-aminolevulinate synthase 1
10673	5,61E-01	2,51E-01	5,20E-01	0,4507	-0,6428722	-0,28973134	14,92	TNFSF13B	TNF superfamily member 13b
29855	1,01E-08	8,00E+00	4,94E-09	0,0495	-5,8491412	-0,28976678	3127,09	UBN1	ubinuclein 1
79411	3,99E-03	2,40E+00	2,75E-03	0,0968	-2,9939582	-0,28993651	400,91	GLB1L	galactosidase beta 1 like
5879	2,05E-15	1,47E+01	7,86E-16	0,036	-8,0563912	-0,2900283	14896,92	RAC1	Rac family small GTPase 1
55696	4,01E-09	8,40E+00	1,92E-09	0,0483	-6,0044254	-0,29011674	3372,25	RBM22	RNA binding motif protein 22
9802	9,67E-12	1,10E+01	4,17E-12	0,0419	-6,9313102	-0,29015858	7463,4	DAZAP2	DAZ associated protein 2
79571	1,47E-05	4,83E+00	8,47E-06	0,0652	-4,4528705	-0,29025683	987,23	GCC1	GRIP and coiled-coil domain containing 1
101928445	4,93E-02	1,31E+00	3,82E-02	0,1401	-2,0725353	-0,29028336	160,08	RUFY1-AS1	RUFY1 antisense RNA 1
53407	1,67E-07	6,78E+00	8,64E-08	0,0542	-5,3532731	-0,29040222	2362,87	STX18	syntaxin 18
105374419	6,13E-01	2,13E-01	5,74E-01	0,517	-0,561728	-0,29040975	10,81	SMIM14-DT	SMIM14 divergent transcript
6218	1,18E-10	9,93E+00	5,32E-11	0,0443	-6,5617891	-0,2906127	29730,99	RPS17	ribosomal protein S17
210	2,31E-08	7,64E+00	1,14E-08	0,0509	-5,7079503	-0,29062813	2009,11	ALAD	aminolevulinate dehydratase
9894	1,50E-04	3,82E+00	9,23E-05	0,0744	-3,9099423	-0,29093361	937,89	TELO2	telomere maintenance 2
105375215	4,77E-01	3,21E-01	4,35E-01	0,3732	-0,7799214	-0,29109633	22,74	FKBP14-AS1	FKBP14 antisense RNA 1
23593	1,31E-06	5,88E+00	7,14E-07	0,0587	-4,9576265	-0,29122426	1455,57	HEBP2	heme binding protein 2
107984248	3,43E-01	4,65E-01	3,03E-01	0,2828	-1,03088	-0,29151299	36,21	LOC107984(	replaced by ID 729262
283575	6,47E-01	1,89E-01	6,10E-01	0,5723	-0,509549	-0,29161754	8,96	LINC02288	long intergenic non-protein coding RNA 2288
3899	6,76E-10	9,17E+00	3,13E-10	0,0464	-6,291981	-0,29167494	2829,08	AFF3	ALF transcription elongation factor 3
5025	3,30E-04	3,48E+00	2,08E-04	0,0787	-3,7085186	-0,29172745	659,23	P2RX4	purinergic receptor P2X 4
4564	2,88E-02	1,54E+00	2,16E-02	0,1271	-2,2965318	-0,29190058	276,08	TRNH	tRNA-His
105377022	6,64E-01	1,78E-01	6,27E-01	0,6014	-0,4853923	-0,29192647	8,69	LOC105377(	replaced by ID 2720
102724149	4,44E-01	3,53E-01	4,03E-01	0,3491	-0,836488	-0,29202673	23,94	LOC102724(	uncharacterized LOC102724149
84134	7,62E-06	5,12E+00	4,31E-06	0,0636	-4,5956735	-0,29208018	993,9	TOMM40L	translocase of outer mitochondrial membrane 40 like
100131378	2,45E-02	1,61E+00	1,83E-02	0,1238	-2,3599162	-0,29211496	275,28	C11orf91	chromosome 11 open reading frame 91
3099	7,46E-13	1,21E+01	3,10E-13	0,0401	-7,2899733	-0,29216148	6727,16	HK2	hexokinase 2
51341	4,62E-08	7,34E+00	2,32E-08	0,0523	-5,5860233	-0,29231247	1866,9	ZBTB7A	zinc finger and BTB domain containing 7A
84293	1,73E-08	7,76E+00	8,52E-09	0,0508	-5,7578477	-0,29241259	2455,26	PRXL2A	peroxiredoxin like 2A
105377663	2,19E-02	1,66E+00	1,63E-02	0,1217	-2,4031358	-0,29242749	241,75	LOC105377(	uncharacterized LOC105377663
23677	3,28E-09	8,48E+00	1,57E-09	0,0485	-6,0374065	-0,29278922	3932,1	SH3BP4	SH3 domain binding protein 4
126661	2,12E-02	1,67E+00	1,57E-02	0,1212	-2,416894	-0,29282308	232,36	CCDC163	CCDC163 homolog
9371	1,15E-10	9,94E+00	5,15E-11	0,0446	-6,5665415	-0,29314836	4927,31	KIF3B	kinesin family member 3B
1822	1,15E-08	7,94E+00	5,60E-09	0,0503	-5,8282554	-0,29324549	4665,01	ATN1	atrophin 1
27336	2,79E-08	7,55E+00	1,39E-08	0,0517	-5,6745394	-0,29328527	6982,35	HTATSF1	HIV-1 Tat specific factor 1
57179	1,78E-11	1,07E+01	7,75E-12	0,0429	-6,8430331	-0,29351711	8008,19	KIAA1191	KIAA1191
2189	1,28E-09	8,89E+00	6,03E-10	0,0475	-6,189553	-0,29386585	2740,3	FANCG	FA complementation group G
114769	3,44E-02	1,46E+00	2,61E-02	0,1321	-2,2245579	-0,29396361	180,34	CARD16	caspase recruitment domain family member 16
55824	5,24E-06	5,28E+00	2,94E-06	0,063	-4,674886	-0,29441455	1043,34	PAG1	phosphoprotein membrane anchor with glycosphingolipid microdomains 1
54994	4,09E-11	1,04E+01	1,81E-11	0,0438	-6,720807	-0,29446132	4316,29	GID8	GID complex subunit 8 homolog
100132406	4,56E-09	8,34E+00	2,19E-09	0,0493	-5,9831594	-0,29482605	2418,72	NBPF10	NBPF member 10
84173	1,42E-04	3,85E+00	8,70E-05	0,0752	-3,9241191	-0,29497802	773,69	ELMOD3	ELMO domain containing 3
84922	2,66E-04	3,58E+00	1,67E-04	0,0784	-3,7642577	-0,29516452	619,11	FIZ1	FLT3 interacting zinc finger 1
105377621	5,09E-01	2,93E-01	4,67E-01	0,4061	-0,7268839	-0,29518468	19,82	LOC105377(	uncharacterized LOC105377621
9970	4,51E-02	1,35E+00	3,48E-02	0,1399	-2,1111195	-0,29526539	158,47	NR1I3	nuclear receptor subfamily 1 group I member 3
6921	3,38E-07	6,47E+00	1,77E-07	0,0566	-5,2217212	-0,2953471	2439,85	ELOC	elongin C
79947	8,53E-09	8,07E+00	4,14E-09	0,0502	-5,8784673	-0,29538773	2162,75	DHDDS	dehydrodolichyl diphosphate synthase subunit
8871	6,04E-15	1,42E+01	2,35E-15	0,0373	-7,9215214	-0,29539243	8891,21	SYNJ2	synaptojanin 2
26503	3,81E-07	6,42E+00	2,01E-07	0,0568	-5,1987562	-0,29546139	2216,9	SLC17A5	solute carrier family 17 member 5
439916	6,72E-01	1,73E-01	6,37E-01	0,6263	-0,4719938	-0,29561974	7,93	LINC00615	long intergenic non-protein coding RNA 615
57171	2,37E-07	6,63E+00	1,23E-07	0,056	-5,2883715	-0,29604843	1617,41	DOLPP1	dolichyldiphosphatase 1
107987095	2,33E-01	6,33E-01	1,99E-01	0,2306	-1,2839702	-0,29607701	59,75	LOC107987(	uncharacterized LOC107987095
100137047	2,36E-01	6,27E-01	2,02E-01	0,2323	-1,2763873	-0,29655458	70,28	JMJD7	jumonji domain containing 7
5465	4,76E-05	4,32E+00	2,82E-05	0,0709	-4,1871708	-0,29669659	823,67	PPARA	peroxisome proliferator activated receptor alpha
10277	9,16E-11	1,00E+01	4,10E-11	0,045	-6,6003643	-0,29690917	3743,26	UBE4B	ubiquitination factor E4B
22838	3,38E-06	5,47E+00	1,87E-06	0,0624	-4,7667493	-0,29761393	1325,2	RNF44	ring finger protein 44
80127	3,32E-03	2,48E+00	2,27E-03	0,0975	-3,0517826	-0,29766527	365,36	BBOF1	basal body orientation factor 1
57555	2,34E-08	7,63E+00	1,16E-08	0,0522	-5,705083	-0,29771335	2397,65	NLGN2	neuroligin 2
10533	2,95E-07	6,53E+00	1,55E-07	0,0567	-5,2469277	-0,29772546	1599,83	ATG7	autophagy related 7
7879	9,75E-11	1,00E+01	4,37E-11	0,0452	-6,5910457	-0,29789635	11025,41	RAB7A	RAB7A, member RAS oncogene family
22864	1,14E-06	5,94E+00	6,15E-07	0,0597	-4,9863319	-0,29792773	1463,78	R3HDM2	R3H domain containing 2
107985358	7,51E-02	1,12E+00	5,96E-02	0,1581	-1,8838799	-0,29792965	121,82	LOC107985(	uncharacterized LOC107985358
4983	9,41E-06	5,03E+00	5,36E-06	0,0655	-4,5502784	-0,29805759	1272,09	OPHN1	oligophrenin 1
54815	4,38E-11	1,04E+01	1,94E-11	0,0444	-6,710479	-0,29825064	6371,7	GATAD2A	GATA zinc finger domain containing 2A
284649	3,29E-01	4,83E-01	2,89E-01	0,2814	-1,0601901	-0,29828963	37,66	SMG7-AS1	SMG7 antisense RNA 1
23682	1,90E-05	4,72E+00	1,10E-05	0,0679	-4,3960822	-0,29829024	1056,5	RAB38	RAB38, member RAS oncogene family
56954	6,75E-08	7,17E+00	3,42E-08	0,0541	-5,5185349	-0,29829947	2280,78	NIT2	nitrilase family member 2
148223	5,02E-03	2,30E+00	3,50E-03	0,1023	-2,9200695	-0,29865029	421,39	C19orf25	chromosome 19 open reading frame 25
79922	3,90E-03	2,41E+00	2,69E-03	0,0995	-3,0013172	-0,29870106	347,24	MRM1	mitochondrial rRNA methyltransferase 1
4824	1,80E-05	4,74E+00	1,04E-05	0,0678	-4,4080737	-0,29885346	971,92	NKX3-1	NK3 homeobox 1
334	4,05E-16	1,54E+01	1,51E-16	0,0362	-8,2553694	-0,29886212	58460,9	APLP2	amyloid beta precursor like protein 2
23194	7,99E-03	2,10E+00	5,67E-03	0,1081	-2,7662753	-0,29894461	309,39	FBXL7	F-box and leucine rich repeat protein 7
84961	5,10E-04	3,29E+00	3,28E-04	0,0832	-3,5925117	-0,29906065	612,66	FBXL20	F-box and leucine rich repeat protein 20
6924	1,62E-09	8,79E+00	7,65E-10	0,0486	-6,1520872	-0,29912566	5474,38	ELOA	elongin A
285352	2,96E-01	5,29E-01	2,58E-01	0,2643	-1,1319658	-0,29916177	43,29	KIF9-AS1	KIF9 antisense RNA 1
107985314	5,62E-01	2,50E-01	5,21E-01	0,4666	-0,6411792	-0,29917975	14,92	LOC107985(	uncharacterized LOC107985314
79135	7,51E-06	5,12E+00	4,25E-06	0,0651	-4,5989114	-0,29933827	1001,99	APOO	apolipoprotein O
107986193	5,79E-01	2,37E-01	5,39E-01	0,4875	-0,6140826	-0,29935648	12,93	LOC107986(	uncharacterized LOC107986193

9761	7,51E-17	1,61E+01	2,74E-17	0,0354	-8,4570381	-0,29953262	20475,54	MLEC	malectin
56652	6,04E-08	7,22E+00	3,05E-08	0,0542	-5,5383669	-0,29994757	1981,06	TWNK	twinkle mtDNA helicase
105377742	2,54E-01	5,95E-01	2,19E-01	0,2442	-1,2296014	-0,30030888	50,11	LOC105377	uncharacterized LOC105377742
8812	1,67E-09	8,78E+00	7,91E-10	0,0489	-6,1467993	-0,30036536	2644,76	CCNK	cyclin K
79987	4,48E-01	3,49E-01	4,06E-01	0,3617	-0,83037	-0,30038099	23,33	SVEP1	sushi, von Willebrand factor type A, EGF and pentraxin domain containing 1
10455	4,03E-11	1,04E+01	1,78E-11	0,0447	-6,7229403	-0,3004706	4638,63	ECI2	enoyl-CoA delta isomerase 2
2733	8,31E-12	1,11E+01	3,57E-12	0,0432	-6,9530875	-0,30070776	4442,17	GLE1	GLE1 RNA export mediator
5683	4,99E-10	9,30E+00	2,30E-10	0,0475	-6,339791	-0,3010188	7129,03	PSMA2	proteasome 20S subunit alpha 2
375190	1,31E-02	1,88E+00	9,49E-03	0,1161	-2,5939507	-0,30111106	234,47	FAM228B	family with sequence similarity 228 member B
645954	6,58E-01	1,82E-01	6,22E-01	0,6103	-0,4933847	-0,30113312	8,09	SVIL2P	supervillin family member 2, pseudogene
653381	8,64E-05	4,06E+00	5,22E-05	0,0745	-4,0456119	-0,30148302	696,41	SORD2P	sorbitol dehydrogenase 2, pseudogene
84124	4,39E-04	3,36E+00	2,80E-04	0,0831	-3,6327841	-0,30183063	512,7	ZNF394	zinc finger protein 394
100302185	4,69E-01	3,29E-01	4,28E-01	0,3806	-0,7933126	-0,30196302	21,26	MIR1204	microRNA 1204
5822	2,85E-05	4,55E+00	1,67E-05	0,0702	-4,3049792	-0,3020585	1175,5	PWP2	PWP2 small subunit processome component
56270	8,07E-15	1,41E+01	3,15E-15	0,0384	-7,8849044	-0,30252419	8572,3	WDR45B	WD repeat domain 45B
2017	3,04E-14	1,35E+01	1,21E-14	0,0392	-7,7152489	-0,30256578	6820,21	CTTN	cortactin
5160	4,38E-12	1,14E+01	1,87E-12	0,043	-7,0439953	-0,30260528	4674,42	PDHA1	pyruvate dehydrogenase E1 subunit alpha 1
283373	2,17E-11	1,07E+01	9,49E-12	0,0444	-6,8140395	-0,30261359	6341,29	ANKRD52	ankyrin repeat domain 52
65057	8,78E-06	5,06E+00	4,99E-06	0,0664	-4,5650428	-0,30306469	1095,98	ACD	ACD shelterin complex subunit and telomerase recruitment factor
8767	7,88E-06	5,10E+00	4,47E-06	0,0661	-4,5884322	-0,30309104	913,87	RIPK2	receptor interacting serine/threonine kinase 2
708	9,47E-13	1,20E+01	3,95E-13	0,0418	-7,257279	-0,30321251	10650,33	C1QBP	complement C1q binding protein
4729	6,91E-11	1,02E+01	3,08E-11	0,0457	-6,6427232	-0,30372862	6725,99	NDUFV2	NADH:ubiquinone oxidoreductase core subunit V2
6229	1,72E-11	1,08E+01	7,50E-12	0,0444	-6,8477594	-0,30382292	56179,42	RPS24	ribosomal protein S24
2677	1,75E-12	1,18E+01	7,37E-13	0,0424	-7,1724224	-0,30390543	4592,44	GGCX	gamma-glutamyl carboxylase
89122	3,46E-05	4,46E+00	2,04E-05	0,0713	-4,2606815	-0,30398687	803,2	TRIM4	tripartite motif containing 4
522	4,08E-09	8,39E+00	1,95E-09	0,0507	-6,0016107	-0,304104	4719,1	ATP5PF	ATP synthase peripheral stalk subunit F6
23081	7,58E-03	2,12E+00	5,37E-03	0,1093	-2,7837815	-0,30413337	306,68	KDM4C	lysine demethylase 4C
6625	1,60E-11	1,08E+01	6,96E-12	0,0444	-6,8584468	-0,30431911	9094,49	SNRNP70	small nuclear ribonucleoprotein U1 subunit 70
84964	6,33E-04	3,20E+00	4,09E-04	0,0861	-3,5341409	-0,30442966	531,46	ALKBH6	alkB homolog 6
107985013	1,84E-01	7,35E-01	1,54E-01	0,2138	-1,4250459	-0,3046745	64,08	LOC107985	uncharacterized LOC107985013
84501	8,30E-03	2,08E+00	5,91E-03	0,1108	-2,7529918	-0,30492344	285,49	SPIRE2	spire type actin nucleation factor 2
9830	2,08E-12	1,17E+01	8,76E-13	0,0427	-7,1486583	-0,30506483	4001,09	TRIM14	tripartite motif containing 14
145567	3,24E-06	5,49E+00	1,80E-06	0,064	-4,7751353	-0,30540337	1125,7	TTC7B	tetratricopeptide repeat domain 7B
102724594	1,09E-09	8,96E+00	5,08E-10	0,0491	-6,2164876	-0,30550291	2932,76	LOC102724	U2 small nuclear RNA auxiliary factor 1 like 5
8737	1,01E-11	1,10E+01	4,35E-12	0,0441	-6,9252696	-0,30553069	3493,97	RIPK1	receptor interacting serine/threonine kinase 1
25937	5,88E-10	9,23E+00	2,72E-10	0,0484	-6,3138583	-0,30555584	4300,57	WWTR1	WW domain containing transcription regulator 1
10505	1,01E-05	5,00E+00	5,74E-06	0,0674	-4,5358828	-0,30556508	898,01	SEMA4F	ssemaphorin 4F
107985338	6,61E-01	1,80E-01	6,25E-01	0,6244	-0,4893767	-0,30558528	8,13	LINC02813	long intergenic non-protein coding RNA 2813
6821	1,76E-08	7,75E+00	8,65E-09	0,0531	-5,755194	-0,30570635	2151,91	SUOX	sulfite oxidase
4293	6,41E-07	6,19E+00	3,42E-07	0,06	-5,0986982	-0,3057263	1456,14	MAP3K9	mitogen-activated protein kinase kinase kinase 9
113419	5,97E-13	1,22E+01	2,47E-13	0,0418	-7,3204128	-0,30580733	4874,64	TEX261	testis expressed 261
101928274	6,58E-03	2,18E+00	4,63E-03	0,1081	-2,831477	-0,30609337	276,61	LOC101928	uncharacterized LOC101928274
26233	7,90E-02	1,10E+00	6,28E-02	0,1646	-1,8603587	-0,30618764	751,17	FBXL6	F-box and leucine rich repeat protein 6
144983	1,52E-07	6,82E+00	7,84E-08	0,057	-5,370709	-0,30618926	1839,33	HNRNPA1L2	heterogeneous nuclear ribonucleoprotein A1 like 2
107986531	6,69E-02	1,17E+00	5,27E-02	0,1581	-1,9372696	-0,30620997	124,79	LOC107986	uncharacterized LOC107986531
23392	6,04E-16	1,52E+01	2,27E-16	0,0373	-8,2068081	-0,30638222	12043,68	ECPAS	Ecm29 proteasome adaptor and scaffold
92691	3,93E-01	4,06E-01	3,51E-01	0,3291	-0,9320541	-0,30675026	27,16	TMEM169	transmembrane protein 169
85320	2,24E-01	6,50E-01	1,91E-01	0,2348	-1,3072336	-0,30694503	54,87	ABCC11	ATP binding cassette subfamily C member 11
23623	5,19E-07	6,28E+00	2,75E-07	0,0597	-5,1396287	-0,30705084	2083,18	RUSC1	RUN and SH3 domain containing 1
23203	7,27E-08	7,14E+00	3,69E-08	0,0558	-5,505146	-0,30730325	2205,71	PMPCA	peptidase, mitochondrial processing subunit alpha
23180	1,63E-11	1,08E+01	7,10E-12	0,0448	-6,8555792	-0,30741747	4022,8	RFTN1	raftlin, lipid raft linker 1
1981	4,69E-18	1,73E+01	1,65E-18	0,0351	-8,7790167	-0,30786285	48446,82	EIF4G1	eukaryotic translation initiation factor 4 gamma 1
100526740	2,05E-08	7,69E+00	1,02E-08	0,0538	-5,728072	-0,30816512	3752,37	ATP5MF-PT(	ATP5MF-PTCD1 readthrough
54903	1,66E-04	3,78E+00	1,03E-04	0,0794	-3,8842228	-0,30831683	618,25	MKS1	MKS transition zone complex subunit 1
23268	5,63E-15	1,42E+01	2,18E-15	0,0389	-7,9303771	-0,30855865	10595,2	DNMBP	dynamin binding protein
22872	4,41E-14	1,34E+01	1,76E-14	0,0402	-7,6670715	-0,30855933	15530,65	SEC31A	SEC31 homolog A, COPII coat complex component
3399	7,68E-04	3,11E+00	5,00E-04	0,0887	-3,4807134	-0,30881972	536,05	ID3	inhibitor of DNA binding 3
105372476	6,03E-01	2,20E-01	5,65E-01	0,5362	-0,5761528	-0,30891986	10,82	ZNF460-AS1	ZNF460 antisense RNA 1
526	3,17E-12	1,15E+01	1,35E-12	0,0436	-7,0895896	-0,30902106	3768,63	ATP6V1B2	ATPase H+ transporting V1 subunit B2
5045	3,76E-07	6,42E+00	1,98E-07	0,0595	-5,2011456	-0,30922799	2226,14	FURIN	furin, paired basic amino acid cleaving enzyme
594842	1,13E-01	9,47E-01	9,19E-02	0,1835	-1,6856914	-0,30925673	92,99	HAS2-AS1	HAS2 antisense RNA 1
4578	4,61E-02	1,34E+00	3,55E-02	0,1471	-2,1022768	-0,30932526	173,9	TRNW	tRNA-Trp
2178	2,12E-09	8,67E+00	1,00E-09	0,0507	-6,1087201	-0,30958763	1954,38	FANCE	FA complementation group E
51547	1,58E-05	4,80E+00	9,12E-06	0,0698	-4,4370131	-0,30971003	909,8	SIRT7	sirtuin 7
105370088	4,68E-01	3,30E-01	4,26E-01	0,3894	-0,7956669	-0,30982872	18,98	LOC105370	uncharacterized LOC105370088
11158	1,22E-03	2,91E+00	8,06E-04	0,0925	-3,3506086	-0,30994078	398,43	RABL2B	RAB, member of RAS oncogene family like 2B
1635	7,58E-15	1,41E+01	2,95E-15	0,0393	-7,8928122	-0,30995679	6150,63	DCTD	dCMP deaminase
8341	3,62E-01	4,41E-01	3,21E-01	0,3126	-0,9922658	-0,31017473	32,57	H2BC15	H2B clustered histone 15
100847042	2,66E-01	5,75E-01	2,30E-01	0,2584	-1,2007124	-0,31031971	47,04	MIR5572	microRNA 5572
5331	2,44E-10	9,61E+00	1,11E-10	0,0481	-6,4508974	-0,31039529	3450,78	PLCB3	phospholipase C beta 3
286128	4,10E-04	3,39E+00	2,61E-04	0,085	-3,6510977	-0,31049248	531,84	ZFP41	ZFP41 zinc finger protein
4097	1,15E-08	7,94E+00	5,62E-09	0,0533	-5,8275545	-0,3107039	2923,11	MAFG	MAF bZIP transcription factor G
8744	1,67E-03	2,78E+00	1,12E-03	0,0954	-3,2593653	-0,31082327	403,78	TNFSF9	TNF superfamily member 9
114790	1,37E-04	3,86E+00	8,41E-05	0,0791	-3,9324609	-0,31090103	728,36	STK11IP	serine/threonine kinase 11 interacting protein
8031	3,06E-13	1,25E+01	1,26E-13	0,042	-7,4108151	-0,3109658	11256,7	NCOA4	nuclear receptor coactivator 4
79939	2,42E-14	1,36E+01	9,58E-15	0,0402	-7,7447176	-0,31117884	6760,58	SLC35E1	solute carrier family 35 member E1
51642	3,79E-08	7,42E+00	1,90E-08	0,0554	-5,6211456	-0,31146299	1737,15	MRPL48	mitochondrial ribosomal protein L48
105375957	1,81E-01	7,42E-01	1,52E-01	0,2176	-1,4317803	-0,31161743	64,71	LOC105375	uncharacterized LOC105375957
5134	1,09E-09	8,96E+00	5,11E-10	0,0503	-6,2156858	-0,31238327	2816,7	PDCD2	programmed cell death 2
949	4,81E-08	7,32E+00	2,42E-08	0,056	-5,5791988	-0,31253093	2024,92	SCARB1	scavenger receptor class B member 1
54847	1,59E-01	7,99E-01	1,33E-01	0,2078	-1,5041029	-0,31259314	68,81	SIDT1	SID1 transmembrane family member 1
9079	3,07E-01	5,13E-01	2,68E-01	0,2825	-1,1070342	-0,31276474	41,12	LDB2	LIM domain binding 2
8650	8,59E-12	1,11E+01	3,69E-12	0,0451	-6,9484355	-0,31308135	5260,54	NUMB	NUMB endocytic adaptor protein
7325	9,34E-08	7,03E+00	4,77E-08	0,0574	-5,4597277	-0,31354452	1344,35	UBE2E2	ubiquitin conjugating enzyme E2 E2
11142	3,53E-07	6,45E+00	1,86E-07	0,0601	-5,2129359	-0,3135554	1355,54	PKIG	cAMP-dependent protein kinase inhibitor gamma
27296	2,33E-01	6,33E-01	1,99E-01	0,2441	-1,2849277	-0,31364469	49,01	TP53TG5	TP53 target 5
9967	1,22E-11	1,09E+01	5,29E-12	0,0455	-6,8975248	-0,31367204	14722,57	THRAP3	thyroid hormone receptor associated protein 3
388152	9,60E-03	2,02E+00	6,88E-03	0,1161	-2,7027115	-0,31372154	243,69	GOLGA2P7	GOLGA2 pseudogene 7
6493	5,65E-02	1,25E+00	4,42E-02	0,1559	-2,0125612	-0,31374685	124,92	SIM2	SIM bHLH transcription factor 2
1487	3,33E-07	6,48E+00	1,75E-07	0,0601	-5,2241768	-0,31384332	3519,21	CTBP1	C-terminal binding protein 1
3855	4,43E-11	1,04E+01	1,96E-11	0,0469	-6,708921	-0,31454683	6826,07	KRT7	keratin 7
5604	4,96E-12	1,13E+01	2,12E-12	0,0448	-7,026246	-0,31456266	3764,08	MAP2K1	mitogen-activated protein kinase kinase 1
339290	2,82E-06	5,55E+00	1,55E-06	0,0655	-4,8042603	-0,31485829	1000,27	LINC00667	long intergenic non-protein coding RNA 667
9020	1,64E-05	4,79E+00	9,50E-06	0,0711	-4,4283435	-0,31489195	870,66	MAP3K14	mitogen-activated protein kinase kinase kinase 14
1994	5,08E-15	1,43E+01	1,97E-15	0,0396	-7,9433047	-0,31492282	6824,06	ELAVL1	ELAV like RNA binding protein 1
7290	3,99E-09	8,40E+00	1,91E-09	0,0524	-6,005202	-0,31494038	2073,35	HIRA	histone cell cycle regulator
653712	4,21E-01	3,76E-01	3,80E-01	0,3587	-0,8780082	-0,31496726	23,94	IFT122P3	IFT122 pseudogene 3
10723	8,98E-05	4,05E+00	5,43E-05	0,078	-4,0362244	-0,31497846	589,79	SLC12A7	solute carrier family 12 member 7
348926	5,16E-02	1,29E+00	4,01E-02	0,1535	-2,052717	-0,31500875	128,18	FAM86EP	family with sequence similarity 86, member A pseudogene
92105	5,91E-09	8,23E+00	2,85E-09	0,053	-5,939734	-0,31503586	2062,44	INTS4	integrator complex subunit 4
55803	1,42E-01	8,48E-01	1,17E-01	0,2012	-1,566589	-0,31513325	73,08	ADAP2	ArfGAP with dual PH domains 2
100532726	3,51E-09	8,45E+00	1,68E-09	0,0523	-6,0260864	-0,31513553	2279,07	NDUFC2-KC	NDUFC2-KCTD14 readthrough
152992	9,10E-04	3,04E+00	5,95E-04	0,0918	-3,4339682	-0,31517858	418,13	TRMT44	tRNA methyltransferase 44 homolog
101927895	5,58E-03	2,25E+00	3,90E-03	0,1093	-2,8858744	-0,31539175	275,05	EMC1-AS1	EMC1 antisense RNA 1
8079	1,33E-11	1,09E+01	5,77E-12	0,0458	-6,8851618	-0,31542939	5803,25	MLF2	myeloid leukemia factor 2
28978	2,40E-05	4,62E+00	1,40E-05	0,0726	-4,3441875	-0,31546892	811,66	TMEM14A	transmembrane protein 14A
1417	2,65E-04	3,58E+00	1,66E-04	0,0839	-3,7653872	-0,31574579	490,68	CRYBB3	crystallin beta B3
9766	3,53E-05	4,45E+00	2,08E-05	0,0742	-4,2560361	-0,31599905	765,06	SUSD6	sushi domain containing 6
10039	6,55E-07	6,18E+00	3,49E-07	0,0621	-5,0946557	-0,3163012	1085,04	PARP3	poly(ADP-ribose) polymerase family member 3
9024	3,62E-01	4,41E-01	3,22E-01	0,3192	-0,9910344	-0,31632801	30,44	BRSK2	BR serine/threonine kinase 2
1571	4,57E-01	3,40E-01	4,16E-01	0,3893	-0,8138883	-0,31681121	20,28	CYP2E1	cytochrome P450 family 2 subfamily E member 1
10675	2,14E-02	1,67E+00	1,58E-02	0,1314	-2,4133066	-0,31702497	180,83	CSPG5	chondroitin sulfate proteoglycan 5
57448	5,86E-13	1,22E+01	2,42E-13	0,0434	-7,3229936	-0,31751093	4964,35	BIRC6	baculoviral IAP repeat containing 6
85414	3,15E-04	3,50E+00	1,99E-04	0,0854	-3,7201994	-0,3177217	551,27	SLC45A3	solute carrier family 45 member 3
1960	6,32E-01	1,99E-01	5,94E-01	0,5964	-0,5327576	-0,31773568	8,43	EGR3	early growth response 3
100532737	1,70E-14	1,38E+01	6,72E-15	0,0408	-7,7895999	-0,31779132	6386,19	ATP6V1G2-I	ATP6V1G2-DDX39B readthrough (NMD candidate)
6125	3,47E-16	1,55E+01	1,29E-16	0,0384	-8,2741772	-0,31791476	47220,22	RPL5	ribosomal protein L5
10098	5,17E-10	9,29E+00	2,39E-10	0,0502	-6,334223	-0,31822026	2342,52	TSPAN5	tetraspanin 5
89866	3,64E-01	4,39E-01	3,24E-01	0,3225	-0,9872863	-0,31835217	27,85	SEC16B	SEC16 homolog B, endoplasmic reticulum export factor
55505	5,28E-09	8,28E+00	2,54E-09	0,0535	-5,9587435	-0,31868354	4022,46	NOP10	NOP10 ribonucleoprotein

3791	2,30E-04	3,64E+00	1,44E-04	0,0839	-3,8016979	-0,31881687	494,73	KDR	kinase insert domain receptor
6804	1,37E-06	5,86E+00	7,46E-07	0,0644	-4,9490789	-0,31884611	1186,92	STX1A	syntaxin 1A
64781	3,91E-09	8,41E+00	1,87E-09	0,0531	-6,0083556	-0,31915839	1854,07	CERK	ceramide kinase
728855	3,83E-03	2,42E+00	2,64E-03	0,1063	-3,0070842	-0,31957323	327,02	LINC00623	long intergenic non-protein coding RNA 623
476	5,33E-21	2,03E+01	1,72E-21	0,0336	-9,5204852	-0,31973393	43166,71	ATP1A1	ATPase Na+/K+ transporting subunit alpha 1
51538	3,55E-09	8,45E+00	1,70E-09	0,0531	-6,024357	-0,31979964	2644	ZCCHC17	zinc finger CCHC-type containing 17
100507381	3,44E-01	4,63E-01	3,04E-01	0,3112	-1,0278065	-0,31986877	31,18	KCNQ5-IT1	KCNQ5 intronic transcript 1
101929516	2,00E-07	6,70E+00	1,04E-07	0,0601	-5,3198736	-0,31989335	1230,93	PABPC4-AS1	PABPC4 antisense RNA 1
646762	2,66E-04	3,58E+00	1,67E-04	0,085	-3,7642471	-0,31990549	583,51	LOC646762	uncharacterized LOC646762
51477	4,83E-04	3,32E+00	3,09E-04	0,0888	-3,607382	-0,32025108	504,27	ISYNA1	inositol-3-phosphate synthase 1
128102	5,61E-01	2,51E-01	5,20E-01	0,498	-0,6432102	-0,32034984	11,81	HSD3BP4	hydroxy-delta-5-steroid dehydrogenase, 3 beta, pseudogene 4
54623	2,30E-11	1,06E+01	1,01E-11	0,0471	-6,8051993	-0,32044686	6761,94	PAF1	PAF1 homolog, Paf1/RNA polymerase II complex component
7919	1,03E-14	1,40E+01	4,04E-15	0,0408	-7,8536958	-0,320459	6349,29	DDX39B	DExD-box helicase 39B
2110	1,26E-05	4,90E+00	7,24E-06	0,0715	-4,4863977	-0,32059344	797,41	ETFDH	electron transfer flavoprotein dehydrogenase
2029	2,63E-15	1,46E+01	1,01E-15	0,04	-8,0256426	-0,32071971	6494,65	ENSA	endosulfine alpha
399694	2,75E-01	5,61E-01	2,38E-01	0,2723	-1,1790218	-0,32107129	41,91	SHC4	SHC adaptor protein 4
3978	7,87E-12	1,11E+01	3,38E-12	0,0461	-6,9608618	-0,32110515	3963,12	LIG1	DNA ligase 1
5147	1,85E-07	6,73E+00	9,57E-08	0,0602	-5,3346749	-0,32123304	1496,94	PDE6D	phosphodiesterase 6D
60386	2,78E-04	3,56E+00	1,75E-04	0,0856	-3,7532156	-0,32124977	516,02	SLC25A19	solute carrier family 25 member 19
5564	3,99E-10	9,40E+00	1,83E-10	0,0504	-6,3746402	-0,32136513	2109,08	PRKAB1	protein kinase AMP-activated non-catalytic subunit beta 1
113452	1,71E-04	3,77E+00	1,05E-04	0,0829	-3,877869	-0,32141038	931,42	TMEM54	transmembrane protein 54
23348	3,30E-16	1,55E+01	1,23E-16	0,0388	-8,2799912	-0,32145863	6838,6	DOCK9	dedicator of cytokinesis 9
107983990	5,92E-01	2,28E-01	5,53E-01	0,5419	-0,5934711	-0,3215754	9,98	LOC107983	uncharacterized LOC107983990
23294	7,26E-10	9,14E+00	3,37E-10	0,0512	-6,2806557	-0,32177688	2344,91	ANKS1A	ankyrin repeat and sterile alpha motif domain containing 1A
6389	2,73E-17	1,66E+01	9,83E-18	0,0375	-8,5759328	-0,32182241	8709,52	SDHA	succinate dehydrogenase complex flavoprotein subunit A
11119	5,64E-08	7,25E+00	2,85E-08	0,058	-5,5505967	-0,32184267	1569,5	BTN3A1	butyrophilin subfamily 3 member A1
5723	4,96E-09	8,30E+00	2,39E-09	0,054	-5,9690389	-0,32234115	1733,28	PSPH	phosphoserine phosphatase
83858	4,36E-07	6,36E+00	2,30E-07	0,0623	-5,173115	-0,32239981	1519,2	ATAD3B	ATPase family AAA domain containing 3B
112	1,61E-06	5,79E+00	8,76E-07	0,0656	-4,9175925	-0,32240644	1049,93	ADCY6	adenylate cyclase 6
55245	1,17E-11	1,09E+01	5,07E-12	0,0467	-6,903558	-0,32258246	3827,07	UQCC1	ubiquinol-cytochrome c reductase complex assembly factor 1
8509	5,89E-06	5,23E+00	3,31E-06	0,0694	-4,6504892	-0,32269919	873,32	NDST2	N-deacetylase and N-sulfotransferase 2
837	4,60E-11	1,03E+01	2,04E-11	0,0481	-6,703248	-0,32272814	3595,93	CASP4	caspase 4
1317	2,99E-12	1,15E+01	1,27E-12	0,0455	-7,0976003	-0,32283681	2973,52	SLC31A1	solute carrier family 31 member 1
105370681	2,10E-01	6,78E-01	1,78E-01	0,2397	-1,347526	-0,3229893	53,18	LINC02323	long intergenic non-protein coding RNA 2323
126526	6,80E-07	6,17E+00	3,63E-07	0,0636	-5,0873953	-0,32370026	1196,41	C19orf47	chromosome 19 open reading frame 47
1124	2,35E-02	1,63E+00	1,75E-02	0,1362	-2,3768525	-0,32370239	176,69	CHN2	chimerin 2
80230	5,95E-12	1,12E+01	2,55E-12	0,0463	-7,0005813	-0,32381707	3031,81	RUFY1	RUN and FYVE domain containing 1
1846	7,49E-18	1,71E+01	2,65E-18	0,0372	-8,7254366	-0,32415241	26728,16	DUSP4	dual specificity phosphatase 4
200916	9,07E-08	7,04E+00	4,63E-08	0,0593	-5,465117	-0,32423977	2140,97	RPL22L1	ribosomal protein L22 like 1
84707	2,22E-03	2,65E+00	1,50E-03	0,1022	-3,1746233	-0,32430869	352,36	BEX2	brain expressed X-linked 2
100506023	3,98E-01	4,00E-01	3,57E-01	0,3519	-0,9217998	-0,32435407	23,76	LOC100506	uncharacterized LOC100506023
645638	4,95E-01	3,05E-01	4,53E-01	0,4324	-0,7502836	-0,32443682	15,53	WFDC21P	WAP four-disulfide core domain 21, pseudogene
23275	2,18E-09	8,66E+00	1,03E-09	0,0532	-6,1042733	-0,32466313	1680,3	POFUT2	protein O-fucosyltransferase 2
48	2,78E-17	1,66E+01	1,00E-17	0,0379	-8,5734618	-0,32515358	9743,89	ACO1	aconitase 1
8940	8,72E-06	5,06E+00	4,96E-06	0,0712	-4,5665922	-0,32525332	792,87	TOP3B	DNA topoisomerase III beta
25790	5,25E-02	1,28E+00	4,08E-02	0,1592	-2,0456265	-0,32557958	120,48	CFAP45	cilia and flagella associated protein 45
105375169	3,44E-01	4,63E-01	3,04E-01	0,3169	-1,0279776	-0,32579671	29,56	LOC105375	uncharacterized LOC105375169
6242	1,39E-06	5,86E+00	7,56E-07	0,0659	-4,9463942	-0,32587803	1071,86	RTKN	rhotekin
29799	1,21E-01	9,17E-01	9,90E-02	0,1976	-1,649877	-0,32605877	83,45	YPEL1	yippee like 1
25970	8,69E-06	5,06E+00	4,94E-06	0,0714	-4,5673254	-0,32614173	969,22	SH2B1	SH2B adaptor protein 1
2874	2,83E-12	1,15E+01	1,20E-12	0,0459	-7,1056504	-0,32637989	4721,57	GPS2	G protein pathway suppressor 2
105379507	5,51E-01	2,59E-01	5,11E-01	0,4963	-0,6580008	-0,32656582	12,2	LOC105379	uncharacterized LOC105379507
93654	9,25E-02	1,03E+00	7,43E-02	0,1831	-1,7850229	-0,32677261	93,23	ST7-AS2	ST7 antisense RNA 2
10450	3,89E-10	9,41E+00	1,78E-10	0,0512	-6,3790002	-0,32683131	2420,97	PPIE	peptidylprolyl isomerase E
170690	4,07E-05	4,39E+00	2,40E-05	0,0774	-4,2235885	-0,32687806	627,93	ADAMTS16	ADAM metallopeptidase with thrombospondin type 1 motif 16
55100	2,84E-07	6,55E+00	1,48E-07	0,0622	-5,2545469	-0,32709167	1292,12	WDR70	WD repeat domain 70
3598	5,06E-01	2,96E-01	4,64E-01	0,4472	-0,731993	-0,32737396	16,08	IL13RA2	interleukin 13 receptor subunit alpha 2
140699	5,79E-06	5,24E+00	3,26E-06	0,0704	-4,6540243	-0,32750158	1105,87	MROH8	maestro heat like repeat family member 8
55229	6,45E-07	6,19E+00	3,44E-07	0,0643	-5,0975611	-0,32759256	1251,1	PANK4	pantothenate kinase 4 (inactive)
56135	4,74E-01	3,24E-01	4,32E-01	0,4173	-0,7851028	-0,3276614	17,37	PCDHAC1	protocadherin alpha subfamily C, 1
23193	9,41E-20	1,90E+01	3,15E-20	0,0356	-9,2138357	-0,32768056	39497,54	GANAB	glucosidase II alpha subunit
5744	3,88E-01	4,11E-01	3,47E-01	0,3495	-0,9405646	-0,32870603	25,85	PTHLH	parathyroid hormone like hormone
3607	4,24E-15	1,44E+01	1,64E-15	0,0413	-7,9658864	-0,32876292	5420,46	FOXK2	forkhead box K2
78998	1,52E-01	8,18E-01	1,26E-01	0,215	-1,5300737	-0,32889154	64,38	RHPN1-AS1	RHPN1 antisense RNA 1 (head to head)
3104	7,25E-04	3,14E+00	4,71E-04	0,0942	-3,4968327	-0,32931937	483,99	ZBTB48	zinc finger and BTB domain containing 48
10838	9,17E-04	3,04E+00	6,00E-04	0,096	-3,4317325	-0,32934909	376,74	ZNF275	zinc finger protein 275
100130172	1,75E-01	7,57E-01	1,46E-01	0,2268	-1,4528049	-0,32956756	59,44	FAM13B-AS	FAM13B antisense RNA 1
5954	3,22E-10	9,49E+00	1,47E-10	0,0515	-6,4082284	-0,32982922	13684,78	RCN1	reticulocalbin 1
105378552	2,33E-01	6,33E-01	1,99E-01	0,2569	-1,284433	-0,32994677	45,79	LOC105378	uncharacterized LOC105378552
7124	4,88E-01	3,12E-01	4,47E-01	0,4339	-0,760959	-0,33021709	15,52	TNF	tumor necrosis factor
4218	1,07E-12	1,20E+01	4,46E-13	0,0456	-7,2407179	-0,33044517	10611,17	RAB8A	RAB8A, member RAS oncogene family
440034	5,44E-01	2,64E-01	5,03E-01	0,4935	-0,6699282	-0,33060641	11,82	PAX6-AS1	PAX6 antisense RNA 1
103	1,24E-16	1,59E+01	4,55E-17	0,0394	-8,3976787	-0,3307553	8366,93	ADAR	adenosine deaminase RNA specific
11182	4,80E-04	3,32E+00	3,07E-04	0,0917	-3,6092523	-0,33091353	519,54	SLC2A6	solute carrier family 2 member 6
101926888	3,02E-01	5,20E-01	2,64E-01	0,2962	-1,1177826	-0,33105248	33,96	RALY-AS1	RALY antisense RNA 1
100505573	6,23E-05	4,21E+00	3,73E-05	0,0803	-4,1238666	-0,33120571	689,06	INAFM2	InaF motif containing 2
8890	7,12E-13	1,21E+01	2,95E-13	0,0454	-7,2964588	-0,3313101	2899,36	EIF2B4	eukaryotic translation initiation factor 2B subunit delta
85002	4,87E-02	1,31E+00	3,77E-02	0,1595	-2,0777973	-0,33132133	119,45	FAM86B1	family with sequence similarity 86 member B1
200186	3,68E-08	7,43E+00	1,84E-08	0,0589	-5,6262882	-0,33161125	2544,02	CRTC2	CREB regulated transcription coactivator 2
84679	2,89E-11	1,05E+01	1,27E-11	0,049	-6,7717786	-0,33161518	2436,93	SLC9A7	solute carrier family 9 member A7
7462	2,42E-02	1,62E+00	1,80E-02	0,1404	-2,3650347	-0,33200053	163,05	LAT2	linker for activation of T cells family member 2
100507316	2,38E-02	1,62E+00	1,77E-02	0,14	-2,3724554	-0,33203167	155,86	MINCR	MYC-induced long non-coding RNA
101929441	1,20E-01	9,21E-01	9,76E-02	0,2005	-1,6563656	-0,33206696	74,65	ERLNC1	estrogen receptor responsive lncRNA 1
497258	1,53E-02	1,82E+00	1,12E-02	0,131	-2,5367065	-0,33227926	193,2	BDNF-AS	BDNF antisense RNA
6838	1,58E-09	8,80E+00	7,46E-10	0,0541	-6,1560227	-0,33284488	2144,62	SURF6	surfeit 6
116151	1,45E-11	1,08E+01	6,31E-12	0,0484	-6,8725576	-0,33292664	2662,46	FAM210B	family with sequence similarity 210 member B
56126	1,36E-01	8,66E-01	1,12E-01	0,2097	-1,5895917	-0,33326693	70,83	PCDHB10	protocadherin beta 10
122961	1,86E-06	5,73E+00	1,02E-06	0,0682	-4,8885951	-0,33330478	844,29	ISCA2	iron-sulfur cluster assembly 2
3725	4,30E-15	1,44E+01	1,67E-15	0,0419	-7,9640261	-0,33340564	5106,04	JUN	Jun proto-oncogene, AP-1 transcription factor subunit
56993	9,09E-11	1,00E+01	4,07E-11	0,0505	-6,6016419	-0,33343414	2247,16	TOMM22	translocase of outer mitochondrial membrane 22
107984643	7,43E-03	2,13E+00	5,26E-03	0,1196	-2,7906298	-0,333638	239,43	LOC107984	uncharacterized LOC107984643
3708	1,24E-06	5,91E+00	6,70E-07	0,0671	-4,9698693	-0,33364199	864,24	ITPR1	inositol 1,4,5-trisphosphate receptor type 1
59271	1,67E-03	2,78E+00	1,12E-03	0,1024	-3,2587288	-0,33364218	313,39	EVA1C	eva-1 homolog C
349136	2,15E-02	1,67E+00	1,59E-02	0,1384	-2,4110801	-0,33366819	164,93	WDR86	WD repeat domain 86
103344931	4,14E-02	1,38E+00	3,18E-02	0,1554	-2,1472109	-0,33368007	135,62	LOC103344	uncharacterized LOC103344931
2923	1,33E-20	1,99E+01	4,35E-21	0,0354	-9,4238928	-0,33371307	22054,8	PDIA3	protein disulfide isomerase family A member 3
283989	1,92E-04	3,72E+00	1,19E-04	0,0867	-3,8485524	-0,3337293	519,2	TSEN54	tRNA splicing endonuclease subunit 54
9656	4,87E-10	9,31E+00	2,24E-10	0,0527	-6,3436815	-0,33436155	5472,45	MDC1	mediator of DNA damage checkpoint 1
51501	9,17E-07	6,04E+00	4,93E-07	0,0665	-5,028964	-0,33447361	1092,22	HIKESHI	heat shock protein nuclear import factor hikeshi
29100	7,07E-06	5,15E+00	3,99E-06	0,0725	-4,6117488	-0,33448654	811,14	TMEM208	transmembrane protein 208
5163	1,01E-06	6,00E+00	5,42E-07	0,0668	-5,0108539	-0,33462528	897,79	PDK1	pyruvate dehydrogenase kinase 1
90416	1,59E-04	3,80E+00	9,79E-05	0,0859	-3,8958187	-0,33471052	523,92	CCDC32	coiled-coil domain containing 32
6872	1,22E-09	8,91E+00	5,73E-10	0,054	-6,1977049	-0,33474496	2483,78	TAF1	TATA-box binding protein associated factor 1
51686	3,99E-04	3,40E+00	2,54E-04	0,0915	-3,6582167	-0,33476363	424,2	OAZ3	ornithine decarboxylase antizyme 3
11124	4,83E-14	1,33E+01	1,93E-14	0,0437	-7,6551208	-0,33479172	3930,31	FAF1	Fas associated factor 1
10954	5,17E-06	5,29E+00	2,90E-06	0,0717	-4,6778831	-0,33534746	745,46	PDIA5	protein disulfide isomerase family A member 5
51561	5,59E-02	1,25E+00	4,36E-02	0,1663	-2,0175453	-0,33553319	112,54	IL23A	interleukin 23 subunit alpha
101929715	2,97E-01	5,27E-01	2,59E-01	0,2975	-1,1285067	-0,33568345	33,33	ODC1-DT	ODC1 divergent transcript
93653	4,08E-02	1,39E+00	3,12E-02	0,156	-2,154097	-0,33599036	125,96	ST7-AS1	ST7 antisense RNA 1
79022	4,91E-14	1,33E+01	1,96E-14	0,0439	-7,6531365	-0,3361186	3957,42	TMEM106C	transmembrane protein 106C
6737	7,29E-06	5,14E+00	4,12E-06	0,073	-4,6052865	-0,33614496	981,29	TRIM21	tripartite motif containing 21
107986587	2,21E-01	6,56E-01	1,88E-01	0,2552	-1,3173202	-0,33619679	47,75	ABCF1-DT	ABCF1 divergent transcript
107985010	5,48E-01	2,61E-01	5,07E-01	0,5073	-0,662749	-0,33622784	12,26	LOC107985	replaced by ID 57690
55848	1,24E-04	3,91E+00	7,55E-05	0,085	-3,9581818	-0,33626487	513,03	PLGRKT	plasminogen receptor with a C-terminal lysine
8802	1,66E-11	1,08E+01	7,24E-12	0,0491	-6,8528487	-0,33626551	3372,67	SUCLG1	succinate-CoA ligase GDP/ADP-forming subunit alpha
84645	9,00E-03	2,05E+00	6,43E-03	0,1234	-2,7251901	-0,33627183	236,45	C22orf23	chromosome 22 open reading frame 23
101928602	5,70E-01	2,44E-01	5,29E-01	0,5355	-0,6287941	-0,33672383	10,32	LINC01775	long intergenic non-protein coding RNA 1775
101929316	4,96E-01	3,05E-01	4,54E-01	0,4498	-0,7487518	-0,33682459	14,33	PRICKLE2-D	PRICKLE2 divergent transcript
107986452	2,13E-01	6,72E-01	1,81E-01	0,2517	-1,3381922	-0,33683601	48,59	LOC107986452	
26147	1,32E-15	1,49E+01	5,00E-16	0,0416	-8,1115115	-0,33716191	6785,95	PHF19	PHD finger protein 19

1466	1,51E-05	4,82E+00	8,68E-06	0,0758	-4,4476103	-0,33721701	747,36	CSRP2	cysteine and glycine rich protein 2
107986985	4,88E-04	3,31E+00	3,13E-04	0,0936	-3,6045691	-0,33721845	416,34	LOC107986	uncharacterized LOC107986985
10566	5,34E-01	2,72E-01	4,93E-01	0,4921	-0,685455	-0,33729009	13,46	AKAP3	A-kinase anchoring protein 3
410	6,54E-03	2,18E+00	4,61E-03	0,1191	-2,8330887	-0,33735033	233,12	ARSA	arylsulfatase A
66035	1,86E-02	1,73E+00	1,37E-02	0,1368	-2,465818	-0,33736815	167,05	SLC2A11	solute carrier family 2 member 11
150221	1,63E-01	7,88E-01	1,36E-01	0,2262	-1,4923505	-0,33750647	59,61	RIMBP3C	RIMS binding protein 3C
8479	4,15E-08	7,38E+00	2,08E-08	0,0602	-5,6054031	-0,33752084	1461,38	HIRIP3	HIRA interacting protein 3
6742	1,24E-12	1,19E+01	5,18E-13	0,0468	-7,220584	-0,33770518	4911,25	SSBP1	single stranded DNA binding protein 1
9050	6,91E-05	4,16E+00	4,15E-05	0,0824	-4,0991394	-0,3377876	685,2	PSTPIP2	proline-serine-threonine phosphatase interacting protein 2
101929540	2,61E-01	5,83E-01	2,25E-01	0,2784	-1,2141466	-0,33800305	42,12	LOC101929	uncharacterized LOC101929540
25839	3,90E-10	9,41E+00	1,79E-10	0,053	-6,3784443	-0,33825007	2115,79	COG4	component of oligomeric golgi complex 4
3703	6,30E-21	2,02E+01	2,04E-21	0,0356	-9,5028954	-0,3384407	18571,85	STT3A	STT3 oligosaccharyltransferase complex catalytic subunit A
767811	3,80E-01	4,20E-01	3,39E-01	0,3546	-0,9553638	-0,33876966	23,94	H2BW4P	H2B.W histone 4, pseudogene
23597	5,02E-15	1,43E+01	1,95E-15	0,0426	-7,9447266	-0,3387736	4433,01	ACOT9	acyl-CoA thioesterase 9
64963	3,17E-09	8,50E+00	1,51E-09	0,0561	-6,0428167	-0,33878555	1643,4	MRPS11	mitochondrial ribosomal protein S11
107986998	5,90E-01	2,29E-01	5,51E-01	0,5682	-0,5966938	-0,33905283	9,12	LOC107986	998
5591	2,55E-19	1,86E+01	8,65E-20	0,0373	-9,1046652	-0,33917167	18011,35	PRKDC	protein kinase, DNA-activated, catalytic subunit
5990	2,10E-02	1,68E+00	1,55E-02	0,1402	-2,4200945	-0,33930001	172,9	RFX2	regulatory factor X2
79913	7,59E-06	5,12E+00	4,30E-06	0,0738	-4,5965209	-0,33933885	695,07	ACTR5	actin related protein 5
3032	1,63E-14	1,38E+01	6,44E-15	0,0435	-7,7951119	-0,33947353	5505,06	HADHB	hydroxyacyl-CoA dehydrogenase trifunctional multienzyme complex subunit beta
124935	1,97E-02	1,71E+00	1,45E-02	0,1389	-2,444333	-0,33948435	185,37	SLC43A2	solute carrier family 43 member 2
10553	1,24E-08	7,91E+00	6,07E-09	0,0584	-5,8147519	-0,33953995	1871,39	HTATIP2	HIV-1 Tat interactive protein 2
81894	1,16E-06	5,94E+00	6,25E-07	0,0682	-4,9833156	-0,3396911	978,86	SLC25A28	solute carrier family 25 member 28
105374880	4,26E-01	3,71E-01	3,84E-01	0,3905	-0,8701335	-0,33981163	19,78	FOXF2-DT	FOXF2 divergent transcript
405	4,55E-11	1,03E+01	2,02E-11	0,0507	-6,7048139	-0,33990351	2392,34	ARNT	aryl hydrocarbon receptor nuclear translocator
91056	3,68E-08	7,43E+00	1,84E-08	0,0605	-5,6262596	-0,34037087	1168,41	AP5B1	adaptor related protein complex 5 subunit beta 1
79906	3,31E-02	1,48E+00	2,51E-02	0,152	-2,240164	-0,34046754	164,77	MORN1	MORN repeat containing 1
4942	5,52E-17	1,63E+01	2,01E-17	0,0401	-8,493141	-0,34072609	6469,48	OAT	ornithine aminotransferase
51650	1,47E-08	7,83E+00	7,23E-09	0,0589	-5,7856007	-0,34103359	1278,18	MRPS33	mitochondrial ribosomal protein S33
29956	3,19E-20	1,95E+01	1,05E-20	0,0366	-9,3305176	-0,34116801	12809,51	CERS2	ceramide synthase 2
55861	8,37E-11	1,01E+01	3,74E-11	0,0516	-6,6140473	-0,34158312	2334,37	DBNDD2	dysbindin domain containing 2
143282	1,40E-02	1,85E+00	1,02E-02	0,1329	-2,5701089	-0,34160484	178,73	FGFBP3	fibroblast growth factor binding protein 3
7007	3,69E-01	4,33E-01	3,28E-01	0,3497	-0,9774109	-0,34182162	24,71	TECTA	tectorin alpha
43	5,34E-01	2,72E-01	4,93E-01	0,4986	-0,6857394	-0,34192815	12,17	ACHE	acetylcholinesterase (Cartwright blood group)
116987	2,03E-10	9,69E+00	9,21E-11	0,0528	-6,4793874	-0,3420311	1918,53	AGAP1	ArfGAP with GTPase domain, ankyrin repeat and PH domain 1
127703	5,16E-06	5,29E+00	2,89E-06	0,0731	-4,6784779	-0,34211482	803,66	C1orf216	chromosome 1 open reading frame 216
23598	3,04E-08	7,52E+00	1,51E-08	0,0605	-5,6600235	-0,34230236	1390,33	PATZ1	POZ/BTB and AT hook containing zinc finger 1
54471	1,54E-10	9,81E+00	6,97E-11	0,0525	-6,5213439	-0,34260127	1912,65	MIEF1	mitochondrial elongation factor 1
8678	5,16E-14	1,33E+01	2,06E-14	0,0448	-7,6466712	-0,34283801	3748,02	BECN1	beclin 1
105379695	1,36E-09	8,87E+00	6,42E-10	0,0555	-6,1797393	-0,34292373	3390,49	IER3-AS1	IER3 antisense RNA 1
54805	4,03E-10	9,39E+00	1,85E-10	0,0538	-6,3730445	-0,34301959	1804,38	CNNM2	cyclin and CBS domain divalent metal cation transport mediator 2
6590	1,49E-01	8,27E-01	1,23E-01	0,2225	-1,5418887	-0,34312882	65,53	SLPI	secretory leukocyte peptidase inhibitor
10471	8,75E-10	9,06E+00	4,08E-10	0,0549	-6,2510482	-0,34314883	4776,9	PFDN6	prefoldin subunit 6
55298	6,21E-07	6,21E+00	3,31E-07	0,0672	-5,1048325	-0,34323893	941,79	RNF121	ring finger protein 121
55116	7,76E-08	7,11E+00	3,94E-08	0,0625	-5,4933101	-0,34338348	1491,5	TMEM39B	transmembrane protein 39B
51133	2,03E-12	1,17E+01	8,58E-13	0,048	-7,151515	-0,34348343	4638,33	KCTD3	potassium channel tetramerization domain containing 3
79971	4,09E-16	1,54E+01	1,53E-16	0,0416	-8,2542115	-0,34350872	4738,8	WLS	Wnt ligand secretion mediator
80086	3,17E-01	4,99E-01	2,78E-01	0,3167	-1,0851126	-0,34369144	29,43	TUBA4B	tubulin alpha 4b
26133	1,91E-15	1,47E+01	7,29E-16	0,0426	-8,0655322	-0,34387446	6956,73	TRPC4AP	transient receptor potential cation channel subfamily C member 4 associated protein
55529	3,60E-04	3,44E+00	2,28E-04	0,0933	-3,6859164	-0,34398388	384,69	PIP4P2	phosphatidylinositol-4,5-bisphosphate 4-phosphatase 2
5550	7,20E-13	1,21E+01	2,99E-13	0,0472	-7,2948255	-0,34426657	3037,99	PREP	prolyl endopeptidase
7579	3,83E-03	2,42E+00	2,64E-03	0,1146	-3,0067912	-0,34457653	242,69	ZSCAN20	zinc finger and SCAN domain containing 20
102724808	5,57E-01	2,54E-01	5,17E-01	0,5315	-0,6484356	-0,34463678	10,64	LOC102724	uncharacterized LOC102724808
57613	1,46E-03	2,84E+00	9,69E-04	0,1045	-3,299431	-0,34468493	329,59	FAM234B	family with sequence similarity 234 member B
1198	5,42E-09	8,27E+00	2,61E-09	0,0579	-5,9544234	-0,3446945	1921,16	CLK3	CDC like kinase 3
441212	2,46E-03	2,61E+00	1,67E-03	0,1096	-3,1438958	-0,34469543	331,54	RP9P	RP9 pseudogene
6152	7,78E-20	1,91E+01	2,60E-20	0,0373	-9,2344649	-0,34478688	23909,38	RPL24	ribosomal protein L24
4666	6,61E-19	1,82E+01	2,27E-19	0,0383	-8,9994746	-0,34490195	23899,26	NACA	nascent polypeptide associated complex subunit alpha
106478956	3,21E-04	3,49E+00	2,03E-04	0,0929	-3,7153471	-0,34500233	425,03	MDC1-AS1	MDC1 antisense RNA 1
105369201	1,11E-02	1,95E+00	7,98E-03	0,1301	-2,6528816	-0,34502945	223,2	GCAWKR	gastric cancer associated WDR5 and KAT2A binding lncRNA
6688	5,48E-01	2,61E-01	5,07E-01	0,5198	-0,6638061	-0,34503713	11,35	SPI1	Spi-1 proto-oncogene
1839	5,37E-17	1,63E+01	1,96E-17	0,0406	-8,4964134	-0,34518382	5105,39	HBEGF	heparin binding EGF like growth factor
321	2,46E-06	5,61E+00	1,35E-06	0,0715	-4,8318243	-0,34544643	944,18	APBA2	amyloid beta precursor protein binding family A member 2
23567	7,81E-07	6,11E+00	4,18E-07	0,0683	-5,0606747	-0,34548727	1016,05	ZNF346	zinc finger protein 346
51693	1,29E-07	6,89E+00	6,64E-08	0,064	-5,4007048	-0,34553816	1231,28	TRAPPC2L	trafficking protein particle complex subunit 2L
105369352	1,10E-05	4,96E+00	6,29E-06	0,0765	-4,5163905	-0,34562731	873,65	KLC2-AS1	KLC2 antisense RNA 1
79831	8,20E-03	2,09E+00	5,83E-03	0,1254	-2,7570021	-0,34573581	202,2	KDM8	lysine demethylase 8
692099	2,35E-05	4,63E+00	1,37E-05	0,0795	-4,3489113	-0,34579928	655,93	FAM86DP	family with sequence similarity 86 member D, pseudogene
55650	1,85E-06	5,73E+00	1,01E-06	0,0707	-4,8896556	-0,34581579	837,86	PIGV	phosphatidylinositol glycan anchor biosynthesis class V
57530	9,00E-03	2,05E+00	6,43E-03	0,1269	-2,7249756	-0,34583391	201,15	CGN	cingulin
2000	5,22E-12	1,13E+01	2,23E-12	0,0493	-7,0190634	-0,34603236	2681,72	ELF4	E74 like ETS transcription factor 4
55178	8,40E-09	8,08E+00	4,08E-09	0,0589	-5,8809222	-0,34615845	1344,61	MRM3	mitochondrial rRNA methyltransferase 3
7178	2,34E-22	2,16E+01	7,27E-23	0,0352	-9,8440742	-0,34629304	52767,41	TPT1	tumor protein, translationally-controlled 1
55716	2,40E-03	2,62E+00	1,62E-03	0,1099	-3,1517531	-0,34629734	293,4	LMBR1L	limb development membrane protein 1 like
9588	2,79E-20	1,96E+01	9,18E-21	0,0371	-9,345048	-0,34655555	10520,36	PRDX6	peroxiredoxin 6
51564	8,93E-11	1,00E+01	3,99E-11	0,0525	-6,6043486	-0,34656962	2429,97	HDAC7	histone deacetylase 7
9901	1,94E-02	1,71E+00	1,43E-02	0,1415	-2,4506495	-0,34688033	155,68	SRGAP3	SLIT-ROBO Rho GTPase activating protein 3
112268052	7,25E-03	2,14E+00	5,13E-03	0,124	-2,7985562	-0,34688743	213,65	LOC112268	052
6452	1,88E-10	9,73E+00	8,53E-11	0,0535	-6,4909508	-0,3469851	2070,6	SH3BP2	SH3 domain binding protein 2
10724	1,18E-15	1,49E+01	4,48E-16	0,0427	-8,124747	-0,34700775	6657,35	OGA	O-GlcNAcase
23199	4,50E-09	8,35E+00	2,16E-09	0,058	-5,9852979	-0,34715151	1360,74	GSE1	Gse1 coiled-coil protein
1268	5,89E-01	2,30E-01	5,49E-01	0,5799	-0,5988304	-0,34726627	8,88	CNR1	cannabinoid receptor 1
1352	1,87E-08	7,73E+00	9,24E-09	0,0605	-5,7441016	-0,34730474	1158,53	COX10	cytochrome c oxidase assembly factor heme A:farnesyltransferase COX10
51005	1,09E-03	2,96E+00	7,15E-04	0,1028	-3,3836431	-0,34774603	315,89	AMDHD2	amidohydrolase domain containing 2
552889	2,46E-13	1,26E+01	1,00E-13	0,0467	-7,4405177	-0,34777314	2767,03	ATXN7L3B	ataxin 7 like 3B
643853	2,64E-04	3,58E+00	1,65E-04	0,0923	-3,7669139	-0,34780731	413,98	TMPPE	transmembrane protein with metallophosphoesterase domain
56981	1,11E-03	2,95E+00	7,31E-04	0,103	-3,3777313	-0,34804802	304,97	PRDM11	PR/SET domain 11
8216	4,47E-09	8,35E+00	2,15E-09	0,0581	-5,9863175	-0,348077	1604,55	LZTR1	leucine zipper like transcription regulator 1
8655	5,15E-15	1,43E+01	2,00E-15	0,0438	-7,9415856	-0,34815315	12063,92	DYNLL1	dynein light chain LC8-type 1
100128385	5,41E-08	7,27E+00	2,73E-08	0,0627	-5,5580858	-0,34850678	1029,54	FAM225B	family with sequence similarity 225 member B
55841	5,76E-15	1,42E+01	2,24E-15	0,044	-7,9274132	-0,34861984	3701,96	WWC3	WWC family member 3
57643	3,70E-02	1,43E+00	2,82E-02	0,1589	-2,1938121	-0,34868621	130,86	ZSWIM5	zinc finger SWIM-type containing 5
90378	7,90E-12	1,11E+01	3,39E-12	0,0501	-6,9603984	-0,34869448	2767,51	SAMD1	sterile alpha motif domain containing 1
987	1,68E-15	1,48E+01	6,39E-16	0,0431	-8,081571	-0,34870772	3895,25	LRBA	LPS responsive beige-like anchor protein
26168	1,74E-12	1,18E+01	7,31E-13	0,0486	-7,1734185	-0,34885005	2930,96	SENP3	SUMO specific peptidase 3
9469	2,25E-12	1,16E+01	9,50E-13	0,0489	-7,1375274	-0,34904864	2883,29	CHST3	carbohydrate sulfotransferase 3
11046	4,92E-04	3,31E+00	3,15E-04	0,0969	-3,6025402	-0,34916284	685,9	SLC35D2	solute carrier family 35 member D2
285033	2,90E-03	2,54E+00	1,98E-03	0,1129	-3,0939057	-0,34928244	261,15	STARD7-AS	STARD7 antisense RNA 1
64170	4,26E-01	3,71E-01	3,85E-01	0,4019	-0,8691598	-0,34929315	18,08	CARD9	caspase recruitment domain family member 9
100129195	4,81E-03	2,32E+00	3,34E-03	0,1191	-2,934173	-0,34942482	248,19	ZSCAN16-A	ZSCAN16 antisense RNA 1
102466720	5,37E-01	2,70E-01	4,96E-01	0,513	-0,6811612	-0,3494459	11,1	MIR6720	microRNA 6720
101929937	3,59E-03	2,44E+00	2,47E-03	0,1155	-3,0272368	-0,34963966	248,86	LOC101929	serine/arginine repetitive matrix protein 2-like
1794	2,87E-07	6,54E+00	1,50E-07	0,0666	-5,2524959	-0,34972388	1123,55	DOCK2	dedicator of cytokinesis 2
79902	1,46E-14	1,38E+01	5,75E-15	0,0448	-7,8093775	-0,34985832	4486,91	NUP85	nucleoporin 85
284233	5,28E-01	2,77E-01	4,87E-01	0,5037	-0,6948662	-0,35003746	12,26	CYP4F35P	cytochrome P450 family 4 subfamily F member 35, pseudogene
101154753	4,46E-01	3,51E-01	4,04E-01	0,4198	-0,8340725	-0,35016511	16,56	PANDAR	promoter of CDKN1A antisense DNA damage activated RNA
107984398	4,39E-01	3,58E-01	3,98E-01	0,4145	-0,8459835	-0,3506742	19,72	LOC107984	uncharacterized LOC107984398
105373939	4,95E-01	3,05E-01	4,53E-01	0,4672	-0,7507101	-0,35073857	13,19	LOC105373	uncharacterized LOC105373939
27077	3,55E-06	5,45E+00	1,97E-06	0,0737	-4,7562641	-0,35076737	755,4	B9D1	B9 domain containing 1
60490	6,38E-05	4,20E+00	3,82E-05	0,0852	-4,118371	-0,35087688	544,57	PPCDC	phosphopantothenoylcysteine decarboxylase
202052	1,04E-06	5,98E+00	5,60E-07	0,0701	-5,0044985	-0,35089461	888,18	DNAJC18	DnaJ heat shock protein family (Hsp40) member C18
51573	6,04E-15	1,42E+01	2,35E-15	0,0443	-7,9215296	-0,35123399	3739,05	GDE1	glycerophosphodiester phosphodiesterase 1
4601	2,13E-07	6,67E+00	1,11E-07	0,0662	-5,3079626	-0,3515077	1143,01	MXI1	MAX interactor 1, dimerization protein
7988	6,57E-06	5,18E+00	3,71E-06	0,076	-4,6272424	-0,35158492	698,87	ZNF212	zinc finger protein 212
10544	2,52E-09	8,60E+00	1,20E-09	0,0578	-6,080186	-0,35171278	1506,72	PROCR	protein C receptor
7186	1,88E-09	8,73E+00	8,92E-10	0,0574	-6,1276829	-0,35171902	1574,87	TRAF2	TNF receptor associated factor 2
51728	2,59E-06	5,59E+00	1,43E-06	0,073	-4,8213092	-0,35189849	770,46	POLR3K	RNA polymerase III subunit K
6777	1,32E-12	1,19E+01	5,53E-13	0,0488	-7,2116131	-0,35191561	2256,07	STAT5B	signal transducer and activator of transcription 5B
4693	1,02E-01	9,91E-01	8,26E-02	0,203	-1,7356266	-0,35227803	74,43	NDP	norrin cystine knot growth factor NDP
100507459	4,68E-02	1,33E+00	3,61E-02	0,1682	-2,0954632	-0,35247573	114,59	NRSN2-AS1	NRSN2 antisense RNA 1

8428	1,66E-16	1,58E+01	6,11E-17	0,0422	-8,3630273	-0,35256541	4780,05	STK24	serine/threonine kinase 24
149840	7,38E-02	1,13E+00	5,84E-02	0,1864	-1,892554	-0,35270869	96,27	SHLD1	shieldin complex subunit 1
5467	3,06E-13	1,25E+01	1,25E-13	0,0476	-7,4111757	-0,35292247	3314,88	PPARD	peroxisome proliferator activated receptor delta
85462	1,01E-02	2,00E+00	7,26E-03	0,1315	-2,6847248	-0,35299506	205,2	FHDC1	FH2 domain containing 1
51125	2,75E-09	8,56E+00	1,31E-09	0,0582	-6,066186	-0,35299792	1424,59	GOLGA7	golgin A7
100129503	1,11E-01	9,55E-01	8,98E-02	0,2083	-1,6966272	-0,35332809	76,3	LOC100129503	
55154	4,43E-10	9,35E+00	2,04E-10	0,0556	-6,3583668	-0,35333963	1616,22	MSTO1	misato mitochondrial distribution and morphology regulator 1
8019	4,21E-10	9,38E+00	1,93E-10	0,0555	-6,3664869	-0,35345192	1528,43	BRD3	bromodomain containing 3
3094	1,84E-13	1,27E+01	7,47E-14	0,0473	-7,4793462	-0,35357472	12613,8	HINT1	histidine triad nucleotide binding protein 1
3913	2,15E-11	1,07E+01	9,42E-12	0,0519	-6,8151696	-0,35382921	14398,5	LAMB2	laminin subunit beta 2
56672	2,23E-08	7,65E+00	1,10E-08	0,0619	-5,7140926	-0,35383654	1174,69	AKIP1	A-kinase interacting protein 1
115290	4,38E-04	3,36E+00	2,79E-04	0,0974	-3,6339738	-0,35386664	415,36	FBXO17	F-box protein 17
101929298	5,27E-01	2,78E-01	4,86E-01	0,508	-0,6967251	-0,35391054	11,41	LOC101929298	uncharacterized LOC101929298
105369194	3,04E-01	5,17E-01	2,66E-01	0,3182	-1,1124709	-0,35399701	30,61	LOC105369194	uncharacterized LOC105369194
255057	6,37E-02	1,20E+00	5,00E-02	0,1807	-1,9595808	-0,35410297	99,1	CBARP	CACN subunit beta associated regulatory protein
92856	2,75E-10	9,56E+00	1,26E-10	0,055	-6,4324847	-0,35410601	2377,18	IMP4	IMP U3 small nucleolar ribonucleoprotein 4
7414	1,67E-21	2,08E+01	5,31E-22	0,0367	-9,6420809	-0,35418419	16099,01	VCL	vinculin
102724479	3,57E-01	4,47E-01	3,16E-01	0,3534	-1,0024454	-0,35426273	25,42	LOC102724479	uncharacterized LOC102724479
55374	5,62E-08	7,25E+00	2,84E-08	0,0639	-5,5512301	-0,35462006	1393,13	TMCO6	transmembrane and coiled-coil domains 6
285	4,34E-01	3,63E-01	3,92E-01	0,4144	-0,8558942	-0,35471905	16,81	ANGPT2	angiopoietin 2
56252	5,15E-11	1,03E+01	2,28E-11	0,0531	-6,6866784	-0,35485784	7191,99	YLPM1	YLP motif containing 1
58528	1,22E-06	5,91E+00	6,59E-07	0,0714	-4,9729904	-0,35490239	775,33	RRAGD	Ras related GTP binding D
6911	2,75E-01	5,61E-01	2,38E-01	0,3012	-1,179182	-0,35518175	35,84	TBX6	T-box transcription factor 6
146857	6,40E-06	5,19E+00	3,61E-06	0,0767	-4,6327773	-0,35519863	645,36	SLFN13	schlafen family member 13
23001	1,96E-12	1,17E+01	8,29E-13	0,0496	-7,1563054	-0,35529045	3002,78	WDFY3	WD repeat and FYVE domain containing 3
11100	6,03E-22	2,12E+01	1,89E-22	0,0365	-9,7472749	-0,35530081	23038,95	HNRNPUL1	heterogeneous nuclear ribonucleoprotein U like 1
6167	2,49E-17	1,66E+01	8,96E-18	0,0414	-8,5866219	-0,35530457	26008,46	RPL37	ribosomal protein L37
23339	2,50E-09	8,60E+00	1,19E-09	0,0584	-6,0818404	-0,35546143	1713,81	VPS39	VPS39 subunit of HOPS complex
26097	1,60E-12	1,18E+01	6,74E-13	0,0495	-7,1846353	-0,35550739	3996,74	CHTOP	chromatin target of PRMT1
51098	2,38E-11	1,06E+01	1,05E-11	0,0523	-6,8000553	-0,35552473	1920,17	IFT52	intraflagellar transport 52
140461	8,66E-07	6,06E+00	4,65E-07	0,0706	-5,040314	-0,35560421	922,68	ASB8	ankyrin repeat and SOCS box containing 8
79086	3,02E-16	1,55E+01	1,12E-16	0,0429	-8,2908335	-0,35580005	6851,63	SMIM7	small integral membrane protein 7
677	1,49E-14	1,38E+01	5,88E-15	0,0456	-7,8064883	-0,35597464	8792,57	ZFP36L1	ZFP36 ring finger protein like 1
9256	7,92E-03	2,10E+00	5,62E-03	0,1286	-2,7691271	-0,35613251	189,17	TSPOAP1	TSPO associated protein 1
100289678	1,35E-05	4,87E+00	7,75E-06	0,0797	-4,4718752	-0,35621623	561,91	ZNF783	zinc finger protein 783
1400	2,58E-03	2,59E+00	1,75E-03	0,1139	-3,1295669	-0,35636668	247,75	CRMP1	collapsin response mediator protein 1
140462	1,51E-03	2,82E+00	1,01E-03	0,1084	-3,2888095	-0,3564728	362,95	ASB9	ankyrin repeat and SOCS box containing 9
100506321	1,50E-04	3,82E+00	9,22E-05	0,0912	-3,9103391	-0,35648304	531,78	LOC100506321	uncharacterized LOC100506321
9790	2,17E-14	1,37E+01	8,57E-15	0,046	-7,7588269	-0,35654802	9788,36	BMS1	BMS1 ribosome biogenesis factor
54859	6,34E-11	1,02E+01	2,82E-11	0,0536	-6,6556742	-0,35673566	2141,66	ELP6	elongator acetyltransferase complex subunit 6
2036	2,91E-08	7,54E+00	1,45E-08	0,063	-5,6677607	-0,35685738	1025,2	EPB41L1	erythrocyte membrane protein band 4.1 like 1
84759	4,03E-07	6,39E+00	2,13E-07	0,0688	-5,1877204	-0,35707412	851,51	PCGF1	polycomb group ring finger 1
94059	7,24E-03	2,14E+00	5,12E-03	0,1276	-2,7993687	-0,35708968	208,36	LENG9	leukocyte receptor cluster member 9
7162	8,45E-12	1,11E+01	3,63E-12	0,0514	-6,9507087	-0,35717285	2777,22	TPBG	trophoblast glycoprotein
101060226	2,16E-10	9,67E+00	9,84E-11	0,0552	-6,469434	-0,3573826	2273,99	NBPF19	NBPF member 19
26175	1,86E-06	5,73E+00	1,02E-06	0,0731	-4,8884495	-0,35745712	705,04	LYSET	lysosomal enzyme trafficking factor
1643	8,69E-10	9,06E+00	4,05E-10	0,0572	-6,2520857	-0,35748577	1431,16	DDB2	damage specific DNA binding protein 2
205	3,07E-15	1,45E+01	1,18E-15	0,0447	-8,006458	-0,35757172	3818,65	AK4	adenylate kinase 4
55192	9,84E-05	4,01E+00	5,97E-05	0,0891	-4,0140456	-0,35767644	485,92	DNAJC17	DnaJ heat shock protein family (Hsp40) member C17
1798	1,32E-13	1,29E+01	5,34E-14	0,0476	-7,5233835	-0,35773737	3622,24	DPAGT1	dolichyl-phosphate N-acetylglucosaminephosphotransferase 1
333929	5,51E-01	2,59E-01	5,10E-01	0,5433	-0,6585203	-0,35776254	9,83	SNAI3	snail family transcriptional repressor 3
25992	1,59E-02	1,80E+00	1,16E-02	0,1417	-2,5242775	-0,35779498	151,28	SNED1	sushi, nidogen and EGF like domains 1
10921	1,06E-14	1,40E+01	4,14E-15	0,0456	-7,8506898	-0,3578017	6562,7	RNPS1	RNA binding protein with serine rich domain 1
51218	3,24E-06	5,49E+00	1,79E-06	0,0749	-4,775709	-0,35791744	1535,76	GLRX5	glutaredoxin 5
115201	9,52E-07	6,02E+00	5,13E-07	0,0713	-5,0215423	-0,35804446	850,08	ATG4A	autophagy related 4A cysteine peptidase
2585	2,82E-05	4,55E+00	1,65E-05	0,0832	-4,3074539	-0,35832846	512,6	GALK2	galactokinase 2
80725	4,26E-01	3,71E-01	3,85E-01	0,4125	-0,8688138	-0,35839805	22,71	SRCIN1	SRC kinase signaling inhibitor 1
79019	6,53E-04	3,19E+00	4,22E-04	0,1017	-3,5257827	-0,35871653	639,63	CENPM	centromere protein M
860	5,53E-11	1,03E+01	2,45E-11	0,0538	-6,6761223	-0,35887173	1786,53	RUNX2	RUNX family transcription factor 2
10717	2,25E-07	6,65E+00	1,17E-07	0,0678	-5,2983439	-0,35903975	907,95	AP4B1	adaptor related protein complex 4 subunit beta 1
80207	6,38E-13	1,22E+01	2,65E-13	0,0491	-7,3112954	-0,35916351	2585,17	OPA3	outer mitochondrial membrane lipid metabolism regulator OPA3
6641	1,38E-08	7,86E+00	6,76E-09	0,062	-5,7966949	-0,35938516	1174,32	SNTB1	syntrophin beta 1
542767	1,81E-01	7,42E-01	1,52E-01	0,2509	-1,4341136	-0,35979451	47,2	PCOTH	prostate and testis expressed opposite C1QTNF9B and MIPEP
105371942	7,09E-03	2,15E+00	5,01E-03	0,1282	-2,80627	-0,35982039	202,91	LOC105371942	uncharacterized LOC105371942
3680	5,58E-01	2,53E-01	5,17E-01	0,5556	-0,6479596	-0,36000551	9,51	ITGA9	integrin subunit alpha 9
25941	4,92E-16	1,53E+01	1,84E-16	0,0437	-8,231828	-0,36003815	5131	TPGS2	tubulin polyglutamylase complex subunit 2
5496	7,25E-20	1,91E+01	2,42E-20	0,039	-9,24207	-0,36043445	17120,69	PPM1G	protein phosphatase, Mg2+/Mn2+ dependent 1G
79703	2,30E-06	5,64E+00	1,26E-06	0,0744	-4,8451838	-0,3606355	690,13	C11orf80	chromosome 11 open reading frame 80
56259	1,57E-12	1,18E+01	6,59E-13	0,0502	-7,1877066	-0,3608234	3823,25	CTNNBL1	catenin beta like 1
57325	2,14E-10	9,67E+00	9,72E-11	0,0558	-6,4712963	-0,36107135	1612,87	KAT14	lysine acetyltransferase 14
387787	5,19E-02	1,28E+00	4,03E-02	0,1762	-2,0504204	-0,3612226	105,79	LIPT2	lipoyl(octanoyl) transferase 2
595	7,38E-24	2,31E+01	2,21E-24	0,0355	-10,189622	-0,36137175	24963,16	CCND1	cyclin D1
1979	2,43E-17	1,66E+01	8,75E-18	0,0421	-8,5893052	-0,3614476	5763,5	EIF4EBP2	eukaryotic translation initiation factor 4E binding protein 2
101927755	3,85E-02	1,41E+00	2,94E-02	0,166	-2,1779479	-0,36150317	116,76	RNFT1-DT	RNFT1 divergent transcript
9725	3,95E-10	9,40E+00	1,81E-10	0,0567	-6,3765938	-0,36169403	2227,45	TMEM63A	transmembrane protein 63A
9704	4,97E-08	7,30E+00	2,50E-08	0,0649	-5,5732624	-0,36175559	1644,34	DHX34	DExH-box helicase 34
8985	2,23E-10	9,65E+00	1,01E-10	0,056	-6,464769	-0,36176567	3961,05	PLOD3	procollagen-lysine,2-oxoglutarate 5-dioxygenase 3
3460	5,21E-13	1,23E+01	2,16E-13	0,0493	-7,3387851	-0,36188744	2149,77	IFNGR2	interferon gamma receptor 2
51531	8,80E-08	7,06E+00	4,49E-08	0,0662	-5,4704843	-0,36196398	904,64	TRMO	tRNA methyltransferase O
3337	2,86E-20	1,95E+01	9,45E-21	0,0388	-9,342081	-0,36241806	13600,07	DNAJB1	DnaJ heat shock protein family (Hsp40) member B1
27301	2,89E-11	1,05E+01	1,27E-11	0,0535	-6,7721831	-0,36249616	2518,31	APEX2	apurinic/apyrimidinic endodeoxyribonuclease 2
55323	1,12E-08	7,95E+00	5,47E-09	0,0622	-5,832236	-0,36250473	1197,34	LARP6	La ribonucleoprotein 6, translational regulator
3547	6,08E-02	1,22E+00	4,77E-02	0,1832	-1,9800024	-0,36280467	92,91	IGSF1	immunoglobulin superfamily member 1
6154	4,58E-15	1,43E+01	1,77E-15	0,0456	-7,9561801	-0,36282658	41906,8	RPL26	ribosomal protein L26
8872	2,48E-18	1,76E+01	8,66E-19	0,041	-8,8512325	-0,36287206	7240,4	CDC123	cell division cycle 123
220074	7,53E-10	9,12E+00	3,50E-10	0,0578	-6,2749644	-0,36291938	1473,17	LRTOMT	leucine rich transmembrane and O-methyltransferase domain containing
255031	2,21E-01	6,56E-01	1,88E-01	0,2756	-1,3172105	-0,36302611	39,66	LINC00957	long intergenic non-protein coding RNA 957
412	6,56E-09	8,18E+00	3,17E-09	0,0614	-5,9224695	-0,36347175	1394,79	STS	steroid sulfatase
2067	1,07E-14	1,40E+01	4,18E-15	0,0463	-7,8494543	-0,36376425	3730,35	ERCC1	ERCC excision repair 1, endonuclease non-catalytic subunit
22983	2,42E-03	2,62E+00	1,64E-03	0,1156	-3,1486529	-0,36393369	268,75	MAST1	microtubule associated serine/threonine kinase 1
644596	5,21E-01	2,83E-01	4,79E-01	0,5147	-0,7071873	-0,3639636	12,78	SMIM10L2B	small integral membrane protein 10 like 2B
112858	7,66E-09	8,12E+00	3,71E-09	0,0618	-5,8965657	-0,3644383	1423,85	TP53RK	TP53 regulating kinase
11176	4,38E-18	1,74E+01	1,54E-18	0,0415	-8,7867549	-0,36447177	5606,65	BAZ2A	bromodomain adjacent to zinc finger domain 2A
1848	3,77E-19	1,84E+01	1,28E-19	0,0402	-9,0617348	-0,36456171	11827,09	DUSP6	dual specificity phosphatase 6
9878	1,32E-14	1,39E+01	5,19E-15	0,0466	-7,8221793	-0,36480284	4552,96	TOX4	TOX high mobility group box family member 4
3753	4,39E-01	3,58E-01	3,98E-01	0,4315	-0,8455259	-0,36484236	15,73	KCNE1	potassium voltage-gated channel subfamily E regulatory subunit 1
57727	1,91E-15	1,47E+01	7,30E-16	0,0452	-8,0654388	-0,36492414	3208,68	NCOA5	nuclear receptor coactivator 5
57553	5,02E-11	1,03E+01	2,23E-11	0,0545	-6,6903577	-0,36494587	1698,19	MICAL3	microtubule associated monooxygenase, calponin and LIM domain containing 3
54442	1,38E-14	1,39E+01	5,42E-15	0,0467	-7,8168199	-0,36494767	3277,28	KCTD5	potassium channel tetramerization domain containing 5
51260	2,60E-09	8,59E+00	1,24E-09	0,0601	-6,0752757	-0,36497976	3822,19	PBDC1	polysaccharide biosynthesis domain containing 1
79177	5,20E-05	4,28E+00	3,09E-05	0,0876	-4,1666171	-0,36500552	450,47	ZNF576	zinc finger protein 576
107987072	1,30E-03	2,89E+00	8,58E-04	0,1095	-3,3332581	-0,36506464	305	LOC107987072	
26504	2,53E-08	7,60E+00	1,26E-08	0,0642	-5,6917225	-0,36537057	1080,57	CNNM4	cyclin and CBS domain divalent metal cation transport mediator 4
5745	4,19E-01	3,78E-01	3,77E-01	0,414	-0,8827063	-0,36545029	18,4	PTH1R	parathyroid hormone 1 receptor
728658	3,40E-02	1,47E+00	2,58E-02	0,1639	-2,2296293	-0,36549266	3292,84	RPL13AP5	ribosomal protein L13a pseudogene 5
22806	3,04E-01	5,17E-01	2,66E-01	0,3285	-1,1130864	-0,36561338	28,37	IKZF3	IKAROS family zinc finger 3
64802	5,02E-07	6,30E+00	2,66E-07	0,0711	-5,1459459	-0,36569966	949,2	NMNAT1	nicotinamide nucleotide adenylyltransferase 1
128	1,42E-14	1,38E+01	5,60E-15	0,0468	-7,8127206	-0,36576752	5107,46	ADH5	alcohol dehydrogenase 5 (class III), chi polypeptide
4712	2,82E-08	7,55E+00	1,40E-08	0,0645	-5,672798	-0,36582802	2070,93	NDUFB6	NADH:ubiquinone oxidoreductase subunit B6
151056	9,39E-07	6,03E+00	5,05E-07	0,0728	-5,0244143	-0,36592197	763,48	PLB1	phospholipase B1
81888	6,76E-10	9,17E+00	3,14E-10	0,0582	-6,2918597	-0,36596841	1376,15	HYI	hydroxypyruvate isomerase (putative)
9410	8,64E-12	1,11E+01	3,72E-12	0,0527	-6,947578	-0,36599554	3535,15	SNRNP40	small nuclear ribonucleoprotein U5 subunit 40
4355	3,68E-03	2,43E+00	2,53E-03	0,1212	-3,0192935	-0,36600824	246,55	MPP2	MAGUK p55 scaffold protein 2
9806	2,41E-01	6,18E-01	2,07E-01	0,2899	-1,2626654	-0,36601685	43,71	SPOCK2	SPARC (osteonectin), cwcv and kazal like domains proteoglycan 2
375260	1,23E-03	2,91E+00	8,14E-04	0,1093	-3,3481446	-0,3660581	290,26	WASH2P	WASP family homolog 2, pseudogene
23261	1,22E-08	7,91E+00	5,97E-09	0,063	-5,817525	-0,36625792	1101,81	CAMTA1	calmodulin binding transcription activator 1
124512	5,58E-08	7,25E+00	2,81E-08	0,066	-5,552611	-0,36636235	1299	METTL23	methyltransferase like 23
57462	3,08E-05	4,51E+00	1,81E-05	0,0855	-4,2869854	-0,36649109	485,46	MYORG	myogenesis regulating glycosidase (putative)
84957	7,47E-06	5,13E+00	4,23E-06	0,0797	-4,5999795	-0,36649214	650,21	RELT	RELT TNF receptor
91050	8,83E-06	5,05E+00	5,02E-06	0,0803	-4,5639546	-0,36654764	674,06	CCDC149	coiled-coil domain containing 149

11066	3,37E-10	9,47E+00	1,54E-10	0,0573	-6,4009432	-0,36681287	1894,29	SNRNP35	small nuclear ribonucleoprotein U11/U12 subunit 35
112268190	2,73E-02	1,56E+00	2,04E-02	0,1583	-2,3184181	-0,36691414	128,4	LOC112268190	
105374261	4,30E-01	3,67E-01	3,89E-01	0,4258	-0,8617489	-0,36692085	16,91	LINC02041	long intergenic non-protein coding RNA 2041
100287559	2,48E-01	6,06E-01	2,13E-01	0,2946	-1,2453659	-0,36693702	33,65	ADPGK-AS1	ADPGK antisense RNA 1
439994	1,52E-03	2,82E+00	1,01E-03	0,1117	-3,2879622	-0,36714368	258,38	LINC00863	long intergenic non-protein coding RNA 863
63932	3,98E-10	9,40E+00	1,83E-10	0,0576	-6,3753308	-0,36717067	1626,75	STEEP1	STING1 ER exit protein 1
196951	3,61E-02	1,44E+00	2,75E-02	0,1666	-2,204038	-0,36721456	109,59	FAM227B	family with sequence similarity 227 member B
221496	7,35E-13	1,21E+01	3,05E-13	0,0504	-7,2920819	-0,36725012	3158,49	LEMD2	LEM domain nuclear envelope protein 2
84126	7,06E-06	5,15E+00	3,98E-06	0,0796	-4,6122068	-0,3673505	564,61	ATRIP	ATR interacting protein
8449	1,87E-16	1,57E+01	6,93E-17	0,044	-8,348302	-0,36765574	5759,99	DHX16	DEAH-box helicase 16
107987135	3,15E-11	1,05E+01	1,39E-11	0,0544	-6,7591932	-0,36769836	1601,95	LOC107987135	
10090	1,87E-04	3,73E+00	1,16E-04	0,0954	-3,8541921	-0,36782867	371,71	UST	uronyl 2-sulfotransferase
101929693	2,50E-01	6,02E-01	2,15E-01	0,2964	-1,2411464	-0,36783451	33,26	RARA-AS1	RARA antisense RNA 1
1677	9,75E-05	4,01E+00	5,91E-05	0,0916	-4,0163678	-0,36795719	441,37	DFFB	DNA fragmentation factor subunit beta
145783	1,61E-02	1,79E+00	1,18E-02	0,1461	-2,518123	-0,36801832	142,73	TCF12-DT	TCF12 divergent transcript
4705	7,11E-14	1,31E+01	2,86E-14	0,0484	-7,604678	-0,3681329	2979,64	NDUFA10	NADH:ubiquinone oxidoreductase subunit A10
54496	8,07E-09	8,09E+00	3,92E-09	0,0626	-5,8877112	-0,36828171	1198,02	PRMT7	protein arginine methyltransferase 7
283871	9,56E-06	5,02E+00	5,44E-06	0,0811	-4,5469379	-0,36883443	807,18	PGP	phosphoglycolate phosphatase
8607	5,93E-21	2,02E+01	1,92E-21	0,0388	-9,5092421	-0,36895156	6718,21	RUVBL1	RuvB like AAA ATPase 1
6837	1,00E-11	1,10E+01	4,31E-12	0,0533	-6,9265514	-0,36939729	2613,52	MED22	mediator complex subunit 22
100873919	3,70E-01	4,32E-01	3,30E-01	0,3789	-0,974868	-0,36941608	20,13	NDP-AS1	NDP antisense RNA 1
607	3,41E-07	6,47E+00	1,79E-07	0,0708	-5,2199557	-0,36954641	1187,4	BCL9	BCL9 transcription coactivator
79697	3,92E-08	7,41E+00	1,96E-08	0,0658	-5,6150879	-0,36968224	1241,82	RIOX1	ribosomal oxygenase 1
54938	2,68E-07	6,57E+00	1,40E-07	0,0702	-5,2654904	-0,36985194	1329,42	SARS2	seryl-tRNA synthetase 2, mitochondrial
79710	4,96E-16	1,53E+01	1,86E-16	0,0449	-8,2307629	-0,36994737	5367,16	MORC4	MORC family CW-type zinc finger 4
4706	3,96E-10	9,40E+00	1,82E-10	0,058	-6,3758863	-0,36997612	1903,25	NDUFAB1	NADH:ubiquinone oxidoreductase subunit AB1
6124	3,51E-28	2,75E+01	9,35E-29	0,0333	-11,1262136	-0,37020132	62883,2	RPL4	ribosomal protein L4
84306	1,26E-06	5,90E+00	6,81E-07	0,0745	-4,9665968	-0,37023914	743,52	PDCD2L	programmed cell death 2 like
27037	6,16E-06	5,21E+00	3,47E-06	0,0798	-4,6409752	-0,37027544	1040,47	TRMT2A	tRNA methyltransferase 2 homolog A
25832	2,06E-11	1,07E+01	9,00E-12	0,0543	-6,8216165	-0,37044561	3213,13	NBPF14	NBPF member 14
3222	1,43E-01	8,45E-01	1,18E-01	0,2371	-1,5637755	-0,37084819	52,67	HOXC5	homeobox C5
101927642	4,09E-03	2,39E+00	2,82E-03	0,1242	-2,9863941	-0,3709741	204,75	LINC01444	long intergenic non-protein coding RNA 1444
1917	5,84E-05	4,23E+00	3,49E-05	0,0896	-4,1391337	-0,37101283	653,71	EEF1A2	eukaryotic translation elongation factor 1 alpha 2
11015	8,89E-07	6,05E+00	4,77E-07	0,0737	-5,0351604	-0,37120846	901,1	KDELR3	KDEL endoplasmic reticulum protein retention receptor 3
10641	6,41E-08	7,19E+00	3,24E-08	0,0672	-5,5278755	-0,37127298	1071	NPRL2	NPR2 like, GATOR1 complex subunit
57680	3,50E-14	1,35E+01	1,39E-14	0,0482	-7,697166	-0,37129458	6868,18	CHD8	chromodomain helicase DNA binding protein 8
105377123	3,02E-02	1,52E+00	2,28E-02	0,1631	-2,2771614	-0,37132727	135,32	LOC105377123	uncharacterized LOC105377123
100529145	2,95E-04	3,53E+00	1,86E-04	0,0994	-3,7371495	-0,37136855	398,41	TEN1-CDK3	TEN1-CDK3 readthrough (NMD candidate)
196993	1,70E-01	7,70E-01	1,42E-01	0,2529	-1,468871	-0,37142337	50,76	CT62	cancer/testis associated 62
138311	7,97E-04	3,10E+00	5,19E-04	0,1071	-3,470657	-0,37162717	293,21	DIPK1B	divergent protein kinase domain 1B
3622	5,15E-08	7,29E+00	2,59E-08	0,0668	-5,5668561	-0,37167006	1105,78	ING2	inhibitor of growth family member 2
389741	1,47E-06	5,83E+00	8,02E-07	0,0755	-4,9348839	-0,37239659	747,66	GLIDR	glioblastoma down-regulated RNA
80775	2,83E-04	3,55E+00	1,78E-04	0,0994	-3,7487448	-0,37272229	387,3	TMEM177	transmembrane protein 177
101927423	2,56E-01	5,92E-01	2,21E-01	0,3043	-1,2250843	-0,37282609	33,42	PANO1	proapoptotic nucleolar protein 1
92070	7,61E-05	4,12E+00	4,58E-05	0,0915	-4,0760927	-0,3730416	404,91	CTBP1-DT	CTBP1 divergent transcript
10861	3,64E-02	1,44E+00	2,77E-02	0,1696	-2,2009287	-0,37322385	104,74	SLC26A1	solute carrier family 26 member 1
403323	3,95E-03	2,40E+00	2,72E-03	0,1245	-2,9975518	-0,37330602	198,95	LERFS	lncRNA negative regulator of fibroblast-like synoviocyte migration, SYNCRIP interacting
257364	6,65E-11	1,02E+01	2,96E-11	0,0562	-6,6486349	-0,37336898	1849,57	SNX33	sorting nexin 33
100113386	6,86E-03	2,16E+00	4,84E-03	0,1326	-2,8174492	-0,37373355	189,82	UCKL1-AS1	UCKL1 antisense RNA 1
100188954	1,42E-05	4,85E+00	8,19E-06	0,0838	-4,4601168	-0,37381703	550,92	DNMBP-AS1	DNMBP antisense RNA 1
11159	1,50E-02	1,82E+00	1,09E-02	0,1469	-2,5450822	-0,37384604	142,61	RABL2A	RAB, member of RAS oncogene family like 2A
84334	3,11E-10	9,51E+00	1,42E-10	0,0583	-6,4133718	-0,37392979	1335,44	COA8	cytochrome c oxidase assembly factor 8
100874212	1,27E-02	1,90E+00	9,18E-03	0,1436	-2,6053671	-0,37403279	153,24	MYCBP2-AS1	MYCBP2 antisense RNA 1
102723576	3,56E-01	4,49E-01	3,16E-01	0,3729	-1,0034551	-0,374156	23,99	LOC102723576	uncharacterized LOC102723576
4135	2,31E-02	1,64E+00	1,72E-02	0,1571	-2,3828079	-0,37444379	126,55	MAP6	microtubule associated protein 6
8498	1,25E-12	1,19E+01	5,21E-13	0,0519	-7,2195773	-0,37469793	3002,54	RANBP3	RAN binding protein 3
197322	9,61E-06	5,02E+00	5,48E-06	0,0825	-4,5456547	-0,37483104	584,32	ACSF3	acyl-CoA synthetase family member 3
386724	3,88E-03	2,41E+00	2,67E-03	0,1248	-3,0031545	-0,37487179	237,09	AMIGO3	adhesion molecule with Ig like domain 3
105369758	4,41E-03	2,36E+00	3,06E-03	0,1266	-2,961876	-0,37488758	197,63	DDN-AS1	DDN and PRKAG1 antisense RNA 1
3326	2,94E-19	1,85E+01	9,98E-20	0,0413	-9,089207	-0,37499956	187282,26	HSP90AB1	heat shock protein 90 alpha family class B member 1
9667	1,88E-11	1,07E+01	8,20E-12	0,0549	-6,8349857	-0,37541039	4361,84	SAFB2	scaffold attachment factor B2
89796	8,21E-16	1,51E+01	3,10E-16	0,046	-8,169321	-0,37547884	3777,24	NAV1	neuron navigator 1
2887	1,04E-14	1,40E+01	4,08E-15	0,0478	-7,852516	-0,37553622	2704,95	GRB10	growth factor receptor bound protein 10
105376235	4,08E-01	3,89E-01	3,67E-01	0,416	-0,9026854	-0,37555332	18,9	LOC105376235	uncharacterized LOC105376235
7266	3,01E-16	1,55E+01	1,12E-16	0,0453	-8,2912209	-0,37558417	7150,62	DNAJC7	DnaJ heat shock protein family (Hsp40) member C7
23543	1,92E-23	2,27E+01	5,81E-24	0,0372	-10,0949742	-0,37564905	9810,42	RBFOX2	RNA binding fox-1 homolog 2
23467	3,09E-03	2,51E+00	2,11E-03	0,1222	-3,0738262	-0,37573324	216,46	NPTXR	neuronal pentraxin receptor
54964	4,95E-04	3,31E+00	3,17E-04	0,1044	-3,6007727	-0,37581326	305,45	C1orf56	chromosome 1 open reading frame 56
65005	3,56E-13	1,24E+01	1,46E-13	0,0509	-7,3903957	-0,37598318	2297,46	MRPL9	mitochondrial ribosomal protein L9
93624	2,90E-10	9,54E+00	1,32E-10	0,0586	-6,4246094	-0,37653049	1426	TADA2B	transcriptional adaptor 2B
102723334	2,88E-01	5,41E-01	2,50E-01	0,3274	-1,1506771	-0,37667509	27,69	LOC102723334	uncharacterized LOC102723334
54082	3,20E-01	4,95E-01	2,81E-01	0,3492	-1,0791182	-0,37682229	24,85	TSPEAR-AS1	TSPEAR antisense RNA 1
151516	5,29E-01	2,77E-01	4,88E-01	0,5436	-0,6933277	-0,37687499	10,11	ASPRV1	aspartic peptidase retroviral like 1
9915	5,42E-12	1,13E+01	2,32E-12	0,0537	-7,013894	-0,3768981	1835,38	ARNT2	aryl hydrocarbon receptor nuclear translocator 2
401288	2,81E-01	5,51E-01	2,44E-01	0,3233	-1,1660352	-0,37692311	29,16	LINC00242	long intergenic non-protein coding RNA 242
102724943	1,73E-01	7,62E-01	1,45E-01	0,2586	-1,4577021	-0,37694419	43,97	LOC102724943	splicing factor 3A subunit 2
389125	2,68E-01	5,72E-01	2,32E-01	0,3153	-1,1960943	-0,3770814	29,39	MUSTN1	musculoskeletal, embryonic nuclear protein 1
55090	1,76E-05	4,75E+00	1,02E-05	0,0854	-4,413394	-0,37709081	563,88	MED9	mediator complex subunit 9
90835	5,27E-02	1,28E+00	4,10E-02	0,1847	-2,0433508	-0,37741483	90,36	CFAP119	cilia and flagella associated protein 119
5493	2,45E-03	2,61E+00	1,66E-03	0,12	-3,1453687	-0,37748933	223,57	PPL	periplakin
9253	1,13E-04	3,95E+00	6,89E-05	0,0949	-3,9799192	-0,37773981	562,74	NUMBL	NUMB like endocytic adaptor protein
102723591	1,50E-01	8,24E-01	1,25E-01	0,246	-1,5361453	-0,3779044	53,51	PLXNB3-AS1	PLXNB3 antisense RNA 1
285830	2,86E-01	5,44E-01	2,48E-01	0,3271	-1,1554402	-0,37799111	27,67	HLA-F-AS1	HLA-F antisense RNA 1
1975	8,01E-23	2,21E+01	2,46E-23	0,038	-9,9524349	-0,37816954	15790,78	EIF4B	eukaryotic translation initiation factor 4B
5690	1,10E-18	1,80E+01	3,79E-19	0,0423	-8,9430244	-0,37820076	13646,83	PSMB2	proteasome 20S subunit beta 2
208	2,59E-12	1,16E+01	1,10E-12	0,0532	-7,1177684	-0,37832923	5535,85	AKT2	AKT serine/threonine kinase 2
401152	7,70E-08	7,11E+00	3,91E-08	0,0689	-5,494698	-0,37838323	2553,36	C4orf3	chromosome 4 open reading frame 3
23326	5,94E-21	2,02E+01	1,92E-21	0,0398	-9,5090556	-0,37851424	14317,54	USP22	ubiquitin specific peptidase 22
2121	9,86E-14	1,30E+01	3,97E-14	0,0501	-7,5618254	-0,37860404	3923,46	EVC	EvC ciliary complex subunit 1
389549	8,07E-03	2,09E+00	5,73E-03	0,1371	-2,7626152	-0,37871052	165,96	FEZF1	FEZ family zinc finger 1
79672	1,79E-11	1,07E+01	7,79E-12	0,0554	-6,8423228	-0,37879194	1936,72	FN3KRP	fructosamine 3 kinase related protein
10367	1,39E-16	1,59E+01	5,10E-17	0,0452	-8,3842837	-0,37883267	3288,22	MICU1	mitochondrial calcium uptake 1
119710	1,09E-04	3,96E+00	6,61E-05	0,095	-3,9899049	-0,37900293	368,14	IFTAP	intraflagellar transport associated protein
643641	8,66E-07	6,06E+00	4,65E-07	0,0752	-5,0402743	-0,37907389	677,17	ZNF862	zinc finger protein 862
128977	1,40E-04	3,85E+00	8,57E-05	0,0965	-3,9278239	-0,37910695	391,85	C22orf39	chromosome 22 open reading frame 39
976	1,09E-18	1,80E+01	3,78E-19	0,0424	-8,9432857	-0,3791325	18756,07	ADGRE5	adhesion G protein-coupled receptor E5
111822955	3,67E-06	5,44E+00	2,04E-06	0,0798	-4,7496604	-0,37921794	561,49	ATRIP-TREX1	ATRIP-TREX1 readthrough
8761	2,13E-18	1,77E+01	7,42E-19	0,0428	-8,8683843	-0,37968312	9156,79	PABPC4	poly(A) binding protein cytoplasmic 4
60312	8,98E-23	2,20E+01	2,76E-23	0,0382	-9,9409431	-0,37980212	7885,64	AFAP1	actin filament associated protein 1
23258	3,09E-16	1,55E+01	1,15E-16	0,0458	-8,2881613	-0,37983695	3900,39	DENND5A	DENN domain containing 5A
56160	1,62E-08	7,79E+00	7,96E-09	0,0659	-5,769385	-0,380301	942,99	NSMCE3	NSE3 homolog, SMC5-SMC6 complex component
5795	1,03E-17	1,70E+01	3,67E-18	0,0438	-8,6884543	-0,38050745	12193,86	PTPRJ	protein tyrosine phosphatase receptor type J
5936	1,81E-15	1,47E+01	6,92E-16	0,0472	-8,0719138	-0,38062777	2844,74	RBM4	RNA binding motif protein 4
113455421	3,54E-14	1,35E+01	1,41E-14	0,0495	-7,6956003	-0,38120942	2345,75	DERPC	DERPC proline and glycine rich nuclear protein
54921	3,54E-14	1,35E+01	1,41E-14	0,0495	-7,6956003	-0,38120942	2345,75	CHTF8	chromosome transmission fidelity factor 8
84246	2,93E-11	1,05E+01	1,29E-11	0,0563	-6,7697519	-0,38143014	1632,81	MED10	mediator complex subunit 10
149465	1,54E-01	8,12E-01	1,28E-01	0,2505	-1,5227806	-0,38143371	49,5	CFAP57	cilia and flagella associated protein 57
407004	1,26E-01	9,00E-01	1,03E-01	0,2343	-1,6293283	-0,38167029	57,53	MIR22	microRNA 22
100507633	4,07E-01	3,90E-01	3,66E-01	0,4223	-0,9040968	-0,38176759	16,37	TNKS2-DT	TNKS2 divergent transcript
55655	3,86E-07	6,41E+00	2,03E-07	0,0735	-5,1963752	-0,38193596	799,83	NLRP2	NLR family pyrin domain containing 2
5347	8,68E-20	1,91E+01	2,90E-20	0,0414	-9,2225607	-0,38208373	8381,53	PLK1	polo like kinase 1
83596	2,55E-10	9,59E+00	1,16E-10	0,0593	-6,4443758	-0,38220218	1980,43	BCL2L12	BCL2 like 12
54820	1,10E-12	1,20E+01	4,60E-13	0,0528	-7,2366405	-0,38227435	2778,05	NDE1	nudE neurodevelopment protein 1
377	7,29E-22	2,11E+01	2,30E-22	0,0393	-9,727698	-0,38238847	7155,85	ARF3	ADP ribosylation factor 3
55070	4,58E-03	2,34E+00	3,18E-03	0,1297	-2,9498673	-0,38255764	205,83	DET1	DET1 partner of COP1 E3 ubiquitin ligase
199953	2,78E-07	6,56E+00	1,45E-07	0,0728	-5,2584453	-0,38302602	1020,29	TMEM201	transmembrane protein 201
1946	2,15E-09	8,67E+00	1,02E-09	0,0628	-6,1063337	-0,38328616	1069,68	EFNA5	ephrin A5
642819	7,42E-02	1,13E+00	5,88E-02	0,203	-1,8898484	-0,38369351	81,07	ZNF487	zinc finger protein 487
3268	3,03E-09	8,52E+00	1,45E-09	0,0635	-6,0503689	-0,38423225	1365,42	AGFG2	ArfGAP with FG repeats 2
23351	8,94E-18	1,70E+01	3,17E-18	0,0442	-8,7051571	-0,38440804	3933,33	KHNYN	KH and NYN domain containing

8893	1,52E-20	1,98E+01	4,97E-21	0,0409	-9,4097303	-0,38445628	5492,98	EIF2B5	eukaryotic translation initiation factor 2B subunit epsilon
175	1,33E-07	6,88E+00	6,82E-08	0,0713	-5,3959369	-0,38465023	880,28	AGA	aspartylglucosaminidase
7060	2,92E-01	5,35E-01	2,54E-01	0,3375	-1,1398493	-0,38467261	28,48	THBS4	thrombospondin 4
598	5,54E-20	1,93E+01	1,84E-20	0,0415	-9,2710442	-0,38478317	18870,76	BCL2L1	BCL2 like 1
10419	1,51E-24	2,38E+01	4,43E-25	0,0372	-10,3445488	-0,38493497	10210,14	PRMT5	protein arginine methyltransferase 5
23381	3,21E-17	1,65E+01	1,16E-17	0,045	-8,556909	-0,38497352	5907,02	SMG5	SMG5 nonsense mediated mRNA decay factor
100505692	3,97E-01	4,01E-01	3,56E-01	0,417	-0,9237182	-0,38520907	17,8	FTO-IT1	FTO intronic transcript 1
25880	1,16E-04	3,94E+00	7,06E-05	0,097	-3,9742126	-0,38561743	369,27	TMEM186	transmembrane protein 186
51433	6,80E-15	1,42E+01	2,65E-15	0,0488	-7,9065232	-0,38564811	8208,38	ANAPC5	anaphase promoting complex subunit 5
51497	1,21E-24	2,39E+01	3,55E-25	0,0372	-10,3658273	-0,38569502	8690,86	NELFCD	negative elongation factor complex member C/D
3491	7,24E-27	2,61E+01	2,00E-27	0,0355	-10,8498574	-0,38570908	37876,28	CCN1	cellular communication network factor 1
57176	2,26E-10	9,65E+00	1,03E-10	0,0597	-6,4625341	-0,3858286	1512,12	VARS2	valyl-tRNA synthetase 2, mitochondrial
3068	4,13E-27	2,64E+01	1,13E-27	0,0354	-10,9017485	-0,38599378	32356,67	HDGF	heparin binding growth factor
101929089	2,77E-03	2,56E+00	1,89E-03	0,1243	-3,1075897	-0,38613085	213,94	TTC36-AS1	TTC36 and KMT2A antisense RNA 1
767557	3,24E-14	1,35E+01	1,29E-14	0,0502	-7,7071827	-0,38653242	2453,62	SYS1-DBND	SYS1-DBNDD2 readthrough (NMD candidate)
5514	3,75E-16	1,54E+01	1,40E-16	0,0468	-8,2647806	-0,38660884	5550,47	PPP1R10	protein phosphatase 1 regulatory subunit 10
90226	4,50E-02	1,35E+00	3,46E-02	0,1831	-2,1127472	-0,38675942	97,46	UCN2	urocortin 2
105377348	2,03E-01	6,93E-01	1,72E-01	0,2832	-1,3656104	-0,38678078	36,86	UBE2D3-AS	UBE2D3 antisense RNA 1
54502	3,20E-06	5,49E+00	1,77E-06	0,081	-4,7779537	-0,38684165	556,88	RBM47	RNA binding motif protein 47
100287036	4,51E-02	1,35E+00	3,48E-02	0,1832	-2,1111506	-0,3868476	88,82	LOC100287(	uncharacterized LOC100287036
50488	6,14E-18	1,72E+01	2,17E-18	0,0442	-8,7481091	-0,38706542	4384,13	MINK1	misshapen like kinase 1
81576	4,34E-09	8,36E+00	2,08E-09	0,0647	-5,9914546	-0,38739189	1297,43	YJU2B	YJU2 splicing factor homolog B
23077	1,71E-16	1,58E+01	6,32E-17	0,0464	-8,3591899	-0,38746246	3546,17	MYCBP2	MYC binding protein 2
5576	4,34E-21	2,04E+01	1,40E-21	0,0406	-9,5421121	-0,38783636	7110,75	PRKAR2A	protein kinase cAMP-dependent type II regulatory subunit alpha
55226	1,17E-19	1,89E+01	3,91E-20	0,0422	-9,1904857	-0,38792344	6104,03	NAT10	N-acetyltransferase 10
149175	1,10E-09	8,96E+00	5,15E-10	0,0624	-6,2144496	-0,38803158	1098,81	MANEAL	mannosidase endo-alpha like
29109	2,88E-09	8,54E+00	1,37E-09	0,0641	-6,0583954	-0,38808956	1708,46	FHOD1	formin homology 2 domain containing 1
643862	1,05E-01	9,79E-01	8,54E-02	0,2256	-1,7203563	-0,38810725	57,78	SPDYE10	speedy/RINGO cell cycle regulator family member E10
388121	3,02E-01	5,20E-01	2,64E-01	0,3473	-1,1177566	-0,38815716	26,98	TNFAIP8L3	TNF alpha induced protein 8 like 3
100190939	1,76E-03	2,75E+00	1,18E-03	0,1197	-3,2436658	-0,38823396	226,71	TPT1-AS1	TPT1 antisense RNA 1
8567	1,44E-20	1,98E+01	4,72E-21	0,0413	-9,415266	-0,38845695	5654,01	MADD	MAP kinase activating death domain
9122	3,59E-01	4,45E-01	3,18E-01	0,3893	-0,9979957	-0,38851519	24,42	SLC16A4	solute carrier family 16 member 4
9048	1,30E-02	1,89E+00	9,40E-03	0,1496	-2,5971517	-0,38859249	142,43	ARTN	artemin
10782	8,64E-14	1,31E+01	3,48E-14	0,0513	-7,5791714	-0,3886007	1944,11	ZNF274	zinc finger protein 274
8891	5,40E-15	1,43E+01	2,10E-15	0,049	-7,9355575	-0,38869985	2607,85	EIF2B3	eukaryotic translation initiation factor 2B subunit gamma
4717	3,79E-10	9,42E+00	1,74E-10	0,0609	-6,3827683	-0,38894144	1598,95	NDUFC1	NADH:ubiquinone oxidoreductase subunit C1
57501	1,09E-04	3,96E+00	6,64E-05	0,0976	-3,9887636	-0,38921322	352,68	CFAP92	cilia and flagella associated protein 92 (putative)
107985115	8,77E-02	1,06E+00	7,02E-02	0,215	-1,8108508	-0,38928669	70,58	ZNF496-DT	ZNF496 divergent transcript
9275	4,85E-13	1,23E+01	2,00E-13	0,053	-7,3487028	-0,3894414	2515,61	BCL7B	BAF chromatin remodeling complex subunit BCL7B
65996	3,05E-11	1,05E+01	1,34E-11	0,0576	-6,7641159	-0,38948941	1644,87	CENPBD2P	CENPB DNA-binding domains containing 2, pseudogene
28976	1,51E-13	1,28E+01	6,14E-14	0,0519	-7,5050159	-0,38955797	1927,57	ACAD9	acyl-CoA dehydrogenase family member 9
9172	8,36E-02	1,08E+00	6,67E-02	0,2125	-1,8335688	-0,38960184	67,34	MYOM2	myomesin 2
90678	9,47E-09	8,02E+00	4,61E-09	0,0665	-5,8608478	-0,38960325	988,89	LRSAM1	leucine rich repeat and sterile alpha motif containing 1
10379	8,16E-08	7,09E+00	4,15E-08	0,0711	-5,484215	-0,38969631	789,32	IRF9	interferon regulatory factor 9
10495	1,06E-08	7,97E+00	5,17E-09	0,0667	-5,8417661	-0,38978078	903,56	ENOX2	ecto-NOX disulfide-thiol exchanger 2
285407	1,20E-01	9,21E-01	9,81E-02	0,2357	-1,6539606	-0,38991674	54,16	ALG1L9P	ALG1 like 9, pseudogene
28957	1,22E-08	7,91E+00	5,95E-09	0,0671	-5,818078	-0,39013997	919,61	MRPS28	mitochondrial ribosomal protein S28
7165	1,18E-26	2,59E+01	3,27E-27	0,0361	-10,8047812	-0,39019172	15627,67	TPD52L2	TPD52 like 2
55738	6,82E-13	1,22E+01	2,83E-13	0,0534	-7,3021772	-0,39028809	3824,09	ARFGAP1	ADP ribosylation factor GTPase activating protein 1
1741	2,70E-10	9,57E+00	1,23E-10	0,0607	-6,4352026	-0,39036213	1282,36	DLG3	discs large MAGUK scaffold protein 3
2306	3,42E-01	4,66E-01	3,02E-01	0,378	-1,0330413	-0,39049189	21,14	FOXD2	forkhead box D2
7918	1,03E-15	1,50E+01	3,90E-16	0,048	-8,1415001	-0,39061556	2857,3	GPANK1	G-patch domain and ankyrin repeats 1
338758	2,65E-02	1,58E+00	1,99E-02	0,1677	-2,328971	-0,39064709	108,26	ATP2B1-AS1	ATP2B1 antisense RNA 1
4710	1,09E-16	1,60E+01	4,00E-17	0,0465	-8,4130128	-0,39081936	3777,38	NDUFB4	NADH:ubiquinone oxidoreductase subunit B4
55281	1,19E-05	4,92E+00	6,84E-06	0,0869	-4,4985248	-0,39104377	447,58	TMEM140	transmembrane protein 140
84674	2,93E-10	9,53E+00	1,34E-10	0,0609	-6,4230113	-0,39112259	1221,05	CARD6	caspase recruitment domain family member 6
5609	7,40E-12	1,11E+01	3,18E-12	0,0561	-6,9696416	-0,39115735	3397,11	MAP2K7	mitogen-activated protein kinase kinase 7
107987388	5,42E-01	2,66E-01	5,01E-01	0,5821	-0,6722655	-0,39131255	8,65	LOC107987	replaced by ID 102724151
78991	8,29E-07	6,08E+00	4,44E-07	0,0775	-5,0489268	-0,39136206	595,17	PCYOX1L	prenylcysteine oxidase 1 like
100302213	2,03E-02	1,69E+00	1,50E-02	0,161	-2,4324617	-0,39165008	1333,35	MIR1181	microRNA 1181
9757	1,83E-10	9,74E+00	8,31E-11	0,0603	-6,494951	-0,39182454	2599,32	KMT2B	lysine methyltransferase 2B
514	1,08E-16	1,60E+01	3,96E-17	0,0466	-8,4141792	-0,39193047	4398,3	ATP5F1E	ATP synthase F1 subunit epsilon
388569	9,27E-05	4,03E+00	5,62E-05	0,0973	-4,0283613	-0,3920058	365,24	ZNF324B	zinc finger protein 324B
55504	7,50E-04	3,12E+00	4,88E-04	0,1125	-3,4874777	-0,39218463	277,69	TNFRSF19	TNF receptor superfamily member 19
594840	1,12E-01	9,51E-01	9,07E-02	0,2318	-1,6919054	-0,39221451	56,12	ZFAT-AS1	ZFAT antisense RNA 1
22821	5,09E-18	1,73E+01	1,80E-18	0,0447	-8,7694556	-0,3922217	3518,62	RASA3	RAS p21 protein activator 3
1666	1,63E-10	9,79E+00	7,38E-11	0,0603	-6,5127994	-0,39242477	1303,01	DECR1	2,4-dienoyl-CoA reductase 1
10574	2,54E-28	2,76E+01	6,74E-29	0,0352	-11,1553777	-0,39242503	27292,69	CCT7	chaperonin containing TCP1 subunit 7
8925	4,40E-11	1,04E+01	1,95E-11	0,0585	-6,7099097	-0,3927369	1589,57	HERC1	HECT and RLD domain containing E3 ubiquitin protein ligase family member 1
284440	1,01E-01	9,96E-01	8,16E-02	0,2255	-1,7416326	-0,392756	75,14	LINC00663	long intergenic non-protein coding RNA 663
245812	2,66E-06	5,58E+00	1,46E-06	0,0815	-4,816317	-0,39276044	538,41	CNPY4	canopy FGF signaling regulator 4
105369807	3,56E-01	4,49E-01	3,16E-01	0,3914	-1,0035377	-0,39276263	19,47	LINC02454	long intergenic non-protein coding RNA 2454
57718	9,24E-03	2,03E+00	6,61E-03	0,1446	-2,7160656	-0,39281721	156,49	PPP4R4	protein phosphatase 4 regulatory subunit 4
2282	5,43E-01	2,65E-01	5,03E-01	0,5862	-0,6702457	-0,39289477	8,66	FKBP1AP1	FKBP prolyl isomerase 1A pseudogene 1
81554	6,07E-13	1,22E+01	2,52E-13	0,0537	-7,3180772	-0,39290568	1776,86	RCC1L	RCC1 like
51807	4,80E-01	3,19E-01	4,38E-01	0,5068	-0,7756359	-0,3930921	12	TUBA8	tubulin alpha 8
23636	5,80E-17	1,62E+01	2,11E-17	0,0463	-8,4874786	-0,39309255	6309,53	NUP62	nucleoporin 62
9400	9,60E-09	8,02E+00	4,67E-09	0,0671	-5,8584581	-0,39326723	978,66	RECQL5	RecQ like helicase 5
10969	1,25E-24	2,39E+01	3,66E-25	0,038	-10,3628607	-0,39336884	12040,79	EBNA1BP2	EBNA1 binding protein 2
221749	5,71E-12	1,12E+01	2,44E-12	0,0561	-7,0064259	-0,39337431	1643,89	PXDC1	PX domain containing 1
100130311	4,80E-01	3,19E-01	4,38E-01	0,5072	-0,7757227	-0,39346021	11,28	C17orf107	chromosome 17 open reading frame 107
84695	5,87E-06	5,23E+00	3,30E-06	0,0847	-4,651239	-0,39380688	490,74	LOXL3	lysyl oxidase like 3
91442	1,40E-04	3,85E+00	8,59E-05	0,1003	-3,9273635	-0,39399912	326,03	FAAP24	FA core complex associated protein 24
26959	2,16E-11	1,07E+01	9,46E-12	0,0578	-6,8144476	-0,39409125	1463,95	HBP1	HMG-box transcription factor 1
59284	1,51E-02	1,82E+00	1,10E-02	0,1549	-2,543791	-0,39413269	145,48	CACNG7	calcium voltage-gated channel auxiliary subunit gamma 7
5283	1,16E-04	3,94E+00	7,06E-05	0,0992	-3,9743823	-0,39430422	386,2	PIGH	phosphatidylinositol glycan anchor biosynthesis class H
102724515	1,26E-01	9,00E-01	1,03E-01	0,2419	-1,630662	-0,39452132	50,82	LINC01291	long intergenic non-protein coding RNA 1291
219771	1,87E-16	1,57E+01	6,90E-17	0,0473	-8,3487242	-0,39461678	3117,8	CCNY	cyclin Y
79932	1,81E-18	1,77E+01	6,29E-19	0,0444	-8,8867601	-0,39461998	3694,2	KIAA0319L	KIAA0319 like
100271927	2,96E-02	1,53E+00	2,23E-02	0,1727	-2,2850787	-0,39467074	106,82	RASA4B	RAS p21 protein activator 4B
399909	2,04E-10	9,69E+00	9,26E-11	0,061	-6,4785564	-0,39498763	2662,46	PCNX3	pecanex 3
201163	6,80E-11	1,02E+01	3,03E-11	0,0595	-6,6450786	-0,39506619	1583,73	FLCN	folliculin
63925	1,98E-10	9,70E+00	8,97E-11	0,061	-6,4834306	-0,39522068	1712,28	ZNF335	zinc finger protein 335
102723750	4,39E-01	3,58E-01	3,98E-01	0,4676	-0,845319	-0,39525938	14,2	LOC102723(	uncharacterized LOC102723750
105371770	4,81E-01	3,18E-01	4,39E-01	0,5107	-0,7740096	-0,39526292	11,82	LOC105371(	uncharacterized LOC105371770
5321	1,24E-04	3,91E+00	7,58E-05	0,0999	-3,9573933	-0,39529327	345,12	PLA2G4A	phospholipase A2 group IVA
100128494	3,91E-14	1,34E+01	1,56E-14	0,0515	-7,6824983	-0,39531434	2462,26	LOC100128(	uncharacterized LOC100128494
51654	5,22E-14	1,33E+01	2,09E-14	0,0517	-7,6450301	-0,3953194	2345,5	CDK5RAP1	CDK5 regulatory subunit associated protein 1
100873952	2,09E-01	6,80E-01	1,77E-01	0,293	-1,3490968	-0,3953489	34,04	SZT2-AS1	SZT2 antisense RNA 1
102724548	1,56E-01	8,07E-01	1,29E-01	0,2609	-1,5167595	-0,39567813	43,16	HHLA3-AS1	HHLA3 antisense RNA 1
100500872	8,09E-02	1,09E+00	6,44E-02	0,214	-1,8493373	-0,39570683	66,46	MIR3911	microRNA 3911
9061	9,43E-18	1,70E+01	3,35E-18	0,0455	-8,6988594	-0,39571923	3337,27	PAPSS1	3'-phosphoadenosine 5'-phosphosulfate synthase 1
10906	6,92E-14	1,32E+01	2,78E-14	0,052	-7,6083463	-0,39583373	2013,23	TRAFD1	TRAF-type zinc finger domain containing 1
8743	2,86E-09	8,54E+00	1,36E-09	0,0653	-6,0596268	-0,39589655	1077,96	TNFSF10	TNF superfamily member 10
441374	5,31E-01	2,75E-01	4,90E-01	0,5737	-0,6902772	-0,39600823	9,1	FLJ42969	uncharacterized LOC441374
55534	3,42E-07	6,47E+00	1,80E-07	0,0759	-5,2190511	-0,39612895	648,32	MAML3	mastermind like transcriptional coactivator 3
10978	4,00E-10	9,40E+00	1,83E-10	0,0622	-6,3745744	-0,39624614	1152,32	CLP1	cleavage factor polyribonucleotide kinase subunit 1
10239	4,23E-09	8,37E+00	2,03E-09	0,0661	-5,9956001	-0,39659091	912,87	AP3S2	adaptor related protein complex 3 subunit sigma 2
100534599	4,36E-11	1,04E+01	1,93E-11	0,0591	-6,7113901	-0,39660796	1226,25	ISY1-RAB43	ISY1-RAB43 readthrough
83861	4,47E-04	3,35E+00	2,86E-04	0,1093	-3,6280288	-0,39666873	281,79	RSPH3	radial spoke head 3
23603	6,41E-26	2,52E+01	1,81E-26	0,0373	-10,6463693	-0,39669504	20608,99	CORO1C	coronin 1C
883	2,83E-04	3,55E+00	1,78E-04	0,1058	-3,7479271	-0,39671414	394,05	KYAT1	kynurenine aminotransferase 1
705	9,55E-22	2,10E+01	3,01E-22	0,0409	-9,7000267	-0,39676972	5053,75	BYSL	bystin like
1213	1,01E-22	2,20E+01	3,12E-23	0,04	-9,9287323	-0,39687985	35586,06	CLTC	clathrin heavy chain
55256	2,38E-22	2,16E+01	7,41E-23	0,0403	-9,8421435	-0,39691042	6993,32	ADI1	acireductone dioxygenase 1
100616210	3,27E-01	4,85E-01	2,88E-01	0,3735	-1,0633631	-0,39717055	20,91	MIR4737	microRNA 4737
105379351	4,70E-01	3,28E-01	4,29E-01	0,502	-0,7912514	-0,39718713	11,59	LINC02948	long intergenic non-protein coding RNA 2948
23	2,01E-25	2,47E+01	5,76E-26	0,0377	-10,5381859	-0,39723772	15969,77	ABCF1	ATP binding cassette subfamily F member 1
9342	5,36E-14	1,33E+01	2,15E-14	0,052	-7,6415765	-0,39733578	2049,03	SNAP29	synaptosome associated protein 29
5575	9,32E-07	6,03E+00	5,01E-07	0,0791	-5,025783	-0,39759559	656,09	PRKAR1B	protein kinase cAMP-dependent type I regulatory subunit beta

124222	1,15E-09	8,94E+00	5,38E-10	0,064	-6,2077238	-0,39760396	1230,1	PAQR4	progestin and adipoQ receptor family member 4
729614	4,34E-03	2,36E+00	3,00E-03	0,134	-2,9673905	-0,39762704	178,85	SPEN-AS1	SPEN antisense RNA 1
271	9,89E-10	9,00E+00	4,62E-10	0,0638	-6,2315851	-0,39787377	2536,74	AMPD2	adenosine monophosphate deaminase 2
10949	6,92E-19	1,82E+01	2,37E-19	0,0442	-8,994456	-0,39794191	7052,62	HNRNPA0	heterogeneous nuclear ribonucleoprotein A0
4904	2,07E-21	2,07E+01	6,63E-22	0,0414	-9,6192852	-0,39805771	50581,7	YBX1	Y-box binding protein 1
51056	1,83E-19	1,87E+01	6,17E-20	0,0436	-9,1413509	-0,39815684	5001,3	LAP3	leucine aminopeptidase 3
101929314	4,84E-07	6,32E+00	2,56E-07	0,0773	-5,1530319	-0,39820627	628,1	LOC1019293	uncharacterized LOC101929314
2048	8,65E-18	1,71E+01	3,07E-18	0,0457	-8,7090006	-0,39824822	4895,45	EPHB2	EPH receptor B2
9463	2,67E-06	5,57E+00	1,47E-06	0,0828	-4,8152322	-0,39861363	554,3	PICK1	protein interacting with PRKCA 1
102466736	1,33E-01	8,76E-01	1,10E-01	0,2492	-1,5995722	-0,39861755	48,16	MIR6789	microRNA 6789
55829	2,43E-12	1,16E+01	1,03E-12	0,056	-7,1266932	-0,39875533	1908,34	SELENOS	selenoprotein S
105379118	5,85E-05	4,23E+00	3,49E-05	0,0964	-4,1386825	-0,39876464	405,42	LOC105379118	
2762	2,35E-13	1,26E+01	9,60E-14	0,0536	-7,4463065	-0,39882694	1858,41	GMDS	GDP-mannose 4,6-dehydratase
83892	7,94E-23	2,21E+01	2,44E-23	0,0401	-9,953312	-0,39958442	5406,78	KCTD10	potassium channel tetramerization domain containing 10
107987141	1,37E-02	1,86E+00	9,97E-03	0,1551	-2,5768538	-0,39965862	141,18	CAMSAP1-D	CAMSAP1 divergent transcript
30827	8,23E-10	9,08E+00	3,83E-10	0,0639	-6,2607621	-0,39996706	1937,23	CXXC1	CXXC finger protein 1
652	1,83E-18	1,77E+01	6,35E-19	0,045	-8,8856719	-0,4000188	3799,72	BMP4	bone morphogenetic protein 4
5797	2,82E-17	1,65E+01	1,02E-17	0,0467	-8,572039	-0,40013988	5315,98	PTPRM	protein tyrosine phosphatase receptor type M
9618	2,55E-11	1,06E+01	1,12E-11	0,0589	-6,7905343	-0,40015878	2136,15	TRAF4	TNF receptor associated factor 4
7097	3,02E-05	4,52E+00	1,77E-05	0,0933	-4,29201	-0,40024816	432,56	TLR2	toll like receptor 2
10007	2,47E-18	1,76E+01	8,61E-19	0,0452	-8,8517889	-0,4003689	3397,74	GNPDA1	glucosamine-6-phosphate deaminase 1
387911	2,22E-01	6,54E-01	1,89E-01	0,3047	-1,3139389	-0,40037719	33,35	C1QTNF9B	C1q and TNF related 9B
54987	1,13E-12	1,19E+01	4,71E-13	0,0554	-7,2334096	-0,40057458	1688,31	CZIB	CXXC motif containing zinc binding protein
63941	1,93E-05	4,71E+00	1,12E-05	0,0912	-4,3929903	-0,40068856	556,21	NECAB3	N-terminal EF-hand calcium binding protein 3
221545	1,77E-12	1,18E+01	7,45E-13	0,0559	-7,1709076	-0,40074472	1971,66	C6orf136	chromosome 6 open reading frame 136
51032	4,58E-01	3,39E-01	4,17E-01	0,4938	-0,8116195	-0,40077171	11,88	CELA2B	chymotrypsin like elastase 2B
55243	1,95E-23	2,27E+01	5,90E-24	0,0397	-10,0934687	-0,40078094	5796,05	KIRREL1	kirre like nephrin family adhesion molecule 1
4697	1,13E-18	1,79E+01	3,90E-19	0,0448	-8,9398768	-0,4008259	5441,14	NDUFA4	NDUFA4 mitochondrial complex associated
57169	1,15E-20	1,99E+01	3,77E-21	0,0425	-9,4389036	-0,40091916	7667,61	ZNFX1	zinc finger NFX1-type containing 1
103021294	1,53E-19	1,88E+01	5,16E-20	0,0438	-9,1606661	-0,4009767	4125,28	ABALON	apoptotic BCL2L1-antisense long non-coding RNA
9363	4,33E-01	3,64E-01	3,92E-01	0,4683	-0,8563315	-0,40105439	15,02	RAB33A	RAB33A, member RAS oncogene family
105373194	1,35E-01	8,70E-01	1,11E-01	0,2517	-1,5932928	-0,40108316	47,95	LOC105373	uncharacterized LOC105373194
26509	4,38E-21	2,04E+01	1,41E-21	0,042	-9,541122	-0,40119359	48573,56	MYOF	myoferlin
284615	2,28E-02	1,64E+00	1,70E-02	0,1681	-2,3874951	-0,40127458	115,52	ANKRD34A	ankyrin repeat domain 34A
3983	7,97E-21	2,01E+01	2,59E-21	0,0423	-9,4779983	-0,40130395	3959,04	ABLIM1	actin binding LIM protein 1
81892	1,59E-12	1,18E+01	6,69E-13	0,0559	-7,1856007	-0,40155715	2774,86	SLIRP	SRA stem-loop interacting RNA binding protein
100506054	3,82E-08	7,42E+00	1,91E-08	0,0715	-5,6198283	-0,40161702	719,93	RNASEH1-D	RNASEH1 divergent transcript
10966	2,35E-03	2,63E+00	1,59E-03	0,1272	-3,1584001	-0,40164531	196,39	RAB40B	RAB40B, member RAS oncogene family
102724064	9,32E-02	1,03E+00	7,48E-02	0,2256	-1,7814148	-0,40185059	58,14	B4GAT1-DT	B4GAT1 divergent transcript
101409257	1,08E-06	5,97E+00	5,83E-07	0,0805	-4,996734	-0,40211536	577,78	EZR-AS1	EZR antisense RNA 1
100134015	2,71E-01	5,67E-01	2,35E-01	0,3384	-1,1887717	-0,40224511	25,92	UBOX5-AS1	UBOX5 antisense RNA 1
3015	2,35E-26	2,56E+01	6,56E-27	0,0375	-10,7405741	-0,40235958	18417,71	H2AZ1	H2A.Z variant histone 1
162282	1,19E-01	9,24E-01	9,67E-02	0,2425	-1,6608734	-0,40272695	55,58	ANKFN1	ankyrin repeat and fibronectin type III domain containing 1
79152	3,46E-01	4,61E-01	3,05E-01	0,393	-1,0247927	-0,40275485	18,74	FA2H	fatty acid 2-hydroxylase
83955	7,93E-02	1,10E+00	6,31E-02	0,2168	-1,8583083	-0,40283642	63,54	NACA4P	NACA family member 4, pseudogene
9945	1,03E-16	1,60E+01	3,77E-17	0,048	-8,4197272	-0,40402035	2643,52	GFPT2	glutamine-fructose-6-phosphate transaminase 2
152007	9,35E-03	2,03E+00	6,69E-03	0,149	-2,7119253	-0,40408472	172,61	GLIPR2	GLI pathogenesis related 2
115273	4,02E-02	1,40E+00	3,08E-02	0,1871	-2,1601227	-0,40419973	86,87	RAB42	RAB42, member RAS oncogene family
112268166	3,38E-02	1,47E+00	2,56E-02	0,1811	-2,2317647	-0,40422136	92,49	LOC112268166	
91010	2,27E-12	1,16E+01	9,59E-13	0,0567	-7,1362089	-0,40433084	1792,05	FMNL3	formin like 3
55486	4,70E-12	1,13E+01	2,01E-12	0,0576	-7,0338065	-0,40504246	2730,99	PARL	presenilin associated rhomboid like
113277	4,44E-04	3,35E+00	2,83E-04	0,1116	-3,6301705	-0,40522316	267,18	TMEM106A	transmembrane protein 106A
92595	1,51E-03	2,82E+00	1,00E-03	0,1232	-3,2892874	-0,40526321	209,75	ZNF764	zinc finger protein 764
107986991	4,95E-04	3,31E+00	3,17E-04	0,1126	-3,6006219	-0,40560025	265,58	LOC107986991	
9764	4,53E-06	5,34E+00	2,53E-06	0,0863	-4,7056048	-0,40591316	500,25	KIAA0513	KIAA0513
107983969	2,99E-01	5,24E-01	2,61E-01	0,3609	-1,1248017	-0,40592114	23,26	LOC107983969	
9322	1,41E-21	2,09E+01	4,48E-22	0,042	-9,6595601	-0,40596912	8702,99	TRIP10	thyroid hormone receptor interactor 10
105376286	6,64E-04	3,18E+00	4,30E-04	0,1154	-3,5210516	-0,40635757	247,29	LOC105376	uncharacterized LOC105376286
100506649	8,23E-10	9,08E+00	3,83E-10	0,0649	-6,2608486	-0,4064378	961,11	PXN-AS1	PXN antisense RNA 1
54949	1,54E-11	1,08E+01	6,68E-12	0,0592	-6,8644243	-0,40649393	2536,55	SDHAF2	succinate dehydrogenase complex assembly factor 2
375607	5,14E-01	2,89E-01	4,72E-01	0,5656	-0,7192986	-0,40686216	9,41	NAT16	N-acetyltransferase 16 (putative)
4926	6,64E-20	1,92E+01	2,21E-20	0,044	-9,2515456	-0,40696073	10289,54	NUMA1	nuclear mitotic apparatus protein 1
100526783	6,84E-11	1,02E+01	3,04E-11	0,0613	-6,6443924	-0,4070009	1107,01	ARPIN-AP3S	ARPIN-AP3S2 readthrough
10156	2,37E-02	1,63E+00	1,76E-02	0,1715	-2,3732724	-0,40709648	107,9	RASA4	RAS p21 protein activator 4
25976	1,40E-20	1,99E+01	4,57E-21	0,0432	-9,4187005	-0,40725142	5016,97	TIPARP	TCDD inducible poly(ADP-ribose) polymerase
84217	3,16E-02	1,50E+00	2,38E-02	0,1802	-2,2597307	-0,40725246	92,91	ZMYND12	zinc finger MYND-type containing 12
11065	1,36E-12	1,19E+01	5,70E-13	0,0565	-7,2073626	-0,40727222	11731,79	UBE2C	ubiquitin conjugating enzyme E2 C
112267936	1,99E-01	7,01E-01	1,68E-01	0,2954	-1,3789434	-0,40735373	33,53	LOC112267	uncharacterized LOC112267936
202658	2,01E-09	8,70E+00	9,54E-10	0,0666	-6,1169433	-0,40750377	1234,78	TRIM39-RPF	TRIM39-RPP21 readthrough
51309	2,55E-13	1,26E+01	1,04E-13	0,0548	-7,4358636	-0,40751791	1777,44	ARMCX1	armadillo repeat containing X-linked 1
2068	8,71E-15	1,41E+01	3,40E-15	0,0518	-7,8751435	-0,40760318	3969,69	ERCC2	ERCC excision repair 2, TFIIH core complex helicase subunit
84726	4,51E-21	2,03E+01	1,46E-21	0,0428	-9,5380401	-0,40797771	6883,37	PRRC2B	proline rich coiled-coil 2B
107282092	3,29E-07	6,48E+00	1,73E-07	0,0781	-5,226691	-0,40809275	650,24	BOLA2-SMG	BOLA2-SMG1P6 readthrough
59277	1,73E-15	1,48E+01	6,60E-16	0,0505	-8,0776575	-0,40826921	2026,88	NTN4	netrin 4
64754	1,31E-13	1,29E+01	5,32E-14	0,0543	-7,5238084	-0,40828591	1578,01	SMYD3	SET and MYND domain containing 3
1605	2,21E-22	2,17E+01	6,86E-23	0,0415	-9,8499897	-0,40870982	15134,18	DAG1	dystroglycan 1
196385	2,35E-02	1,63E+00	1,75E-02	0,1721	-2,3767752	-0,40900164	110,1	DNAH10	dynein axonemal heavy chain 10
27434	1,31E-07	6,88E+00	6,75E-08	0,0758	-5,3975995	-0,40900223	822,94	POLM	DNA polymerase mu
8349	8,94E-03	2,05E+00	6,38E-03	0,15	-2,7273333	-0,40914756	139,96	H2BC21	H2B clustered histone 21
7982	2,36E-09	8,63E+00	1,12E-09	0,0672	-6,091243	-0,40922105	915,53	ST7	suppression of tumorigenicity 7
105373583	4,01E-01	3,97E-01	3,59E-01	0,4469	-0,9166867	-0,40963071	14,68	LOC105373	uncharacterized LOC105373583
5890	2,67E-04	3,57E+00	1,68E-04	0,1089	-3,7633613	-0,40964753	290,91	RAD51B	RAD51 paralog B
6631	2,97E-24	2,35E+01	8,80E-25	0,0399	-10,2785493	-0,40965993	9520,26	SNRPC	small nuclear ribonucleoprotein polypeptide C
9895	4,36E-13	1,24E+01	1,80E-13	0,0557	-7,3632063	-0,40993029	1856,28	TECPR2	tectonin beta-propeller repeat containing 2
10238	1,38E-28	2,79E+01	3,64E-29	0,0366	-11,2100017	-0,41038729	11755,32	DCAF7	DDB1 and CUL4 associated factor 7
85449	3,34E-02	1,48E+00	2,53E-02	0,1835	-2,2368989	-0,41053182	93,63	KIAA1755	KIAA1755
100128822	1,28E-02	1,89E+00	9,25E-03	0,1578	-2,6024994	-0,41055661	126,92	LINC01003	long intergenic non-protein coding RNA 1003
6517	1,77E-01	7,52E-01	1,48E-01	0,2839	-1,446383	-0,41057469	37,15	SLC2A4	solute carrier family 2 member 4
112268179	2,93E-01	5,33E-01	2,55E-01	0,3605	-1,1389307	-0,41059896	22,64	LOC112268	uncharacterized LOC112268179
79714	8,85E-10	9,05E+00	4,12E-10	0,0657	-6,2493026	-0,41061434	923,65	CCDC51	coiled-coil domain containing 51
5686	1,02E-20	2,00E+01	3,33E-21	0,0434	-9,4519221	-0,4106629	8766,19	PSMA5	proteasome 20S subunit alpha 5
6230	6,83E-25	2,42E+01	1,99E-25	0,0394	-10,4211222	-0,41078632	30138,64	RPS25	ribosomal protein S25
56937	9,40E-16	1,50E+01	3,56E-16	0,0504	-8,1527271	-0,4108844	2228,25	PMEPA1	prostate transmembrane protein, androgen induced 1
10062	4,43E-06	5,35E+00	2,47E-06	0,0873	-4,7103265	-0,41103856	543,98	NR1H3	nuclear receptor subfamily 1 group H member 3
9883	1,17E-19	1,89E+01	3,92E-20	0,0447	-9,1903341	-0,41107771	4634,58	POM121	POM121 transmembrane nucleoporin
150383	1,51E-03	2,82E+00	1,00E-03	0,125	-3,2895029	-0,41110027	210,13	CDPF1	cysteine rich DPF motif domain containing 1
10687	5,22E-12	1,13E+01	2,23E-12	0,0586	-7,0191722	-0,41134866	1451,82	PNMA2	PNMA family member 2
113444	1,76E-16	1,58E+01	6,50E-17	0,0493	-8,3558239	-0,41173374	2342,94	SMIM12	small integral membrane protein 12
25793	4,94E-20	1,93E+01	1,64E-20	0,0444	-9,2834515	-0,41179413	4165,12	FBXO7	F-box protein 7
117145	1,48E-08	7,83E+00	7,30E-09	0,0712	-5,7839367	-0,41187276	945,87	THEM4	thioesterase superfamily member 4
23211	9,63E-15	1,40E+01	3,77E-15	0,0524	-7,8624806	-0,41206172	1866,01	ZC3H4	zinc finger CCCH-type containing 4
10324	2,92E-01	5,35E-01	2,54E-01	0,3613	-1,1415464	-0,4124821	23,31	KLHL41	kelch like family member 41
378884	2,79E-02	1,55E+00	2,09E-02	0,1788	-2,3089897	-0,41285419	98,62	NHLRC1	NHL repeat containing E3 ubiquitin protein ligase 1
1773	7,62E-10	9,12E+00	3,54E-10	0,0659	-6,2730793	-0,41326949	1030,26	DNASE1	deoxyribonuclease 1
389119	2,53E-01	5,97E-01	2,18E-01	0,3354	-1,2324233	-0,41331003	28,22	INKA1	inka box actin regulator 1
2804	8,61E-16	1,51E+01	3,25E-16	0,0506	-8,1634922	-0,41333933	4975,84	GOLGB1	golgin B1
5098	5,48E-04	3,26E+00	3,52E-04	0,1157	-3,573692	-0,41350675	247,09	PCDHGC3	protocadherin gamma subfamily C, 3
647024	2,37E-13	1,26E+01	9,67E-14	0,0556	-7,4452785	-0,41359113	1774,83	C6orf132	chromosome 6 open reading frame 132
100291105	2,10E-02	1,68E+00	1,55E-02	0,1711	-2,4199822	-0,41403302	104,66	RBM38-AS1	RBM38 antisense RNA 1
55080	2,05E-03	2,69E+00	1,38E-03	0,1294	-3,1991402	-0,414036	184,88	TAPBPL	TAP binding protein like
403	1,30E-12	1,19E+01	5,44E-13	0,0574	-7,213878	-0,41415253	1535,72	ARL3	ADP ribosylation factor like GTPase 3
2011	6,86E-16	1,52E+01	2,58E-16	0,0506	-8,1913295	-0,41430123	2833,93	MARK2	microtubule affinity regulating kinase 2
100631383	3,76E-06	5,42E+00	2,09E-06	0,0873	-4,744581	-0,41437207	458,37	FAM47E-STE	FAM47E-STBD1 readthrough
3304	2,55E-15	1,46E+01	9,79E-16	0,0516	-8,0294993	-0,41441243	6444,2	HSPA1B	heat shock protein family A (Hsp70) member 1B
24137	1,01E-19	1,90E+01	3,39E-20	0,045	-9,2059835	-0,41451256	6564,81	KIF4A	kinesin family member 4A
219854	5,90E-09	8,23E+00	2,85E-09	0,0698	-5,9401406	-0,41461631	763,16	TMEM218	transmembrane protein 218
100130581	1,01E-01	9,96E-01	8,17E-02	0,2382	-1,7406832	-0,41471021	54,17	LINC00910	long intergenic non-protein coding RNA 910
78995	1,00E-07	7,00E+00	5,13E-08	0,0761	-5,4467167	-0,41471971	699,16	HROB	homologous recombination factor with OB-fold
149095	1,21E-01	9,17E-01	9,91E-02	0,2516	-1,6491655	-0,41500608	46,77	DCST1	DC-STAMP domain containing 1
51593	5,28E-19	1,83E+01	1,81E-19	0,046	-9,0244413	-0,41502951	7046	SRRT	serrate, RNA effector molecule

55852	2,72E-18	1,76E+01	9,51E-19	0,0469	-8,840739	-0,41503553	3391,53	TEX2	testis expressed 2
101929691	3,52E-01	4,53E-01	3,12E-01	0,4103	-1,0115705	-0,41509135	19,96	LOC101929691	uncharacterized LOC101929691
958	7,44E-11	1,01E+01	3,32E-11	0,0626	-6,631724	-0,41513186	1213,84	CD40	CD40 molecule
107984660	6,70E-02	1,17E+00	5,29E-02	0,2145	-1,9360771	-0,41519651	64,11	AJUBA-DT	AJUBA divergent transcript
4731	5,91E-17	1,62E+01	2,15E-17	0,0489	-8,485124	-0,41525414	2503,12	NDUFV3	NADH:ubiquinone oxidoreductase subunit V3
60412	6,55E-17	1,62E+01	2,39E-17	0,049	-8,4731261	-0,41529883	2284,84	EXOC4	exocyst complex component 4
28955	1,59E-04	3,80E+00	9,77E-05	0,1066	-3,8962031	-0,4153945	329,69	DEXI	Dexi homolog
4968	4,02E-09	8,40E+00	1,92E-09	0,0692	-6,0040622	-0,41550476	852,1	OGG1	8-oxoguanine DNA glycosylase
55659	1,38E-05	4,86E+00	7,92E-06	0,0931	-4,4672931	-0,41578146	393,19	ZNF416	zinc finger protein 416
65220	2,95E-13	1,25E+01	1,21E-13	0,0561	-7,4160709	-0,41582737	3361,76	NADK	NAD kinase
662	1,39E-10	9,86E+00	6,25E-11	0,0636	-6,5375474	-0,41597228	995,32	BNIP1	BCL2 interacting protein 1
100132774	1,22E-03	2,91E+00	8,03E-04	0,1242	-3,351632	-0,41623902	210,19	KDM4A-AS1	KDM4A antisense RNA 1
79400	1,39E-06	5,86E+00	7,55E-07	0,0842	-4,9465307	-0,41651533	592,17	NOX5	NADPH oxidase 5
79693	1,70E-13	1,28E+01	6,90E-14	0,0556	-7,4897578	-0,41660106	1515,35	YRDC	yrdC N6-threonylcarbamoyltransferase domain containing
1820	1,49E-03	2,83E+00	9,89E-04	0,1265	-3,2936853	-0,41663491	226,43	ARID3A	AT-rich interaction domain 3A
11153	7,43E-08	7,13E+00	3,77E-08	0,0758	-5,5012146	-0,41676909	622,74	FICD	FIC domain protein adenylyltransferase
107986710	1,13E-01	9,47E-01	9,18E-02	0,2473	-1,6860345	-0,4170007	47,9	LOC107986710	uncharacterized LOC107986710
439931	9,12E-02	1,04E+00	7,31E-02	0,2328	-1,7919042	-0,41710517	54,45	THAP7-AS1	THAP7 antisense RNA 1
2782	2,42E-25	2,46E+01	6,96E-26	0,0397	-10,5203726	-0,41795981	27725,37	GNB1	G protein subunit beta 1
339231	5,82E-11	1,02E+01	2,58E-11	0,0627	-6,668509	-0,41813666	1283,43	ARL16	ADP ribosylation factor like GTPase 16
102723729	8,49E-03	2,07E+00	6,04E-03	0,1523	-2,7454673	-0,41817519	131,97	GPAT4-AS1	GPAT4 and GINS4 antisense RNA 1
22928	1,27E-15	1,49E+01	4,83E-16	0,0515	-8,1157916	-0,41826911	2299	SEPHS2	selenophosphate synthetase 2
10460	2,93E-26	2,55E+01	8,20E-27	0,039	-10,7199693	-0,41846269	7135,01	TACC3	transforming acidic coiled-coil containing protein 3
440278	3,62E-01	4,41E-01	3,22E-01	0,4222	-0,9912756	-0,41848393	17,7	CATSPER2P	cation channel sperm associated 2 pseudogene 1
84167	1,19E-13	1,29E+01	4,81E-14	0,0556	-7,5369789	-0,41869209	1551,1	C19orf44	chromosome 19 open reading frame 44
29114	1,36E-01	8,66E-01	1,12E-01	0,2636	-1,5886147	-0,4188281	53,03	TAGLN3	transgelin 3
22809	1,03E-16	1,60E+01	3,79E-17	0,0498	-8,4191539	-0,41901536	2180,01	ATF5	activating transcription factor 5
7005	6,23E-12	1,12E+01	2,67E-12	0,0599	-6,9941863	-0,41906443	2178,13	TEAD3	TEA domain transcription factor 3
23020	6,08E-32	3,12E+01	1,47E-32	0,0353	-11,881816	-0,41937353	27111,66	SNRNP200	small nuclear ribonucleoprotein U5 subunit 200
11108	5,06E-18	1,73E+01	1,78E-18	0,0478	-8,7701752	-0,41947029	3662,38	PRDM4	PR/SET domain 4
78994	2,31E-13	1,26E+01	9,43E-14	0,0563	-7,4485951	-0,41949178	1559,97	PRR14	proline rich 14
105373428	4,83E-01	3,16E-01	4,41E-01	0,5446	-0,7703263	-0,41950776	10,16	LOC105373428	uncharacterized LOC105373428
8455	3,81E-22	2,14E+01	1,19E-22	0,0428	-9,7942759	-0,41954211	3822,66	ATRN	attractin
22794	7,39E-24	2,31E+01	2,21E-24	0,0412	-10,1894847	-0,41954593	6693,44	CASC3	CASC3 exon junction complex subunit
83592	9,32E-03	2,03E+00	6,67E-03	0,1548	-2,7131145	-0,42005303	135	AKR1E2	aldo-keto reductase family 1 member E2
117246	1,34E-23	2,29E+01	4,04E-24	0,0415	-10,130739	-0,4201509	9783,78	FTSJ3	FtsJ RNA 2'-O-methyltransferase 3
100506564	4,90E-01	3,10E-01	4,48E-01	0,5538	-0,7589198	-0,42026717	9,77	THEGL	theg spermatid protein like
644815	3,18E-16	1,55E+01	1,19E-16	0,0507	-8,2845424	-0,42027462	2191,97	FAM83G	family with sequence similarity 83 member G
4779	9,76E-30	2,90E+01	2,50E-30	0,0367	-11,4448576	-0,42033005	25596,81	NFE2L1	NFE2 like bZIP transcription factor 1
9538	2,61E-20	1,96E+01	8,61E-21	0,045	-9,3519275	-0,42079629	8926,8	EI24	EI24 autophagy associated transmembrane protein
5829	1,70E-24	2,38E+01	4,98E-25	0,0407	-10,3332854	-0,42086086	16292,52	PXN	paxillin
8648	3,87E-14	1,34E+01	1,54E-14	0,0548	-7,683892	-0,42106635	1719,24	NCOA1	nuclear receptor coactivator 1
116447	4,19E-11	1,04E+01	1,85E-11	0,0627	-6,7173148	-0,42119021	1242,49	TOP1MT	DNA topoisomerase I mitochondrial
106821730	2,00E-06	5,70E+00	1,09E-06	0,0865	-4,8740463	-0,42138974	465,37	BUB1B-PAK6	BUB1B-PAK6 readthrough
55181	6,69E-16	1,52E+01	2,52E-16	0,0514	-8,1944108	-0,42154163	1949,4	SMG8	SMG8 nonsense mediated mRNA decay factor
102724015	1,05E-02	1,98E+00	7,51E-03	0,1577	-2,6731771	-0,42155666	129,82	SIPA1L1-AS1	SIPA1L1 antisense RNA 1
2157	3,03E-05	4,52E+00	1,78E-05	0,0983	-4,2912373	-0,42200576	378,09	F8	coagulation factor VIII
79685	7,74E-13	1,21E+01	3,22E-13	0,058	-7,2848571	-0,42233597	1329,25	SAP30L	SAP30 like
5536	8,58E-23	2,21E+01	2,64E-23	0,0425	-9,9454536	-0,42242233	6513,82	PPP5C	protein phosphatase 5 catalytic subunit
1345	3,18E-15	1,45E+01	1,22E-15	0,0528	-8,0020182	-0,42258466	4085,6	COX6C	cytochrome c oxidase subunit 6C
54455	2,56E-13	1,26E+01	1,04E-13	0,0568	-7,4352763	-0,42268438	1386,31	FBXO42	F-box protein 42
503538	5,99E-02	1,22E+00	4,69E-02	0,2127	-1,9872441	-0,42269051	65,03	A1BG-AS1	A1BG antisense RNA 1
29925	1,98E-11	1,07E+01	8,62E-12	0,062	-6,8278548	-0,42323156	1385,93	GMPPB	GDP-mannose pyrophosphorylase B
79159	4,03E-06	5,39E+00	2,24E-06	0,0896	-4,7303014	-0,42384477	629,87	NOL12	nucleolar protein 12
10847	2,96E-20	1,95E+01	9,77E-21	0,0454	-9,3384684	-0,423974	6509,77	SRCAP	Snf2 related CREBBP activator protein
342538	2,45E-01	6,11E-01	2,10E-01	0,3386	-1,2524215	-0,4241009	27,18	NACA2	nascent polypeptide associated complex subunit alpha 2
284023	1,11E-03	2,95E+00	7,33E-04	0,1256	-3,3768117	-0,42417487	199,86	RNF227	ring finger protein 227
5266	2,18E-02	1,66E+00	1,62E-02	0,1764	-2,4048013	-0,42425831	98,17	PI3	peptidase inhibitor 3
84790	2,91E-25	2,45E+01	8,38E-26	0,0404	-10,5028888	-0,4243744	61219,63	TUBA1C	tubulin alpha 1c
112268056	3,05E-01	5,16E-01	2,67E-01	0,382	-1,1108499	-0,42437981	20,1	LOC112268056	
100996746	2,23E-01	6,52E-01	1,89E-01	0,3235	-1,3122784	-0,42446309	28,08	SPDYE11	speedy/RINGO cell cycle regulator family member E11
79603	2,47E-02	1,61E+00	1,84E-02	0,1801	-2,3566484	-0,42451589	98,4	CERS4	ceramide synthase 4
55257	1,18E-17	1,69E+01	4,21E-18	0,049	-8,6730863	-0,42488473	3908,86	MRGBP	MRG domain binding protein
26227	5,15E-06	5,29E+00	2,89E-06	0,0908	-4,6787208	-0,42493457	457,58	PHGDH	phosphoglycerate dehydrogenase
5871	1,70E-09	8,77E+00	8,02E-10	0,0692	-6,1445552	-0,42497939	871,75	MAP4K2	mitogen-activated protein kinase kinase kinase kinase 2
283229	8,03E-06	5,10E+00	4,55E-06	0,0927	-4,5844075	-0,42499184	389,46	CRACR2B	calcium release activated channel regulator 2B
84223	1,65E-05	4,78E+00	9,54E-06	0,096	-4,4274377	-0,42501585	390,9	IQCG	IQ motif containing G
55937	1,23E-10	9,91E+00	5,53E-11	0,0648	-6,5558652	-0,42513348	1107,66	APOM	apolipoprotein M
6300	6,91E-07	6,16E+00	3,69E-07	0,0837	-5,0843079	-0,42537999	583,42	MAPK12	mitogen-activated protein kinase 12
80228	6,85E-11	1,02E+01	3,05E-11	0,064	-6,6440951	-0,42538915	1149,61	ORAI2	ORAI calcium release-activated calcium modulator 2
171523	4,49E-01	3,48E-01	4,08E-01	0,5143	-0,8277197	-0,42570928	11,87	CYP2T1P	cytochrome P450 family 2 subfamily T member 1, pseudogene
9759	3,04E-07	6,52E+00	1,59E-07	0,0812	-5,2416358	-0,42585127	667,4	HDAC4	histone deacetylase 4
646450	3,88E-03	2,41E+00	2,68E-03	0,1419	-3,0025572	-0,4259609	158,5	ARIH2OS	ARIH2 opposite strand lncRNA
27351	9,13E-18	1,70E+01	3,24E-18	0,049	-8,7027639	-0,42606322	3429,67	DESI1	desumoylating isopeptidase 1
137964	9,88E-23	2,20E+01	3,04E-23	0,0429	-9,9312722	-0,42629197	4701,3	GPAT4	glycerol-3-phosphate acyltransferase 4
3188	7,76E-20	1,91E+01	2,59E-20	0,0462	-9,2348446	-0,42653067	3397,85	HNRNPH2	heterogeneous nuclear ribonucleoprotein H2
81853	3,45E-20	1,95E+01	1,14E-20	0,0458	-9,3221553	-0,42672283	5214,51	TMEM14B	transmembrane protein 14B
55176	1,45E-10	9,84E+00	6,54E-11	0,0653	-6,5308274	-0,42678271	1100,04	SEC61A2	SEC61 translocon subunit alpha 2
23212	2,93E-14	1,35E+01	1,16E-14	0,0553	-7,7199859	-0,42680406	1667,81	RRS1	ribosome biogenesis regulator 1 homolog
100287042	5,80E-04	3,24E+00	3,74E-04	0,12	-3,5578363	-0,42705955	224,75	MIF4GD-DT	MIF4GD divergent transcript
100506190	1,85E-03	2,73E+00	1,24E-03	0,1323	-3,2291931	-0,42708817	179,82	LINC00963	long intergenic non-protein coding RNA 963
389203	3,52E-07	6,45E+00	1,85E-07	0,0819	-5,2137479	-0,42713222	584,06	SMIM20	small integral membrane protein 20
51588	2,01E-09	8,70E+00	9,54E-10	0,0698	-6,1169424	-0,42725853	903,33	PIAS4	protein inhibitor of activated STAT 4
102723539	9,39E-03	2,03E+00	6,72E-03	0,1576	-2,710549	-0,42726361	122,99	LOC102723539	
51307	1,52E-19	1,88E+01	5,10E-20	0,0467	-9,1618071	-0,42748063	3600,43	FAM53C	family with sequence similarity 53 member C
400804	4,52E-01	3,45E-01	4,11E-01	0,5199	-0,8223242	-0,4275127	10,72	LINC02817	long intergenic non-protein coding RNA 2817
399664	6,84E-06	5,16E+00	3,86E-06	0,0926	-4,6188349	-0,42757178	515,98	MEX3D	mex-3 RNA binding family member D
5826	3,30E-17	1,65E+01	1,19E-17	0,05	-8,5535061	-0,42762709	2454,36	ABCD4	ATP binding cassette subfamily D member 4
116115	2,28E-09	8,64E+00	1,08E-09	0,0702	-6,096567	-0,42776877	812,18	ZNF526	zinc finger protein 526
54850	6,74E-11	1,02E+01	3,00E-11	0,0644	-6,6464912	-0,42798503	1066,83	FBXL12	F-box and leucine rich repeat protein 12
56342	3,10E-13	1,25E+01	1,27E-13	0,0578	-7,4092305	-0,42804836	1455,72	PPAN	peter pan homolog
9553	4,67E-17	1,63E+01	1,69E-17	0,0503	-8,5130647	-0,42839304	3844,49	MRPL33	mitochondrial ribosomal protein L33
2817	7,70E-07	6,11E+00	4,12E-07	0,0847	-5,0632407	-0,42861711	559,32	GPC1	glypican 1
80153	3,13E-16	1,55E+01	1,17E-16	0,0518	-8,2864935	-0,42884859	2153,52	EDC3	enhancer of mRNA decapping 3
340591	9,56E-07	6,02E+00	5,15E-07	0,0854	-5,0206639	-0,42897863	479,61	CA5BP1	carbonic anhydrase 5B pseudogene 1
79650	1,03E-25	2,50E+01	2,93E-26	0,0405	-10,6016192	-0,42900482	6816,75	USB1	U6 snRNA biogenesis phosphodiesterase 1
105369914	3,10E-01	5,09E-01	2,71E-01	0,3901	-1,0998849	-0,42907671	18,98	LOC105369914	uncharacterized LOC105369914
23710	8,15E-11	1,01E+01	3,64E-11	0,0648	-6,6180185	-0,42909828	1150,98	GABARAPL1	GABA type A receptor associated protein like 1
644242	3,85E-01	4,15E-01	3,44E-01	0,4535	-0,946822	-0,42938552	15,08	LINC00622	long intergenic non-protein coding RNA 622
105374464	2,53E-01	5,97E-01	2,17E-01	0,3482	-1,2336033	-0,42956953	23,94	LINC03063	long intergenic non-protein coding RNA 3063
79934	6,92E-05	4,16E+00	4,15E-05	0,1048	-4,0988626	-0,42957192	448,69	COQ8B	coenzyme Q8B
64324	9,59E-18	1,70E+01	3,41E-18	0,0494	-8,6967908	-0,42964268	3729,36	NSD1	nuclear receptor binding SET domain protein 1
101928403	2,76E-01	5,59E-01	2,39E-01	0,3649	-1,1782422	-0,429882	22,14	EIF2AK3-DT	EIF2AK3 divergent transcript
105371701	4,41E-01	3,56E-01	3,99E-01	0,5101	-0,8430172	-0,43002911	11,07	LOC105371701	uncharacterized LOC105371701
60672	4,56E-08	7,34E+00	2,29E-08	0,077	-5,5883388	-0,4302913	758,99	MIIP	migration and invasion inhibitory protein
55527	4,41E-13	1,24E+01	1,82E-13	0,0585	-7,361551	-0,43063075	1459,36	FEM1A	fem-1 homolog A
317648	1,09E-14	1,40E+01	4,26E-15	0,0549	-7,8471523	-0,43064457	1761,64	NOP14-AS1	NOP14 antisense RNA 1
100507507	3,30E-03	2,48E+00	2,26E-03	0,1411	-3,0532369	-0,43072148	168,43	FAM131B-AS	FAM131B antisense RNA 2
5052	1,57E-25	2,48E+01	4,48E-26	0,0408	-10,5617698	-0,43075824	16229,51	PRDX1	peroxiredoxin 1
116444	1,52E-01	8,18E-01	1,26E-01	0,2815	-1,5305526	-0,43087922	36,91	GRIN3B	glutamate ionotropic receptor NMDA type subunit 3B
100129583	1,94E-01	7,12E-01	1,64E-01	0,3093	-1,3932832	-0,43092025	31,92	FAM47E	family with sequence similarity 47 member E
84962	4,71E-30	2,93E+01	1,19E-30	0,0374	-11,5086731	-0,43094307	9594,96	AJUBA	ajuba LIM protein
1431	3,12E-28	2,75E+01	8,29E-29	0,0387	-11,1369143	-0,43102734	9475,14	CS	citrate synthase
808	2,09E-31	3,07E+01	5,12E-32	0,0366	-11,7771921	-0,43108432	15092,39	CALM3	calmodulin 3
51082	1,54E-18	1,78E+01	5,35E-19	0,0484	-8,9047166	-0,43125927	2691,93	POLR1D	RNA polymerase I and III subunit D
432	3,13E-01	5,04E-01	2,74E-01	0,3948	-1,0933766	-0,43171579	19,07	ASGR1	asialoglycoprotein receptor 1
2909	2,56E-27	2,66E+01	6,97E-28	0,0394	-10,9456651	-0,43171658	7784,33	ARHGAP35	Rho GTPase activating protein 35
9552	6,42E-18	1,72E+01	2,27E-18	0,0494	-8,7431118	-0,43192798	2306,17	SPAG7	sperm associated antigen 7
5007	1,45E-26	2,58E+01	4,04E-27	0,0401	-10,7853753	-0,43195821	6144,63	OSBP	oxysterol binding protein
7538	5,30E-07	6,28E+00	2,81E-07	0,0841	-5,1357511	-0,43200257	525,77	ZFP36	ZFP36 ring finger protein

6144	1,87E-16	1,57E+01	6,93E-17	0,0518	-8,3482694	-0,43221244	11959,4	RPL21	ribosomal protein L21
283507	3,51E-01	4,55E-01	3,10E-01	0,4259	-1,0148057	-0,43221617	16,45	SUGT1P3	SUGT1 pseudogene 3
51228	3,59E-23	2,24E+01	1,09E-23	0,0431	-10,0329867	-0,43226857	4605,95	GLTP	glycolipid transfer protein
2859	2,40E-01	6,20E-01	2,05E-01	0,3413	-1,2664929	-0,43229267	26,62	GPR35	G protein-coupled receptor 35
219654	1,17E-12	1,19E+01	4,90E-13	0,0598	-7,2280663	-0,43239215	1429,65	ZCCHC24	zinc finger CCHC-type containing 24
80868	1,29E-03	2,89E+00	8,53E-04	0,1297	-3,334933	-0,43248313	210,79	HCG4B	HLA complex group 4B
1609	1,40E-05	4,85E+00	8,06E-06	0,0969	-4,4635217	-0,43250016	515,16	DGKQ	diacylglycerol kinase theta
144404	1,98E-16	1,57E+01	7,34E-17	0,0519	-8,3414232	-0,43285666	2486,4	TMEM120B	transmembrane protein 120B
57446	2,22E-24	2,37E+01	6,54E-25	0,042	-10,3071531	-0,43286691	4717,95	NDRG3	NDRG family member 3
2590	9,38E-29	2,80E+01	2,45E-29	0,0385	-11,2448669	-0,43305063	7464,17	GALNT2	polypeptide N-acetylgalactosaminyltransferase 2
100873935	4,78E-02	1,32E+00	3,69E-02	0,2076	-2,0863802	-0,43311616	68,66	MTOR-AS1	MTOR antisense RNA 1
286319	1,00E-04	4,00E+00	6,07E-05	0,108	-4,0100893	-0,43328346	282,72	TUSC1	tumor suppressor candidate 1
100526842	1,19E-29	2,89E+01	3,04E-30	0,0379	-11,4276355	-0,43332829	12997,58	RPL17-C18o	RPL17-C18orf32 readthrough
2802	1,35E-16	1,59E+01	4,96E-17	0,0517	-8,3876394	-0,43357142	3036,03	GOLGA3	golgin A3
57017	8,81E-14	1,31E+01	3,55E-14	0,0572	-7,5765828	-0,43373804	1526,87	COQ9	coenzyme Q9
10612	5,71E-07	6,24E+00	3,04E-07	0,0847	-5,1210941	-0,43383315	510,07	TRIM3	tripartite motif containing 3
51300	2,61E-16	1,56E+01	9,68E-17	0,0522	-8,30863	-0,43408946	1799,26	TIMMDC1	translocase of inner mitochondrial membrane domain containing 1
100506603	2,61E-02	1,58E+00	1,95E-02	0,186	-2,3358643	-0,43449471	87,17	VASH1-AS1	VASH1 antisense RNA 1
9904	4,06E-15	1,44E+01	1,57E-15	0,0545	-7,971124	-0,43450977	1611,6	RBM19	RNA binding motif protein 19
30011	2,84E-22	2,15E+01	8,83E-23	0,0442	-9,8244692	-0,43470229	6217,18	SH3KBP1	SH3 domain containing kinase binding protein 1
1181	8,85E-06	5,05E+00	5,04E-06	0,0954	-4,5632788	-0,43526648	440,76	CLCN2	chloride voltage-gated channel 2
2644	6,13E-02	1,21E+00	4,81E-02	0,2203	-1,9767141	-0,43549095	60,73	GCHFR	GTP cyclohydrolase I feedback regulator
23788	2,50E-24	2,36E+01	7,38E-25	0,0424	-10,2955704	-0,43622049	7601,91	MTCH2	mitochondrial carrier 2
23139	1,44E-13	1,28E+01	5,82E-14	0,0581	-7,5121244	-0,4362292	3187,68	MAST2	microtubule associated serine/threonine kinase 2
105374888	2,92E-01	5,35E-01	2,54E-01	0,3825	-1,1405579	-0,43628419	19,71	NQO2-AS1	NQO2 antisense RNA 1
22993	1,08E-20	2,00E+01	3,53E-21	0,0462	-9,445607	-0,43641798	4021,56	HMGXB3	HMG-box containing 3
84630	4,88E-01	3,12E-01	4,46E-01	0,5727	-0,7621843	-0,43648102	8,91	TTBK1	tau tubulin kinase 1
85417	9,65E-04	3,02E+00	6,32E-04	0,1277	-3,4174095	-0,43650606	210,96	CCNB3	cyclin B3
7161	1,40E-04	3,85E+00	8,58E-05	0,1112	-3,9275807	-0,43656879	298,2	TP73	tumor protein p73
84820	1,76E-09	8,75E+00	8,33E-10	0,0712	-6,1384597	-0,43687769	984,24	POLR2J4	RNA polymerase II subunit J4, pseudogene
3275	2,60E-22	2,16E+01	8,09E-23	0,0444	-9,8332765	-0,43705695	4428,93	PRMT2	protein arginine methyltransferase 2
54991	5,72E-06	5,24E+00	3,21E-06	0,0939	-4,656781	-0,43706372	466,84	C1orf159	chromosome 1 open reading frame 159
93621	1,58E-23	2,28E+01	4,77E-24	0,0432	-10,1143214	-0,4371462	15459,85	MRFAP1	Morf4 family associated protein 1
6717	4,67E-17	1,63E+01	1,70E-17	0,0514	-8,5128405	-0,43734298	2135,65	SRI	sorcin
8336	9,74E-02	1,01E+00	7,85E-02	0,2487	-1,7594188	-0,43755472	50,13	H2AC17	H2A clustered histone 17
100505483	2,11E-01	6,76E-01	1,79E-01	0,3256	-1,3444491	-0,43769498	28,21	PRKAG2-AS	PRKAG2 antisense RNA 1
55810	4,42E-13	1,24E+01	1,82E-13	0,0595	-7,3610575	-0,43808758	1361,79	FOXJ2	forkhead box J2
54986	1,62E-04	3,79E+00	9,99E-05	0,1126	-3,8907736	-0,43811173	254,8	ULK4	unc-51 like kinase 4
23191	8,68E-25	2,41E+01	2,53E-25	0,0422	-10,3981778	-0,43836889	5911,37	CYFIP1	cytoplasmic FMR1 interacting protein 1
79098	9,46E-02	1,02E+00	7,61E-02	0,2472	-1,7739933	-0,43848987	49,49	C1orf116	chromosome 1 open reading frame 116
65083	3,33E-16	1,55E+01	1,24E-16	0,053	-8,279036	-0,43850634	5532,19	NOL6	nucleolar protein 6
29888	3,78E-19	1,84E+01	1,29E-19	0,0484	-9,0613239	-0,43850643	6015,7	STRN4	striatin 4
440574	1,21E-12	1,19E+01	5,08E-13	0,0607	-7,2232299	-0,43858109	1630,19	MICOS10	mitochondrial contact site and cristae organizing system subunit 10
7203	4,81E-36	3,53E+01	1,05E-36	0,0347	-12,6548389	-0,43871643	26911,58	CCT3	chaperonin containing TCP1 subunit 3
102465666	2,86E-01	5,44E-01	2,48E-01	0,3803	-1,1546012	-0,43903998	22,07	MIR7109	microRNA 7109
2810	5,11E-15	1,43E+01	1,98E-15	0,0553	-7,9425812	-0,43906621	3237,2	SFN	stratifin
339175	3,23E-15	1,45E+01	1,25E-15	0,0549	-7,9998541	-0,43916161	1641,01	METTL2A	methyltransferase 2A, methylcytidine
105374060	1,16E-01	9,36E-01	9,41E-02	0,2624	-1,673942	-0,43926597	42,25	LOC105374(	uncharacterized LOC105374060
23505	1,75E-25	2,48E+01	5,01E-26	0,0416	-10,5512104	-0,43935635	5734,44	TMEM131	transmembrane protein 131
22929	3,23E-21	2,05E+01	1,04E-21	0,0459	-9,5730771	-0,43957387	3918,14	SEPHS1	selenophosphate synthetase 1
84749	2,18E-05	4,66E+00	1,27E-05	0,1007	-4,3654394	-0,43961444	349,36	USP30	ubiquitin specific peptidase 30
9825	5,45E-09	8,26E+00	2,63E-09	0,0739	-5,9532984	-0,43968154	827,32	SPATA2	spermatogenesis associated 2
100505624	1,83E-06	5,74E+00	9,98E-07	0,0899	-4,8919631	-0,4397186	433,16	GTF3C2-AS	GTF3C2 antisense RNA 1
2976	1,07E-20	2,00E+01	3,49E-21	0,0466	-9,4468623	-0,43980546	3723,7	GTF3C2	general transcription factor IIIC subunit 2
114971	1,30E-17	1,69E+01	4,64E-18	0,0508	-8,661962	-0,44010481	2215,9	PTPMT1	protein tyrosine phosphatase mitochondrial 1
255512	3,91E-01	4,08E-01	3,49E-01	0,4708	-0,935682	-0,44051323	13,94	TOLLIP-DT	TOLLIP divergent transcript
102723870	2,04E-01	6,90E-01	1,73E-01	0,3232	-1,3633497	-0,44065571	30,1	LOC102723(	uncharacterized LOC102723870
100507303	7,67E-03	2,12E+00	5,44E-03	0,1586	-2,7797808	-0,44083679	119,47	SNHG19	small nucleolar RNA host gene 19
91949	1,85E-08	7,73E+00	9,14E-09	0,0767	-5,7459371	-0,44088989	720,77	COG7	component of oligomeric golgi complex 7
9929	2,64E-25	2,46E+01	7,61E-26	0,042	-10,5119803	-0,44102957	5202,03	JOSD1	Josephin domain containing 1
414208	9,00E-03	2,05E+00	6,43E-03	0,1619	-2,7249583	-0,44119907	121,79	ZNF32-AS2	ZNF32 antisense RNA 2
4176	2,09E-27	2,67E+01	5,68E-28	0,0403	-10,9641656	-0,44140985	13105,23	MCM7	minichromosome maintenance complex component 7
831	8,98E-16	1,50E+01	3,40E-16	0,0541	-8,1583213	-0,44155266	14673,2	CAST	calpastatin
11161	1,22E-11	1,09E+01	5,27E-12	0,0641	-6,8979773	-0,44185223	1098,77	ERG28	ergosterol biosynthesis 28 homolog
11261	1,69E-20	1,98E+01	5,54E-21	0,047	-9,3984265	-0,44187996	3745,84	CHP1	calcineurin like EF-hand protein 1
399473	3,42E-10	9,47E+00	1,56E-10	0,0691	-6,3990118	-0,44193549	876,81	SPRED3	sprouty related EVH1 domain containing 3
91445	5,61E-14	1,33E+01	2,25E-14	0,0579	-7,6355452	-0,44212988	1627,07	RNF185	ring finger protein 185
25946	3,35E-04	3,47E+00	2,12E-04	0,1194	-3,7042895	-0,44226571	221,79	ZNF385A	zinc finger protein 385A
29928	2,15E-16	1,57E+01	7,99E-17	0,0531	-8,3313914	-0,44249388	1803,45	TIMM22	translocase of inner mitochondrial membrane 22
23371	7,52E-13	1,21E+01	3,13E-13	0,0607	-7,2888526	-0,44250518	1660,32	TNS2	tensin 2
23013	7,35E-23	2,21E+01	2,25E-23	0,0444	-9,9611808	-0,44254346	4851,07	SPEN	spen family transcriptional repressor
414236	7,72E-24	2,31E+01	2,31E-24	0,0435	-10,1851516	-0,44264711	3573,18	C10orf55	chromosome 10 putative open reading frame 55
317781	2,37E-11	1,06E+01	1,04E-11	0,0651	-6,8008045	-0,44297662	973,87	DDX51	DEAD-box helicase 51
144097	5,35E-15	1,43E+01	2,08E-15	0,0558	-7,9366568	-0,4429768	1858,39	SPINDOC	spindlin interactor and repressor of chromatin binding
25766	1,94E-06	5,71E+00	1,06E-06	0,0908	-4,8795751	-0,44299067	437,69	PRPF40B	pre-mRNA processing factor 40 homolog B
84265	1,43E-09	8,84E+00	6,74E-10	0,0718	-6,1721354	-0,44300743	1218,4	POLR3GL	RNA polymerase III subunit GL
9567	3,26E-17	1,65E+01	1,18E-17	0,0518	-8,5552722	-0,44302954	2532,18	GTPBP1	GTP binding protein 1
29904	2,28E-11	1,06E+01	1,00E-11	0,0651	-6,8065343	-0,44317065	1051,02	EEF2K	eukaryotic elongation factor 2 kinase
101926895	1,77E-01	7,52E-01	1,48E-01	0,3063	-1,4469243	-0,44320624	31,47	CRTC3-AS1	CRTC3 antisense RNA 1
57827	2,57E-14	1,36E+01	1,02E-14	0,0573	-7,7371358	-0,4433321	1603,75	C6orf47	chromosome 6 open reading frame 47
10370	8,00E-21	2,01E+01	2,60E-21	0,0468	-9,4775646	-0,44347054	3894,55	CITED2	Cbp/p300 interacting transactivator with Glu/Asp rich carboxy-terminal domain 2
65123	1,93E-21	2,07E+01	6,18E-22	0,0461	-9,626524	-0,443517	3433,12	INTS3	integrator complex subunit 3
105371481	1,84E-04	3,74E+00	1,14E-04	0,115	-3,8582885	-0,44368279	254,73	LOC105371(	uncharacterized LOC105371481
64960	9,14E-18	1,70E+01	3,25E-18	0,051	-8,702502	-0,44398854	3705	MRPS15	mitochondrial ribosomal protein S15
740	1,55E-24	2,38E+01	4,56E-25	0,0429	-10,3418067	-0,44408165	4958,45	MRPL49	mitochondrial ribosomal protein L49
9783	5,69E-03	2,24E+00	3,98E-03	0,1542	-2,8795788	-0,44409371	149,01	RIMS3	regulating synaptic membrane exocytosis 3
64979	7,26E-14	1,31E+01	2,92E-14	0,0584	-7,6019406	-0,44412514	1967,64	MRPL36	mitochondrial ribosomal protein L36
54059	1,52E-09	8,82E+00	7,17E-10	0,0721	-6,162206	-0,4442731	768,89	YBEY	ybeY metalloendoribonuclease
79369	1,92E-12	1,17E+01	8,11E-13	0,0621	-7,1592242	-0,44436694	1229,76	B3GNT4	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 4
9978	1,90E-16	1,57E+01	7,04E-17	0,0533	-8,346313	-0,44479644	1968,52	RBX1	ring-box 1
5603	3,69E-25	2,44E+01	1,07E-25	0,0424	-10,4802041	-0,44484382	4025,55	MAPK13	mitogen-activated protein kinase 13
113230	7,06E-02	1,15E+00	5,59E-02	0,2327	-1,9121054	-0,44497767	54,95	MISP3	MISP family member 3
107986599	1,12E-04	3,95E+00	6,80E-05	0,1117	-3,9831813	-0,44499412	273,29	LOC107986(	uncharacterized LOC107986599
91012	2,30E-11	1,06E+01	1,01E-11	0,0654	-6,8055659	-0,44519812	1088,95	CERS5	ceramide synthase 5
55509	6,73E-03	2,17E+00	4,75E-03	0,1578	-2,8235738	-0,4455235	124,72	BATF3	basic leucine zipper ATF-like transcription factor 3
6448	2,44E-11	1,06E+01	1,07E-11	0,0656	-6,7969413	-0,44556381	1350,95	SGSH	N-sulfoglucosamine sulfohydrolase
84617	1,90E-31	3,07E+01	4,66E-32	0,0378	-11,7850287	-0,44557994	15222,15	TUBB6	tubulin beta 6 class V
1363	9,99E-10	9,00E+00	4,67E-10	0,0716	-6,2299061	-0,44581363	835,01	CPE	carboxypeptidase E
51008	9,50E-18	1,70E+01	3,38E-18	0,0513	-8,6979907	-0,44612029	2068,81	ASCC1	activating signal cointegrator 1 complex subunit 1
9397	3,83E-17	1,64E+01	1,39E-17	0,0523	-8,5361832	-0,44619816	2275,44	NMT2	N-myristoyltransferase 2
80305	1,20E-09	8,92E+00	5,61E-10	0,072	-6,201047	-0,44623799	1047,46	TRABD	TraB domain containing
1445	1,08E-14	1,40E+01	4,21E-15	0,0569	-7,848392	-0,44625555	3138,89	CSK	C-terminal Src kinase
105376222	4,26E-02	1,37E+00	3,27E-02	0,2091	-2,136157	-0,44662193	70,73	LOC105376(	uncharacterized LOC105376222
155435	9,83E-21	2,00E+01	3,20E-21	0,0473	-9,4558655	-0,4469242	2960,88	RBM33	RNA binding motif protein 33
51192	1,16E-10	9,94E+00	5,21E-11	0,0681	-6,5647008	-0,44693492	898,71	CKLF	chemokine like factor
100506736	2,39E-01	6,22E-01	2,05E-01	0,3525	-1,2681479	-0,44705781	28,36	SLFN12L	schlafen family member 12 like
144193	9,70E-03	2,01E+00	6,95E-03	0,1657	-2,6990785	-0,44710879	118,37	AMDHD1	amidohydrolase domain containing 1
22	9,54E-12	1,10E+01	4,11E-12	0,0645	-6,9332169	-0,44732981	1202,69	ABCB7	ATP binding cassette subfamily B member 7
1478	4,79E-21	2,03E+01	1,55E-21	0,0469	-9,5318066	-0,4473605	2674,87	CSTF2	cleavage stimulation factor subunit 2
100302210	1,48E-01	8,30E-01	1,22E-01	0,2895	-1,5455599	-0,44746998	35,03	MIR1909	microRNA 1909
2235	2,39E-12	1,16E+01	1,01E-12	0,0628	-7,1292758	-0,44747975	1207,25	FECH	ferrochelatase
80830	1,15E-16	1,59E+01	4,23E-17	0,0532	-8,4063613	-0,44753796	1768,77	APOL6	apolipoprotein L6
100529251	1,25E-10	9,90E+00	5,63E-11	0,0683	-6,5533406	-0,44787906	868,75	CKLF-CMTM	CKLF-CMTM1 readthrough
11243	1,49E-14	1,38E+01	5,85E-15	0,0574	-7,8072154	-0,44791055	1429,54	PMF1	polyamine modulated factor 1
100286844	6,90E-02	1,16E+00	5,45E-02	0,2329	-1,9231406	-0,4479365	54,77	BCDIN3D-AS	BCDIN3D antisense RNA 1
107987175	2,38E-04	3,62E+00	1,49E-04	0,1182	-3,7925963	-0,44814163	242,07	LOC107987	replaced by ID 140465
7402	4,70E-17	1,63E+01	1,71E-17	0,0527	-8,5121175	-0,44840873	4051,89	UTRN	utrophin
100500888	1,59E-10	9,80E+00	7,18E-11	0,0688	-6,5168104	-0,44843678	870,1	MIR3940	microRNA 3940
1513	4,26E-02	1,37E+00	3,27E-02	0,2099	-2,1361883	-0,4484614	74,94	CTSK	cathepsin K
5306	6,04E-27	2,62E+01	1,66E-27	0,0413	-10,866581	-0,4485225	5729,83	PITPNA	phosphatidylinositol transfer protein alpha

3092	2,45E-07	6,61E+00	1,28E-07	0,0849	-5,2819586	-0,44854805	495,42	HIP1	huntingtin interacting protein 1
79595	5,49E-19	1,83E+01	1,88E-19	0,0497	-9,0201407	-0,44867473	2839,72	SAP130	Sin3A associated protein 130
51154	1,17E-24	2,39E+01	3,41E-25	0,0433	-10,3695997	-0,44869717	4980,2	MRTO4	MRT4 homolog, ribosome maturation factor
105371871	4,63E-01	3,34E-01	4,21E-01	0,5581	-0,8043108	-0,44885703	9,23	LOC105371871	
259307	2,56E-07	6,59E+00	1,33E-07	0,0851	-5,2742638	-0,44893874	480,01	IL4I1	interleukin 4 induced 1
2665	1,85E-31	3,07E+01	4,54E-32	0,0381	-11,7873431	-0,44920297	18419,26	GDI2	GDP dissociation inhibitor 2
79147	2,83E-11	1,05E+01	1,24E-11	0,0663	-6,7751592	-0,44942784	1022,39	FKRP	fukutin related protein
56971	1,21E-02	1,92E+00	8,73E-03	0,1714	-2,6225978	-0,44959706	112,65	CEACAM19	CEA cell adhesion molecule 19
54707	5,07E-15	1,43E+01	1,97E-15	0,0566	-7,9434222	-0,44964826	1575,82	GPN2	GPN-loop GTPase 2
107984220	2,40E-01	6,20E-01	2,05E-01	0,3551	-1,2670583	-0,44995563	31,37	LOC107984220	uncharacterized LOC107984220
56948	6,00E-11	1,02E+01	2,67E-11	0,0676	-6,6637898	-0,45028549	890,04	SDR39U1	short chain dehydrogenase/reductase family 39U member 1
1742	8,27E-13	1,21E+01	3,44E-13	0,0619	-7,2759535	-0,45040849	1123,5	DLG4	discs large MAGUK scaffold protein 4
89958	3,94E-20	1,94E+01	1,31E-20	0,0484	-9,3077586	-0,45093461	2332,53	SAPCD2	suppressor APC domain containing 2
104355135	4,50E-01	3,47E-01	4,08E-01	0,5459	-0,8267503	-0,45130498	9,97	LINC00431	long intergenic non-protein coding RNA 431
9696	7,22E-05	4,14E+00	4,34E-05	0,1104	-4,0888046	-0,45152406	314,65	CROCC	ciliary rootlet coiled-coil, rootletin
127544	2,16E-14	1,37E+01	8,56E-15	0,0582	-7,7590763	-0,45156316	1499,79	RNF19B	ring finger protein 19B
6047	4,03E-26	2,54E+01	1,13E-26	0,0423	-10,6899141	-0,45165791	6188,21	RNF4	ring finger protein 4
105370447	2,21E-05	4,66E+00	1,29E-05	0,1036	-4,362549	-0,45179962	299,4	LOC105370447	uncharacterized LOC105370447
388524	2,25E-19	1,86E+01	7,61E-20	0,0496	-9,1185383	-0,45225145	2697,28	RPSA2	ribosomal protein SA 2
7841	5,09E-17	1,63E+01	1,85E-17	0,0532	-8,5029294	-0,45245068	4023,84	MOGS	mannosyl-oligosaccharide glucosidase
133396	4,58E-16	1,53E+01	1,71E-16	0,0549	-8,2405182	-0,45260569	1531,49	IL31RA	interleukin 31 receptor A
80273	1,04E-25	2,50E+01	2,96E-26	0,0427	-10,6006087	-0,45267261	4475,52	GRPEL1	GrpE like 1, mitochondrial
10253	3,32E-25	2,45E+01	9,58E-26	0,0432	-10,4902345	-0,4526778	5064,76	SPRY2	sprouty RTK signaling antagonist 2
441072	5,36E-02	1,27E+00	4,17E-02	0,2226	-2,0362573	-0,4532319	61,05	IL6ST-DT	IL6ST divergent transcript
90632	2,49E-01	6,04E-01	2,13E-01	0,3643	-1,2443336	-0,4532518	23,47	LINC00473	long intergenic non-protein coding RNA 473
114785	5,18E-11	1,03E+01	2,30E-11	0,0678	-6,6856525	-0,45354248	1265,8	MBD6	methyl-CpG binding domain protein 6
107985921	2,79E-05	4,55E+00	1,63E-05	0,1053	-4,3100184	-0,45384465	329,26	LOC107985921	
8969	8,00E-02	1,10E+00	6,37E-02	0,2451	-1,8546139	-0,45452558	50,73	H2AC11	H2A clustered histone 11
129138	1,97E-09	8,71E+00	9,34E-10	0,0744	-6,120301	-0,45515213	678,53	ANKRD54	ankyrin repeat domain 54
132160	4,48E-07	6,35E+00	2,37E-07	0,0881	-5,1677891	-0,45515346	445,45	PPM1M	protein phosphatase, Mg2+/Mn2+ dependent 1M
314	2,85E-02	1,55E+00	2,14E-02	0,1982	-2,3007341	-0,45590929	80,57	AOC2	amine oxidase copper containing 2
8834	3,32E-15	1,45E+01	1,28E-15	0,057	-7,9965783	-0,45594669	1525,75	TMEM11	transmembrane protein 11
728229	3,92E-01	4,07E-01	3,50E-01	0,4883	-0,9336983	-0,45595924	12,4	TMEM191B	transmembrane protein 191B
47	2,86E-35	3,45E+01	6,38E-36	0,0364	-12,5124845	-0,45597893	20287,89	ACLY	ATP citrate lyase
127262	1,84E-17	1,67E+01	6,61E-18	0,0529	-8,6215518	-0,4561977	2108,44	TPRG1L	tumor protein p63 regulated 1 like
107984329	1,44E-02	1,84E+00	1,05E-02	0,1784	-2,559124	-0,45648108	93,52	LOC107984329	
6257	1,18E-25	2,49E+01	3,37E-26	0,0431	-10,5884821	-0,45669278	4674,39	RXRB	retinoid X receptor beta
10251	4,91E-02	1,31E+00	3,81E-02	0,2204	-2,0741471	-0,45712977	63,49	SPRY3	sprouty RTK signaling antagonist 3
24147	5,46E-15	1,43E+01	2,12E-15	0,0576	-7,9342236	-0,45722103	1810,01	FJX1	four-jointed box kinase 1
8877	2,80E-04	3,55E+00	1,76E-04	0,1219	-3,7509895	-0,45728856	397,86	SPHK1	sphingosine kinase 1
29095	5,38E-12	1,13E+01	2,30E-12	0,0652	-7,0148363	-0,45749825	1014,55	ORMDL2	ORMDL sphingolipid biosynthesis regulator 2
54855	3,63E-12	1,14E+01	1,54E-12	0,0648	-7,0704723	-0,45791483	982,8	TENT5C	terminal nucleotidyltransferase 5C
140685	2,69E-03	2,57E+00	1,83E-03	0,1469	-3,1164556	-0,45795061	142,94	ZBTB46	zinc finger and BTB domain containing 46
105375751	3,49E-02	1,46E+00	2,66E-02	0,2065	-2,2180208	-0,45797981	70,39	LOC105375751	uncharacterized LOC105375751
23043	7,75E-06	5,11E+00	4,39E-06	0,0998	-4,5920043	-0,45822729	336,78	TNIK	TRAF2 and NCK interacting kinase
25764	9,50E-12	1,10E+01	4,09E-12	0,0661	-6,9339562	-0,45828845	1374,46	HYPK	huntingtin interacting protein K
100996717	2,48E-07	6,61E+00	1,29E-07	0,0868	-5,2798745	-0,45829842	464,61	NOTCH2NLC	notch 2 N-terminal like C
83660	4,43E-09	8,35E+00	2,13E-09	0,0765	-5,9877965	-0,45836561	701,2	TLN2	talin 2
10632	5,37E-25	2,43E+01	1,56E-25	0,0439	-10,444056	-0,45889088	10027,19	ATP5MG	ATP synthase membrane subunit g
7955	3,25E-01	4,88E-01	2,86E-01	0,4301	-1,0670611	-0,45894069	15,62	RNF217-AS1	RNF217 antisense RNA 1 (head to head)
5673	2,40E-01	6,20E-01	2,05E-01	0,3626	-1,2660387	-0,45903092	22,5	PSG5	pregnancy specific beta-1-glycoprotein 5
665	1,83E-19	1,87E+01	6,19E-20	0,0502	-9,1409602	-0,45909696	5327,27	BNIP3L	BCL2 interacting protein 3 like
6647	6,95E-30	2,92E+01	1,77E-30	0,04	-11,4747081	-0,45921085	9520,17	SOD1	superoxide dismutase 1
81704	3,38E-01	4,71E-01	2,98E-01	0,4411	-1,041258	-0,45930548	15,37	DOCK8	dedicator of cytokinesis 8
51271	2,08E-19	1,87E+01	7,04E-20	0,0504	-9,1270548	-0,45957305	3777,35	UBAP1	ubiquitin associated protein 1
136853	2,75E-01	5,61E-01	2,38E-01	0,3894	-1,1811737	-0,45992217	19,21	SSC4D	scavenger receptor cysteine rich family member with 4 domains
63891	2,42E-15	1,46E+01	9,30E-16	0,0572	-8,0358118	-0,45992226	1905,72	RNF123	ring finger protein 123
90196	9,57E-18	1,70E+01	3,40E-18	0,0529	-8,6971237	-0,46030445	2101,76	SYS1	SYS1 golgi trafficking protein
29777	7,63E-18	1,71E+01	2,70E-18	0,0528	-8,7233997	-0,46055706	2384,36	ABT1	activator of basal transcription 1
1809	3,77E-04	3,42E+00	2,40E-04	0,1254	-3,6731623	-0,46065799	201,37	DPYSL3	dihydropyrimidinase like 3
2780	2,96E-01	5,29E-01	2,57E-01	0,4068	-1,1327118	-0,46074555	18,08	GNAT2	G protein subunit alpha transducin 2
79142	3,04E-23	2,25E+01	9,23E-24	0,0459	-10,0494975	-0,4608006	3283,42	PHF23	PHD finger protein 23
63894	4,60E-15	1,43E+01	1,78E-15	0,0579	-7,9556967	-0,46090443	1521,68	VIPAS39	VPS33B interacting protein, apical-basolateral polarity regulator, spe-39 homolog
107985200	2,51E-01	6,00E-01	2,16E-01	0,3727	-1,2374449	-0,46120706	21,67	LOC107985200	uncharacterized LOC107985200
26259	5,65E-20	1,92E+01	1,88E-20	0,0498	-9,2688898	-0,46132769	2212,64	FBXW8	F-box and WD repeat domain containing 8
29093	2,54E-17	1,66E+01	9,13E-18	0,0538	-8,5843631	-0,461602	1791,38	MRPL22	mitochondrial ribosomal protein L22
89910	3,17E-23	2,25E+01	9,62E-24	0,046	-10,04542	-0,46166601	2879,8	UBE3B	ubiquitin protein ligase E3B
283345	1,43E-02	1,84E+00	1,04E-02	0,1801	-2,5629862	-0,46168776	92,35	RPL13P5	ribosomal protein L13 pseudogene 5
25960	3,00E-03	2,52E+00	2,04E-03	0,1498	-3,0836383	-0,46185551	142,66	ADGRA2	adhesion G protein-coupled receptor A2
4288	3,58E-13	1,24E+01	1,47E-13	0,0626	-7,3898446	-0,46228374	32628,12	MKI67	marker of proliferation Ki-67
51081	3,16E-24	2,35E+01	9,39E-25	0,045	-10,2723376	-0,46232272	3997,85	MRPS7	mitochondrial ribosomal protein S7
6201	4,38E-33	3,24E+01	1,03E-33	0,0382	-12,1019254	-0,46246807	34137,53	RPS7	ribosomal protein S7
4512	3,98E-33	3,24E+01	9,36E-34	0,0382	-12,1099426	-0,46252371	343119,02	COX1	cytochrome c oxidase subunit I
10487	7,19E-35	3,41E+01	1,62E-35	0,0372	-12,438245	-0,46292249	25390,22	CAP1	cyclase associated actin cytoskeleton regulatory protein 1
29797	1,96E-01	7,08E-01	1,65E-01	0,3336	-1,3879379	-0,46296767	25,97	POM121L8P	POM121 transmembrane nucleoporin like 8, pseudogene
131583	3,89E-09	8,41E+00	1,86E-09	0,0771	-6,0091816	-0,46303315	708,55	FAM43A	family with sequence similarity 43 member A
286333	2,56E-13	1,26E+01	1,04E-13	0,0623	-7,435306	-0,46303568	1052,43	FAM225A	family with sequence similarity 225 member A
92170	7,63E-12	1,11E+01	3,27E-12	0,0665	-6,9654356	-0,4630779	1015,57	MTG1	mitochondrial ribosome associated GTPase 1
58515	1,24E-10	9,91E+00	5,58E-11	0,0707	-6,5544854	-0,46342181	1051,17	SELENOK	selenoprotein K
21	2,06E-16	1,57E+01	7,65E-17	0,0556	-8,336532	-0,46348202	2056,81	ABCA3	ATP binding cassette subfamily A member 3
3720	2,12E-24	2,37E+01	6,26E-25	0,045	-10,3113951	-0,4635552	3432,76	JARID2	jumonji and AT-rich interaction domain containing 2
22994	8,36E-07	6,08E+00	4,48E-07	0,0919	-5,0473197	-0,46369909	542,21	CEP131	centrosomal protein 131
100507747	1,03E-01	9,87E-01	8,32E-02	0,2677	-1,7322874	-0,46370058	42,78	C13orf46	chromosome 13 open reading frame 46
687	8,22E-10	9,09E+00	3,83E-10	0,0741	-6,2609702	-0,46395675	759,69	KLF9	KLF transcription factor 9
10826	1,73E-09	8,76E+00	8,18E-10	0,0756	-6,1413839	-0,46445417	803,45	FAXDC2	fatty acid hydroxylase domain containing 2
56997	4,05E-13	1,24E+01	1,67E-13	0,063	-7,3730094	-0,46451971	1144,16	COQ8A	coenzyme Q8A
2348	2,34E-02	1,63E+00	1,74E-02	0,1954	-2,3785451	-0,46486221	82,43	FOLR1	folate receptor alpha
10577	1,31E-25	2,49E+01	3,74E-26	0,044	-10,5786139	-0,46503835	4226,78	NPC2	NPC intracellular cholesterol transporter 2
5687	2,13E-27	2,67E+01	5,79E-28	0,0424	-10,9624339	-0,46511725	10806,03	PSMA6	proteasome 20S subunit alpha 6
6470	7,32E-17	1,61E+01	2,68E-17	0,055	-8,4599427	-0,46514611	1593,88	SHMT1	serine hydroxymethyltransferase 1
6310	3,99E-15	1,44E+01	1,54E-15	0,0583	-7,9734571	-0,4652177	1400,5	ATXN1	ataxin 1
105376106	3,34E-02	1,48E+00	2,53E-02	0,2081	-2,2363452	-0,46529144	72,54	LOC105376106	uncharacterized LOC105376106
7043	1,58E-02	1,80E+00	1,15E-02	0,1843	-2,5256753	-0,46548418	87,27	TGFB3	transforming growth factor beta 3
65987	1,25E-09	8,90E+00	5,86E-10	0,0752	-6,1941087	-0,46567286	729,39	KCTD14	potassium channel tetramerization domain containing 14
5037	5,97E-32	3,12E+01	1,44E-32	0,0392	-11,883506	-0,46582229	10226,01	PEBP1	phosphatidylethanolamine binding protein 1
91133	3,66E-01	4,37E-01	3,25E-01	0,4737	-0,9834798	-0,46582816	15,03	L3MBTL4	L3MBTL histone methyl-lysine binding protein 4
154313	4,47E-01	3,50E-01	4,06E-01	0,5602	-0,8315902	-0,46588941	9,65	CFAP206	cilia and flagella associated protein 206
84243	1,97E-15	1,47E+01	7,56E-16	0,0578	-8,061187	-0,46591949	1423,47	ZDHHC18	zinc finger DHHC-type palmitoyltransferase 18
51321	1,54E-28	2,78E+01	4,07E-29	0,0416	-11,2002545	-0,4659578	5546,57	AMZ2	archaelysin family metallopeptidase 2
22888	4,89E-08	7,31E+00	2,46E-08	0,0836	-5,5761019	-0,46601807	503,73	UBOX5	U-box domain containing 5
85453	4,86E-10	9,31E+00	2,24E-10	0,0735	-6,3439665	-0,46627424	820,78	TSPYL5	TSPY like 5
107984200	6,00E-04	3,22E+00	3,87E-04	0,1314	-3,548894	-0,46634874	201,23	LOC107984200	uncharacterized LOC107984200
192111	1,26E-16	1,59E+01	4,63E-17	0,0556	-8,3957142	-0,46640053	2394,06	PGAM5	PGAM family member 5, mitochondrial serine/threonine protein phosphatase
1318	4,99E-08	7,30E+00	2,51E-08	0,0837	-5,5726566	-0,46646597	514,59	SLC31A2	solute carrier family 31 member 2
100527943	1,51E-23	2,28E+01	4,55E-24	0,0461	-10,1189657	-0,46678195	2944,32	TGIF2-RAB5	TGIF2-RAB5IF readthrough
84062	3,70E-16	1,54E+01	1,38E-16	0,0565	-8,2663961	-0,46684956	1584,9	DTNBP1	dystrobrevin binding protein 1
100505758	1,20E-19	1,89E+01	4,03E-20	0,0508	-9,187199	-0,46686334	2028,58	PRMT5-AS1	PRMT5 antisense RNA 1
6165	6,66E-32	3,12E+01	1,61E-32	0,0394	-11,87412	-0,46725072	20707,65	RPL35A	ribosomal protein L35a
64776	4,16E-11	1,04E+01	1,84E-11	0,0696	-6,7183549	-0,46732553	892,48	CFAP68	cilia and flagella associated protein 68
102800317	3,62E-18	1,74E+01	1,27E-18	0,0531	-8,8082956	-0,46753582	2167,03	TPTEP2-CSI	TPTEP2-CSNK1E readthrough
64689	8,26E-16	1,51E+01	3,12E-16	0,0572	-8,1685696	-0,46758709	1572,99	GORASP1	golgi reassembly stacking protein 1
102465524	1,53E-01	8,15E-01	1,27E-01	0,3065	-1,5257339	-0,46765741	30,79	MIR6869	microRNA 6869
9711	1,21E-15	1,49E+01	4,59E-16	0,0576	-8,1219938	-0,46765982	1549,18	RUBCN	rubicon autophagy regulator
134147	3,48E-17	1,65E+01	1,26E-17	0,0547	-8,5475482	-0,46770394	1932,71	CMBL	carboxymethylenebutenolidase homolog
2801	3,91E-27	2,64E+01	1,07E-27	0,0429	-10,9067592	-0,4677774	4655	GOLGA2	golgin A2
10330	6,53E-17	1,62E+01	2,38E-17	0,0552	-8,4735097	-0,46778657	1551,59	CNPY2	canopy FGF signaling regulator 2
85379	1,41E-19	1,89E+01	4,75E-20	0,051	-9,1695924	-0,46789917	2002,58	KIAA1671	KIAA1671
105376527	3,05E-01	5,16E-01	2,67E-01	0,4215	-1,1101443	-0,46789954	16,32	STIM1-AS1	STIM1 antisense RNA 1
2687	1,10E-10	9,96E+00	4,96E-11	0,0712	-6,5722307	-0,46791331	1505,33	GGT5	gamma-glutamyltransferase 5
3371	1,36E-31	3,09E+01	3,31E-32	0,0396	-11,8138127	-0,46801381	12676,42	TNC	tenascin C

1856	4,41E-19	1,84E+01	1,50E-19	0,0517	-9,0443925	-0,46802717	2607,59	DVL2	dishevelled segment polarity protein 2
118980	1,18E-09	8,93E+00	5,55E-10	0,0755	-6,2025963	-0,46831679	639,54	SFXN2	sideroflexin 2
51076	2,15E-13	1,27E+01	8,74E-14	0,0628	-7,4586664	-0,46844801	1203,83	CUTC	cutC copper transporter
112268196	1,53E-05	4,82E+00	8,85E-06	0,1056	-4,4436303	-0,46918299	306,55	LOC112268196	
9791	8,27E-29	2,81E+01	2,16E-29	0,0417	-11,2561239	-0,46927264	6218,4	PTDSS1	phosphatidylserine synthase 1
54460	1,93E-13	1,27E+01	7,86E-14	0,0628	-7,4726393	-0,46929619	1156,4	MRPS21	mitochondrial ribosomal protein S21
267004	3,45E-03	2,46E+00	2,37E-03	0,1544	-3,0395924	-0,46940992	130,66	PGBD3	piggyBac transposable element derived 3
5298	8,89E-21	2,01E+01	2,90E-21	0,0496	-9,4664291	-0,4694113	4159,93	PI4KB	phosphatidylinositol 4-kinase beta
285154	2,94E-01	5,32E-01	2,56E-01	0,4137	-1,1351044	-0,46954296	16,96	CYP1B1-AS	CYP1B1 antisense RNA 1
105377763	3,33E-01	4,78E-01	2,93E-01	0,4468	-1,0514258	-0,46976398	15,78	LOC105377	uncharacterized LOC105377763
107986588	8,16E-08	7,09E+00	4,15E-08	0,0857	-5,4842285	-0,46976949	510,95	EHMT2-AS1	EHMT2 and SLC44A4 antisense RNA 1
147463	6,08E-09	8,22E+00	2,94E-09	0,0792	-5,9351649	-0,46987126	603,54	ANKRD29	ankyrin repeat domain 29
5998	1,94E-18	1,77E+01	6,74E-19	0,0529	-8,8790678	-0,47005472	2116,64	RGS3	regulator of G protein signaling 3
283078	8,71E-03	2,06E+00	6,21E-03	0,1718	-2,7363846	-0,47015057	123,26	MKX	mohawk homeobox
2975	1,50E-27	2,68E+01	4,06E-28	0,0428	-10,9946424	-0,47033761	5047,98	GTF3C1	general transcription factor IIIC subunit 1
285905	5,52E-02	1,26E+00	4,31E-02	0,2326	-2,0229419	-0,47046372	54,77	INTS4P1	integrator complex subunit 4 pseudogene 1
5054	5,26E-22	2,13E+01	1,65E-22	0,0482	-9,76137	-0,47050563	17634,76	SERPINE1	serpin family E member 1
9739	1,51E-18	1,78E+01	5,22E-19	0,0528	-8,9075211	-0,47058136	2059,96	SETD1A	SET domain containing 1A, histone lysine methyltransferase
4798	3,55E-22	2,14E+01	1,11E-22	0,048	-9,8015504	-0,47070181	2717,53	NFRKB	nuclear factor related to kappaB binding protein
51075	3,78E-29	2,84E+01	9,79E-30	0,0416	-11,3257194	-0,47072682	5766,4	TMX2	thioredoxin related transmembrane protein 2
286480	5,97E-05	4,22E+00	3,56E-05	0,1139	-4,134015	-0,47085147	249,75	UBE2E4P	ubiquitin conjugating enzyme E2 E4 pseudogene
80728	3,71E-11	1,04E+01	1,64E-11	0,0699	-6,7351709	-0,4709114	837,05	ARHGAP39	Rho GTPase activating protein 39
2354	6,12E-02	1,21E+00	4,80E-02	0,2382	-1,9774179	-0,4710052	59,06	FOSB	FosB proto-oncogene, AP-1 transcription factor subunit
100101267	1,21E-18	1,79E+01	4,18E-19	0,0528	-8,9321896	-0,4712478	3490,92	POM121C	POM121 transmembrane nucleoporin C
150365	2,14E-01	6,70E-01	1,82E-01	0,353	-1,334997	-0,47128239	25,36	MEI1	meiotic double-stranded break formation protein 1
25776	6,55E-12	1,12E+01	2,81E-12	0,0675	-6,9871129	-0,47147243	904,06	CBY1	chibby family member 1, beta catenin antagonist
619208	2,45E-03	2,61E+00	1,66E-03	0,1499	-3,1457441	-0,47152	143,89	FAM229B	family with sequence similarity 229 member B
23331	7,92E-11	1,01E+01	3,54E-11	0,0712	-6,622291	-0,47167648	969,2	TTC28	tetratricopeptide repeat domain 28
3038	1,38E-09	8,86E+00	6,51E-10	0,0764	-6,1776519	-0,47167997	635,34	HAS3	hyaluronan synthase 3
340544	1,00E-02	2,00E+00	7,17E-03	0,1755	-2,6886514	-0,47184426	98,91	MORF4L2-A	MORF4L2 antisense RNA 1
105375591	7,05E-02	1,15E+00	5,58E-02	0,2467	-1,9129411	-0,47195673	53,86	INSIG1-DT	INSIG1 divergent transcript
55709	9,45E-13	1,20E+01	3,94E-13	0,065	-7,2577072	-0,47205474	1055,84	KBTBD4	kelch repeat and BTB domain containing 4
1454	1,89E-18	1,77E+01	6,57E-19	0,0532	-8,881971	-0,47226514	2145,72	CSNK1E	casein kinase 1 epsilon
285961	4,20E-01	3,77E-01	3,78E-01	0,5363	-0,8810409	-0,47249665	10,66	SEPTIN7P9	septin 7 pseudogene 9
100131187	1,74E-03	2,76E+00	1,16E-03	0,1455	-3,2481685	-0,47257353	145,8	TSTD1	thiosulfate sulfurtransferase like domain containing 1
100132288	9,04E-02	1,04E+00	7,25E-02	0,2632	-1,7957862	-0,47257837	43,16	TEKT4P2	tektin 4 pseudogene 2
4700	5,69E-20	1,92E+01	1,89E-20	0,051	-9,2682185	-0,47280737	2130,66	NDUFA6	NADH:ubiquinone oxidoreductase subunit A6
1649	1,57E-10	9,80E+00	7,11E-11	0,0725	-6,518386	-0,47281974	776,41	DDIT3	DNA damage inducible transcript 3
6774	1,37E-35	3,49E+01	3,03E-36	0,0376	-12,5713575	-0,4728673	8628,35	STAT3	signal transducer and activator of transcription 3
8570	3,69E-35	3,44E+01	8,26E-36	0,0379	-12,4919641	-0,47287386	17681,99	KHSRP	KH-type splicing regulatory protein
22808	5,64E-07	6,25E+00	3,00E-07	0,0923	-5,1236046	-0,47287926	412,69	MRAS	muscle RAS oncogene homolog
102725180	1,22E-03	2,91E+00	8,04E-04	0,1411	-3,3514667	-0,47301085	158,94	LOC102725	collagen alpha-1(VII) chain
84329	3,44E-04	3,46E+00	2,17E-04	0,1279	-3,697891	-0,47303416	191,86	HVCN1	hydrogen voltage gated channel 1
132299	7,62E-24	2,31E+01	2,28E-24	0,0464	-10,1864434	-0,47306699	3126	OCIAD2	OCIA domain containing 2
55833	1,78E-24	2,37E+01	5,24E-25	0,0458	-10,3285134	-0,47321022	5516,4	UBAP2	ubiquitin associated protein 2
6450	6,35E-02	1,20E+00	4,99E-02	0,2413	-1,9611164	-0,47327301	51,51	SH3BGR	SH3 domain binding glutamate rich protein
23389	1,89E-22	2,17E+01	5,85E-23	0,048	-9,8658971	-0,47330825	3423,84	MED13L	mediator complex subunit 13L
83742	3,73E-15	1,44E+01	1,44E-15	0,0593	-7,9820743	-0,47354864	1413,87	MARVELD1	MARVEL domain containing 1
23221	2,99E-13	1,25E+01	1,23E-13	0,0639	-7,4140335	-0,47355651	1292,22	RHOBTB2	Rho related BTB domain containing 2
29890	3,95E-21	2,04E+01	1,27E-21	0,0496	-9,5520079	-0,47361316	3574,29	RBM15B	RNA binding motif protein 15B
10597	1,12E-06	5,95E+00	6,04E-07	0,0949	-4,9900793	-0,47374615	402,53	TRAPPC2B	trafficking protein particle complex subunit 2B
7009	1,04E-31	3,10E+01	2,52E-32	0,04	-11,8367459	-0,47403797	25543,38	TMBIM6	transmembrane BAX inhibitor motif containing 6
6566	2,17E-01	6,64E-01	1,85E-01	0,3573	-1,3267282	-0,47404228	23,32	SLC16A1	solute carrier family 16 member 1
93974	3,92E-27	2,64E+01	1,07E-27	0,0435	-10,9065327	-0,47404674	4188,88	ATP5IF1	ATP synthase inhibitory factor subunit 1
8314	3,72E-25	2,44E+01	1,08E-25	0,0452	-10,4791817	-0,47406228	5490,83	BAP1	BRCA1 associated protein 1
84296	1,72E-22	2,18E+01	5,33E-23	0,048	-9,8751576	-0,47411823	3397,26	GINS4	GINS complex subunit 4
84320	1,29E-21	2,09E+01	4,10E-22	0,0491	-9,6686371	-0,47434828	2771,24	ACBD6	acyl-CoA binding domain containing 6
518	2,19E-16	1,57E+01	8,13E-17	0,057	-8,3293131	-0,47442472	5527,62	ATP5MC3	ATP synthase membrane subunit c locus 3
4833	6,69E-13	1,22E+01	2,77E-13	0,065	-7,3049334	-0,47481703	1410,11	NME4	NME/NM23 nucleoside diphosphate kinase 4
28999	1,14E-02	1,94E+00	8,22E-03	0,1797	-2,6428561	-0,47488326	94,25	KLF15	KLF transcription factor 15
26528	1,17E-26	2,59E+01	3,24E-27	0,044	-10,8055346	-0,47499932	6006,07	DAZAP1	DAZ associated protein 1
56253	4,28E-02	1,37E+00	3,29E-02	0,2227	-2,1335781	-0,47505563	64,88	CRTAM	cytotoxic and regulatory T cell molecule
6709	1,23E-33	3,29E+01	2,86E-34	0,0389	-12,2067042	-0,47514814	24509,36	SPTAN1	spectrin alpha, non-erythrocytic 1
155061	2,32E-10	9,63E+00	1,05E-10	0,0736	-6,4589122	-0,47515689	808,8	ZNF746	zinc finger protein 746
284325	3,08E-20	1,95E+01	1,02E-20	0,0509	-9,334293	-0,47538941	2460,28	ACTMAP	actin maturation protease
7386	1,41E-25	2,49E+01	4,03E-26	0,045	-10,5716839	-0,47546477	5637,29	UQCRFS1	ubiquinol-cytochrome c reductase, Rieske iron-sulfur polypeptide 1
25792	7,75E-21	2,01E+01	2,52E-21	0,0502	-9,4810569	-0,47599282	7261,02	CIZ1	CDKN1A interacting zinc finger protein 1
8312	3,93E-14	1,34E+01	1,57E-14	0,062	-7,6819806	-0,47629803	1306,64	AXIN1	axin 1
54984	8,99E-11	1,00E+01	4,02E-11	0,0721	-6,6033055	-0,47638739	793,7	PINX1	PIN2 (TERF1) interacting telomerase inhibitor 1
649	1,23E-14	1,39E+01	4,85E-15	0,0609	-7,830851	-0,47683711	1318,03	BMP1	bone morphogenetic protein 1
9466	4,60E-16	1,53E+01	1,72E-16	0,0579	-8,2398052	-0,47692775	1369,42	IL27RA	interleukin 27 receptor subunit alpha
162417	1,14E-08	7,94E+00	5,59E-09	0,0818	-5,8287194	-0,47703126	609,97	NAGS	N-acetylglutamate synthase
100126338	6,02E-03	2,22E+00	4,22E-03	0,1669	-2,8609273	-0,47742383	108,68	MIR937	microRNA 937
164684	1,73E-03	2,76E+00	1,16E-03	0,147	-3,2487873	-0,47745936	146,26	WBP2NL	WBP2 N-terminal like
1951	3,27E-08	7,49E+00	1,63E-08	0,0846	-5,6472369	-0,47749292	503,56	CELSR3	cadherin EGF LAG seven-pass G-type receptor 3
105371060	4,06E-01	3,91E-01	3,65E-01	0,5271	-0,9062862	-0,47767509	10,91	LOC105371	uncharacterized LOC105371060
221092	6,13E-28	2,72E+01	1,64E-28	0,0431	-11,0759589	-0,47780058	6713,25	HNRNPUL2	heterogeneous nuclear ribonucleoprotein U like 2
149473	2,25E-05	4,65E+00	1,31E-05	0,1096	-4,3590182	-0,47788778	269,68	CCDC24	coiled-coil domain containing 24
7409	2,15E-01	6,68E-01	1,83E-01	0,3585	-1,3330409	-0,47794107	22,57	VAV1	vav guanine nucleotide exchange factor 1
117144	1,19E-04	3,92E+00	7,23E-05	0,1204	-3,9685586	-0,47796216	224,49	CATSPER1	cation channel sperm associated 1
7088	2,93E-25	2,45E+01	8,46E-26	0,0455	-10,5019579	-0,47812901	3073,64	TLE1	TLE family member 1, transcriptional corepressor
107986447	3,08E-01	5,11E-01	2,69E-01	0,433	-1,1044721	-0,47820285	17,11	PPIC-AS1	PPIC antisense RNA 1
54752	1,26E-01	9,00E-01	1,03E-01	0,2934	-1,6302618	-0,47824561	35,58	FNDC8	fibronectin type III domain containing 8
6128	4,88E-40	3,93E+01	9,77E-41	0,0358	-13,3643634	-0,47846249	50540,71	RPL6	ribosomal protein L6
2475	7,06E-31	3,02E+01	1,76E-31	0,041	-11,6727815	-0,47851175	5580,52	MTOR	mechanistic target of rapamycin kinase
50650	3,33E-12	1,15E+01	1,41E-12	0,0676	-7,0826182	-0,47873936	900,74	ARHGEF3	Rho guanine nucleotide exchange factor 3
79724	2,15E-12	1,17E+01	9,08E-13	0,067	-7,1437146	-0,47878934	1334,58	ZNF768	zinc finger protein 768
53918	5,67E-24	2,32E+01	1,69E-24	0,0469	-10,2153984	-0,47882678	2999,56	PELO	pelota mRNA surveillance and ribosome rescue factor
3151	3,51E-29	2,85E+01	9,08E-30	0,0423	-11,3322977	-0,47895342	19018,91	HMGN2	high mobility group nucleosomal binding domain 2
23361	4,40E-13	1,24E+01	1,81E-13	0,0651	-7,3618074	-0,47897421	1477,72	ZNF629	zinc finger protein 629
219293	9,95E-03	2,00E+00	7,13E-03	0,178	-2,6905615	-0,47904164	109,44	ATAD3C	ATPase family AAA domain containing 3C
105369312	2,65E-01	5,77E-01	2,29E-01	0,3985	-1,2029594	-0,47935072	18,68	LOC105369312	
10280	6,70E-31	3,02E+01	1,67E-31	0,0411	-11,6772986	-0,47943124	7150,16	SIGMAR1	sigma non-opioid intracellular receptor 1
9551	3,50E-19	1,85E+01	1,19E-19	0,0529	-9,0698972	-0,47944638	3800,46	ATP5MF	ATP synthase membrane subunit f
10557	1,10E-11	1,10E+01	4,73E-12	0,0694	-6,9134968	-0,47952566	805,06	RPP38	ribonuclease P/MRP subunit p38
55086	5,59E-04	3,25E+00	3,60E-04	0,1344	-3,5681178	-0,47964929	191,43	RADX	RPA1 related single stranded DNA binding protein, X-linked
57670	1,82E-12	1,17E+01	7,66E-13	0,067	-7,1671016	-0,4799538	911,19	KIAA1549	KIAA1549
4329	1,21E-10	9,92E+00	5,43E-11	0,0732	-6,5586078	-0,47999512	797,52	ALDH6A1	aldehyde dehydrogenase 6 family member A1
80178	7,97E-07	6,10E+00	4,27E-07	0,0949	-5,0565327	-0,48003029	370,87	TEDC2	tubulin epsilon and delta complex 2
7922	1,45E-38	3,78E+01	3,00E-39	0,0366	-13,1070032	-0,48012628	14239,62	SLC39A7	solute carrier family 39 member 7
23385	9,09E-36	3,50E+01	2,01E-36	0,0381	-12,6039943	-0,4801988	9946,62	NCSTN	nicastrin
467	9,89E-05	4,00E+00	6,00E-05	0,1197	-4,0128524	-0,48047158	247,22	ATF3	activating transcription factor 3
6139	9,39E-36	3,50E+01	2,07E-36	0,0381	-12,6014788	-0,4805586	12889,33	RPL17	ribosomal protein L17
100506844	4,57E-03	2,34E+00	3,18E-03	0,1629	-2,9502629	-0,48057777	114,17	GIHCG	GIHCG inhibitor of miR-200b/200a/429 expression
7190	6,43E-02	1,19E+00	5,06E-02	0,2458	-1,9551462	-0,48063016	50,01	HSP90B2P	heat shock protein 90 beta family member 2, pseudogene
5641	3,12E-26	2,55E+01	8,75E-27	0,0449	-10,7140323	-0,48064767	3258,27	LGMN	legumain
2885	6,72E-34	3,32E+01	1,55E-34	0,0392	-12,2565164	-0,480729	6255,91	GRB2	growth factor receptor bound protein 2
51019	1,08E-20	2,00E+01	3,53E-21	0,0509	-9,4457805	-0,48078848	1970,45	WASHC3	WASH complex subunit 3
399687	5,90E-26	2,52E+01	1,67E-26	0,0452	-10,6542499	-0,48116198	3541,83	MYO18A	myosin XVIIIA
29115	1,22E-23	2,29E+01	3,67E-24	0,0475	-10,1401552	-0,48133418	3703,12	SAP30BP	SAP30 binding protein
100289361	2,92E-01	5,35E-01	2,54E-01	0,4224	-1,1397429	-0,48142318	17,02	LOC100289	uncharacterized LOC100289361
154	2,74E-18	1,76E+01	9,60E-19	0,0545	-8,839669	-0,48166414	2799,37	ADRB2	adrenoceptor beta 2
50485	3,69E-14	1,34E+01	1,47E-14	0,0627	-7,6901394	-0,48188362	1242,57	SMARCAL1	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a like 1
1796	8,28E-11	1,01E+01	3,70E-11	0,0729	-6,6155525	-0,48199929	712,82	DOK1	docking protein 1
9034	4,02E-14	1,34E+01	1,60E-14	0,0628	-7,6790375	-0,48209649	1150,63	CCRL2	C-C motif chemokine receptor like 2
693149	2,61E-01	5,83E-01	2,25E-01	0,3973	-1,213343	-0,48210405	19,62	MIR564	microRNA 564
84271	1,19E-25	2,49E+01	3,40E-26	0,0455	-10,587635	-0,48213448	4540,46	POLDIP3	DNA polymerase delta interacting protein 3
8382	3,09E-01	5,10E-01	2,70E-01	0,4375	-1,102079	-0,4821922	15,45	NME5	NME/NM23 family member 5
79676	1,69E-08	7,77E+00	8,33E-09	0,0838	-5,761715	-0,48273206	634,24	OGFOD2	2-oxoglutarate and iron dependent oxygenase domain containing 2
106865373	1,07E-05	4,97E+00	6,10E-06	0,1067	-4,5228241	-0,48274297	294,18	GET1-SH3B	GET1-SH3BGR readthrough

8897	2,91E-17	1,65E+01	1,05E-17	0,0563	-8,5684813	-0,4828107	1654,96	MTMR3	myotubularin related protein 3
63897	3,75E-22	2,14E+01	1,17E-22	0,0493	-9,7959964	-0,48289963	2184,16	HEATR6	HEAT repeat containing 6
112267864	7,40E-03	2,13E+00	5,24E-03	0,173	-2,7917295	-0,48294156	104,31	LOC112267864	
26267	1,30E-09	8,89E+00	6,09E-10	0,0781	-6,1880694	-0,48298809	632,32	FBXO10	F-box protein 10
114902	3,90E-01	4,09E-01	3,49E-01	0,5156	-0,937387	-0,48334046	11,03	C1QTNF5	C1q and TNF related 5
83552	3,90E-01	4,09E-01	3,49E-01	0,5156	-0,937387	-0,48334046	11,03	MFRP	membrane frizzled-related protein
9556	1,01E-23	2,30E+01	3,04E-24	0,0476	-10,1584224	-0,48386659	3334,91	ATP5MJ	ATP synthase membrane subunit j
567	1,95E-31	3,07E+01	4,78E-32	0,0411	-11,7828877	-0,48388908	30367,75	B2M	beta-2-microglobulin
54963	3,71E-17	1,64E+01	1,34E-17	0,0567	-8,5400722	-0,48396474	3143,9	UCKL1	uridine-cytidine kinase 1 like 1
9643	1,57E-25	2,48E+01	4,48E-26	0,0459	-10,56183	-0,48441804	15025,68	MORF4L2	mortality factor 4 like 2
339230	1,29E-17	1,69E+01	4,61E-18	0,0559	-8,6625743	-0,48451203	2054,38	CCDC137	coiled-coil domain containing 137
400685	4,53E-01	3,44E-01	4,12E-01	0,5908	-0,82045	-0,48468744	9,33	LINC01801	long intergenic non-protein coding RNA 1801
5327	9,28E-40	3,90E+01	1,87E-40	0,0364	-13,3159229	-0,48471425	18472,33	PLAT	plasminogen activator, tissue type
80326	2,85E-01	5,45E-01	2,47E-01	0,4188	-1,1576716	-0,48484189	18,18	WNT10A	Wnt family member 10A
79883	2,17E-01	6,64E-01	1,84E-01	0,3654	-1,3270475	-0,48493358	22,15	PODNL1	podocan like 1
26024	1,52E-11	1,08E+01	6,60E-12	0,0707	-6,8661038	-0,48510896	838,86	PTCD1	pentatricopeptide repeat domain 1
7430	6,92E-36	3,52E+01	1,52E-36	0,0384	-12,625742	-0,48526757	18574,48	EZR	ezrin
83743	1,39E-21	2,09E+01	4,42E-22	0,0502	-9,6608544	-0,48527092	3531,5	GRWD1	glutamate rich WD repeat containing 1
30815	1,77E-21	2,08E+01	5,66E-22	0,0504	-9,6355871	-0,48557174	2263,14	ST6GALNAC	ST6 N-acetylgalactosaminide alpha-2,6-sialyltransferase 6
107986876	4,10E-05	4,39E+00	2,43E-05	0,115	-4,221423	-0,48565719	246,44	LOC107986	uncharacterized LOC107986876
3664	1,30E-01	8,86E-01	1,06E-01	0,3009	-1,6146614	-0,48588233	34,9	IRF6	interferon regulatory factor 6
89797	2,74E-25	2,46E+01	7,88E-26	0,0462	-10,5086957	-0,48593543	5365,71	NAV2	neuron navigator 2
8568	4,39E-16	1,54E+01	1,64E-16	0,0589	-8,2456652	-0,48597366	2071,09	RRP1	ribosomal RNA processing 1
51372	2,17E-24	2,37E+01	6,39E-25	0,0471	-10,3094337	-0,48604426	4348,68	TMA7	translation machinery associated 7 homolog
54952	5,36E-14	1,33E+01	2,15E-14	0,0636	-7,6416151	-0,48618953	1060,68	TRNAU1AP	tRNA selenocysteine 1 associated protein 1
8637	1,40E-02	1,85E+00	1,02E-02	0,1892	-2,5704739	-0,4862953	88,32	EIF4EBP3	eukaryotic translation initiation factor 4E binding protein 3
26119	2,85E-16	1,55E+01	1,06E-16	0,0586	-8,2977245	-0,48638228	1430,97	LDLRAP1	low density lipoprotein receptor adaptor protein 1
4538	4,50E-21	2,03E+01	1,45E-21	0,051	-9,5383184	-0,48671912	246489,47	ND4	NADH dehydrogenase subunit 4
100128640	4,48E-02	1,35E+00	3,45E-02	0,2304	-2,1140548	-0,48704551	58,62	ACVR2B-AS	ACVR2B antisense RNA 1
55588	1,62E-25	2,48E+01	4,64E-26	0,0461	-10,5584429	-0,48722557	3057,25	MED29	mediator complex subunit 29
729375	1,16E-01	9,36E-01	9,42E-02	0,2912	-1,6734432	-0,48730446	35,79	FAM86HP	family with sequence similarity 86, member A pseudogene
55135	2,15E-16	1,57E+01	7,95E-17	0,0585	-8,3319119	-0,48734777	1869,08	WRAP53	WD repeat containing antisense to TP53
200150	5,61E-05	4,25E+00	3,34E-05	0,1175	-4,1487842	-0,48763143	245,32	PLD5	phospholipase D family member 5
9827	1,07E-25	2,50E+01	3,04E-26	0,0461	-10,5982503	-0,48808868	4289,38	RGP1	RGP1 homolog, RAB6A GEF complex partner 1
26205	3,41E-15	1,45E+01	1,32E-15	0,0611	-7,993105	-0,48812704	1138,93	GMEB2	glucocorticoid modulatory element binding protein 2
10783	4,49E-26	2,53E+01	1,26E-26	0,0457	-10,6798617	-0,48829656	3316,17	NEK6	NIMA related kinase 6
7625	7,08E-07	6,15E+00	3,78E-07	0,0961	-5,079574	-0,48839447	352,18	ZNF74	zinc finger protein 74
150291	7,46E-02	1,13E+00	5,92E-02	0,2589	-1,8868565	-0,48858014	43,8	MORC2-AS1	MORC2 antisense RNA 1
1522	4,92E-30	2,93E+01	1,25E-30	0,0425	-11,5048062	-0,48862931	14421,6	CTSZ	cathepsin Z
641371	8,46E-06	5,07E+00	4,80E-06	0,1069	-4,5733088	-0,48903657	284,43	ACOT1	acyl-CoA thioesterase 1
200205	1,17E-05	4,93E+00	6,68E-06	0,1086	-4,5037005	-0,489221	297	IBA57	iron-sulfur cluster assembly factor IBA57
1362	1,03E-39	3,90E+01	2,07E-40	0,0368	-13,3083051	-0,48937339	15869,22	CPD	carboxypeptidase D
11133	3,44E-07	6,46E+00	1,81E-07	0,0938	-5,2182565	-0,48948333	479,24	KPTN	kaptin, actin binding protein
90379	9,28E-19	1,80E+01	3,20E-19	0,0546	-8,961715	-0,48951248	3129,95	DCAF15	DDB1 and CUL4 associated factor 15
4636	5,79E-15	1,42E+01	2,25E-15	0,0618	-7,9268596	-0,48957515	1145,5	MYL5	myosin light chain 5
149111	3,04E-09	8,52E+00	1,45E-09	0,081	-6,0499648	-0,48986419	580,07	CNIH3	cornichon family AMPA receptor auxiliary protein 3
64215	2,10E-17	1,67E+01	7,54E-18	0,0569	-8,6064551	-0,48986622	1638,83	DNAJC1	DnaJ heat shock protein family (Hsp40) member C1
286204	3,30E-02	1,48E+00	2,50E-02	0,2185	-2,2419806	-0,48986949	65,38	CRB2	crumbs cell polarity complex component 2
254100	2,62E-01	5,82E-01	2,26E-01	0,4045	-1,2119731	-0,49019966	18,44	ZNRD2-DT	ZNRD2 divergent transcript
55825	2,63E-05	4,58E+00	1,54E-05	0,1134	-4,3231795	-0,49024236	256,64	PECR	peroxisomal trans-2-enoyl-CoA reductase
54509	4,79E-17	1,63E+01	1,74E-17	0,0576	-8,5100229	-0,49030843	1716,58	RHOF	ras homolog family member F, filopodia associated
107987209	3,56E-08	7,45E+00	1,78E-08	0,0871	-5,632424	-0,49055377	485,12	LOC107987	uncharacterized LOC107987209
114781	1,06E-16	1,60E+01	3,90E-17	0,0583	-8,4158099	-0,49095509	1507,45	BTBD9	BTB domain containing 9
54478	5,83E-15	1,42E+01	2,27E-15	0,062	-7,9258747	-0,49105391	1205,05	PIMREG	PICALM interacting mitotic regulator
10645	6,63E-23	2,22E+01	2,03E-23	0,0493	-9,9714247	-0,49131438	2609,66	CAMKK2	calcium/calmodulin dependent protein kinase kinase 2
51647	1,03E-13	1,30E+01	4,16E-14	0,065	-7,5557912	-0,49137874	1812,43	CIAO2B	cytosolic iron-sulfur assembly component 2B
116835	7,91E-02	1,10E+00	6,29E-02	0,2642	-1,8598461	-0,49140748	45,15	HSPA12B	heat shock protein family A (Hsp70) member 12B
548644	9,14E-13	1,20E+01	3,81E-13	0,0677	-7,262166	-0,49159529	885,22	POLR2J3	RNA polymerase II subunit J3
28969	6,55E-21	2,02E+01	2,12E-21	0,0518	-9,4987554	-0,49201315	3828,07	BZW2	basic leucine zipper and W2 domains 2
105369225	1,96E-01	7,08E-01	1,66E-01	0,355	-1,3863564	-0,49208748	24,84	LOC105369	uncharacterized LOC105369225
100533496	8,05E-09	8,09E+00	3,90E-09	0,0836	-5,8882833	-0,49210458	528,45	TVP23C-CD	TVP23C-CDRT4 readthrough
100506356	1,48E-01	8,30E-01	1,22E-01	0,3184	-1,5459435	-0,492181	28,78	ARSD-AS1	ARSD antisense RNA 1
8738	2,67E-06	5,57E+00	1,47E-06	0,1022	-4,8155299	-0,49224845	318,02	CRADD	CASP2 and RIPK1 domain containing adaptor with death domain
440804	4,63E-02	1,33E+00	3,57E-02	0,2347	-2,0998092	-0,49291699	54,49	RIMBP3B	RIMS binding protein 3B
23245	4,50E-03	2,35E+00	3,12E-03	0,1668	-2,9556947	-0,49299004	122,43	ASTN2	astrotactin 2
5255	1,19E-18	1,79E+01	4,10E-19	0,0552	-8,9341339	-0,49309991	1524,7	PHKA1	phosphorylase kinase regulatory subunit alpha 1
5796	1,52E-30	2,98E+01	3,81E-31	0,0425	-11,6066637	-0,49322266	4596,83	PTPRK	protein tyrosine phosphatase receptor type K
100126332	1,87E-02	1,73E+00	1,37E-02	0,2001	-2,4645867	-0,49323437	74,45	MIR943	microRNA 943
3035	5,70E-29	2,82E+01	1,48E-29	0,0437	-11,2893203	-0,49329067	6165,37	HARS1	histidyl-tRNA synthetase 1
81789	1,89E-03	2,72E+00	1,27E-03	0,1531	-3,223761	-0,49342856	140,7	TIGD6	tigger transposable element derived 6
83786	2,33E-11	1,06E+01	1,02E-11	0,0726	-6,8037097	-0,4938304	853,22	FERMD8	FERM domain containing 8
10869	8,62E-25	2,41E+01	2,51E-25	0,0475	-10,3988517	-0,49397863	2984,2	USP19	ubiquitin specific peptidase 19
109729180	7,60E-03	2,12E+00	5,38E-03	0,1775	-2,7830741	-0,49404727	102,77	SNHG26	small nucleolar RNA host gene 26
81552	1,11E-27	2,70E+01	2,99E-28	0,0448	-11,0222115	-0,49410144	3487,52	VOPP1	VOPP1 WW domain binding protein
3185	2,29E-34	3,36E+01	5,22E-35	0,04	-12,3444922	-0,49414084	16296	HNRNPF	heterogeneous nuclear ribonucleoprotein F
100133005	3,49E-02	1,46E+00	2,65E-02	0,2228	-2,2184677	-0,49427834	61,31	RASA4DP	RAS p21 protein activator 4D, pseudogene
54930	3,16E-21	2,05E+01	1,02E-21	0,0517	-9,5753336	-0,49467284	1974,3	HAUS4	HAUS augmin like complex subunit 4
105371763	6,52E-03	2,19E+00	4,59E-03	0,1745	-2,8344675	-0,49474344	100,05	LOC105371	uncharacterized LOC105371763
85455	6,28E-07	6,20E+00	3,35E-07	0,097	-5,1026123	-0,49497042	398,56	DISP2	dispatched RND transporter family member 2
81890	1,57E-11	1,08E+01	6,83E-12	0,0721	-6,8611726	-0,49500959	1316,54	QTRT1	queuine tRNA-ribosyltransferase catalytic subunit 1
8683	3,02E-27	2,65E+01	8,24E-28	0,0453	-10,930526	-0,49534511	5363,87	SRSF9	serine and arginine rich splicing factor 9
2737	1,65E-13	1,28E+01	6,70E-14	0,0661	-7,4936772	-0,49542013	1087,1	GLI3	GLI family zinc finger 3
8987	8,60E-09	8,07E+00	4,18E-09	0,0843	-5,8770294	-0,49560725	497,04	STBD1	starch binding domain 1
4615	7,61E-23	2,21E+01	2,34E-23	0,0498	-9,9576207	-0,49578024	2360,08	MYD88	MYD88 innate immune signal transduction adaptor
103908605	4,92E-02	1,31E+00	3,81E-02	0,2392	-2,0736385	-0,49593575	53,96	FAM88E	family with sequence similarity 88 member E
101929243	2,34E-08	7,63E+00	1,16E-08	0,0869	-5,7056744	-0,4959931	465,47	ILRUN-AS1	ILRUN antisense RNA 1
387521	2,03E-18	1,77E+01	7,05E-19	0,0559	-8,8741321	-0,49600239	1939,95	PEDS1	plasmanylethanolamine desaturase 1
55218	1,26E-15	1,49E+01	4,79E-16	0,0611	-8,1167087	-0,49607084	1139,06	EXD2	exonuclease 3'-5' domain containing 2
56136	4,44E-01	3,53E-01	4,02E-01	0,5927	-0,8374265	-0,49633326	8,97	PCDHA13	protocadherin alpha 13
112268123	1,29E-03	2,89E+00	8,52E-04	0,1489	-3,3353972	-0,49653785	140,93	LOC112268	uncharacterized LOC112268123
107985898	2,54E-01	5,95E-01	2,19E-01	0,4036	-1,2304826	-0,49659014	18,18	LOC107985	898
1933	4,78E-34	3,33E+01	1,10E-34	0,0404	-12,2843523	-0,49662305	24231,92	EEF1B2	eukaryotic translation elongation factor 1 beta 2
144699	1,09E-06	5,96E+00	5,87E-07	0,0994	-4,9956006	-0,49666351	339,73	FBXL14	F-box and leucine rich repeat protein 14
284129	4,07E-05	4,39E+00	2,41E-05	0,1176	-4,2231671	-0,4967421	271,11	SLC26A11	solute carrier family 26 member 11
55662	5,44E-26	2,53E+01	1,53E-26	0,0466	-10,6618977	-0,49715199	3832,84	HIF1AN	hypoxia inducible factor 1 subunit alpha inhibitor
105370027	8,81E-03	2,06E+00	6,28E-03	0,1819	-2,7328171	-0,4972216	90,01	LOC105370	uncharacterized LOC105370027
10139	6,50E-16	1,52E+01	2,44E-16	0,0607	-8,1979934	-0,49728701	1830,15	ARFRP1	ADP ribosylation factor related protein 1
6720	1,43E-19	1,88E+01	4,82E-20	0,0543	-9,1679144	-0,49774824	3421,16	SREBF1	sterol regulatory element binding transcription factor 1
140290	3,44E-01	4,63E-01	3,04E-01	0,4848	-1,0270687	-0,49797223	12,33	TCP10L	t-complex 10 like
90952	3,68E-22	2,14E+01	1,15E-22	0,0508	-9,7979904	-0,49807454	8334,35	ESAM	endothelial cell adhesion molecule
399512	2,89E-10	9,54E+00	1,32E-10	0,0775	-6,4249799	-0,49817537	670,02	SLC25A35	solute carrier family 25 member 35
28973	2,35E-28	2,76E+01	6,23E-29	0,0446	-11,1623761	-0,49820902	6402,31	MRPS18B	mitochondrial ribosomal protein S18B
342945	3,58E-08	7,45E+00	1,79E-08	0,0885	-5,6310356	-0,49843969	440,28	ZSCAN22	zinc finger and SCAN domain containing 22
79616	2,19E-22	2,17E+01	6,81E-23	0,0506	-9,8506352	-0,49847081	2739,05	CCNJL	cyclin J like
55869	1,72E-14	1,38E+01	6,77E-15	0,064	-7,7886979	-0,49860703	1177,3	HDAC8	histone deacetylase 8
23621	5,77E-29	2,82E+01	1,50E-29	0,0442	-11,2881782	-0,49901051	3609,13	BACE1	beta-secretase 1
539	2,47E-29	2,86E+01	6,36E-30	0,0439	-11,3634747	-0,49913394	5528,71	ATP5PO	ATP synthase peripheral stalk subunit OSCP
28964	3,85E-18	1,74E+01	1,35E-18	0,0567	-8,8012472	-0,49931735	2705,88	GIT1	GIT ArfGAP 1
2877	4,46E-01	3,51E-01	4,04E-01	0,5989	-0,8340677	-0,49949358	8,76	GPX2	glutathione peroxidase 2
3386	2,22E-03	2,65E+00	1,50E-03	0,1574	-3,1747568	-0,49963825	130,86	ICAM4	intercellular adhesion molecule 4 (Landsteiner-Wiener blood group)
6297	6,29E-06	5,20E+00	3,54E-06	0,1078	-4,6365727	-0,4997314	333,06	SALL2	spalt like transcription factor 2
51236	2,21E-10	9,66E+00	1,01E-10	0,0773	-6,4660878	-0,49980093	1470,97	HGH1	HGH1 homolog
58477	3,26E-22	2,15E+01	1,02E-22	0,051	-9,8102207	-0,49983961	2357,53	SRPRB	SRP receptor subunit beta
25805	1,99E-05	4,70E+00	1,16E-05	0,114	-4,3858258	-0,49989356	314,8	BAMBI	BMP and activin membrane bound inhibitor
116986	3,17E-07	6,50E+00	1,66E-07	0,0955	-5,2337183	-0,4998947	421,23	AGAP2	ArfGAP with GTPase domain, ankyrin repeat and PH domain 2
85376	1,89E-02	1,72E+00	1,39E-02	0,2033	-2,4596429	-0,49993794	71,58	RIMBP3	RIMS binding protein 3
51522	7,32E-28	2,71E+01	1,96E-28	0,0452	-11,0599028	-0,49994938	5376,74	TMEM14C	transmembrane protein 14C
100528031	1,11E-15	1,50E+01	4,21E-16	0,0615	-8,1325064	-0,49997889	1924,78	FKBP1A-SD	FKBP1A-SDCBP2 readthrough (NMD candidate)
9019	7,96E-36	3,51E+01	1,75E-36	0,0396	-12,6146686	-0,5000048	7554,67	MPZL1	myelin protein zero like 1
79443	2,58E-19	1,86E+01	8,74E-20	0,0549	-9,1035764	-0,50009703	2083,7	FYCO1	FYVE and coiled-coil domain autophagy adaptor 1

4809	2,44E-31	3,06E+01	5,99E-32	0,0425	-11,7639184	-0,5002469	6131,06	SNU13	small nuclear ribonucleoprotein 13
347862	1,09E-20	2,00E+01	3,56E-21	0,053	-9,4447556	-0,50026402	2054,44	GATD1	glutamine amidotransferase class 1 domain containing 1
80737	4,42E-02	1,35E+00	3,40E-02	0,236	-2,1198126	-0,50037931	55,5	VWA7	von Willebrand factor A domain containing 7
6722	1,47E-24	2,38E+01	4,30E-25	0,0484	-10,3473075	-0,50057843	5475,78	SRF	serum response factor
28227	6,49E-11	1,02E+01	2,89E-11	0,0753	-6,6521039	-0,50059112	841,44	PPP2R3B	protein phosphatase 2 regulatory subunit B"beta
100128253	1,90E-01	7,21E-01	1,60E-01	0,3563	-1,4057781	-0,50088537	23,14	LOC100128	uncharacterized LOC100128253
102724593	2,64E-01	5,78E-01	2,27E-01	0,415	-1,2071079	-0,50099898	17,6	LOC102724	uncharacterized LOC102724593
10517	4,32E-01	3,65E-01	3,91E-01	0,5839	-0,8580329	-0,50104335	8,82	FBXW10	F-box and WD repeat domain containing 10
54982	1,26E-13	1,29E+01	5,10E-14	0,0666	-7,5292563	-0,50139906	2030,49	CLN6	CLN6 transmembrane ER protein
84983	3,96E-01	4,02E-01	3,55E-01	0,5416	-0,9257615	-0,50140002	10,13	FAM222A-AS	FAM222A antisense RNA 1
55199	4,97E-09	8,30E+00	2,39E-09	0,084	-5,9686232	-0,50157694	580,96	FAM86C1P	family with sequence similarity 86 member C1, pseudogene
8841	4,79E-31	3,03E+01	1,19E-31	0,0429	-11,706066	-0,50168068	4795,59	HDAC3	histone deacetylase 3
11221	2,07E-18	1,77E+01	7,21E-19	0,0566	-8,8716593	-0,50185103	1426,79	DUSP10	dual specificity phosphatase 10
10452	3,51E-22	2,15E+01	1,09E-22	0,0512	-9,8029661	-0,50193247	7060,13	TOMM40	translocase of outer mitochondrial membrane 40
107984659	3,40E-02	1,47E+00	2,58E-02	0,2252	-2,2294447	-0,50197649	63,67	LOC107984	659
56155	1,28E-01	8,93E-01	1,05E-01	0,3097	-1,6207591	-0,5019891	30,53	TEX14	testis expressed 14, intercellular bridge forming factor
100505741	8,04E-03	2,09E+00	5,71E-03	0,1817	-2,7638715	-0,50227975	95,54	SPATA1	spermatogenesis associated 1
2132	2,00E-35	3,47E+01	4,44E-36	0,0401	-12,5413227	-0,5023027	6542,33	EXT2	exostosin glycosyltransferase 2
5598	5,88E-12	1,12E+01	2,52E-12	0,0718	-7,0023634	-0,50260159	1185,16	MAPK7	mitogen-activated protein kinase 7
29087	8,02E-21	2,01E+01	2,61E-21	0,053	-9,4773368	-0,50263815	2496,72	THYN1	thymocyte nuclear protein 1
131616	6,46E-07	6,19E+00	3,45E-07	0,0986	-5,0971829	-0,5028098	377,82	TMEM42	transmembrane protein 42
79154	5,45E-10	9,26E+00	2,52E-10	0,0795	-6,3258702	-0,50295835	617,44	DHRS11	dehydrogenase/reductase 11
60528	6,85E-34	3,32E+01	1,58E-34	0,0411	-12,2548211	-0,50356676	7650,96	ELAC2	elaC ribonuclease Z 2
102723340	4,04E-09	8,39E+00	1,93E-09	0,0839	-6,0032706	-0,50360335	514,09	LOC102723	uncharacterized LOC102723340
80115	2,50E-01	6,02E-01	2,15E-01	0,4061	-1,240691	-0,50382847	18,01	BAIAP2L2	BAR/IMD domain containing adaptor protein 2 like 2
80227	7,32E-14	1,31E+01	2,94E-14	0,0663	-7,6008982	-0,50391036	962,62	PAAF1	proteasomal ATPase associated factor 1
5860	4,81E-17	1,63E+01	1,75E-17	0,0592	-8,5093664	-0,50410592	1443,9	QDPR	quinoid dihydropteridine reductase
50628	1,38E-24	2,39E+01	4,04E-25	0,0487	-10,3533477	-0,50416388	3794,54	GEMIN4	gem nuclear organelle associated protein 4
23247	9,68E-10	9,01E+00	4,52E-10	0,0809	-6,2350375	-0,50419619	666,52	KATNIP	katanin interacting protein
400999	2,58E-01	5,88E-01	2,22E-01	0,4128	-1,2218415	-0,50436403	17,31	SLC20A1-DT	SLC20A1 divergent transcript
114483834	2,91E-29	2,85E+01	7,52E-30	0,0444	-11,3488016	-0,50437035	3312,12	ABCF2-H2BI	ABCF2-H2BK1 readthrough
55653	2,42E-08	7,62E+00	1,20E-08	0,0885	-5,6998332	-0,50449232	442,3	BCAS4	breast carcinoma amplified sequence 4
90525	3,33E-01	4,78E-01	2,93E-01	0,4803	-1,050797	-0,50469879	13,01	SHF	Src homology 2 domain containing F
5681	4,16E-10	9,38E+00	1,91E-10	0,0793	-6,3681	-0,50522519	1014,42	PSKH1	protein serine kinase H1
4192	5,57E-09	8,25E+00	2,69E-09	0,085	-5,9496823	-0,50547194	508,57	MDK	midkine
11014	2,11E-30	2,97E+01	5,31E-31	0,0437	-11,5783505	-0,50559009	7390,69	KDELR2	KDEL endoplasmic reticulum protein retention receptor 2
157574	5,08E-02	1,29E+00	3,95E-02	0,2455	-2,0594582	-0,50566818	50,34	FBXO16	F-box protein 16
92703	1,22E-26	2,59E+01	3,37E-27	0,0468	-10,8019074	-0,50573039	3267,34	TMEM183A	transmembrane protein 183A
5261	8,38E-13	1,21E+01	3,49E-13	0,0695	-7,2741916	-0,505754	895,89	PHKG2	phosphorylase kinase catalytic subunit gamma 2
84444	9,24E-20	1,90E+01	3,09E-20	0,0549	-9,2158285	-0,50585943	2069,78	DOT1L	DOT1 like histone lysine methyltransferase
439990	3,74E-11	1,04E+01	1,65E-11	0,0752	-6,7340673	-0,50616413	690,48	LINC00857	long intergenic non-protein coding RNA 857
6954	4,50E-01	3,47E-01	4,09E-01	0,6129	-0,8259995	-0,50624155	9,56	TCP11	t-complex 11
332	6,02E-38	3,72E+01	1,26E-38	0,0389	-12,9976209	-0,50624745	7352,61	BIRC5	baculoviral IAP repeat containing 5
389362	1,82E-12	1,17E+01	7,66E-13	0,0706	-7,1671079	-0,50627169	792,93	PSMG4	proteasome assembly chaperone 4
11194	3,49E-10	9,46E+00	1,60E-10	0,0792	-6,3959059	-0,50638788	887,96	ABCB8	ATP binding cassette subfamily B member 8
102724009	1,44E-09	8,84E+00	6,79E-10	0,0821	-6,1709229	-0,5065598	520,22	KIF1C-AS1	KIF1C antisense RNA 1
7846	8,08E-29	2,81E+01	2,11E-29	0,045	-11,2581483	-0,50678934	24109,94	TUBA1A	tubulin alpha 1a
9045	2,37E-46	4,56E+01	4,10E-47	0,0352	-14,4161363	-0,50682738	31714,7	RPL14	ribosomal protein L14
723972	3,99E-01	3,99E-01	3,58E-01	0,5518	-0,9193222	-0,50724413	9,46	ANP32AP1	acidic nuclear phosphoprotein 32 family member A pseudogene 1
105372426	1,31E-04	3,88E+00	7,99E-05	0,1286	-3,9447559	-0,50746937	187,63	LOC105372	uncharacterized LOC105372426
5976	1,13E-27	2,69E+01	3,04E-28	0,0461	-11,0205424	-0,50776973	6174,74	UPF1	UPF1 RNA helicase and ATPase
8861	1,95E-16	1,57E+01	7,20E-17	0,0609	-8,3436932	-0,50809745	2536,28	LDB1	LIM domain binding 1
100126351	1,25E-02	1,90E+00	9,04E-03	0,1947	-2,6106007	-0,50819577	83,85	MIR939	microRNA 939
84067	2,00E-12	1,17E+01	8,43E-13	0,0711	-7,1539392	-0,50832347	1016,29	FHIP1B	FHF complex subunit HOOK interacting protein 1B
107985361	5,28E-04	3,28E+00	3,39E-04	0,142	-3,5834128	-0,5090215	154,87	LOC107985	uncharacterized LOC107985361
10193	9,82E-22	2,10E+01	3,10E-22	0,0525	-9,6971326	-0,50914883	1945,99	RNF41	ring finger protein 41
9220	1,34E-07	6,87E+00	6,89E-08	0,0944	-5,3941061	-0,50924566	387,6	TIAF1	replaced by ID 399687
51367	7,45E-15	1,41E+01	2,90E-15	0,0645	-7,894981	-0,50925463	1023,04	POP5	POP5 homolog, ribonuclease P/MRP subunit
54920	2,84E-13	1,25E+01	1,16E-13	0,0686	-7,4208634	-0,50930781	863,67	DUS2	dihydrouridine synthase 2
89801	1,09E-08	7,96E+00	5,34E-09	0,0873	-5,8362346	-0,50940912	470,22	PPP1R3F	protein phosphatase 1 regulatory subunit 3F
54933	1,64E-03	2,79E+00	1,10E-03	0,156	-3,2648598	-0,50944297	133,65	RHBDL2	rhomboid like 2
573	2,19E-18	1,77E+01	7,62E-19	0,0575	-8,8654718	-0,50956476	2466,39	BAG1	BAG cochaperone 1
57221	3,29E-15	1,45E+01	1,27E-15	0,0637	-7,9977641	-0,50959815	1013,67	ARFGEF3	ARFGEF family member 3
64063	8,85E-02	1,05E+00	7,09E-02	0,2824	-1,8059878	-0,50995995	37,11	PRSS22	serine protease 22
145788	9,90E-02	1,00E+00	7,99E-02	0,2914	-1,7512192	-0,51028504	36,19	PIERCE2	piercer of microtubule wall 2
158787	9,65E-02	1,02E+00	7,77E-02	0,2893	-1,7640852	-0,51039318	38,61	RIBC1	RIB43A domain with coiled-coils 1
22845	1,75E-15	1,48E+01	6,67E-16	0,0632	-8,0764782	-0,51057662	1110,67	DOLK	dolichol kinase
102725044	5,51E-05	4,26E+00	3,28E-05	0,123	-4,1530162	-0,51064239	245,52	LOC102725	replaced by ID 161424
664709	1,91E-21	2,07E+01	6,09E-22	0,053	-9,627935	-0,51071153	2593,38	HNRNPA1P	heterogeneous nuclear ribonucleoprotein A1 pseudogene 10
100422991	6,45E-02	1,19E+00	5,08E-02	0,2615	-1,9535493	-0,51078037	44,33	MIR1260B	microRNA 1260b
54880	1,40E-18	1,79E+01	4,84E-19	0,0573	-8,9158249	-0,51078157	2150,36	BCOR	BCL6 corepressor
107985034	1,01E-21	2,10E+01	3,20E-22	0,0527	-9,6938692	-0,51079667	2681,43	LOC107985	uncharacterized LOC107985034
51239	1,55E-07	6,81E+00	8,03E-08	0,0952	-5,3665534	-0,51091997	381,68	ANKRD39	ankyrin repeat domain 39
101930100	4,03E-01	3,95E-01	3,62E-01	0,5603	-0,9119141	-0,51093495	9,39	LOC101930	uncharacterized LOC101930100
4802	3,59E-20	1,94E+01	1,19E-20	0,0549	-9,3177181	-0,51124747	2736,33	NFYC	nuclear transcription factor Y subunit gamma
7536	4,17E-45	4,44E+01	7,45E-46	0,036	-14,2145195	-0,51148474	14386,25	SF1	splicing factor 1
729013	1,87E-08	7,73E+00	9,25E-09	0,0891	-5,743971	-0,51152085	870,86	ZBED5-AS1	ZBED5 antisense RNA 1
140809	7,12E-32	3,11E+01	1,72E-32	0,0431	-11,8685524	-0,51161847	4371,6	SRXN1	sulfiredoxin 1
79791	1,31E-13	1,29E+01	5,29E-14	0,068	-7,5246263	-0,5117975	949,56	FBXO31	F-box protein 31
196463	1,29E-28	2,79E+01	3,39E-29	0,0456	-11,2164667	-0,51192566	5785,34	PLBD2	phospholipase B domain containing 2
105371452	4,41E-03	2,36E+00	3,06E-03	0,1729	-2,9621045	-0,51205743	108,62	LOC105371	uncharacterized LOC105371452
116988	1,02E-19	1,90E+01	3,42E-20	0,0556	-9,2047932	-0,51209342	2417,84	AGAP3	ArfGAP with GTPase domain, ankyrin repeat and PH domain 3
390637	2,37E-02	1,63E+00	1,76E-02	0,2158	-2,3733553	-0,5121863	66,85	GDPGP1	GDP-D-glucose phosphorylase 1
163154	9,13E-02	1,04E+00	7,33E-02	0,286	-1,7912622	-0,51233117	42,33	PRR22	proline rich 22
6233	6,51E-38	3,72E+01	1,37E-38	0,0394	-12,9915876	-0,51234789	32060,55	RPS27A	ribosomal protein S27a
683	1,56E-03	2,81E+00	1,04E-03	0,1562	-3,279801	-0,51238297	125,73	BST1	bone marrow stromal cell antigen 1
2972	1,61E-16	1,58E+01	5,94E-17	0,0612	-8,3663867	-0,51238835	1218,84	BRF1	BRF1 RNA polymerase III transcription initiation factor subunit
84074	6,32E-03	2,20E+00	4,45E-03	0,1803	-2,8447203	-0,51277895	100,2	QRICH2	glutamine rich 2
8601	1,70E-04	3,77E+00	1,05E-04	0,1323	-3,8779949	-0,51315711	202,74	RGS20	regulator of G protein signaling 20
26094	9,13E-18	1,70E+01	3,24E-18	0,059	-8,7027297	-0,51316528	1411,25	DCAF4	DDB1 and CUL4 associated factor 4
101928669	2,20E-01	6,58E-01	1,87E-01	0,3889	-1,3202555	-0,51340383	19,22	LOC101928	uncharacterized LOC101928669
23410	1,17E-12	1,19E+01	4,88E-13	0,071	-7,2286564	-0,51341115	866,08	SIRT3	sirtuin 3
3065	1,19E-36	3,59E+01	2,55E-37	0,0402	-12,7655873	-0,51342096	7455,66	HDAC1	histone deacetylase 1
92922	4,38E-06	5,36E+00	2,44E-06	0,1089	-4,7127114	-0,51343581	274,41	CCDC102A	coiled-coil domain containing 102A
105374104	2,15E-01	6,68E-01	1,82E-01	0,3852	-1,3336766	-0,5137823	21,48	LINC02021	long intergenic non-protein coding RNA 2021
84522	6,74E-20	1,92E+01	2,25E-20	0,0556	-9,2499244	-0,5142215	1664,8	JAGN1	jagunal homolog 1
131408	9,67E-15	1,40E+01	3,78E-15	0,0654	-7,8619552	-0,51455737	1024,18	FAM131A	family with sequence similarity 131 member A
60626	1,45E-24	2,38E+01	4,26E-25	0,0497	-10,3481947	-0,51458528	8603,64	RIC8A	RIC8 guanine nucleotide exchange factor A
90701	2,03E-19	1,87E+01	6,85E-20	0,0564	-9,1300522	-0,51464614	1664,59	SEC11C	SEC11 homolog C, signal peptidase complex subunit
4704	1,49E-25	2,48E+01	4,24E-26	0,0487	-10,5668635	-0,51465428	2765,98	NDUFA9	NADH:ubiquinone oxidoreductase subunit A9
5768	5,01E-22	2,13E+01	1,57E-22	0,0527	-9,7663084	-0,51468725	27866,62	QSOX1	quiescin sulfhydryl oxidase 1
119559	2,48E-15	1,46E+01	9,52E-16	0,0641	-8,0329549	-0,51477001	1131,42	SFXN4	sideroflexin 4
115362	6,38E-03	2,20E+00	4,49E-03	0,1813	-2,8413813	-0,51517638	95,41	GBP5	guanylate binding protein 5
460	1,42E-01	8,48E-01	1,17E-01	0,3287	-1,5676922	-0,51524864	27,51	ASTN1	astrotactin 1
105370624	1,60E-01	7,96E-01	1,33E-01	0,3427	-1,5037684	-0,51528601	26,76	LOC105370	uncharacterized LOC105370624
498	3,50E-47	4,65E+01	5,93E-48	0,0354	-14,5489495	-0,51533484	25495,32	ATP5F1A	ATP synthase F1 subunit alpha
23513	1,84E-23	2,27E+01	5,55E-24	0,051	-10,0995636	-0,5154261	4577,01	SCRIB	scribble planar cell polarity protein
9088	8,04E-17	1,61E+01	2,94E-17	0,061	-8,4489492	-0,515652	1337,95	PKMYT1	protein kinase, membrane associated tyrosine/threonine 1
90637	2,28E-13	1,26E+01	9,28E-14	0,0693	-7,4507384	-0,5161369	822,5	ZFAND2A	zinc finger AN1-type containing 2A
93664	3,84E-07	6,42E+00	2,02E-07	0,0993	-5,1974532	-0,51617776	387,55	CADPS2	calcium dependent secretion activator 2
328	8,65E-35	3,41E+01	1,95E-35	0,0415	-12,4233724	-0,51618289	9795,01	APEX1	apurinic/apyrimidinic endodeoxyribonuclease 1
121665	3,59E-23	2,24E+01	1,09E-23	0,0515	-10,0329109	-0,51649472	3046,83	SPPL3	signal peptide peptidase like 3
151903	2,51E-15	1,46E+01	9,62E-16	0,0643	-8,0315986	-0,51653315	1222,52	CCDC12	coiled-coil domain containing 12
5328	5,88E-46	4,52E+01	1,03E-46	0,036	-14,3524588	-0,51655509	16627,42	PLAU	plasminogen activator, urokinase
58508	2,95E-20	1,95E+01	9,72E-21	0,0553	-9,3390468	-0,51668411	2639,89	KMT2C	lysine methyltransferase 2C
3954	7,32E-30	2,91E+01	1,86E-30	0,0451	-11,4701861	-0,51696864	3324,74	LETM1	leucine zipper and EF-hand containing transmembrane protein 1
103695366	3,66E-01	4,37E-01	3,25E-01	0,5254	-0,9841222	-0,51702005	10,47	LINC01461	long intergenic non-protein coding RNA 1461
107985405	4,47E-12	1,13E+01	1,91E-12	0,0734	-7,0408811	-0,51708072	1051,48	LOC107985	uncharacterized LOC107985405
150274	8,49E-07	6,07E+00	4,56E-07	0,1025	-5,0441269	-0,51718738	357,04	HSCB	HscB mitochondrial iron-sulfur cluster cochaperone
2634	1,71E-15	1,48E+01	6,53E-16	0,064	-8,0790836	-0,51722889	1656,42	GBP2	guanylate binding protein 2

23054	6,04E-27	2,62E+01	1,66E-27	0,0476	-10,8666691	-0,51723338	5289,64	NCOA6	nuclear receptor coactivator 6
54776	9,35E-16	1,50E+01	3,54E-16	0,0634	-8,1534197	-0,51726753	2378,61	PPP1R12C	protein phosphatase 1 regulatory subunit 12C
5689	4,44E-17	1,64E+01	1,61E-17	0,0607	-8,5189076	-0,5173642	9870,66	PSMB1	proteasome 20S subunit beta 1
57794	8,87E-18	1,71E+01	3,15E-18	0,0594	-8,705985	-0,51738559	1912,03	SUGP1	SURP and G-patch domain containing 1
107986372	4,76E-02	1,32E+00	3,68E-02	0,2479	-2,0879601	-0,51769706	48,97	LOC107986	mitochondrial import receptor subunit TOM5 homolog
92689	1,30E-26	2,59E+01	3,62E-27	0,048	-10,7954033	-0,51776717	2917,61	FAM114A1	family with sequence similarity 114 member A1
1069	1,32E-21	2,09E+01	4,20E-22	0,0536	-9,666216	-0,51789858	2218,59	CETN2	centrin 2
339366	2,44E-06	5,61E+00	1,34E-06	0,1072	-4,8333228	-0,51813658	298,62	ADAMTSL5	ADAMTS like 5
9413	1,01E-01	9,96E-01	8,16E-02	0,2976	-1,741343	-0,51830354	35,65	ENTREP1	endosomal transmembrane epsin interactor 1
10551	4,00E-14	1,34E+01	1,59E-14	0,0675	-7,6796809	-0,51847751	1092,61	AGR2	anterior gradient 2, protein disulphide isomerase family member
84292	6,58E-16	1,52E+01	2,48E-16	0,0633	-8,1964116	-0,51857479	2355,65	WDR83	WD repeat domain 83
105375740	1,29E-01	8,89E-01	1,06E-01	0,3207	-1,6177171	-0,51876944	29,65	LOC105375	uncharacterized LOC105375740
9486	4,70E-22	2,13E+01	1,47E-22	0,0531	-9,7728207	-0,51886109	1905,7	CHST10	carbohydrate sulfotransferase 10
107986373	4,58E-02	1,34E+00	3,53E-02	0,2465	-2,1050566	-0,51894436	49,68	LOC107986	mitochondrial import receptor subunit TOM5 homolog
83549	7,88E-19	1,81E+01	2,71E-19	0,0578	-8,9800365	-0,51900528	1682,98	UCK1	uridine-cytidine kinase 1
107984950	3,31E-13	1,25E+01	1,36E-13	0,0701	-7,4004106	-0,51906773	795,95	LOC107984	uncharacterized LOC107984950
125150	5,93E-12	1,12E+01	2,54E-12	0,0741	-7,0011378	-0,51907495	689,39	ZSWIM7	zinc finger SWIM-type containing 7
94009	1,95E-08	7,71E+00	9,65E-09	0,0905	-5,7368119	-0,51913327	467,28	SERHL	serine hydrolase like (pseudogene)
4094	1,89E-01	7,24E-01	1,59E-01	0,3691	-1,4072978	-0,51940453	23,14	MAF	MAF bZIP transcription factor
388886	1,30E-02	1,89E+00	9,42E-03	0,2001	-2,5963511	-0,51940683	76,68	LRRC75B	leucine rich repeat containing 75B
27241	2,64E-08	7,58E+00	1,31E-08	0,0914	-5,6844359	-0,51981765	436,53	BBS9	Bardet-Biedl syndrome 9
8569	5,73E-20	1,92E+01	1,91E-20	0,0561	-9,2673923	-0,51998597	1519,31	MKNK1	MAPK interacting serine/threonine kinase 1
5303	2,84E-12	1,15E+01	1,21E-12	0,0732	-7,1046709	-0,52002305	1722,26	PIN4	peptidylprolyl cis/trans isomerase, NIMA-interacting 4
107985388	4,00E-03	2,40E+00	2,76E-03	0,1738	-2,9929684	-0,5202589	103,48	LOC107985	pre-mRNA-splicing factor cwc22-like
105378662	1,42E-01	8,48E-01	1,18E-01	0,3325	-1,5649396	-0,52032427	26,8	LOC105378	uncharacterized LOC105378662
3706	1,23E-02	1,91E+00	8,88E-03	0,1989	-2,6166922	-0,52052052	83,26	ITPKA	inositol-trisphosphate 3-kinase A
4725	3,25E-31	3,05E+01	8,02E-32	0,0444	-11,7392956	-0,52172709	7472,25	NDUFS5	NADH:ubiquinone oxidoreductase subunit S5
4322	2,66E-01	5,75E-01	2,29E-01	0,4342	-1,2026528	-0,52224631	16,5	MMP13	matrix metallopeptidase 13
6944	4,23E-19	1,84E+01	1,44E-19	0,0578	-9,0490874	-0,52280316	2715,36	VPS72	vacuolar protein sorting 72 homolog
143425	2,23E-01	6,52E-01	1,90E-01	0,3988	-1,3119747	-0,52326051	19,56	SYT9	synaptotagmin 9
25874	2,45E-19	1,86E+01	8,31E-20	0,0574	-9,1091198	-0,52326516	2117,33	MPC2	mitochondrial pyruvate carrier 2
55819	9,13E-19	1,80E+01	3,14E-19	0,0584	-8,9635587	-0,52331003	1829,44	RNF130	ring finger protein 130
284207	5,59E-04	3,25E+00	3,60E-04	0,1467	-3,5678813	-0,52333104	157,39	METRNL	meteorin like, glial cell differentiation regulator
390877	9,55E-02	1,02E+00	7,69E-02	0,2959	-1,7691879	-0,5234382	33,49	LOC390877	adenylate kinase isoenzyme 1-like
9124	3,18E-32	3,15E+01	7,64E-33	0,0439	-11,9364368	-0,52365956	3421,1	PDLIM1	PDZ and LIM domain 1
11140	6,79E-30	2,92E+01	1,73E-30	0,0456	-11,4767686	-0,52376962	15745,59	CDC37	cell division cycle 37, HSP90 cochaperone
101929609	2,19E-04	3,66E+00	1,37E-04	0,1373	-3,8142665	-0,52385253	176,45	LOC101929	uncharacterized LOC101929609
1907	3,08E-02	1,51E+00	2,32E-02	0,2308	-2,2698114	-0,5238857	58,86	EDN2	endothelin 2
23580	6,09E-28	2,72E+01	1,63E-28	0,0473	-11,0765279	-0,52404575	2850,53	CDC42EP4	CDC42 effector protein 4
102723885	8,17E-09	8,09E+00	3,96E-09	0,089	-5,8857139	-0,52405006	435,78	SRI-AS1	SRI antisense RNA 1
10174	1,06E-22	2,20E+01	3,27E-23	0,0528	-9,9241305	-0,52411547	2088,39	SORBS3	sorbin and SH3 domain containing 3
1349	5,34E-31	3,03E+01	1,32E-31	0,0448	-11,6967645	-0,52439298	6179,95	COX7B	cytochrome c oxidase subunit 7B
6830	3,96E-35	3,44E+01	8,88E-36	0,042	-12,4862263	-0,52465948	12217,52	SUPT6H	SPT6 homolog, histone chaperone and transcription elongation factor
11143	5,55E-34	3,33E+01	1,28E-34	0,0428	-12,2721674	-0,52477159	4099,36	KAT7	lysine acetyltransferase 7
100506551	1,32E-02	1,88E+00	9,55E-03	0,2025	-2,5916346	-0,52479398	72,29	LOC100506	uncharacterized LOC100506551
11328	1,20E-30	2,99E+01	3,01E-31	0,0451	-11,6268459	-0,52479942	4971,56	FKBP9	FKBP prolyl isomerase 9
112268170	5,43E-20	1,93E+01	1,81E-20	0,0566	-9,2731968	-0,52489529	1760,96	LOC112268	translation initiation factor IF-2-like
9587	9,98E-22	2,10E+01	3,15E-22	0,0541	-9,6954049	-0,52490339	1821,17	MAD2L1BP	MAD2L1 binding protein
4513	2,67E-33	3,26E+01	6,26E-34	0,0432	-12,1428596	-0,52502159	242087,47	COX2	cytochrome c oxidase subunit II
10726	1,34E-40	3,99E+01	2,64E-41	0,039	-13,4613517	-0,52508549	13281,91	NUDC	nuclear distribution C, dynein complex regulator
3815	3,25E-01	4,88E-01	2,86E-01	0,4923	-1,0666065	-0,52509034	12,21	KIT	KIT proto-oncogene, receptor tyrosine kinase
64968	1,48E-26	2,58E+01	4,10E-27	0,0487	-10,7838206	-0,525325	2675,39	MRPS6	mitochondrial ribosomal protein S6
11145	5,66E-21	2,02E+01	1,83E-21	0,0552	-9,5141125	-0,52539367	2628,57	PLAAT3	phospholipase A and acyltransferase 3
9349	7,56E-46	4,51E+01	1,33E-46	0,0367	-14,3348117	-0,52548615	31040,35	RPL23	ribosomal protein L23
138151	2,12E-18	1,77E+01	7,39E-19	0,0593	-8,8688377	-0,52571657	1407,8	NACC2	NACC family member 2
90423	2,59E-05	4,59E+00	1,51E-05	0,1216	-4,3270924	-0,52603944	219,43	ATP6V1E2	ATPase H+ transporting V1 subunit E2
81544	5,46E-09	8,26E+00	2,63E-09	0,0884	-5,9530302	-0,5261992	510,25	GDPD5	glycerophosphodiester phosphodiesterase domain containing 5
25828	3,19E-22	2,15E+01	9,94E-23	0,0536	-9,8125469	-0,52640944	3251,74	TXN2	thioredoxin 2
1455	1,44E-23	2,28E+01	4,35E-24	0,052	-10,1233661	-0,52657763	2310,17	CSNK1G2	casein kinase 1 gamma 2
102465447	7,35E-01	1,34E-01	7,04E-01	1,3847	-0,3803551	-0,52666027	64,35	MIR6747	microRNA 6747
6461	2,17E-26	2,57E+01	6,07E-27	0,049	-10,7478552	-0,52679017	2489,84	SHB	SH2 domain containing adaptor protein B
1390	2,78E-15	1,46E+01	1,07E-15	0,0657	-8,0185784	-0,5269288	1115,52	CREM	cAMP responsive element modulator
29763	9,46E-18	1,70E+01	3,36E-18	0,0606	-8,6984577	-0,52700501	1661,75	PACSIN3	protein kinase C and casein kinase substrate in neurons 3
84314	2,60E-08	7,59E+00	1,29E-08	0,0927	-5,6868597	-0,52714996	443,75	TMEM107	transmembrane protein 107
100885850	1,44E-16	1,58E+01	5,32E-17	0,0629	-8,3793692	-0,52716496	1116,57	PTGES3L-A	PTGES3L-AARSD1 readthrough
101927632	2,75E-05	4,56E+00	1,61E-05	0,1222	-4,3128341	-0,52723222	249,21	PPP1R35-AS	PPP1R35 antisense RNA 1
730013	1,70E-01	7,70E-01	1,42E-01	0,3591	-1,4686188	-0,52733606	23,43	ABCC6P2	ATP binding cassette subfamily C member 6 pseudogene 2
100128176	3,31E-01	4,80E-01	2,92E-01	0,5004	-1,054266	-0,52755145	11,52	UST-AS1	UST antisense RNA 1
91409	3,39E-01	4,70E-01	2,99E-01	0,5085	-1,0376941	-0,52761821	11,85	CCDC74B	coiled-coil domain containing 74B
101928837	2,87E-01	5,42E-01	2,49E-01	0,458	-1,1520202	-0,52766864	15,16	TSKU-AS1	TSKU antisense RNA 1
81037	7,40E-24	2,31E+01	2,21E-24	0,0518	-10,1892956	-0,52789672	6278,62	CLPTM1L	CLPTM1 like
6166	4,72E-37	3,63E+01	1,01E-37	0,0411	-12,8377556	-0,52809171	11610,31	RPL36AL	ribosomal protein L36a like
56917	3,10E-01	5,09E-01	2,71E-01	0,4805	-1,0998803	-0,52849259	13,97	MEIS3	Meis homeobox 3
107984340	2,97E-15	1,45E+01	1,14E-15	0,066	-8,0104587	-0,52858489	2942,4	LOC107984	uncharacterized LOC107984340
4363	1,43E-30	2,98E+01	3,58E-31	0,0455	-11,612147	-0,52873808	3275,28	ABCC1	ATP binding cassette subfamily C member 1
132014	2,15E-06	5,67E+00	1,18E-06	0,1088	-4,8593262	-0,52881898	322,37	IL17RE	interleukin 17 receptor E
79140	1,73E-04	3,76E+00	1,07E-04	0,1365	-3,8748746	-0,52897521	195,78	CCDC28B	coiled-coil domain containing 28B
84626	4,65E-06	5,33E+00	2,60E-06	0,1125	-4,7003985	-0,52902194	254,48	KRBA1	KRAB-A domain containing 1
6210	5,05E-32	3,13E+01	1,22E-32	0,0445	-11,8975105	-0,52904253	22381,52	RPS15A	ribosomal protein S15a
1145	1,21E-03	2,92E+00	8,02E-04	0,1579	-3,3519857	-0,52917378	126,17	CHRNE	cholinergic receptor nicotinic epsilon subunit
10514	8,23E-26	2,51E+01	2,33E-26	0,0498	-10,6228382	-0,52927268	4949,29	MYBBP1A	MYB binding protein 1a
2787	3,04E-26	2,55E+01	8,53E-27	0,0494	-10,7163671	-0,52927789	3583,11	GNG5	G protein subunit gamma 5
3693	6,56E-28	2,72E+01	1,76E-28	0,0478	-11,0698477	-0,52942626	4542,26	ITGB5	integrin subunit beta 5
6603	3,34E-28	2,75E+01	8,88E-29	0,0476	-11,1307913	-0,52944488	3210,81	SMARCD2	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 2
10361	2,03E-01	6,93E-01	1,72E-01	0,3876	-1,3664311	-0,5295891	20,93	NPM2	nucleophosmin/nucleoplasmin 2
101928034	3,06E-16	1,55E+01	1,14E-16	0,0639	-8,2893046	-0,52959051	1780,05	LOC101928	uncharacterized LOC101928034
285386	3,25E-01	4,88E-01	2,86E-01	0,4969	-1,0667471	-0,53005533	12,67	TPRG1	tumor protein p63 regulated 1
646962	2,97E-01	5,27E-01	2,59E-01	0,4694	-1,1297581	-0,53033232	13,24	HRCT1	histidine rich carboxyl terminus 1
579	6,82E-03	2,17E+00	4,81E-03	0,1882	-2,8194736	-0,530545	85,84	NKX3-2	NK3 homeobox 2
3916	3,10E-39	3,85E+01	6,32E-40	0,0402	-13,2246556	-0,530991	9676,33	LAMP1	lysosomal associated membrane protein 1
107987254	3,36E-01	4,74E-01	2,96E-01	0,5079	-1,0455693	-0,53104035	11,85	LOC107987	254
2971	1,95E-33	3,27E+01	4,56E-34	0,0436	-12,1687944	-0,53115728	5165,69	GTF3A	general transcription factor IIIA
84996	2,66E-04	3,58E+00	1,67E-04	0,1412	-3,7641308	-0,53136104	158,54	URB1-AS1	URB1 antisense RNA 1 (head to head)
4302	5,92E-36	3,52E+01	1,30E-36	0,0421	-12,638404	-0,53152863	4942,52	MLLT6	MLLT6, PHD finger containing
10016	6,52E-26	2,52E+01	1,84E-26	0,0499	-10,6448785	-0,53153292	2432,73	PDCD6	programmed cell death 6
401127	3,19E-01	4,96E-01	2,80E-01	0,492	-1,0809597	-0,53186482	12,27	LOC401127	WD repeat domain 5 pseudogene
80023	1,07E-21	2,10E+01	3,39E-22	0,0549	-9,6880141	-0,53206911	2207,47	NRSN2	neurensin 2
53838	1,80E-26	2,57E+01	5,02E-27	0,0494	-10,7653262	-0,53210888	3161,07	C11orf24	chromosome 11 open reading frame 24
100506178	6,50E-10	9,19E+00	3,01E-10	0,0845	-6,298069	-0,5323086	516,67	STEAP1B-AS	STEAP1B antisense RNA 1
613	3,44E-20	1,95E+01	1,14E-20	0,0571	-9,3225869	-0,53247308	2202,27	BCR	BCR activator of RhoGEF and GTPase
10123	8,77E-27	2,61E+01	2,42E-27	0,0492	-10,8322082	-0,5324806	5195,94	ARL4C	ADP ribosylation factor like GTPase 4C
8061	1,41E-37	3,69E+01	2,97E-38	0,0412	-12,9319006	-0,53249735	18788,47	FOSL1	FOS like 1, AP-1 transcription factor subunit
25812	3,03E-02	1,52E+00	2,28E-02	0,234	-2,2764011	-0,53256831	55,42	POM121L1P	POM121 transmembrane nucleoporin like 1, pseudogene
5213	4,06E-30	2,94E+01	1,03E-30	0,0462	-11,5215962	-0,53274308	3349,41	PFKM	phosphofructokinase, muscle
3554	1,33E-11	1,09E+01	5,76E-12	0,0774	-6,8853594	-0,53309596	612,09	IL1R1	interleukin 1 receptor type 1
8331	1,39E-01	8,57E-01	1,15E-01	0,3378	-1,5782289	-0,53312743	27,11	H2AC14	H2A clustered histone 14
51507	2,60E-41	4,06E+01	5,05E-42	0,0393	-13,5830069	-0,53319357	7051,85	RTF2	replication termination factor 2
81619	1,74E-35	3,48E+01	3,86E-36	0,0425	-12,5523312	-0,53327479	4892,78	TSPAN14	tetraspanin 14
105370203	1,70E-02	1,77E+00	1,25E-02	0,2135	-2,4978394	-0,53339323	68,8	LOC105370	uncharacterized LOC105370203
8904	9,39E-44	4,30E+01	1,73E-44	0,0381	-13,9925155	-0,53356515	13513,06	CPNE1	copine 1
90853	4,11E-11	1,04E+01	1,82E-11	0,0794	-6,7201457	-0,5337493	621,76	SPOCD1	SPOC domain containing 1
105375798	2,98E-01	5,26E-01	2,60E-01	0,4734	-1,1275349	-0,53376451	14,62	LOC105375	uncharacterized LOC105375798
100507071	1,42E-01	8,48E-01	1,17E-01	0,3407	-1,5671805	-0,53387805	26,34	PIWIL2-DT	PIWIL2 divergent transcript
79777	3,45E-06	5,46E+00	1,91E-06	0,1122	-4,7625581	-0,53417498	310,3	ACBD4	acyl-CoA binding domain containing 4
112755	3,13E-01	5,04E-01	2,74E-01	0,4884	-1,0938373	-0,5342031	12,25	STX1B	syntaxin 1B
4629	1,93E-05	4,71E+00	1,12E-05	0,1216	-4,3926467	-0,53430638	218,38	MYH11	myosin heavy chain 11
2074	5,83E-14	1,32E+01	2,34E-14	0,0701	-7,6305978	-0,53455005	836,33	ERCC6	ERCC excision repair 6, chromatin remodeling factor
80758	6,15E-06	5,21E+00	3,46E-06	0,1152	-4,6414285	-0,53456328	272,25	PRR7	proline rich 7, synaptic
55353	4,05E-23	2,24E+01	1,23E-23	0,0534	-10,0210449	-0,53463138	3332,9	LAPTM4B	lysosomal protein transmembrane 4 beta
11336	1,85E-21	2,07E+01	5,90E-22	0,0555	-9,6312873	-0,53478544	2077,33	EXOC3	exocyst complex component 3

107984834	1,81E-01	7,42E-01	1,51E-01	0,3729	-1,4346821	-0,53492125	21,77	CORO1A-AS	CORO1A antisense RNA 1
27304	2,14E-11	1,07E+01	9,34E-12	0,0785	-6,8163145	-0,53503977	636,21	MOCS3	molybdenum cofactor synthesis 3
78999	9,06E-13	1,20E+01	3,77E-13	0,0737	-7,263399	-0,5350781	788,98	LRFN4	leucine rich repeat and fibronectin type III domain containing 4
1388	9,61E-21	2,00E+01	3,13E-21	0,0566	-9,4582802	-0,53545649	6977,32	ATF6B	activating transcription factor 6 beta
57062	5,01E-37	3,63E+01	1,07E-37	0,0417	-12,8330011	-0,53569096	15131,5	DDX24	DEAD-box helicase 24
11237	8,89E-21	2,01E+01	2,90E-21	0,0566	-9,4664438	-0,53573868	1511,66	RNF24	ring finger protein 24
374655	2,95E-13	1,25E+01	1,21E-13	0,0722	-7,4160259	-0,53580469	758	ZNF710	zinc finger protein 710
91748	3,31E-27	2,65E+01	9,05E-28	0,0491	-10,9219851	-0,53590774	2187,51	MIDEAS	mitotic deacetylase associated SANT domain protein
100507246	6,21E-29	2,82E+01	1,62E-29	0,0475	-11,2815755	-0,5359731	3484,01	SNHG16	small nucleolar RNA host gene 16
107985064	2,92E-04	3,53E+00	1,84E-04	0,1433	-3,739888	-0,53600781	155,28	LOC107985	064
107983993	5,37E-07	6,27E+00	2,85E-07	0,1045	-5,1331387	-0,53616165	295,91	UPK3BL2	uroplakin 3B like 2
54620	4,24E-16	1,54E+01	1,59E-16	0,065	-8,2497723	-0,53619176	1192,51	FBXL19	F-box and leucine rich repeat protein 19
107987244	6,32E-02	1,20E+00	4,96E-02	0,2732	-1,9630367	-0,53627065	39,76	LOC107987	uncharacterized LOC107987244
170954	9,66E-45	4,40E+01	1,74E-45	0,0379	-14,1548674	-0,5362717	12254,46	PPP1R18	protein phosphatase 1 regulatory subunit 18
105371814	1,48E-05	4,83E+00	8,55E-06	0,1205	-4,4510298	-0,5362784	215,95	LOC105371	uncharacterized LOC105371814
25973	1,01E-09	9,00E+00	4,73E-10	0,0861	-6,2278212	-0,53639075	489,59	PARS2	prolyl-tRNA synthetase 2, mitochondrial
2542	2,75E-21	2,06E+01	8,81E-22	0,0559	-9,5899937	-0,53647504	3013,72	SLC37A4	solute carrier family 37 member 4
6136	8,06E-42	4,11E+01	1,55E-42	0,0393	-13,6691157	-0,53652397	43161,13	RPL12	ribosomal protein L12
56181	4,35E-20	1,94E+01	1,44E-20	0,0577	-9,2971318	-0,53682671	1602,6	MTFR1L	mitochondrial fission regulator 1 like
10469	8,95E-25	2,40E+01	2,61E-25	0,0516	-10,3952047	-0,53683001	3495,99	TIMM44	translocase of inner mitochondrial membrane 44
5830	5,81E-18	1,72E+01	2,05E-18	0,0613	-8,7545192	-0,53690935	1373,66	PEX5	peroxisomal biogenesis factor 5
51594	7,48E-25	2,41E+01	2,18E-25	0,0516	-10,4124249	-0,53698006	2711,64	NBAS	NBAS subunit of NRZ tethering complex
81	1,43E-28	2,78E+01	3,75E-29	0,0479	-11,207366	-0,53710723	47574,01	ACTN4	actinin alpha 4
619570	2,48E-01	6,06E-01	2,13E-01	0,4315	-1,2456044	-0,53746712	16,71	SNORD95	small nucleolar RNA, C/D box 95
2194	1,06E-19	1,90E+01	3,54E-20	0,0584	-9,2012087	-0,53752585	10418,77	FASN	fatty acid synthase
55572	1,81E-25	2,47E+01	5,20E-26	0,051	-10,5477338	-0,53775417	2232,57	FOXRED1	FAD dependent oxidoreductase domain containing 1
3770	8,12E-04	3,09E+00	5,30E-04	0,1553	-3,4653089	-0,53809537	129,5	KCNJ14	potassium inwardly rectifying channel subfamily J member 14
1387	5,20E-31	3,03E+01	1,29E-31	0,046	-11,6991386	-0,53820188	3381,27	CREBBP	CREB binding protein
112939	5,53E-28	2,73E+01	1,48E-28	0,0486	-11,0852948	-0,53874418	9569,23	NACC1	nucleus accumbens associated 1
140831	3,50E-08	7,46E+00	1,75E-08	0,0956	-5,6352463	-0,53883257	404,03	ZSWIM3	zinc finger SWIM-type containing 3
51493	1,69E-40	3,98E+01	3,33E-41	0,0401	-13,4442781	-0,53887889	5223,96	RTCB	RNA 2',3'-cyclic phosphate and 5'-OH ligase
203062	3,61E-11	1,04E+01	1,59E-11	0,08	-6,7391559	-0,5389539	623,84	TSNARE1	t-SNARE domain containing 1
80212	4,12E-21	2,04E+01	1,33E-21	0,0565	-9,5475702	-0,53907345	1839,79	CCDC92	coiled-coil domain containing 92
23503	1,80E-20	1,97E+01	5,90E-21	0,0574	-9,3918078	-0,53909872	1659,57	ZFYVE26	zinc finger FYVE-type containing 26
23210	1,39E-22	2,19E+01	4,29E-23	0,0545	-9,8968812	-0,53917644	1723,26	JMJD6	jumonji domain containing 6, arginine demethylase and lysine hydroxylase
84798	1,32E-17	1,69E+01	4,71E-18	0,0623	-8,6602697	-0,53935628	3349,25	C19orf48	multidrug resistance-related protein
105369380	1,13E-01	9,47E-01	9,21E-02	0,3203	-1,684503	-0,53953021	31,39	LOC105369	380
5096	5,85E-23	2,22E+01	1,79E-23	0,054	-9,9840266	-0,5395631	1883,92	PCCB	propionyl-CoA carboxylase subunit beta
5872	3,10E-22	2,15E+01	9,66E-23	0,055	-9,8154107	-0,53977046	4503,43	RAB13	RAB13, member RAS oncogene family
619190	2,67E-01	5,73E-01	2,31E-01	0,4506	-1,1983311	-0,53994467	14,26	FDPSP2	farnesyl diphosphate synthase pseudogene 2
333926	1,06E-01	9,75E-01	8,59E-02	0,3144	-1,7174971	-0,54006244	30,92	PPM1J	protein phosphatase, Mg2+/Mn2+ dependent 1J
7318	4,85E-11	1,03E+01	2,15E-11	0,0807	-6,6954531	-0,54020027	681,79	UBA7	ubiquitin like modifier activating enzyme 7
9459	4,43E-04	3,35E+00	2,83E-04	0,1488	-3,6305342	-0,54020409	144,22	ARHGEF6	Rac/Cdc42 guanine nucleotide exchange factor 6
51599	5,51E-14	1,33E+01	2,21E-14	0,0707	-7,6379235	-0,54021656	1439,33	LSR	lipolysis stimulated lipoprotein receptor
3614	2,67E-18	1,76E+01	9,36E-19	0,0611	-8,8425043	-0,54024422	1845,39	IMPDH1	inosine monophosphate dehydrogenase 1
4306	9,64E-14	1,30E+01	3,89E-14	0,0714	-7,5647673	-0,54031532	920,45	NR3C2	nuclear receptor subfamily 3 group C member 2
729991	5,06E-07	6,30E+00	2,68E-07	0,1052	-5,144343	-0,5409475	374,34	BORCS8	BLOC-1 related complex subunit 8
4508	2,48E-28	2,76E+01	6,58E-29	0,0485	-11,1575792	-0,54096187	134503,52	ATP6	ATP synthase F0 subunit 6
55316	3,93E-18	1,74E+01	1,38E-18	0,0615	-8,7989623	-0,54103229	1517,39	RSAD1	radical S-adenosyl methionine domain containing 1
6697	1,17E-19	1,89E+01	3,92E-20	0,0589	-9,1902731	-0,54118951	1461,02	SPR	sepiapterin reductase
80114	8,35E-11	1,01E+01	3,73E-11	0,0818	-6,6143335	-0,54136048	566,05	BICC1	BicC family RNA binding protein 1
401398	1,12E-01	9,51E-01	9,11E-02	0,3204	-1,6896575	-0,54136404	28,41	POT1-AS1	POT1 antisense RNA 1
5883	4,21E-13	1,24E+01	1,74E-13	0,0735	-7,3677352	-0,5414719	878,87	RAD9A	RAD9 checkpoint clamp component A
253725	8,94E-25	2,40E+01	2,60E-25	0,0521	-10,3953361	-0,54157048	3601,94	WASHC2C	WASH complex subunit 2C
80325	9,79E-10	9,01E+00	4,57E-10	0,0869	-6,2330761	-0,54157368	659,43	ABTB1	ankyrin repeat and BTB domain containing 1
56172	2,91E-24	2,35E+01	8,63E-25	0,0527	-10,2804864	-0,5417063	1723,72	ANKH	ANKH inorganic pyrophosphate transport regulator
57533	8,81E-28	2,71E+01	2,37E-28	0,0491	-11,0430205	-0,5417869	2972,85	TBC1D14	TBC1 domain family member 14
54097	3,91E-01	4,08E-01	3,50E-01	0,5799	-0,9344026	-0,54183852	9,53	FAM3B	FAM3 metabolism regulating signaling molecule B
100533955	2,17E-52	5,17E+01	3,27E-53	0,0353	-15,3551819	-0,54218874	40584,18	SENP3-EIF4	SENP3-EIF4A1 readthrough (NMD candidate)
201164	4,52E-09	8,34E+00	2,17E-09	0,0906	-5,9845136	-0,5422777	441,88	PLD6	phospholipase D family member 6
57222	1,45E-26	2,58E+01	4,03E-27	0,0503	-10,7854537	-0,54227905	6883,83	ERGIC1	endoplasmic reticulum-golgi intermediate compartment 1
4053	1,10E-14	1,40E+01	4,31E-15	0,0691	-7,8456588	-0,54230726	902,44	LTBP2	latent transforming growth factor beta binding protein 2
147968	4,52E-10	9,34E+00	2,08E-10	0,0853	-6,3553432	-0,54235465	1113,72	CAPN12	calpain 12
107985877	5,62E-02	1,25E+00	4,38E-02	0,2691	-2,015562	-0,54240484	41,79	LOC107985	877
6480	1,73E-12	1,18E+01	7,27E-13	0,0756	-7,1743405	-0,54245177	700,32	ST6GAL1	ST6 beta-galactoside alpha-2,6-sialyltransferase 1
60681	1,52E-01	8,18E-01	1,26E-01	0,355	-1,5284642	-0,54253316	23,18	FKBP10	FKBP prolyl isomerase 10
6464	4,14E-34	3,34E+01	9,49E-35	0,0441	-12,2961929	-0,5426248	6906,03	SHC1	SHC adaptor protein 1
84752	1,18E-06	5,93E+00	6,41E-07	0,109	-4,9783551	-0,54263619	268,69	B3GNT9	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 9
10347	1,49E-07	6,83E+00	7,70E-08	0,101	-5,3740252	-0,54297508	354,36	ABCA7	ATP binding cassette subfamily A member 7
55969	3,98E-32	3,14E+01	9,59E-33	0,0456	-11,91754	-0,54300292	3230,49	RAB5IF	RAB5 interacting factor
9314	9,02E-19	1,80E+01	3,11E-19	0,0606	-8,9649039	-0,54355665	1174,83	KLF4	KLF transcription factor 4
4650	2,73E-40	3,96E+01	5,43E-41	0,0406	-13,4079955	-0,54369553	6674,82	MYO9B	myosin IXB
80210	1,35E-17	1,69E+01	4,83E-18	0,0628	-8,6573029	-0,54396656	1084,47	ARMC9	armadillo repeat containing 9
4817	1,68E-15	1,48E+01	6,41E-16	0,0673	-8,0812697	-0,54396888	1052,79	NIT1	nitrilase 1
2979	7,72E-03	2,11E+00	5,48E-03	0,1961	-2,7774276	-0,54455916	78,38	GUCA1B	guanylate cyclase activator 1B
1108	4,35E-42	4,14E+01	8,33E-43	0,0397	-13,7143999	-0,54461321	14876,78	CHD4	chromodomain helicase DNA binding protein 4
254263	2,11E-01	6,76E-01	1,79E-01	0,4054	-1,3435071	-0,54469305	19,27	CNIH2	cornichon family AMPA receptor auxiliary protein 2
6238	4,66E-36	3,53E+01	1,02E-36	0,043	-12,6573427	-0,54475989	21733,56	RRBP1	ribosome binding protein 1
55731	5,99E-19	1,82E+01	2,05E-19	0,0605	-9,0104378	-0,54495271	1317,63	FAM222B	family with sequence similarity 222 member B
10919	6,35E-31	3,02E+01	1,58E-31	0,0467	-11,6820001	-0,54499961	3778,41	EHMT2	euchromatic histone lysine methyltransferase 2
8671	1,74E-05	4,76E+00	1,01E-05	0,1234	-4,4157273	-0,54501438	214,55	SLC4A4	solute carrier family 4 member 4
285590	1,16E-10	9,94E+00	5,20E-11	0,083	-6,5650767	-0,54509843	550,85	SH3PXD2B	SH3 and PX domains 2B
154810	8,82E-42	4,11E+01	1,70E-42	0,0399	-13,6624917	-0,54528823	6222,68	AMOTL1	angiomotin like 1
7515	5,05E-17	1,63E+01	1,84E-17	0,0641	-8,5037226	-0,54536388	1202,56	XRCC1	X-ray repair cross complementing 1
101927861	1,01E-06	6,00E+00	5,45E-07	0,1089	-5,0095774	-0,54571394	303,06	LINC01293	long intergenic non-protein coding RNA 1293
57234	1,30E-06	5,89E+00	7,08E-07	0,1101	-4,9592297	-0,5458031	292,03	LINC00869	long intergenic non-protein coding RNA 869
643314	2,43E-18	1,76E+01	8,49E-19	0,0616	-8,8534082	-0,54581039	2086,42	KIAA0754	replaced by ID 23499
85360	5,88E-31	3,02E+01	1,46E-31	0,0467	-11,6886142	-0,54606833	5222,92	SYDE1	synapse defective Rho GTPase homolog 1
80755	2,15E-17	1,67E+01	7,74E-18	0,0635	-8,6033674	-0,54639457	1083,61	AARSD1	alanyl-tRNA synthetase domain containing 1
23632	1,54E-11	1,08E+01	6,69E-12	0,0796	-6,8642011	-0,54650952	715,65	CA14	carbonic anhydrase 14
2882	2,48E-01	6,06E-01	2,12E-01	0,4384	-1,2469253	-0,54666517	18,07	GPX7	glutathione peroxidase 7
2767	7,82E-26	2,51E+01	2,22E-26	0,0514	-10,6276355	-0,54677994	4064,94	GNA11	G protein subunit alpha 11
6388	9,88E-27	2,60E+01	2,73E-27	0,0506	-10,8212267	-0,54712097	2195,33	SDF2	stromal cell derived factor 2
283254	3,27E-08	7,49E+00	1,63E-08	0,0969	-5,6471013	-0,54712273	375,77	HARBI1	harbinger transposase derived 1
8310	1,11E-08	7,95E+00	5,42E-09	0,0938	-5,8338823	-0,54737742	415,66	ACOX3	acyl-CoA oxidase 3, pristanoyl
1326	4,57E-08	7,34E+00	2,30E-08	0,098	-5,5879586	-0,54755758	446,88	MAP3K8	mitogen-activated protein kinase kinase kinase 8
1969	5,68E-28	2,72E+01	1,52E-28	0,0494	-11,082817	-0,5476998	21634,15	EPHA2	EPH receptor A2
27352	1,53E-15	1,48E+01	5,84E-16	0,0677	-8,0925499	-0,54777653	931,12	SGSM3	small G protein signaling modulator 3
84915	1,18E-04	3,93E+00	7,18E-05	0,138	-3,9701092	-0,54790802	177,2	FAM222A	family with sequence similarity 222 member A
7296	2,04E-46	4,57E+01	3,52E-47	0,038	-14,4265528	-0,54836991	18677,54	TXNRD1	thioredoxin reductase 1
310	4,84E-40	3,93E+01	9,69E-41	0,041	-13,3649802	-0,54862385	7985,37	ANXA7	annexin A7
4537	1,93E-36	3,57E+01	4,17E-37	0,0431	-12,7272646	-0,5487402	18604,92	ND3	NADH dehydrogenase subunit 3
653333	6,74E-02	1,17E+00	5,31E-02	0,2837	-1,9339911	-0,54874654	37,15	FAM86B2	family with sequence similarity 86 member B2
2592	7,39E-15	1,41E+01	2,88E-15	0,0695	-7,8960926	-0,54902841	940,78	GALT	galactose-1-phosphate uridylyltransferase
55275	2,55E-28	2,76E+01	6,78E-29	0,0493	-11,1548829	-0,54969515	2762,96	VPS53	VPS53 subunit of GARP complex
28991	2,20E-18	1,77E+01	7,68E-19	0,0621	-8,864581	-0,55022721	1759,79	COMMD5	COMM domain containing 5
57109	7,85E-27	2,61E+01	2,16E-27	0,0508	-10,8424897	-0,55029629	2039,5	REXO4	REX4 homolog, 3'-5' exonuclease
9569	9,18E-18	1,70E+01	3,26E-18	0,0632	-8,7019918	-0,55035706	1119,99	GTF2IRD1	GTF2I repeat domain containing 1
107080638	1,40E-07	6,85E+00	7,19E-08	0,1022	-5,3864018	-0,55040781	331,57	TBC1D7-LO	TBC1D7-LOC100130357 readthrough
23612	4,81E-06	5,32E+00	2,69E-06	0,1174	-4,6932328	-0,55097929	248,61	PHLDA3	pleckstrin homology like domain family A member 3
51112	5,35E-24	2,33E+01	1,60E-24	0,0539	-10,2210465	-0,55108908	1639,59	TRAPPC12	trafficking protein particle complex subunit 12
94097	3,41E-11	1,05E+01	1,50E-11	0,0817	-6,7478946	-0,55109024	556,95	SFXN5	sideroflexin 5
6776	3,32E-18	1,75E+01	1,16E-18	0,0625	-8,8181198	-0,55114457	1209,31	STAT5A	signal transducer and activator of transcription 5A
112268469	1,29E-01	8,89E-01	1,06E-01	0,3411	-1,6161074	-0,55120627	26,76	LOC112268	uncharacterized LOC112268469
64852	1,46E-15	1,48E+01	5,54E-16	0,0681	-8,0990155	-0,55130765	991,34	TUT1	terminal uridylyl transferase 1, U6 snRNA-specific
11190	3,20E-36	3,55E+01	6,95E-37	0,0435	-12,68733	-0,55157703	5950,72	CEP250	centrosomal protein 250
10055	2,76E-47	4,66E+01	4,67E-48	0,0379	-14,5652968	-0,55167683	12025,13	SAE1	SUMO1 activating enzyme subunit 1
105375787	3,60E-01	4,44E-01	3,19E-01	0,5536	-0,9965769	-0,55168099	9,62	LOC105375	uncharacterized LOC105375787
79979	2,25E-27	2,66E+01	6,11E-28	0,0504	-10,9575909	-0,55254141	2094,62	TRMT2B	tRNA methyltransferase 2 homolog B
10300	1,02E-17	1,70E+01	3,64E-18	0,0636	-8,6895285	-0,55298174	1696,14	KATNB1	katanin regulatory subunit B1

88745	1,70E-42	4,18E+01	3,23E-43	0,0401	-13,7829789	-0,55306632	5620,09	RRP36	ribosomal RNA processing 36
55290	7,61E-08	7,12E+00	3,86E-08	0,1006	-5,4970247	-0,5530829	357,33	BRF2	BRF2 RNA polymerase III transcription initiation factor subunit
348180	2,16E-11	1,07E+01	9,45E-12	0,0812	-6,8146994	-0,55313711	670,23	CTU2	cytosolic thiouridylase subunit 2
102465538	3,44E-01	4,63E-01	3,04E-01	0,5392	-1,0273575	-0,55395903	10,03	MIR6892	microRNA 6892
1476	1,30E-29	2,89E+01	3,34E-30	0,0485	-11,4195562	-0,55399852	6932,23	CSTB	cystatin B
105371906	9,10E-04	3,04E+00	5,95E-04	0,1613	-3,4339414	-0,55402646	125,85	LACAT1	lung adenocarcinoma-associated transcript 1
5094	1,08E-51	5,10E+01	1,64E-52	0,0363	-15,2501106	-0,55408299	15469,69	PCBP2	poly(rC) binding protein 2
64759	5,82E-43	4,22E+01	1,09E-43	0,04	-13,8609796	-0,55420907	6812,18	TNS3	tensin 3
60509	9,33E-22	2,10E+01	2,94E-22	0,0571	-9,7024265	-0,55439242	2031,24	AGBL5	AGBL carboxypeptidase 5
9167	8,91E-34	3,31E+01	2,06E-34	0,0453	-12,2333203	-0,55450108	4687,36	COX7A2L	cytochrome c oxidase subunit 7A2 like
57470	1,24E-20	1,99E+01	4,07E-21	0,0588	-9,4308284	-0,55453898	2380,33	LRRC47	leucine rich repeat containing 47
7431	1,85E-57	5,67E+01	2,50E-58	0,0344	-16,1012072	-0,5546774	127974,34	VIM	vimentin
1675	1,67E-01	7,77E-01	1,39E-01	0,3752	-1,4783411	-0,55468812	23,5	CFD	complement factor D
51234	1,32E-23	2,29E+01	3,98E-24	0,0547	-10,1322182	-0,55472517	1737,09	EMC4	ER membrane protein complex subunit 4
400569	2,91E-17	1,65E+01	1,05E-17	0,0648	-8,5683112	-0,55486998	1025,12	MED11	mediator complex subunit 11
5437	4,95E-31	3,03E+01	1,22E-31	0,0474	-11,7033784	-0,55502321	2641,78	POLR2H	RNA polymerase II, I and III subunit H
9448	1,35E-34	3,39E+01	3,07E-35	0,0448	-12,3871823	-0,55503763	18882,75	MAP4K4	mitogen-activated protein kinase kinase kinase kinase 4
3420	4,89E-36	3,53E+01	1,07E-36	0,0439	-12,653499	-0,55519322	4872,47	IDH3B	isocitrate dehydrogenase (NAD(+)) 3 non-catalytic subunit beta
5373	7,24E-28	2,71E+01	1,94E-28	0,0502	-11,0608962	-0,55539303	2338,85	PMM2	phosphomannomutase 2
23383	3,56E-26	2,54E+01	1,00E-26	0,0519	-10,7015612	-0,55556959	2190,94	MAU2	MAU2 sister chromatid cohesion factor
57463	1,93E-12	1,17E+01	8,13E-13	0,0776	-7,1588748	-0,55565831	665,7	AMIGO1	adhesion molecule with Ig like domain 1
7032	3,98E-05	4,40E+00	2,35E-05	0,1315	-4,2287064	-0,55591647	184,86	TFF2	trefoil factor 2
2115	4,41E-20	1,94E+01	1,46E-20	0,0598	-9,2956579	-0,55616634	3244,42	ETV1	ETS variant transcription factor 1
6812	2,42E-23	2,26E+01	7,34E-24	0,0552	-10,0720793	-0,55633725	1780,54	STXBP1	syntaxin binding protein 1
24144	2,38E-28	2,76E+01	6,30E-29	0,0499	-11,1614224	-0,55654075	2306,11	TFIP11	tuftelin interacting protein 11
105371416	2,04E-01	6,90E-01	1,73E-01	0,4088	-1,3627205	-0,55704968	19,18	LINC02166	long intergenic non-protein coding RNA 2166
92979	1,69E-09	8,77E+00	7,96E-10	0,0906	-6,1457044	-0,55707341	443,82	MARCHF9	membrane associated ring-CH-type finger 9
154664	2,86E-02	1,54E+00	2,15E-02	0,2424	-2,2989286	-0,55715084	52,73	ABCA13	ATP binding cassette subfamily A member 13
93643	5,98E-22	2,12E+01	1,88E-22	0,0572	-9,7482151	-0,55734172	2590,28	TJAP1	tight junction associated protein 1
6138	7,44E-54	5,31E+01	1,09E-54	0,0358	-15,5742588	-0,55746705	43970,62	RPL15	ribosomal protein L15
9315	2,20E-16	1,57E+01	8,16E-17	0,067	-8,3289122	-0,55805619	965,3	NREP	neuronal regeneration related protein
93100	2,77E-09	8,56E+00	1,32E-09	0,0921	-6,0647086	-0,5583196	649,98	NAPRT	nicotinate phosphoribosyltransferase
114915	1,47E-11	1,08E+01	6,37E-12	0,0813	-6,8710251	-0,55849675	573,87	EPB41L4A-A	EPB41L4A antisense RNA 1
132228	3,97E-07	6,40E+00	2,09E-07	0,1076	-5,1907475	-0,55868684	371,11	LSMEM2	leucine rich single-pass membrane protein 2
26608	3,36E-26	2,55E+01	9,43E-27	0,0522	-10,7071089	-0,55884249	1957,64	TBL2	transducin beta like 2
1973	5,20E-55	5,43E+01	7,44E-56	0,0355	-15,744939	-0,55895845	37919,92	EIF4A1	eukaryotic translation initiation factor 4A1
57217	2,88E-14	1,35E+01	1,14E-14	0,0724	-7,7225008	-0,55924674	1331,98	TTC7A	tetratricopeptide repeat domain 7A
473	1,65E-33	3,28E+01	3,85E-34	0,0459	-12,18249	-0,55927085	3111,87	RERE	arginine-glutamic acid dipeptide repeats
80161	6,91E-03	2,16E+00	4,88E-03	0,1987	-2,8150365	-0,55930784	78,75	ASMTL-AS1	ASMTL antisense RNA 1
5414	5,17E-02	1,29E+00	4,01E-02	0,2725	-2,0523511	-0,55934128	40,87	SEPTIN4	septin 4
8566	9,98E-30	2,90E+01	2,55E-30	0,0489	-11,4429043	-0,55951624	3238,4	PDXK	pyridoxal kinase
159195	1,59E-19	1,88E+01	5,35E-20	0,0611	-9,156675	-0,55956234	1235,04	USP54	ubiquitin specific peptidase 54
10243	9,61E-23	2,20E+01	2,96E-23	0,0563	-9,9340514	-0,55960589	1489,43	GPHN	gephyrin
9513	1,79E-39	3,87E+01	3,62E-40	0,0422	-13,2664842	-0,55968947	5886,06	FXR2	FMR1 autosomal homolog 2
6878	2,66E-26	2,56E+01	7,44E-27	0,0522	-10,7289683	-0,55983383	2430,5	TAF6	TATA-box binding protein associated factor 6
63916	1,03E-28	2,80E+01	2,71E-29	0,0498	-11,236204	-0,55990407	3599,03	ELMO2	engulfment and cell motility 2
22907	1,63E-34	3,38E+01	3,71E-35	0,0453	-12,3719164	-0,5600243	7653,21	DHX30	DExH-box helicase 30
24139	1,61E-16	1,58E+01	5,94E-17	0,067	-8,3663468	-0,56034738	1717,4	EML2	EMAP like 2
357	1,78E-10	9,75E+00	8,07E-11	0,0862	-6,4993773	-0,56036321	582,5	SHROOM2	shroom family member 2
55052	1,28E-29	2,89E+01	3,29E-30	0,0491	-11,420858	-0,5603832	2632,73	MRPL20	mitochondrial ribosomal protein L20
784	3,05E-05	4,52E+00	1,79E-05	0,1307	-4,2892145	-0,56050061	203,82	CACNB3	calcium voltage-gated channel auxiliary subunit beta 3
105379243	1,30E-01	8,86E-01	1,06E-01	0,3472	-1,6150612	-0,56072075	25,88	LOC105379	uncharacterized LOC105379243
6633	2,48E-34	3,36E+01	5,65E-35	0,0455	-12,3380247	-0,56086558	8282,87	SNRPD2	small nuclear ribonucleoprotein D2 polypeptide
116496	8,81E-39	3,81E+01	1,81E-39	0,0427	-13,145305	-0,56110327	5151,31	NIBAN1	niban apoptosis regulator 1
100272147	1,87E-05	4,73E+00	1,09E-05	0,1276	-4,399106	-0,56130608	222,51	CMC4	C-X9-C motif containing 4
10749	1,41E-38	3,79E+01	2,90E-39	0,0428	-13,1095807	-0,56139338	9968,52	KIF1C	kinesin family member 1C
202051	1,82E-04	3,74E+00	1,13E-04	0,1454	-3,860918	-0,56146584	151,08	SPATA24	spermatogenesis associated 24
642938	1,34E-01	8,73E-01	1,11E-01	0,3521	-1,5957337	-0,56183693	24,89	INSYN2A	inhibitory synaptic factor 2A
23765	2,80E-12	1,16E+01	1,19E-12	0,0791	-7,1070941	-0,56187673	602	IL17RA	interleukin 17 receptor A
23195	2,94E-26	2,55E+01	8,23E-27	0,0524	-10,719635	-0,56189303	2544,89	MDN1	midasin AAA ATPase 1
9709	4,17E-30	2,94E+01	1,06E-30	0,0488	-11,5192082	-0,56210049	2418,59	HERPUD1	homocysteine inducible ER protein with ubiquitin like domain 1
1495	1,68E-46	4,58E+01	2,90E-47	0,0389	-14,4399933	-0,5622671	37320,81	CTNNA1	catenin alpha 1
9064	1,46E-14	1,38E+01	5,75E-15	0,072	-7,809387	-0,56232601	1115,51	MAP3K6	mitogen-activated protein kinase kinase kinase 6
4174	1,52E-30	2,98E+01	3,81E-31	0,0485	-11,6067565	-0,56305906	4700,41	MCM5	minichromosome maintenance complex component 5
161835	1,70E-03	2,77E+00	1,14E-03	0,173	-3,2542445	-0,56307547	102,96	FSIP1	fibrous sheath interacting protein 1
7283	1,43E-25	2,48E+01	4,08E-26	0,0533	-10,5704673	-0,56331403	10617,89	TUBG1	tubulin gamma 1
144233	6,79E-03	2,17E+00	4,79E-03	0,1997	-2,8207955	-0,56332029	74,43	BCDIN3D	BCDIN3 domain containing RNA methyltransferase
142678	3,79E-13	1,24E+01	1,56E-13	0,0763	-7,3821086	-0,56345957	1091,15	MIB2	MIB E3 ubiquitin protein ligase 2
27341	4,51E-27	2,63E+01	1,24E-27	0,0517	-10,893644	-0,56347337	4016,57	RRP7A	ribosomal RNA processing 7 homolog A
7726	2,48E-30	2,96E+01	6,24E-31	0,0487	-11,5643978	-0,56352799	3459,54	TRIM26	tripartite motif containing 26
150368	4,79E-06	5,32E+00	2,68E-06	0,1201	-4,6937904	-0,56357775	228,11	PHETA2	PH domain containing endocytic trafficking adaptor 2
3667	2,44E-37	3,66E+01	5,18E-38	0,0437	-12,8891794	-0,56369131	4794,74	IRS1	insulin receptor substrate 1
101926935	1,66E-01	7,80E-01	1,38E-01	0,3805	-1,4819477	-0,56391951	21,07	LOC101926	uncharacterized LOC101926935
728975	3,26E-06	5,49E+00	1,81E-06	0,1181	-4,7737359	-0,56395578	241,57	CAPN1-AS1	CAPN1 antisense RNA 1
3061	5,95E-06	5,23E+00	3,35E-06	0,1214	-4,6483638	-0,56410775	250,74	HCRTR1	hypocretin receptor 1
57597	2,51E-17	1,66E+01	9,03E-18	0,0657	-8,585643	-0,56416136	921,37	BAHCC1	BAH domain and coiled-coil containing 1
100287932	1,46E-40	3,98E+01	2,88E-41	0,0419	-13,4549646	-0,56418914	4558,47	TIMM23	translocase of inner mitochondrial membrane 23
101927830	3,25E-01	4,88E-01	2,86E-01	0,5288	-1,067112	-0,56431248	10,33	LOC101927	uncharacterized LOC101927830
5051	8,49E-10	9,07E+00	3,95E-10	0,0902	-6,2558289	-0,56441867	411,23	PAFAH2	platelet activating factor acetylhydrolase 2
1952	2,36E-14	1,36E+01	9,35E-15	0,0729	-7,7477945	-0,56456346	709,08	CELSR2	cadherin EGF LAG seven-pass G-type receptor 2
102724889	3,92E-02	1,41E+00	3,00E-02	0,2601	-2,1703457	-0,5645799	43,84	LOC102724	889
6794	2,23E-24	2,37E+01	6,57E-25	0,0548	-10,3067372	-0,56498073	1925,58	STK11	serine/threonine kinase 11
100126784	1,66E-09	8,78E+00	7,86E-10	0,0919	-6,1478196	-0,56512167	444,02	NAV2-AS6	NAV2 antisense RNA 6
26578	6,78E-24	2,32E+01	2,03E-24	0,0554	-10,1979116	-0,56526858	2401,38	OSTF1	osteoclast stimulating factor 1
8848	1,58E-47	4,68E+01	2,65E-48	0,0387	-14,6040779	-0,56542162	8592,45	TSC22D1	TSC22 domain family member 1
29960	1,39E-28	2,79E+01	3,66E-29	0,0504	-11,2096438	-0,56550815	2109,29	MRM2	mitochondrial rRNA methyltransferase 2
9875	8,01E-31	3,01E+01	1,99E-31	0,0485	-11,6619617	-0,5656805	3212,67	URB1	URB1 ribosome biogenesis homolog
83943	6,77E-05	4,17E+00	4,06E-05	0,1378	-4,1042412	-0,56568799	162,84	IMMP2L	inner mitochondrial membrane peptidase subunit 2
57186	7,22E-16	1,51E+01	2,72E-16	0,0691	-8,18513	-0,56582635	917,82	RALGAPA2	Ral GTPase activating protein catalytic subunit alpha 2
100874048	1,86E-11	1,07E+01	8,12E-12	0,0828	-6,8363849	-0,565947	538,75	DGUOK-AS1	DGUOK antisense RNA 1
90780	5,92E-25	2,42E+01	1,72E-25	0,0542	-10,4347353	-0,5660111	2233	PYGO2	pygopus family PHD finger 2
51550	7,13E-19	1,81E+01	2,45E-19	0,063	-8,9910983	-0,56606541	1191,84	CINP	cyclin dependent kinase 2 interacting protein
54606	1,74E-31	3,08E+01	4,26E-32	0,048	-11,7927303	-0,56618168	4851,3	DDX56	DEAD-box helicase 56
51491	1,30E-32	3,19E+01	3,10E-33	0,0471	-12,011276	-0,5662769	3687,29	NOP16	NOP16 nucleolar protein
101927509	1,36E-11	1,09E+01	5,89E-12	0,0823	-6,8822918	-0,56637307	539,78	HDLBP-AS1	HDLBP antisense RNA 1
115286	2,04E-18	1,77E+01	7,11E-19	0,0638	-8,8731339	-0,56641009	994,04	SLC25A26	solute carrier family 25 member 26
112268022	2,80E-01	5,53E-01	2,42E-01	0,4847	-1,1691929	-0,56674269	12,38	LOC112268	uncharacterized LOC112268022
29978	4,36E-26	2,54E+01	1,23E-26	0,0531	-10,6826051	-0,56689976	1731,56	UBQLN2	ubiquilin 2
6730	6,88E-48	4,72E+01	1,15E-48	0,0387	-14,660981	-0,56729581	7570,05	SRP68	signal recognition particle 68
79165	4,18E-12	1,14E+01	1,78E-12	0,0805	-7,0505407	-0,56749918	609,19	LENG1	leukocyte receptor cluster member 1
23112	4,15E-20	1,94E+01	1,37E-20	0,061	-9,3023744	-0,56754251	1522,45	TNRC6B	trinucleotide repeat containing adaptor 6B
5719	2,21E-45	4,47E+01	3,93E-46	0,0398	-14,2592124	-0,56766924	10002,32	PSMD13	proteasome 26S subunit, non-ATPase 13
4221	6,77E-28	2,72E+01	1,81E-28	0,0513	-11,0670228	-0,56768853	2955,81	MEN1	menin 1
647033	1,52E-04	3,82E+00	9,33E-05	0,1454	-3,9074884	-0,56803878	155,94	PA2G4P4	proliferation-associated 2G4 pseudogene 4
55613	8,04E-03	2,09E+00	5,71E-03	0,2055	-2,7638357	-0,56807794	74,25	MTMR8	myotubularin related protein 8
22984	4,71E-44	4,33E+01	8,64E-45	0,0405	-14,0418821	-0,56814393	5021,9	PDCD11	programmed cell death 11
85474	2,18E-03	2,66E+00	1,47E-03	0,1786	-3,1811022	-0,56830322	99,19	LBX2	ladybird homeobox 2
100996763	6,40E-12	1,12E+01	2,74E-12	0,0813	-6,9902071	-0,56859423	604,34	NOTCH2NLE	notch 2 N-terminal like B
25988	7,07E-19	1,82E+01	2,42E-19	0,0632	-8,9921339	-0,5686569	1055,12	HINFP	histone H4 transcription factor
8506	2,96E-26	2,55E+01	8,29E-27	0,0531	-10,7189683	-0,56884822	2287,1	CNTNAP1	contactin associated protein 1
107985487	3,29E-01	4,83E-01	2,90E-01	0,5374	-1,0588467	-0,56897971	10,04	LOC107985	487
105379327	2,25E-01	6,48E-01	1,91E-01	0,4357	-1,3067976	-0,56932073	16,68	LOC105379	uncharacterized LOC105379327
7408	2,04E-40	3,97E+01	4,05E-41	0,0424	-13,4297376	-0,56938824	5375,47	VASP	vasodilator stimulated phosphoprotein
9328	9,59E-32	3,10E+01	2,33E-32	0,0481	-11,8433	-0,56948666	3743,29	GTF3C5	general transcription factor IIIC subunit 5
5792	1,07E-44	4,40E+01	1,93E-45	0,0403	-14,1476002	-0,56963835	16808,45	PTPRF	protein tyrosine phosphatase receptor type F
7048	1,18E-57	5,69E+01	1,58E-58	0,0353	-16,1295059	-0,56969736	18267,21	TGFBR2	transforming growth factor beta receptor 2
3276	1,61E-25	2,48E+01	4,62E-26	0,054	-10,5589624	-0,5702131	13722,6	PRMT1	protein arginine methyltransferase 1
200407	1,49E-01	8,27E-01	1,23E-01	0,3702	-1,5403466	-0,57026653	22,28	CREG2	cellular repressor of E1A stimulated genes 2
100506637	4,32E-03	2,36E+00	2,99E-03	0,1921	-2,9683263	-0,57033744	87,34	PRKAR2A-A	PRKAR2A antisense RNA 1
26499	2,37E-21	2,06E+01	7,60E-22	0,0594	-9,6052764	-0,57053862	1810,27	PLEK2	pleckstrin 2

57699	2,95E-04	3,53E+00	1,86E-04	0,1528	-3,737631	-0,57124339	131,83	CPNE5	copine 5
5763	3,73E-29	2,84E+01	9,66E-30	0,0505	-11,3268568	-0,5717014	4496,75	PTMS	parathymosin
3303	1,21E-24	2,39E+01	3,54E-25	0,0552	-10,3659032	-0,57170278	4960,65	HSPA1A	heat shock protein family A (Hsp70) member 1A
550	5,10E-36	3,53E+01	1,12E-36	0,0452	-12,6501482	-0,57170668	6539,2	AUP1	AUP1 lipid droplet regulating VLDL assembly factor
64792	1,90E-11	1,07E+01	8,27E-12	0,0837	-6,8337776	-0,5717187	526,21	IFT22	intraflagellar transport 22
6390	3,70E-40	3,94E+01	7,38E-41	0,0427	-13,3852276	-0,57191565	5200,62	SDHB	succinate dehydrogenase complex iron sulfur subunit B
339983	4,24E-06	5,37E+00	2,37E-06	0,1212	-4,7194218	-0,57204876	214,24	NAT8L	N-acetyltransferase 8 like
51634	2,33E-21	2,06E+01	7,46E-22	0,0596	-9,6071102	-0,57219548	1744,49	RBMX2	RNA binding motif protein X-linked 2
105371849	2,42E-01	6,16E-01	2,08E-01	0,4542	-1,2604028	-0,57248626	14,1	HEATR6-DT	HEATR6 divergent transcript
719	2,30E-01	6,38E-01	1,97E-01	0,4435	-1,2910669	-0,57253333	15,43	C3AR1	complement C3a receptor 1
1939	5,37E-34	3,33E+01	1,24E-34	0,0466	-12,2748698	-0,57256983	3232,06	EIF2D	eukaryotic translation initiation factor 2D
100996301	2,01E-04	3,70E+00	1,25E-04	0,1493	-3,8359988	-0,57269215	144,3	FOXD3-AS1	FOXD3 antisense RNA 1
9277	3,76E-39	3,84E+01	7,67E-40	0,0434	-13,2100755	-0,57275709	7032,79	WDR46	WD repeat domain 46
23524	4,89E-39	3,83E+01	1,00E-39	0,0434	-13,190072	-0,57275874	24770,69	SRRM2	serine/arginine repetitive matrix 2
56114	1,11E-02	1,95E+00	7,96E-03	0,2159	-2,6537483	-0,57306535	63,91	PCDHGA1	protocadherin gamma subfamily A, 1
4092	1,71E-07	6,77E+00	8,85E-08	0,1071	-5,3489288	-0,57307398	297,23	SMAD7	SMAD family member 7
2937	1,76E-45	4,48E+01	3,10E-46	0,0402	-14,2756358	-0,57337925	6568,53	GSS	glutathione synthetase
6382	3,46E-36	3,55E+01	7,55E-37	0,0452	-12,680877	-0,57346189	5304,46	SDC1	syndecan 1
100288077	1,68E-44	4,38E+01	3,05E-45	0,0406	-14,115442	-0,57351387	15985,74	WTAPP1	Wilms tumor 1 associated protein pseudogene 1
102725201	8,09E-07	6,09E+00	4,33E-07	0,1135	-5,0537233	-0,57363738	248,39	CEP250-AS1	CEP250 antisense RNA 1
10667	3,70E-17	1,64E+01	1,34E-17	0,0672	-8,5402338	-0,57384389	948,84	FARS2	phenylalanyl-tRNA synthetase 2, mitochondrial
4720	4,35E-42	4,14E+01	8,32E-43	0,0418	-13,7144827	-0,57384502	4312,03	NDUFS2	NADH:ubiquinone oxidoreductase core subunit S2
11251	5,89E-08	7,23E+00	2,97E-08	0,1035	-5,5429391	-0,57392058	315,28	PTGDR2	prostaglandin D2 receptor 2
9179	5,50E-17	1,63E+01	2,00E-17	0,0676	-8,4935265	-0,57393945	1017,43	AP4M1	adaptor related protein complex 4 subunit mu 1
221184	1,00E-20	2,00E+01	3,26E-21	0,0607	-9,4540186	-0,57418583	1258,86	CPNE2	copine 2
5600	6,93E-04	3,16E+00	4,49E-04	0,1636	-3,5094363	-0,57428714	173,84	MAPK11	mitogen-activated protein kinase 11
389538	1,93E-10	9,71E+00	8,77E-11	0,0885	-6,4868374	-0,57436409	455,26	CCZ1P-OR7	CCZ1P-OR7E38P readthrough
100421577	2,05E-01	6,88E-01	1,74E-01	0,4226	-1,360105	-0,57483022	17,02	FAM21EP	family with sequence similarity 21, member A pseudogene
85377	7,79E-27	2,61E+01	2,15E-27	0,053	-10,8431983	-0,57521945	1857,94	MICALL1	MICAL like 1
126792	1,42E-21	2,08E+01	4,50E-22	0,0596	-9,6589669	-0,57528034	1262,61	B3GALT6	beta-1,3-galactosyltransferase 6
10130	4,07E-52	5,14E+01	6,16E-53	0,0376	-15,3140613	-0,57564836	15956,66	PDIA6	protein disulfide isomerase family A member 6
5589	1,88E-30	2,97E+01	4,72E-31	0,0497	-11,5882942	-0,57584462	17440,62	PRKCSH	protein kinase C substrate 80K-H
728769	1,82E-07	6,74E+00	9,41E-08	0,1079	-5,3377455	-0,57594793	313,07	SCAMP1-AS	SCAMP1 antisense RNA 1
10241	1,57E-42	4,18E+01	2,97E-43	0,0418	-13,7890094	-0,57594926	6134,11	CALCOCO2	calcium binding and coiled-coil domain 2
105372876	7,40E-02	1,13E+00	5,86E-02	0,3047	-1,8909336	-0,57618126	31,85	DYRK3-AS1	DYRK3 antisense RNA 1
100287177	4,66E-04	3,33E+00	2,98E-04	0,1593	-3,6171438	-0,57626774	121,64	EML2-AS1	EML2 antisense RNA 1
23264	1,54E-27	2,68E+01	4,16E-28	0,0524	-10,9923404	-0,57637126	4662,07	ZC3H7B	zinc finger CCCH-type containing 7B
9016	3,49E-09	8,46E+00	1,67E-09	0,0956	-6,0273101	-0,57641555	371,87	SLC25A14	solute carrier family 25 member 14
55929	9,70E-18	1,70E+01	3,45E-18	0,0663	-8,6954617	-0,57654275	1313,67	DMAP1	DNA methyltransferase 1 associated protein 1
55095	7,17E-31	3,01E+01	1,78E-31	0,0494	-11,6714834	-0,57673055	5286,55	SAMD4B	sterile alpha motif domain containing 4B
27339	4,94E-43	4,23E+01	9,25E-44	0,0416	-13,8728923	-0,57679524	9929,58	PRPF19	pre-mRNA processing factor 19
10094	5,73E-56	5,52E+01	8,01E-57	0,0364	-15,885301	-0,57745216	13605,13	ARPC3	actin related protein 2/3 complex subunit 3
1915	3,64E-67	6,64E+01	3,96E-68	0,0331	-17,4419607	-0,57771916	489185,45	EEF1A1	eukaryotic translation elongation factor 1 alpha 1
9881	1,04E-10	9,98E+00	4,66E-11	0,0878	-6,5814801	-0,57797676	509,8	TRANK1	tetratricopeptide repeat and ankyrin repeat containing 1
693140	8,08E-02	1,09E+00	6,44E-02	0,3127	-1,8495265	-0,57837174	29,9	MIR555	microRNA 555
637	1,04E-23	2,30E+01	3,11E-24	0,0569	-10,1562705	-0,57837785	1576,73	BID	BH3 interacting domain death agonist
57647	7,13E-21	2,01E+01	2,32E-21	0,061	-9,4897766	-0,57854279	1567,51	DHX37	DEAH-box helicase 37
283008	1,02E-03	2,99E+00	6,69E-04	0,1701	-3,4021133	-0,57867166	105,91	NUTM2E	NUT family member 2E
1725	4,20E-29	2,84E+01	1,09E-29	0,0512	-11,316273	-0,57896451	4295,39	DHPS	deoxyhypusine synthase
79644	3,51E-13	1,25E+01	1,44E-13	0,0783	-7,3923151	-0,57917543	836,76	SRD5A3	steroid 5 alpha-reductase 3
112268236	1,69E-01	7,72E-01	1,41E-01	0,3933	-1,4731357	-0,57934381	18,87	LOC112268236	
54884	2,93E-32	3,15E+01	7,02E-33	0,0485	-11,9435508	-0,57949018	2274,91	RETSAT	retinol saturase
101060091	3,39E-01	4,70E-01	2,99E-01	0,5584	-1,0380256	-0,57967074	10,34	ACTR3-AS1	ACTR3 antisense RNA 1
645426	2,39E-01	6,22E-01	2,04E-01	0,4567	-1,2695991	-0,57976296	14,11	TMEM191C	transmembrane protein 191C
9820	9,15E-29	2,80E+01	2,39E-29	0,0515	-11,2470527	-0,57977832	4042,37	CUL7	cullin 7
27445	1,50E-12	1,18E+01	6,28E-13	0,0806	-7,1942771	-0,57978143	560,21	PCLO	piccolo presynaptic cytomatrix protein
105375216	1,88E-01	7,26E-01	1,58E-01	0,4106	-1,4120591	-0,57980513	17,4	LOC105375216	uncharacterized LOC105375216
83756	8,92E-02	1,05E+00	7,15E-02	0,3218	-1,8020757	-0,57986522	29,14	TAS1R3	taste 1 receptor member 3
9605	6,55E-09	8,18E+00	3,17E-09	0,0979	-5,9226974	-0,58000145	392	VPS9D1	VPS9 domain containing 1
6239	8,58E-27	2,61E+01	2,37E-27	0,0535	-10,8342555	-0,58004537	1727,61	RREB1	ras responsive element binding protein 1
152579	7,43E-16	1,51E+01	2,80E-16	0,0709	-8,1815204	-0,58032146	887,12	SCFD2	sec1 family domain containing 2
11060	6,99E-32	3,12E+01	1,69E-32	0,0489	-11,8701038	-0,58037497	2480,76	WWP2	WW domain containing E3 ubiquitin protein ligase 2
80741	1,41E-02	1,85E+00	1,03E-02	0,2263	-2,5660739	-0,58057868	60,86	LY6G5C	lymphocyte antigen 6 family member G5C
8938	2,08E-08	7,68E+00	1,03E-08	0,1014	-5,726221	-0,58065342	376,78	BAIAP3	BAI1 associated protein 3
55544	2,18E-14	1,37E+01	8,62E-15	0,0749	-7,7581757	-0,58080317	752,57	RBM38	RNA binding motif protein 38
10956	1,88E-45	4,47E+01	3,33E-46	0,0407	-14,2706579	-0,58085366	5998,68	OS9	OS9 endoplasmic reticulum lectin
6119	1,75E-17	1,68E+01	6,27E-18	0,0673	-8,6274509	-0,58092265	1169	RPA3	replication protein A3
105370947	1,38E-01	8,60E-01	1,14E-01	0,3675	-1,5809386	-0,58103174	21,94	LOC105370947	uncharacterized LOC105370947
54475	1,22E-23	2,29E+01	3,67E-24	0,0573	-10,1399655	-0,58104235	1778,2	NLE1	notchless homolog 1
105372233	2,70E-05	4,57E+00	1,58E-05	0,1346	-4,3170176	-0,58114859	175,67	BSG-AS1	BSG antisense RNA 1
9238	4,30E-24	2,34E+01	1,28E-24	0,0568	-10,2425081	-0,58149263	4640,07	TBRG4	transforming growth factor beta regulator 4
55644	8,35E-30	2,91E+01	2,13E-30	0,0508	-11,4585712	-0,58171181	2631,29	OSGEP	O-sialoglycoprotein endopeptidase
26099	5,97E-36	3,52E+01	1,31E-36	0,046	-12,6377296	-0,58179033	7624,63	SZRD1	SUZ RNA binding domain containing 1
9382	2,51E-32	3,16E+01	6,02E-33	0,0487	-11,9562465	-0,58208822	2696,06	COG1	component of oligomeric golgi complex 1
221120	7,74E-24	2,31E+01	2,32E-24	0,0572	-10,1848761	-0,58222723	1462,84	ALKBH3	alkB homolog 3, alpha-ketoglutarate dependent dioxygenase
23274	1,39E-19	1,89E+01	4,68E-20	0,0635	-9,171254	-0,58239809	1114,47	CLEC16A	C-type lectin domain containing 16A
374955	2,30E-36	3,56E+01	4,96E-37	0,0458	-12,7136947	-0,58251346	3894,06	SPATA21	spermatogenesis associated 21
23229	2,42E-22	2,16E+01	7,52E-23	0,0592	-9,8406147	-0,5826792	1265,53	ARHGEF9	Cdc42 guanine nucleotide exchange factor 9
54784	2,02E-08	7,69E+00	1,00E-08	0,1017	-5,730721	-0,58292341	344,06	ALKBH4	alkB homolog 4, lysine demethylase
54946	1,85E-28	2,77E+01	4,90E-29	0,0522	-11,1837701	-0,58331006	2061,73	SLC41A3	solute carrier family 41 member 3
106635683	2,41E-02	1,62E+00	1,80E-02	0,2466	-2,366568	-0,58359691	459,59	SNORD141A	small nucleolar RNA, C/D box 141A
55286	2,61E-18	1,76E+01	9,12E-19	0,066	-8,8453745	-0,58396785	1064,55	C4orf19	chromosome 4 open reading frame 19
728621	5,22E-07	6,28E+00	2,77E-07	0,1137	-5,1385024	-0,58410626	246,33	CCDC30	coiled-coil domain containing 30
6626	8,01E-38	3,71E+01	1,68E-38	0,045	-12,9755175	-0,58440038	3453,66	SNRPA	small nuclear ribonucleoprotein polypeptide A
692094	2,16E-11	1,07E+01	9,46E-12	0,0858	-6,8145231	-0,58443972	485,74	MSMP	microseminoprotein, prostate associated
8352	6,60E-03	2,18E+00	4,65E-03	0,2065	-2,8303633	-0,58448127	71,88	H3C3	H3 clustered histone 3
112268055	9,62E-07	6,02E+00	5,18E-07	0,1165	-5,0194125	-0,58452969	269,08	LOC112268055	uncharacterized LOC112268055
55845	2,56E-33	3,26E+01	6,00E-34	0,0481	-12,1463775	-0,58467112	6364,95	BRK1	BRICK1 subunit of SCAR/WAVE actin nucleating complex
64320	5,24E-18	1,73E+01	1,85E-18	0,0667	-8,7663426	-0,5846884	1413,01	RNF25	ring finger protein 25
23151	7,04E-12	1,12E+01	3,02E-12	0,0838	-6,9768231	-0,58481471	513,17	GRAMD4	GRAM domain containing 4
9903	1,62E-26	2,58E+01	4,51E-27	0,0543	-10,7751328	-0,58494114	2576,76	KLHL21	kelch like family member 21
64834	1,61E-37	3,68E+01	3,40E-38	0,0453	-12,9215141	-0,58502145	7577,89	ELOVL1	ELOVL fatty acid elongase 1
643866	6,09E-02	1,22E+00	4,78E-02	0,2956	-1,979443	-0,58504402	35,4	CBLN3	cerebellin 3 precursor
10867	6,72E-26	2,52E+01	1,90E-26	0,055	-10,6419879	-0,585119	1837,77	TSPAN9	tetraspanin 9
1514	3,42E-42	4,15E+01	6,53E-43	0,0426	-13,7319666	-0,58514857	6061,09	CTSL	cathepsin L
221937	5,26E-22	2,13E+01	1,65E-22	0,0599	-9,7611717	-0,58516882	1982,43	FOXK1	forkhead box K1
85012	1,42E-19	1,88E+01	4,77E-20	0,0638	-9,1690619	-0,58523152	2693,51	TCEAL3	transcription elongation factor A like 3
101928707	2,92E-02	1,53E+00	2,20E-02	0,2555	-2,2909483	-0,58527826	47,18	CD2BP2-DT	CD2BP2 divergent transcript
100526772	7,09E-06	5,15E+00	4,00E-06	0,1269	-4,6112387	-0,58536571	203,79	STIMATE-MU	STIMATE-MUSTN1 readthrough
57862	1,55E-28	2,78E+01	4,10E-29	0,0523	-11,1995787	-0,5855223	2228,09	ZNF410	zinc finger protein 410
152002	8,25E-32	3,11E+01	2,00E-32	0,0494	-11,8561254	-0,58557412	2698,58	XXYLT1	xyloside xylosyltransferase 1
14	2,07E-28	2,77E+01	5,47E-29	0,0524	-11,1738878	-0,58575602	4102,61	AAMP	angio associated migratory cell protein
441168	4,72E-02	1,33E+00	3,65E-02	0,2801	-2,0913977	-0,585813	40,51	CALHM6	calcium homeostasis modulator family member 6
201176	1,24E-21	2,09E+01	3,93E-22	0,0606	-9,6729388	-0,58586636	1633,79	ARHGAP27	Rho GTPase activating protein 27
166647	1,17E-41	4,09E+01	2,26E-42	0,043	-13,6418923	-0,5860647	5247,96	ADGRA3	adhesion G protein-coupled receptor A3
9578	5,84E-45	4,42E+01	1,05E-45	0,0413	-14,1906483	-0,58636519	6250,73	CDC42BPB	CDC42 binding protein kinase beta
10540	1,13E-47	4,69E+01	1,89E-48	0,0401	-14,6268274	-0,586372	6601,29	DCTN2	dynactin subunit 2
53	4,93E-23	2,23E+01	1,50E-23	0,0586	-10,0013191	-0,58654671	1793,33	ACP2	acid phosphatase 2, lysosomal
8021	3,57E-36	3,54E+01	7,80E-37	0,0463	-12,6783422	-0,58658539	5477,94	NUP214	nucleoporin 214
102465511	4,92E-03	2,31E+00	3,42E-03	0,2006	-2,9267822	-0,58706851	74,63	MIR6848	microRNA 6848
8638	7,70E-26	2,51E+01	2,18E-26	0,0552	-10,6291331	-0,58724914	1887,05	OASL	2'-5'-oligoadenylate synthetase like
25886	1,26E-27	2,69E+01	3,40E-28	0,0533	-11,0106003	-0,58735083	2531,7	POC1A	POC1 centriolar protein A
221060	2,15E-01	6,68E-01	1,82E-01	0,4403	-1,3340356	-0,58738383	15,56	RPP38-DT	RPP38 divergent transcript
2962	1,60E-45	4,48E+01	2,83E-46	0,0411	-14,2821908	-0,58768427	7975,45	GTF2F1	general transcription factor IIF subunit 1
100379571	5,11E-05	4,29E+00	3,04E-05	0,1409	-4,1707457	-0,58769398	171,99	BACE1-AS	BACE1 antisense RNA
4524	1,21E-13	1,29E+01	4,91E-14	0,078	-7,5343398	-0,58803716	626,86	MTHFR	methylenetetrahydrofolate reductase
56850	2,71E-26	2,56E+01	7,59E-27	0,0548	-10,7271689	-0,58829495	2230,57	GRIPAP1	GRIP1 associated protein 1
6222	1,16E-40	3,99E+01	2,28E-41	0,0437	-13,4722035	-0,5883672	77345,98	RPS18	ribosomal protein S18
84944	2,21E-02	1,66E+00	1,63E-02	0,2453	-2,4010361	-0,58886163	51,14	MAEL	maelstrom spermatogenic transposon silencer
23309	6,56E-39	3,82E+01	1,35E-39	0,0447	-13,1677112	-0,588991	4979,61	SIN3B	SIN3 transcription regulator family member B

100126793	2,08E-02	1,68E+00	1,53E-02	0,243	-2,4242055	-0,58915848	52,52	GHRLOS	ghrelin opposite strand/antisense RNA
10970	1,18E-57	5,69E+01	1,58E-58	0,0365	-16,1295565	-0,58936516	15019,29	CKAP4	cytoskeleton associated protein 4
2805	1,42E-39	3,88E+01	2,87E-40	0,0444	-13,283987	-0,58937945	3780,07	GOT1	glutamic-oxaloacetic transaminase 1
127829	5,79E-18	1,72E+01	2,04E-18	0,0673	-8,7549242	-0,58940737	1027,71	ARL8A	ADP ribosylation factor like GTPase 8A
10524	1,67E-38	3,78E+01	3,44E-39	0,045	-13,0965692	-0,5897072	3306,42	KAT5	lysine acetyltransferase 5
57715	4,88E-05	4,31E+00	2,90E-05	0,1411	-4,1814178	-0,58994615	161,08	SEMA4G	semaphorin 4G
56246	4,94E-04	3,31E+00	3,17E-04	0,1638	-3,6012857	-0,58998239	112,37	MRAP	melanocortin 2 receptor accessory protein
124056	9,15E-02	1,04E+00	7,34E-02	0,3296	-1,790312	-0,59001776	28,66	NOXO1	NADPH oxidase organizer 1
80724	2,95E-13	1,25E+01	1,21E-13	0,0796	-7,4159993	-0,59003448	570,23	ACAD10	acyl-CoA dehydrogenase family member 10
2738	1,14E-08	7,94E+00	5,55E-09	0,1012	-5,8299296	-0,59013279	335,54	GLI4	GLI family zinc finger 4
57095	3,96E-25	2,44E+01	1,14E-25	0,0563	-10,4734117	-0,59015376	1555,86	PITHD1	PITH domain containing 1
10106	1,99E-41	4,07E+01	3,86E-42	0,0434	-13,6026247	-0,59032971	5756,69	CTDSP2	CTD small phosphatase 2
102724668	2,57E-02	1,59E+00	1,92E-02	0,2521	-2,3416357	-0,59040303	46,46	DPY19L1P2	DPY19L1 pseudogene 2
145853	1,24E-03	2,91E+00	8,20E-04	0,1765	-3,3458192	-0,59069509	116,83	C15orf61	chromosome 15 open reading frame 61
85016	4,63E-02	1,33E+00	3,57E-02	0,2813	-2,1001316	-0,59079167	38,36	CFAP300	cilia and flagella associated protein 300
4733	7,92E-37	3,61E+01	1,70E-37	0,0462	-12,7971577	-0,59086483	3187,43	DRG1	developmentally regulated GTP binding protein 1
842	8,79E-16	1,51E+01	3,32E-16	0,0724	-8,1609754	-0,59092165	740,89	CASP9	caspase 9
16	2,00E-53	5,27E+01	2,95E-54	0,0381	-15,5103679	-0,59092448	8576,76	AARS1	alanyl-tRNA synthetase 1
286140	6,07E-02	1,22E+00	4,76E-02	0,2983	-1,9813172	-0,5910306	35,06	RNF5P1	ring finger protein 5 pseudogene 1
5724	1,22E-01	9,14E-01	1,00E-01	0,3595	-1,6443958	-0,59118235	23,23	PTAFR	platelet activating factor receptor
26088	1,01E-17	1,70E+01	3,61E-18	0,0681	-8,6903125	-0,59157659	1214,16	GGA1	golgi associated, gamma adaptin ear containing, ARF binding protein 1
23082	1,60E-29	2,88E+01	4,12E-30	0,0519	-11,4013335	-0,59159708	3988,77	PPRC1	PPARG related coactivator 1
7706	7,69E-55	5,41E+01	1,10E-55	0,0376	-15,7199412	-0,59160748	10021,95	TRIM25	tripartite motif containing 25
201255	7,50E-15	1,41E+01	2,92E-15	0,075	-7,8940997	-0,59181402	699,27	LRRC45	leucine rich repeat containing 45
6184	2,83E-51	5,05E+01	4,35E-52	0,039	-15,18642	-0,59186616	11564,48	RPN1	ribophorin I
8692	4,26E-23	2,24E+01	1,30E-23	0,0591	-10,0159573	-0,59197649	2099,08	HYAL2	hyaluronidase 2
10287	9,30E-15	1,40E+01	3,64E-15	0,0753	-7,8667862	-0,59202631	776,06	RGS19	regulator of G protein signaling 19
1762	1,34E-19	1,89E+01	4,51E-20	0,0646	-9,1750538	-0,59227278	1070,84	DMWD	DM1 locus, WD repeat containing
474338	2,72E-03	2,57E+00	1,85E-03	0,1903	-3,1131662	-0,59229377	134,78	SUMO1P3	SUMO1 pseudogene 3
285368	2,01E-04	3,70E+00	1,25E-04	0,1545	-3,8357111	-0,5925785	138,34	PRRT3	proline rich transmembrane protein 3
55280	3,44E-26	2,55E+01	9,68E-27	0,0554	-10,7046675	-0,59274386	1493,45	CWF19L1	CWF19 like cell cycle control factor 1
6207	6,80E-43	4,22E+01	1,28E-43	0,0428	-13,8496433	-0,59297843	13924,93	RPS13	ribosomal protein S13
65059	1,16E-32	3,19E+01	2,76E-33	0,0493	-12,0209779	-0,59310431	3739,41	RAPH1	Ras association (RalGDS/AF-6) and pleckstrin homology domains 1
51253	4,40E-43	4,24E+01	8,22E-44	0,0428	-13,8813308	-0,59342964	5841,47	MRPL37	mitochondrial ribosomal protein L37
64976	9,69E-22	2,10E+01	3,06E-22	0,0612	-9,6985033	-0,59346704	1225,96	MRPL40	mitochondrial ribosomal protein L40
51256	9,77E-09	8,01E+00	4,75E-09	0,1014	-5,8555959	-0,59353849	339,72	TBC1D7	TBC1 domain family member 7
22839	1,70E-38	3,78E+01	3,51E-39	0,0453	-13,0951976	-0,59361684	5345,83	DLGAP4	DLG associated protein 4
105376860	1,49E-07	6,83E+00	7,66E-08	0,1105	-5,3748711	-0,59367355	285,88	LOC105376	uncharacterized LOC105376860
9145	4,54E-03	2,34E+00	3,15E-03	0,2011	-2,9524221	-0,59370076	76,74	SYNGR1	synaptogyrin 1
1327	5,15E-35	3,43E+01	1,16E-35	0,0477	-12,4651587	-0,59411103	6304,65	COX4I1	cytochrome c oxidase subunit 4I1
100506668	8,79E-11	1,01E+01	3,93E-11	0,09	-6,6066628	-0,59454479	447,22	NRAV	negative regulator of antiviral response
8189	4,30E-27	2,64E+01	1,18E-27	0,0546	-10,8980272	-0,59459581	5892,17	SYMPK	symplekin scaffold protein
10548	5,16E-43	4,23E+01	9,67E-44	0,0429	-13,8696568	-0,59460977	4474,66	TM9SF1	transmembrane 9 superfamily member 1
55182	3,35E-30	2,95E+01	8,47E-31	0,0515	-11,5381842	-0,59462558	2486,72	RNF220	ring finger protein 220
84993	6,78E-21	2,02E+01	2,20E-21	0,0626	-9,4950646	-0,59474591	1904,47	UBL7	ubiquitin like 7
1032	1,60E-30	2,98E+01	4,01E-31	0,0513	-11,6023622	-0,59513514	2201,84	CDKN2D	cyclin dependent kinase inhibitor 2D
22818	4,75E-42	4,13E+01	9,10E-43	0,0434	-13,7079428	-0,59514007	5168,78	COPZ1	COPI coat complex subunit zeta 1
261734	2,97E-13	1,25E+01	1,22E-13	0,0803	-7,4149638	-0,59527153	627,62	NPHP4	nephrocystin 4
54932	9,42E-08	7,03E+00	4,81E-08	0,1091	-5,4581287	-0,59556949	308,85	EXD3	exonuclease 3'-5' domain containing 3
10272	4,46E-15	1,44E+01	1,73E-15	0,0748	-7,959595	-0,59576767	1075,33	FSTL3	follistatin like 3
5977	1,47E-33	3,28E+01	3,43E-34	0,0489	-12,1919725	-0,59584509	2891,4	DPF2	double PHD fingers 2
7436	3,62E-21	2,04E+01	1,17E-21	0,0624	-9,5610847	-0,59636368	1152,38	VLDLR	very low density lipoprotein receptor
51231	3,56E-20	1,94E+01	1,18E-20	0,064	-9,3186484	-0,59654814	1228,57	VRK3	VRK serine/threonine kinase 3
100528064	2,59E-36	3,56E+01	5,61E-37	0,047	-12,7041093	-0,59658979	3076,43	NEDD8-MDF	NEDD8-MDP1 readthrough
102724397	9,17E-03	2,04E+00	6,56E-03	0,2195	-2,7184803	-0,59659093	69,54	TWSG1-DT	TWSG1 divergent transcript
100125556	5,29E-03	2,28E+00	3,69E-03	0,2055	-2,903409	-0,59675832	75,27	FAM86JP	family with sequence similarity 86, member A pseudogene
51343	4,26E-25	2,44E+01	1,23E-25	0,0571	-10,4664332	-0,59716279	2095,75	FZR1	fizzy and cell division cycle 20 related 1
4540	9,63E-22	2,10E+01	3,04E-22	0,0616	-9,6992172	-0,59729917	110224,43	ND5	NADH dehydrogenase subunit 5
3131	6,47E-02	1,19E+00	5,09E-02	0,3061	-1,9525108	-0,5975857	31,43	HLF	HLF transcription factor, PAR bZIP family member
56006	2,49E-28	2,76E+01	6,60E-29	0,0536	-11,1573004	-0,59761582	3822,84	SMG9	SMG9 nonsense mediated mRNA decay factor
145483	1,34E-13	1,29E+01	5,44E-14	0,0795	-7,5209259	-0,59804054	569,66	FAM161B	FAM161 centrosomal protein B
101928953	2,97E-08	7,53E+00	1,48E-08	0,1056	-5,6637673	-0,59836294	331	LOC101928	uncharacterized LOC101928953
3712	8,02E-36	3,51E+01	1,77E-36	0,0474	-12,6140727	-0,59843225	2534,51	IVD	isovaleryl-CoA dehydrogenase
102723342	5,97E-22	2,12E+01	1,88E-22	0,0614	-9,748281	-0,5987801	1445,83	LOC102723	uncharacterized LOC102723342
57513	1,36E-16	1,59E+01	4,99E-17	0,0714	-8,3868222	-0,59891469	850,7	CASKIN2	CASK interacting protein 2
139596	1,09E-15	1,50E+01	4,12E-16	0,0737	-8,1349835	-0,5992537	734,8	UPRT	uracil phosphoribosyltransferase homolog
653162	2,21E-09	8,66E+00	1,05E-09	0,0982	-6,1017634	-0,59940306	380,1	RPSAP9	ribosomal protein SA pseudogene 9
105378912	6,88E-05	4,16E+00	4,13E-05	0,1462	-4,1001233	-0,59963676	144,58	LINC01357	long intergenic non-protein coding RNA 1357
60685	3,58E-57	5,64E+01	4,88E-58	0,0373	-16,0598619	-0,59968632	9131,92	ZFAND3	zinc finger AN1-type containing 3
55568	3,81E-56	5,54E+01	5,31E-57	0,0377	-15,9110611	-0,59984981	8595,34	GALNT10	polypeptide N-acetylgalactosaminyltransferase 10
388789	1,39E-16	1,59E+01	5,11E-17	0,0716	-8,3841022	-0,60006512	1200,08	SMIM26	small integral membrane protein 26
26995	1,11E-31	3,10E+01	2,71E-32	0,0507	-11,8305972	-0,60016528	2250,42	TRUB2	TruB pseudouridine synthase family member 2
23098	2,13E-10	9,67E+00	9,70E-11	0,0928	-6,4715457	-0,60032288	403,09	SARM1	sterile alpha and TIR motif containing 1
105372245	6,58E-03	2,18E+00	4,64E-03	0,2121	-2,8313007	-0,60048721	67,83	LOC105372	uncharacterized LOC105372245
100506555	2,80E-01	5,53E-01	2,43E-01	0,5146	-1,1675533	-0,60080517	11,89	NECTIN3-AS	NECTIN3 antisense RNA 1
3780	2,86E-01	5,44E-01	2,48E-01	0,5205	-1,1550829	-0,60122201	11,35	KCNN1	potassium calcium-activated channel subfamily N member 1
29796	2,41E-39	3,86E+01	4,92E-40	0,0454	-13,2435622	-0,60144063	3542,45	UQCR10	ubiquinol-cytochrome c reductase, complex III subunit X
164091	1,01E-21	2,10E+01	3,19E-22	0,062	-9,6941896	-0,60145796	1166,03	PAQR7	progestin and adipoQ receptor family member 7
90007	1,48E-21	2,08E+01	4,72E-22	0,0623	-9,6541902	-0,60165815	1235,06	MIDN	midnolin
441869	4,31E-02	1,37E+00	3,31E-02	0,2825	-2,1307542	-0,60198418	38,51	ANKRD65	ankyrin repeat domain 65
207	4,74E-33	3,23E+01	1,12E-33	0,0498	-12,095387	-0,60217186	6950,24	AKT1	AKT serine/threonine kinase 1
221908	5,12E-07	6,29E+00	2,71E-07	0,1171	-5,1422575	-0,60220114	280,49	PPP1R35	protein phosphatase 1 regulatory subunit 35
4351	4,74E-35	3,43E+01	1,06E-35	0,0483	-12,4717598	-0,60231413	2409,34	MPI	mannose phosphate isomerase
6548	1,30E-25	2,49E+01	3,71E-26	0,0569	-10,5795633	-0,60238742	2181,08	SLC9A1	solute carrier family 9 member A1
100861541	3,00E-01	5,23E-01	2,62E-01	0,5368	-1,1224468	-0,60255362	10,63	DOCK9-DT	DOCK9 divergent transcript
84905	9,39E-08	7,03E+00	4,79E-08	0,1104	-5,458862	-0,60275086	314,92	ZNF341	zinc finger protein 341
1743	4,05E-51	5,04E+01	6,25E-52	0,0398	-15,1626687	-0,60276659	7289,23	DLST	dihydrolipoamide S-succinyltransferase
26037	1,53E-41	4,08E+01	2,97E-42	0,0443	-13,6219017	-0,60278474	4394,01	SIPA1L1	signal induced proliferation associated 1 like 1
8798	1,51E-17	1,68E+01	5,41E-18	0,0697	-8,6444699	-0,60287973	812,06	DYRK4	dual specificity tyrosine phosphorylation regulated kinase 4
5832	2,93E-50	4,95E+01	4,62E-51	0,0401	-15,0306648	-0,60300137	5395,85	ALDH18A1	aldehyde dehydrogenase 18 family member A1
3225	2,53E-01	5,97E-01	2,18E-01	0,4893	-1,2329278	-0,60331126	13,39	HOXC9	homeobox C9
1374	1,14E-48	4,79E+01	1,86E-49	0,0408	-14,7837795	-0,60337794	6308,29	CPT1A	carnitine palmitoyltransferase 1A
23420	4,60E-47	4,63E+01	7,81E-48	0,0415	-14,5301133	-0,60338834	9986,73	NOMO1	NODAL modulator 1
55794	3,71E-14	1,34E+01	1,48E-14	0,0785	-7,6893872	-0,60342479	587,69	DDX28	DEAD-box helicase 28
1437	2,61E-27	2,66E+01	7,10E-28	0,0551	-10,9440449	-0,60345921	2393,15	CSF2	colony stimulating factor 2
5546	3,59E-34	3,34E+01	8,22E-35	0,049	-12,3078362	-0,60359732	3000,62	PRCC	proline rich mitotic checkpoint control factor
101927098	3,45E-03	2,46E+00	2,37E-03	0,1986	-3,039717	-0,60375183	79,68	LOC101927	uncharacterized LOC101927098
2195	1,04E-48	4,80E+01	1,70E-49	0,0408	-14,7901124	-0,60379058	24497,32	FAT1	FAT atypical cadherin 1
9181	9,56E-53	5,20E+01	1,43E-53	0,0392	-15,4087687	-0,60379518	7008,69	ARHGEF2	Rho/Rac guanine nucleotide exchange factor 2
4239	1,69E-02	1,77E+00	1,23E-02	0,2414	-2,5022186	-0,60397514	53,3	MFAP4	microfibril associated protein 4
105372141	1,20E-02	1,92E+00	8,65E-03	0,2301	-2,6254177	-0,60398063	56,79	LOC105372	uncharacterized LOC105372141
79109	2,32E-50	4,96E+01	3,65E-51	0,0402	-15,0463363	-0,60432855	7747,7	MAPKAP1	MAPK associated protein 1
55651	1,61E-34	3,38E+01	3,65E-35	0,0488	-12,3731448	-0,60434041	3896,42	NHP2	NHP2 ribonucleoprotein
100507002	5,25E-06	5,28E+00	2,95E-06	0,1293	-4,6745048	-0,6045327	207,8	LOC100507	uncharacterized LOC100507002
9921	2,26E-60	5,96E+01	2,87E-61	0,0366	-16,5147884	-0,60464354	11727,54	RNF10	ring finger protein 10
7355	5,92E-20	1,92E+01	1,97E-20	0,0653	-9,263863	-0,6047512	1358,14	SLC35A2	solute carrier family 35 member A2
4297	1,92E-36	3,57E+01	4,15E-37	0,0475	-12,7277462	-0,60481418	8183,21	KMT2A	lysine methyltransferase 2A
10491	2,48E-55	5,46E+01	3,51E-56	0,0383	-15,7923192	-0,6049713	14896,96	CRTAP	cartilage associated protein
10628	8,84E-55	5,41E+01	1,27E-55	0,0385	-15,7110845	-0,6052355	15590,98	TXNIP	thioredoxin interacting protein
55147	3,02E-34	3,35E+01	6,90E-35	0,0491	-12,3219123	-0,60532961	4354,28	RBM23	RNA binding motif protein 23
101927245	6,08E-02	1,22E+00	4,76E-02	0,3056	-1,9806633	-0,60537374	32,86	LOC101927	uncharacterized LOC101927245
55974	7,29E-37	3,61E+01	1,56E-37	0,0473	-12,8037895	-0,6055676	2656,64	SLC50A1	solute carrier family 50 member 1
10383	7,43E-37	3,61E+01	1,59E-37	0,0473	-12,8022081	-0,60567641	39043,76	TUBB4B	tubulin beta 4B class IVb
8992	1,30E-27	2,69E+01	3,51E-28	0,055	-11,0076114	-0,60572473	6161,7	ATP6V0E1	ATPase H+ transporting V0 subunit e1
54978	1,72E-21	2,08E+01	5,48E-22	0,0629	-9,6389349	-0,60584752	1480,03	SLC35F6	solute carrier family 35 member F6
57506	7,53E-50	4,91E+01	1,20E-50	0,0405	-14,9674555	-0,6061935	8949,88	MAVS	mitochondrial antiviral signaling protein
9600	1,71E-20	1,98E+01	5,61E-21	0,0645	-9,3971486	-0,60622714	1589,46	PITPNM1	phosphatidylinositol transfer protein membrane associated 1
8664	9,47E-60	5,90E+01	1,22E-60	0,0369	-16,427326	-0,606349	13735,36	EIF3D	eukaryotic translation initiation factor 3 subunit D
2683	2,81E-50	4,96E+01	4,42E-51	0,0404	-15,0336414	-0,60675165	7178,52	B4GALT1	beta-1,4-galactosyltransferase 1
4597	4,30E-14	1,34E+01	1,72E-14	0,0791	-7,6702073	-0,60707147	864,64	MVD	mevalonate diphosphate decarboxylase

8544	7,57E-04	3,12E+00	4,92E-04	0,1742	-3,4848757	-0,60713031	101,81	PIR	pirin
7709	8,74E-22	2,11E+01	2,76E-22	0,0625	-9,7091144	-0,6072083	1218,34	ZBTB17	zinc finger and BTB domain containing 17
646019	2,00E-01	6,99E-01	1,69E-01	0,4417	-1,3749058	-0,60724498	14,94	CBY3	chibby family member 3
4547	2,35E-01	6,29E-01	2,01E-01	0,4748	-1,2789511	-0,60730632	12,92	MTTP	microsomal triglyceride transfer protein
55260	1,18E-07	6,93E+00	6,05E-08	0,1121	-5,4172231	-0,60733321	278,01	TMEM143	transmembrane protein 143
129563	3,55E-24	2,34E+01	1,05E-24	0,0592	-10,2611007	-0,60734911	1310,95	DIS3L2	DIS3 like 3'-5' exoribonuclease 2
156	2,95E-29	2,85E+01	7,61E-30	0,0535	-11,3477991	-0,60748022	2062,28	GRK2	G protein-coupled receptor kinase 2
102723475	2,30E-01	6,38E-01	1,96E-01	0,4698	-1,2936634	-0,60771017	14,1	LOC102723	potassium voltage-gated channel subfamily E regulatory subunit 1B
22859	1,69E-22	2,18E+01	5,23E-23	0,0615	-9,8770679	-0,60792375	1328,07	ADGRL1	adhesion G protein-coupled receptor L1
10296	1,93E-35	3,47E+01	4,28E-36	0,0485	-12,5441396	-0,60798918	3878,46	MAEA	macrophage erythroblast attacher, E3 ubiquitin ligase
991	1,32E-55	5,49E+01	1,87E-56	0,0384	-15,832176	-0,60811616	15427	CDC20	cell division cycle 20
22884	3,66E-23	2,24E+01	1,11E-23	0,0606	-10,0311424	-0,60829725	1194,64	WDR37	WD repeat domain 37
5739	8,58E-23	2,21E+01	2,64E-23	0,0612	-9,9454294	-0,6083912	1663,48	PTGIR	prostaglandin I2 receptor
729438	1,53E-06	5,82E+00	8,34E-07	0,1235	-4,9271293	-0,60841342	214,92	CASTOR2	cytosolic arginine sensor for mTORC1 subunit 2
55654	9,17E-42	4,10E+01	1,77E-42	0,0445	-13,6595007	-0,60852178	4338,53	TMEM127	transmembrane protein 127
5447	3,74E-16	1,54E+01	1,40E-16	0,0737	-8,264954	-0,60936557	1222,04	POR	cytochrome p450 oxidoreductase
92675	3,08E-38	3,75E+01	6,42E-39	0,0467	-13,049271	-0,60940347	3544,27	DTD1	D-aminoacyl-tRNA deacylase 1
23085	9,06E-32	3,10E+01	2,20E-32	0,0514	-11,8481709	-0,60947674	3342,79	ERC1	ELKS/RAB6-interacting/CAST family member 1
102724316	1,09E-28	2,80E+01	2,87E-29	0,0543	-11,2310206	-0,60971697	1584,05	SVIL-AS1	SVIL antisense RNA 1
788	7,24E-12	1,11E+01	3,11E-12	0,0875	-6,9727632	-0,60992587	626,15	SLC25A20	solute carrier family 25 member 20
4234	2,18E-18	1,77E+01	7,61E-19	0,0688	-8,8656518	-0,61008636	830	METTL1	methyltransferase 1, tRNA methylguanosine
54458	1,18E-33	3,29E+01	2,75E-34	0,05	-12,209874	-0,61012203	3280,97	PRR13	proline rich 13
105371841	2,99E-01	5,24E-01	2,61E-01	0,5424	-1,1250837	-0,61020144	9,83	LOC105371	uncharacterized LOC105371841
59342	1,37E-33	3,29E+01	3,20E-34	0,05	-12,1976142	-0,61038174	2302,84	SCPEP1	serine carboxypeptidase 1
29946	5,02E-19	1,83E+01	1,72E-19	0,0676	-9,0300958	-0,61040149	890,47	SERTAD3	SERTA domain containing 3
105379271	2,37E-01	6,25E-01	2,03E-01	0,4797	-1,2727472	-0,61049557	12,58	LOC105379	uncharacterized LOC105379271
8668	2,12E-52	5,17E+01	3,19E-53	0,0398	-15,3567164	-0,61067849	16868,21	EIF3I	eukaryotic translation initiation factor 3 subunit I
57136	2,33E-55	5,46E+01	3,31E-56	0,0387	-15,7960951	-0,61071187	7746,14	APMAP	adipocyte plasma membrane associated protein
9817	4,35E-34	3,34E+01	9,99E-35	0,0497	-12,292103	-0,61114543	5034,25	KEAP1	kelch like ECH associated protein 1
130557	2,44E-05	4,61E+00	1,42E-05	0,1409	-4,3402412	-0,61141214	169,1	ZNF513	zinc finger protein 513
9727	1,07E-20	2,00E+01	3,50E-21	0,0647	-9,4465602	-0,61141675	1181,3	RAB11FIP3	RAB11 family interacting protein 3
8892	6,25E-45	4,42E+01	1,12E-45	0,0431	-14,1858528	-0,61169512	4081,24	EIF2B2	eukaryotic translation initiation factor 2B subunit beta
23762	1,88E-03	2,73E+00	1,26E-03	0,1898	-3,2252537	-0,6120414	84,6	OSBP2	oxysterol binding protein 2
3566	1,03E-28	2,80E+01	2,69E-29	0,0545	-11,2369268	-0,61208576	2253,36	IL4R	interleukin 4 receptor
140459	8,01E-23	2,21E+01	2,46E-23	0,0616	-9,9523766	-0,61284764	2018,08	ASB6	ankyrin repeat and SOCS box containing 6
100289092	6,39E-03	2,19E+00	4,50E-03	0,2158	-2,8407751	-0,61302094	64,57	ATP2A1-AS1	ATP2A1 antisense RNA 1
81618	7,56E-34	3,31E+01	1,75E-34	0,0501	-12,2467444	-0,61315323	2558,43	ITM2C	integral membrane protein 2C
203245	4,67E-12	1,13E+01	1,99E-12	0,0872	-7,0348497	-0,613194	463,76	NAIF1	nuclear apoptosis inducing factor 1
162461	6,88E-14	1,32E+01	2,76E-14	0,0806	-7,6090953	-0,61322564	857,86	TMEM92	transmembrane protein 92
105377016	1,70E-01	7,70E-01	1,42E-01	0,4175	-1,4688815	-0,61328536	16,75	LOC105377	uncharacterized LOC105377016
30818	3,40E-14	1,35E+01	1,35E-14	0,0797	-7,7007637	-0,61351241	742,44	KCNIP3	potassium voltage-gated channel interacting protein 3
135154	5,80E-11	1,02E+01	2,58E-11	0,092	-6,669027	-0,61357921	527,84	SDHAF4	succinate dehydrogenase complex assembly factor 4
26191	3,91E-10	9,41E+00	1,80E-10	0,0962	-6,3779106	-0,61383427	385,55	PTPN22	protein tyrosine phosphatase non-receptor type 22
100505826	9,70E-02	1,01E+00	7,81E-02	0,3485	-1,761744	-0,61405384	24,48	STK4-DT	STK4 divergent transcript
6302	7,62E-30	2,91E+01	1,94E-30	0,0536	-11,4665711	-0,61413033	2156,36	TSPAN31	tetraspanin 31
151534	1,18E-06	5,93E+00	6,37E-07	0,1233	-4,9797601	-0,61416465	234,17	LBX2-AS1	LBX2 antisense RNA 1
51317	1,29E-17	1,69E+01	4,61E-18	0,0709	-8,662695	-0,61432774	1137,43	PHF21A	PHD finger protein 21A
23583	4,92E-13	1,23E+01	2,03E-13	0,0836	-7,3467587	-0,61445013	521,55	SMUG1	single-strand-selective monofunctional uracil-DNA glycosylase 1
90809	3,95E-22	2,14E+01	1,23E-22	0,0628	-9,7907346	-0,61446861	1436,81	PIP4P1	phosphatidylinositol-4,5-bisphosphate 4-phosphatase 1
5935	1,11E-61	6,10E+01	1,37E-62	0,0368	-16,6974438	-0,6147731	20385,77	RBM3	RNA binding motif protein 3
643246	4,27E-04	3,37E+00	2,72E-04	0,1689	-3,6404975	-0,6148679	116,4	MAP1LC3B2	microtubule associated protein 1 light chain 3 beta 2
100506100	1,58E-09	8,80E+00	7,43E-10	0,0999	-6,1566266	-0,61510018	332,75	ZDHHC12-D	ZDHHC12 divergent transcript
101928378	7,11E-17	1,61E+01	2,60E-17	0,0727	-8,4634671	-0,61513549	761,75	PTOV1-AS2	PTOV1 antisense RNA 2
57805	1,83E-40	3,97E+01	3,62E-41	0,0458	-13,4381075	-0,61520278	5600,72	CCAR2	cell cycle and apoptosis regulator 2
307	3,92E-27	2,64E+01	1,07E-27	0,0564	-10,9066483	-0,61531746	1673,64	ANXA4	annexin A4
8228	3,35E-14	1,35E+01	1,33E-14	0,0799	-7,702846	-0,61531771	560,98	PNPLA4	patatin like phospholipase domain containing 4
107985355	2,49E-01	6,04E-01	2,14E-01	0,4951	-1,2428722	-0,61535982	11,93	LOC107985	uncharacterized LOC107985355
4566	7,90E-06	5,10E+00	4,48E-06	0,1341	-4,5878006	-0,61538717	184,65	TRNK	tRNA-Lys
118813	5,99E-21	2,02E+01	1,94E-21	0,0647	-9,5081444	-0,61545906	1007,7	ZFYVE27	zinc finger FYVE-type containing 27
2288	2,44E-48	4,76E+01	4,03E-49	0,0418	-14,7317436	-0,61546968	5852,46	FKBP4	FKBP prolyl isomerase 4
10456	2,55E-40	3,96E+01	5,06E-41	0,0459	-13,4132288	-0,61557587	4302,73	HAX1	HCLS1 associated protein X-1
11343	2,59E-43	4,26E+01	4,83E-44	0,0442	-13,9194386	-0,61558258	3832,71	MGLL	monoglyceride lipase
7916	7,94E-43	4,21E+01	1,50E-43	0,0445	-13,8383783	-0,61565519	27914,39	PRRC2A	proline rich coiled-coil 2A
7353	6,93E-40	3,92E+01	1,39E-40	0,0462	-13,3379639	-0,61575198	2910,06	UFD1	ubiquitin recognition factor in ER associated degradation 1
23293	7,66E-36	3,51E+01	1,69E-36	0,0488	-12,617677	-0,61621545	2777,28	SMG6	SMG6 nonsense mediated mRNA decay factor
128240	4,89E-36	3,53E+01	1,07E-36	0,0487	-12,6534369	-0,61622112	3026,48	NAXE	NAD(P)HX epimerase
54531	3,05E-21	2,05E+01	9,79E-22	0,0644	-9,5790507	-0,61672839	1094,25	MIER2	MIER family member 2
79132	9,67E-06	5,01E+00	5,51E-06	0,1358	-4,5443398	-0,61693967	192,75	DHX58	DExH-box helicase 58
9755	7,90E-06	5,10E+00	4,48E-06	0,1345	-4,5878282	-0,617113	188,26	TBKBP1	TBK1 binding protein 1
79845	1,34E-02	1,87E+00	9,72E-03	0,2387	-2,5856986	-0,6171341	58,13	RNF122	ring finger protein 122
5305	5,21E-34	3,33E+01	1,20E-34	0,0503	-12,2773796	-0,6171463	2693,52	PIP4K2A	phosphatidylinositol-5-phosphate 4-kinase type 2 alpha
81570	5,71E-31	3,02E+01	1,41E-31	0,0528	-11,691166	-0,61721283	2279,07	CLPB	caseinolytic mitochondrial matrix peptidase chaperone subunit B
83658	1,08E-32	3,20E+01	2,58E-33	0,0513	-12,026532	-0,61730334	8563,25	DYNLRB1	dynein light chain roadblock-type 1
2931	4,77E-34	3,33E+01	1,10E-34	0,0503	-12,2846155	-0,61783548	5041,34	GSK3A	glycogen synthase kinase 3 alpha
2533	3,05E-01	5,16E-01	2,67E-01	0,5564	-1,1106367	-0,61792369	9,81	FYB1	FYN binding protein 1
55707	7,56E-42	4,11E+01	1,46E-42	0,0452	-13,6738194	-0,61798732	4335,59	NECAP2	NECAP endocytosis associated 2
506	4,13E-60	5,94E+01	5,28E-61	0,0375	-16,4780564	-0,61815427	30185,73	ATP5F1B	ATP synthase F1 subunit beta
146330	4,78E-02	1,32E+00	3,69E-02	0,2964	-2,0863967	-0,61842329	36,79	FBXL16	F-box and leucine rich repeat protein 16
287	1,27E-21	2,09E+01	4,03E-22	0,064	-9,6702529	-0,61848244	1035,6	ANK2	ankyrin 2
387680	5,65E-42	4,12E+01	1,08E-42	0,0452	-13,695262	-0,61853418	3949,62	WASHC2A	WASH complex subunit 2A
8663	1,74E-61	6,08E+01	2,15E-62	0,0371	-16,6703956	-0,61856	13431,19	EIF3C	eukaryotic translation initiation factor 3 subunit C
26519	2,26E-24	2,36E+01	6,67E-25	0,0601	-10,3053002	-0,61885596	1542,85	TIMM10	translocase of inner mitochondrial membrane 10
83606	6,18E-39	3,82E+01	1,27E-39	0,047	-13,17221	-0,61907377	4515,71	GUCD1	guanylyl cyclase domain containing 1
102465248	2,64E-05	4,58E+00	1,55E-05	0,1432	-4,3220638	-0,61912627	157,1	MIR6501	microRNA 6501
152641	1,61E-01	7,93E-01	1,33E-01	0,4126	-1,500658	-0,61918424	17,33	WWC2-AS2	WWC2 antisense RNA 2
100996702	7,94E-09	8,10E+00	3,85E-09	0,1051	-5,8905599	-0,61929715	308,46	LINC01356	long intergenic non-protein coding RNA 1356
11333	2,47E-45	4,46E+01	4,38E-46	0,0435	-14,251545	-0,61938195	7106,92	PDAP1	PDGFA associated protein 1
339344	9,67E-10	9,01E+00	4,51E-10	0,0994	-6,2351619	-0,61952632	335	MYPOP	Myb related transcription factor, partner of profilin
148979	1,18E-01	9,28E-01	9,60E-02	0,3723	-1,6647874	-0,61977018	22,02	GLIS1	GLIS family zinc finger 1
2749	2,40E-02	1,62E+00	1,78E-02	0,2617	-2,3692504	-0,61995306	45,75	GLUD1P3	glutamate dehydrogenase 1 pseudogene 3
670	4,66E-14	1,33E+01	1,86E-14	0,081	-7,6598537	-0,6201277	576,2	BPHL	biphenyl hydrolase like
10965	5,35E-23	2,23E+01	1,63E-23	0,0621	-9,9930572	-0,62016881	1281,63	ACOT2	acyl-CoA thioesterase 2
129804	1,52E-05	4,82E+00	8,79E-06	0,1397	-4,4448771	-0,62082686	161,47	FBLN7	fibulin 7
100874014	1,72E-07	6,76E+00	8,93E-08	0,1161	-5,3472737	-0,62095079	271,7	NAV2-AS2	NAV2 antisense RNA 2
100289341	6,05E-05	4,22E+00	3,61E-05	0,1503	-4,1308196	-0,62105598	135,56	MAN1B1-DT	MAN1B1 divergent transcript
10276	6,42E-33	3,22E+01	1,52E-33	0,0515	-12,0703012	-0,62113524	7827,12	NET1	neuroepithelial cell transforming 1
8536	6,62E-21	2,02E+01	2,15E-21	0,0654	-9,4976643	-0,62128983	984,82	CAMK1	calcium/calmodulin dependent protein kinase I
100506779	4,52E-22	2,13E+01	1,42E-22	0,0636	-9,7767706	-0,62131891	1054,22	TSPOAP1-A	TSPOAP1, SUPT4H1 and RNF43 antisense RNA 1
105372935	9,70E-02	1,01E+00	7,81E-02	0,3527	-1,7617557	-0,62136351	24,3	FAM247A	family with sequence similarity 247 member A
83886	1,42E-01	8,48E-01	1,17E-01	0,3962	-1,5683176	-0,62142166	19,03	PRSS27	serine protease 27
80346	1,38E-26	2,59E+01	3,83E-27	0,0576	-10,7901208	-0,62162728	1374,31	REEP4	receptor accessory protein 4
101928525	1,20E-14	1,39E+01	4,71E-15	0,0794	-7,8344896	-0,62168633	874,24	LOC101928	uncharacterized LOC101928525
118812	2,41E-14	1,36E+01	9,54E-15	0,0803	-7,7451829	-0,6217423	601,59	MORN4	MORN repeat containing 4
10765	1,93E-42	4,17E+01	3,65E-43	0,0451	-13,7739848	-0,62175769	3833,74	KDM5B	lysine demethylase 5B
414918	2,19E-02	1,66E+00	1,62E-02	0,2586	-2,4041386	-0,62177377	44,64	DENND6B	DENN domain containing 6B
8602	1,70E-55	5,48E+01	2,40E-56	0,0394	-15,8163722	-0,62238766	6749,66	NOP14	NOP14 nucleolar protein
280664	1,26E-01	9,00E-01	1,03E-01	0,3825	-1,6301635	-0,62350262	21,64	WFDC10B	WAP four-disulfide core domain 10B
5688	7,31E-46	4,51E+01	1,28E-46	0,0435	-14,3371557	-0,62376821	11374,31	PSMA7	proteasome 20S subunit alpha 7
5224	1,59E-01	7,99E-01	1,32E-01	0,4141	-1,5062593	-0,62379409	18,18	PGAM2	phosphoglycerate mutase 2
283820	8,63E-55	5,41E+01	1,24E-55	0,0397	-15,7126011	-0,62387726	8801,22	NOMO2	NODAL modulator 2
10061	5,30E-51	5,03E+01	8,20E-52	0,0412	-15,1447738	-0,62404687	4649,05	ABCF2	ATP binding cassette subfamily F member 2
23208	2,15E-03	2,67E+00	1,45E-03	0,1961	-3,1846205	-0,62442547	79,04	SYT11	synaptotagmin 11
54663	3,13E-34	3,35E+01	7,16E-35	0,0507	-12,3189285	-0,62446341	2218,79	WDR74	WD repeat domain 74
79591	7,07E-31	3,02E+01	1,76E-31	0,0535	-11,6727409	-0,6244817	1729,68	ARMH3	armadillo like helical domain containing 3
79877	1,08E-12	1,20E+01	4,51E-13	0,0863	-7,2392128	-0,6248546	624,43	DCAKD	dephospho-CoA kinase domain containing
11000	2,28E-04	3,64E+00	1,43E-04	0,1644	-3,8036283	-0,62525185	123,42	SLC27A3	solute carrier family 27 member 3
100505771	9,92E-05	4,00E+00	6,02E-05	0,1559	-4,0119601	-0,6253094	131,68	MHENCR	melanoma highly expressed competing endogenous lncRNA for miR-425 and miR-489
128866	5,12E-54	5,33E+01	7,46E-55	0,0401	-15,5984251	-0,62566036	8381,95	CHMP4B	charged multivesicular body protein 4B
5920	2,82E-11	1,05E+01	1,24E-11	0,0924	-6,7757578	-0,62577002	453,33	PLAAT4	phospholipase A and acyltransferase 4
4574	1,09E-33	3,30E+01	2,54E-34	0,0513	-12,2165064	-0,62634662	3977,13	TRNS1	tRNA-Ser

164284	1,25E-24	2,39E+01	3,67E-25	0,0605	-10,3626859	-0,62654419	1798,75	APCDD1L	APC down-regulated 1 like
2661	3,94E-16	1,54E+01	1,47E-16	0,0759	-8,2587432	-0,62722595	1155,48	GDF9	growth differentiation factor 9
80709	7,24E-13	1,21E+01	3,01E-13	0,086	-7,2941337	-0,62764479	656,41	AKNA	AT-hook transcription factor
23608	4,52E-38	3,73E+01	9,45E-39	0,0482	-13,0197279	-0,62769678	2536,44	MKRN1	makorin ring finger protein 1
6827	1,47E-41	4,08E+01	2,85E-42	0,0461	-13,6248497	-0,62770093	3122,07	SUPT4H1	SPT4 homolog, DSIF elongation factor subunit
8535	9,74E-15	1,40E+01	3,81E-15	0,0799	-7,8609497	-0,62776039	595,48	CBX4	chromobox 4
1984	3,44E-55	5,45E+01	4,90E-56	0,0398	-15,7713788	-0,62779302	30356,85	EIF5A	eukaryotic translation initiation factor 5A
55111	1,97E-16	1,57E+01	7,29E-17	0,0753	-8,3422535	-0,6281375	748,96	PLEKHJ1	pleckstrin homology domain containing J1
51428	2,41E-37	3,66E+01	5,12E-38	0,0487	-12,8900539	-0,62815101	3394,28	DDX41	DEAD-box helicase 41
1877	1,59E-13	1,28E+01	6,46E-14	0,0838	-7,4983507	-0,62852725	580,55	E4F1	E4F transcription factor 1
516	4,43E-29	2,84E+01	1,15E-29	0,0556	-11,3116226	-0,62855983	5872,26	ATP5MC1	ATP synthase membrane subunit c locus 1
84284	3,01E-21	2,05E+01	9,67E-22	0,0656	-9,5803229	-0,62871474	949,22	NTPCR	nucleoside-triphosphatase, cancer-related
100313837	1,73E-02	1,76E+00	1,27E-02	0,2522	-2,4925581	-0,62873178	46,66	MIR762	microRNA 762
115110	2,27E-03	2,64E+00	1,54E-03	0,1985	-3,1679583	-0,62893013	78,44	TNFRSF14-A	TNFRSF14 antisense RNA 1
84536	2,53E-06	5,60E+00	1,39E-06	0,1304	-4,82627	-0,62930091	208,72	LINC01547	long intergenic non-protein coding RNA 1547
101929270	1,91E-01	7,19E-01	1,60E-01	0,4485	-1,4036448	-0,62952776	16,22	LOC101929	uncharacterized LOC101929270
5702	3,64E-60	5,94E+01	4,66E-61	0,0382	-16,4856132	-0,62954321	12697,38	PSMC3	proteasome 26S subunit, ATPase 3
7407	7,58E-34	3,31E+01	1,75E-34	0,0514	-12,2465113	-0,62959208	12009,95	VARS1	valyl-tRNA synthetase 1
10516	7,55E-04	3,12E+00	4,91E-04	0,1806	-3,48547	-0,62963227	99,13	FBLN5	fibulin 5
55743	7,22E-23	2,21E+01	2,22E-23	0,0632	-9,9628743	-0,62964349	1323,13	CHFR	checkpoint with forkhead and ring finger domains
80020	6,12E-29	2,82E+01	1,59E-29	0,0558	-11,2829203	-0,62976314	1724,15	FOXRED2	FAD dependent oxidoreductase domain containing 2
51287	6,57E-34	3,32E+01	1,51E-34	0,0514	-12,2584305	-0,62993172	2729,38	COA4	cytochrome c oxidase assembly factor 4 homolog
9701	6,71E-26	2,52E+01	1,90E-26	0,0592	-10,6421407	-0,62994874	1408,36	PPP6R2	protein phosphatase 6 regulatory subunit 2
101928745	1,51E-01	8,21E-01	1,25E-01	0,4112	-1,5321602	-0,63003272	17,55	LL21NC02-2	uncharacterized LL21NC02-21A1.1
9616	1,01E-29	2,90E+01	2,57E-30	0,0551	-11,44225	-0,6301543	2216,51	RNF7	ring finger protein 7
11315	5,54E-55	5,43E+01	7,93E-56	0,04	-15,7409076	-0,63025294	8988,37	PARK7	Parkinsonism associated deglycase
3588	2,88E-28	2,75E+01	7,67E-29	0,0566	-11,1438983	-0,63025315	1438,69	IL10RB	interleukin 10 receptor subunit beta
9435	8,94E-16	1,50E+01	3,38E-16	0,0772	-8,1589749	-0,63027185	618,54	CHST2	carbohydrate sulfotransferase 2
667	5,55E-40	3,93E+01	1,11E-40	0,0472	-13,3546848	-0,63031039	21177,41	DST	dystonin
91039	1,11E-44	4,40E+01	2,00E-45	0,0446	-14,1450097	-0,630335	4935,81	DPP9	dipeptidyl peptidase 9
25974	1,43E-40	3,98E+01	2,81E-41	0,0468	-13,4566597	-0,6304395	3716,39	MMACHC	metabolism of cobalamin associated C
57659	1,94E-44	4,37E+01	3,53E-45	0,0447	-14,1051322	-0,63061463	5426,55	ZBTB4	zinc finger and BTB domain containing 4
955	1,71E-35	3,48E+01	3,80E-36	0,0502	-12,5536553	-0,63068213	2928,1	ENTPD6	ectonucleoside triphosphate diphosphohydrolase 6
161	2,71E-38	3,76E+01	5,64E-39	0,0483	-13,0590567	-0,63091343	4042,74	AP2A2	adaptor related protein complex 2 subunit alpha 2
25906	1,54E-21	2,08E+01	4,91E-22	0,0654	-9,6501573	-0,63104209	966,95	ANAPC15	anaphase promoting complex subunit 15
9796	2,60E-02	1,59E+00	1,94E-02	0,2701	-2,3370359	-0,63113496	40,54	PHYHIP	phytanoyl-CoA 2-hydroxylase interacting protein
4555	2,53E-02	1,60E+00	1,89E-02	0,2689	-2,347284	-0,6311661	216,83	TRND	tRNA-Asp
642658	4,51E-09	8,35E+00	2,16E-09	0,1055	-5,985001	-0,63131977	309,12	SCX	scleraxis bHLH transcription factor
283951	1,13E-09	8,95E+00	5,30E-10	0,1017	-6,209879	-0,63144296	417,76	UQCC4	ubiquinol-cytochrome c reductase complex assembly factor 4
4849	9,27E-38	3,70E+01	1,95E-38	0,0487	-12,9642585	-0,63147676	3242,24	CNOT3	CCR4-NOT transcription complex subunit 3
5338	5,27E-20	1,93E+01	1,75E-20	0,0681	-9,2765446	-0,63156553	1026,78	PLD2	phospholipase D2
54704	1,20E-31	3,09E+01	2,93E-32	0,0534	-11,8241308	-0,63196664	2361,12	PDP1	pyruvate dehydrogenase phosphatase catalytic subunit 1
51292	4,36E-46	4,54E+01	7,59E-47	0,044	-14,3734517	-0,63235477	3669,91	GMPR2	guanosine monophosphate reductase 2
107984537	1,06E-04	3,97E+00	6,43E-05	0,1583	-3,9964327	-0,6328156	126,12	LOC107984	uncharacterized LOC107984537
1613	9,47E-18	1,70E+01	3,37E-18	0,0728	-8,6983488	-0,6329171	1764,18	DAPK3	death associated protein kinase 3
51090	5,19E-11	1,03E+01	2,30E-11	0,0947	-6,685524	-0,63298447	381,01	PLLP	plasmolipin
2778	1,24E-51	5,09E+01	1,90E-52	0,0415	-15,2407629	-0,63310871	40225,57	GNAS	GNAS complex locus
3300	2,48E-18	1,76E+01	8,65E-19	0,0715	-8,8513256	-0,63319127	938,77	DNAJB2	DnaJ heat shock protein family (Hsp40) member B2
253980	3,61E-14	1,34E+01	1,44E-14	0,0823	-7,6928694	-0,63323645	588,7	KCTD13	potassium channel tetramerization domain containing 13
4675	1,98E-09	8,70E+00	9,38E-10	0,1035	-6,1195384	-0,63332629	415,42	NAP1L3	nucleosome assembly protein 1 like 3
10980	5,12E-47	4,63E+01	8,69E-48	0,0436	-14,5227544	-0,63345788	4681,75	COPS6	COP9 signalosome subunit 6
102465256	3,01E-04	3,52E+00	1,90E-04	0,1697	-3,7325225	-0,63355713	107,02	MIR6513	microRNA 6513
100532742	1,26E-03	2,90E+00	8,33E-04	0,1897	-3,3417376	-0,6338267	85,83	PIR-FIGF	PIR-FIGF readthrough
283219	1,85E-17	1,67E+01	6,63E-18	0,0736	-8,6210913	-0,63423934	690,59	KCTD21	potassium channel tetramerization domain containing 21
7965	3,24E-30	2,95E+01	8,20E-31	0,055	-11,540997	-0,63430422	1987,37	AIMP2	aminoacyl tRNA synthetase complex interacting multifunctional protein 2
51006	1,90E-37	3,67E+01	4,02E-38	0,0491	-12,908611	-0,63433631	3546,31	SLC35C2	solute carrier family 35 member C2
90736	9,00E-11	1,00E+01	4,03E-11	0,0961	-6,6031476	-0,6346496	385,17	FAM104B	family with sequence similarity 104 member B
58476	3,32E-39	3,85E+01	6,78E-40	0,048	-13,219419	-0,63473168	2575,41	TP53INP2	tumor protein p53 inducible nuclear protein 2
730183	2,90E-03	2,54E+00	1,97E-03	0,2052	-3,0940041	-0,63480013	74,04	LOC730183	uncharacterized LOC730183
1020	9,24E-19	1,80E+01	3,18E-19	0,0708	-8,9621281	-0,63480383	1226,22	CDK5	cyclin dependent kinase 5
54977	9,55E-35	3,40E+01	2,16E-35	0,0511	-12,415332	-0,63481082	2080,6	SLC25A38	solute carrier family 25 member 38
1267	3,83E-51	5,04E+01	5,91E-52	0,0419	-15,1663177	-0,63489408	6077,2	CNP	2',3'-cyclic nucleotide 3' phosphodiesterase
101928845	1,82E-01	7,40E-01	1,53E-01	0,444	-1,4300991	-0,63489956	15,56	LINC01842	long intergenic non-protein coding RNA 1842
100534595	1,52E-44	4,38E+01	2,75E-45	0,045	-14,1227326	-0,6351477	5349,17	HNRNPUL2-	HNRNPUL2-BSCL2 readthrough (NMD candidate)
4682	1,23E-26	2,59E+01	3,40E-27	0,0588	-10,8011448	-0,63517343	1397,8	NUBP1	NUBP iron-sulfur cluster assembly factor 1, cytosolic
5452	9,63E-36	3,50E+01	2,13E-36	0,0504	-12,5993763	-0,63530958	3962,56	POU2F2	POU class 2 homeobox 2
8793	1,67E-50	4,98E+01	2,62E-51	0,0422	-15,0681894	-0,63547233	4334,19	TNFRSF10D	TNF receptor superfamily member 10d
8425	4,10E-27	2,64E+01	1,12E-27	0,0583	-10,9022575	-0,63575565	2646,26	LTBP4	latent transforming growth factor beta binding protein 4
22883	6,78E-63	6,22E+01	8,07E-64	0,0377	-16,8655396	-0,63605004	12496,95	CLSTN1	calsyntenin 1
408050	2,71E-52	5,16E+01	4,09E-53	0,0415	-15,3406823	-0,63624219	6585,18	NOMO3	NODAL modulator 3
8557	1,77E-01	7,52E-01	1,49E-01	0,4404	-1,4447912	-0,63630531	16,36	TCAP	titin-cap
84247	4,38E-34	3,34E+01	1,00E-34	0,0518	-12,2916063	-0,63654038	2469,76	RTL6	retrotransposon Gag like 6
100526693	2,63E-34	3,36E+01	6,00E-35	0,0516	-12,3331955	-0,63662104	2172,89	ARPC4-TTLI	ARPC4-TTLL3 readthrough
57507	5,26E-17	1,63E+01	1,91E-17	0,075	-8,4988831	-0,63711233	676,51	ZNF608	zinc finger protein 608
113189	3,95E-23	2,24E+01	1,20E-23	0,0636	-10,0235764	-0,63711681	1160,43	CHST14	carbohydrate sulfotransferase 14
754	2,53E-70	6,96E+01	2,57E-71	0,0357	-17,8565852	-0,63719009	31526,56	PTTG1IP	PTTG1 interacting protein
441263	1,36E-11	1,09E+01	5,89E-12	0,0926	-6,8823614	-0,63723109	441,88	DTX2P1-UPI	DTX2P1-UPK3BP1-PMS2P11 readthrough, transcribed pseudogene
8882	7,38E-53	5,21E+01	1,10E-53	0,0413	-15,4256383	-0,63744123	5233,33	ZPR1	ZPR1 zinc finger
105376810	1,51E-01	8,21E-01	1,25E-01	0,4154	-1,5348719	-0,63761356	16,9	LOC105376	uncharacterized LOC105376810
91272	2,21E-49	4,87E+01	3,53E-50	0,0428	-14,8953405	-0,63764561	4003,35	BOD1	biorientation of chromosomes in cell division 1
51409	9,06E-13	1,20E+01	3,77E-13	0,0878	-7,2634466	-0,63772594	556,68	HEMK1	HemK methyltransferase family member 1
203069	1,41E-19	1,89E+01	4,73E-20	0,0695	-9,169904	-0,63775823	1024,97	R3HCC1	R3H domain and coiled-coil containing 1
80764	6,61E-17	1,62E+01	2,41E-17	0,0753	-8,4719345	-0,63783661	813,85	THAP7	THAP domain containing 7
5264	2,03E-20	1,97E+01	6,67E-21	0,068	-9,378819	-0,63793743	866,3	PHYH	phytanoyl-CoA 2-hydroxylase
338692	4,78E-19	1,83E+01	1,63E-19	0,0706	-9,035379	-0,63793944	1014,52	ANKRD13D	ankyrin repeat domain 13D
119504	7,58E-40	3,91E+01	1,52E-40	0,0479	-13,3311978	-0,63808123	2766,71	ANAPC16	anaphase promoting complex subunit 16
125206	3,69E-07	6,43E+00	1,94E-07	0,1226	-5,2046917	-0,63817683	218,91	SLC5A10	solute carrier family 5 member 10
55701	2,02E-28	2,77E+01	5,35E-29	0,0571	-11,1758714	-0,6384926	1422,62	ARHGEF40	Rho guanine nucleotide exchange factor 40
162989	4,57E-25	2,43E+01	1,32E-25	0,0611	-10,4595806	-0,63857721	1411,03	DEDD2	death effector domain containing 2
246721	1,76E-16	1,58E+01	6,52E-17	0,0765	-8,3554839	-0,63881312	723,02	POLR2J2	RNA polymerase II subunit J2
644619	3,98E-02	1,40E+00	3,04E-02	0,2952	-2,1645062	-0,63887534	34,3	INTS4P2	integrator complex subunit 4 pseudogene 2
8996	1,34E-17	1,69E+01	4,80E-18	0,0738	-8,6581155	-0,63892779	753,27	NOL3	nucleolar protein 3
109729181	2,95E-04	3,53E+00	1,86E-04	0,171	-3,7373847	-0,63926599	103,28	ZNF710-AS1	ZNF710 antisense RNA 1
6228	2,38E-58	5,76E+01	3,14E-59	0,0395	-16,2290686	-0,64040124	33691,55	RPS23	ribosomal protein S23
105372419	2,61E-09	8,58E+00	1,24E-09	0,1054	-6,0743436	-0,64040138	302,53	GEMIN7-AS	GEMIN7 antisense RNA 1
402682	5,01E-02	1,30E+00	3,88E-02	0,31	-2,0661742	-0,64054494	34,4	UFSP1	UFM1 specific peptidase 1 (inactive)
8501	4,24E-12	1,14E+01	1,81E-12	0,0909	-7,0484161	-0,6405513	442,94	SLC43A1	solute carrier family 43 member 1
107984504	1,84E-02	1,74E+00	1,35E-02	0,2594	-2,4697823	-0,6406388	45,42	CPNE8-AS1	CPNE8 antisense RNA 1
11277	1,65E-04	3,78E+00	1,02E-04	0,1649	-3,886556	-0,64107471	115,77	TREX1	three prime repair exonuclease 1
8398	1,10E-03	2,96E+00	7,23E-04	0,1897	-3,3807854	-0,64124738	85,93	PLA2G6	phospholipase A2 group VI
54961	8,70E-10	9,06E+00	4,05E-10	0,1026	-6,2519234	-0,64133302	368,84	SSH3	slingshot protein phosphatase 3
58488	9,81E-29	2,80E+01	2,57E-29	0,0571	-11,2408148	-0,64136925	1333,73	PCTP	phosphatidylcholine transfer protein
389058	1,40E-04	3,85E+00	8,61E-05	0,1633	-3,9267066	-0,64141399	123,06	SP5	Sp5 transcription factor
84274	5,69E-24	2,32E+01	1,70E-24	0,0628	-10,21511	-0,6416012	1107,27	COQ5	coenzyme Q5, methyltransferase
9775	1,15E-54	5,39E+01	1,66E-55	0,0409	-15,6941253	-0,64170053	6418,19	EIF4A3	eukaryotic translation initiation factor 4A3
10580	2,41E-04	3,62E+00	1,51E-04	0,1693	-3,7897565	-0,64173533	108,58	SORBS1	sorbin and SH3 domain containing 1
105370707	9,81E-02	1,01E+00	7,91E-02	0,3655	-1,7560461	-0,6418103	23,76	LOC105370	707
105377769	1,14E-01	9,43E-01	9,25E-02	0,3815	-1,68252	-0,64182354	20,63	TRIM7-AS2	TRIM7 antisense RNA 2
9772	1,13E-25	2,49E+01	3,21E-26	0,0606	-10,5929027	-0,64205953	2159,07	TMEM94	transmembrane protein 94
100132948	3,28E-03	2,48E+00	2,25E-03	0,2101	-3,0556877	-0,64206852	69,76	FAM27C	family with sequence similarity 27 member C
26277	1,43E-34	3,38E+01	3,25E-35	0,0519	-12,3825041	-0,64227133	2487,39	TINF2	TERF1 interacting nuclear factor 2
169792	4,98E-11	1,03E+01	2,21E-11	0,0961	-6,6916467	-0,64310562	396,71	GLIS3	GLIS family zinc finger 3
1659	1,64E-51	5,08E+01	2,50E-52	0,0423	-15,2227367	-0,64328466	6704,05	DHX8	DEAH-box helicase 8
283551	3,90E-10	9,41E+00	1,79E-10	0,1009	-6,3784247	-0,64347252	343,09	LINC01588	long intergenic non-protein coding RNA 1588
5269	1,63E-56	5,58E+01	2,25E-57	0,0403	-15,9646726	-0,64355095	6710,89	SERPINB6	serpin family B member 6
3856	6,74E-51	5,02E+01	1,05E-51	0,0425	-15,1287883	-0,64355578	24184,67	KRT8	keratin 8
23466	2,39E-38	3,76E+01	4,97E-39	0,0492	-13,0687805	-0,64357405	2605,77	CBX6	chromobox 6
105379036	2,66E-01	5,75E-01	2,29E-01	0,5354	-1,2020749	-0,64361315	10,44	LINC02122	long intergenic non-protein coding RNA 2122
3090	4,45E-18	1,74E+01	1,57E-18	0,0733	-8,7848851	-0,64373728	747,07	HIC1	HIC ZBTB transcriptional repressor 1
79192	3,41E-02	1,47E+00	2,59E-02	0,289	-2,2278399	-0,64373908	36,97	IRX1	iroquois homeobox 1

220136	1,05E-01	9,79E-01	8,54E-02	0,3742	-1,7203734	-0,64376792	21,81	CFAP53	cilia and flagella associated protein 53
84973	5,22E-23	2,23E+01	1,59E-23	0,0644	-9,9955603	-0,643769	1096,03	SNHG7	small nucleolar RNA host gene 7
92659	1,92E-07	6,72E+00	9,94E-08	0,1209	-5,3278973	-0,64426846	229,22	MILIP	MYC inducible lncRNA inactivating p53
29	2,67E-51	5,06E+01	4,10E-52	0,0424	-15,1903502	-0,64455802	6976,89	ABR	ABR activator of RhoGEF and GTPase
5463	7,97E-07	6,10E+00	4,27E-07	0,1275	-5,0566387	-0,64493748	202,19	POU6F1	POU class 6 homeobox 1
5909	7,89E-02	1,10E+00	6,27E-02	0,3467	-1,8613285	-0,64524541	31,7	RAP1GAP	RAP1 GTPase activating protein
107986152	1,89E-01	7,24E-01	1,59E-01	0,4583	-1,4078961	-0,64528227	15,33	LOC107986152	
23406	5,39E-62	6,13E+01	6,57E-63	0,0386	-16,7411992	-0,64537907	15602,19	COTL1	coactosin like F-actin binding protein 1
84447	3,28E-31	3,05E+01	8,09E-32	0,055	-11,7384994	-0,64549126	3184,64	SYVN1	synoviolin 1
25813	7,45E-28	2,71E+01	2,00E-28	0,0584	-11,0582278	-0,64576796	2461,94	SAMM50	SAMM50 sorting and assembly machinery component
27106	1,16E-26	2,59E+01	3,21E-27	0,0598	-10,8065282	-0,64584407	1253,14	ARRDC2	arrestin domain containing 2
27153	7,52E-22	2,11E+01	2,37E-22	0,0664	-9,7245515	-0,64587697	1144,39	ZNF777	zinc finger protein 777
113235	1,18E-14	1,39E+01	4,62E-15	0,0824	-7,8367312	-0,64592878	567,93	SLC46A1	solute carrier family 46 member 1
222699	8,58E-08	7,07E+00	4,37E-08	0,118	-5,4751107	-0,64593281	231,04	TOB2P1	transducer of ERBB2, 2 pseudogene 1
8291	3,93E-33	3,24E+01	9,24E-34	0,0533	-12,1109282	-0,64594952	1883,98	DYSF	dysferlin
5093	5,25E-62	6,13E+01	6,39E-63	0,0386	-16,742785	-0,64604318	15542,57	PCBP1	poly(rC) binding protein 1
100506544	4,23E-06	5,37E+00	2,36E-06	0,1369	-4,7202659	-0,64615577	175,98	L3MBTL2-AS	L3MBTL2 antisense RNA 1
84287	1,53E-43	4,28E+01	2,84E-44	0,0463	-13,9572805	-0,64622872	3538,21	ZDHHC16	zinc finger DHHC-type palmitoyltransferase 16
8227	5,27E-20	1,93E+01	1,75E-20	0,0697	-9,2764738	-0,6462682	898,06	AKAP17A	A-kinase anchoring protein 17A
10189	5,90E-41	4,02E+01	1,16E-41	0,0478	-13,5222919	-0,6463937	3601,88	ALYREF	Aly/REF export factor
7084	2,23E-28	2,77E+01	5,91E-29	0,0579	-11,1670792	-0,64653564	1547,32	TK2	thymidine kinase 2
6497	3,01E-47	4,65E+01	5,09E-48	0,0444	-14,5593408	-0,64700517	3896,38	SKI	SKI proto-oncogene
790	7,93E-48	4,71E+01	1,32E-48	0,0442	-14,651318	-0,6470693	9354,43	CAD	carbamoyl-phosphate synthetase 2, aspartate transcarbamylase, and dihydroorotase
9261	6,20E-60	5,92E+01	7,95E-61	0,0393	-16,4532626	-0,64722278	8116,13	MAPKAPK2	MAPK activated protein kinase 2
770	1,65E-04	3,78E+00	1,02E-04	0,1667	-3,8857906	-0,64760467	129,69	CA11	carbonic anhydrase 11
10525	6,37E-68	6,72E+01	6,79E-69	0,0369	-17,542463	-0,64799805	27903,7	HYOU1	hypoxia up-regulated 1
22870	8,38E-49	4,81E+01	1,37E-49	0,0438	-14,8046828	-0,6480071	6979,67	PPP6R1	protein phosphatase 6 regulatory subunit 1
694	7,67E-37	3,61E+01	1,65E-37	0,0506	-12,7996757	-0,64805066	2689,97	BTG1	BTG anti-proliferation factor 1
105373335	5,49E-06	5,26E+00	3,08E-06	0,139	-4,6653	-0,64826587	196,14	LOC105373	uncharacterized LOC105373335
9094	4,65E-18	1,73E+01	1,64E-18	0,0739	-8,779831	-0,64843529	788,92	UNC119	unc-119 lipid binding chaperone
83451	7,26E-13	1,21E+01	3,01E-13	0,0889	-7,2937517	-0,64846739	481,14	ABHD11	abhydrolase domain containing 11
55362	2,14E-39	3,87E+01	4,34E-40	0,049	-13,252911	-0,64897521	2898,74	TMEM63B	transmembrane protein 63B
64147	1,57E-08	7,80E+00	7,74E-09	0,1125	-5,7739261	-0,64928374	279,25	KIF9	kinesin family member 9
9912	7,91E-02	1,10E+00	6,29E-02	0,3492	-1,8598361	-0,64943054	24,59	ARHGAP44	Rho GTPase activating protein 44
6251	2,25E-46	4,56E+01	3,89E-47	0,0451	-14,4197319	-0,64962804	5480,61	RSU1	Ras suppressor protein 1
100506164	1,83E-01	7,38E-01	1,53E-01	0,4549	-1,4281669	-0,64963601	14,41	HSFX1	heat shock transcription factor family, X-linked 1
8178	5,17E-29	2,83E+01	1,34E-29	0,0575	-11,2979174	-0,64976739	1574,38	ELL	elongation factor for RNA polymerase II
1153	4,66E-48	4,73E+01	7,74E-49	0,0442	-14,6876125	-0,64981089	4664,31	CIRBP	cold inducible RNA binding protein
11331	6,67E-48	4,72E+01	1,11E-48	0,0443	-14,6631862	-0,64986422	7474,69	PHB2	prohibitin 2
10248	4,48E-28	2,73E+01	1,20E-28	0,0585	-11,104247	-0,64993766	1513,27	POP7	POP7 homolog, ribonuclease P/MRP subunit
23654	1,82E-46	4,57E+01	3,14E-47	0,045	-14,4345096	-0,65004053	8521,34	PLXNB2	plexin B2
105376367	3,59E-04	3,44E+00	2,28E-04	0,1764	-3,686286	-0,65011867	100,16	LOC105376	uncharacterized LOC105376367
20	2,11E-22	2,17E+01	6,53E-23	0,066	-9,8548932	-0,65022321	1303,31	ABCA2	ATP binding cassette subfamily A member 2
55735	7,13E-54	5,31E+01	1,04E-54	0,0418	-15,5771359	-0,6504474	4401,57	DNAJC11	DnaJ heat shock protein family (Hsp40) member C11
9682	1,29E-37	3,69E+01	2,71E-38	0,0503	-12,9389159	-0,65048958	2169,31	KDM4A	lysine demethylase 4A
9120	2,67E-03	2,57E+00	1,81E-03	0,2086	-3,1192772	-0,65062301	71,87	SLC16A6	solute carrier family 16 member 6
6499	3,43E-36	3,55E+01	7,46E-37	0,0513	-12,6817642	-0,65069975	4460,46	SKIC2	SKI2 subunit of superkiller complex
56262	2,51E-42	4,16E+01	4,79E-43	0,0473	-13,7544927	-0,65071436	5317,92	LRRC8A	leucine rich repeat containing 8 VRAC subunit A
84687	5,70E-45	4,42E+01	1,02E-45	0,0459	-14,1923511	-0,65073016	3486,26	PPP1R9B	protein phosphatase 1 regulatory subunit 9B
284040	2,95E-10	9,53E+00	1,35E-10	0,1013	-6,4219492	-0,65081282	340,03	CDRT4	CMT1A duplicated region transcript 4
65988	3,91E-10	9,41E+00	1,79E-10	0,1021	-6,3781773	-0,65124171	319,44	ZNF747	zinc finger protein 747
25959	4,45E-55	5,44E+01	6,35E-56	0,0413	-15,7549334	-0,65125714	6545,64	KANK2	KN motif and ankyrin repeat domains 2
139285	6,21E-16	1,52E+01	2,34E-16	0,0794	-8,2034452	-0,65130674	639,6	AMER1	APC membrane recruitment protein 1
8711	2,06E-08	7,69E+00	1,02E-08	0,1138	-5,7279861	-0,65187153	262,3	TNK1	tyrosine kinase non receptor 1
100996842	1,47E-11	1,08E+01	6,36E-12	0,0949	-6,8714034	-0,65207862	381,8	LOC100996	uncharacterized LOC100996842
5705	9,63E-64	6,30E+01	1,13E-64	0,0384	-16,9814141	-0,65249545	11082,62	PSMC5	proteasome 26S subunit, ATPase 5
400892	2,07E-01	6,84E-01	1,75E-01	0,4811	-1,3564877	-0,65261336	12,78	BCRP2	BCR pseudogene 2
28989	4,51E-22	2,13E+01	1,41E-22	0,0668	-9,7771459	-0,65307445	1788,61	NTMT1	N-terminal Xaa-Pro-Lys N-methyltransferase 1
26469	1,66E-24	2,38E+01	4,89E-25	0,0632	-10,3350905	-0,65318517	1255,64	PTPN18	protein tyrosine phosphatase non-receptor type 18
50515	1,33E-64	6,39E+01	1,53E-65	0,0382	-17,0980539	-0,6533641	8483,21	CHST11	carbohydrate sulfotransferase 11
55723	4,28E-53	5,24E+01	6,37E-54	0,0423	-15,4609216	-0,6533819	6280,03	ASF1B	anti-silencing function 1B histone chaperone
1528	9,89E-25	2,40E+01	2,89E-25	0,063	-10,3854908	-0,65403176	1408,59	CYB5A	cytochrome b5 type A
7461	4,70E-28	2,73E+01	1,26E-28	0,0589	-11,0998956	-0,65408023	1584,56	CLIP2	CAP-Gly domain containing linker protein 2
100130987	1,06E-01	9,75E-01	8,63E-02	0,3816	-1,7152482	-0,65446992	20,47	LOC100130	uncharacterized LOC100130987
91373	8,69E-26	2,51E+01	2,47E-26	0,0616	-10,6177174	-0,65450519	1280,59	UAP1L1	UDP-N-acetylglucosamine pyrophosphorylase 1 like 1
30834	1,37E-23	2,29E+01	4,12E-24	0,0646	-10,1287332	-0,654538	1057,9	POLR1H	RNA polymerase I subunit H
64771	3,39E-64	6,35E+01	3,93E-65	0,0384	-17,0430942	-0,65467655	9052,51	ILRUN	inflammation and lipid regulator with UBA-like and NBR1-like domains
11021	8,06E-46	4,51E+01	1,42E-46	0,0457	-14,3302462	-0,65508144	6036,42	RAB35	RAB35, member RAS oncogene family
100506020	1,48E-04	3,83E+00	9,08E-05	0,1674	-3,9139719	-0,65534469	116,52	ARAP1-AS2	ARAP1 antisense RNA 2
50636	2,50E-17	1,66E+01	8,99E-18	0,0764	-8,5861614	-0,65563291	645,34	ANO7	anoctamin 7
51155	5,12E-62	6,13E+01	6,23E-63	0,0392	-16,7443468	-0,65569017	6810,99	JPT1	Jupiter microtubule associated homolog 1
90121	5,73E-39	3,82E+01	1,17E-39	0,0498	-13,1779806	-0,6557925	3002,7	TSR2	TSR2 ribosome maturation factor
25902	3,29E-46	4,55E+01	5,71E-47	0,0456	-14,393211	-0,65583269	3363,57	MTHFD1L	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 1 like
22893	1,56E-25	2,48E+01	4,47E-26	0,0621	-10,5620287	-0,65594478	1210,04	BAHD1	bromo adjacent homology domain containing 1
26073	6,72E-48	4,72E+01	1,12E-48	0,0447	-14,6626173	-0,65596741	7778,61	POLDIP2	DNA polymerase delta interacting protein 2
105378116	3,72E-02	1,43E+00	2,83E-02	0,2992	-2,1924216	-0,65598148	32,67	LOC105378	uncharacterized LOC105378116
6665	8,18E-03	2,09E+00	5,82E-03	0,2379	-2,7579579	-0,65609414	54,25	SOX15	SRY-box transcription factor 15
23386	9,23E-56	5,50E+01	1,30E-56	0,0414	-15,8550709	-0,65660084	6056,56	NUDCD3	NudC domain containing 3
152217	3,99E-18	1,74E+01	1,40E-18	0,0747	-8,7972964	-0,65676283	711,65	NCBP2AS2	NCBP2 antisense 2 (head to head)
7146	1,14E-01	9,43E-01	9,28E-02	0,3907	-1,6810605	-0,65681082	19,94	TNXA	tenascin XA (pseudogene)
6135	4,57E-71	7,03E+01	4,58E-72	0,0366	-17,9525753	-0,65683262	34342,77	RPL11	ribosomal protein L11
29082	2,15E-22	2,17E+01	6,67E-23	0,0667	-9,8527932	-0,65692464	1421,27	CHMP4A	charged multivesicular body protein 4A
107984432	2,06E-01	6,86E-01	1,75E-01	0,4842	-1,3569194	-0,65700854	13,23	LOC107984	uncharacterized LOC107984432
84164	1,53E-34	3,38E+01	3,47E-35	0,0531	-12,3773395	-0,65731166	2064,75	ASCC2	activating signal cointegrator 1 complex subunit 2
6194	1,58E-66	6,58E+01	1,74E-67	0,0379	-17,3573397	-0,6574401	40107,95	RPS6	ribosomal protein S6
29920	3,22E-33	3,25E+01	7,55E-34	0,0542	-12,1274772	-0,65778071	3569,31	PYCR2	pyrroline-5-carboxylate reductase 2
56109	3,86E-03	2,41E+00	2,66E-03	0,2191	-3,0045363	-0,65818529	62,78	PCDHGA6	protocadherin gamma subfamily A, 6
650669	9,97E-24	2,30E+01	2,99E-24	0,0648	-10,1600339	-0,65825082	1196,67	GAS6-AS1	GAS6 antisense RNA 1
105371781	2,33E-01	6,33E-01	1,99E-01	0,5128	-1,2838754	-0,65840792	11,12	RAB5C-AS1	RAB5C antisense RNA 1
100874111	2,56E-10	9,59E+00	1,16E-10	0,1022	-6,4439082	-0,65872808	337,57	STEAP3-AS	STEAP3 antisense RNA 1
105377182	3,98E-02	1,40E+00	3,05E-02	0,3044	-2,1639327	-0,65876782	33,74	FAM247C	family with sequence similarity 247 member C
401074	2,29E-05	4,64E+00	1,33E-05	0,1513	-4,3550503	-0,65883706	202,9	LINC00960	long intergenic non-protein coding RNA 960
9526	4,94E-37	3,63E+01	1,05E-37	0,0513	-12,8342289	-0,65893189	3535,65	MPDU1	mannose-P-dolichol utilization defect 1
55968	1,40E-56	5,59E+01	1,94E-57	0,0413	-15,9740677	-0,65901722	5318,39	NSFL1C	NSFL1 cofactor
90850	4,28E-22	2,14E+01	1,34E-22	0,0674	-9,7823406	-0,65970176	1728,28	ZNF598	zinc finger protein 598, E3 ubiquitin ligase
255104	1,78E-25	2,47E+01	5,11E-26	0,0625	-10,5494187	-0,65974644	1413,16	TMCO4	transmembrane and coiled-coil domains 4
286207	5,96E-06	5,22E+00	3,35E-06	0,142	-4,6479126	-0,65981338	170,17	CFAP157	cilia and flagella associated protein 157
4609	1,52E-53	5,28E+01	2,24E-54	0,0425	-15,5279724	-0,66006334	8701,59	MYC	MYC proto-oncogene, bHLH transcription factor
126129	1,07E-12	1,20E+01	4,49E-13	0,0912	-7,239854	-0,66044125	449,53	CPT1C	carnitine palmitoyltransferase 1C
10985	3,24E-53	5,25E+01	4,80E-54	0,0427	-15,4791095	-0,66092246	13802,5	GCN1	GCN1 activator of EIF2AK4
80017	5,67E-23	2,22E+01	1,74E-23	0,0662	-9,9870885	-0,6610052	1089,79	DGLUCY	D-glutamate cyclase
414	1,93E-07	6,71E+00	1,00E-07	0,1241	-5,326437	-0,66110215	204,71	ARSD	arylsulfatase D
107984247	7,66E-18	1,71E+01	2,71E-18	0,0758	-8,7228816	-0,66127282	633,61	LOC107984	247
5720	2,11E-49	4,87E+01	3,37E-50	0,0444	-14,8984497	-0,66133446	9118,02	PSME1	proteasome activator subunit 1
102723983	1,12E-07	6,95E+00	5,72E-08	0,1219	-5,4272399	-0,66142599	237,16	LOC102723	983
285362	1,65E-24	2,38E+01	4,85E-25	0,064	-10,3358915	-0,66159511	1010,63	SUMF1	sulfatase modifying factor 1
8220	5,46E-17	1,63E+01	1,99E-17	0,0779	-8,4945233	-0,66198033	678,2	ESS2	ess-2 splicing factor homolog
26284	4,59E-36	3,53E+01	1,00E-36	0,0523	-12,6585858	-0,66198942	3961,25	ERAL1	Era like 12S mitochondrial rRNA chaperone 1
404665	3,73E-07	6,43E+00	1,96E-07	0,1272	-5,2028222	-0,66205448	202,3	CACTIN-AS	CACTIN antisense RNA 1
4541	1,69E-28	2,78E+01	4,47E-29	0,0592	-11,1918643	-0,66215799	23931,15	ND6	NADH dehydrogenase subunit 6
148327	6,28E-07	6,20E+00	3,35E-07	0,1298	-5,1026365	-0,66229764	231,54	CREB3L4	cAMP responsive element binding protein 3 like 4
79885	1,54E-13	1,28E+01	6,24E-14	0,0883	-7,5028707	-0,66279247	459,75	HDAC11	histone deacetylase 11
90135	1,71E-30	2,98E+01	4,29E-31	0,0572	-11,5966474	-0,66293566	1846,32	BTBD6	BTB domain containing 6
165545	1,22E-01	9,14E-01	1,00E-01	0,4031	-1,6447712	-0,66298185	18,15	DQX1	DEAQ-box RNA dependent ATPase 1
54919	2,09E-22	2,17E+01	6,48E-23	0,0673	-9,8556462	-0,66299704	2036,95	DNAAF5	dynein axonemal assembly factor 5
5900	6,75E-26	2,52E+01	1,91E-26	0,0623	-10,6414966	-0,66319984	1546,79	RALGDS	ral guanine nucleotide dissociation stimulator
79080	9,78E-39	3,80E+01	2,02E-39	0,0505	-13,1372116	-0,66355127	3970,07	CCDC86	coiled-coil domain containing 86
10523	1,34E-43	4,29E+01	2,48E-44	0,0476	-13,9670694	-0,66432132	5030,19	CHERP	calcium homeostasis endoplasmic reticulum protein
100616168	1,74E-01	7,59E-01	1,46E-01	0,4565	-1,4554229	-0,66437107	17,94	MIR4754	microRNA 4754
11164	2,88E-57	5,65E+01	3,90E-58	0,0413	-16,0737261	-0,66438008	6429,52	NUDT5	nudix hydrolase 5

55818	7,64E-50	4,91E+01	1,22E-50	0,0444	-14,9664237	-0,66468718	3581,47	KDM3A	lysine demethylase 3A
255411	5,66E-08	7,25E+00	2,86E-08	0,1198	-5,5500799	-0,66490428	221,25	TEX49	testis expressed 49
64210	6,79E-55	5,42E+01	9,74E-56	0,0423	-15,7278783	-0,664942	5426,57	MMS19	MMS19 homolog, cytosolic iron-sulfur assembly component
108783645	1,67E-02	1,78E+00	1,22E-02	0,2653	-2,5065379	-0,66502239	42,6	HFE-AS1	HFE antisense RNA 1
653689	9,59E-13	1,20E+01	4,00E-13	0,0917	-7,2556416	-0,66537471	434,5	GSTT2B	glutathione S-transferase theta 2B
728689	2,39E-70	6,96E+01	2,42E-71	0,0373	-17,859845	-0,66537725	12657,93	EIF3CL	eukaryotic translation initiation factor 3 subunit C like
27151	1,28E-01	8,93E-01	1,05E-01	0,4103	-1,6219694	-0,66546674	18,1	CPAMD8	C3 and PZP like alpha-2-macroglobulin domain containing 8
643596	3,81E-02	1,42E+00	2,91E-02	0,3052	-2,1820088	-0,66588315	34,44	RNF224	ring finger protein 224
2788	7,31E-02	1,14E+00	5,79E-02	0,3512	-1,8967846	-0,66606239	27,42	GNG7	G protein subunit gamma 7
19	9,11E-33	3,20E+01	2,16E-33	0,0553	-12,0411151	-0,66631905	2290,11	ABCA1	ATP binding cassette subfamily A member 1
101928120	3,67E-15	1,44E+01	1,42E-15	0,0835	-7,9838235	-0,66654493	553,68	LOC101928	uncharacterized LOC101928120
57706	1,41E-30	2,99E+01	3,53E-31	0,0574	-11,6131539	-0,66659866	1559,51	DENND1A	DENN domain containing 1A
10498	4,11E-48	4,74E+01	6,81E-49	0,0454	-14,6962899	-0,66666858	4852,04	CARM1	coactivator associated arginine methyltransferase 1
9501	2,35E-27	2,66E+01	6,40E-28	0,0609	-10,9533985	-0,66692048	1559,84	RPH3AL	rabphilin 3A like (without C2 domains)
10317	1,09E-14	1,40E+01	4,29E-15	0,085	-7,8461958	-0,66710319	530,12	B3GALT5	beta-1,3-galactosyltransferase 5
6583	2,10E-12	1,17E+01	8,86E-13	0,0934	-7,1471719	-0,66722617	401,94	SLC22A4	solute carrier family 22 member 4
79948	1,53E-37	3,68E+01	3,24E-38	0,0516	-12,9252202	-0,66726439	2463,76	PLPPR3	phospholipid phosphatase related 3
64928	1,84E-48	4,77E+01	3,03E-49	0,0453	-14,7510428	-0,66819204	4701,29	MRPL14	mitochondrial ribosomal protein L14
11226	3,32E-32	3,15E+01	7,99E-33	0,056	-11,9327882	-0,6684474	1578,72	GALNT6	polypeptide N-acetylgalactosaminyltransferase 6
79073	1,13E-52	5,19E+01	1,69E-53	0,0434	-15,3980062	-0,66858523	8323,22	TMEM109	transmembrane protein 109
56935	3,33E-08	7,48E+00	1,66E-08	0,1185	-5,643783	-0,6686258	248,63	SMCO4	single-pass membrane protein with coiled-coil domains 4
11252	3,12E-52	5,15E+01	4,71E-53	0,0436	-15,3315249	-0,66882399	4333,02	PACSIN2	protein kinase C and casein kinase substrate in neurons 2
105377105	1,68E-32	3,18E+01	4,02E-33	0,0558	-11,9898701	-0,66942197	1805,03	FLNB-AS1	FLNB antisense RNA 1
2180	6,67E-36	3,52E+01	1,47E-36	0,053	-12,6287496	-0,66953491	1792,14	ACSL1	acyl-CoA synthetase long chain family member 1
112268109	4,44E-12	1,14E+01	1,89E-12	0,0951	-7,0420313	-0,66957145	508,08	LOC112268	109
83642	6,40E-10	9,19E+00	2,96E-10	0,1063	-6,3006995	-0,66959697	317,22	SELENOO	selenoprotein O
6189	5,20E-78	7,73E+01	4,48E-79	0,0356	-18,8276509	-0,66962992	54186,36	RPS3A	ribosomal protein S3A
64175	3,98E-44	4,34E+01	7,28E-45	0,0476	-14,053974	-0,66963737	6004,99	P3H1	prolyl 3-hydroxylase 1
4782	3,73E-40	3,94E+01	7,44E-41	0,05	-13,3846107	-0,66967733	4775,87	NFIC	nuclear factor I C
23413	6,19E-27	2,62E+01	1,70E-27	0,0616	-10,8643629	-0,6697184	1541,48	NCS1	neuronal calcium sensor 1
54480	1,06E-24	2,40E+01	3,08E-25	0,0645	-10,3791709	-0,6699323	2973,77	CHPF2	chondroitin polymerizing factor 2
203259	4,17E-29	2,84E+01	1,08E-29	0,0592	-11,3170296	-0,66996505	1336,7	FAM219A	family with sequence similarity 219 member A
284069	3,06E-03	2,51E+00	2,09E-03	0,2177	-3,0773033	-0,67001776	75,94	FAM171A2	family with sequence similarity 171 member A2
100874249	2,68E-03	2,57E+00	1,82E-03	0,2151	-3,1177395	-0,67047144	64,51	DENND5B-A	DENND5B antisense RNA 1
5436	3,70E-52	5,14E+01	5,60E-53	0,0438	-15,3202893	-0,67049398	4080,95	POLR2G	RNA polymerase II subunit G
4201	1,02E-71	7,10E+01	1,00E-72	0,0372	-18,0367592	-0,67067097	12669,71	MEA1	male-enhanced antigen 1
201266	4,61E-12	1,13E+01	1,97E-12	0,0953	-7,0365356	-0,67070933	370,6	SLC39A11	solute carrier family 39 member 11
100129931	1,82E-25	2,47E+01	5,22E-26	0,0636	-10,5474653	-0,67076626	1125,79	LOC100129	uncharacterized LOC100129931
3797	7,23E-30	2,91E+01	1,84E-30	0,0585	-11,4712208	-0,67078717	2017,89	KIF3C	kinesin family member 3C
81928	3,81E-25	2,44E+01	1,10E-25	0,064	-10,4768931	-0,6709887	1121,82	CABLES2	Cdk5 and Abl enzyme substrate 2
105376322	6,22E-02	1,21E+00	4,89E-02	0,3406	-1,9698547	-0,67101949	26,65	LOC105376	322
5165	9,19E-20	1,90E+01	3,07E-20	0,0728	-9,2164084	-0,67110878	757,82	PDK3	pyruvate dehydrogenase kinase 3
23587	2,07E-33	3,27E+01	4,83E-34	0,0552	-12,1640319	-0,67167068	1943,4	ELP5	elongator acetyltransferase complex subunit 5
2260	6,04E-65	6,42E+01	6,88E-66	0,0392	-17,1447823	-0,67187521	6955,31	FGFR1	fibroblast growth factor receptor 1
112268430	5,94E-12	1,12E+01	2,54E-12	0,096	-7,0009817	-0,67218575	428,98	LOC112268	430
629	3,84E-42	4,14E+01	7,35E-43	0,049	-13,7234509	-0,67218583	2743,96	CFB	complement factor B
55756	7,74E-22	2,11E+01	2,44E-22	0,0691	-9,7215611	-0,67218756	915,5	INTS9	integrator complex subunit 9
6446	1,13E-34	3,39E+01	2,56E-35	0,0542	-12,4017566	-0,67225459	1773,94	SGK1	serum/glucocorticoid regulated kinase 1
10262	1,20E-47	4,69E+01	2,01E-48	0,046	-14,6228839	-0,67243255	7175,47	SF3B4	splicing factor 3b subunit 4
5693	3,65E-49	4,84E+01	5,88E-50	0,0453	-14,8612211	-0,67255087	8184,23	PSMB5	proteasome 20S subunit beta 5
10322	9,95E-45	4,40E+01	1,80E-45	0,0475	-14,1527216	-0,67276038	2898,06	SMYD5	SMYD family member 5
65061	1,27E-03	2,90E+00	8,40E-04	0,2017	-3,3394173	-0,67349906	86,25	CDK15	cyclin dependent kinase 15
105378983	2,00E-02	1,70E+00	1,47E-02	0,2761	-2,4391575	-0,67357164	39,12	LOC105378	uncharacterized LOC105378983
9986	1,21E-15	1,49E+01	4,60E-16	0,0829	-8,1217125	-0,67358181	725,23	RCE1	Ras converting CAAX endopeptidase 1
220979	2,03E-07	6,69E+00	1,05E-07	0,1267	-5,3170254	-0,67358986	202,96	ZNF22-AS1	ZNF22 antisense RNA 1
23201	1,62E-42	4,18E+01	3,07E-43	0,0489	-13,7866128	-0,67372106	3419,63	FAM168A	family with sequence similarity 168 member A
25885	1,52E-61	6,08E+01	1,87E-62	0,0404	-16,6786648	-0,67385736	7603,78	POLR1A	RNA polymerase I subunit A
8787	2,49E-03	2,60E+00	1,69E-03	0,2146	-3,1401413	-0,67398813	66,41	RGS9	regulator of G protein signaling 9
170691	1,94E-03	2,71E+00	1,30E-03	0,2096	-3,2158072	-0,67410192	75,29	ADAMTS17	ADAM metallopeptidase with thrombospondin type 1 motif 17
3425	1,05E-09	8,98E+00	4,93E-10	0,1085	-6,2214579	-0,67483731	290,76	IDUA	alpha-L-iduronidase
199720	2,87E-02	1,54E+00	2,15E-02	0,2936	-2,2985158	-0,67486631	34,97	GGN	gametogenetin
3073	2,95E-47	4,65E+01	4,99E-48	0,0464	-14,5607779	-0,67500591	3995,44	HEXA	hexosaminidase subunit alpha
1603	1,17E-28	2,79E+01	3,06E-29	0,0601	-11,2253252	-0,67505255	4763,33	DAD1	defender against cell death 1
55152	6,62E-34	3,32E+01	1,53E-34	0,0551	-12,2577812	-0,67509564	1716,14	DALRD3	DALR anticodon binding domain containing 3
63935	1,69E-25	2,48E+01	4,83E-26	0,064	-10,5548179	-0,67516981	2826,5	PCIF1	phosphorylated CTD interacting factor 1
54960	8,42E-05	4,07E+00	5,08E-05	0,1667	-4,0517512	-0,67533372	153,68	GEMIN8	gem nuclear organelle associated protein 8
5092	2,83E-29	2,85E+01	7,31E-30	0,0595	-11,351278	-0,67536481	1269,29	PCBD1	pterin-4 alpha-carbinolamine dehydratase 1
6927	4,03E-03	2,39E+00	2,78E-03	0,2259	-2,9910651	-0,67555461	60,87	HNF1A	HNF1 homeobox A
100616424	2,38E-04	3,62E+00	1,49E-04	0,1781	-3,7929201	-0,67556541	104,34	MIR4707	microRNA 4707
610	8,42E-02	1,07E+00	6,72E-02	0,3692	-1,8304826	-0,67572877	21,69	HCN2	hyperpolarization activated cyclic nucleotide gated potassium and sodium channel 2
100506428	3,76E-08	7,42E+00	1,88E-08	0,1202	-5,6226831	-0,67595364	225,68	CBR3-AS1	CBR3 antisense RNA 1
84080	3,09E-07	6,51E+00	1,62E-07	0,1291	-5,2381802	-0,67628001	218,63	ENKD1	enkurin domain containing 1
10992	3,50E-61	6,05E+01	4,38E-62	0,0407	-16,627876	-0,67631804	18631,46	SF3B2	splicing factor 3b subunit 2
100131801	1,16E-24	2,39E+01	3,40E-25	0,0653	-10,3698208	-0,67675113	1043,91	PET100	PET100 cytochrome c oxidase chaperone
146664	2,86E-16	1,55E+01	1,06E-16	0,0816	-8,2975932	-0,6768208	613,59	MGAT5B	alpha-1,6-mannosylglycoprotein 6-beta-N-acetylglucosaminyltransferase B
1627	2,37E-35	3,46E+01	5,27E-36	0,054	-12,5276649	-0,67683268	5912,44	DBN1	drebrin 1
107986597	1,35E-01	8,70E-01	1,11E-01	0,4244	-1,5948554	-0,67684752	16,44	LOC107986	597
7157	6,10E-62	6,12E+01	7,45E-63	0,0405	-16,733651	-0,67699547	6891,06	TP53	tumor protein p53
440689	5,88E-03	2,23E+00	4,12E-03	0,236	-2,8686872	-0,67703692	58,96	H2BC18	H2B clustered histone 18
8772	5,48E-35	3,43E+01	1,23E-35	0,0543	-12,4601641	-0,67707795	2483,84	FADD	Fas associated via death domain
147179	3,96E-53	5,24E+01	5,87E-54	0,0438	-15,466136	-0,67730744	3684,1	WIPF2	WAS/WASL interacting protein family member 2
107984224	1,70E-01	7,70E-01	1,42E-01	0,4608	-1,4699286	-0,67737422	14	LOC107984	224
283807	8,80E-02	1,06E+00	7,05E-02	0,3745	-1,8088729	-0,67743406	21,06	FBXL22	F-box and leucine rich repeat protein 22
3801	8,34E-35	3,41E+01	1,88E-35	0,0545	-12,4263742	-0,67777291	7095,25	KIFC3	kinesin family member C3
3486	1,99E-44	4,37E+01	3,61E-45	0,0481	-14,1035341	-0,67788225	3054,03	IGFBP3	insulin like growth factor binding protein 3
6305	1,95E-26	2,57E+01	5,45E-27	0,063	-10,7577414	-0,67793364	3633,46	SBF1	SET binding factor 1
100130894	9,75E-06	5,01E+00	5,56E-06	0,1492	-4,5425938	-0,67796453	150,66	VAC14-AS1	VAC14 antisense RNA 1
100499489	6,38E-07	6,20E+00	3,40E-07	0,1329	-5,0997726	-0,67796564	209,75	LINC03027	long intergenic non-protein coding RNA 3027
100534012	1,25E-21	2,09E+01	3,97E-22	0,0701	-9,6717817	-0,67799753	826,91	TNFAIP8L2-S	TNFAIP8L2-SCNM1 readthrough
100507331	3,93E-11	1,04E+01	1,74E-11	0,1008	-6,7267382	-0,67800736	344,65	ZSWIM8-AS	ZSWIM8 antisense RNA 1
10133	5,17E-57	5,63E+01	7,05E-58	0,0423	-16,037011	-0,67806981	5961,57	OPTN	optineurin
4204	1,56E-49	4,88E+01	2,50E-50	0,0455	-14,9184466	-0,67823824	3223,07	MECP2	methyl-CpG binding protein 2
54869	1,99E-09	8,70E+00	9,40E-10	0,1108	-6,119199	-0,67825399	272,6	EPS8L1	EPS8 like 1
441549	1,62E-01	7,90E-01	1,35E-01	0,4538	-1,4951627	-0,6785271	14,4	CDNF	cerebral dopamine neurotrophic factor
643387	7,80E-02	1,11E+00	6,19E-02	0,3635	-1,8666629	-0,67861151	25,16	TARDBPP3	TARDBP pseudogene 3
107984745	1,39E-01	8,57E-01	1,15E-01	0,4305	-1,5764791	-0,67861977	16,51	LOC107984	745
9902	5,93E-32	3,12E+01	1,43E-32	0,0571	-11,8840933	-0,67872425	1527,15	MRC2	mannose receptor C type 2
100996740	3,51E-03	2,45E+00	2,41E-03	0,2237	-3,0343789	-0,67882391	60,78	LOC100996	uncharacterized LOC100996740
25797	2,02E-10	9,69E+00	9,15E-11	0,1048	-6,4803686	-0,67886854	305,88	QPCT	glutaminyl-peptide cyclotransferase
2794	3,34E-45	4,45E+01	5,94E-46	0,0477	-14,2303568	-0,67888739	3577,99	GNL1	G protein nucleolar 1 (putative)
11128	3,98E-44	4,34E+01	7,28E-45	0,0483	-14,0540511	-0,6790181	2360,22	POLR3A	RNA polymerase III subunit A
105221694	2,38E-15	1,46E+01	9,11E-16	0,0845	-8,0383208	-0,67905864	542,89	BISPR	BST2 interferon stimulated positive regulator
8416	5,66E-07	6,25E+00	3,01E-07	0,1326	-5,1229602	-0,67911253	196,58	ANXA9	annexin A9
26048	8,11E-10	9,09E+00	3,77E-10	0,1084	-6,2630935	-0,67916582	298,6	ZNF500	zinc finger protein 500
2947	7,29E-45	4,41E+01	1,31E-45	0,0479	-14,1748536	-0,67924851	2747,82	GSTM3	glutathione S-transferase mu 3
100506385	1,24E-04	3,91E+00	7,57E-05	0,1717	-3,9577117	-0,679359	108,27	LINC01426	long intergenic non-protein coding RNA 1426
55379	8,95E-51	5,00E+01	1,39E-51	0,045	-15,1098858	-0,6796953	18932,78	LRRC59	leucine rich repeat containing 59
132	1,03E-46	4,60E+01	1,77E-47	0,047	-14,4740897	-0,67972531	3678,89	ADK	adenosine kinase
64837	3,68E-32	3,14E+01	8,86E-33	0,057	-11,9241776	-0,67981186	3618,98	KLC2	kinesin light chain 2
64506	2,26E-04	3,65E+00	1,41E-04	0,1786	-3,8064982	-0,67984018	94,38	CPEB1	cytoplasmic polyadenylation element binding protein 1
4836	2,31E-61	6,06E+01	2,87E-62	0,0408	-16,6531786	-0,6799354	10872,93	NMT1	N-myristoyltransferase 1
2021	5,27E-14	1,33E+01	2,11E-14	0,089	-7,6439404	-0,67998429	438,63	ENDOG	endonuclease G
284346	6,02E-03	2,22E+00	4,23E-03	0,2377	-2,8604866	-0,68006338	57,38	ZNF575	zinc finger protein 575
79447	3,14E-40	3,95E+01	6,26E-41	0,0508	-13,397471	-0,68013445	2298,87	PAGR1	PAXIP1 associated glutamate rich protein 1
22897	2,47E-48	4,76E+01	4,08E-49	0,0462	-14,730965	-0,68019704	2906,07	CEP164	centrosomal protein 164
79005	1,20E-21	2,09E+01	3,81E-22	0,0703	-9,6761704	-0,68036871	838,55	SCNM1	sodium channel modifier 1
284119	1,09E-72	7,20E+01	1,05E-73	0,0375	-18,1609206	-0,68044146	28198,1	CAVIN1	caveolae associated protein 1
6301	6,52E-71	7,02E+01	6,56E-72	0,0379	-17,932615	-0,68050471	11841,3	SARS1	seryl-tRNA synthetase 1
100129540	6,67E-03	2,18E+00	4,70E-03	0,2408	-2,8267309	-0,68061631	53,51	LOC100129	uncharacterized LOC100129540
9973	1,39E-14	1,39E+01	5,47E-15	0,0871	-7,8155226	-0,68066304	616,12	CCS	copper chaperone for superoxide dismutase

79897	8,76E-19	1,81E+01	3,01E-19	0,0759	-8,9682424	-0,68080082	847,29	RPP21	ribonuclease P/MRP subunit p21
340075	4,86E-02	1,31E+00	3,76E-02	0,3276	-2,0787904	-0,68105351	33,55	ARSI	arylsulfatase family member I
79085	8,74E-46	4,51E+01	1,54E-46	0,0475	-14,3245754	-0,68109054	4454,28	SLC25A23	solute carrier family 25 member 23
79081	5,22E-37	3,63E+01	1,12E-37	0,0531	-12,8299041	-0,68110514	2178,15	LBHD1	LBH domain containing 1
64207	1,96E-30	2,97E+01	4,92E-31	0,0588	-11,5847499	-0,68118329	1406,08	IRF2BPL	interferon regulatory factor 2 binding protein like
8427	1,55E-24	2,38E+01	4,56E-25	0,0659	-10,3418406	-0,68168418	1436,9	ZNF282	zinc finger protein 282
10743	7,32E-41	4,01E+01	1,43E-41	0,0505	-13,5063403	-0,6817187	2047,48	RAI1	retinoic acid induced 1
55898	2,88E-39	3,85E+01	5,88E-40	0,0515	-13,2301446	-0,6817567	2994,89	UNC45A	unc-45 myosin chaperone A
644165	9,40E-02	1,03E+00	7,56E-02	0,3838	-1,7768139	-0,68187862	20,01	BCRP3	BCR pseudogene 3
54587	6,04E-32	3,12E+01	1,46E-32	0,0574	-11,8824777	-0,68196164	1858,02	MXRA8	matrix remodeling associated 8
113026	1,97E-38	3,77E+01	4,08E-39	0,0521	-13,0837011	-0,68198596	3189,29	PLCD3	phospholipase C delta 3
6273	6,52E-27	2,62E+01	1,79E-27	0,0628	-10,8596591	-0,68202631	1124,91	S100A2	S100 calcium binding protein A2
7064	7,36E-36	3,51E+01	1,62E-36	0,0541	-12,6208299	-0,68230486	2960,03	THOP1	thimet oligopeptidase 1
53834	1,65E-40	3,98E+01	3,25E-41	0,0508	-13,4460555	-0,68263583	2851,28	FGFRL1	fibroblast growth factor receptor like 1
8225	2,10E-21	2,07E+01	6,71E-22	0,071	-9,6179944	-0,6827231	1584,31	GTPBP6	GTP binding protein 6 (putative)
55224	8,92E-22	2,10E+01	2,81E-22	0,0704	-9,7070511	-0,6829273	851,1	ETNK2	ethanolamine kinase 2
9871	5,07E-62	6,13E+01	6,16E-63	0,0408	-16,7449709	-0,68298541	5477,69	SEC24D	SEC24 homolog D, COPII coat complex component
978	4,07E-34	3,34E+01	9,33E-35	0,0556	-12,2975808	-0,68323965	2430,97	CDA	cytidine deaminase
23557	9,52E-32	3,10E+01	2,31E-32	0,0577	-11,8439294	-0,68349895	1397,3	SNAPIN	SNAP associated protein
53917	2,18E-20	1,97E+01	7,15E-21	0,073	-9,3715188	-0,68380136	717,03	RAB24	RAB24, member RAS oncogene family
2314	2,04E-61	6,07E+01	2,53E-62	0,041	-16,6607909	-0,68383731	29515,45	FLII	FLII actin remodeling protein
5881	2,14E-15	1,47E+01	8,21E-16	0,085	-8,0509649	-0,68399465	774,03	RAC3	Rac family small GTPase 3
6232	3,06E-74	7,35E+01	2,85E-75	0,0373	-18,3579417	-0,68407476	26205,26	RPS27	ribosomal protein S27
11186	1,26E-29	2,89E+01	3,23E-30	0,0599	-11,4224365	-0,68407977	1486,13	RASSF1	Ras association domain family member 1
80352	2,74E-12	1,16E+01	1,16E-12	0,0962	-7,1098638	-0,68431909	377,9	RNF39	ring finger protein 39
27242	1,15E-75	7,49E+01	1,04E-76	0,0369	-18,5367572	-0,6843729	9314,6	TNFRSF21	TNF receptor superfamily member 21
7417	8,31E-58	5,71E+01	1,11E-58	0,0424	-16,1511957	-0,68442222	7421,03	VDAC2	voltage dependent anion channel 2
7873	1,82E-55	5,47E+01	2,58E-56	0,0433	-15,8118108	-0,6845402	4256,48	MANF	mesencephalic astrocyte derived neurotrophic factor
6628	1,03E-50	5,00E+01	1,61E-51	0,0453	-15,1005296	-0,68459061	14383,66	SNRPB	small nuclear ribonucleoprotein polypeptides B and B1
10211	4,89E-61	6,03E+01	6,13E-62	0,0412	-16,6076526	-0,6848264	7471,06	FLOT1	flotillin 1
92017	1,58E-17	1,68E+01	5,65E-18	0,0793	-8,6393519	-0,68487561	678,15	SNX29	sorting nexin 29
10120	3,45E-44	4,35E+01	6,30E-45	0,0487	-14,0642516	-0,68511172	4054,77	ACTR1B	actin related protein 1B
11187	2,78E-17	1,66E+01	1,00E-17	0,0799	-8,5734898	-0,68517064	939,62	PKP3	plakophilin 3
105373113	1,34E-01	8,73E-01	1,10E-01	0,4289	-1,598254	-0,68546191	17,16	LINC01703	long intergenic non-protein coding RNA 1703
23363	1,86E-26	2,57E+01	5,19E-27	0,0637	-10,7622751	-0,68566091	1276,58	OBSL1	obscurin like cytoskeletal adaptor 1
8370	2,05E-03	2,69E+00	1,38E-03	0,2144	-3,1989722	-0,68571646	64,73	H4C14	H4 clustered histone 14
56052	3,13E-30	2,95E+01	7,89E-31	0,0594	-11,5442579	-0,68573539	1288,52	ALG1	ALG1 chitobiosyldiphosphodolichol beta-mannosyltransferase
100874032	1,16E-04	3,94E+00	7,08E-05	0,1726	-3,9736924	-0,68585678	103,07	PRRT3-AS1	PRRT3 antisense RNA 1
4330	1,59E-01	7,99E-01	1,32E-01	0,4559	-1,504447	-0,68591709	14,42	MN1	MN1 proto-oncogene, transcriptional regulator
113218503	3,23E-03	2,49E+00	2,21E-03	0,2241	-3,0605886	-0,68594808	61,83	MIR10399	microRNA 10399
57447	3,18E-05	4,50E+00	1,87E-05	0,1603	-4,2802766	-0,68616167	122,83	NDRG2	NDRG family member 2
102157401	2,65E-26	2,56E+01	7,40E-27	0,064	-10,7295389	-0,68622613	1315,15	PCBP2-OT1	PCBP2 overlapping transcript 1
101928963	8,81E-02	1,06E+00	7,05E-02	0,3796	-1,8084482	-0,6865007	22,73	HNRNPD-DT	HNRNPD divergent transcript
283316	6,74E-25	2,42E+01	1,96E-25	0,0659	-10,4225175	-0,68657136	1145,12	CD163L1	CD163 molecule like 1
5818	3,02E-21	2,05E+01	9,68E-22	0,0717	-9,5802092	-0,68657218	1514,64	NECTIN1	nectin cell adhesion molecule 1
107985303	8,82E-02	1,05E+00	7,06E-02	0,3798	-1,8078486	-0,68668061	31,3	LOC107985	IQ motif and SEC7 domain-containing protein 2-like
100529261	1,47E-28	2,78E+01	3,86E-29	0,0613	-11,2048183	-0,68686851	1144,52	CHURC1-FN	CHURC1-FNTB readthrough
2137	9,24E-50	4,90E+01	1,47E-50	0,0459	-14,9537149	-0,6870877	3295,99	EXTL3	exostosin like glycosyltransferase 3
56257	7,91E-45	4,41E+01	1,42E-45	0,0485	-14,1690416	-0,68764843	3079,91	MEPCE	methylphosphate capping enzyme
57118	7,47E-21	2,01E+01	2,42E-21	0,0725	-9,4849681	-0,68771177	722,13	CAMK1D	calcium/calmodulin dependent protein kinase ID
3991	1,67E-06	5,78E+00	9,13E-07	0,1401	-4,9095966	-0,68790634	165,08	LIPE	lipase E, hormone sensitive type
27238	1,25E-28	2,79E+01	3,28E-29	0,0613	-11,2191595	-0,68790828	1145,3	GPKOW	G-patch domain and KOW motifs
10922	2,85E-25	2,45E+01	8,20E-26	0,0655	-10,5049609	-0,68803479	1805,94	FASTK	Fas activated serine/threonine kinase
55101	6,67E-40	3,92E+01	1,34E-40	0,0516	-13,3409236	-0,68804994	3261,7	DMAC2	distal membrane arm assembly component 2
80024	6,56E-33	3,22E+01	1,55E-33	0,057	-12,0684155	-0,68838855	2284,58	SLC8B1	solute carrier family 8 member B1
1716	6,42E-39	3,82E+01	1,32E-39	0,0523	-13,169367	-0,68843226	2405,48	DGUOK	deoxyguanosine kinase
100129464	1,13E-01	9,47E-01	9,22E-02	0,4089	-1,6839122	-0,68862466	17,67	LINC01546	long intergenic non-protein coding RNA 1546
644634	3,49E-02	1,46E+00	2,66E-02	0,3105	-2,2179259	-0,6886485	30,86	LOC644634	uncharacterized LOC644634
11147	4,42E-14	1,34E+01	1,77E-14	0,0898	-7,6665888	-0,68870169	440,85	HHLA3	HERV-H LTR-associating 3
100131094	1,88E-12	1,17E+01	7,93E-13	0,0962	-7,1622886	-0,68909039	402,72	DPP9-AS1	DPP9 antisense RNA 1
5863	6,18E-43	4,22E+01	1,16E-43	0,0497	-13,8566996	-0,68909929	3228,52	RGL2	ral guanine nucleotide dissociation stimulator like 2
4938	2,55E-06	5,59E+00	1,40E-06	0,1429	-4,8245196	-0,68920869	157	OAS1	2'-5'-oligoadenylate synthetase 1
27173	6,90E-74	7,32E+01	6,47E-75	0,0376	-18,3134228	-0,68929849	10229,7	SLC39A1	solute carrier family 39 member 1
30	8,60E-27	2,61E+01	2,38E-27	0,0636	-10,8339987	-0,68931057	1101,76	ACAA1	acetyl-CoA acyltransferase 1
51004	5,78E-19	1,82E+01	1,98E-19	0,0765	-9,0143305	-0,68945472	613,86	COQ6	coenzyme Q6, monooxygenase
309	2,78E-59	5,86E+01	3,61E-60	0,0422	-16,361401	-0,6896474	25434,14	ANXA6	annexin A6
6839	1,21E-29	2,89E+01	3,10E-30	0,0604	-11,4259283	-0,68975829	1629,28	SUV39H1	SUV39H1 histone lysine methyltransferase
55210	1,00E-33	3,30E+01	2,32E-34	0,0565	-12,223739	-0,69007912	3266,41	ATAD3A	ATPase family AAA domain containing 3A
100533970	1,08E-42	4,20E+01	2,04E-43	0,05	-13,8161013	-0,69065756	3851,79	P2RX5-TAX1	P2RX5-TAX1BP3 readthrough (NMD candidate)
23072	1,02E-07	6,99E+00	5,22E-08	0,1269	-5,4436148	-0,69066068	202,65	HECW1	HECT, C2 and WW domain containing E3 ubiquitin protein ligase 1
26355	3,25E-32	3,15E+01	7,81E-33	0,0579	-11,9346669	-0,69076829	1705,03	FAM162A	family with sequence similarity 162 member A
5886	7,29E-38	3,71E+01	1,53E-38	0,0532	-12,9828856	-0,69086346	11972,49	RAD23A	RAD23 homolog A, nucleotide excision repair protein
2050	5,75E-39	3,82E+01	1,18E-39	0,0524	-13,1776916	-0,69095735	2040,08	EPHB4	EPH receptor B4
401303	1,52E-04	3,82E+00	9,33E-05	0,1769	-3,9073847	-0,69109091	98,45	ZNF815P	zinc finger protein 815, pseudogene
375790	7,00E-44	4,32E+01	1,29E-44	0,0493	-14,0135409	-0,69123895	11305,09	AGRN	agrin
84337	1,22E-33	3,29E+01	2,84E-34	0,0566	-12,207342	-0,69148557	3052,54	ELOF1	elongation factor 1
27095	5,34E-54	5,33E+01	7,78E-55	0,0443	-15,5957205	-0,69157459	3340,15	TRAPPC3	trafficking protein particle complex subunit 3
26090	6,38E-43	4,22E+01	1,20E-43	0,0499	-13,8543623	-0,69158081	2350,15	ABHD12	abhydrolase domain containing 12, lysophospholipase
1278	1,48E-01	8,30E-01	1,22E-01	0,4477	-1,5450881	-0,69171234	15,79	COL1A2	collagen type I alpha 2 chain
5725	7,23E-68	6,71E+01	7,73E-69	0,0395	-17,5351173	-0,69185817	15392,38	PTBP1	polypyrimidine tract binding protein 1
54970	4,66E-32	3,13E+01	1,12E-32	0,0581	-11,9043635	-0,691879	1434,29	TTC12	tetratricopeptide repeat domain 12
55311	3,08E-20	1,95E+01	1,02E-20	0,0741	-9,3343355	-0,69198851	834,22	ZNF444	zinc finger protein 444
143244	8,43E-28	2,71E+01	2,27E-28	0,0627	-11,0470056	-0,69225725	1382,34	EIF5AL1	eukaryotic translation initiation factor 5A like 1
116092	9,10E-40	3,90E+01	1,83E-40	0,052	-13,3173687	-0,69229907	3320,43	DNTTIP1	deoxynucleotidyltransferase terminal interacting protein 1
64925	1,24E-18	1,79E+01	4,28E-19	0,0775	-8,9295887	-0,69238133	803,65	CCDC71	coiled-coil domain containing 71
4853	3,11E-76	7,55E+01	2,79E-77	0,0372	-18,6075263	-0,69238677	15986,15	NOTCH2	notch receptor 2
1785	1,64E-56	5,58E+01	2,27E-57	0,0434	-15,9642224	-0,69249565	13797,01	DNM2	dynamin 2
3033	2,74E-46	4,56E+01	4,74E-47	0,0481	-14,4059896	-0,69298262	2729,69	HADH	hydroxyacyl-CoA dehydrogenase
5566	9,11E-48	4,70E+01	1,52E-48	0,0473	-14,6417531	-0,69298784	8117,87	PRKACA	protein kinase cAMP-activated catalytic subunit alpha
196483	2,53E-19	1,86E+01	8,60E-20	0,0762	-9,1053773	-0,69354578	644,25	EEF2KMT	eukaryotic elongation factor 2 lysine methyltransferase
9776	6,33E-53	5,22E+01	9,45E-54	0,0449	-15,4354993	-0,69365604	4132,46	ATG13	autophagy related 13
55449	1,07E-12	1,20E+01	4,48E-13	0,0959	-7,2402605	-0,69424615	418,81	DHRS4-AS1	DHRS4 antisense RNA 1
122616	5,62E-13	1,23E+01	2,33E-13	0,0948	-7,3285667	-0,69444115	375,57	CLBA1	clathrin binding box of aftiphilin containing 1
105373422	7,92E-06	5,10E+00	4,49E-06	0,1514	-4,587277	-0,69449137	140,66	LOC105373	uncharacterized LOC105373422
55022	2,45E-18	1,76E+01	8,56E-19	0,0785	-8,8524597	-0,69459594	590,52	PID1	phosphotyrosine interaction domain containing 1
23510	2,59E-39	3,86E+01	5,27E-40	0,0525	-13,2383854	-0,69462397	2355,73	KCTD2	potassium channel tetramerization domain containing 2
105371887	5,35E-04	3,27E+00	3,44E-04	0,1941	-3,5800033	-0,69470454	80,41	LOC105371	uncharacterized LOC105371887
92305	2,96E-32	3,15E+01	7,10E-33	0,0582	-11,9425263	-0,69476758	1709,21	TMEM129	transmembrane protein 129, E3 ubiquitin ligase
28960	5,70E-45	4,42E+01	1,02E-45	0,049	-14,1923885	-0,69494955	3108,15	DCPS	decapping enzyme, scavenger
84861	4,82E-15	1,43E+01	1,87E-15	0,0874	-7,9499467	-0,69498146	651,02	KLHL22	kelch like family member 22
27315	4,75E-16	1,53E+01	1,78E-16	0,0844	-8,2360677	-0,69536344	550,28	PGAP2	post-GPI attachment to proteins 2
468	9,71E-64	6,30E+01	1,14E-64	0,041	-16,9808886	-0,69541705	13811,77	ATF4	activating transcription factor 4
112970	1,47E-10	9,83E+00	6,64E-11	0,1066	-6,5284631	-0,69567365	283,06	KTI12	KTI12 chromatin associated homolog
1192	1,04E-60	6,00E+01	1,31E-61	0,042	-16,561942	-0,69591878	50762,58	CLIC1	chloride intracellular channel 1
84446	1,44E-11	1,08E+01	6,25E-12	0,1012	-6,8737209	-0,69595576	328,96	BRSK1	BR serine/threonine kinase 1
51649	1,02E-48	4,80E+01	1,66E-49	0,0471	-14,7913967	-0,69599445	3275,95	MRPS23	mitochondrial ribosomal protein S23
10131	4,12E-37	3,64E+01	8,79E-38	0,0542	-12,8483383	-0,69607003	4824,36	TRAP1	TNF receptor associated protein 1
9807	1,27E-50	4,99E+01	1,98E-51	0,0461	-15,0867661	-0,69625063	4061,68	IP6K1	inositol hexakisphosphate kinase 1
105371793	2,06E-01	6,86E-01	1,74E-01	0,5126	-1,3582382	-0,69625652	11,23	LOC105371	uncharacterized LOC105371793
23170	9,64E-35	3,40E+01	2,18E-35	0,0561	-12,4145389	-0,69634527	3547,62	TTLL12	tubulin tyrosine ligase like 12
112268105	4,07E-02	1,39E+00	3,12E-02	0,3232	-2,1547541	-0,6964235	29,09	SBNO1-AS1	SBNO1 antisense RNA 1
9703	1,71E-83	8,28E+01	1,32E-84	0,0357	-19,490583	-0,69663045	20326,61	BLTP2	bridge-like lipid transfer protein family member 2
81562	1,88E-33	3,27E+01	4,39E-34	0,0572	-12,1718331	-0,69670351	1534,71	LMAN2L	lectin, mannose binding 2 like
84277	6,05E-10	9,22E+00	2,80E-10	0,1104	-6,3094958	-0,69678457	300,62	DNAJC30	DnaJ heat shock protein family (Hsp40) member C30
347404	1,75E-06	5,76E+00	9,58E-07	0,1422	-4,9000156	-0,69681084	162,92	LANCL3	LanC like family member 3
57658	2,44E-31	3,06E+01	5,99E-32	0,0592	-11,7639594	-0,69688527	1313,79	CALCOCO1	calcium binding and coiled-coil domain 1
105372480	1,01E-11	1,10E+01	4,38E-12	0,1007	-6,9244244	-0,69694638	356,95	LOC105372	uncharacterized LOC105372480
10066	1,76E-38	3,78E+01	3,65E-39	0,0532	-13,0922721	-0,69697958	3390,4	SCAMP2	secretory carrier membrane protein 2
6810	6,43E-33	3,22E+01	1,52E-33	0,0578	-12,0701704	-0,69718316	1613,52	STX4	syntaxin 4
51291	1,49E-16	1,58E+01	5,50E-17	0,0833	-8,3755635	-0,69743011	530,33	GMIP	GEM interacting protein

79637	5,70E-22	2,12E+01	1,79E-22	0,0715	-9,753135	-0,6975598	785,28	ARMC7	armadillo repeat containing 7
727856	2,24E-01	6,50E-01	1,91E-01	0,5329	-1,3089385	-0,69758039	10,54	DDX11L16	DEAD/H-box helicase 11 like 16 (pseudogene)
5912	1,29E-31	3,09E+01	3,13E-32	0,059	-11,8184987	-0,69779748	1546,72	RAP2B	RAP2B, member of RAS oncogene family
54973	2,48E-32	3,16E+01	5,93E-33	0,0584	-11,957521	-0,69843326	3922,57	INTS11	integrator complex subunit 11
55793	7,11E-16	1,51E+01	2,68E-16	0,0853	-8,1869262	-0,69851879	550,27	MINDY1	MINDY lysine 48 deubiquitinase 1
9473	6,74E-08	7,17E+00	3,42E-08	0,1266	-5,5186864	-0,6985782	200,22	THEMIS2	thymocyte selection associated family member 2
83475	1,26E-11	1,09E+01	5,46E-12	0,1014	-6,8929851	-0,6986812	529,95	DOHH	deoxyhypusine hydroxylase
58986	4,57E-24	2,33E+01	1,36E-24	0,0683	-10,2365627	-0,69872808	2048,52	PGAP6	post-GPI attachment to proteins 6
6668	6,71E-30	2,92E+01	1,71E-30	0,0609	-11,4777106	-0,6991068	1908,15	SP2	Sp2 transcription factor
2012	1,81E-64	6,37E+01	2,09E-65	0,0409	-17,0800646	-0,69936206	14455,68	EMP1	epithelial membrane protein 1
28974	1,25E-35	3,49E+01	2,77E-36	0,0556	-12,5785913	-0,69945514	4180,92	C19orf53	chromosome 19 open reading frame 53
373156	4,00E-34	3,34E+01	9,16E-35	0,0569	-12,299068	-0,6996152	1477,96	GSTK1	glutathione S-transferase kappa 1
100529097	4,85E-64	6,33E+01	5,64E-65	0,0411	-17,0219667	-0,69973073	12062,3	RPL36A-HNI	RPL36A-HNRNPH2 readthrough
89853	3,84E-07	6,42E+00	2,02E-07	0,1347	-5,1970391	-0,69984999	176,56	MVB12B	multivesicular body subunit 12B
7114	6,78E-52	5,12E+01	1,03E-52	0,0458	-15,2804959	-0,69997994	40027,41	TMSB4X	thymosin beta 4 X-linked
374	3,51E-33	3,25E+01	8,23E-34	0,0578	-12,1204247	-0,70002908	1800,54	AREG	amphiregulin
644890	1,03E-01	9,87E-01	8,32E-02	0,4041	-1,7326652	-0,70018192	18,36	MEIG1	meiosis/spermiogenesis associated 1
79042	6,58E-30	2,92E+01	1,67E-30	0,061	-11,4794893	-0,70021264	2272,52	TSEN34	tRNA splicing endonuclease subunit 34
105379251	2,97E-02	1,53E+00	2,24E-02	0,3068	-2,2838809	-0,70058935	31,98	LOC105379	replaced by ID 220869
84706	5,12E-24	2,33E+01	1,53E-24	0,0685	-10,2254436	-0,70071808	1118,26	GPT2	glutamic--pyruvic transaminase 2
125061	3,88E-28	2,74E+01	1,03E-28	0,063	-11,117264	-0,70080869	2258,26	AFMID	arylformamidase
25822	3,05E-21	2,05E+01	9,80E-22	0,0732	-9,5789539	-0,70088618	874,54	DNAJB5	DnaJ heat shock protein family (Hsp40) member B5
4150	1,77E-50	4,98E+01	2,77E-51	0,0465	-15,0646102	-0,70104414	5088,83	MAZ	MYC associated zinc finger protein
84812	1,43E-06	5,84E+00	7,76E-07	0,1419	-4,9412804	-0,70130113	152,06	PLCD4	phospholipase C delta 4
1019	2,50E-51	5,06E+01	3,84E-52	0,0462	-15,1945569	-0,70188231	5035,82	CDK4	cyclin dependent kinase 4
4125	2,36E-47	4,66E+01	3,98E-48	0,0482	-14,5762125	-0,70202532	4873	MAN2B1	mannosidase alpha class 2B member 1
1869	1,77E-44	4,38E+01	3,20E-45	0,0497	-14,1119772	-0,70205444	3595,99	E2F1	E2F transcription factor 1
9762	2,67E-15	1,46E+01	1,02E-15	0,0876	-8,023928	-0,70255842	508,94	LZTS3	leucine zipper tumor suppressor family member 3
6147	7,47E-69	6,81E+01	7,84E-70	0,0398	-17,6647145	-0,70270328	39773,62	RPL23A	ribosomal protein L23a
552900	1,46E-16	1,58E+01	5,40E-17	0,0839	-8,3777135	-0,70298227	545,79	BOLA2	bolA family member 2
2639	1,00E-25	2,50E+01	2,84E-26	0,0663	-10,6043568	-0,70325495	1099,21	GCDH	glutaryl-CoA dehydrogenase
4668	2,74E-28	2,76E+01	7,29E-29	0,0631	-11,1484109	-0,70329407	1039,86	NAGA	alpha-N-acetylgalactosaminidase
64763	6,75E-21	2,02E+01	2,19E-21	0,0741	-9,4955434	-0,70343433	1083,79	ZNF574	zinc finger protein 574
26297	7,23E-18	1,71E+01	2,56E-18	0,0806	-8,7294929	-0,7036263	623,34	SERGEF	secretion regulating guanine nucleotide exchange factor
124995	9,91E-42	4,10E+01	1,91E-42	0,0515	-13,6538551	-0,70377697	2759,23	MRPL10	mitochondrial ribosomal protein L10
222229	4,61E-23	2,23E+01	1,41E-23	0,0704	-10,0078765	-0,70407027	892,39	LRWD1	leucine rich repeats and WD repeat domain containing 1
3939	4,03E-99	9,84E+01	2,33E-100	0,0331	-21,2662667	-0,70407793	147481,7	LDHA	lactate dehydrogenase A
9278	3,98E-30	2,94E+01	1,01E-30	0,0611	-11,5233486	-0,70422816	1384,25	ZBTB22	zinc finger and BTB domain containing 22
401585	6,69E-02	1,17E+00	5,27E-02	0,3638	-1,9369846	-0,7045796	22,9	LINC02595	long intergenic non-protein coding RNA 2595
5260	1,40E-30	2,99E+01	3,51E-31	0,0607	-11,6136909	-0,70461649	1397,47	PHKG1	phosphorylase kinase catalytic subunit gamma 1
1200	4,04E-33	3,24E+01	9,49E-34	0,0582	-12,1087385	-0,704755	4640,13	TPP1	tripeptidyl peptidase 1
285971	4,84E-05	4,32E+00	2,87E-05	0,1685	-4,1831742	-0,70476811	109,06	ZNF775	zinc finger protein 775
5695	7,64E-63	6,21E+01	9,10E-64	0,0418	-16,8583894	-0,70515867	7800,03	PSMB7	proteasome 20S subunit beta 7
51021	8,54E-54	5,31E+01	1,25E-54	0,0453	-15,5652974	-0,70534575	4193,75	MRPS16	mitochondrial ribosomal protein S16
7205	2,94E-25	2,45E+01	8,48E-26	0,0672	-10,5017147	-0,70537869	1513,66	TRIP6	thyroid hormone receptor interactor 6
105373020	5,97E-03	2,22E+00	4,19E-03	0,2464	-2,8633801	-0,70539865	51,46	LOC105373	uncharacterized LOC105373020
7280	1,93E-39	3,87E+01	3,92E-40	0,0532	-13,2606185	-0,70565821	2201,44	TUBB2A	tubulin beta 2A class IIa
643669	3,31E-07	6,48E+00	1,74E-07	0,1351	-5,2252362	-0,70607779	174,32	CCER2	coiled-coil glutamate rich protein 2
1802	6,57E-34	3,32E+01	1,52E-34	0,0576	-12,2583102	-0,70607987	2354,04	DPH2	diphthamide biosynthesis 2
123	3,28E-61	6,05E+01	4,09E-62	0,0425	-16,6319193	-0,70610689	7521,8	PLIN2	perilipin 2
105370917	3,11E-02	1,51E+00	2,35E-02	0,3118	-2,2656863	-0,70649822	31,01	LOC105370	uncharacterized LOC105370917
151393	2,20E-23	2,27E+01	6,66E-24	0,0701	-10,0816592	-0,70657494	1433,78	RMDN2	regulator of microtubule dynamics 2
8603	1,54E-38	3,78E+01	3,19E-39	0,054	-13,1023122	-0,70703221	1703,91	FAM193A	family with sequence similarity 193 member A
10406	1,02E-02	1,99E+00	7,33E-03	0,2637	-2,681589	-0,70724745	44,2	WFDC2	WAP four-disulfide core domain 2
7390	1,06E-47	4,70E+01	1,78E-48	0,0483	-14,6312107	-0,70724932	2678,95	UROS	uroporphyrinogen III synthase
2335	5,70E-49	4,82E+01	9,25E-50	0,0477	-14,830895	-0,70728007	28786,4	FN1	fibronectin 1
25912	6,69E-73	7,22E+01	6,42E-74	0,0389	-18,1880543	-0,70750754	8409,57	C1orf43	chromosome 1 open reading frame 43
101929291	1,11E-05	4,95E+00	6,35E-06	0,1568	-4,5145402	-0,70768582	124,22	LOC101929	uncharacterized LOC101929291
6449	3,74E-42	4,14E+01	7,15E-43	0,0516	-13,725424	-0,70772787	4405,59	SGTA	small glutamine rich tetratricopeptide repeat co-chaperone alpha
105378949	9,24E-02	1,03E+00	7,42E-02	0,3964	-1,7854522	-0,70774384	20,77	GNB1-DT	GNB1 divergent transcript
6051	2,24E-49	4,86E+01	3,58E-50	0,0475	-14,8944164	-0,70782996	3126,8	RNPEP	arginyl aminopeptidase
107985219	2,23E-13	1,27E+01	9,08E-14	0,095	-7,4536135	-0,70804314	535,25	LOC107985	uncharacterized LOC107985219
2868	3,25E-06	5,49E+00	1,80E-06	0,1483	-4,7747694	-0,70806957	153,65	GRK4	G protein-coupled receptor kinase 4
57692	3,04E-10	9,52E+00	1,39E-10	0,1103	-6,4172415	-0,70810616	269,96	MAGEE1	MAGE family member E1
10500	8,18E-04	3,09E+00	5,33E-04	0,2045	-3,4634517	-0,70820792	74,18	SEMA6C	semaphorin 6C
4215	7,01E-50	4,92E+01	1,12E-50	0,0473	-14,9722328	-0,70849301	2829,42	MAP3K3	mitogen-activated protein kinase kinase kinase 3
100507607	7,64E-09	8,12E+00	3,70E-09	0,1202	-5,8970443	-0,70868192	228,78	NPIPB9	nuclear pore complex interacting protein family member B9
54106	1,80E-01	7,45E-01	1,51E-01	0,494	-1,435481	-0,70915201	12,83	TLR9	toll like receptor 9
1435	3,37E-56	5,55E+01	4,69E-57	0,0446	-15,9188381	-0,70919922	21780,75	CSF1	colony stimulating factor 1
100131234	1,17E-01	9,32E-01	9,50E-02	0,4247	-1,669734	-0,70920459	17,35	MIR181A1H(	MIR181A1 host gene
7703	2,18E-42	4,17E+01	4,14E-43	0,0515	-13,7649808	-0,70925087	2252,36	PCGF2	polycomb group ring finger 2
550631	1,10E-09	8,96E+00	5,16E-10	0,1141	-6,2142309	-0,70930461	270,03	CCDC157	coiled-coil domain containing 157
10670	1,20E-44	4,39E+01	2,17E-45	0,0502	-14,1395544	-0,70935468	3293,47	RRAGA	Ras related GTP binding A
8510	4,67E-03	2,33E+00	3,25E-03	0,241	-2,9432552	-0,70936126	50,76	MMP23B	matrix metallopeptidase 23B
10454	2,87E-22	2,15E+01	8,94E-23	0,0722	-9,82325	-0,70938967	1120,2	TAB1	TGF-beta activated kinase 1 (MAP3K7) binding protein 1
771	1,79E-27	2,67E+01	4,85E-28	0,0646	-10,9784946	-0,70943411	1147,88	CA12	carbonic anhydrase 12
8241	7,52E-43	4,21E+01	1,42E-43	0,0513	-13,8423385	-0,70946932	3210,8	RBM10	RNA binding motif protein 10
3601	2,57E-24	2,36E+01	7,60E-25	0,0689	-10,2927647	-0,70949384	819,9	IL15RA	interleukin 15 receptor subunit alpha
5754	5,43E-57	5,63E+01	7,41E-58	0,0443	-16,0339027	-0,70968999	9098,74	PTK7	protein tyrosine kinase 7 (inactive)
4641	7,83E-69	6,81E+01	8,23E-70	0,0402	-17,6620123	-0,7099916	15823,31	MYO1C	myosin IC
55577	6,68E-31	3,02E+01	1,66E-31	0,0608	-11,6776368	-0,71012023	1576,62	NAGK	N-acetylglucosamine kinase
101409261	8,70E-02	1,06E+00	6,96E-02	0,3913	-1,8147132	-0,71012647	22,43	OGFR-AS1	OGFR antisense RNA 1
100529067	1,25E-46	4,59E+01	2,14E-47	0,0491	-14,4607361	-0,71013642	3235,91	SERF2-C15(	SERF2-C15orf63 readthrough
5424	1,10E-27	2,70E+01	2,97E-28	0,0644	-11,0225732	-0,71022327	2739,25	POLD1	DNA polymerase delta 1, catalytic subunit
22877	2,49E-59	5,86E+01	3,23E-60	0,0434	-16,3681044	-0,71041586	4124,41	MLXIP	MLX interacting protein
3897	3,55E-36	3,54E+01	7,74E-37	0,0561	-12,6789529	-0,7107017	2143,08	L1CAM	L1 cell adhesion molecule
6094	5,63E-04	3,25E+00	3,62E-04	0,1994	-3,5662099	-0,7111441	77,45	ROM1	retinal outer segment membrane protein 1
29882	3,01E-25	2,45E+01	8,69E-26	0,0677	-10,4994392	-0,71128943	1365,03	ANAPC2	anaphase promoting complex subunit 2
285463	3,21E-19	1,85E+01	1,09E-19	0,0784	-9,0792124	-0,7116084	672,25	CTBP1-AS	CTBP1 antisense RNA
3656	9,35E-34	3,30E+01	2,17E-34	0,0583	-12,2293627	-0,71239201	1786,68	IRAK2	interleukin 1 receptor associated kinase 2
2717	1,85E-42	4,17E+01	3,50E-43	0,0517	-13,7770784	-0,71241824	1992,56	GLA	galactosidase alpha
50865	9,88E-41	4,00E+01	1,94E-41	0,0528	-13,4840378	-0,71247245	1740,81	HEBP1	heme binding protein 1
84971	1,78E-31	3,07E+01	4,35E-32	0,0604	-11,7908734	-0,71255948	1342,06	ATG4D	autophagy related 4D cysteine peptidase
100131213	1,22E-02	1,91E+00	8,77E-03	0,2719	-2,6207046	-0,71261019	41,78	ZNF503-AS2	ZNF503 antisense RNA 2
9343	1,55E-84	8,38E+01	1,17E-85	0,0363	-19,6141058	-0,71276688	14071,44	EFTUD2	elongation factor Tu GTP binding domain containing 2
101927393	3,27E-12	1,15E+01	1,39E-12	0,1006	-7,0851578	-0,71292601	343,5	LOC101927	uncharacterized LOC101927393
107984124	1,68E-01	7,75E-01	1,40E-01	0,4833	-1,4752853	-0,71295211	13,1	LOC107984	uncharacterized LOC107984124
84875	1,97E-21	2,07E+01	6,29E-22	0,0741	-9,6246435	-0,71298372	1239,02	PARP10	poly(ADP-ribose) polymerase family member 10
9754	1,55E-31	3,08E+01	3,79E-32	0,0604	-11,8024521	-0,71310214	1190,62	STARD8	StAR related lipid transfer domain containing 8
108570035	2,89E-24	2,35E+01	8,57E-25	0,0694	-10,2811209	-0,7134792	865,91	LINP1	lncRNA in non-homologous end joining pathway 1
57661	4,29E-45	4,44E+01	7,66E-46	0,0502	-14,2124971	-0,71369864	3259,16	PHRF1	PHD and ring finger domains 1
246330	1,19E-10	9,92E+00	5,34E-11	0,1088	-6,5612095	-0,71375746	276,75	PELI3	pellino E3 ubiquitin protein ligase family member 3
58525	3,05E-40	3,95E+01	6,07E-41	0,0533	-13,3996612	-0,7138525	4088,93	WIZ	WIZ zinc finger
102288414	8,73E-36	3,51E+01	1,93E-36	0,0566	-12,6072137	-0,71404305	2001,56	C11orf98	chromosome 11 open reading frame 98
10399	5,03E-71	7,03E+01	5,05E-72	0,0398	-17,947138	-0,71410246	70124,48	RACK1	receptor for activated C kinase 1
56144	2,36E-01	6,27E-01	2,02E-01	0,5592	-1,277045	-0,71412473	9,55	PCDHA4	protocadherin alpha 4
55011	8,42E-47	4,61E+01	1,44E-47	0,0493	-14,4882073	-0,71429333	4367,98	PIH1D1	PIH1 domain containing 1
23157	3,08E-35	3,45E+01	6,88E-36	0,0572	-12,5065313	-0,71488624	1495,58	SEPTIN6	septin 6
54939	4,54E-21	2,03E+01	1,46E-21	0,075	-9,5373714	-0,71508801	1358,78	COMMD4	COMM domain containing 4
129303	2,87E-11	1,05E+01	1,26E-11	0,1056	-6,77305	-0,71518674	361,86	TMEM150A	transmembrane protein 150A
116841	1,30E-33	3,29E+01	3,03E-34	0,0586	-12,2020217	-0,71524471	1654,13	SNAP47	synaptosome associated protein 47
107987269	2,86E-04	3,54E+00	1,80E-04	0,1911	-3,7457709	-0,71576963	88,02	LOC107987	uncharacterized LOC107987269
23220	1,09E-02	1,96E+00	7,87E-03	0,2693	-2,6576737	-0,71577878	42,25	DTX4	deltex E3 ubiquitin ligase 4
90326	1,06E-34	3,40E+01	2,40E-35	0,0577	-12,4066891	-0,7158457	1351,06	THAP3	THAP domain containing 3
4674	8,74E-02	1,06E+00	7,00E-02	0,3951	-1,812167	-0,71593659	19,65	NAP1L2	nucleosome assembly protein 1 like 2
140701	4,36E-05	4,36E+00	2,58E-05	0,1702	-4,207278	-0,71606186	109,21	ABHD16B	abhydrolase domain containing 16B
100652768	2,70E-06	5,57E+00	1,49E-06	0,1488	-4,8131457	-0,71623176	145,11	LOC100652	uncharacterized LOC100652768
8876	2,61E-20	1,96E+01	8,59E-21	0,0766	-9,3521845	-0,71628878	676,56	VNN1	vanin 1
79705	1,17E-27	2,69E+01	3,16E-28	0,065	-11,0169977	-0,71641479	1054,15	LRRK1	leucine rich repeat kinase 1
4258	1,27E-23	2,29E+01	3,81E-24	0,0707	-10,1363086	-0,71650345	879,9	MGST2	microsomal glutathione S-transferase 2

105373748	5,07E-02	1,29E+00	3,93E-02	0,3478	-2,0608287	-0,71680408	25,79	GPR155-DT	GPR155 divergent transcript
54662	2,35E-42	4,16E+01	4,46E-43	0,0521	-13,7595524	-0,71689793	2356,65	TBC1D13	TBC1 domain family member 13
439921	6,75E-69	6,82E+01	7,07E-70	0,0406	-17,6705249	-0,71695375	7008,7	MXRA7	matrix remodeling associated 7
10113	4,10E-39	3,84E+01	8,37E-40	0,0543	-13,203529	-0,71728539	2930,95	PREB	prolactin regulatory element binding
4298	4,46E-44	4,34E+01	8,17E-45	0,0511	-14,0458099	-0,71770694	3172,92	MLLT1	MLLT1 super elongation complex subunit
92335	1,26E-37	3,69E+01	2,65E-38	0,0555	-12,9406682	-0,71822375	1477,9	STRADA	STE20 related adaptor alpha
64847	3,14E-31	3,05E+01	7,74E-32	0,0612	-11,742277	-0,71834807	2264,95	SPATA20	spermatogenesis associated 20
4055	2,87E-45	4,45E+01	5,10E-46	0,0504	-14,2409227	-0,71835333	3858,9	LTBR	lymphotoxin beta receptor
7866	1,89E-32	3,17E+01	4,52E-33	0,06	-11,9800195	-0,71838303	4329,2	IFRD2	interferon related developmental regulator 2
7132	2,29E-37	3,66E+01	4,86E-38	0,0557	-12,894037	-0,71840021	5773,15	TNFRSF1A	TNF receptor superfamily member 1A
147040	1,91E-12	1,17E+01	8,04E-13	0,1003	-7,16052	-0,71843285	351,38	KCTD11	potassium channel tetramerization domain containing 11
3689	1,77E-25	2,48E+01	5,07E-26	0,0681	-10,550112	-0,71850862	1539,49	ITGB2	integrin subunit beta 2
83444	4,63E-13	1,23E+01	1,91E-13	0,0978	-7,3549204	-0,71916301	401,89	INO80B	INO80 complex subunit B
4134	3,25E-58	5,75E+01	4,31E-59	0,0444	-16,2096234	-0,71924196	24466,91	MAP4	microtubule associated protein 4
256281	9,82E-09	8,01E+00	4,78E-09	0,1229	-5,8546812	-0,71925733	243,88	NUDT14	nudix hydrolase 14
94005	6,56E-42	4,12E+01	1,26E-42	0,0526	-13,6842997	-0,71951883	2771,6	PIGS	phosphatidylinositol glycan anchor biosynthesis class S
6525	3,92E-49	4,84E+01	6,34E-50	0,0485	-14,8562534	-0,71980701	4454,49	SMTN	smoothelin
112950	6,42E-43	4,22E+01	1,20E-43	0,052	-13,8539055	-0,71992546	1863,78	MED8	mediator complex subunit 8
158584	9,47E-02	1,02E+00	7,62E-02	0,4061	-1,7732487	-0,72007617	18,07	FAAH2	fatty acid amide hydrolase 2
105379273	1,00E-01	1,00E+00	8,08E-02	0,4127	-1,745822	-0,72051178	17,46	LOC10537927	uncharacterized LOC105379273
5195	5,18E-33	3,23E+01	1,22E-33	0,0596	-12,0881425	-0,72064951	1613,86	PEX14	peroxisomal biogenesis factor 14
107984655	2,07E-04	3,68E+00	1,29E-04	0,1883	-3,8283716	-0,72069803	88,59	LOC10798465	uncharacterized LOC107984655
30851	6,84E-32	3,12E+01	1,66E-32	0,0607	-11,8719659	-0,72088148	2852,57	TAX1BP3	Tax1 binding protein 3
9911	4,11E-11	1,04E+01	1,82E-11	0,1073	-6,7199856	-0,721143	294,21	TMCC2	transmembrane and coiled-coil domain family 2
79016	3,50E-68	6,75E+01	3,72E-69	0,041	-17,5766268	-0,72122185	6840,77	DDA1	DET1 and DDB1 associated 1
284498	3,45E-05	4,46E+00	2,03E-05	0,1692	-4,2617674	-0,72129134	112,21	C1orf167	chromosome 1 open reading frame 167
79102	1,61E-50	4,98E+01	2,52E-51	0,0479	-15,0706894	-0,7214492	5393,99	RNF26	ring finger protein 26
80381	2,64E-32	3,16E+01	6,31E-33	0,0604	-11,9523478	-0,72151571	2893,66	CD276	CD276 molecule
692312	5,74E-31	3,02E+01	1,42E-31	0,0617	-11,6906163	-0,72184076	1674,3	PPAN-P2RY	PPAN-P2RY11 readthrough
57410	6,94E-35	3,42E+01	1,56E-35	0,058	-12,44116	-0,72206822	3939,82	SCYL1	SCY1 like pseudokinase 1
3659	1,91E-47	4,67E+01	3,21E-48	0,0495	-14,5909619	-0,72284521	2970,83	IRF1	interferon regulatory factor 1
102724322	5,41E-02	1,27E+00	4,21E-02	0,3557	-2,0325171	-0,7229691	30,81	LOC10272432	uncharacterized LOC102724322
100129046	2,56E-18	1,76E+01	8,95E-19	0,0818	-8,8475008	-0,72332178	566,3	BCAR3-AS1	BCAR3 antisense RNA 1
5435	1,20E-33	3,29E+01	2,78E-34	0,0593	-12,2090334	-0,72395384	1506,59	POLR2F	RNA polymerase II, I and III subunit F
65982	1,79E-22	2,17E+01	5,56E-23	0,0734	-9,8710869	-0,72413899	995,06	ZSCAN18	zinc finger and SCAN domain containing 18
1949	5,28E-04	3,28E+00	3,39E-04	0,2021	-3,5833873	-0,72428925	83,91	EFNB3	ephrin B3
79607	1,42E-62	6,18E+01	1,71E-63	0,0431	-16,8211864	-0,72479475	4735,53	FAM118B	family with sequence similarity 118 member B
112936	1,25E-39	3,89E+01	2,52E-40	0,0545	-13,2935127	-0,72493914	2740,97	VPS26B	VPS26 retromer complex component B
100847073	4,58E-02	1,34E+00	3,53E-02	0,3445	-2,1046828	-0,7251236	25,16	MIR5090	microRNA 5090
284338	3,84E-16	1,54E+01	1,43E-16	0,0878	-8,2619143	-0,72514298	474,13	PRR19	proline rich 19
3875	4,47E-81	8,03E+01	3,63E-82	0,0378	-19,2010737	-0,72545584	14000,95	KRT18	keratin 18
6598	8,58E-62	6,11E+01	1,05E-62	0,0434	-16,7130973	-0,72548611	4649,94	SMARCB1	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily b, member 1
84313	7,57E-63	6,21E+01	9,02E-64	0,043	-16,8589411	-0,72562078	4158,42	VPS25	vacuolar protein sorting 25 homolog
84317	2,32E-21	2,06E+01	7,42E-22	0,0756	-9,6076216	-0,72591605	736,55	CCDC115	coiled-coil domain containing 115
375	5,34E-61	6,03E+01	6,70E-62	0,0437	-16,6023663	-0,72603034	23881,81	ARF1	ADP ribosylation factor 1
26155	1,97E-47	4,67E+01	3,32E-48	0,0498	-14,5886402	-0,72628689	9580,97	NOC2L	NOC2 like nucleolar associated transcriptional repressor
79178	1,95E-20	1,97E+01	6,41E-21	0,0774	-9,383092	-0,72637116	643,7	THTPA	thiamine triphosphatase
91289	1,50E-38	3,78E+01	3,10E-39	0,0554	-13,1044876	-0,72649521	2202,13	LMF2	lipase maturation factor 2
780	7,55E-37	3,61E+01	1,62E-37	0,0568	-12,8009125	-0,72652821	1539,75	DDR1	discoidin domain receptor tyrosine kinase 1
56110	1,79E-03	2,75E+00	1,20E-03	0,2243	-3,2398658	-0,72657416	59,33	PCDHGA5	protocadherin gamma subfamily A, 5
100507423	2,30E-06	5,64E+00	1,27E-06	0,15	-4,8451134	-0,7265777	140,62	MKNK1-AS1	MKNK1 antisense RNA 1
318	1,24E-27	2,69E+01	3,34E-28	0,066	-11,0121783	-0,7265806	1049,42	NUDT2	nudix hydrolase 2
158	1,90E-67	6,67E+01	2,06E-68	0,0416	-17,4793138	-0,72671239	6729,28	ADSL	adenylosuccinate lyase
29086	2,72E-62	6,16E+01	3,28E-63	0,0433	-16,7825136	-0,72672416	8583,55	BABAM1	BRISC and BRCA1 A complex member 1
578	4,46E-44	4,34E+01	8,16E-45	0,0517	-14,0459132	-0,72672491	4226,51	BAK1	BCL2 antagonist/killer 1
5296	2,98E-70	6,95E+01	3,03E-71	0,0407	-17,847422	-0,7268103	8222,16	PIK3R2	phosphoinositide-3-kinase regulatory subunit 2
63943	3,49E-22	2,15E+01	1,09E-22	0,0741	-9,803412	-0,72681082	835,7	FKBPL	FKBP prolyl isomerase like
3611	4,32E-55	5,44E+01	6,16E-56	0,0461	-15,7568297	-0,72683855	6792,29	ILK	integrin linked kinase
440567	1,04E-18	1,80E+01	3,59E-19	0,0812	-8,9489349	-0,72701333	713,42	UQCRHL	ubiquinol-cytochrome c reductase hinge protein like
6836	4,28E-51	5,04E+01	6,61E-52	0,048	-15,1589637	-0,72713193	18105,04	SURF4	surfeit 4
149076	9,04E-22	2,10E+01	2,85E-22	0,0749	-9,7056941	-0,7271543	717,31	ZNF362	zinc finger protein 362
54470	8,76E-40	3,91E+01	1,76E-40	0,0546	-13,3202763	-0,72718612	2040,2	ARMCX6	armadillo repeat containing X-linked 6
65992	1,54E-46	4,58E+01	2,65E-47	0,0503	-14,446295	-0,72718725	2354,3	DDRGK1	DDRGK domain containing 1
2746	3,66E-70	6,94E+01	3,73E-71	0,0408	-17,8357924	-0,72720942	9234,85	GLUD1	glutamate dehydrogenase 1
100505666	2,17E-06	5,66E+00	1,19E-06	0,1498	-4,8567925	-0,72751498	141,43	DCST1-AS1	DCST1 antisense RNA 1
29927	1,52E-74	7,38E+01	1,41E-75	0,0396	-18,3963354	-0,72766809	15489,63	SEC61A1	SEC61 translocon subunit alpha 1
81620	1,51E-27	2,68E+01	4,09E-28	0,0662	-10,9939665	-0,72767505	1417,44	CDT1	chromatin licensing and DNA replication factor 1
85027	7,31E-18	1,71E+01	2,58E-18	0,0834	-8,7283472	-0,72774004	565,48	SMIM3	small integral membrane protein 3
3340	1,10E-54	5,40E+01	1,58E-55	0,0464	-15,6971249	-0,7278287	7677,39	NDST1	N-deacetylase and N-sulfotransferase 1
81559	9,01E-30	2,90E+01	2,30E-30	0,0636	-11,4519191	-0,72800676	1022,14	TRIM11	tripartite motif containing 11
26999	2,94E-14	1,35E+01	1,17E-14	0,0943	-7,7198042	-0,72819671	394,56	CYFIP2	cytoplasmic FMR1 interacting protein 2
5480	2,38E-22	2,16E+01	7,40E-23	0,074	-9,8423636	-0,72830674	833,28	PPIC	peptidylprolyl isomerase C
101928000	2,76E-03	2,56E+00	1,88E-03	0,2343	-3,1092469	-0,72835271	63,2	ZNF232-AS1	ZNF232 antisense RNA 1
3749	7,03E-09	8,15E+00	3,40E-09	0,1233	-5,9109216	-0,72856642	225,09	KCNC4	potassium voltage-gated channel subfamily C member 4
26093	3,55E-20	1,94E+01	1,17E-20	0,0782	-9,3189515	-0,72862375	708,91	CCDC9	coiled-coil domain containing 9
6892	1,20E-74	7,39E+01	1,11E-75	0,0396	-18,4091867	-0,72865889	12913,37	TAPBP	TAP binding protein
387	1,06E-87	8,70E+01	7,56E-89	0,0365	-19,9841644	-0,72886758	31673,89	RHOA	ras homolog family member A
4837	1,31E-23	2,29E+01	3,94E-24	0,0719	-10,133042	-0,72896421	795,56	NNMT	nicotinamide N-methyltransferase
6161	1,02E-77	7,70E+01	8,91E-79	0,0388	-18,7912513	-0,72902722	29799,1	RPL32	ribosomal protein L32
4478	9,21E-82	8,10E+01	7,37E-83	0,0378	-19,2836503	-0,72906158	71286,81	MSN	moesin
3191	8,67E-87	8,61E+01	6,31E-88	0,0367	-19,8780369	-0,72908915	13389,41	HNRNPL	heterogeneous nuclear ribonucleoprotein L
100507412	1,57E-01	8,04E-01	1,30E-01	0,4817	-1,5137068	-0,72912493	12,52	LOC10050741	uncharacterized LOC100507412
10432	3,48E-31	3,05E+01	8,59E-32	0,0621	-11,7334549	-0,72912943	2981,99	RBM14	RNA binding motif protein 14
100506289	2,84E-05	4,55E+00	1,66E-05	0,1694	-4,3059952	-0,7292712	105,86	LOC10050628	uncharacterized LOC100506289
11338	1,86E-65	6,47E+01	2,10E-66	0,0424	-17,2136132	-0,72995671	10465,27	U2AF2	U2 small nuclear RNA auxiliary factor 2
90864	2,95E-15	1,45E+01	1,13E-15	0,0911	-8,0114285	-0,730208	645,94	SPSB3	splA/ryanodine receptor domain and SOCS box containing 3
57623	3,40E-21	2,05E+01	1,09E-21	0,0763	-9,5676727	-0,73023925	683,97	ZFAT	zinc finger and AT-hook domain containing
115416	1,37E-34	3,39E+01	3,11E-35	0,059	-12,385933	-0,73040469	1383,78	MALSU1	mitochondrial assembly of ribosomal large subunit 1
284613	4,01E-24	2,34E+01	1,19E-24	0,0713	-10,2494447	-0,73058532	744,23	CYB561D1	cytochrome b561 family member D1
105375020	2,67E-02	1,57E+00	2,00E-02	0,3141	-2,3262197	-0,73062352	30,41	LOC10537502	uncharacterized LOC105375020
780851	6,56E-03	2,18E+00	4,62E-03	0,258	-2,832401	-0,73077672	47,63	SNORD3A	small nucleolar RNA, C/D box 3A
80320	1,43E-06	5,84E+00	7,78E-07	0,1479	-4,9406986	-0,73088247	145,5	SP6	Sp6 transcription factor
23313	4,72E-27	2,63E+01	1,30E-27	0,0672	-10,8893753	-0,73123831	1215,27	KIAA0930	KIAA0930
6610	4,07E-10	9,39E+00	1,87E-10	0,1148	-6,3715668	-0,73134253	263,96	SMPD2	sphingomyelin phosphodiesterase 2
9138	7,78E-46	4,51E+01	1,37E-46	0,051	-14,3326649	-0,73145201	5197,9	ARHGEF1	Rho guanine nucleotide exchange factor 1
196410	2,40E-02	1,62E+00	1,79E-02	0,309	-2,3683025	-0,73174036	36,49	METTL7B	methyltransferase like 7B
54896	4,11E-24	2,34E+01	1,22E-24	0,0714	-10,2469268	-0,73206654	1192,03	SLC66A1	solute carrier family 66 member 1
643339	1,02E-01	9,91E-01	8,22E-02	0,4216	-1,737815	-0,73273583	16,79	LOC643339	uncharacterized LOC643339
112268184	4,17E-32	3,14E+01	1,00E-32	0,0615	-11,9136846	-0,73276961	1136,28	KPNB1-DT	KPNB1 divergent transcript
168455	9,56E-18	1,70E+01	3,40E-18	0,0843	-8,6971866	-0,73281249	541,28	CCDC71L	coiled-coil domain containing 71 like
91107	1,73E-21	2,08E+01	5,51E-22	0,076	-9,6382276	-0,73290433	897,41	TRIM47	tripartite motif containing 47
2535	8,49E-40	3,91E+01	1,71E-40	0,055	-13,3227179	-0,73303323	2169,97	FZD2	frizzled class receptor 2
84219	1,62E-18	1,78E+01	5,63E-19	0,0824	-8,8990807	-0,73304738	614,19	WDR24	WD repeat domain 24
102723728	4,32E-52	5,14E+01	6,55E-53	0,0479	-15,3101103	-0,73376595	2796,55	LOC10272373	nodal modulator 3-like
55967	3,97E-46	4,54E+01	6,92E-47	0,051	-14,3799214	-0,73389531	3856,26	NDUFA12	NADH:ubiquinone oxidoreductase subunit A12
1337	8,87E-68	6,71E+01	9,52E-69	0,0419	-17,5232624	-0,73404819	9817,8	COX6A1	cytochrome c oxidase subunit 6A1
220082	1,46E-01	8,36E-01	1,21E-01	0,4733	-1,5509515	-0,73410997	14,33	CBY2	chibby family member 2
5510	9,67E-39	3,80E+01	1,99E-39	0,0559	-13,138146	-0,73421429	1719,89	PPP1R7	protein phosphatase 1 regulatory subunit 7
112268412	8,37E-05	4,08E+00	5,05E-05	0,1812	-4,0530999	-0,73429835	104,85	LOC11226842	uncharacterized LOC112268412
107986148	4,61E-02	1,34E+00	3,55E-02	0,3493	-2,102304	-0,7343296	25,67	LOC10798617	replaced by ID 25976
100130086	1,52E-01	8,18E-01	1,26E-01	0,4804	-1,5285692	-0,73435813	12,84	HSFX2	heat shock transcription factor family, X-linked 2
102465134	8,54E-03	2,07E+00	6,08E-03	0,2677	-2,7432408	-0,73435891	44,45	MIR6126	microRNA 6126
105376579	5,79E-02	1,24E+00	4,52E-02	0,3668	-2,0023662	-0,73448046	23,49	LOC10537652	replaced by ID 144110
654483	1,30E-23	2,29E+01	3,90E-24	0,0725	-10,1340582	-0,73448768	797,33	BOLA2B	bolA family member 2B
100505783	4,25E-12	1,14E+01	1,81E-12	0,1042	-7,0480844	-0,73463418	299,55	OSER1-DT	OSER1 divergent transcript
26121	3,39E-57	5,65E+01	4,60E-58	0,0457	-16,0634564	-0,73489869	4800,73	PRPF31	pre-mRNA processing factor 31
102724102	8,93E-03	2,05E+00	6,37E-03	0,2695	-2,7278858	-0,73529326	42,34	LOC10272410	uncharacterized LOC102724102
26157	1,27E-01	8,96E-01	1,04E-01	0,452	-1,6266973	-0,73530446	14,72	GIMAP2	GTPase, IMAP family member 2
4783	3,30E-30	2,95E+01	8,35E-31	0,0637	-11,5394298	-0,73531135	1140,33	NFIL3	nuclear factor, interleukin 3 regulated
101928238	1,34E-02	1,87E+00	9,70E-03	0,2843	-2,5862952	-0,73535485	39,37	ZNF426-DT	ZNF426 divergent transcript

255394	2,09E-13	1,27E+01	8,50E-14	0,0985	-7,4622845	-0,73539559	344,68	TCP11L2	t-complex 11 like 2
5692	1,44E-71	7,08E+01	1,42E-72	0,0408	-18,0176646	-0,73570657	9862,57	PSMB4	proteasome 20S subunit beta 4
288	8,04E-08	7,09E+00	4,09E-08	0,1341	-5,4869352	-0,73587737	180,83	ANK3	ankyrin 3
6650	1,33E-29	2,89E+01	3,40E-30	0,0645	-11,4178818	-0,73614195	1577,27	CAPN15	calpain 15
9377	3,70E-40	3,94E+01	7,38E-41	0,055	-13,3852278	-0,7363718	4146,9	COX5A	cytochrome c oxidase subunit 5A
133	2,93E-50	4,95E+01	4,63E-51	0,049	-15,0306131	-0,73660293	2628,19	ADM	adrenomedullin
91647	8,34E-15	1,41E+01	3,26E-15	0,0935	-7,8806515	-0,73664298	468,25	ATPAF2	ATP synthase mitochondrial F1 complex assembly factor 2
83590	3,27E-28	2,75E+01	8,69E-29	0,0662	-11,1327276	-0,73664373	1366,54	TMUB1	transmembrane and ubiquitin like domain containing 1
196051	4,53E-13	1,23E+01	1,87E-13	0,1002	-7,3579005	-0,73698352	332,31	PLPP4	phospholipid phosphatase 4
100861518	1,54E-06	5,81E+00	8,37E-07	0,1496	-4,9264793	-0,73702856	141,66	P4HA2-AS1	P4HA2 antisense RNA 1
26579	1,32E-47	4,69E+01	2,21E-48	0,0505	-14,6162448	-0,73740374	6733,11	MYEOV	myeloma overexpressed
5664	2,56E-35	3,46E+01	5,71E-36	0,0589	-12,5212774	-0,73743849	1279,95	PSEN2	presenilin 2
57455	2,56E-31	3,06E+01	6,28E-32	0,0627	-11,7598857	-0,73746459	1055,35	REXO1	RNA exonuclease 1 homolog
90871	5,68E-16	1,52E+01	2,13E-16	0,0898	-8,2144475	-0,73781761	461,77	DMAC1	distal membrane arm assembly component 1
201294	2,69E-38	3,76E+01	5,59E-39	0,0565	-13,0597329	-0,73813338	11026,02	UNC13D	unc-13 homolog D
252969	1,84E-18	1,77E+01	6,38E-19	0,0831	-8,8852186	-0,73819519	542,78	NEIL2	nei like DNA glycosylase 2
23373	4,06E-36	3,54E+01	8,86E-37	0,0583	-12,668326	-0,73820884	1732,84	CRTC1	CREB regulated transcription coactivator 1
162427	3,00E-43	4,25E+01	5,59E-44	0,0531	-13,9089284	-0,73832175	2325,19	RETREG3	reticulophagy regulator family member 3
107984210	3,03E-05	4,52E+00	1,78E-05	0,1721	-4,291022	-0,73843984	109,01	LOC107984210	uncharacterized LOC107984210
414197	9,62E-04	3,02E+00	6,30E-04	0,216	-3,4182984	-0,73847649	64,88	ZNF32-AS1	ZNF32 antisense RNA 1
1728	2,52E-69	6,86E+01	2,62E-70	0,0417	-17,7263853	-0,73851958	8933,5	NQO1	NAD(P)H quinone dehydrogenase 1
9985	1,05E-08	7,98E+00	5,13E-09	0,1264	-5,8429058	-0,73873438	207,58	REC8	REC8 meiotic recombination protein
80233	4,05E-24	2,34E+01	1,21E-24	0,0722	-10,2482478	-0,73966037	1419,79	FAAP100	FA core complex associated protein 100
9531	1,06E-64	6,40E+01	1,21E-65	0,0432	-17,1118073	-0,73986079	5808,58	BAG3	BAG cochaperone 3
105372266	1,93E-04	3,71E+00	1,20E-04	0,1925	-3,8461655	-0,7403984	84,16	LOC105372	uncharacterized LOC105372266
435	4,09E-27	2,64E+01	1,12E-27	0,0679	-10,9026642	-0,74078361	1231,41	ASL	argininosuccinate lyase
653659	1,07E-16	1,60E+01	3,93E-17	0,0881	-8,4148199	-0,74109649	453,87	TMEM183BP	transmembrane protein 183B, pseudogene
196383	2,31E-45	4,46E+01	4,10E-46	0,052	-14,2562501	-0,7413573	2003,88	RILPL2	Rab interacting lysosomal protein like 2
151887	9,35E-58	5,70E+01	1,25E-58	0,0459	-16,1438776	-0,74138519	4196,66	CCDC80	coiled-coil domain containing 80
23370	1,94E-54	5,37E+01	2,81E-55	0,0473	-15,6605781	-0,74143481	5738,04	ARHGEF18	Rho/Rac guanine nucleotide exchange factor 18
5859	8,65E-68	6,71E+01	9,28E-69	0,0423	-17,5247152	-0,74147352	9913,31	QARS1	glutaminyl-tRNA synthetase 1
29107	2,40E-40	3,96E+01	4,76E-41	0,0553	-13,4177536	-0,74163234	1490,95	NXT1	nuclear transport factor 2 like export factor 1
55020	4,89E-43	4,23E+01	9,15E-44	0,0535	-13,8736264	-0,74166363	2353,98	TTC38	tetratricopeptide repeat domain 38
8974	6,27E-56	5,52E+01	8,77E-57	0,0467	-15,8796372	-0,74177272	3316,09	P4HA2	prolyl 4-hydroxylase subunit alpha 2
1460	6,86E-54	5,32E+01	1,00E-54	0,0476	-15,5796303	-0,74222949	10328,05	CSNK2B	casein kinase 2 beta
1650	1,31E-67	6,69E+01	1,41E-68	0,0424	-17,500824	-0,74285426	17722,32	DDOST	dolichyl-diphosphooligosaccharide--protein glycosyltransferase non-catalytic subunit
79903	2,09E-35	3,47E+01	4,65E-36	0,0593	-12,5376412	-0,74304574	1310,26	NAA60	N-alpha-acetyltransferase 60, NatF catalytic subunit
339122	4,75E-18	1,73E+01	1,67E-18	0,0847	-8,7773938	-0,74315559	562,95	RAB43	RAB43, member RAS oncogene family
126382	3,60E-31	3,04E+01	8,88E-32	0,0634	-11,7306099	-0,74321777	1097,43	NR2C2AP	nuclear receptor 2C2 associated protein
92999	2,87E-21	2,05E+01	9,22E-22	0,0775	-9,5852839	-0,74326831	898,47	ZBTB47	zinc finger and BTB domain containing 47
81854	1,93E-03	2,71E+00	1,30E-03	0,2311	-3,2165769	-0,74348519	58,59	ZNF205-AS1	ZNF205 antisense RNA 1
1329	4,63E-64	6,33E+01	5,38E-65	0,0437	-17,0247555	-0,74379309	3746,87	COX5B	cytochrome c oxidase subunit 5B
64777	2,27E-38	3,76E+01	4,71E-39	0,0569	-13,0727973	-0,74390828	1547,56	RMND5B	required for meiotic nuclear division 5 homolog B
130617	4,15E-20	1,94E+01	1,37E-20	0,08	-9,3022591	-0,74397453	815,4	ZFAND2B	zinc finger AN1-type containing 2B
100302133	1,11E-01	9,55E-01	8,97E-02	0,4385	-1,6969098	-0,74402971	15,12	MIR1287	microRNA 1287
2091	5,03E-73	7,23E+01	4,81E-74	0,0409	-18,2038293	-0,74414028	11061,43	FBL	fibrillarin
10616	1,92E-48	4,77E+01	3,17E-49	0,0505	-14,7480819	-0,74440619	2961,62	RBCK1	RANBP2-type and C3HC4-type zinc finger containing 1
94103	1,75E-32	3,18E+01	4,17E-33	0,0621	-11,9867779	-0,74440878	1385,82	ORMDL3	ORMDL sphingolipid biosynthesis regulator 3
92154	1,40E-48	4,79E+01	2,29E-49	0,0504	-14,7698589	-0,74441438	3031,02	MTSS2	MTSS I-BAR domain containing 2
105371224	2,56E-02	1,59E+00	1,91E-02	0,3179	-2,3426733	-0,74463863	30,53	LOC105371	uncharacterized LOC105371224
10212	2,29E-52	5,16E+01	3,45E-53	0,0485	-15,3517085	-0,74484732	8790,6	DDX39A	DExD-box helicase 39A
100170229	6,49E-10	9,19E+00	3,01E-10	0,1183	-6,2983953	-0,74490661	247,54	SRRM5	serine/arginine repetitive matrix 5
8242	3,33E-56	5,55E+01	4,63E-57	0,0468	-15,9196753	-0,74504625	5495,95	KDM5C	lysine demethylase 5C
5694	4,23E-51	5,04E+01	6,53E-52	0,0492	-15,159762	-0,74511389	8548,92	PSMB6	proteasome 20S subunit beta 6
115572	2,70E-11	1,06E+01	1,19E-11	0,1099	-6,7817804	-0,74528273	278,65	TENT5B	terminal nucleotidyltransferase 5B
641467	6,67E-05	4,18E+00	4,00E-05	0,1815	-4,1074802	-0,74539707	92,66	TSC22D1-AS	TSC22D1 antisense RNA 1
100130705	1,69E-02	1,77E+00	1,24E-02	0,2982	-2,5003114	-0,74549436	33,45	ATP6V1FNB	ATP6V1F neighbor
105371764	5,87E-02	1,23E+00	4,59E-02	0,3735	-1,9959764	-0,74552959	23,31	LOC105371764	
115024	4,71E-54	5,33E+01	6,87E-55	0,0478	-15,6037385	-0,74565227	2396,98	NT5C3B	5'-nucleotidase, cytosolic IIIB
79797	8,83E-16	1,51E+01	3,34E-16	0,0914	-8,1604247	-0,74579662	555,62	ZNF408	zinc finger protein 408
401647	4,06E-02	1,39E+00	3,11E-02	0,346	-2,1558294	-0,74582533	25,84	GOLGA7B	golgin A7 family member B
221955	7,71E-32	3,11E+01	1,87E-32	0,0629	-11,8618462	-0,74592147	1589,51	DAGLB	diacylglycerol lipase beta
79228	7,46E-34	3,31E+01	1,72E-34	0,0609	-12,2478571	-0,74629635	1821,56	THOC6	THO complex subunit 6
23087	1,67E-27	2,68E+01	4,52E-28	0,0679	-10,9848635	-0,74632047	855,03	TRIM35	tripartite motif containing 35
114904	5,23E-12	1,13E+01	2,24E-12	0,1064	-7,0189469	-0,74651198	331,74	C1QTNF6	C1q and TNF related 6
51706	7,10E-42	4,11E+01	1,37E-42	0,0546	-13,6784604	-0,74698807	1775,29	CYB5R1	cytochrome b5 reductase 1
4209	6,66E-46	4,52E+01	1,17E-46	0,0521	-14,3436939	-0,74709492	3213,98	MEF2D	myocyte enhancer factor 2D
4598	5,67E-26	2,52E+01	1,60E-26	0,0701	-10,6579247	-0,74716013	869,23	MVK	mevalonate kinase
53833	2,52E-02	1,60E+00	1,88E-02	0,318	-2,3498125	-0,74728903	33,66	IL20RB	interleukin 20 receptor subunit beta
55502	7,69E-04	3,11E+00	5,00E-04	0,2147	-3,4805762	-0,7474167	66,91	HES6	hes family bHLH transcription factor 6
58509	1,19E-22	2,19E+01	3,68E-23	0,0754	-9,9123294	-0,74744362	787,61	CACTIN	cactin, spliceosome C complex subunit
5287	2,32E-12	1,16E+01	9,82E-13	0,1049	-7,1329769	-0,74800701	321,19	PIK3C2B	phosphatidylinositol-4-phosphate 3-kinase catalytic subunit type 2 beta
91663	1,96E-47	4,67E+01	3,29E-48	0,0513	-14,5891288	-0,74857841	10977,01	MYADM	myeloid associated differentiation marker
81857	1,53E-41	4,08E+01	2,96E-42	0,055	-13,6220748	-0,74868608	2035,83	MED25	mediator complex subunit 25
1314	5,05E-84	8,33E+01	3,85E-85	0,0383	-19,5534786	-0,74886785	12283,39	COPA	COPI coat complex subunit alpha
9447	1,48E-11	1,08E+01	6,44E-12	0,1091	-6,8695939	-0,7493231	324,64	AIM2	absent in melanoma 2
5018	1,05E-53	5,30E+01	1,54E-54	0,0482	-15,5522344	-0,74935991	4931,52	OXA1L	OXA1L mitochondrial inner membrane protein
27429	1,22E-40	3,99E+01	2,39E-41	0,0556	-13,4685855	-0,74938193	1816,06	HTRA2	HtrA serine peptidase 2
8815	5,03E-73	7,23E+01	4,81E-74	0,0412	-18,2038716	-0,74943489	10567,23	BANF1	BAF nuclear assembly factor 1
84858	4,28E-07	6,37E+00	2,26E-07	0,1448	-5,1764185	-0,74944078	153,02	ZNF503	zinc finger protein 503
81848	1,84E-52	5,17E+01	2,76E-53	0,0488	-15,3661996	-0,74983225	4006,79	SPRY4	sprouty RTK signaling antagonist 4
9647	1,38E-51	5,09E+01	2,11E-52	0,0492	-15,2337837	-0,749983	3202,08	PPM1F	protein phosphatase, Mg2+/Mn2+ dependent 1F
100861548	2,96E-55	5,45E+01	4,21E-56	0,0475	-15,7808959	-0,75010331	3087,05	PINK1-AS	PINK1 antisense RNA
84893	1,52E-53	5,28E+01	2,24E-54	0,0483	-15,5279482	-0,75017895	2435,47	FBH1	F-box DNA helicase 1
10497	2,41E-48	4,76E+01	3,98E-49	0,0509	-14,7325904	-0,75032833	2469,17	UNC13B	unc-13 homolog B
23125	1,15E-38	3,79E+01	2,38E-39	0,0572	-13,1247021	-0,75070641	2467,2	CAMTA2	calmodulin binding transcription activator 2
7284	2,20E-69	6,87E+01	2,28E-70	0,0423	-17,7341834	-0,75077789	9040,66	TUFM	Tu translation elongation factor, mitochondrial
266655	1,36E-30	2,99E+01	3,40E-31	0,0646	-11,6164221	-0,75098045	1070,7	BRD3OS	BRD3 opposite strand
148709	1,66E-02	1,78E+00	1,22E-02	0,2996	-2,5067941	-0,75108378	33,11	ACTG1P25	actin gamma 1 pseudogene 25
200312	2,91E-14	1,35E+01	1,15E-14	0,0973	-7,721179	-0,75127918	356,38	RNF215	ring finger protein 215
27018	5,98E-61	6,02E+01	7,52E-62	0,0453	-16,5954676	-0,7513874	4118,59	BEX3	brain expressed X-linked 3
440465	1,40E-15	1,49E+01	5,33E-16	0,0927	-8,1038102	-0,7514574	403,16	BAIAP2-DT	BAIAP2 divergent transcript
92949	2,49E-32	3,16E+01	5,95E-33	0,0629	-11,9572091	-0,75154311	1170,86	ADAMTSL1	ADAMTS like 1
100289495	5,06E-02	1,30E+00	3,92E-02	0,3645	-2,0616902	-0,75157265	23,04	LOC100289	uncharacterized LOC100289495
57060	2,32E-38	3,76E+01	4,81E-39	0,0575	-13,0712017	-0,75195774	1554,15	PCBP4	poly(rC) binding protein 4
23476	1,70E-57	5,68E+01	2,29E-58	0,0467	-16,1066514	-0,75202599	7439,71	BRD4	bromodomain containing 4
8879	1,67E-53	5,28E+01	2,46E-54	0,0485	-15,5220279	-0,75210456	2728,76	SGPL1	sphingosine-1-phosphate lyase 1
107986126	4,45E-24	2,34E+01	1,32E-24	0,0735	-10,2390944	-0,75228486	842,08	LOC107986	uncharacterized LOC107986126
80301	1,81E-23	2,27E+01	5,46E-24	0,0746	-10,1011205	-0,75315414	800,91	PLEKHO2	pleckstrin homology domain containing O2
100129034	9,50E-65	6,40E+01	1,09E-65	0,044	-17,1181675	-0,75369558	4665,75	LOC100129	uncharacterized LOC100129034
149951	2,49E-58	5,76E+01	3,29E-59	0,0465	-16,2262266	-0,75414034	3725,79	COMMD7	COMM domain containing 7
8666	8,79E-82	8,11E+01	7,03E-83	0,0391	-19,2861093	-0,75414736	11980,87	EIF3G	eukaryotic translation initiation factor 3 subunit G
56940	2,58E-36	3,56E+01	5,59E-37	0,0594	-12,7044235	-0,7542411	1203,72	DUSP22	dual specificity phosphatase 22
146547	1,98E-01	7,03E-01	1,67E-01	0,5463	-1,3808379	-0,75430541	10,22	PRSS36	serine protease 36
6157	1,02E-73	7,30E+01	9,63E-75	0,0413	-18,2917474	-0,75488991	33428,67	RPL27A	ribosomal protein L27a
541565	9,00E-12	1,10E+01	3,88E-12	0,1088	-6,9416077	-0,75511333	271,1	C8orf58	chromosome 8 open reading frame 58
8531	6,65E-64	6,32E+01	7,76E-65	0,0444	-17,0033434	-0,75533253	6665,56	YBX3	Y-box binding protein 3
7805	4,95E-48	4,73E+01	8,23E-49	0,0514	-14,6834703	-0,75535977	5813,71	LAPTM5	lysosomal protein transmembrane 5
9744	2,30E-15	1,46E+01	8,81E-16	0,0939	-8,0424329	-0,75543154	414,95	ACAP1	ArfGAP with coiled-coil, ankyrin repeat and PH domains 1
105369332	1,26E-14	1,39E+01	4,95E-15	0,0965	-7,8282469	-0,75551181	370,39	STX5-DT	STX5 divergent transcript
6015	1,81E-40	3,97E+01	3,58E-41	0,0562	-13,4388891	-0,75566361	2601,71	RING1	ring finger protein 1
79991	2,91E-41	4,05E+01	5,67E-42	0,0557	-13,5745003	-0,75578897	2168,27	STN1	STN1 subunit of CST complex
100134259	1,55E-01	8,10E-01	1,29E-01	0,4979	-1,5181132	-0,75580213	12,45	LINC01119	long intergenic non-protein coding RNA 1119
9564	4,13E-58	5,74E+01	5,50E-59	0,0467	-16,1946415	-0,75580363	4032,1	BCAR1	BCAR1 scaffold protein, Cas family member
7389	2,34E-50	4,96E+01	3,69E-51	0,0502	-15,0456705	-0,75593456	5313,79	UROD	uroporphyrinogen decarboxylase
8859	9,31E-28	2,70E+01	2,51E-28	0,0685	-11,0379725	-0,75642188	938,66	STK19	serine/threonine kinase 19
100526737	1,04E-37	3,70E+01	2,19E-38	0,0585	-12,9552755	-0,75749608	1525,28	RBM14-RBM	RBM14-RBM4 readthrough
10244	3,29E-40	3,95E+01	6,55E-41	0,0566	-13,394063	-0,75774487	1546,85	RABEPK	Rab9 effector protein with kelch motifs
201633	5,10E-04	3,29E+00	3,27E-04	0,211	-3,5927255	-0,75796604	70,63	TIGIT	T cell immunoreceptor with Ig and ITIM domains
55666	8,56E-63	6,21E+01	1,02E-63	0,045	-16,8516173	-0,75799228	11057,42	NPLOC4	NPL4 homolog, ubiquitin recognition factor

154791	3,38E-09	8,47E+00	1,62E-09	0,1257	-6,0321517	-0,7583643	209,87	FMC1	formation of mitochondrial complex V assembly factor 1 homolog
10531	6,08E-77	7,62E+01	5,39E-78	0,0406	-18,6954317	-0,7585418	7562,55	PITRM1	pitrilysin metallopeptidase 1
100134934	9,86E-12	1,10E+01	4,25E-12	0,1096	-6,9285215	-0,75911782	320,76	TEN1	TEN1 subunit of CST complex
5923	7,91E-20	1,91E+01	2,64E-20	0,0822	-9,2326855	-0,75911813	625,98	RASGRF1	Ras protein specific guanine nucleotide releasing factor 1
23207	8,78E-47	4,61E+01	1,50E-47	0,0524	-14,4852967	-0,75916374	3306,81	PLEKHM2	pleckstrin homology and RUN domain containing M2
2671	9,39E-19	1,80E+01	3,24E-19	0,0848	-8,960363	-0,75950162	700,36	GFER	growth factor, augmenter of liver regeneration
10775	2,42E-42	4,16E+01	4,59E-43	0,0552	-13,7574577	-0,75979669	2006,45	POP4	POP4 homolog, ribonuclease P/MRP subunit
58472	1,02E-54	5,40E+01	1,47E-55	0,0484	-15,701653	-0,75992026	4038,36	SQOR	sulfide quinone oxidoreductase
56111	8,51E-06	5,07E+00	4,83E-06	0,1663	-4,5718244	-0,76012168	113,29	PCDHGA4	protocadherin gamma subfamily A, 4
92609	1,49E-55	5,48E+01	2,10E-56	0,048	-15,8246258	-0,76014925	4498,81	TIMM50	translocase of inner mitochondrial membrane 50
727957	1,69E-29	2,88E+01	4,35E-30	0,0667	-11,3965677	-0,76047713	1528,74	MROH1	maestro heat like repeat family member 1
6168	1,50E-88	8,78E+01	1,05E-89	0,0379	-20,0824559	-0,76048205	21552,07	RPL37A	ribosomal protein L37a
90580	1,51E-21	2,08E+01	4,80E-22	0,0788	-9,6525417	-0,76049201	682,06	TIMM29	translocase of inner mitochondrial membrane 29
51619	5,52E-32	3,13E+01	1,33E-32	0,064	-11,8901558	-0,76085453	1112,89	UBE2D4	ubiquitin conjugating enzyme E2 D4 (putative)
2014	6,97E-46	4,52E+01	1,22E-46	0,0531	-14,3405336	-0,76090058	11537,46	EMP3	epithelial membrane protein 3
10021	3,52E-02	1,45E+00	2,68E-02	0,3436	-2,2150657	-0,76099889	25,93	HCN4	hyperpolarization activated cyclic nucleotide gated potassium channel 4
1954	3,75E-36	3,54E+01	8,19E-37	0,0601	-12,6744848	-0,76128074	1370,86	MEGF8	multiple EGF like domains 8
4643	7,85E-42	4,11E+01	1,51E-42	0,0557	-13,6710396	-0,76129366	2357,34	MYO1E	myosin IE
8337	5,04E-07	6,30E+00	2,67E-07	0,148	-5,1453716	-0,76145375	150,18	H2AC18	H2A clustered histone 18
100130744	7,42E-09	8,13E+00	3,59E-09	0,129	-5,9019678	-0,76156397	194,8	LOC1001307	uncharacterized LOC100130744
4835	2,41E-36	3,56E+01	5,22E-37	0,0599	-12,7097923	-0,76157668	1312,17	NQO2	N-ribosyldihydronicotinamide:quinone reductase 2
387646	1,69E-04	3,77E+00	1,04E-04	0,1964	-3,8800107	-0,76188956	81,88	LRRC37A6P	leucine rich repeat containing 37 member A6, pseudogene
81029	5,57E-23	2,23E+01	1,70E-23	0,0763	-9,9889707	-0,76211003	734,02	WNT5B	Wnt family member 5B
170384	1,34E-22	2,19E+01	4,15E-23	0,077	-9,9002789	-0,76232786	712,4	FUT11	fucosyltransferase 11
56102	1,08E-03	2,97E+00	7,13E-04	0,2253	-3,3846085	-0,76252454	58,8	PCDHGB3	protocadherin gamma subfamily B, 3
55324	8,69E-61	6,01E+01	1,09E-61	0,046	-16,5729039	-0,76255396	3429,1	ABCF3	ATP binding cassette subfamily F member 3
8525	1,07E-36	3,60E+01	2,30E-37	0,0597	-12,7738497	-0,76271929	2529,37	DGKZ	diacylglycerol kinase zeta
9442	4,80E-51	5,03E+01	7,43E-52	0,0503	-15,151316	-0,76276268	2130,07	MED27	mediator complex subunit 27
55831	3,66E-50	4,94E+01	5,79E-51	0,0508	-15,0158017	-0,76278422	2586,41	EMC3	ER membrane protein complex subunit 3
29099	9,75E-45	4,40E+01	1,76E-45	0,0539	-14,1541602	-0,76284734	1649,95	COMMD9	COMM domain containing 9
23617	6,56E-02	1,18E+00	5,16E-02	0,3921	-1,946321	-0,76323157	19,94	TSSK2	testis specific serine kinase 2
100129196	1,46E-02	1,84E+00	1,06E-02	0,2988	-2,5545296	-0,76332948	34,08	MATN1-AS1	MATN1 antisense RNA 1
51272	1,75E-57	5,68E+01	2,36E-58	0,0474	-16,1049289	-0,76361635	2792,21	BET1L	Bet1 golgi vesicular membrane trafficking protein like
101927279	7,92E-02	1,10E+00	6,30E-02	0,4109	-1,8589227	-0,76383373	18,85	EP300-AS1	EP300 antisense RNA 1
2720	2,87E-72	7,15E+01	2,80E-73	0,0422	-18,1071914	-0,76385309	4826,5	GLB1	galactosidase beta 1
23154	6,91E-35	3,42E+01	1,56E-35	0,0614	-12,4415144	-0,76438963	2028,57	NCDN	neurochondrin
100885776	4,53E-04	3,34E+00	2,89E-04	0,211	-3,6247835	-0,76474415	69,72	UGDH-AS1	UGDH antisense RNA 1
9429	1,27E-27	2,69E+01	3,43E-28	0,0695	-11,0098147	-0,76492093	854,74	ABCG2	ATP binding cassette subfamily G member 2 (Junior blood group)
79173	5,99E-07	6,22E+00	3,19E-07	0,1496	-5,1120616	-0,76492797	153,41	BRME1	break repair meiotic recombinase recruitment factor 1
23401	1,31E-24	2,39E+01	3,85E-25	0,0739	-10,3580583	-0,76495033	715,2	FRAT2	FRAT regulator of WNT signaling pathway 2
10758	2,90E-35	3,45E+01	6,46E-36	0,0612	-12,5114328	-0,76518701	1343,38	TRAF3IP2	TRAF3 interacting protein 2
54522	1,29E-13	1,29E+01	5,23E-14	0,1017	-7,5259272	-0,76535724	335,7	ANKRD16	ankyrin repeat domain 16
1808	9,16E-68	6,70E+01	9,83E-69	0,0437	-17,5214165	-0,76548509	4755,85	DPYSL2	dihydropyrimidinase like 2
112268006	4,10E-03	2,39E+00	2,83E-03	0,2564	-2,9852453	-0,76551461	46,82	LOC112268006	
29015	4,16E-105	1,04E+02	2,15E-106	0,0349	-21,9086796	-0,76560502	24241,6	SLC43A3	solute carrier family 43 member 3
105375666	2,31E-02	1,64E+00	1,71E-02	0,3214	-2,3837534	-0,76609212	28,68	VPS13B-DT	VPS13B divergent transcript
644	1,06E-44	4,40E+01	1,91E-45	0,0542	-14,1485666	-0,76615981	1689,01	BLVRA	biliverdin reductase A
101929770	1,74E-04	3,76E+00	1,07E-04	0,1979	-3,8733388	-0,76648994	77,11	LOC101929770	uncharacterized LOC101929770
105372432	5,07E-10	9,29E+00	2,34E-10	0,121	-6,3371314	-0,76663711	261,97	LOC105372432	uncharacterized LOC105372432
9582	1,06E-35	3,50E+01	2,34E-36	0,0609	-12,5919903	-0,76677083	1177,45	APOBEC3B	apolipoprotein B mRNA editing enzyme catalytic subunit 3B
4327	3,76E-09	8,42E+00	1,80E-09	0,1275	-6,0148115	-0,76685622	192,21	MMP19	matrix metallopeptidase 19
8038	4,76E-02	1,32E+00	3,68E-02	0,3673	-2,0881877	-0,76697277	22,47	ADAM12	ADAM metallopeptidase domain 12
63906	1,04E-22	2,20E+01	3,20E-23	0,0773	-9,9262891	-0,76745753	747,7	GPATCH3	G-patch domain containing 3
5310	5,72E-25	2,42E+01	1,66E-25	0,0735	-10,4380557	-0,76760901	870,55	PKD1	polycystin 1, transient receptor potential channel interacting
7469	1,13E-35	3,49E+01	2,51E-36	0,061	-12,5864333	-0,76765886	1228,62	NELFA	negative elongation factor complex member A
105375563	1,06E-01	9,75E-01	8,58E-02	0,4469	-1,7179456	-0,76778715	15,34	REPIN1-AS1	REPIN1 antisense RNA 1
6385	6,23E-96	9,52E+01	3,81E-97	0,0367	-20,9163014	-0,76780379	13801,81	SDC4	syndecan 4
4171	1,07E-54	5,40E+01	1,54E-55	0,0489	-15,698868	-0,76781885	4535,47	MCM2	minichromosome maintenance complex component 2
4312	6,29E-114	1,13E+02	2,78E-115	0,0337	-22,8219265	-0,76800336	64462,4	MMP1	matrix metallopeptidase 1
126074	1,02E-09	8,99E+00	4,78E-10	0,1234	-6,2262035	-0,76818304	214,16	SWSAP1	SWIM-type zinc finger 7 associated protein 1
78992	2,91E-41	4,05E+01	5,66E-42	0,0566	-13,5746265	-0,768471	2207,29	YIPF2	Yip1 domain family member 2
441089	6,61E-12	1,12E+01	2,83E-12	0,11	-6,9857918	-0,7685853	281,11	CRSP8P	mediator complex subunit 27 pseudogene
79937	1,75E-17	1,68E+01	6,29E-18	0,0891	-8,6272304	-0,76861682	429,83	CNTNAP3	contactin associated protein family member 3
10445	1,94E-42	4,17E+01	3,68E-43	0,0558	-13,7733978	-0,76867862	2502,79	MCRS1	microspherule protein 1
101928156	2,49E-05	4,60E+00	1,45E-05	0,1773	-4,3359548	-0,76870545	121,18	LOC101928	uncharacterized LOC101928156
105376018	2,73E-02	1,56E+00	2,05E-02	0,3317	-2,3174396	-0,76872162	27,89	LOC105376	uncharacterized LOC105376018
79817	4,47E-06	5,35E+00	2,50E-06	0,1633	-4,7084767	-0,76883983	119,36	MOB3B	MOB kinase activator 3B
5365	5,03E-21	2,03E+01	1,63E-21	0,0807	-9,526568	-0,76894902	633,65	PLXNB3	plexin B3
11041	2,84E-32	3,15E+01	6,80E-33	0,0644	-11,9461303	-0,76897888	1063,31	B4GAT1	beta-1,4-glucuronyltransferase 1
5875	1,14E-26	2,59E+01	3,15E-27	0,0712	-10,8080095	-0,76900214	1588,75	RABGGTA	Rab geranylgeranyltransferase subunit alpha
4902	4,21E-03	2,38E+00	2,91E-03	0,2584	-2,9767244	-0,76915158	46,1	NRTN	neurturin
100507140	4,70E-02	1,33E+00	3,64E-02	0,3678	-2,0929866	-0,76974894	22,32	LINC01792	long intergenic non-protein coding RNA 1792
84892	2,01E-30	2,97E+01	5,05E-31	0,0665	-11,5826145	-0,76984552	1201,05	POMGNT2	protein O-linked mannose N-acetylglucosaminyltransferase 2 (beta 1,4-)
2317	1,70E-102	1,02E+02	9,24E-104	0,0356	-21,6306821	-0,77018298	48220,48	FLNB	filamin B
896	1,34E-63	6,29E+01	1,57E-64	0,0454	-16,962071	-0,77023847	6444,3	CCND3	cyclin D3
23277	2,53E-40	3,96E+01	5,03E-41	0,0574	-13,4136787	-0,77028822	5499,36	CLUH	clustered mitochondria homolog
7264	3,49E-39	3,85E+01	7,11E-40	0,0583	-13,2157903	-0,77053616	2607,83	GFUS	GDP-L-fucose synthase
645166	2,29E-02	1,64E+00	1,70E-02	0,3231	-2,3859763	-0,77081208	45,68	LSP1P5	LSP1 pseudogene 5
342346	1,64E-02	1,79E+00	1,20E-02	0,3068	-2,512938	-0,77090372	33,71	C16orf96	chromosome 16 open reading frame 96
79064	6,85E-36	3,52E+01	1,51E-36	0,0611	-12,6266219	-0,77095587	1141,63	TMEM223	transmembrane protein 223
65264	1,73E-92	9,18E+01	1,13E-93	0,0376	-20,531211	-0,77100972	10613,73	UBE2Z	ubiquitin conjugating enzyme E2 Z
101927685	1,46E-03	2,84E+00	9,71E-04	0,2338	-3,298881	-0,77117802	55,23	HSFX4	heat shock transcription factor family, X-linked member 4
191	1,19E-67	6,69E+01	1,28E-68	0,0441	-17,5062	-0,77123673	18552,81	AHCY	adenosylhomocysteinase
101930071	3,12E-02	1,51E+00	2,36E-02	0,3408	-2,2639898	-0,77148517	25,12	LOC101930	uncharacterized LOC101930071
8406	1,53E-37	3,68E+01	3,24E-38	0,0597	-12,9253276	-0,77165599	1283,24	SRPX	sushi repeat containing protein X-linked
6829	3,87E-71	7,04E+01	3,87E-72	0,043	-17,9618999	-0,77165801	8955,19	SUPT5H	SPT5 homolog, DSIF elongation factor subunit
55663	5,80E-14	1,32E+01	2,33E-14	0,1011	-7,6311884	-0,77184803	346,82	ZNF446	zinc finger protein 446
4722	4,22E-53	5,24E+01	6,26E-54	0,0499	-15,4620079	-0,77187492	2268,85	NDUFS3	NADH:ubiquinone oxidoreductase core subunit S3
347517	8,57E-03	2,07E+00	6,10E-03	0,2815	-2,7422167	-0,77188579	40,86	RAB41	RAB41, member RAS oncogene family
692087	2,31E-25	2,46E+01	6,64E-26	0,0734	-10,5247399	-0,77207622	926,78	SNORD49B	small nucleolar RNA, C/D box 49B
2811	3,21E-02	1,49E+00	2,43E-02	0,343	-2,2524259	-0,77253577	25,94	GP1BA	glycoprotein Ib platelet subunit alpha
11214	6,33E-58	5,72E+01	8,46E-59	0,0478	-16,168139	-0,77255884	2829,19	AKAP13	A-kinase anchoring protein 13
51150	1,97E-46	4,57E+01	3,40E-47	0,0536	-14,4289359	-0,77271706	6587,67	SDF4	stromal cell derived factor 4
84300	3,31E-35	3,45E+01	7,41E-36	0,0618	-12,5006369	-0,77286677	1426,46	UQCC2	ubiquinol-cytochrome c reductase complex assembly factor 2
91300	4,11E-33	3,24E+01	9,67E-34	0,0639	-12,1072176	-0,77309386	1519,87	R3HDM4	R3H domain containing 4
30817	2,80E-14	1,36E+01	1,11E-14	0,1001	-7,7260791	-0,77331783	341,82	ADGRE2	adhesion G protein-coupled receptor E2
11273	5,77E-75	7,42E+01	5,30E-76	0,0419	-18,4491045	-0,77336624	7343,59	ATXN2L	ataxin 2 like
23659	8,84E-32	3,11E+01	2,15E-32	0,0653	-11,8502561	-0,7734529	1204,64	PLA2G15	phospholipase A2 group XV
8943	5,64E-82	8,12E+01	4,48E-83	0,0401	-19,3093331	-0,77353854	6813,99	AP3D1	adaptor related protein complex 3 subunit delta 1
843	4,39E-14	1,34E+01	1,75E-14	0,1009	-7,6675213	-0,77363585	397,52	CASP10	caspase 10
101926977	1,06E-01	9,75E-01	8,57E-02	0,4502	-1,7186171	-0,77375258	16,67	VIRMA-DT	VIRMA divergent transcript
55240	2,49E-55	5,46E+01	3,53E-56	0,049	-15,7919822	-0,77390591	3001,98	STEAP3	STEAP3 metalloreductase
606551	1,31E-09	8,88E+00	6,18E-10	0,1251	-6,1858142	-0,77391209	236,81	UBE2MP1	ubiquitin conjugating enzyme E2 M pseudogene 1
4841	1,14E-97	9,69E+01	6,76E-99	0,0367	-21,107667	-0,77447609	25424,83	NONO	non-POU domain containing octamer binding
5315	7,67E-102	1,01E+02	4,23E-103	0,0359	-21,5604364	-0,7747284	163093,87	PKM	pyruvate kinase M1/2
89953	1,00E-30	3,00E+01	2,51E-31	0,0665	-11,6423777	-0,77477146	1146,26	KLC4	kinesin light chain 4
116349	1,73E-06	5,76E+00	9,45E-07	0,158	-4,9026635	-0,77477194	134,09	EXOC3-AS1	EXOC3 antisense RNA 1
388677	1,19E-21	2,09E+01	3,77E-22	0,0801	-9,677305	-0,7752432	584,28	NOTCH2NLA	notch 2 N-terminal like A
5442	3,66E-28	2,74E+01	9,75E-29	0,0697	-11,122464	-0,77533131	1166,47	POLRMT	RNA polymerase mitochondrial
8907	1,06E-59	5,90E+01	1,36E-60	0,0472	-16,4207347	-0,77538172	10672,54	AP1M1	adaptor related protein complex 1 subunit mu 1
11079	4,67E-64	6,33E+01	5,44E-65	0,0455	-17,0241714	-0,77542774	5468,88	RER1	retention in endoplasmic reticulum sorting receptor 1
6844	1,98E-48	4,77E+01	3,26E-49	0,0526	-14,7459909	-0,77574657	2097,98	VAMP2	vesicle associated membrane protein 2
57048	3,59E-24	2,34E+01	1,07E-24	0,0756	-10,2601156	-0,77592527	719,26	PLSCR3	phospholipid scramblase 3
5528	2,86E-74	7,35E+01	2,67E-75	0,0423	-18,3616033	-0,77599716	8849,2	PPP2R5D	protein phosphatase 2 regulatory subunit B'delta
2953	1,36E-11	1,09E+01	5,88E-12	0,1128	-6,8825129	-0,77609167	252,18	GSTT2	glutathione S-transferase theta 2 (gene/pseudogene)
55163	2,45E-54	5,36E+01	3,56E-55	0,0496	-15,6456633	-0,77632205	2377,14	PNPO	pyridoxamine 5'-phosphate oxidase
54432	2,35E-46	4,56E+01	4,06E-47	0,0539	-14,4167798	-0,77644618	1850,58	YIPF1	Yip1 domain family member 1
125170	3,98E-19	1,84E+01	1,36E-19	0,0858	-9,055815	-0,77698302	810,9	MIEF2	mitochondrial elongation factor 2
121642	4,00E-25	2,44E+01	1,16E-25	0,0742	-10,4723569	-0,77708171	818,15	ALKBH2	alkB homolog 2, alpha-ketoglutarate dependent dioxygenase
3069	1,51E-105	1,05E+02	7,73E-107	0,0354	-21,9551587	-0,77761215	27249,98	HDLBP	high density lipoprotein binding protein

26112	3,17E-76	7,55E+01	2,84E-77	0,0418	-18,6066237	-0,77764516	5245,83	CCDC69	coiled-coil domain containing 69
80308	1,17E-27	2,69E+01	3,16E-28	0,0706	-11,0171747	-0,77767994	1102,15	FLAD1	flavin adenine dinucleotide synthetase 1
54862	1,91E-46	4,57E+01	3,29E-47	0,0539	-14,4312879	-0,77799342	2871,64	CC2D1A	coiled-coil and C2 domain containing 1A
4702	3,39E-57	5,65E+01	4,60E-58	0,0485	-16,0634395	-0,77856945	2823,79	NDUFA8	NADH:ubiquinone oxidoreductase subunit A8
56243	4,64E-39	3,83E+01	9,49E-40	0,059	-13,1940519	-0,77862431	2059,98	KIAA1217	KIAA1217
256710	1,04E-01	9,83E-01	8,39E-02	0,4504	-1,7287495	-0,77868373	14,68	GLIPR1L1	GLIPR1 like 1
79894	4,84E-27	2,63E+01	1,33E-27	0,0715	-10,887101	-0,77881362	1003,53	ZNF672	zinc finger protein 672
100529239	6,24E-89	8,82E+01	4,34E-90	0,0387	-20,1263082	-0,77929827	22396,26	RPS10-NUD	RPS10-NUDT3 readthrough
105376323	1,13E-01	9,47E-01	9,22E-02	0,4628	-1,6839056	-0,77937171	14,38	LINC02846	long intergenic non-protein coding RNA 2846
6155	1,79E-63	6,27E+01	2,10E-64	0,046	-16,9447678	-0,7797283	32125,74	RPL27	ribosomal protein L27
122416	2,25E-19	1,86E+01	7,64E-20	0,0855	-9,1181944	-0,77991644	589,42	ANKRD9	ankyrin repeat domain 9
4536	7,99E-70	6,91E+01	8,23E-71	0,0438	-17,7914715	-0,78002046	97264,96	ND2	NADH dehydrogenase subunit 2
51363	8,55E-70	6,91E+01	8,81E-71	0,0439	-17,787671	-0,78003764	3643,04	CHST15	carbohydrate sulfotransferase 15
125144	1,19E-82	8,19E+01	9,34E-84	0,0402	-19,3901789	-0,78011691	14862,26	SNHG29	small nucleolar RNA host gene 29
9131	7,69E-67	6,61E+01	8,42E-68	0,0449	-17,3988427	-0,78042349	3099,92	AIFM1	apoptosis inducing factor mitochondria associated 1
84364	2,29E-50	4,96E+01	3,60E-51	0,0519	-15,0472383	-0,78054255	2581,68	ARFGAP2	ADP ribosylation factor GTPase activating protein 2
51035	8,42E-54	5,31E+01	1,23E-54	0,0502	-15,5662331	-0,78075232	4151,58	UBXN1	UBX domain protein 1
54797	6,31E-36	3,52E+01	1,38E-36	0,0618	-12,6332254	-0,7808722	1229,81	MED18	mediator complex subunit 18
100133286	2,88E-16	1,55E+01	1,07E-16	0,0941	-8,2966321	-0,7810233	548,33	CBR1-AS1	CBR1 antisense RNA 1
283050	1,37E-03	2,86E+00	9,10E-04	0,2355	-3,317024	-0,7810677	57,83	ZMIZ1-AS1	ZMIZ1 antisense RNA 1
23787	4,85E-92	9,13E+01	3,20E-93	0,0381	-20,4806871	-0,78114465	23031,92	MTCH1	mitochondrial carrier 1
51116	1,54E-39	3,88E+01	3,11E-40	0,0588	-13,2778721	-0,78115727	2578,52	MRPS2	mitochondrial ribosomal protein S2
25870	5,96E-84	8,32E+01	4,55E-85	0,04	-19,5449606	-0,78119786	7278,18	SUMF2	sulfatase modifying factor 2
57228	5,12E-40	3,93E+01	1,02E-40	0,0585	-13,3607803	-0,78121722	1765,59	SMAGP	small cell adhesion glycoprotein
6415	5,22E-45	4,43E+01	9,33E-46	0,055	-14,198742	-0,78141983	1731,22	SELENOW	selenoprotein W
9670	1,75E-38	3,78E+01	3,62E-39	0,0597	-13,0928569	-0,78164657	1799,81	IPO13	importin 13
9146	4,17E-65	6,44E+01	4,74E-66	0,0455	-17,1664394	-0,78173375	7783,23	HGS	hepatocyte growth factor-regulated tyrosine kinase substrate
80774	2,91E-27	2,65E+01	7,93E-28	0,0715	-10,9339628	-0,78219695	847,5	LIMD2	LIM domain containing 2
6205	9,22E-70	6,90E+01	9,51E-71	0,044	-17,7833884	-0,78225765	43841,34	RPS11	ribosomal protein S11
220965	4,19E-02	1,38E+00	3,22E-02	0,3653	-2,1422738	-0,78259856	24,44	FAM13C	family with sequence similarity 13 member C
400619	5,68E-02	1,25E+00	4,43E-02	0,3893	-2,0109874	-0,78283245	19,84	LINC00511	long intergenic non-protein coding RNA 511
79077	5,76E-36	3,52E+01	1,26E-36	0,0619	-12,640571	-0,78299732	1413,52	DCTPP1	dCTP pyrophosphatase 1
23523	1,38E-42	4,19E+01	2,61E-43	0,0568	-13,7982205	-0,78308621	1726,97	CABIN1	calcineurin binding protein 1
8576	4,69E-38	3,73E+01	9,80E-39	0,0602	-13,0169451	-0,7831566	1438,88	STK16	serine/threonine kinase 16
1774	2,10E-26	2,57E+01	5,87E-27	0,0729	-10,7509187	-0,78326219	872,41	DNASE1L1	deoxyribonuclease 1 like 1
6524	8,31E-15	1,41E+01	3,24E-15	0,0995	-7,881182	-0,78379591	355,74	SLC5A2	solute carrier family 5 member 2
254896	9,26E-03	2,03E+00	6,62E-03	0,2887	-2,7151787	-0,78391848	37,97	LOC254896	uncharacterized LOC254896
4794	4,74E-42	4,13E+01	9,08E-43	0,0572	-13,7080697	-0,78396201	2031,67	NFKBIE	NFKB inhibitor epsilon
11313	1,20E-35	3,49E+01	2,65E-36	0,0623	-12,5820725	-0,78411807	3100,76	LYPLA2	lysophospholipase 2
79570	1,28E-01	8,93E-01	1,05E-01	0,4841	-1,6208139	-0,78459291	14,73	NKAIN1	sodium/potassium transporting ATPase interacting 1
55748	5,34E-79	7,83E+01	4,50E-80	0,0414	-18,9490125	-0,78464279	7417,72	CNDP2	carnosine dipeptidase 2
57605	1,66E-28	2,78E+01	4,38E-29	0,0701	-11,1936814	-0,78464732	819,35	PITPNM2	phosphatidylinositol transfer protein membrane associated 2
23387	3,07E-43	4,25E+01	5,73E-44	0,0564	-13,9072229	-0,78492825	2233,29	SIK3	SIK family kinase 3
6048	5,51E-46	4,53E+01	9,62E-47	0,0547	-14,3570477	-0,78525334	3947,56	RNF5	ring finger protein 5
8870	1,36E-71	7,09E+01	1,34E-72	0,0436	-18,0205851	-0,78527614	28106,57	IER3	immediate early response 3
79096	3,05E-37	3,65E+01	6,48E-38	0,061	-12,8718624	-0,78556288	1126,63	CSTPP1	centriolar satellite-associated tubulin polyglutamylase complex regulator 1
54768	1,56E-04	3,81E+00	9,61E-05	0,2015	-3,9003204	-0,78572752	79,14	HYDIN	HYDIN axonemal central pair apparatus protein
25865	7,50E-28	2,71E+01	2,01E-28	0,0711	-11,0576444	-0,78584573	1209,73	PRKD2	protein kinase D2
682	4,43E-67	6,64E+01	4,83E-68	0,0451	-17,4306254	-0,78585022	20428,35	BSG	basigin (Ok blood group)
581	1,58E-49	4,88E+01	2,52E-50	0,0527	-14,917937	-0,78602117	3083,81	BAX	BCL2 associated X, apoptosis regulator
728118	3,14E-09	8,50E+00	1,50E-09	0,13	-6,0444444	-0,7860222	193,75	NUTM2A	NUT family member 2A
55501	3,30E-31	3,05E+01	8,13E-32	0,067	-11,7380803	-0,78603507	960	CHST12	carbohydrate sulfotransferase 12
284612	3,99E-08	7,40E+00	2,00E-08	0,1401	-5,6121212	-0,78614469	162,74	SYPL2	synaptophysin like 2
10652	3,87E-88	8,74E+01	2,74E-89	0,0392	-20,0347393	-0,78620541	6862,41	YKT6	YKT6 v-SNARE homolog
8794	1,14E-05	4,94E+00	6,54E-06	0,1744	-4,5080092	-0,7862746	99,69	TNFRSF10C	TNF receptor superfamily member 10c
162968	1,34E-05	4,87E+00	7,68E-06	0,1758	-4,4739185	-0,78636587	104,44	ZNF497	zinc finger protein 497
116238	7,87E-31	3,01E+01	1,96E-31	0,0674	-11,663496	-0,78639138	1038,88	TLCD1	TLC domain containing 1
5753	9,06E-16	1,50E+01	3,43E-16	0,0964	-8,1572891	-0,78650355	458,46	PTK6	protein tyrosine kinase 6
4048	1,08E-93	9,30E+01	6,89E-95	0,0381	-20,6668158	-0,78656159	8008,64	LTA4H	leukotriene A4 hydrolase
1211	5,92E-82	8,12E+01	4,72E-83	0,0407	-19,3067278	-0,78659885	8364,17	CLTA	clathrin light chain A
3615	7,04E-105	1,04E+02	3,65E-106	0,0359	-21,8845514	-0,78661445	22679,86	IMPDH2	inosine monophosphate dehydrogenase 2
7593	2,16E-17	1,67E+01	7,76E-18	0,0915	-8,603109	-0,78706229	446,4	MZF1	myeloid zinc finger 1
50	5,56E-72	7,13E+01	5,44E-73	0,0436	-18,0705405	-0,7871	4397,38	ACO2	aconitase 2
7920	2,14E-36	3,57E+01	4,63E-37	0,0619	-12,7191255	-0,7872504	2342,86	ABHD16A	abhydrolase domain containing 16A, phospholipase
6855	2,10E-03	2,68E+00	1,41E-03	0,2466	-3,1921171	-0,78729509	49,78	SYP	synaptophysin
100133121	6,47E-08	7,19E+00	3,27E-08	0,1425	-5,5261878	-0,78748559	156,58	FAM27B	family with sequence similarity 27 member B
101926925	3,59E-02	1,44E+00	2,73E-02	0,3569	-2,2070719	-0,78777057	24,19	LINC01358	long intergenic non-protein coding RNA 1358
65993	4,66E-45	4,43E+01	8,33E-46	0,0555	-14,2066579	-0,78779557	2695,15	MRPS34	mitochondrial ribosomal protein S34
8499	3,17E-06	5,50E+00	1,75E-06	0,1648	-4,7801663	-0,78785501	128,84	PPFIA2	PTPRF interacting protein alpha 2
10573	6,48E-50	4,92E+01	1,03E-50	0,0526	-14,9776002	-0,7881596	3056,49	MRPL28	mitochondrial ribosomal protein L28
6895	1,35E-26	2,59E+01	3,76E-27	0,0731	-10,7919333	-0,7884889	931,75	TARBP2	TARBP2 subunit of RISC loading complex
54858	3,41E-50	4,95E+01	5,38E-51	0,0525	-15,0206057	-0,78861089	2477,97	PGPEP1	pyroglutamyl-peptidase I
100529211	6,04E-33	3,22E+01	1,43E-33	0,0653	-12,0753443	-0,78884619	1160,71	TMEM256-P	TMEM256-PLSCR3 readthrough (NMD candidate)
122953	6,06E-13	1,22E+01	2,51E-13	0,1078	-7,3183749	-0,78900671	294,04	JDP2	Jun dimerization protein 2
105377659	1,61E-01	7,93E-01	1,34E-01	0,5269	-1,4974608	-0,78900958	11,36	LINC02928	long intergenic non-protein coding RNA 2928
105378235	3,01E-04	3,52E+00	1,90E-04	0,2114	-3,7323573	-0,78906611	76,78	ATOX1-AS1	ATOX1 antisense RNA 1
112268218	1,79E-09	8,75E+00	8,47E-10	0,1286	-6,1357808	-0,78911011	210,65	LOC112268	uncharacterized LOC112268218
26240	3,70E-07	6,43E+00	1,95E-07	0,1516	-5,2045083	-0,78911575	139,97	FAM50B	family with sequence similarity 50 member B
28587	1,42E-01	8,48E-01	1,17E-01	0,5038	-1,5668515	-0,789309	11,75	TRBV8-2	T cell receptor beta variable 8-2 (pseudogene)
6202	3,45E-78	7,75E+01	2,96E-79	0,0419	-18,8495897	-0,78939717	29527,62	RPS8	ribosomal protein S8
24140	6,28E-54	5,32E+01	9,16E-55	0,0507	-15,5853477	-0,78946292	4318,17	FTSJ1	FtsJ RNA 2'-O-methyltransferase 1
3490	4,03E-65	6,44E+01	4,57E-66	0,046	-17,1684509	-0,78976518	7479,89	IGFBP7	insulin like growth factor binding protein 7
11047	3,53E-36	3,55E+01	7,69E-37	0,0623	-12,6794134	-0,78988549	9833,36	ADRM1	ADRM1 26S proteasome ubiquitin receptor
30008	1,18E-06	5,93E+00	6,39E-07	0,1587	-4,979066	-0,78995171	123,05	EFEMP2	EGF containing fibulin extracellular matrix protein 2
83460	6,60E-27	2,62E+01	1,82E-27	0,0728	-10,858518	-0,79008863	821,17	EMC6	ER membrane protein complex subunit 6
2629	5,21E-53	5,23E+01	7,75E-54	0,0511	-15,448245	-0,7900969	5929,46	GBA1	glucosylceramidase beta 1
23412	4,32E-41	4,04E+01	8,43E-42	0,0583	-13,5454342	-0,7901685	1445,04	COMMD3	COMM domain containing 3
84948	2,41E-21	2,06E+01	7,71E-22	0,0823	-9,6037934	-0,79025733	637,1	TIGD5	tigger transposable element derived 5
726	2,98E-27	2,65E+01	8,13E-28	0,0723	-10,9316841	-0,79051354	765,48	CAPN5	calpain 5
107985020	7,87E-02	1,10E+00	6,25E-02	0,4245	-1,8625883	-0,79072419	16,65	LOC107985	uncharacterized LOC107985020
375387	2,50E-19	1,86E+01	8,48E-20	0,0868	-9,1068428	-0,79072659	493,38	NRROS	negative regulator of reactive oxygen species
9098	1,40E-01	8,54E-01	1,15E-01	0,5019	-1,5756248	-0,79079757	11,72	USP6	ubiquitin specific peptidase 6
199786	2,89E-05	4,54E+00	1,70E-05	0,1838	-4,3014768	-0,79080506	99,59	NIBAN3	niban apoptosis regulator 3
102724378	2,13E-02	1,67E+00	1,57E-02	0,3276	-2,4149035	-0,79106197	27,54	LOC102724	uncharacterized LOC102724378
6274	1,87E-17	1,67E+01	6,73E-18	0,0918	-8,619431	-0,79118408	501,84	S100A3	S100 calcium binding protein A3
780776	2,65E-21	2,06E+01	8,51E-22	0,0825	-9,5935916	-0,7912854	541,81	TVP23A	trans-golgi network vesicle protein 23 homolog A
107984208	4,60E-02	1,34E+00	3,54E-02	0,3763	-2,1032703	-0,79145334	21,64	USP6NL-AS	USP6NL antisense RNA 1
55658	2,03E-37	3,67E+01	4,31E-38	0,0614	-12,9033264	-0,79194616	1493,62	RNF126	ring finger protein 126
723790	5,02E-08	7,30E+00	2,52E-08	0,1422	-5,5715553	-0,79219736	164,03	H2AC19	H2A clustered histone 19
54681	1,03E-27	2,70E+01	2,79E-28	0,0718	-11,028467	-0,79222457	816,56	P4HTM	prolyl 4-hydroxylase, transmembrane
100506581	2,63E-05	4,58E+00	1,54E-05	0,1833	-4,3233287	-0,79240963	95,06	C16orf95	chromosome 16 open reading frame 95
280636	1,35E-43	4,29E+01	2,50E-44	0,0568	-13,9663047	-0,79291339	1902,18	SELENOH	selenoprotein H
105371932	7,63E-04	3,12E+00	4,96E-04	0,2278	-3,482663	-0,79331805	59,24	LOC105371	uncharacterized LOC105371932
109729182	6,82E-04	3,17E+00	4,42E-04	0,2258	-3,5138203	-0,79337701	60,14	DM1-AS	DM1 locus antisense RNA
83638	1,87E-30	2,97E+01	4,70E-31	0,0685	-11,5886572	-0,79422081	2869,04	C11orf68	chromosome 11 open reading frame 68
9482	5,86E-32	3,12E+01	1,41E-32	0,0668	-11,8850918	-0,79446361	1264,86	STX8	syntaxin 8
58513	1,81E-63	6,27E+01	2,13E-64	0,0469	-16,9440305	-0,79462481	4912,6	EPS15L1	epidermal growth factor receptor pathway substrate 15 like 1
64223	7,72E-26	2,51E+01	2,19E-26	0,0748	-10,6288413	-0,79492474	2218,24	MLST8	MTOR associated protein, LST8 homolog
112812	7,94E-38	3,71E+01	1,67E-38	0,0613	-12,976224	-0,7950155	1202,55	FDX2	ferredoxin 2
100129534	4,20E-04	3,38E+00	2,67E-04	0,2182	-3,6450722	-0,79532223	75,38	LOC100129	small nuclear ribonucleoprotein polypeptide N pseudogene
10163	3,63E-74	7,34E+01	3,38E-75	0,0434	-18,348659	-0,79545547	11392,69	WASF2	WASP family member 2
112268447	1,61E-04	3,79E+00	9,94E-05	0,2044	-3,8921476	-0,79546981	72,34	LOC112268447	
100526830	5,51E-11	1,03E+01	2,45E-11	0,1192	-6,6766098	-0,79561018	225,03	SLX1A-SULT	SLX1A-SULT1A3 readthrough (NMD candidate)
55558	3,23E-29	2,85E+01	8,34E-30	0,0702	-11,3397043	-0,79570911	1286,81	PLXNA3	plexin A3
79875	5,18E-57	5,63E+01	7,07E-58	0,0496	-16,0367986	-0,79590991	2712,56	THSD4	thrombospondin type 1 domain containing 4
51172	3,50E-15	1,45E+01	1,35E-15	0,0996	-7,9899136	-0,79611498	384,63	NAGPA	N-acetylglucosamine-1-phosphodiester alpha-N-acetylglucosaminidase
1889	2,42E-81	8,06E+01	1,95E-82	0,0414	-19,2333635	-0,79616606	15595,83	ECE1	endothelin converting enzyme 1
10420	8,80E-19	1,81E+01	3,03E-19	0,0888	-8,9676647	-0,7961681	440,99	TESK2	testis associated actin remodelling kinase 2
55695	1,29E-24	2,39E+01	3,77E-25	0,0769	-10,3601091	-0,79642006	926,3	NSUN5	NOP2/Sun RNA methyltransferase 5
9274	7,85E-29	2,81E+01	2,05E-29	0,0707	-11,2608339	-0,79643258	848,59	BCL7C	BAF chromatin remodeling complex subunit BCL7C

3704	1,14E-44	4,39E+01	2,07E-45	0,0563	-14,1428429	-0,79648138	1961,99	ITPA	inosine triphosphatase
10398	8,28E-62	6,11E+01	1,02E-62	0,0477	-16,7152354	-0,79648444	4079,24	MYL9	myosin light chain 9
10643	2,97E-47	4,65E+01	5,02E-48	0,0547	-14,5603183	-0,79673028	1835,93	IGF2BP3	insulin like growth factor 2 mRNA binding protein 3
28988	7,17E-67	6,61E+01	7,84E-68	0,0458	-17,4029018	-0,79689904	3852,28	DBNL	drebrin like
730202	2,06E-02	1,69E+00	1,52E-02	0,3285	-2,4264381	-0,79709117	27,66	PAPOLA-DT	PAPOLA divergent transcript
4738	1,29E-69	6,89E+01	1,34E-70	0,0449	-17,7643354	-0,79714287	3591,06	NEDD8	NEDD8 ubiquitin like modifier
84231	2,38E-47	4,66E+01	4,01E-48	0,0547	-14,575703	-0,7975135	3770,09	TRAF7	TNF receptor associated factor 7
352954	5,51E-13	1,23E+01	2,28E-13	0,1088	-7,3313531	-0,79765465	276,89	CASTOR3P	CASTOR family member 3, pseudogene
113451	5,81E-19	1,82E+01	1,99E-19	0,0885	-9,0138707	-0,79779384	446,13	AZIN2	antizyme inhibitor 2
107984638	4,85E-08	7,31E+00	2,44E-08	0,1431	-5,5777554	-0,7979011	152,13	LOC107984	arf-GAP with GTPase, ANK repeat and PH domain-containing protein 2
283571	5,55E-03	2,26E+00	3,88E-03	0,2763	-2,8876346	-0,7979074	47,78	PROX2	prospero homeobox 2
113000	2,98E-35	3,45E+01	6,67E-36	0,0638	-12,5089984	-0,79793592	1302,59	RPUSD1	RNA pseudouridine synthase domain containing 1
9424	3,07E-23	2,25E+01	9,31E-24	0,0794	-10,0486607	-0,79800847	655,5	KCNK6	potassium two pore domain channel subfamily K member 6
3077	8,83E-24	2,31E+01	2,64E-24	0,0785	-10,1719889	-0,79840261	581,24	HFE	homeostatic iron regulator
23764	2,38E-61	6,06E+01	2,96E-62	0,048	-16,6513881	-0,79853088	3638,77	MAFF	MAF bZIP transcription factor F
63875	2,56E-65	6,46E+01	2,89E-66	0,0464	-17,1950938	-0,79856476	5436,14	MRPL17	mitochondrial ribosomal protein L17
5606	3,27E-61	6,05E+01	4,08E-62	0,048	-16,632117	-0,7987261	3538,81	MAP2K3	mitogen-activated protein kinase kinase 3
84282	2,31E-39	3,86E+01	4,70E-40	0,0603	-13,2469076	-0,79882154	1219,57	RNF135	ring finger protein 135
64943	3,09E-44	4,35E+01	5,64E-45	0,0568	-14,0720669	-0,79915556	3869,15	NT5DC2	5'-nucleotidase domain containing 2
79137	6,39E-57	5,62E+01	8,74E-58	0,0499	-16,0236419	-0,79917007	3021,4	RETREG2	reticulophagy regulator family member 2
11264	1,60E-25	2,48E+01	4,58E-26	0,0757	-10,559691	-0,79918698	698,81	PXMP4	peroxisomal membrane protein 4
693196	5,60E-26	2,53E+01	1,58E-26	0,075	-10,6590681	-0,79931041	742,75	MIR611	microRNA 611
54890	2,63E-64	6,36E+01	3,05E-65	0,0469	-17,0580595	-0,79936696	5451,93	ALKBH5	alkB homolog 5, RNA demethylase
84262	4,46E-32	3,14E+01	1,08E-32	0,0671	-11,9080005	-0,79940892	1186,66	PSMG3	proteasome assembly chaperone 3
100526831	1,12E-10	9,95E+00	5,04E-11	0,1217	-6,5698117	-0,79951355	215,79	SLX1B-SULT	SLX1B-SULT1A4 readthrough (NMD candidate)
11224	3,69E-85	8,44E+01	2,75E-86	0,0406	-19,6876443	-0,79956973	30613,76	RPL35	ribosomal protein L35
125875	2,95E-03	2,53E+00	2,01E-03	0,259	-3,0880466	-0,79965186	45,73	CLDND2	claudin domain containing 2
25980	1,52E-69	6,88E+01	1,57E-70	0,045	-17,7552103	-0,79977329	3558,02	AAR2	AAR2 splicing factor
118487	9,46E-29	2,80E+01	2,48E-29	0,0711	-11,2440918	-0,79995724	1333,68	CHCHD1	coiled-coil-helix-coiled-coil-helix domain containing 1
2033	2,82E-49	4,85E+01	4,53E-50	0,0538	-14,878659	-0,80055658	4112,81	EP300	E1A binding protein p300
150381	2,75E-09	8,56E+00	1,31E-09	0,132	-6,0660471	-0,80071212	190,33	PRR34-AS1	PRR34 antisense RNA 1
23481	2,56E-65	6,46E+01	2,89E-66	0,0466	-17,1950178	-0,80086564	5238,99	PES1	pescadillo ribosomal biogenesis factor 1
105372295	2,00E-04	3,70E+00	1,24E-04	0,2087	-3,8382013	-0,80090075	74,65	LOC105372	uncharacterized LOC105372295
1059	9,97E-54	5,30E+01	1,46E-54	0,0515	-15,5552954	-0,80093964	3598,07	CENPB	centromere protein B
389199	3,61E-03	2,44E+00	2,48E-03	0,2648	-3,0254842	-0,80103437	47,94	LOC389199	uncharacterized LOC389199
55076	3,85E-12	1,14E+01	1,64E-12	0,1136	-7,0623337	-0,8019742	274,67	TMEM45A	transmembrane protein 45A
10067	2,64E-62	6,16E+01	3,19E-63	0,0478	-16,7841786	-0,80235412	4192,17	SCAMP3	secretory carrier membrane protein 3
79711	3,54E-55	5,45E+01	5,06E-56	0,0509	-15,7693544	-0,80249448	5238,41	IPO4	importin 4
105372707	9,55E-21	2,00E+01	3,11E-21	0,0849	-9,4589063	-0,80261242	669,22	LOC105372	707
51386	8,16E-106	1,05E+02	4,15E-107	0,0365	-21,9834645	-0,80267465	11526,42	EIF3L	eukaryotic translation initiation factor 3 subunit L
84153	7,56E-61	6,01E+01	9,52E-62	0,0484	-16,5812797	-0,80294675	2446,41	RNASEH2C	ribonuclease H2 subunit C
163732	5,22E-03	2,28E+00	3,64E-03	0,2762	-2,9076624	-0,80302345	41,17	CITED4	Cbp/p300 interacting transactivator with Glu/Asp rich carboxy-terminal domain 4
6888	2,03E-79	7,87E+01	1,70E-80	0,0423	-19,0001604	-0,80321813	9553,02	TALDO1	transaldolase 1
101929444	1,18E-01	9,28E-01	9,66E-02	0,4834	-1,6616694	-0,80329854	14,58	LOC101929	uncharacterized LOC101929444
4542	6,95E-07	6,16E+00	3,71E-07	0,158	-5,0832389	-0,80333326	135,95	MYO1F	myosin IF
5866	2,72E-07	6,57E+00	1,42E-07	0,1527	-5,2626077	-0,80343436	173,83	RAB3IL1	RAB3A interacting protein like 1
5715	9,49E-69	6,80E+01	9,98E-70	0,0455	-17,65111	-0,8034638	4179,74	PSMD9	proteasome 26S subunit, non-ATPase 9
3030	3,15E-91	9,05E+01	2,10E-92	0,0394	-20,3888771	-0,803755	13065,06	HADHA	hydroxyacyl-CoA dehydrogenase trifunctional multienzyme complex subunit alpha
23416	7,13E-03	2,15E+00	5,05E-03	0,2867	-2,8041186	-0,8038066	37,48	KCNH3	potassium voltage-gated channel subfamily H member 3
582	5,96E-19	1,82E+01	2,04E-19	0,0893	-9,0109167	-0,80424398	448,11	BBS1	Bardet-Biedl syndrome 1
6903	5,59E-66	6,53E+01	6,23E-67	0,0465	-17,2838175	-0,80445823	3129,84	TBCC	tubulin folding cofactor C
3309	1,11E-107	1,07E+02	5,47E-109	0,0363	-22,1790994	-0,80468469	58138,6	HSPA5	heat shock protein family A (Hsp70) member 5
105378083	4,24E-02	1,37E+00	3,26E-02	0,3767	-2,1372404	-0,80504335	21,03	TAGAP-AS1	TAGAP antisense RNA 1
106635684	6,84E-04	3,16E+00	4,43E-04	0,2292	-3,5127598	-0,80528059	66,09	SNORD141E	small nucleolar RNA, C/D box 141B
92249	1,97E-28	2,77E+01	5,20E-29	0,072	-11,1785084	-0,80538875	810,02	LINC01278	long intergenic non-protein coding RNA 1278
114796	5,55E-05	4,26E+00	3,31E-05	0,194	-4,1510554	-0,80539902	86,04	PSMG3-AS1	PSMG3 antisense RNA 1 (head to head)
92714	1,70E-34	3,38E+01	3,86E-35	0,0651	-12,3686492	-0,80573947	1259,45	ARRDC1	arrestin domain containing 1
30833	4,79E-35	3,43E+01	1,08E-35	0,0646	-12,4709237	-0,80574931	1152,98	NT5C	5', 3'-nucleotidase, cytosolic
79622	1,26E-29	2,89E+01	3,23E-30	0,0705	-11,4223743	-0,80579144	845,79	SNRNP25	small nuclear ribonucleoprotein U11/U12 subunit 25
84717	1,68E-48	4,78E+01	2,75E-49	0,0546	-14,7575218	-0,80610951	2024,9	HDGFL2	HDGF like 2
164832	7,09E-05	4,15E+00	4,26E-05	0,1969	-4,0931011	-0,80611445	91,28	LONRF2	LON peptidase N-terminal domain and ring finger 2
84769	5,65E-28	2,72E+01	1,51E-28	0,0727	-11,0832906	-0,80625617	1768,69	MPV17L2	MPV17 mitochondrial inner membrane protein like 2
56104	9,83E-17	1,60E+01	3,60E-17	0,0957	-8,4252786	-0,80626899	392,74	PCDHGB1	protocadherin gamma subfamily B, 1
23635	2,66E-13	1,26E+01	1,09E-13	0,1085	-7,4296478	-0,80633108	289,78	SSBP2	single stranded DNA binding protein 2
101929767	1,50E-05	4,82E+00	8,65E-06	0,1813	-4,448327	-0,80640561	95,38	LOC101929	uncharacterized LOC101929767
27076	5,30E-03	2,28E+00	3,70E-03	0,2779	-2,9024791	-0,80648541	49,68	LYPD3	LY6/PLAUR domain containing 3
55690	7,35E-61	6,01E+01	9,24E-62	0,0486	-16,583045	-0,80666347	4699,47	PACS1	phosphofurin acidic cluster sorting protein 1
11247	1,31E-02	1,88E+00	9,49E-03	0,311	-2,5940559	-0,80683595	30,38	NXPH4	neurexophilin 4
128153	8,97E-03	2,05E+00	6,41E-03	0,296	-2,7261676	-0,80697636	33,69	SPATA17	spermatogenesis associated 17
107986929	9,47E-04	3,02E+00	6,20E-04	0,2358	-3,4227116	-0,80720845	56,37	LOC107986	929
7030	9,23E-65	6,40E+01	1,06E-65	0,0472	-17,1198447	-0,80758034	4861,93	TFE3	transcription factor binding to IGHM enhancer 3
400451	1,28E-18	1,79E+01	4,43E-19	0,0905	-8,9257378	-0,80766695	418,1	FAM174B	family with sequence similarity 174 member B
26768	3,56E-02	1,45E+00	2,71E-02	0,3654	-2,2101899	-0,80769385	26,46	SNORA73B	small nucleolar RNA, H/ACA box 73B
51398	2,40E-41	4,06E+01	4,67E-42	0,0594	-13,5887286	-0,80769786	3177	WDR83OS	WD repeat domain 83 opposite strand
10594	1,12E-107	1,07E+02	5,49E-109	0,0364	-22,1788988	-0,80827284	37677,51	PRPF8	pre-mRNA processing factor 8
79874	3,40E-13	1,25E+01	1,40E-13	0,1093	-7,3967223	-0,80836978	318,54	RABEP2	rabaptin, RAB GTPase binding effector protein 2
6173	9,70E-68	6,70E+01	1,04E-68	0,0461	-17,5180623	-0,80840091	8687,46	RPL36A	ribosomal protein L36a
10362	2,24E-63	6,26E+01	2,64E-64	0,0478	-16,9314693	-0,80897782	2835,41	HMG20B	high mobility group 20B
5127	4,70E-63	6,23E+01	5,58E-64	0,0479	-16,8873198	-0,80909316	6627,4	CDK16	cyclin dependent kinase 16
4714	1,56E-69	6,88E+01	1,61E-70	0,0456	-17,7538327	-0,80962304	3129,74	NDUFB8	NADH:ubiquinone oxidoreductase subunit B8
105369606	8,38E-05	4,08E+00	5,06E-05	0,1999	-4,052942	-0,8100133	80,84	LINC02827	long intergenic non-protein coding RNA 2827
55902	7,41E-45	4,41E+01	1,33E-45	0,0572	-14,1737105	-0,81014978	1802,35	ACSS2	acyl-CoA synthetase short chain family member 2
5029	2,46E-31	3,06E+01	6,03E-32	0,0689	-11,7632806	-0,81033385	1025,87	P2RY2	purinergic receptor P2Y2
6204	2,68E-90	8,96E+01	1,82E-91	0,04	-20,2830491	-0,81069686	21983,57	RPS10	ribosomal protein S10
26000	8,29E-58	5,71E+01	1,11E-58	0,0502	-16,1513609	-0,81077778	2409,35	TBC1D10B	TBC1 domain family member 10B
10763	1,55E-22	2,18E+01	4,81E-23	0,082	-9,8855636	-0,81086146	661,86	NES	nestin
9203	5,39E-57	5,63E+01	7,36E-58	0,0506	-16,0343185	-0,81127029	3341,06	ZMYM3	zinc finger MYM-type containing 3
170679	6,24E-05	4,20E+00	3,73E-05	0,1968	-4,1236413	-0,81146251	80,39	PSORS1C1	psoriasis susceptibility 1 candidate 1
9368	2,91E-37	3,65E+01	6,19E-38	0,063	-12,8753736	-0,8114666	1726,32	NHERF1	NHERF family PDZ scaffold protein 1
6171	1,27E-77	7,69E+01	1,11E-78	0,0432	-18,7796423	-0,81156067	15669,55	RPL41	ribosomal protein L41
3396	1,54E-50	4,98E+01	2,41E-51	0,0538	-15,0738098	-0,81163964	2121,23	MRPL58	mitochondrial ribosomal protein L58
303	1,61E-08	7,79E+00	7,91E-09	0,1407	-5,7702832	-0,81177283	171,1	ANXA2P1	annexin A2 pseudogene 1
344887	8,87E-02	1,05E+00	7,11E-02	0,4499	-1,8049023	-0,81195806	15,42	NMRAL2P	NmrA like redox sensor 2, pseudogene
4343	8,71E-62	6,11E+01	1,07E-62	0,0486	-16,7121604	-0,81202512	5325,12	MOV10	Mov10 RISC complex RNA helicase
100287216	5,63E-03	2,25E+00	3,94E-03	0,2818	-2,88291	-0,81238243	39,25	SH3RF3-AS	SH3RF3 antisense RNA 1
79760	4,74E-30	2,93E+01	1,20E-30	0,0706	-11,5080862	-0,81247918	821,01	GEMIN7	gem nuclear organelle associated protein 7
126375	1,91E-31	3,07E+01	4,68E-32	0,069	-11,7847911	-0,81290543	849,01	ZNF792	zinc finger protein 792
197407	4,96E-16	1,53E+01	1,86E-16	0,0988	-8,2306806	-0,81294581	436,2	ZNF48	zinc finger protein 48
93185	6,27E-22	2,12E+01	1,97E-22	0,0834	-9,7432434	-0,81301298	741,97	IGSF8	immunoglobulin superfamily member 8
56912	3,04E-49	4,85E+01	4,89E-50	0,0547	-14,8735893	-0,81319984	1606,37	IFT46	intraflagellar transport 46
9993	3,69E-49	4,84E+01	5,96E-50	0,0547	-14,8603127	-0,81328265	2049,52	DGCR2	DiGeorge syndrome critical region gene 2
2064	1,73E-68	6,78E+01	1,83E-69	0,0462	-17,6168355	-0,81354881	3183,49	ERBB2	erb-b2 receptor tyrosine kinase 2
828	1,97E-02	1,71E+00	1,45E-02	0,3329	-2,4442699	-0,81373767	27,44	CAPS	calcyphosine
553115	9,39E-58	5,70E+01	1,26E-58	0,0504	-16,14354	-0,81384358	2913,93	PEF1	penta-EF-hand domain containing 1
23265	6,27E-79	7,82E+01	5,30E-80	0,043	-18,9404322	-0,81430388	8194,53	EXOC7	exocyst complex component 7
116985	8,03E-43	4,21E+01	1,51E-43	0,0589	-13,8375212	-0,81439611	3911,75	ARAP1	ArfGAP with RhoGAP domain, ankyrin repeat and PH domain 1
90060	6,61E-16	1,52E+01	2,49E-16	0,0994	-8,1957785	-0,81451696	408,16	CCDC120	coiled-coil domain containing 120
5721	4,53E-79	7,83E+01	3,82E-80	0,043	-18,9576645	-0,81458286	6990,42	PSME2	proteasome activator subunit 2
10952	1,35E-37	3,69E+01	2,86E-38	0,063	-12,9349039	-0,81461689	3764,75	SEC61B	SEC61 translocon subunit beta
339123	8,52E-40	3,91E+01	1,72E-40	0,0612	-13,3223979	-0,81485283	2092,01	JMJD8	jumonji domain containing 8
391356	8,36E-32	3,11E+01	2,03E-32	0,0687	-11,8549483	-0,8148731	839,69	PTRHD1	peptidyl-tRNA hydrolase domain containing 1
64236	3,61E-16	1,54E+01	1,35E-16	0,0986	-8,2691315	-0,81515363	458,68	PDLIM2	PDZ and LIM domain 2
100130933	2,24E-01	6,50E-01	1,91E-01	0,6233	-1,3089784	-0,81593949	8,99	SMIM6	small integral membrane protein 6
3958	1,69E-60	5,98E+01	2,14E-61	0,0494	-16,5324629	-0,81605727	3610,35	LGALS3	galectin 3
57666	2,45E-30	2,96E+01	6,18E-31	0,0706	-11,5653079	-0,81613694	858,7	FBRSL1	fibrosin like 1
5033	1,12E-71	7,10E+01	1,10E-72	0,0453	-18,0314699	-0,81615284	3951,86	P4HA1	prolyl 4-hydroxylase subunit alpha 1
2948	2,59E-38	3,76E+01	5,39E-39	0,0625	-13,0625099	-0,81674434	1318,33	GSTM4	glutathione S-transferase mu 4
3732	3,47E-76	7,55E+01	3,11E-77	0,0439	-18,6017106	-0,8168467	5664,33	CD82	CD82 molecule
81932	6,48E-16	1,52E+01	2,44E-16	0,0996	-8,1983994	-0,81690718	468,31	HDHD3	haloacid dehalogenase like hydrolase domain containing 3
5580	6,64E-51	5,02E+01	1,03E-51	0,054	-15,1297825	-0,81696599	2479,46	PRKCD	protein kinase C delta

1152	1,80E-34	3,37E+01	4,09E-35	0,0661	-12,3640903	-0,8171804	2592,76	CKB	creatine kinase B
51107	6,24E-60	5,92E+01	8,01E-61	0,0497	-16,452778	-0,81724687	5691,78	APH1A	aph-1 homolog A, gamma-secretase subunit
55072	2,40E-36	3,56E+01	5,19E-37	0,0643	-12,7102018	-0,81727251	1749,75	RNF31	ring finger protein 31
23237	2,05E-01	6,88E-01	1,73E-01	0,6	-1,3621863	-0,81736573	10,35	ARC	activity regulated cytoskeleton associated protein
83956	1,62E-01	7,90E-01	1,35E-01	0,5472	-1,4949126	-0,81795007	10	RACGAP1P	Rac GTPase activating protein 1 pseudogene 1
26574	5,54E-78	7,73E+01	4,80E-79	0,0435	-18,8240351	-0,81814243	9705,16	AATF	apoptosis antagonizing transcription factor
8175	1,22E-64	6,39E+01	1,40E-65	0,0478	-17,103221	-0,81838323	3065,15	SF3A2	splicing factor 3a subunit 2
84803	6,87E-69	6,82E+01	7,20E-70	0,0463	-17,669505	-0,81838682	3813,19	GPAT3	glycerol-3-phosphate acyltransferase 3
196	2,79E-78	7,76E+01	2,39E-79	0,0434	-18,8610242	-0,81860232	6299,47	AHR	aryl hydrocarbon receptor
51586	6,28E-54	5,32E+01	9,16E-55	0,0525	-15,585302	-0,818751	4053,11	MED15	mediator complex subunit 15
255043	1,19E-06	5,92E+00	6,44E-07	0,1646	-4,9774935	-0,81905154	117,4	TMEM86B	transmembrane protein 86B
51604	7,17E-50	4,91E+01	1,14E-50	0,0547	-14,9707259	-0,81912122	10836,64	PIGT	phosphatidylinositol glycan anchor biosynthesis class T
56103	5,17E-23	2,23E+01	1,58E-23	0,082	-9,9965598	-0,81921877	546,23	PCDHGB2	protocadherin gamma subfamily B, 2
201229	9,18E-02	1,04E+00	7,37E-02	0,4582	-1,7882819	-0,8194463	15,34	LYRM9	LYR motif containing 9
57591	5,32E-29	2,83E+01	1,38E-29	0,0726	-11,2953835	-0,81963911	1040,74	MRTFA	myocardin related transcription factor A
83605	2,79E-41	4,06E+01	5,43E-42	0,0604	-13,5777342	-0,8202314	1776,77	CCM2	CCM2 scaffold protein
105374296	1,67E-01	7,77E-01	1,39E-01	0,5541	-1,48052	-0,82029878	10,42	LOC105374	uncharacterized LOC105374296
5042	2,83E-03	2,55E+00	1,93E-03	0,2647	-3,1012359	-0,82081281	42,61	PABPC3	poly(A) binding protein cytoplasmic 3
100507144	8,73E-02	1,06E+00	6,98E-02	0,4528	-1,8130262	-0,820905	14,46	CD44-DT	CD44 divergent transcript
4514	2,25E-70	6,96E+01	2,28E-71	0,046	-17,863251	-0,82096975	163002,93	COX3	cytochrome c oxidase subunit III
90441	3,94E-49	4,84E+01	6,37E-50	0,0553	-14,8558924	-0,8211237	1710,16	ZNF622	zinc finger protein 622
8045	2,75E-24	2,36E+01	8,12E-25	0,0798	-10,2863326	-0,82135874	878,84	RASSF7	Ras association domain family member 7
84913	9,14E-08	7,04E+00	4,66E-08	0,1504	-5,4638037	-0,82173413	144,35	ATOH8	atonal bHLH transcription factor 8
66000	1,31E-02	1,88E+00	9,48E-03	0,3168	-2,5940951	-0,82179473	32,39	TMEM108	transmembrane protein 108
101928736	3,61E-16	1,54E+01	1,35E-16	0,0994	-8,2692017	-0,821852	375,3	MIR762HG	MIR762 host gene
26261	9,27E-02	1,03E+00	7,45E-02	0,461	-1,7835507	-0,82225812	14,24	FBXO24	F-box protein 24
55624	3,76E-80	7,94E+01	3,10E-81	0,0431	-19,0892983	-0,82233891	6535,97	POMGNT1	protein O-linked mannose N-acetylglucosaminyltransferase 1 (beta 1,2-)
252839	4,87E-44	4,33E+01	8,93E-45	0,0586	-14,0395601	-0,82254937	1402,61	TMEM9	transmembrane protein 9
285819	3,66E-02	1,44E+00	2,79E-02	0,3743	-2,1981149	-0,82268251	21,81	LOC285819	uncharacterized LOC285819
25981	5,11E-05	4,29E+00	3,04E-05	0,1973	-4,1705913	-0,82277204	91,28	DNAH1	dynein axonemal heavy chain 1
55048	2,20E-39	3,87E+01	4,47E-40	0,0621	-13,2506501	-0,82299237	1323,21	VPS37C	VPS37C subunit of ESCRT-I
27079	2,03E-19	1,87E+01	6,84E-20	0,0901	-9,1301225	-0,82302588	475,89	RPUSD2	RNA pseudouridine synthase domain containing 2
4482	1,33E-33	3,29E+01	3,11E-34	0,0675	-12,2000171	-0,82305774	972,75	MSRA	methionine sulfoxide reductase A
8565	3,06E-97	9,65E+01	1,83E-98	0,0391	-21,0605724	-0,8230707	10724,86	YARS1	tyrosyl-tRNA synthetase 1
10585	1,24E-47	4,69E+01	2,07E-48	0,0563	-14,6207941	-0,82315155	1724,03	POMT1	protein O-mannosyltransferase 1
8209	2,25E-28	2,76E+01	5,94E-29	0,0737	-11,1665566	-0,82338096	918,29	GATD3	glutamine amidotransferase class 1 domain containing 3
51504	3,40E-78	7,75E+01	2,92E-79	0,0437	-18,8503278	-0,82352937	5423,33	TRMT112	tRNA methyltransferase activator subunit 11-2
101927051	7,32E-07	6,14E+00	3,91E-07	0,1623	-5,073194	-0,82357811	124,74	PDXP-DT	PDXP divergent transcript
27338	4,53E-98	9,73E+01	2,67E-99	0,039	-21,151473	-0,8242135	10698,21	UBE2S	ubiquitin conjugating enzyme E2 S
203260	3,40E-28	2,75E+01	9,06E-29	0,0741	-11,1290089	-0,82454444	741,59	CCDC107	coiled-coil domain containing 107
130612	4,75E-04	3,32E+00	3,04E-04	0,2284	-3,6118891	-0,82500377	63,13	TMEM198	transmembrane protein 198
80347	1,15E-60	5,99E+01	1,46E-61	0,0498	-16,5556661	-0,82510847	3843,34	COASY	Coenzyme A synthase
170082	4,33E-02	1,36E+00	3,33E-02	0,3877	-2,1283228	-0,82519837	20,51	TCEANC	transcription elongation factor A N-terminal and central domain containing
5819	2,20E-69	6,87E+01	2,28E-70	0,0465	-17,7343763	-0,82550961	6812,45	NECTIN2	nectin cell adhesion molecule 2
9104	6,34E-02	1,20E+00	4,98E-02	0,4209	-1,9616997	-0,82574128	17,52	RGN	regucalcin
352999	1,67E-01	7,77E-01	1,39E-01	0,5582	-1,4796323	-0,82589029	10,06	C6orf58	chromosome 6 open reading frame 58
116113	1,49E-49	4,88E+01	2,39E-50	0,0554	-14,9215683	-0,82619018	4133,58	FOXP4	forkhead box P4
84657	3,58E-02	1,45E+00	2,72E-02	0,3742	-2,2083554	-0,82634029	21,28	LINC00852	long intergenic non-protein coding RNA 852
101243545	8,21E-62	6,11E+01	1,01E-62	0,0495	-16,7157986	-0,82661273	2805,15	LINC02067	long intergenic non-protein coding RNA 2067
201232	6,08E-06	5,22E+00	3,42E-06	0,1781	-4,6437804	-0,82690205	165,36	SLC16A13	solute carrier family 16 member 13
100862671	3,25E-08	7,49E+00	1,62E-08	0,1465	-5,6480358	-0,82720116	153,67	TMEM265	transmembrane protein 265
10712	3,54E-51	5,05E+01	5,45E-52	0,0545	-15,1716098	-0,82725003	2311,64	ENTREP3	endosomal transmembrane epsin interactor 3
1537	7,81E-63	6,21E+01	9,31E-64	0,0491	-16,8570709	-0,82727717	8482,71	CYC1	cytochrome c1
93436	2,56E-41	4,06E+01	4,98E-42	0,0609	-13,5840455	-0,82770678	3353,03	ARMC6	armadillo repeat containing 6
79594	4,19E-59	5,84E+01	5,47E-60	0,0507	-16,3360227	-0,82785303	2026,62	MUL1	mitochondrial E3 ubiquitin protein ligase 1
100507421	1,67E-01	7,77E-01	1,40E-01	0,5604	-1,4774705	-0,82798322	9,33	TMEM178B	transmembrane protein 178B
64208	1,69E-23	2,28E+01	5,12E-24	0,0819	-10,1075165	-0,82803396	712	POPDC3	popeye domain containing 3
9091	4,47E-21	2,03E+01	1,44E-21	0,0868	-9,5389454	-0,82828457	803,76	PIGQ	phosphatidylinositol glycan anchor biosynthesis class Q
51248	3,03E-59	5,85E+01	3,94E-60	0,0506	-16,3559787	-0,82828756	3009,05	PDZD11	PDZ domain containing 11
64428	1,04E-19	1,90E+01	3,47E-20	0,09	-9,2034213	-0,82835329	694,37	CIAO3	cytosolic iron-sulfur assembly component 3
5578	3,53E-91	9,05E+01	2,36E-92	0,0406	-20,3832374	-0,82837511	7506,36	PRKCA	protein kinase C alpha
55168	2,22E-47	4,67E+01	3,75E-48	0,0568	-14,5803251	-0,82863224	1769,64	MRPS18A	mitochondrial ribosomal protein S18A
26056	3,57E-67	6,64E+01	3,88E-68	0,0475	-17,4431074	-0,82898018	5367,87	RAB11FIP5	RAB11 family interacting protein 5
283899	9,25E-47	4,60E+01	1,58E-47	0,0573	-14,4816452	-0,82907719	1767,75	INO80E	INO80 complex subunit E
51330	2,86E-86	8,55E+01	2,09E-87	0,0419	-19,8177896	-0,82956961	6760,23	TNFRSF12A	TNF receptor superfamily member 12A
100652739	1,70E-03	2,77E+00	1,14E-03	0,2549	-3,2543641	-0,82957397	46	RAET1E-AS	RAET1E antisense RNA 1
24148	1,02E-81	8,10E+01	8,15E-83	0,043	-19,2784591	-0,82962099	7882,17	PRPF6	pre-mRNA processing factor 6
84900	1,02E-06	5,99E+00	5,51E-07	0,1658	-5,0077483	-0,83047388	116,64	RNFT2	ring finger protein, transmembrane 2
7090	2,13E-60	5,97E+01	2,70E-61	0,0503	-16,5184538	-0,8307187	2454,8	TLE3	TLE family member 3, transcriptional corepressor
79087	1,87E-24	2,37E+01	5,52E-25	0,0805	-10,3235115	-0,83088853	693,08	ALG12	ALG12 alpha-1,6-mannosyltransferase
84335	2,84E-60	5,95E+01	3,61E-61	0,0504	-16,5009255	-0,83103671	4662,45	AKT1S1	AKT1 substrate 1
374378	3,28E-42	4,15E+01	6,25E-43	0,0605	-13,7351988	-0,83107327	1301,81	GALNT18	polypeptide N-acetylgalactosaminyltransferase 18
4793	1,46E-36	3,58E+01	3,15E-37	0,0652	-12,7492656	-0,83162871	1230,23	NFKBIB	NFKB inhibitor beta
27433	1,67E-18	1,78E+01	5,80E-19	0,0935	-8,8958763	-0,83168533	443,28	TOR2A	torsin family 2 member A
5138	4,66E-14	1,33E+01	1,86E-14	0,1086	-7,6598829	-0,83170847	275,68	PDE2A	phosphodiesterase 2A
55146	7,53E-56	5,51E+01	1,05E-56	0,0524	-15,8680548	-0,83184674	1843,1	ZDHHC4	zinc finger DHHC-type palmitoyltransferase 4
83986	2,13E-44	4,37E+01	3,87E-45	0,059	-14,098629	-0,83198966	1998,76	FAM234A	family with sequence similarity 234 member A
29098	6,29E-19	1,82E+01	2,16E-19	0,0924	-9,0050205	-0,83200366	450,83	RANGRF	RAN guanine nucleotide release factor
23555	4,30E-37	3,64E+01	9,18E-38	0,0648	-12,8449619	-0,83212342	1138,24	TSPAN15	tetraspanin 15
284385	2,62E-08	7,58E+00	1,30E-08	0,1464	-5,6856523	-0,83217524	151,61	ZNF561-AS1	ZNF561 antisense RNA 1 (head to head)
100616256	3,00E-21	2,05E+01	9,62E-22	0,0869	-9,5809072	-0,83277098	575,05	MIR4721	microRNA 4721
57535	6,09E-03	2,22E+00	4,28E-03	0,2915	-2,8567497	-0,83283263	37,93	ELAPOR1	endosome-lysosome associated apoptosis and autophagy regulator 1
101927751	3,41E-17	1,65E+01	1,23E-17	0,0974	-8,5498429	-0,8329463	368,18	ALDH1A3-AS	ALDH1A3 antisense RNA 1
107985734	2,74E-02	1,56E+00	2,06E-02	0,3597	-2,3156263	-0,83296274	23,91	LOC107985734	
81693	1,35E-22	2,19E+01	4,17E-23	0,0842	-9,8997652	-0,83332342	496,55	AMN	amnion associated transmembrane protein
29985	2,93E-28	2,75E+01	7,80E-29	0,0748	-11,1423929	-0,83363714	811,2	SLC39A3	solute carrier family 39 member 3
87	4,35E-96	9,54E+01	2,66E-97	0,0398	-20,9334118	-0,83373041	35184,14	ACTN1	actinin alpha 1
125111	4,02E-15	1,44E+01	1,55E-15	0,1046	-7,9726073	-0,83391707	343,16	GJD3	gap junction protein delta 3
107984333	1,35E-01	8,70E-01	1,11E-01	0,5241	-1,5922274	-0,83442091	11,38	PRPF19-DT	PRPF19 divergent transcript
23492	2,73E-18	1,76E+01	9,55E-19	0,0944	-8,8402369	-0,83444052	391,27	CBX7	chromobox 7
5714	3,84E-96	9,54E+01	2,34E-97	0,0399	-20,9395031	-0,8346195	12327,76	PSMD8	proteasome 26S subunit, non-ATPase 8
57210	9,89E-25	2,40E+01	2,89E-25	0,0804	-10,385493	-0,83523023	553,78	SLC45A4	solute carrier family 45 member 4
23499	1,05E-52	5,20E+01	1,57E-53	0,0542	-15,4027865	-0,83523452	13796,04	MACF1	microtubule actin crosslinking factor 1
51024	2,59E-40	3,96E+01	5,13E-41	0,0623	-13,4121333	-0,8352987	1922,03	FIS1	fission, mitochondrial 1
118424	1,39E-61	6,09E+01	1,71E-62	0,0501	-16,6840531	-0,8354087	3227,04	UBE2J2	ubiquitin conjugating enzyme E2 J2
26015	1,07E-32	3,20E+01	2,54E-33	0,0695	-12,0276761	-0,83543876	1195,2	RPAP1	RNA polymerase II associated protein 1
414919	2,02E-29	2,87E+01	5,19E-30	0,0734	-11,3812167	-0,83544	759	C8orf82	chromosome 8 open reading frame 82
10126	4,81E-12	1,13E+01	2,06E-12	0,1189	-7,0306299	-0,8356784	242,33	DNAL4	dynein axonemal light chain 4
25825	4,02E-81	8,04E+01	3,25E-82	0,0435	-19,2066949	-0,83577912	3927,2	BACE2	beta-secretase 2
10629	3,67E-29	2,84E+01	9,51E-30	0,0738	-11,3282411	-0,83609122	903,49	TAF6L	TATA-box binding protein associated factor 6 like
6734	1,79E-109	1,09E+02	8,51E-111	0,0374	-22,3656343	-0,83609323	9786,95	SRPRA	SRP receptor subunit alpha
57190	1,33E-60	5,99E+01	1,68E-61	0,0505	-16,5471652	-0,83614022	4788,26	SELENON	selenoprotein N
105377068	1,78E-10	9,75E+00	8,08E-11	0,1288	-6,499128	-0,83689486	320,22	LINC02009	long intergenic non-protein coding RNA 2009
8408	2,81E-26	2,56E+01	7,87E-27	0,0781	-10,7238382	-0,83706021	828,55	ULK1	unc-51 like autophagy activating kinase 1
1642	5,63E-132	1,31E+02	1,76E-133	0,0341	-24,5865644	-0,83736393	25580,19	DDB1	damage specific DNA binding protein 1
64651	5,42E-29	2,83E+01	1,41E-29	0,0741	-11,2937868	-0,83737435	680,8	CSRNP1	cysteine and serine rich nuclear protein 1
5207	1,24E-02	1,91E+00	8,98E-03	0,3205	-2,6127215	-0,8374852	30,75	PFKFB1	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 1
11270	1,15E-49	4,89E+01	1,84E-50	0,0561	-14,938984	-0,83784634	2332,7	NRM	nurim
100506436	4,30E-38	3,74E+01	8,97E-39	0,0643	-13,0236926	-0,83787558	999,04	SPAG5-AS1	SPAG5 antisense RNA 1
101929918	4,56E-08	7,34E+00	2,29E-08	0,1499	-5,5883412	-0,83788705	229,67	LOC101929	uncharacterized LOC101929918
84179	1,71E-13	1,28E+01	6,95E-14	0,1119	-7,488875	-0,83824198	257,17	SLC49A3	solute carrier family 49 member 3
5184	1,99E-53	5,27E+01	2,93E-54	0,054	-15,5107964	-0,83828451	2222,37	PEPD	peptidase D
23053	1,30E-46	4,59E+01	2,23E-47	0,058	-14,4580539	-0,83832538	1588,61	ZSWIM8	zinc finger SWIM-type containing 8
6231	1,73E-73	7,28E+01	1,64E-74	0,0459	-18,2627986	-0,83845611	8589,94	RPS26	ribosomal protein S26
693221	6,22E-06	5,21E+00	3,50E-06	0,1808	-4,6388891	-0,8385485	94,73	MIR636	microRNA 636
51013	3,28E-44	4,35E+01	5,99E-45	0,0597	-14,0677843	-0,83918291	1357,34	EXOSC1	exosome component 1
6195	1,09E-63	6,30E+01	1,28E-64	0,0494	-16,9741222	-0,83931711	2345,59	RPS6KA1	ribosomal protein S6 kinase A1
5119	1,86E-57	5,67E+01	2,51E-58	0,0521	-16,1010269	-0,83932003	3657,84	CHMP1A	charged multivesicular body protein 1A
5226	1,24E-107	1,07E+02	6,10E-109	0,0379	-22,1741336	-0,83950032	12183,83	PGD	phosphogluconate dehydrogenase
285367	3,10E-38	3,75E+01	6,46E-39	0,0644	-13,0487073	-0,83974906	1381,55	RPUSD3	RNA pseudouridine synthase D3

57130	1,64E-45	4,48E+01	2,90E-46	0,0588	-14,2805023	-0,83978589	3344,67	ATP13A1	ATPase 13A1
768211	1,68E-26	2,58E+01	4,67E-27	0,078	-10,7719112	-0,84002326	842,25	RELL1	RELT like 1
94107	3,30E-40	3,95E+01	6,58E-41	0,0627	-13,3936984	-0,84006299	1333,18	TMEM203	transmembrane protein 203
2081	8,84E-46	4,51E+01	1,56E-46	0,0587	-14,3236524	-0,84013694	1307,81	ERN1	endoplasmic reticulum to nucleus signaling 1
22904	1,04E-57	5,70E+01	1,40E-58	0,0521	-16,1371026	-0,840625	3594,95	SBNO2	strawberry notch homolog 2
55526	1,02E-57	5,70E+01	1,37E-58	0,0521	-16,1384007	-0,84097655	2014,31	DHTKD1	dehydrogenase E1 and transketolase domain containing 1
170393	1,02E-01	9,91E-01	8,21E-02	0,4837	-1,7385879	-0,84102886	12,9	LINC02870	long intergenic non-protein coding RNA 2870
1371	2,79E-59	5,86E+01	3,62E-60	0,0514	-16,3611889	-0,84160261	3064,06	CPOX	coproporphyrinogen oxidase
2664	1,99E-70	6,97E+01	2,01E-71	0,0471	-17,87018	-0,84167465	7432,74	GDI1	GDP dissociation inhibitor 1
23399	7,58E-87	8,61E+01	5,51E-88	0,0423	-19,8848217	-0,84180055	6182,65	CTDNEP1	CTD nuclear envelope phosphatase 1
8694	4,48E-34	3,33E+01	1,03E-34	0,0685	-12,2897109	-0,84188276	1520,9	DGAT1	diacylglycerol O-acyltransferase 1
9283	1,25E-01	9,03E-01	1,02E-01	0,5155	-1,6332754	-0,84201883	11,55	GPR37L1	G protein-coupled receptor 37 like 1
51734	5,67E-27	2,62E+01	1,56E-27	0,0774	-10,8724822	-0,8420406	692,2	MSRB1	methionine sulfoxide reductase B1
56949	3,02E-48	4,75E+01	4,99E-49	0,0572	-14,7173308	-0,84220322	3980,97	XAB2	XPA binding protein 2
1265	9,55E-82	8,10E+01	7,65E-83	0,0437	-19,2817376	-0,8423182	5580,87	CNN2	calponin 2
8407	1,61E-93	9,28E+01	1,03E-94	0,0408	-20,6472003	-0,84233043	28288,67	TAGLN2	transgelin 2
107984839	8,45E-03	2,07E+00	6,02E-03	0,3067	-2,746872	-0,84237445	34,33	LOC107984	uncharacterized LOC107984839
105377732	5,85E-03	2,23E+00	4,10E-03	0,2935	-2,8703821	-0,84247815	36,11	LOC105377	uncharacterized LOC105377732
55272	4,01E-49	4,84E+01	6,49E-50	0,0567	-14,8546501	-0,84265612	1687,65	IMP3	IMP U3 small nucleolar ribonucleoprotein 3
92359	6,07E-02	1,22E+00	4,76E-02	0,4256	-1,9808839	-0,84316029	16,69	CRB3	crumbs cell polarity complex component 3
105378687	3,93E-02	1,41E+00	3,00E-02	0,3889	-2,169517	-0,84382541	19,98	CDC20-DT	CDC20 divergent transcript
147184	4,57E-25	2,43E+01	1,33E-25	0,0807	-10,4595146	-0,84413804	677,65	KRT10-AS1	KRT10 antisense RNA 1
5639	6,40E-02	1,19E+00	5,03E-02	0,4314	-1,957533	-0,84447708	16,92	PRRG2	proline rich and Gla domain 2
26100	5,63E-77	7,62E+01	4,99E-78	0,0452	-18,699532	-0,8453847	3412,25	WIPI2	WD repeat domain, phosphoinositide interacting 2
51329	6,53E-80	7,92E+01	5,41E-81	0,0444	-19,0601408	-0,84567834	6135,77	ARL6IP4	ADP ribosylation factor like GTPase 6 interacting protein 4
5710	1,02E-101	1,01E+02	5,65E-103	0,0393	-21,5469872	-0,84577347	7369,93	PSMD4	proteasome 26S subunit ubiquitin receptor, non-ATPase 4
10554	3,47E-71	7,05E+01	3,46E-72	0,0471	-17,9681858	-0,84592545	7738,58	AGPAT1	1-acylglycerol-3-phosphate O-acyltransferase 1
57617	2,71E-33	3,26E+01	6,34E-34	0,0697	-12,1417836	-0,84605637	1427,56	VPS18	VPS18 core subunit of CORVET and HOPS complexes
6169	3,53E-99	9,85E+01	2,04E-100	0,0398	-21,2726158	-0,84663512	14686,12	RPL38	ribosomal protein L38
23647	6,63E-74	7,32E+01	6,20E-75	0,0462	-18,3156865	-0,84680024	4580,05	ARFIP2	ADP ribosylation factor interacting protein 2
8741	4,91E-16	1,53E+01	1,84E-16	0,1029	-8,2319116	-0,8468607	316,26	TNFSF13	TNF superfamily member 13
5476	1,76E-97	9,68E+01	1,05E-98	0,0402	-21,0868314	-0,84694131	8557,57	CTSA	cathepsin A
91252	6,22E-52	5,12E+01	9,46E-53	0,0554	-15,2861666	-0,84699729	3305,83	SLC39A13	solute carrier family 39 member 13
80331	8,88E-85	8,41E+01	6,67E-86	0,0431	-19,6427606	-0,84732408	7349,87	DNAJC5	DnaJ heat shock protein family (Hsp40) member C5
284352	1,08E-38	3,80E+01	2,23E-39	0,0645	-13,1294014	-0,84743373	1012,44	PPP1R37	protein phosphatase 1 regulatory subunit 37
8764	5,03E-15	1,43E+01	1,95E-15	0,1067	-7,9444935	-0,84761841	393,6	TNFRSF14	TNF receptor superfamily member 14
200634	7,53E-03	2,12E+00	5,33E-03	0,3043	-2,7862017	-0,84776095	34,43	KRTCAP3	keratinocyte associated protein 3
63940	5,47E-52	5,13E+01	8,30E-53	0,0555	-15,2946575	-0,84814779	3288,91	GPSM3	G protein signaling modulator 3
1639	5,27E-118	1,17E+02	2,18E-119	0,0365	-23,231745	-0,84846696	14521,59	DCTN1	dynactin subunit 1
64423	2,12E-63	6,27E+01	2,50E-64	0,0501	-16,934633	-0,84885797	5681,11	INF2	inverted formin 2
27090	2,80E-27	2,66E+01	7,62E-28	0,0776	-10,9375305	-0,84916766	1032,45	ST6GALNAC	ST6 N-acetylgalactosaminide alpha-2,6-sialyltransferase 4
51690	3,22E-32	3,15E+01	7,72E-33	0,0712	-11,9355635	-0,84927624	1211,57	LSM7	LSM7 homolog, U6 small nuclear RNA and mRNA degradation associated
653784	1,02E-29	2,90E+01	2,61E-30	0,0742	-11,4409106	-0,84936284	808,23	MZT2A	mitotic spindle organizing protein 2A
6881	4,08E-77	7,64E+01	3,60E-78	0,0454	-18,7169516	-0,84985135	7203,85	TAF10	TATA-box binding protein associated factor 10
10105	4,07E-79	7,84E+01	3,43E-80	0,0448	-18,9633579	-0,84986447	8618,31	PPIF	peptidylprolyl isomerase F
5188	7,54E-48	4,71E+01	1,26E-48	0,058	-14,654788	-0,84988637	1420,9	GATB	glutamyl-tRNA amidotransferase subunit B
25864	2,35E-20	1,96E+01	7,73E-21	0,0908	-9,3632586	-0,8499933	487,96	ABHD14A	abhydrolase domain containing 14A
25920	1,83E-50	4,97E+01	2,87E-51	0,0565	-15,0621825	-0,85052048	3917,67	NELFB	negative elongation factor complex member B
145553	1,10E-15	1,50E+01	4,16E-16	0,1046	-8,133779	-0,85056744	305,98	MDP1	magnesium dependent phosphatase 1
81532	7,97E-29	2,81E+01	2,08E-29	0,0755	-11,2594903	-0,85058599	991,77	MOB2	MOB kinase activator 2
83401	1,39E-02	1,86E+00	1,01E-02	0,3306	-2,5732302	-0,85069594	29,53	ELOVL3	ELOVL fatty acid elongase 3
521	1,30E-45	4,49E+01	2,30E-46	0,0595	-14,2964047	-0,85080166	1391,18	ATP5ME	ATP synthase membrane subunit e
7415	5,95E-138	1,37E+02	1,72E-139	0,0338	-25,1421399	-0,85093026	33831	VCP	valosin containing protein
1844	1,48E-02	1,83E+00	1,08E-02	0,3338	-2,5501082	-0,85127413	26,76	DUSP2	dual specificity phosphatase 2
105376714	7,80E-06	5,11E+00	4,42E-06	0,1855	-4,5907487	-0,85151311	98,87	LOC105376	uncharacterized LOC105376714
105755954	1,93E-12	1,17E+01	8,14E-13	0,119	-7,1587905	-0,85163683	235,17	ADGRD1-AS	ADGRD1 antisense RNA 1
11334	1,74E-38	3,78E+01	3,60E-39	0,0651	-13,0933068	-0,85206216	1154,07	TUSC2	tumor suppressor 2, mitochondrial calcium regulator
5245	4,14E-63	6,24E+01	4,91E-64	0,0504	-16,8948201	-0,85217899	12409,68	PHB1	prohibitin 1
6130	5,49E-99	9,83E+01	3,18E-100	0,0401	-21,2516546	-0,85227727	58058,78	RPL7A	ribosomal protein L7a
64219	8,92E-30	2,90E+01	2,28E-30	0,0744	-11,4527852	-0,85232064	909,6	PJA1	praja ring finger ubiquitin ligase 1
4141	1,21E-95	9,49E+01	7,40E-97	0,0408	-20,8845605	-0,85293436	7824,73	MARS1	methionyl-tRNA synthetase 1
10856	5,56E-50	4,93E+01	8,82E-51	0,0569	-14,9877957	-0,85337474	8498,67	RUVBL2	RuvB like AAA ATPase 2
5777	2,48E-06	5,61E+00	1,36E-06	0,1767	-4,8304138	-0,85339216	103,44	PTPN6	protein tyrosine phosphatase non-receptor type 6
90313	2,82E-35	3,45E+01	6,29E-36	0,0682	-12,5135905	-0,85345203	1043,9	TP53I13	tumor protein p53 inducible protein 13
653583	1,16E-10	9,94E+00	5,23E-11	0,1301	-6,5641608	-0,85392164	249,28	PHLDB3	pleckstrin homology like domain family B member 3
106144593	8,87E-02	1,05E+00	7,11E-02	0,4732	-1,8050734	-0,85417192	13,69	NOP53-AS1	NOP53 antisense RNA 1
51147	4,29E-23	2,24E+01	1,31E-23	0,0853	-10,0150505	-0,85450932	529,99	ING4	inhibitor of growth family member 4
101928158	3,98E-07	6,40E+00	2,10E-07	0,1646	-5,1903649	-0,85452536	116,67	LAMA5-AS1	LAMA5 antisense RNA 1
2771	2,78E-99	9,86E+01	1,60E-100	0,0402	-21,2840314	-0,85455999	17280,43	GNAI2	G protein subunit alpha i2
1841	7,67E-54	5,31E+01	1,12E-54	0,0549	-15,57231	-0,85475565	2534,13	DTYMK	deoxythymidylate kinase
1340	8,95E-79	7,80E+01	7,58E-80	0,0452	-18,9215395	-0,85481421	6947,53	COX6B1	cytochrome c oxidase subunit 6B1
166	1,27E-75	7,49E+01	1,15E-76	0,0461	-18,5313915	-0,85488	5417,59	TLE5	TLE family member 5, transcriptional modulator
23061	2,05E-79	7,87E+01	1,71E-80	0,045	-18,9997574	-0,85505506	6350,52	TBC1D9B	TBC1 domain family member 9B
11078	1,48E-72	7,18E+01	1,43E-73	0,0471	-18,1442489	-0,855417	2706,05	TRIOBP	TRIO and F-actin binding protein
24142	1,54E-22	2,18E+01	4,75E-23	0,0866	-9,8867772	-0,85576714	624,52	NAA80	N-alpha-acetyltransferase 80, NatH catalytic subunit
51063	8,20E-25	2,41E+01	2,39E-25	0,0823	-10,4036806	-0,85594762	560,12	CALHM2	calcium homeostasis modulator family member 2
9470	2,06E-75	7,47E+01	1,88E-76	0,0463	-18,505183	-0,85597159	4207,36	EIF4E2	eukaryotic translation initiation factor 4E family member 2
105376308	6,28E-03	2,20E+00	4,41E-03	0,3007	-2,8470221	-0,85610593	33,2	LOC105376308	
101927086	8,76E-02	1,06E+00	7,01E-02	0,4728	-1,8110178	-0,85620379	13,66	KLF9-DT	KLF9 divergent transcript
284358	1,45E-05	4,84E+00	8,38E-06	0,1922	-4,4552969	-0,85652115	86,6	MAMSTR	MEF2 activating motif and SAP domain containing transcriptional regulator
6281	8,68E-58	5,71E+01	1,16E-58	0,053	-16,1484714	-0,85653856	18245,91	S100A10	S100 calcium binding protein A10
440925	2,00E-02	1,70E+00	1,47E-02	0,3513	-2,4388619	-0,856833	24,3	LINC01124	long intergenic non-protein coding RNA 1124
83862	2,11E-24	2,37E+01	6,21E-25	0,0831	-10,3121683	-0,85687689	534,93	TMEM120A	transmembrane protein 120A
10998	6,99E-07	6,16E+00	3,73E-07	0,1686	-5,082077	-0,85691445	127,71	SLC27A5	solute carrier family 27 member 5
4707	5,81E-28	2,72E+01	1,55E-28	0,0774	-11,0808378	-0,85731569	871,87	NDUFB1	NADH:ubiquinone oxidoreductase subunit B1
79754	2,66E-41	4,06E+01	5,17E-42	0,0631	-13,5813034	-0,85742733	1174,32	ASB13	ankyrin repeat and SOCS box containing 13
1855	2,55E-60	5,96E+01	3,24E-61	0,0519	-16,5074263	-0,85749757	3953,4	DVL1	dishevelled segment polarity protein 1
6487	1,26E-41	4,09E+01	2,43E-42	0,0629	-13,6364549	-0,85752716	1193,83	ST3GAL3	ST3 beta-galactoside alpha-2,3-sialyltransferase 3
8412	8,91E-88	8,71E+01	6,34E-89	0,0429	-19,9929993	-0,85778582	8012,08	BCAR3	BCAR3 adaptor protein, NSP family member
54936	1,48E-54	5,38E+01	2,14E-55	0,0547	-15,6779584	-0,8578485	2018,69	ADPRS	ADP-ribosylserine hydrolase
6505	1,30E-12	1,19E+01	5,45E-13	0,1189	-7,2136461	-0,8579697	235,35	SLC1A1	solute carrier family 1 member 1
102723724	1,89E-02	1,72E+00	1,39E-02	0,3488	-2,4597331	-0,85799438	24,93	LOC102723	uncharacterized LOC102723724
7378	1,15E-41	4,09E+01	2,23E-42	0,0629	-13,6427968	-0,85802154	1854,76	UPP1	uridine phosphorylase 1
27349	1,30E-21	2,09E+01	4,13E-22	0,0888	-9,6679312	-0,85805008	538,37	MCAT	malonyl-CoA-acyl carrier protein transacylase
8402	2,42E-54	5,36E+01	3,51E-55	0,0548	-15,6465069	-0,85808618	2922,07	SLC25A11	solute carrier family 25 member 11
5905	1,21E-92	9,19E+01	7,94E-94	0,0418	-20,5484869	-0,85823627	10604,7	RANGAP1	Ran GTPase activating protein 1
102465480	4,98E-05	4,30E+00	2,96E-05	0,2055	-4,1765061	-0,85844778	72,23	MIR6800	microRNA 6800
6597	9,63E-106	1,05E+02	4,90E-107	0,0391	-21,9758643	-0,85844963	13626,49	SMARCA4	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 4
57561	2,52E-54	5,36E+01	3,65E-55	0,0549	-15,6439725	-0,85859498	1719,24	ARRDC3	arrestin domain containing 3
3217	7,18E-04	3,14E+00	4,66E-04	0,2453	-3,4996047	-0,85862701	53,91	HOXB7	homeobox B7
327	2,80E-90	8,96E+01	1,90E-91	0,0423	-20,2807568	-0,85869194	5117,73	APEH	acylaminoacyl-peptide hydrolase
5691	2,70E-75	7,46E+01	2,47E-76	0,0464	-18,4903062	-0,85883745	6629,59	PSMB3	proteasome 20S subunit beta 3
4715	2,62E-49	4,86E+01	4,21E-50	0,0577	-14,8836548	-0,85910233	1472,1	NDUFB9	NADH:ubiquinone oxidoreductase subunit B9
399972	1,36E-03	2,87E+00	8,99E-04	0,2588	-3,3203123	-0,85921877	47,09	GSEC	G-quadruplex forming sequence containing lncRNA
100507034	1,14E-34	3,39E+01	2,58E-35	0,0693	-12,4010369	-0,85942495	850,51	PITRM1-AS1	PITRM1 antisense RNA 1
25777	2,72E-50	4,96E+01	4,28E-51	0,0572	-15,035793	-0,85955141	3233,15	SUN2	Sad1 and UNC84 domain containing 2
534	1,50E-04	3,82E+00	9,21E-05	0,2198	-3,9106301	-0,85964081	63,54	ATP6V1G2	ATPase H+ transporting V1 subunit G2
100133957	1,24E-17	1,69E+01	4,43E-18	0,0992	-8,6672667	-0,85964633	409,06	UXT-AS1	UXT antisense RNA 1
51368	1,15E-63	6,29E+01	1,35E-64	0,0507	-16,9709601	-0,85967973	2495,44	TEX264	testis expressed 264, ER-phagy receptor
8131	2,00E-48	4,77E+01	3,30E-49	0,0583	-14,7451737	-0,85970834	2228,6	NPRL3	NPR3 like, GATOR1 complex subunit
9189	6,01E-29	2,82E+01	1,56E-29	0,0762	-11,2846264	-0,85975383	733,7	ZBED1	zinc finger BED-type containing 1
9114	8,16E-64	6,31E+01	9,53E-65	0,0506	-16,9912727	-0,86014418	4011,47	ATP6V0D1	ATPase H+ transporting V0 subunit d1
254427	5,52E-48	4,73E+01	9,17E-49	0,0586	-14,676089	-0,86017522	1340,87	PROSER2	proline and serine rich 2
23031	1,81E-33	3,27E+01	4,22E-34	0,0707	-12,1750261	-0,86024755	798,46	MAST3	microtubule associated serine/threonine kinase 3
23549	5,31E-49	4,83E+01	8,61E-50	0,058	-14,8356875	-0,86026296	2229,66	DNPEP	aspartyl aminopeptidase
10994	1,15E-51	5,09E+01	1,75E-52	0,0564	-15,2459602	-0,86055749	3259,44	ILVBL	ilvB acetolactate synthase like
558	1,89E-102	1,02E+02	1,03E-103	0,0398	-21,6256588	-0,86098038	46422,2	AXL	AXL receptor tyrosine kinase
3914	6,60E-93	9,22E+01	4,29E-94	0,0419	-20,5783434	-0,86156899	25558,6	LAMB3	laminin subunit beta 3
116832	3,99E-39	3,84E+01	8,14E-40	0,0653	-13,205618	-0,86173662	1079,14	RPL39L	ribosomal protein L39 like
6396	5,25E-75	7,43E+01	4,82E-76	0,0467	-18,454293	-0,86208209	6690,42	SEC13	SEC13 homolog, nuclear pore and COPII coat complex component

8295	4,66E-76	7,53E+01	4,21E-77	0,0464	-18,5855425	-0,86227236	3414,86	TRRAP	transformation/transcription domain associated protein
10489	5,81E-56	5,52E+01	8,12E-57	0,0543	-15,8844597	-0,86252454	3056,18	LRRC41	leucine rich repeat containing 41
3029	2,43E-43	4,26E+01	4,52E-44	0,062	-13,9241015	-0,86264075	1434,05	HAGH	hydroxyacylglutathione hydrolase
91543	3,63E-03	2,44E+00	2,49E-03	0,2853	-3,0241928	-0,8628145	44,32	RSAD2	radical S-adenosyl methionine domain containing 2
11262	8,36E-35	3,41E+01	1,89E-35	0,0694	-12,4260842	-0,86297271	799,21	SP140	SP140 nuclear body protein
1470	2,54E-02	1,60E+00	1,89E-02	0,368	-2,3466578	-0,86364703	1067,44	CST2	cystatin SA
9296	1,07E-56	5,60E+01	1,47E-57	0,054	-15,9910967	-0,86386734	2691,53	ATP6V1F	ATPase H+ transporting V1 subunit F
56904	1,98E-45	4,47E+01	3,51E-46	0,0606	-14,2671119	-0,86389353	2481,51	SH3GLB2	SH3 domain containing GRB2 like, endophilin B2
5087	4,50E-31	3,03E+01	1,11E-31	0,0738	-11,7114106	-0,86394385	859,8	PBX1	PBX homeobox 1
102723480	5,00E-08	7,30E+00	2,52E-08	0,1551	-5,571985	-0,86446665	131,2	LOC102723	uncharacterized LOC102723480
26086	3,46E-23	2,25E+01	1,05E-23	0,0861	-10,0365931	-0,86459486	561,18	GPSM1	G protein signaling modulator 1
1132	2,22E-02	1,65E+00	1,65E-02	0,3605	-2,3981773	-0,86461082	23,44	CHRM4	cholinergic receptor muscarinic 4
2617	4,40E-108	1,07E+02	2,14E-109	0,0389	-22,2213005	-0,86466283	13386,73	GARS1	glycyl-tRNA synthetase 1
9948	1,86E-111	1,11E+02	8,49E-113	0,0383	-22,5702712	-0,86469106	37200,1	WDR1	WD repeat domain 1
115	3,46E-48	4,75E+01	5,72E-49	0,0588	-14,7080715	-0,86484633	1351,05	ADCY9	adenylate cyclase 9
64755	2,59E-47	4,66E+01	4,37E-48	0,0594	-14,569901	-0,86508588	1884,2	RUSF1	RUS family member 1
6901	1,04E-28	2,80E+01	2,74E-29	0,077	-11,2352826	-0,86528228	760,79	TAFAZZIN	tafazzin, phospholipid-lysophospholipid transacylase
9810	2,01E-74	7,37E+01	1,87E-75	0,0471	-18,3809864	-0,8653925	3910,42	RNF40	ring finger protein 40
57524	4,05E-21	2,04E+01	1,30E-21	0,0906	-9,5494067	-0,86554982	426,71	CASKIN1	CASK interacting protein 1
832	3,28E-95	9,45E+01	2,04E-96	0,0416	-20,8361452	-0,86592227	10978,04	CAPZB	capping actin protein of muscle Z-line subunit beta
5091	3,69E-47	4,64E+01	6,26E-48	0,0595	-14,5452709	-0,86594514	3188,96	PC	pyruvate carboxylase
57192	1,36E-35	3,49E+01	3,01E-36	0,0689	-12,5719793	-0,86659356	1391,32	MCOLN1	mucolipin TRP cation channel 1
9940	2,37E-13	1,26E+01	9,65E-14	0,1164	-7,4456684	-0,86680351	242,72	DLEC1	DLEC1 cilia and flagella associated protein
105377644	3,86E-07	6,41E+00	2,03E-07	0,1668	-5,1962002	-0,86681241	111,67	LOC105377	uncharacterized LOC105377644
55697	1,94E-61	6,07E+01	2,40E-62	0,052	-16,6639469	-0,86705047	3592,8	VAC14	VAC14 component of PIKFYVE complex
100423004	2,76E-04	3,56E+00	1,74E-04	0,231	-3,7547234	-0,86743266	59,67	MIR4315-1	microRNA 4315-1
27293	1,35E-04	3,87E+00	8,24E-05	0,2203	-3,9372717	-0,86745584	63,97	SMPDL3B	sphingomyelin phosphodiesterase acid like 3B
79034	3,62E-27	2,64E+01	9,90E-28	0,0795	-10,9138641	-0,86787535	742,5	INTS15	integrator complex subunit 15
747	1,42E-28	2,78E+01	3,73E-29	0,0775	-11,2078036	-0,86805284	741,4	DAGLA	diacylglycerol lipase alpha
200810	7,14E-02	1,15E+00	5,65E-02	0,4551	-1,9074684	-0,86812989	15,24	ALG1L1P	ALG1 like 1, pseudogene
1173	6,64E-103	1,02E+02	3,57E-104	0,0401	-21,6745588	-0,8682038	16244,58	AP2M1	adaptor related protein complex 2 subunit mu 1
3661	5,21E-58	5,73E+01	6,95E-59	0,0537	-16,1802198	-0,86851234	2455,76	IRF3	interferon regulatory factor 3
51657	3,17E-44	4,35E+01	5,79E-45	0,0618	-14,0702354	-0,86883937	1429,1	STYXL1	serine/threonine/tyrosine interacting like 1
80142	2,46E-36	3,56E+01	5,33E-37	0,0684	-12,7081918	-0,86888953	2091,27	PTGES2	prostaglandin E synthase 2
50617	4,47E-12	1,13E+01	1,91E-12	0,1234	-7,0409068	-0,86892183	256,89	ATP6V0A4	ATPase H+ transporting V0 subunit a4
105371941	3,56E-04	3,45E+00	2,25E-04	0,2357	-3,6886386	-0,86949707	62,12	NARF-AS2	NARF antisense RNA 2
23338	5,67E-93	9,22E+01	3,68E-94	0,0423	-20,5858187	-0,87035372	5794,6	JADE2	jade family PHD finger 2
3669	5,23E-17	1,63E+01	1,90E-17	0,1024	-8,4996242	-0,8704597	343,74	ISG20	interferon stimulated exonuclease gene 20
9040	3,88E-97	9,64E+01	2,33E-98	0,0414	-21,0491841	-0,87078684	5404,51	UBE2M	ubiquitin conjugating enzyme E2 M
100134938	3,67E-15	1,44E+01	1,42E-15	0,1091	-7,9840925	-0,87118485	302,05	UPK3BL1	uroplakin 3B like 1
79735	1,15E-46	4,59E+01	1,97E-47	0,0602	-14,4665475	-0,8715305	1325,52	TBC1D17	TBC1 domain family member 17
57799	3,45E-27	2,65E+01	9,43E-28	0,0798	-10,9182342	-0,87155569	623,51	RAB40C	RAB40C, member RAS oncogene family
79701	1,24E-52	5,19E+01	1,86E-53	0,0566	-15,3917666	-0,87159623	1723,3	OGFOD3	2-oxoglutarate and iron dependent oxygenase domain containing 3
84336	6,48E-37	3,62E+01	1,39E-37	0,0681	-12,8129528	-0,87213501	1317,22	TMEM101	transmembrane protein 101
26030	2,74E-47	4,66E+01	4,63E-48	0,0599	-14,5659371	-0,87231435	1305,72	PLEKHG3	pleckstrin homology and RhoGEF domain containing G3
65003	3,44E-61	6,05E+01	4,30E-62	0,0525	-16,6290065	-0,87243436	2704,69	MRPL11	mitochondrial ribosomal protein L11
89927	2,94E-35	3,45E+01	6,56E-36	0,0698	-12,5102231	-0,87285014	798,71	BMERB1	bMERB domain containing 1
2889	6,91E-80	7,92E+01	5,73E-81	0,0458	-19,057147	-0,87293749	3374,55	RAPGEF1	Rap guanine nucleotide exchange factor 1
23324	1,87E-72	7,17E+01	1,81E-73	0,0481	-18,1311756	-0,8729732	2886	MAN2B2	mannosidase alpha class 2B member 2
113218482	2,81E-24	2,36E+01	8,30E-25	0,0849	-10,2841877	-0,87306075	743,37	MIR9898	microRNA 9898
78987	4,06E-33	3,24E+01	9,55E-34	0,0721	-12,1082268	-0,87311328	999,23	CRELD1	cysteine rich with EGF like domains 1
2527	3,60E-02	1,44E+00	2,74E-02	0,396	-2,2051059	-0,87311712	19,08	FUT5	fucosyltransferase 5
2523	3,80E-08	7,42E+00	1,90E-08	0,1553	-5,6206271	-0,87315204	145,77	FUT1	fucosyltransferase 1 (H blood group)
27286	1,42E-31	3,08E+01	3,47E-32	0,0739	-11,8098747	-0,87326165	731,23	SRPX2	sushi repeat containing protein X-linked 2
6188	2,51E-98	9,76E+01	1,48E-99	0,0413	-21,1795036	-0,87397487	56987,11	RPS3	ribosomal protein S3
115399	2,14E-02	1,67E+00	1,58E-02	0,3622	-2,4129284	-0,87399628	23,67	LRRC56	leucine rich repeat containing 56
56996	1,46E-22	2,18E+01	4,51E-23	0,0884	-9,8920411	-0,87426226	678,33	SLC12A9	solute carrier family 12 member 9
9241	2,03E-50	4,97E+01	3,20E-51	0,0581	-15,0550998	-0,87437529	1438,4	NOG	noggin
63905	1,77E-82	8,18E+01	1,39E-83	0,0452	-19,3697456	-0,87457264	4149,48	MANBAL	mannosidase beta like
219743	1,55E-36	3,58E+01	3,34E-37	0,0686	-12,7445225	-0,87477171	1245,19	TYSND1	trypsin like peroxisomal matrix peptidase 1
4967	3,62E-87	8,64E+01	2,61E-88	0,0439	-19,9222447	-0,87477975	11401,85	OGDH	oxoglutarate dehydrogenase
171425	5,25E-03	2,28E+00	3,66E-03	0,3012	-2,9058084	-0,87516527	35,57	CLYBL	citramalyl-CoA lyase
729870	1,03E-01	9,87E-01	8,33E-02	0,5053	-1,7320632	-0,87528861	11,8	LOC729870	uncharacterized LOC729870
8924	1,73E-73	7,28E+01	1,63E-74	0,0479	-18,2629633	-0,87542258	3895,8	HERC2	HECT and RLD domain containing E3 ubiquitin protein ligase 2
79576	4,27E-45	4,44E+01	7,62E-46	0,0616	-14,2128845	-0,87544913	1331,04	NKAP	NFKB activating protein
6714	2,22E-59	5,87E+01	2,87E-60	0,0535	-16,3752434	-0,8759833	1789,12	SRC	SRC proto-oncogene, non-receptor tyrosine kinase
171568	2,50E-63	6,26E+01	2,94E-64	0,0518	-16,9249922	-0,8761387	2757,01	POLR3H	RNA polymerase III subunit H
118	1,24E-125	1,25E+02	4,43E-127	0,0365	-23,9806229	-0,87613983	10697,79	ADD1	adducin 1
222962	4,59E-02	1,34E+00	3,54E-02	0,4166	-2,1034798	-0,87630876	18,18	SLC29A4	solute carrier family 29 member 4
6160	7,36E-109	1,08E+02	3,51E-110	0,0393	-22,302279	-0,87636373	22643,05	RPL31	ribosomal protein L31
345222	9,20E-09	8,04E+00	4,47E-09	0,1494	-5,8656638	-0,87655415	140,08	MSANTD1	Myb/SANT DNA binding domain containing 1
219539	1,53E-01	8,15E-01	1,27E-01	0,5744	-1,5261292	-0,87663851	9,42	YPEL4	yippee like 4
6256	5,65E-45	4,42E+01	1,01E-45	0,0618	-14,1930139	-0,87678077	2299,26	RXRA	retinoid X receptor alpha
102465801	1,16E-23	2,29E+01	3,49E-24	0,0865	-10,1448894	-0,87718937	486,52	MIR7703	microRNA 7703
22846	9,74E-17	1,60E+01	3,56E-17	0,1041	-8,4263995	-0,87724438	318,24	VASH1	vasohibin 1
60314	3,80E-39	3,84E+01	7,76E-40	0,0664	-13,2092764	-0,8772968	1345,97	MYG1	MYG1 exonuclease
10297	4,21E-14	1,34E+01	1,68E-14	0,1143	-7,6730478	-0,87736246	336,58	APC2	APC regulator of WNT signaling pathway 2
6482	2,74E-96	9,56E+01	1,67E-97	0,0419	-20,9556546	-0,87752967	4810,15	ST3GAL1	ST3 beta-galactoside alpha-2,3-sialyltransferase 1
335	1,39E-01	8,57E-01	1,14E-01	0,5555	-1,5798193	-0,87757194	10,59	APOA1	apolipoprotein A1
112267958	1,25E-08	7,90E+00	6,11E-09	0,151	-5,8137333	-0,87787597	140,51	KLC4-AS1	KLC4 antisense RNA 1
27111	4,78E-05	4,32E+00	2,83E-05	0,2098	-4,186343	-0,87813098	72,21	SDCBP2	syndecan binding protein 2
56834	2,79E-47	4,66E+01	4,71E-48	0,0603	-14,5646758	-0,87831855	2369,81	GPR137	G protein-coupled receptor 137
1819	8,70E-56	5,51E+01	1,22E-56	0,0554	-15,8588087	-0,87862815	1749,46	DRG2	developmentally regulated GTP binding protein 2
11152	5,40E-51	5,03E+01	8,36E-52	0,058	-15,1435332	-0,87868613	1992,52	WDR45	WD repeat domain 45
729723	7,89E-02	1,10E+00	6,28E-02	0,4723	-1,8608212	-0,87887633	13,79	DNAJC27-AS	DNAJC27 antisense RNA 1
83733	6,24E-09	8,20E+00	3,02E-09	0,1482	-5,9307319	-0,8789783	148,78	SLC25A18	solute carrier family 25 member 18
58491	6,73E-26	2,52E+01	1,90E-26	0,0826	-10,6418509	-0,87921253	540,89	ZNF71	zinc finger protein 71
100128927	1,73E-09	8,76E+00	8,17E-10	0,1432	-6,1415318	-0,87935329	162,92	ZBTB42	zinc finger and BTB domain containing 42
29993	8,98E-02	1,05E+00	7,20E-02	0,4888	-1,7991956	-0,87938585	14,2	PACSIN1	protein kinase C and casein kinase substrate in neurons 1
100507420	1,25E-26	2,59E+01	3,46E-27	0,0814	-10,7994169	-0,87940088	591,61	LINC01605	long intergenic non-protein coding RNA 1605
6159	1,95E-88	8,77E+01	1,37E-89	0,0438	-20,0693594	-0,88001413	28311,9	RPL29	ribosomal protein L29
283638	1,89E-40	3,97E+01	3,75E-41	0,0655	-13,4354187	-0,88008535	1424,56	CEP170B	centrosomal protein 170B
101927021	8,11E-08	7,09E+00	4,13E-08	0,1605	-5,485293	-0,8804565	123,29	ZFAND2A-D	ZFAND2A divergent transcript
107986250	1,14E-01	9,43E-01	9,31E-02	0,5244	-1,6791232	-0,88054541	11,09	LOC107986	uncharacterized LOC107986250
9143	5,48E-02	1,26E+00	4,27E-02	0,4345	-2,026555	-0,88060306	17,82	SYNGR3	synaptogyrin 3
100505994	2,18E-09	8,66E+00	1,04E-09	0,1443	-6,1037887	-0,88071004	178,36	LUCAT1	lung cancer associated transcript 1
90507	4,15E-34	3,34E+01	9,52E-35	0,0716	-12,2959657	-0,88093021	897,01	SCRN2	secernin 2
6992	1,07E-76	7,60E+01	9,54E-78	0,0472	-18,6649663	-0,88102299	5552,2	PPP1R11	protein phosphatase 1 regulatory inhibitor subunit 11
3927	2,23E-140	1,40E+02	6,23E-142	0,0348	-25,3643987	-0,88157239	41163,36	LASP1	LIM and SH3 protein 1
54863	5,72E-60	5,92E+01	7,33E-61	0,0536	-16,4581698	-0,88170363	2816,41	TOR4A	torsin family 4 member A
81887	1,79E-82	8,17E+01	1,41E-83	0,0455	-19,3690141	-0,88183403	4236,29	LAS1L	LAS1 like ribosome biogenesis factor
112268097	9,35E-25	2,40E+01	2,72E-25	0,0849	-10,3910147	-0,88188315	545,01	MYG1-AS1	MYG1 antisense RNA 1
6038	1,86E-13	1,27E+01	7,55E-14	0,1179	-7,4779079	-0,8819005	286,05	RNASE4	ribonuclease A family member 4
105372486	1,27E-05	4,90E+00	7,29E-06	0,1966	-4,4849414	-0,88195643	80,66	LOC105372	486
4191	8,75E-80	7,91E+01	7,27E-81	0,0463	-19,0447162	-0,88235036	9612,48	MDH2	malate dehydrogenase 2
554313	3,68E-04	3,43E+00	2,33E-04	0,2398	-3,6798504	-0,88236558	51,71	H4C15	H4 clustered histone 15
51264	6,00E-64	6,32E+01	6,99E-65	0,0519	-17,0094507	-0,88264855	2018,02	MRPL27	mitochondrial ribosomal protein L27
10981	3,54E-49	4,85E+01	5,71E-50	0,0594	-14,8632514	-0,88269907	1714,24	RAB32	RAB32, member RAS oncogene family
23152	1,98E-66	6,57E+01	2,19E-67	0,0509	-17,3440308	-0,88270937	3691,73	CIC	capicua transcriptional repressor
100996307	3,44E-02	1,46E+00	2,61E-02	0,3969	-2,2242815	-0,88272978	19,51	LIPE-AS1	LIPE antisense RNA 1
6376	8,84E-09	8,05E+00	4,30E-09	0,1503	-5,872336	-0,88279368	137,33	CX3CL1	C-X3-C motif chemokine ligand 1
107984384	1,55E-01	8,10E-01	1,29E-01	0,5816	-1,5179394	-0,88285451	9,65	LOC107984	384
102724450	4,53E-02	1,34E+00	3,49E-02	0,4187	-2,1093046	-0,8830819	16,85	RNF207-AS1	RNF207 antisense RNA 1
84975	8,52E-38	3,71E+01	1,79E-38	0,0681	-12,9707121	-0,88321657	1045,47	MFSD5	major facilitator superfamily domain containing 5
4335	1,21E-38	3,79E+01	2,50E-39	0,0673	-13,1207793	-0,88337821	962,37	MNT	MAX network transcriptional repressor
3710	7,31E-84	8,31E+01	5,61E-85	0,0452	-19,5342803	-0,88355225	22323,54	ITPR3	inositol 1,4,5-trisphosphate receptor type 3
441455	1,46E-01	8,36E-01	1,20E-01	0,5688	-1,55356	-0,8837416	9,14	LOC441455	makorin ring finger protein 1 pseudogene
107986828	1,25E-02	1,90E+00	9,05E-03	0,3386	-2,6099976	-0,88377215	26,67	LOC107986	828
9612	3,31E-99	9,85E+01	1,90E-100	0,0415	-21,2757854	-0,88380602	8234,61	NCOR2	nuclear receptor corepressor 2
83983	2,86E-04	3,54E+00	1,80E-04	0,236	-3,7454878	-0,88406745	55,6	TSSK6	testis specific serine kinase 6

997	9,48E-49	4,80E+01	1,55E-49	0,0598	-14,7962782	-0,88413512	1973,39	CDC34	cell division cycle 34, ubiqiutin conjugating enzyme
5293	1,92E-59	5,87E+01	2,49E-60	0,054	-16,3840629	-0,88420727	1887,04	PIK3CD	phosphatidylinositol-4,5-bisphosphate 3-kinase catalytic subunit delta
10005	2,17E-32	3,17E+01	5,20E-33	0,0739	-11,9684525	-0,88442428	799,03	ACOT8	acyl-CoA thioesterase 8
4637	1,98E-148	1,48E+02	4,97E-150	0,0339	-26,0881072	-0,8847063	33866,13	MYL6	myosin light chain 6
90506	2,06E-04	3,69E+00	1,28E-04	0,2311	-3,8297518	-0,88515979	56,5	LRRC46	leucine rich repeat containing 46
112268171	2,05E-04	3,69E+00	1,28E-04	0,2311	-3,8311274	-0,88527848	62,58	LOC112268	replaced by ID 728689
3208	1,12E-02	1,95E+00	8,03E-03	0,334	-2,6506115	-0,88531696	26,91	HPCA	hippocalcin
8078	2,42E-86	8,56E+01	1,76E-87	0,0447	-19,8263412	-0,88564333	6089,67	USP5	ubiquitin specific peptidase 5
644096	4,10E-20	1,94E+01	1,36E-20	0,0952	-9,3034562	-0,88564386	377,56	SDHAF1	succinate dehydrogenase complex assembly factor 1
284106	4,67E-54	5,33E+01	6,80E-55	0,0568	-15,604302	-0,88577488	2085,06	CISD3	CDGSH iron sulfur domain 3
56905	8,65E-49	4,81E+01	1,41E-49	0,0598	-14,8025286	-0,88582425	2150,52	C15orf39	chromosome 15 open reading frame 39
100128731	2,90E-75	7,45E+01	2,66E-76	0,0479	-18,4863963	-0,88586416	3324,68	OST4	oligosaccharyltransferase complex subunit 4, non-catalytic
54187	1,15E-75	7,49E+01	1,04E-76	0,0478	-18,5367594	-0,88606552	3035,58	NANS	N-acetylneuraminate synthase
51069	9,06E-71	7,00E+01	9,12E-72	0,0495	-17,9142971	-0,8862066	4350,69	MRPL2	mitochondrial ribosomal protein L2
400684	1,32E-04	3,88E+00	8,10E-05	0,2249	-3,9413541	-0,88624117	59,88	DPY19L3-D1	DPY19L3 divergent transcript
55357	8,72E-64	6,31E+01	1,02E-64	0,0522	-16,9873015	-0,88627987	2798,59	TBC1D2	TBC1 domain family member 2
9609	3,72E-12	1,14E+01	1,58E-12	0,1254	-7,0669752	-0,88649941	256,59	RAB36	RAB36, member RAS oncogene family
6513	3,49E-104	1,03E+02	1,84E-105	0,0407	-21,8106948	-0,88670839	25707,89	SLC2A1	solute carrier family 2 member 1
29959	2,85E-118	1,18E+02	1,17E-119	0,0381	-23,2583212	-0,88673356	12582,23	NRBP1	nuclear receptor binding protein 1
124790	1,47E-15	1,48E+01	5,61E-16	0,1095	-8,0974398	-0,88707216	288,32	HEXIM2	HEXIM P-TEFb complex subunit 2
79050	2,42E-28	2,76E+01	6,43E-29	0,0795	-11,1596349	-0,88756283	669,14	NOC4L	nucleolar complex associated 4 homolog
79083	4,68E-87	8,63E+01	3,38E-88	0,0446	-19,9093319	-0,88756968	4121,2	MLPH	melanophilin
26249	5,70E-08	7,24E+00	2,88E-08	0,16	-5,5487479	-0,88760932	122,27	KLHL3	kelch like family member 3
111216286	8,97E-05	4,05E+00	5,43E-05	0,2199	-4,0364769	-0,88761517	66,19	LINC02575	long intergenic non-protein coding RNA 2575
22885	4,17E-82	8,14E+01	3,31E-83	0,0459	-19,3250626	-0,8877855	4357,14	ABLIM3	actin binding LIM protein family member 3
100505681	1,58E-16	1,58E+01	5,84E-17	0,1062	-8,3684169	-0,88912821	312,13	NAPA-AS1	NAPA antisense RNA 1
101928595	1,13E-01	9,47E-01	9,19E-02	0,5276	-1,685658	-0,88935499	11,04	YPEL3-DT	YPEL3 divergent transcript
79751	1,16E-36	3,59E+01	2,49E-37	0,0697	-12,7674218	-0,88958607	2356,88	SLC25A22	solute carrier family 25 member 22
5834	4,55E-112	1,11E+02	2,06E-113	0,0393	-22,6328101	-0,88963905	14612,54	PYGB	glycogen phosphorylase B
84727	1,56E-15	1,48E+01	5,94E-16	0,11	-8,090469	-0,89004434	308,96	SPSB2	splA/ryanodine receptor domain and SOCS box containing 2
80028	7,18E-47	4,61E+01	1,22E-47	0,0614	-14,4992897	-0,89030259	1796,08	FBXL18	F-box and leucine rich repeat protein 18
125950	3,46E-88	8,75E+01	2,45E-89	0,0444	-20,040305	-0,8905061	7187,64	RAVER1	ribonucleoprotein, PTB binding 1
115950	1,48E-19	1,88E+01	5,00E-20	0,0972	-9,1640469	-0,8905204	482,65	ZNF653	zinc finger protein 653
84696	1,15E-19	1,89E+01	3,87E-20	0,0969	-9,1915728	-0,89056589	370,88	ABHD1	abhydrolase domain containing 1
157285	5,26E-56	5,53E+01	7,34E-57	0,0561	-15,8908133	-0,89091072	1845,55	PRAG1	PEAK1 related, kinase-activating pseudokinase 1
57491	8,84E-33	3,21E+01	2,10E-33	0,074	-12,0436265	-0,89128991	778,07	AHRR	aryl hydrocarbon receptor repressor
6494	1,07E-44	4,40E+01	1,93E-45	0,063	-14,1475346	-0,89177266	1416,35	SIPA1	signal-induced proliferation-associated 1
56108	3,67E-04	3,44E+00	2,33E-04	0,2423	-3,680418	-0,89182844	51,82	PCDHGA7	protocadherin gamma subfamily A, 7
128272	2,72E-21	2,06E+01	8,73E-22	0,093	-9,5909781	-0,89193235	418,64	ARHGEF19	Rho guanine nucleotide exchange factor 19
219927	3,31E-57	5,65E+01	4,49E-58	0,0555	-16,064948	-0,89202242	1875,77	MRPL21	mitochondrial ribosomal protein L21
26137	4,56E-08	7,34E+00	2,29E-08	0,1596	-5,5884264	-0,89217094	121,48	ZBTB20	zinc finger and BTB domain containing 20
81876	2,40E-56	5,56E+01	3,32E-57	0,056	-15,9403544	-0,89223635	13148,75	RAB1B	RAB1B, member RAS oncogene family
641649	3,37E-06	5,47E+00	1,87E-06	0,1872	-4,7670307	-0,89224126	90,28	TMEM91	transmembrane protein 91
84305	2,33E-25	2,46E+01	6,69E-26	0,0848	-10,5240549	-0,89236256	528,42	PYM1	PYM homolog 1, exon junction complex associated factor
105376146	1,20E-01	9,21E-01	9,81E-02	0,5398	-1,6539211	-0,89276763	10,52	LOC105376	synapsin-1
9632	1,73E-98	9,78E+01	1,01E-99	0,0421	-21,1971636	-0,89283456	8896,77	SEC24C	SEC24 homolog C, COPII coat complex component
8991	2,94E-17	1,65E+01	1,06E-17	0,1043	-8,5673062	-0,89324764	332,45	SELENBP1	selenium binding protein 1
22982	5,57E-42	4,13E+01	1,07E-42	0,0652	-13,696245	-0,89325983	951,48	DIP2C	disco interacting protein 2 homolog C
57458	3,52E-57	5,65E+01	4,78E-58	0,0556	-16,0610408	-0,89370794	1721,71	TMCC3	transmembrane and coiled-coil domain family 3
10488	4,54E-86	8,53E+01	3,33E-87	0,0452	-19,7943278	-0,89377083	3247,84	CREB3	cAMP responsive element binding protein 3
55611	9,83E-78	7,70E+01	8,56E-79	0,0476	-18,7933555	-0,89384741	3682,19	OTUB1	OTU deubiquitinase, ubiquitin aldehyde binding 1
6208	8,58E-89	8,81E+01	5,99E-90	0,0445	-20,1103772	-0,89414249	20849,38	RPS14	ribosomal protein S14
105369340	3,16E-13	1,25E+01	1,30E-13	0,1207	-7,4066179	-0,89433686	221,17	PPP1R14B-A	PPP1R14B antisense RNA 1
106144598	1,32E-17	1,69E+01	4,73E-18	0,1033	-8,6596063	-0,8943967	369,1	FARSA-AS1	FARSA antisense RNA 1
6472	1,92E-73	7,27E+01	1,81E-74	0,049	-18,2572196	-0,89441694	9567,93	SHMT2	serine hydroxymethyltransferase 2
55823	2,22E-84	8,37E+01	1,68E-85	0,0457	-19,5956685	-0,89461077	3871,42	VPS11	VPS11 core subunit of CORVET and HOPS complexes
1801	1,14E-62	6,19E+01	1,37E-63	0,0531	-16,8342126	-0,89471628	1855,88	DPH1	diphthamide biosynthesis 1
128308	4,36E-34	3,34E+01	1,00E-34	0,0728	-12,2919774	-0,89480102	817,07	MRPL55	mitochondrial ribosomal protein L55
2870	2,18E-33	3,27E+01	5,10E-34	0,0736	-12,1595901	-0,89483529	1873,9	GRK6	G protein-coupled receptor kinase 6
3482	7,38E-130	1,29E+02	2,42E-131	0,0367	-24,3857684	-0,89501311	11242,94	IGF2R	insulin like growth factor 2 receptor
2355	1,10E-131	1,31E+02	3,47E-133	0,0365	-24,5589941	-0,89519217	14655,73	FOSL2	FOS like 2, AP-1 transcription factor subunit
79746	8,35E-29	2,81E+01	2,18E-29	0,0796	-11,2552679	-0,89556126	692,28	ECHDC3	enoyl-CoA hydratase domain containing 3
30968	1,32E-72	7,19E+01	1,27E-73	0,0493	-18,150628	-0,89560016	5516,46	STOML2	stomatin like 2
55766	1,33E-28	2,79E+01	3,49E-29	0,0799	-11,2137045	-0,89595045	1097,49	H2AJ	H2A.J histone
79758	2,07E-14	1,37E+01	8,19E-15	0,1155	-7,7645679	-0,89647309	251	DHRS12	dehydrogenase/reductase 12
84443	8,47E-04	3,07E+00	5,53E-04	0,2596	-3,4538651	-0,89667133	44,33	FRMPD3	FERM and PDZ domain containing 3
80206	2,80E-86	8,56E+01	2,05E-87	0,0452	-19,8188954	-0,89678085	3173,17	FHOD3	formin homology 2 domain containing 3
23135	2,72E-24	2,36E+01	8,04E-25	0,0872	-10,2873353	-0,89718897	472	KDM6B	lysine demethylase 6B
8864	3,99E-15	1,44E+01	1,54E-15	0,1126	-7,9734194	-0,89769697	260,93	PER2	period circadian regulator 2
5434	1,44E-54	5,38E+01	2,08E-55	0,0573	-15,67983	-0,89772653	5073,79	POLR2E	RNA polymerase II, I and III subunit E
63035	1,74E-40	3,98E+01	3,45E-41	0,0668	-13,4416755	-0,89804761	1316,87	BCORL1	BCL6 corepressor like 1
257407	7,53E-03	2,12E+00	5,33E-03	0,3224	-2,7862562	-0,89829587	31,88	C2orf72	chromosome 2 open reading frame 72
9577	1,92E-62	6,17E+01	2,32E-63	0,0535	-16,8030809	-0,89836289	2039,85	BABAM2	BRISC and BRCA1 A complex member 2
8372	1,78E-13	1,27E+01	7,23E-14	0,1201	-7,4836735	-0,89849823	283,32	HYAL3	hyaluronidase 3
388323	3,76E-02	1,42E+00	2,87E-02	0,4108	-2,187593	-0,89856691	18,42	GLTPD2	glycolipid transfer protein domain containing 2
3790	5,50E-35	3,43E+01	1,24E-35	0,0721	-12,4598318	-0,89874147	752,86	KCNS3	potassium voltage-gated channel modifier subfamily S member 3
5251	4,52E-04	3,34E+00	2,89E-04	0,2479	-3,6249447	-0,89877744	58,5	PHEX	phosphate regulating endopeptidase X-linked
51204	1,33E-59	5,89E+01	1,71E-60	0,0548	-16,4068005	-0,89886602	1733,91	TACO1	translational activator of cytochrome c oxidase I
4946	1,76E-72	7,18E+01	1,70E-73	0,0496	-18,1345651	-0,89898631	13860,32	OAZ1	ornithine decarboxylase antizyme 1
4685	1,03E-02	1,99E+00	7,42E-03	0,3358	-2,677445	-0,89906643	26,25	NCAM2	neural cell adhesion molecule 2
283416	9,82E-02	1,01E+00	7,92E-02	0,5124	-1,7554396	-0,89940601	12,09	LINC01465	long intergenic non-protein coding RNA 1465
221061	4,88E-50	4,93E+01	7,73E-51	0,06	-14,9966217	-0,89947068	1972,41	FAM171A1	family with sequence similarity 171 member A1
107985092	6,82E-02	1,17E+00	5,38E-02	0,4665	-1,928303	-0,89964651	14,15	ARHGAP29-	ARHGAP29 antisense RNA 1
6746	6,90E-116	1,15E+02	2,95E-117	0,0391	-23,0197944	-0,89971111	10739,33	SSR2	signal sequence receptor subunit 2
6183	7,00E-50	4,92E+01	1,11E-50	0,0601	-14,9724084	-0,89984459	2244,34	MRPS12	mitochondrial ribosomal protein S12
51162	2,15E-17	1,67E+01	7,74E-18	0,1046	-8,6033253	-0,89991748	327,9	EGFL7	EGF like domain multiple 7
79698	8,73E-02	1,06E+00	6,99E-02	0,4967	-1,8128468	-0,900487	13,09	ZMAT4	zinc finger matrin-type 4
353322	7,25E-08	7,14E+00	3,68E-08	0,1636	-5,5055609	-0,90057485	122,17	ANKRD37	ankyrin repeat domain 37
8508	4,85E-59	5,83E+01	6,34E-60	0,0552	-16,3270266	-0,90057971	1535,66	NIPSNAP1	nipsnap homolog 1
100093630	1,16E-66	6,59E+01	1,27E-67	0,0518	-17,3752313	-0,90064562	1953,24	SNHG8	small nucleolar RNA host gene 8
2745	6,07E-58	5,72E+01	8,10E-59	0,0557	-16,1708067	-0,90067598	1858,05	GLRX	glutaredoxin
29844	1,54E-36	3,58E+01	3,31E-37	0,0707	-12,7452849	-0,90082659	909,73	TFPT	TCF3 fusion partner
26251	5,39E-14	1,33E+01	2,16E-14	0,1179	-7,6409088	-0,90091792	238,56	KCNG2	potassium voltage-gated channel modifier subfamily G member 2
5192	5,26E-41	4,03E+01	1,03E-41	0,0666	-13,5308754	-0,90100669	1079,87	PEX10	peroxisomal biogenesis factor 10
26150	1,32E-05	4,88E+00	7,59E-06	0,2014	-4,4764034	-0,90134554	84,95	RIBC2	RIB43A domain with coiled-coils 2
7314	2,09E-88	8,77E+01	1,47E-89	0,0449	-20,0656911	-0,90187828	43194,37	UBB	ubiquitin B
5479	4,54E-117	1,16E+02	1,90E-118	0,039	-23,1385341	-0,90203725	11139,03	PPIB	peptidylprolyl isomerase B
1308	7,37E-30	2,91E+01	1,88E-30	0,0787	-11,4695371	-0,9021413	596,13	COL17A1	collagen type XVII alpha 1 chain
22913	1,41E-75	7,49E+01	1,28E-76	0,0487	-18,525764	-0,90225972	7982,63	RALY	RALY heterogeneous nuclear ribonucleoprotein
340061	3,13E-52	5,15E+01	4,72E-53	0,0589	-15,3312989	-0,90229479	1454,85	STING1	stimulator of interferon response cGAMP interactor 1
421	1,64E-05	4,79E+00	9,50E-06	0,2038	-4,4281724	-0,90263836	73,33	ARVCF	ARVCF delta catenin family member
56288	3,51E-83	8,25E+01	2,72E-84	0,0464	-19,4535179	-0,9031436	4146,66	PARD3	par-3 family cell polarity regulator
1298	3,05E-17	1,65E+01	1,10E-17	0,1055	-8,5627435	-0,90321782	309,95	COL9A2	collagen type IX alpha 2 chain
6778	2,03E-75	7,47E+01	1,85E-76	0,0488	-18,5058846	-0,90329981	5811,31	STAT6	signal transducer and activator of transcription 6
23645	1,59E-125	1,25E+02	5,71E-127	0,0377	-23,9700546	-0,90339715	9830,23	PPP1R15A	protein phosphatase 1 regulatory subunit 15A
5297	2,17E-93	9,27E+01	1,40E-94	0,0438	-20,6325994	-0,90436706	3982,72	PI4KA	phosphatidylinositol 4-kinase alpha
4940	3,00E-79	7,85E+01	2,52E-80	0,0477	-18,9795053	-0,90466501	2589,87	OAS3	2'-5'-oligoadenylate synthetase 3
81605	2,20E-65	6,47E+01	2,49E-66	0,0526	-17,2037715	-0,90470588	3067,25	URM1	ubiquitin related modifier 1
730098	1,13E-03	2,95E+00	7,48E-04	0,2684	-3,3714556	-0,90483123	43,5	LOC730098	uncharacterized LOC730098
3290	6,52E-02	1,19E+00	5,13E-02	0,4643	-1,9488337	-0,9049258	14,19	HSD11B1	hydroxysteroid 11-beta dehydrogenase 1
27440	7,57E-42	4,11E+01	1,46E-42	0,0662	-13,6737327	-0,90494575	1683,7	HDHD5	haloacid dehalogenase like hydrolase domain containing 5
9136	1,68E-50	4,98E+01	2,64E-51	0,0601	-15,0678229	-0,90495114	1906,31	RRP9	ribosomal RNA processing 9, U3 small nucleolar RNA binding protein
729262	8,43E-05	4,07E+00	5,09E-05	0,2234	-4,0514659	-0,90501934	61,24	NUTM2B	NUT family member 2B
27335	1,67E-82	8,18E+01	1,31E-83	0,0467	-19,3727723	-0,90503429	8322,91	EIF3K	eukaryotic translation initiation factor 3 subunit K
10961	3,45E-92	9,15E+01	2,27E-93	0,0442	-20,4974415	-0,90515869	8827,63	ERP29	endoplasmic reticulum protein 29
4605	1,25E-79	7,89E+01	1,04E-80	0,0476	-19,0257209	-0,90526086	5418,44	MYBL2	MYB proto-oncogene like 2
57819	8,23E-82	8,11E+01	6,57E-83	0,0469	-19,2895828	-0,90530078	2967,12	LSM2	LSM2 homolog, U6 small nuclear RNA and mRNA degradation associated
285755	3,12E-04	3,51E+00	1,97E-04	0,2433	-3,722712	-0,90572297	56,49	PPIL6	peptidylprolyl isomerase like 6
6764	4,11E-49	4,84E+01	6,66E-50	0,061	-14,8529564	-0,90613313	1350,74	DENND2B	DENN domain containing 2B
9150	6,02E-37	3,62E+01	1,29E-37	0,0707	-12,8186743	-0,90638447	877,16	CTDP1	CTD phosphatase subunit 1

347733	4,23E-28	2,74E+01	1,13E-28	0,0816	-11,1095038	-0,906442	894,63	TUBB2B	tubulin beta 2B class IIb
353	9,95E-14	1,30E+01	4,01E-14	0,1199	-7,5606474	-0,90650856	2883,91	APRT	adenine phosphoribosyltransferase
554206	4,46E-02	1,35E+00	3,43E-02	0,4284	-2,11613	-0,90655368	17,97	LOC554206	leucine carboxyl methyltransferase 1 pseudogene
57701	4,27E-43	4,24E+01	7,98E-44	0,0654	-13,8834455	-0,90729153	1052,85	NCKAP5L	NCK associated protein 5 like
100507602	4,32E-29	2,84E+01	1,12E-29	0,0802	-11,3138231	-0,90740485	577,3	TRIM52-AS1	TRIM52 antisense RNA 1 (head to head)
55665	7,01E-62	6,12E+01	8,57E-63	0,0543	-16,7253297	-0,90760757	2421,39	URGCP	upregulator of cell proliferation
27245	5,66E-44	4,32E+01	1,04E-44	0,0647	-14,0287068	-0,90766091	1222,58	AHDC1	AT-hook DNA binding motif containing 1
8140	3,81E-68	6,74E+01	4,05E-69	0,0517	-17,5717719	-0,90771536	19094,6	SLC7A5	solute carrier family 7 member 5
9092	5,39E-81	8,03E+01	4,38E-82	0,0473	-19,1912663	-0,90780507	4533,16	SART1	spliceosome associated factor 1, recruiter of U4/U6.U5 tri-snRNP
5157	6,06E-16	1,52E+01	2,28E-16	0,1106	-8,2064514	-0,90783323	317,55	PDGFRL	platelet derived growth factor receptor like
65018	8,22E-68	6,71E+01	8,81E-69	0,0518	-17,5276998	-0,90830416	3707,32	PINK1	PTEN induced kinase 1
4556	1,27E-35	3,49E+01	2,81E-36	0,0722	-12,5774309	-0,90846783	1979,8	TRNE	tRNA-Glu
56106	2,82E-04	3,55E+00	1,77E-04	0,2426	-3,7493777	-0,90945332	51,05	PCDHGA10	protocadherin gamma subfamily A, 10
83463	7,25E-85	8,41E+01	5,44E-86	0,0463	-19,653093	-0,91046143	2984,69	MXD3	MAX dimerization protein 3
79798	1,35E-27	2,69E+01	3,66E-28	0,0828	-11,0038995	-0,91064043	597,09	ARMC5	armadillo repeat containing 5
1347	1,20E-104	1,04E+02	6,27E-106	0,0417	-21,8598135	-0,91100398	5700,32	COX7A2	cytochrome c oxidase subunit 7A2
4259	2,50E-59	5,86E+01	3,23E-60	0,0557	-16,368062	-0,91116655	2244,89	MGST3	microsomal glutathione S-transferase 3
2582	1,73E-62	6,18E+01	2,08E-63	0,0542	-16,8095949	-0,91165281	3144,41	GALE	UDP-galactose-4-epimerase
51027	1,62E-03	2,79E+00	1,08E-03	0,279	-3,2691093	-0,91202397	39,14	BOLA1	bolA family member 1
2766	2,80E-41	4,06E+01	5,46E-42	0,0672	-13,5773349	-0,91207191	945,44	GMPR	guanosine monophosphate reductase
56099	9,98E-05	4,00E+00	6,06E-05	0,2274	-4,0105673	-0,91210436	59,59	PCDHGB7	protocadherin gamma subfamily B, 7
10899	6,72E-85	8,42E+01	5,03E-86	0,0464	-19,6570588	-0,91239654	2845,27	JTB	jumping translocation breakpoint
51374	4,87E-82	8,13E+01	3,86E-83	0,0472	-19,3170661	-0,91247894	5275,55	ATRAID	all-trans retinoic acid induced differentiation factor
84256	1,65E-24	2,38E+01	4,85E-25	0,0883	-10,3358853	-0,91287409	604,09	FLYWCH1	FLYWCH-type zinc finger 1
100852407	1,00E-25	2,50E+01	2,85E-26	0,0861	-10,6043128	-0,91316655	466,63	CARS1-AS1	CARS1 antisense RNA 1
811	9,83E-101	1,00E+02	5,50E-102	0,0426	-21,441354	-0,91319894	111479,59	CALR	calreticulin
84941	9,41E-07	6,03E+00	5,06E-07	0,1818	-5,0238445	-0,91341888	95,5	HSH2D	hematopoietic SH2 domain containing
91607	3,13E-03	2,50E+00	2,14E-03	0,2975	-3,0698557	-0,91343394	35,69	SLFN11	schlafen family member 11
1850	2,62E-07	6,58E+00	1,37E-07	0,1734	-5,269416	-0,91368333	105,27	DUSP8	dual specificity phosphatase 8
10422	2,25E-60	5,96E+01	2,85E-61	0,0554	-16,5151722	-0,91443369	1629,78	UBAC1	UBA domain containing 1
9130	2,60E-85	8,46E+01	1,93E-86	0,0464	-19,7055125	-0,91455891	5386,2	FAM50A	family with sequence similarity 50 member A
79641	6,26E-16	1,52E+01	2,35E-16	0,1115	-8,2024962	-0,91477519	306,05	ROGDI	rogdi atypical leucine zipper
493	6,26E-77	7,62E+01	5,56E-78	0,049	-18,6938315	-0,91522084	3130,3	ATP2B4	ATPase plasma membrane Ca2+ transporting 4
5152	1,26E-02	1,90E+00	9,08E-03	0,3508	-2,6090365	-0,91536044	30,3	PDE9A	phosphodiesterase 9A
284076	1,04E-01	9,83E-01	8,42E-02	0,5301	-1,7267207	-0,91540173	12,28	TTLL6	tubulin tyrosine ligase like 6
441108	6,26E-06	5,20E+00	3,53E-06	0,1975	-4,6375375	-0,91578742	88,01	IRF1-AS1	IRF1 antisense RNA 1
51043	1,22E-37	3,69E+01	2,57E-38	0,0708	-12,9431745	-0,91582675	1062,97	ZBTB7B	zinc finger and BTB domain containing 7B
115708	9,54E-31	3,00E+01	2,38E-31	0,0786	-11,6469025	-0,91595466	970,44	TRMT61A	tRNA methyltransferase 61A
51399	3,88E-86	8,54E+01	2,85E-87	0,0463	-19,8022574	-0,91608697	3160,1	TRAPPC4	trafficking protein particle complex subunit 4
1936	4,88E-55	5,43E+01	6,99E-56	0,0582	-15,7489227	-0,91623649	19532,11	EEF1D	eukaryotic translation elongation factor 1 delta
162466	7,40E-02	1,13E+00	5,86E-02	0,4846	-1,8909969	-0,91633015	14,07	PHOSPHO1	phosphoethanolamine/phosphocholine phosphatase 1
105378286	1,05E-03	2,98E+00	6,93E-04	0,2701	-3,3925064	-0,916482	41,2	LOC105378	uncharacterized LOC105378286
4294	2,44E-27	2,66E+01	6,63E-28	0,0837	-10,9501841	-0,91691255	601,35	MAP3K10	mitogen-activated protein kinase kinase kinase 10
2256	2,50E-03	2,60E+00	1,69E-03	0,2922	-3,1393903	-0,91744628	36,38	FGF11	fibroblast growth factor 11
55893	8,28E-81	8,01E+01	6,75E-82	0,0479	-19,1687877	-0,9175603	3446,32	ZNF395	zinc finger protein 395
6468	7,31E-40	3,91E+01	1,47E-40	0,0688	-13,3339758	-0,91772194	960,2	FBXW4	F-box and WD repeat domain containing 4
4694	3,30E-82	8,15E+01	2,61E-83	0,0475	-19,33735	-0,91783503	4746,95	NDUFA1	NADH:ubiquinone oxidoreductase subunit A1
219541	1,35E-48	4,79E+01	2,20E-49	0,0621	-14,7724708	-0,9178481	1158,08	MED19	mediator complex subunit 19
10813	2,42E-53	5,26E+01	3,58E-54	0,0592	-15,49796	-0,9179785	3237,28	UTP14A	UTP14A small subunit processome component
11070	2,10E-60	5,97E+01	2,67E-61	0,0556	-16,5192111	-0,91802409	2356,83	TMEM115	transmembrane protein 115
8972	9,11E-03	2,04E+00	6,52E-03	0,3375	-2,7206686	-0,91824385	27,18	MGAM	maltase-glucoamylase
25851	1,09E-28	2,80E+01	2,85E-29	0,0818	-11,2315892	-0,91825974	702	TECPR1	tectonin beta-propeller repeat containing 1
326625	1,95E-45	4,47E+01	3,46E-46	0,0644	-14,2681269	-0,91864878	970,89	MMAB	metabolism of cobalamin associated B
101928453	2,47E-03	2,61E+00	1,67E-03	0,2923	-3,1432544	-0,91880214	37,3	LOC101928	uncharacterized LOC101928453
105376843	7,56E-05	4,12E+00	4,55E-05	0,2254	-4,0776991	-0,91906583	62,87	SNHG25	small nucleolar RNA host gene 25
3383	5,06E-115	1,14E+02	2,21E-116	0,0401	-22,9324582	-0,91913695	11416,98	ICAM1	intercellular adhesion molecule 1
6490	5,26E-06	5,28E+00	2,95E-06	0,1968	-4,6743737	-0,91999041	78,62	PMEL	premelanosome protein
100037417	6,97E-37	3,62E+01	1,49E-37	0,0718	-12,807264	-0,92006811	775,7	DDTL	D-dopachrome tautomerase like
3163	3,26E-69	6,85E+01	3,40E-70	0,052	-17,7117565	-0,92034854	2569,6	HMOX2	heme oxygenase 2
5595	1,31E-61	6,09E+01	1,61E-62	0,0552	-16,6875672	-0,92047477	1987,45	MAPK3	mitogen-activated protein kinase 3
4791	4,31E-97	9,64E+01	2,58E-98	0,0438	-21,0442213	-0,92082733	4765,34	NFKB2	nuclear factor kappa B subunit 2
873	5,96E-76	7,52E+01	5,39E-77	0,0496	-18,5722868	-0,92126942	2233,65	CBR1	carbonyl reductase 1
105371795	1,26E-11	1,09E+01	5,45E-12	0,1337	-6,8934203	-0,9217343	191,65	LOC105371	uncharacterized LOC105371795
105373366	1,27E-05	4,90E+00	7,27E-06	0,2055	-4,485574	-0,92190976	73,44	IDS2	uncharacterized IDS2
81558	3,38E-09	8,47E+00	1,61E-09	0,1529	-6,0324466	-0,92208747	157,94	FAM117A	family with sequence similarity 117 member A
56953	3,41E-07	6,47E+00	1,79E-07	0,1767	-5,2197513	-0,92222645	104,92	NT5M	5',3'-nucleotidase, mitochondrial
399665	1,46E-55	5,48E+01	2,06E-56	0,0583	-15,825903	-0,92249602	2067,86	EEIG1	estrogen-induced osteoclastogenesis regulator 1
107984947	1,81E-11	1,07E+01	7,88E-12	0,1349	-6,8407055	-0,92273883	172,41	MED8-AS1	MED8 antisense RNA 1
107985872	2,65E-04	3,58E+00	1,67E-04	0,2451	-3,7650199	-0,9228063	57,24	LOC107985872	
122509	2,16E-32	3,17E+01	5,16E-33	0,0771	-11,9690218	-0,92309147	692,48	IFI27L1	interferon alpha inducible protein 27 like 1
2052	4,55E-38	3,73E+01	9,51E-39	0,0709	-13,0192331	-0,92338499	954,64	EPHX1	epoxide hydrolase 1
107986196	3,44E-02	1,46E+00	2,61E-02	0,4151	-2,2247083	-0,92349159	115,53	LOC107986	uncharacterized LOC107986196
5696	5,10E-90	8,93E+01	3,48E-91	0,0456	-20,2510357	-0,92361161	3153,91	PSMB8	proteasome 20S subunit beta 8
4943	3,20E-51	5,05E+01	4,93E-52	0,0609	-15,1781882	-0,9237985	1445,12	TBC1D25	TBC1 domain family member 25
50814	2,11E-60	5,97E+01	2,68E-61	0,0559	-16,5189789	-0,92381895	1789,21	NSDHL	NAD(P) dependent steroid dehydrogenase-like
1489	2,16E-22	2,17E+01	6,69E-23	0,0938	-9,8523796	-0,9238607	383,37	CTF1	cardiotrophin 1
401551	9,30E-18	1,70E+01	3,30E-18	0,1062	-8,7005594	-0,92386442	383,41	WDR38	WD repeat domain 38
4047	1,75E-62	6,18E+01	2,10E-63	0,055	-16,8088598	-0,92405596	3580,59	LSS	lanosterol synthase
4580	1,33E-50	4,99E+01	2,08E-51	0,0613	-15,0833544	-0,92414484	1407,94	MTX1	metaxin 1
6520	5,17E-80	7,93E+01	4,27E-81	0,0485	-19,0725485	-0,9243119	7545,08	SLC3A2	solute carrier family 3 member 2
65989	4,99E-18	1,73E+01	1,76E-18	0,1054	-8,7719293	-0,92433464	325,93	DLK2	delta like non-canonical Notch ligand 2
826	2,29E-78	7,76E+01	1,95E-79	0,049	-18,871568	-0,92437397	29511,19	CAPNS1	calpain small subunit 1
138428	9,11E-17	1,60E+01	3,33E-17	0,1096	-8,4343256	-0,92456897	282,85	PTRH1	peptidyl-tRNA hydrolase 1 homolog
768206	5,72E-04	3,24E+00	3,68E-04	0,2596	-3,5617874	-0,92465359	45,3	PRCD	photoreceptor disc component
100289373	1,47E-02	1,83E+00	1,07E-02	0,3625	-2,5518184	-0,92498763	22,64	UBAC2-AS1	UBAC2 antisense RNA 1
2872	1,43E-67	6,68E+01	1,54E-68	0,0529	-17,4958308	-0,92547489	2825,14	MKNK2	MAPK interacting serine/threonine kinase 2
871	3,46E-99	9,85E+01	1,99E-100	0,0435	-21,2736035	-0,92549452	9289,98	SERPINH1	serpin family H member 1
10298	2,81E-74	7,36E+01	2,61E-75	0,0504	-18,3627772	-0,92560476	2812,18	PAK4	p21 (RAC1) activated kinase 4
7260	1,68E-70	6,98E+01	1,69E-71	0,0518	-17,8798045	-0,92645434	2172,8	EIPR1	EARP complex and GARP complex interacting protein 1
55113	3,73E-40	3,94E+01	7,44E-41	0,0692	-13,3846322	-0,92652259	1010,39	XKR8	XK related 8
58526	7,34E-51	5,01E+01	1,14E-51	0,0613	-15,1230832	-0,92654961	1779,12	MID1IP1	MID1 interacting protein 1
90956	2,61E-35	3,46E+01	5,82E-36	0,074	-12,5198004	-0,92703939	719,23	ADCK2	aarF domain containing kinase 2
25979	2,57E-44	4,36E+01	4,67E-45	0,0658	-14,0853554	-0,92714873	1117,56	DHRS7B	dehydrogenase/reductase 7B
54504	1,04E-47	4,70E+01	1,73E-48	0,0634	-14,632839	-0,92716627	1352,24	CPVL	carboxypeptidase vitellogenic like
253982	2,11E-18	1,77E+01	7,33E-19	0,1046	-8,8696944	-0,9276783	359,18	ASPHD1	aspartate beta-hydroxylase domain containing 1
56129	3,90E-02	1,41E+00	2,98E-02	0,4272	-2,1721247	-0,92797167	16,97	PCDHB7	protocadherin beta 7
54868	3,59E-52	5,14E+01	5,43E-53	0,0606	-15,3222056	-0,92809882	2038,26	TMEM104	transmembrane protein 104
105378281	3,84E-04	3,42E+00	2,44E-04	0,253	-3,6687691	-0,92811692	48,04	LOC105378	uncharacterized LOC105378281
10868	1,27E-41	4,09E+01	2,46E-42	0,0681	-13,6356482	-0,92814114	1081,03	USP20	ubiquitin specific peptidase 20
100127888	4,69E-42	4,13E+01	8,97E-43	0,0677	-13,7089852	-0,92852951	956,24	SLCO4A1-A	SLCO4A1 antisense RNA 1
90231	1,08E-60	6,00E+01	1,36E-61	0,0561	-16,5596601	-0,92857766	3088,29	KIAA2013	KIAA2013
4901	8,48E-10	9,07E+00	3,95E-10	0,1484	-6,2560192	-0,92869742	146,75	NRL	neural retina leucine zipper
8329	6,95E-03	2,16E+00	4,91E-03	0,3303	-2,8128351	-0,92894251	29,06	H2AC13	H2A clustered histone 13
100532736	2,07E-49	4,87E+01	3,32E-50	0,0623	-14,8995157	-0,9289565	1601,92	MICOS10-NB	MICOS10-NBL1 readthrough
10538	3,63E-05	4,44E+00	2,14E-05	0,2186	-4,2499401	-0,92914774	75,5	BATF	basic leucine zipper ATF-like transcription factor
100132116	8,43E-05	4,07E+00	5,09E-05	0,2294	-4,0514256	-0,92920137	57,16	ACTA2-AS1	ACTA2 antisense RNA 1
55295	3,23E-25	2,45E+01	9,32E-26	0,0886	-10,492807	-0,92951621	544,51	KLHL26	kelch like family member 26
149773	2,58E-07	6,59E+00	1,35E-07	0,1765	-5,2722845	-0,93043445	121,9	APCDD1L-D	APCDD1L divergent transcript
977	2,53E-58	5,76E+01	3,35E-59	0,0574	-16,2250487	-0,93061267	10731,33	CD151	CD151 molecule (Raph blood group)
54913	2,95E-56	5,55E+01	4,09E-57	0,0584	-15,9274201	-0,93084883	1277,4	RPP25	ribonuclease P and MRP subunit p25
28595	3,86E-02	1,41E+00	2,95E-02	0,4277	-2,1767052	-0,9309605	17,1	TRBV7-3	T cell receptor beta variable 7-3
716	1,32E-10	9,88E+00	5,96E-11	0,1423	-6,5447513	-0,9310672	160,3	C1S	complement C1s
140465	8,00E-46	4,51E+01	1,41E-46	0,065	-14,3307855	-0,93127813	1911,38	MYL6B	myosin light chain 6B
83719	2,37E-19	1,86E+01	8,05E-20	0,1023	-9,1125257	-0,93188105	328,32	YPEL3	yippee like 3
11253	2,36E-75	7,46E+01	2,15E-76	0,0504	-18,4977798	-0,93206719	6058,62	MAN1B1	mannosidase alpha class 1B member 1
400512	1,22E-01	9,14E-01	9,93E-02	0,5655	-1,6483106	-0,93214042	9,35	NSMCE1-DT	NSMCE1 divergent transcript
102724800	1,50E-02	1,82E+00	1,09E-02	0,3663	-2,5456871	-0,93243313	22,66	LOC102724	uncharacterized LOC102724800
53349	2,74E-52	5,16E+01	4,13E-53	0,0608	-15,339964	-0,93244983	1225,91	ZFYVE1	zinc finger FYVE-type containing 1
51078	1,21E-57	5,69E+01	1,63E-58	0,0578	-16,1276867	-0,93250224	2093,16	THAP4	THAP domain containing 4
55150	4,17E-03	2,38E+00	2,88E-03	0,313	-2,9798465	-0,93256905	31,02	C19orf73	chromosome 19 open reading frame 73

2353	3,90E-07	6,41E+00	2,06E-07	0,1796	-5,1940748	-0,93272941	100,38	FOS	Fos proto-oncogene, AP-1 transcription factor subunit
7311	4,42E-81	8,04E+01	3,58E-82	0,0486	-19,2016825	-0,93296236	31483,92	UBA52	ubiquitin A-52 residue ribosomal protein fusion product 1
1293	2,83E-71	7,05E+01	2,81E-72	0,0519	-17,9796484	-0,93311388	1887,5	COL6A3	collagen type VI alpha 3 chain
339229	3,54E-23	2,25E+01	1,08E-23	0,093	-10,0343336	-0,93313575	425,69	OXLD1	oxidoreductase like domain containing 1
112869	2,79E-31	3,06E+01	6,87E-32	0,0794	-11,7523721	-0,93322794	610,39	SGF29	SAGA complex associated factor 29
90203	1,26E-47	4,69E+01	2,11E-48	0,0639	-14,6196394	-0,93378747	1237,86	SNX21	sorting nexin family member 21
79036	4,44E-65	6,44E+01	5,04E-66	0,0544	-17,1628353	-0,93418171	6650,9	KXD1	KxDL motif containing 1
3921	2,02E-137	1,37E+02	5,91E-139	0,0372	-25,0931036	-0,93427631	45741,18	RPSA	ribosomal protein SA
7917	2,36E-102	1,02E+02	1,29E-103	0,0432	-21,6151321	-0,93454092	28655,83	BAG6	BAG cochaperone 6
55277	3,40E-07	6,47E+00	1,79E-07	0,179	-5,2201554	-0,93456248	101,14	FGGY	FGGY carbohydrate kinase domain containing
441204	3,22E-02	1,49E+00	2,43E-02	0,415	-2,2520507	-0,93462073	17,19	LINC02981	long intergenic non-protein coding RNA 2981
4207	4,11E-14	1,34E+01	1,64E-14	0,1218	-7,6762583	-0,93508312	247,77	BORCS8-ME	BORCS8-MEF2B readthrough
64866	1,12E-152	1,52E+02	2,63E-154	0,0353	-26,462314	-0,93516047	24886,12	CDCP1	CUB domain containing protein 1
94120	1,40E-37	3,69E+01	2,96E-38	0,0723	-12,9321916	-0,9351741	741,16	SYTL3	synaptotagmin like 3
27343	3,58E-37	3,64E+01	7,63E-38	0,0727	-12,8592564	-0,93529632	804,15	POLL	DNA polymerase lambda
114818278	1,00E-03	3,00E+00	6,57E-04	0,2746	-3,4067153	-0,93537503	41,45	ZNF71-SMIM	ZNF71-SMIM17 readthrough (NMD candidate)
28511	2,01E-78	7,77E+01	1,71E-79	0,0496	-18,8785735	-0,93562539	3552,37	NKIRAS2	NFKB inhibitor interacting Ras like 2
1523	9,13E-103	1,02E+02	4,93E-104	0,0432	-21,6596788	-0,93576192	4037,73	CUX1	cut like homeobox 1
64114	3,35E-115	1,14E+02	1,46E-116	0,0408	-22,9505318	-0,93584054	6759,56	TMBIM1	transmembrane BAX inhibitor motif containing 1
10155	5,00E-83	8,23E+01	3,88E-84	0,0482	-19,4353408	-0,93584383	18058,24	TRIM28	tripartite motif containing 28
7453	2,97E-124	1,24E+02	1,10E-125	0,0392	-23,846566	-0,93592262	8949,41	WARS1	tryptophanyl-tRNA synthetase 1
6235	1,85E-78	7,77E+01	1,58E-79	0,0496	-18,8828611	-0,93599774	11880,59	RPS29	ribosomal protein S29
8704	3,71E-61	6,04E+01	4,63E-62	0,0563	-16,6244719	-0,93611981	2864,66	B4GALT2	beta-1,4-galactosyltransferase 2
10273	5,19E-55	5,43E+01	7,42E-56	0,0595	-15,7450813	-0,93616367	2298,51	STUB1	STIP1 homology and U-box containing protein 1
100170841	3,43E-46	4,55E+01	5,96E-47	0,0651	-14,390272	-0,93677311	1134,95	EPOP	elongin BC and polycomb repressive complex 2 associated protein
6282	3,74E-90	8,94E+01	2,54E-91	0,0462	-20,26648	-0,93713184	20404,59	S100A11	S100 calcium binding protein A11
128439	7,91E-16	1,51E+01	2,99E-16	0,1147	-8,1738428	-0,93739933	273,15	SNHG11	small nucleolar RNA host gene 11
10384	3,33E-49	4,85E+01	5,36E-50	0,0631	-14,8674629	-0,93773357	1042,6	BTN3A3	butyrophilin subfamily 3 member A3
84572	1,97E-37	3,67E+01	4,18E-38	0,0727	-12,905765	-0,93799266	830,07	GNPTG	N-acetylglucosamine-1-phosphate transferase subunit gamma
59	5,70E-10	9,24E+00	2,64E-10	0,1485	-6,3187323	-0,93802617	144,53	ACTA2	actin alpha 2, smooth muscle
26160	8,07E-45	4,41E+01	1,45E-45	0,0662	-14,167584	-0,93831834	1311,88	IFT172	intraflagellar transport 172
64319	4,61E-72	7,13E+01	4,50E-73	0,0519	-18,0809381	-0,93837442	3215,89	FBRS	fibrosin
107986125	1,89E-02	1,72E+00	1,39E-02	0,3815	-2,4599324	-0,93846585	22,29	LINC02034	long intergenic non-protein coding RNA 2034
26811	2,96E-01	5,29E-01	2,58E-01	0,8294	-1,1314862	-0,93850559	66,3	SNORD55	small nucleolar RNA, C/D box 55
4041	2,51E-85	8,46E+01	1,87E-86	0,0476	-19,7072674	-0,93903237	6611,97	LRP5	LDL receptor related protein 5
60673	3,92E-40	3,94E+01	7,84E-41	0,0702	-13,3807131	-0,93949373	1023,93	ATG101	autophagy related 101
4037	3,58E-05	4,45E+00	2,11E-05	0,2209	-4,2532622	-0,93969556	65,48	LRP3	LDL receptor related protein 3
102725238	5,45E-18	1,73E+01	1,92E-18	0,1073	-8,7617788	-0,93975682	401,06	LOC1027252	uncharacterized LOC102725238
53615	1,70E-59	5,88E+01	2,19E-60	0,0574	-16,3917932	-0,94105243	3777,98	MBD3	methyl-CpG binding domain protein 3
5678	3,12E-02	1,51E+00	2,35E-02	0,4163	-2,2649294	-0,94287793	19,01	PSG9	pregnancy specific beta-1-glycoprotein 9
51703	1,13E-108	1,08E+02	5,43E-110	0,0423	-22,2827681	-0,9429598	6460,98	ACSL5	acyl-CoA synthetase long chain family member 5
100303728	1,54E-43	4,28E+01	2,86E-44	0,0676	-13,9567136	-0,94305429	2247,4	SLC25A5-AS	SLC25A5 antisense RNA 1
51016	9,73E-31	3,00E+01	2,43E-31	0,081	-11,6451598	-0,94305505	541,22	EMC9	ER membrane protein complex subunit 9
5704	5,13E-130	1,29E+02	1,67E-131	0,0386	-24,4008578	-0,94306319	7703,16	PSMC4	proteasome 26S subunit, ATPase 4
602	4,25E-36	3,54E+01	9,28E-37	0,0745	-12,6646501	-0,94334092	952,42	BCL3	BCL3 transcription coactivator
201299	4,27E-04	3,37E+00	2,72E-04	0,2591	-3,6407041	-0,94337527	46,19	RDM1	RAD52 motif containing 1
1174	1,18E-88	8,79E+01	8,29E-90	0,047	-20,0942352	-0,94394613	2671,61	AP1S1	adaptor related protein complex 1 subunit sigma 1
6156	3,96E-93	9,24E+01	2,56E-94	0,0458	-20,6034349	-0,94459677	23092,2	RPL30	ribosomal protein L30
4726	5,41E-46	4,53E+01	9,44E-47	0,0658	-14,3583643	-0,94480029	1885,76	NDUFS6	NADH:ubiquinone oxidoreductase subunit S6
7040	4,46E-84	8,34E+01	3,40E-85	0,0483	-19,5598326	-0,94494542	4299,93	TGFB1	transforming growth factor beta 1
100422894	2,70E-25	2,46E+01	7,77E-26	0,0899	-10,510035	-0,94511013	504,55	MIR4260	microRNA 4260
101927609	7,50E-02	1,12E+00	5,95E-02	0,5018	-1,8846264	-0,94561429	13,24	LOC101927(	uncharacterized LOC101927609
254359	7,92E-26	2,51E+01	2,24E-26	0,089	-10,6264625	-0,94565535	450,04	ZDHHC24	zinc finger DHHC-type containing 24
57143	1,67E-10	9,78E+00	7,58E-11	0,1453	-6,5087343	-0,94577282	152,44	ADCK1	aarF domain containing kinase 1
23140	7,06E-68	6,72E+01	7,54E-69	0,0539	-17,5365582	-0,94577564	2181,62	ZZEF1	zinc finger ZZ-type and EF-hand domain containing 1
23589	6,45E-68	6,72E+01	6,88E-69	0,0539	-17,5416944	-0,94625865	1959,49	CARHSP1	calcium regulated heat stable protein 1
374659	3,90E-31	3,04E+01	9,65E-32	0,0807	-11,7236209	-0,94648025	596,11	HDDC3	HD domain containing 3
155368	1,64E-04	3,79E+00	1,01E-04	0,2435	-3,888515	-0,94687683	57,06	METTL27	methyltransferase like 27
219731	1,24E-08	7,91E+00	6,06E-09	0,163	-5,815013	-0,94770913	122,16	PROSER2-A	PROSER2 antisense RNA 1
7384	2,33E-95	9,46E+01	1,44E-96	0,0455	-20,8525922	-0,94779735	6224,82	UQCRC1	ubiquinol-cytochrome c reductase core protein 1
286257	2,32E-47	4,66E+01	3,91E-48	0,065	-14,5774867	-0,94787441	1052,18	PAXX	PAXX non-homologous end joining factor
54867	6,62E-92	9,12E+01	4,38E-93	0,0463	-20,4654219	-0,94796377	4824,26	TMEM214	transmembrane protein 214
22827	3,43E-71	7,05E+01	3,41E-72	0,0528	-17,9688975	-0,94813212	8003,05	PUF60	poly(U) binding splicing factor 60
105378481	7,56E-02	1,12E+00	6,00E-02	0,5042	-1,8809284	-0,94838023	11,93	DUSP5-DT	DUSP5 divergent transcript
10501	3,78E-35	3,44E+01	8,46E-36	0,0759	-12,4900118	-0,94850062	775,07	SEMA6B	semaphorin 6B
55626	2,29E-53	5,26E+01	3,38E-54	0,0612	-15,5016213	-0,94852274	1607,39	AMBRA1	autophagy and beclin 1 regulator 1
105376805	7,83E-08	7,11E+00	3,98E-08	0,1728	-5,4915944	-0,94896019	106,76	LOC105376(	uncharacterized LOC105376805
100526825	5,91E-08	7,23E+00	2,99E-08	0,1713	-5,5421728	-0,94924633	111,73	INMT-MINDY	INMT-MINDY4 readthrough (NMD candidate)
29952	5,95E-45	4,42E+01	1,07E-45	0,0669	-14,1893632	-0,94978537	2417,68	DPP7	dipeptidyl peptidase 7
57716	2,75E-13	1,26E+01	1,12E-13	0,1279	-7,4256433	-0,94990448	208,16	PRX	periaxin
83746	2,56E-46	4,56E+01	4,44E-47	0,0659	-14,4106517	-0,95003375	936,93	L3MBTL2	L3MBTL histone methyl-lysine binding protein 2
3145	3,33E-83	8,25E+01	2,58E-84	0,0488	-19,4562454	-0,95004862	2987,85	HMBS	hydroxymethylbilane synthase
9645	1,56E-160	1,60E+02	3,31E-162	0,035	-27,1401758	-0,95046747	18870,81	MICAL2	microtubule associated monooxygenase, calponin and LIM domain containing 2
6510	3,86E-121	1,20E+02	1,50E-122	0,0404	-23,5424652	-0,95069906	11680,5	SLC1A5	solute carrier family 1 member 5
26270	2,64E-06	5,58E+00	1,45E-06	0,1974	-4,8176485	-0,95077914	82,88	FBXO6	F-box protein 6
101929470	6,47E-03	2,19E+00	4,56E-03	0,3352	-2,8366358	-0,95097535	26,57	LOC1019294	uncharacterized LOC101929470
10587	8,42E-25	2,41E+01	2,45E-25	0,0914	-10,4011258	-0,95106695	533,48	TXNRD2	thioredoxin reductase 2
93210	9,22E-18	1,70E+01	3,28E-18	0,1094	-8,7014796	-0,95167179	315,36	PGAP3	post-GPI attachment to proteins phospholipase 3
5050	4,91E-50	4,93E+01	7,77E-51	0,0635	-14,9962251	-0,95171081	1479,84	PAFAH1B3	platelet activating factor acetylhydrolase 1b catalytic subunit 3
387066	5,02E-97	9,63E+01	3,01E-98	0,0452	-21,0368958	-0,95183591	4332,43	SNHG5	small nucleolar RNA host gene 5
8625	5,17E-51	5,03E+01	8,00E-52	0,0628	-15,1464232	-0,95185225	1804,01	RFXANK	regulatory factor X associated ankyrin containing protein
1945	8,10E-14	1,31E+01	3,26E-14	0,1255	-7,5875938	-0,9518686	202,2	EFNA4	ephrin A4
100289098	3,47E-04	3,46E+00	2,20E-04	0,2576	-3,6952668	-0,9519669	48,61	LINC03011	long intergenic non-protein coding RNA 3011
7849	3,07E-25	2,45E+01	8,86E-26	0,0907	-10,4976475	-0,95205682	448,29	PAX8	paired box 8
7511	2,39E-95	9,46E+01	1,48E-96	0,0457	-20,8513693	-0,95208195	3305,88	XPNPEP1	X-prolyl aminopeptidase 1
152302	4,67E-25	2,43E+01	1,35E-25	0,0911	-10,4575115	-0,9521636	587,8	CIDECP1	CIDEC pseudogene 1
654364	1,32E-128	1,28E+02	4,41E-130	0,0392	-24,2666403	-0,95216928	17073,4	NME1-NME2	NME1-NME2 readthrough
112770	4,46E-65	6,44E+01	5,07E-66	0,0555	-17,1625163	-0,95233407	2596,25	GLMP	glycosylated lysosomal membrane protein
146691	2,06E-64	6,37E+01	2,37E-65	0,0558	-17,0725959	-0,9523469	2098,25	TOM1L2	target of myb1 like 2 membrane trafficking protein
196872	1,82E-04	3,74E+00	1,13E-04	0,2467	-3,861523	-0,95248549	55,73	LINC00638	long intergenic non-protein coding RNA 638
83546	2,64E-03	2,58E+00	1,79E-03	0,3052	-3,1226081	-0,95296352	34,61	RTBDN	retbindin
3292	1,62E-18	1,78E+01	5,64E-19	0,1071	-8,898974	-0,95306884	285,73	HSD17B1	hydroxysteroid 17-beta dehydrogenase 1
55957	5,41E-23	2,23E+01	1,65E-23	0,0954	-9,9918363	-0,95309669	470,84	LIN37	lin-37 DREAM MuvB core complex component
100506046	1,81E-07	6,74E+00	9,37E-08	0,1785	-5,3385716	-0,95315831	103,23	GAS5-AS1	GAS5 antisense RNA 1
127281	5,50E-63	6,23E+01	6,54E-64	0,0565	-16,8779728	-0,95378016	2420,74	PRXL2B	peroxiredoxin like 2B
26207	2,65E-41	4,06E+01	5,17E-42	0,0702	-13,5813548	-0,95408319	952,96	PITPNC1	phosphatidylinositol transfer protein cytoplasmic 1
5524	7,14E-86	8,51E+01	5,26E-87	0,0483	-19,771285	-0,95497323	5388,93	PTPA	protein phosphatase 2 phosphatase activator
91582	4,18E-49	4,84E+01	6,77E-50	0,0643	-14,8517956	-0,95515064	1633,19	RPS19BP1	ribosomal protein S19 binding protein 1
4701	2,37E-11	1,06E+01	1,04E-11	0,1405	-6,801262	-0,95524061	1677,4	NDUFA7	NADH:ubiquinone oxidoreductase subunit A7
84182	3,96E-08	7,40E+00	1,98E-08	0,1702	-5,6133457	-0,95528326	112,86	MINDY4	MINDY lysine 48 deubiquitinase 4
9491	6,02E-113	1,12E+02	2,68E-114	0,042	-22,7226353	-0,95536889	7039,26	PSMF1	proteasome inhibitor subunit 1
100874530	8,76E-14	1,31E+01	3,53E-14	0,1261	-7,5773973	-0,95576528	200,89	APOBEC3B-	APOBEC3B antisense RNA 1
8775	4,56E-77	7,63E+01	4,04E-78	0,0511	-18,7108273	-0,95636642	3613,97	NAPA	NSF attachment protein alpha
8829	2,55E-122	1,22E+02	9,77E-124	0,0404	-23,6579829	-0,95649087	20259,57	NRP1	neuropilin 1
5032	2,99E-26	2,55E+01	8,39E-27	0,0893	-10,7179152	-0,95662982	690,87	P2RY11	purinergic receptor P2Y11
1186	1,64E-47	4,68E+01	2,75E-48	0,0655	-14,6014127	-0,95666807	2322,26	CLCN7	chloride voltage-gated channel 7
55593	2,46E-94	9,36E+01	1,56E-95	0,0461	-20,7385124	-0,95693261	3009,49	OTUD5	OTU deubiquitinase 5
84303	6,38E-23	2,22E+01	1,96E-23	0,0959	-9,9752852	-0,95696288	405,15	CHCHD6	coiled-coil-helix-coiled-coil-helix domain containing 6
2356	1,62E-55	5,48E+01	2,29E-56	0,0605	-15,8192442	-0,95696382	3228,13	FPGS	folylpolyglutamate synthase
90324	8,12E-77	7,61E+01	7,23E-78	0,0513	-18,6797874	-0,95811969	1971,27	CCDC97	coiled-coil domain containing 97
79143	5,09E-91	9,03E+01	3,40E-92	0,047	-20,3652642	-0,95817094	6777,55	MBOAT7	membrane bound O-acyltransferase domain containing 7
6536	7,06E-36	3,52E+01	1,55E-36	0,076	-12,624146	-0,95899397	788,84	SLC6A9	solute carrier family 6 member 9
79720	1,75E-92	9,18E+01	1,15E-93	0,0467	-20,5305709	-0,95932297	4403,39	VPS37B	VPS37B subunit of ESCRT-I
284029	1,20E-04	3,92E+00	7,30E-05	0,2419	-3,9663663	-0,95944275	53,65	LINC00324	long intergenic non-protein coding RNA 324
6337	3,84E-22	2,14E+01	1,20E-22	0,098	-9,7936435	-0,95954972	357,14	SCNN1A	sodium channel epithelial 1 subunit alpha
80148	1,83E-31	3,07E+01	4,47E-32	0,0814	-11,7885931	-0,95963314	725,75	SLC66A2	solute carrier family 66 member 2
57020	2,70E-74	7,36E+01	2,51E-75	0,0523	-18,3648548	-0,95975068	2001,75	VPS35L	VPS35 endosomal protein sorting factor like
83931	4,10E-80	7,94E+01	3,38E-81	0,0503	-19,0847301	-0,95987661	5916,18	STK40	serine/threonine kinase 40
25833	5,60E-02	1,25E+00	4,37E-02	0,4761	-2,0166497	-0,96015613	13,49	POU2F3	POU class 2 homeobox 3
10975	6,32E-74	7,32E+01	5,91E-75	0,0524	-18,3183219	-0,96027576	2552,91	UQCR11	ubiquinol-cytochrome c reductase, complex III subunit XI

2193	2,76E-63	6,26E+01	3,25E-64	0,0568	-16,9191043	-0,96054557	9169,1	FARSA	phenylalanyl-tRNA synthetase subunit alpha
8662	4,91E-156	1,55E+02	1,11E-157	0,0359	-26,7541381	-0,96077123	16055,02	EIF3B	eukaryotic translation initiation factor 3 subunit B
10509	1,14E-62	6,19E+01	1,37E-63	0,0571	-16,8343514	-0,96135907	2898,76	SEMA4B	semaphorin 4B
23328	3,43E-65	6,45E+01	3,89E-66	0,056	-17,1778751	-0,96148258	1725,67	SASH1	SAM and SH3 domain containing 1
7045	2,15E-98	9,77E+01	1,26E-99	0,0454	-21,1869705	-0,96152439	3714,88	TGFBI	transforming growth factor beta induced
55223	2,07E-19	1,87E+01	6,99E-20	0,1053	-9,1278396	-0,96152627	373,61	TRIM62	tripartite motif containing 62
400236	1,12E-03	2,95E+00	7,35E-04	0,2849	-3,3762335	-0,96188054	38,09	FOXN3-AS1	FOXN3 antisense RNA 1
79065	2,78E-62	6,16E+01	3,36E-63	0,0573	-16,7810624	-0,96210354	3410,55	ATG9A	autophagy related 9A
2768	7,60E-93	9,21E+01	4,95E-94	0,0468	-20,5714454	-0,9621345	5341,63	GNA12	G protein subunit alpha 12
5864	1,11E-15	1,50E+01	4,20E-16	0,1184	-8,1327252	-0,96251358	242,97	RAB3A	RAB3A, member RAS oncogene family
440359	3,79E-06	5,42E+00	2,11E-06	0,2029	-4,7429202	-0,96251843	78,46	YBX3P1	Y-box binding protein 3 pseudogene 1
107987223	1,64E-03	2,79E+00	1,10E-03	0,2948	-3,2646998	-0,96251869	37,1	LOC107987	uncharacterized LOC107987223
54472	5,80E-73	7,22E+01	5,55E-74	0,0529	-18,1959824	-0,96255121	2545,54	TOLLIP	toll interacting protein
5155	5,03E-02	1,30E+00	3,90E-02	0,4664	-2,0636726	-0,96255329	15,63	PDGFB	platelet derived growth factor subunit B
83637	2,43E-89	8,86E+01	1,68E-90	0,0477	-20,1732118	-0,96262883	4641,62	ZMIZ2	zinc finger MIZ-type containing 2
541578	3,26E-59	5,85E+01	4,24E-60	0,0589	-16,3515949	-0,96271015	1373,97	EOLA2	endothelium and lymphocyte associated ASCH domain 2
10423	2,00E-48	4,77E+01	3,29E-49	0,0653	-14,7454707	-0,962893	1330,42	CDIPT	CDP-diacylglycerol--inositol 3-phosphatidyltransferase
645432	1,27E-13	1,29E+01	5,16E-14	0,1279	-7,527932	-0,96293527	264,93	ARRDC5	arrestin domain containing 5
100526760	3,75E-36	3,54E+01	8,18E-37	0,076	-12,6745855	-0,96371858	868,45	ABHD14A-A	ABHD14A-ACY1 readthrough
10848	2,75E-71	7,06E+01	2,73E-72	0,0536	-17,9813218	-0,96389103	2096,96	PPP1R13L	protein phosphatase 1 regulatory subunit 13 like
107986852	2,22E-03	2,65E+00	1,50E-03	0,3038	-3,1749474	-0,96446174	37,73	LOC107986	uncharacterized LOC107986852
347734	8,16E-97	9,61E+01	4,92E-98	0,0459	-21,0136869	-0,96451611	6844,79	SLC35B2	solute carrier family 35 member B2
7936	8,05E-113	1,12E+02	3,59E-114	0,0425	-22,7097063	-0,96500576	6271,17	NELFE	negative elongation factor complex member E
100288805	1,68E-02	1,77E+00	1,23E-02	0,3857	-2,5038509	-0,965715	19,95	HYDIN2	HYDIN axonemal central pair apparatus protein 2 (pseudogene)
6143	2,14E-127	1,27E+02	7,39E-129	0,04	-24,1504518	-0,96572765	50926,4	RPL19	ribosomal protein L19
26521	1,77E-69	6,88E+01	1,82E-70	0,0544	-17,7467964	-0,96581587	1778,7	TIMM8B	translocase of inner mitochondrial membrane 8 homolog B
9380	2,71E-80	7,96E+01	2,22E-81	0,0506	-19,1066241	-0,96595817	3747,8	GRHPR	glyoxylate and hydroxypyruvate reductase
285556	7,51E-02	1,12E+00	5,95E-02	0,5129	-1,8841346	-0,96635981	11,96	C4orf54	chromosome 4 open reading frame 54
10476	5,41E-119	1,18E+02	2,19E-120	0,0414	-23,330148	-0,96635986	5077,15	ATP5PD	ATP synthase peripheral stalk subunit d
440093	6,33E-10	9,20E+00	2,93E-10	0,1533	-6,3022895	-0,96641681	145,91	H3-5	H3.5 histone
284948	4,44E-02	1,35E+00	3,42E-02	0,4564	-2,1176358	-0,96655297	14,28	SH2D6	SH2 domain containing 6
344967	9,02E-03	2,04E+00	6,45E-03	0,3549	-2,7241899	-0,96691225	24,65	LOC344967	acyl-CoA thioesterase 7 pseudogene
29988	4,12E-23	2,24E+01	1,25E-23	0,0965	-10,0192328	-0,96695964	362,72	SLC2A8	solute carrier family 2 member 8
3064	8,12E-106	1,05E+02	4,12E-107	0,044	-21,9838025	-0,96704181	4368,27	HTT	huntingtin
107080644	1,89E-48	4,77E+01	3,11E-49	0,0656	-14,7492069	-0,96710834	972,81	CNPY3-GNM	CNPY3-GNMT readthrough
23396	1,05E-58	5,80E+01	1,38E-59	0,0594	-16,2794164	-0,96716261	1468,81	PIP5K1C	phosphatidylinositol-4-phosphate 5-kinase type 1 gamma
368	1,04E-03	2,98E+00	6,85E-04	0,2848	-3,3955793	-0,96719987	38,48	ABCC6	ATP binding cassette subfamily C member 6
25930	3,69E-77	7,64E+01	3,26E-78	0,0517	-18,7222648	-0,96744657	4318,38	PTPN23	protein tyrosine phosphatase non-receptor type 23
1366	4,42E-71	7,04E+01	4,42E-72	0,0539	-17,9545194	-0,96810264	1787,41	CLDN7	claudin 7
146754	3,26E-61	6,05E+01	4,07E-62	0,0582	-16,6322593	-0,96830136	2335,86	DNAH2	dynein axonemal heavy chain 2
94137	1,70E-07	6,77E+00	8,81E-08	0,181	-5,3497508	-0,9685588	96,57	RP1L1	RP1 like 1
112267874	8,67E-06	5,06E+00	4,93E-06	0,2121	-4,5679003	-0,96868337	72,7	LOC112267	replaced by ID 105378948
64981	1,42E-88	8,78E+01	9,99E-90	0,0482	-20,0849557	-0,96874398	2604,27	MRPL34	mitochondrial ribosomal protein L34
29903	1,42E-47	4,68E+01	2,38E-48	0,0663	-14,6112741	-0,96904891	959,72	CCDC106	coiled-coil domain containing 106
56970	1,54E-91	9,08E+01	1,02E-92	0,0474	-20,4241995	-0,96905642	4154,21	ATXN7L3	ataxin 7 like 3
10908	3,82E-70	6,94E+01	3,89E-71	0,0543	-17,8333434	-0,96911385	6385,34	PNPLA6	patatin like phospholipase domain containing 6
56113	3,17E-05	4,50E+00	1,86E-05	0,2264	-4,2805405	-0,96916897	59,06	PCDHGA2	protocadherin gamma subfamily A, 2
6904	6,42E-87	8,62E+01	4,66E-88	0,0487	-19,8932136	-0,96958168	4299,69	TBCD	tubulin folding cofactor D
4314	9,24E-07	6,03E+00	4,97E-07	0,1929	-5,027538	-0,96968842	90,23	MMP3	matrix metallopeptidase 3
5571	9,25E-99	9,80E+01	5,39E-100	0,0457	-21,2269103	-0,96974395	3268,32	PRKAG1	protein kinase AMP-activated non-catalytic subunit gamma 1
55361	1,85E-73	7,27E+01	1,74E-74	0,0531	-18,2593124	-0,96996868	2353,61	PI4K2A	phosphatidylinositol 4-kinase type 2 alpha
105372926	2,97E-02	1,53E+00	2,24E-02	0,4247	-2,2839534	-0,96998004	16,77	LOC105372	uncharacterized LOC105372926
84286	5,06E-26	2,53E+01	1,43E-26	0,0909	-10,6686993	-0,97012243	471,28	TMEM175	transmembrane protein 175
10581	5,02E-56	5,53E+01	7,00E-57	0,061	-15,8937295	-0,97020072	3033	IFITM2	interferon induced transmembrane protein 2
23400	4,94E-73	7,23E+01	4,72E-74	0,0533	-18,2048902	-0,97030227	3798,4	ATP13A2	ATPase cation transporting 13A2
54434	1,89E-119	1,19E+02	7,53E-121	0,0415	-23,3757981	-0,97046248	5272,59	SSH1	slingshot protein phosphatase 1
833	2,24E-103	1,03E+02	1,19E-104	0,0447	-21,7249356	-0,97049088	4357,94	CARS1	cysteinyl-tRNA synthetase 1
8572	3,10E-31	3,05E+01	7,63E-32	0,0827	-11,7434577	-0,9706276	737,2	PDLIM4	PDZ and LIM domain 4
6835	1,96E-34	3,37E+01	4,47E-35	0,0786	-12,3568243	-0,97146054	858,42	SURF2	surfeit 2
126075	1,87E-06	5,73E+00	1,03E-06	0,1988	-4,8866793	-0,97149942	77,35	CCDC159	coiled-coil domain containing 159
3476	1,78E-89	8,87E+01	1,23E-90	0,0481	-20,1889031	-0,97177316	2545,53	IGBP1	immunoglobulin binding protein 1
155066	1,06E-56	5,60E+01	1,45E-57	0,0608	-15,9920368	-0,97212662	2050,2	ATP6V0E2	ATPase H+ transporting V0 subunit e2
5878	3,29E-75	7,45E+01	3,01E-76	0,0526	-18,4796468	-0,9721945	9963,6	RAB5C	RAB5C, member RAS oncogene family
10227	2,81E-51	5,06E+01	4,33E-52	0,0641	-15,186755	-0,97298763	2207,56	MFSD10	major facilitator superfamily domain containing 10
56105	2,08E-04	3,68E+00	1,29E-04	0,2542	-3,8276224	-0,97312384	46,33	PCDHGA11	protocadherin gamma subfamily A, 11
9520	6,20E-108	1,07E+02	3,02E-109	0,0438	-22,2057819	-0,97314645	5612,43	NPEPPS	aminopeptidase puromycin sensitive
10552	5,27E-111	1,10E+02	2,43E-112	0,0432	-22,5237255	-0,97318148	5244,5	ARPC1A	actin related protein 2/3 complex subunit 1A
84872	4,79E-24	2,33E+01	1,43E-24	0,0951	-10,2318654	-0,97345867	417,11	ZC3H10	zinc finger CCCH-type containing 10
5618	1,22E-08	7,91E+00	5,98E-09	0,1674	-5,8173163	-0,9736438	113,43	PRLR	prolactin receptor
11267	2,22E-106	1,06E+02	1,11E-107	0,0442	-22,0432378	-0,97365954	4343,74	SNF8	SNF8 subunit of ESCRT-II
6224	2,68E-119	1,19E+02	1,08E-120	0,0417	-23,3604776	-0,97369892	15045,15	RPS20	ribosomal protein S20
221393	1,21E-09	8,92E+00	5,69E-10	0,1571	-6,1986597	-0,97388611	135,29	ADGRF4	adhesion G protein-coupled receptor F4
100859930	2,02E-37	3,67E+01	4,27E-38	0,0755	-12,904027	-0,97389956	692,78	HEIH	hepatocellular carcinoma up-regulated EZH2-associated long non-coding RNA
6786	1,26E-86	8,59E+01	9,21E-88	0,049	-19,85903	-0,97402102	3026,23	STIM1	stromal interaction molecule 1
3418	2,00E-47	4,67E+01	3,36E-48	0,0668	-14,5876803	-0,97477464	1007,58	IDH2	isocitrate dehydrogenase (NADP(+)) 2
107984948	4,80E-02	1,32E+00	3,71E-02	0,4678	-2,0842727	-0,97491876	14,24	LOC107984	uncharacterized LOC107984948
23457	1,70E-32	3,18E+01	4,06E-33	0,0813	-11,9888762	-0,97511491	651,16	ABCB9	ATP binding cassette subfamily B member 9
79002	2,32E-126	1,26E+02	8,19E-128	0,0406	-24,0508083	-0,97539045	8676,77	TRIR	telomerase RNA component interacting RNase
1611	5,93E-120	1,19E+02	2,34E-121	0,0416	-23,4256381	-0,97541095	16821,73	DAP	death associated protein
10291	8,70E-126	1,25E+02	3,11E-127	0,0407	-23,9953845	-0,97662217	7884,75	SF3A1	splicing factor 3a subunit 1
6623	3,24E-07	6,49E+00	1,70E-07	0,1868	-5,229808	-0,97673798	91,8	SNCG	synuclein gamma
55160	7,94E-18	1,71E+01	2,81E-18	0,1121	-8,7187791	-0,97718936	290,89	ARHGEF10L	Rho guanine nucleotide exchange factor 10 like
3014	1,01E-96	9,60E+01	6,10E-98	0,0466	-21,0034307	-0,97794106	5458,39	H2AX	H2A.X variant histone
101929705	1,99E-08	7,70E+00	9,82E-09	0,1706	-5,733811	-0,97825975	113,93	SCIRT	stem cell inhibitory RNA transcript
1727	3,49E-87	8,65E+01	2,51E-88	0,0491	-19,9242163	-0,97881013	9873,92	CYB5R3	cytochrome b5 reductase 3
6227	4,47E-78	7,73E+01	3,85E-79	0,052	-18,8356994	-0,97913779	12099,24	RPS21	ribosomal protein S21
7016	2,95E-56	5,55E+01	4,09E-57	0,0615	-15,9273571	-0,97915472	1360,54	TESK1	testis associated actin remodelling kinase 1
1937	1,09E-153	1,53E+02	2,52E-155	0,0369	-26,5507299	-0,97940733	75627,83	EEF1G	eukaryotic translation elongation factor 1 gamma
339456	2,54E-02	1,60E+00	1,89E-02	0,4174	-2,3465578	-0,97950114	23,53	TMEM52	transmembrane protein 52
100313887	9,82E-02	1,01E+00	7,92E-02	0,558	-1,7554598	-0,97959831	9,55	MIR2277	microRNA 2277
2342	4,02E-37	3,64E+01	8,57E-38	0,0762	-12,8502961	-0,97969192	651,38	FNTB	farnesyltransferase, CAAX box, beta
1512	1,25E-53	5,29E+01	1,83E-54	0,0631	-15,5409899	-0,98031643	1123,21	CTSH	cathepsin H
7867	3,42E-103	1,02E+02	1,83E-104	0,0452	-21,7053579	-0,98081933	5229,51	MAPKAPK3	MAPK activated protein kinase 3
4669	5,88E-57	5,62E+01	8,04E-58	0,0612	-16,0288398	-0,98095399	1516,25	NAGLU	N-acetyl-alpha-glucosaminidase
84545	3,82E-62	6,14E+01	4,63E-63	0,0585	-16,7619905	-0,98123915	2320,04	MRPL43	mitochondrial ribosomal protein L43
8641	2,28E-04	3,64E+00	1,42E-04	0,258	-3,8041789	-0,98141107	45,23	PCDHGB4	protocadherin gamma subfamily B, 4
2625	9,64E-26	2,50E+01	2,74E-26	0,0925	-10,6078523	-0,9815816	510,87	GATA3	GATA binding protein 3
80344	1,71E-101	1,01E+02	9,47E-103	0,0456	-21,5230691	-0,98181455	3303,21	DCAF11	DDB1 and CUL4 associated factor 11
85001	4,32E-03	2,36E+00	2,99E-03	0,3308	-2,968313	-0,98187477	27,51	MGC16275	uncharacterized protein MGC16275
55702	1,91E-44	4,37E+01	3,47E-45	0,0696	-14,1062659	-0,98204923	810,61	YJU2	YJU2 splicing factor homolog
101927572	3,36E-03	2,47E+00	2,31E-03	0,3223	-3,04762	-0,98212365	28,8	LOC101927	uncharacterized LOC101927572
10437	1,67E-57	5,68E+01	2,25E-58	0,061	-16,1076895	-0,98239523	1998,54	IFI30	IFI30 lysosomal thiol reductase
105378753	8,77E-04	3,06E+00	5,73E-04	0,2853	-3,4441593	-0,98247197	39,8	LINC02777	long intergenic non-protein coding RNA 2777
4831	4,12E-137	1,36E+02	1,21E-138	0,0392	-25,0646871	-0,98247787	13352,27	NME2	NME/NM23 nucleoside diphosphate kinase 2
10019	8,83E-129	1,28E+02	2,95E-130	0,0405	-24,2832225	-0,98261414	8289,67	SH2B3	SH2B adaptor protein 3
353174	2,50E-45	4,46E+01	4,44E-46	0,069	-14,2507061	-0,98271094	1081,8	ZACN	zinc activated ion channel
619351	1,11E-02	1,95E+00	8,02E-03	0,3707	-2,6510428	-0,98278125	22,01	LINC00589	long intergenic non-protein coding RNA 589
101060179	9,87E-15	1,40E+01	3,86E-15	0,1251	-7,8593226	-0,98283913	211,11	LOC101060	replaced by ID 56981
517	2,11E-102	1,02E+02	1,15E-103	0,0455	-21,6206058	-0,98309675	6996,73	ATP5MC2	ATP synthase membrane subunit c locus 2
29934	3,21E-99	9,85E+01	1,84E-100	0,0462	-21,2772883	-0,98309869	3653,62	SNX12	sorting nexin 12
100874085	1,14E-50	4,99E+01	1,78E-51	0,0651	-15,093805	-0,98331514	994,65	NUCB1-AS1	NUCB1 antisense RNA 1
643723	4,49E-08	7,35E+00	2,25E-08	0,1759	-5,5914414	-0,98335752	106,18	LYPLAL1-DT	LYPLAL1 divergent transcript
79827	1,14E-87	8,69E+01	8,13E-89	0,0492	-19,9805767	-0,9834508	2909,28	CLMP	CXADR like membrane protein
83855	2,04E-67	6,67E+01	2,21E-68	0,0563	-17,4752795	-0,98345991	1579,93	KLF16	KLF transcription factor 16
960	1,10E-139	1,39E+02	3,11E-141	0,0389	-25,3010743	-0,98376014	64774,44	CD44	CD44 molecule (Indian blood group)
102724023	4,91E-45	4,43E+01	8,78E-46	0,0693	-14,2029824	-0,9841039	1107,91	LOC102724	glutamine amidotransferase class 1 domain containing 3B
283870	2,94E-05	4,53E+00	1,72E-05	0,229	-4,2978267	-0,98440061	59,81	BRICD5	BRICHOS domain containing 5
101929796	4,81E-06	5,32E+00	2,69E-06	0,2098	-4,6931759	-0,984484	71,07	NOTCH2NLF	notch 2 N-terminal like R
256949	4,86E-06	5,31E+00	2,72E-06	0,2099	-4,6907721	-0,98449807	69,9	KANK3	KN motif and ankyrin repeat domains 3
51614	1,18E-126	1,26E+02	4,12E-128	0,0409	-24,0792748	-0,98455032	9998,53	ERGIC3	ERGIC and golgi 3

445577	6,30E-09	8,20E+00	3,05E-09	0,1661	-5,92903	-0,98485717	118,07	FAM120A2P	family with sequence similarity 120A2, pseudogene
51255	1,80E-79	7,87E+01	1,50E-80	0,0518	-19,0067284	-0,98495456	3211,77	RNF181	ring finger protein 181
29070	3,17E-08	7,50E+00	1,58E-08	0,1744	-5,6525146	-0,98578655	107,35	CCDC113	coiled-coil domain containing 113
150223	6,37E-34	3,32E+01	1,47E-34	0,0804	-12,260904	-0,985924	664,5	YDJC	YdjC chitooligosaccharide deacetylase homolog
64132	7,91E-48	4,71E+01	1,32E-48	0,0673	-14,6515059	-0,98633725	1386,55	XYLT2	xylosyltransferase 2
790955	3,94E-27	2,64E+01	1,08E-27	0,0905	-10,9060689	-0,9865378	563,59	UQCC3	ubiquinol-cytochrome c reductase complex assembly factor 3
1305	1,76E-87	8,68E+01	1,26E-88	0,0494	-19,9586978	-0,98682729	9135,41	COL13A1	collagen type XIII alpha 1 chain
100506621	1,59E-05	4,80E+00	9,19E-06	0,2226	-4,4353072	-0,98711525	61,76	LINC01279	replaced by ID 151887
25	8,97E-109	1,08E+02	4,30E-110	0,0443	-22,2932246	-0,98716397	6373,48	ABL1	ABL proto-oncogene 1, non-receptor tyrosine kinase
57634	9,65E-83	8,20E+01	7,54E-84	0,0509	-19,401202	-0,98826706	3219,56	EP400	E1A binding protein p400
51332	1,09E-05	4,96E+00	6,25E-06	0,2188	-4,5176701	-0,98858872	66,21	SPTBN5	spectrin beta, non-erythrocytic 5
84842	8,71E-02	1,06E+00	6,96E-02	0,545	-1,8142649	-0,98873798	10,47	HPDL	4-hydroxyphenylpyruvate dioxygenase like
5141	1,50E-84	8,38E+01	1,13E-85	0,0504	-19,615945	-0,98922964	2288,32	PDE4A	phosphodiesterase 4A
56931	1,27E-43	4,29E+01	2,35E-44	0,0708	-13,9707227	-0,98944845	1082,25	DUS3L	dihydrouridine synthase 3 like
26517	1,07E-50	5,00E+01	1,67E-51	0,0655	-15,0981618	-0,98950802	1823,89	TIMM13	translocase of inner mitochondrial membrane 13
57409	1,05E-53	5,30E+01	1,54E-54	0,0637	-15,5520917	-0,99021999	1225,96	MIF4GD	MIF4G domain containing
25873	8,40E-71	7,01E+01	8,45E-72	0,0553	-17,9185562	-0,99133474	14693	RPL36	ribosomal protein L36
645644	4,13E-21	2,04E+01	1,33E-21	0,1039	-9,5471709	-0,99179835	349,45	FLJ42627	uncharacterized LOC645644
28956	4,19E-60	5,94E+01	5,35E-61	0,0602	-16,4771708	-0,99232962	1549,92	LAMTOR2	late endosomal/lysosomal adaptor, MAPK and MTOR activator 2
5250	5,23E-159	1,58E+02	1,13E-160	0,0367	-27,0097682	-0,99233064	29276,9	SLC25A3	solute carrier family 25 member 3
59286	3,38E-80	7,95E+01	2,78E-81	0,052	-19,0950543	-0,99236896	5215,49	UBL5	ubiquitin like 5
108783654	1,20E-31	3,09E+01	2,91E-32	0,084	-11,8245537	-0,99267523	519,46	HSD17B1-AS	HSD17B1 antisense RNA 1
107986639	8,71E-02	1,06E+00	6,97E-02	0,5473	-1,8139161	-0,99277219	10,47	LOC107986(	uncharacterized LOC107986639
28992	1,36E-28	2,79E+01	3,57E-29	0,0886	-11,2116645	-0,99317186	477,89	MACROD1	mono-ADP ribosylhydrolase 1
50813	3,69E-84	8,34E+01	2,81E-85	0,0508	-19,5696506	-0,99318991	2727,42	COPS7A	COP9 signalosome subunit 7A
222901	1,74E-04	3,76E+00	1,07E-04	0,2565	-3,8731179	-0,99334444	51,92	RPL23P8	ribosomal protein L23 pseudogene 8
57414	5,28E-47	4,63E+01	8,97E-48	0,0684	-14,5206374	-0,99347712	1318,08	RHBDD2	rhomboid domain containing 2
105378539	7,71E-08	7,11E+00	3,92E-08	0,1809	-5,494584	-0,99372882	95,24	LOC105378539	
55083	1,60E-03	2,80E+00	1,07E-03	0,3037	-3,272008	-0,99377635	32,97	KIF26B	kinesin family member 26B
5802	4,54E-86	8,53E+01	3,33E-87	0,0502	-19,7943381	-0,99397728	2240,23	PTPRS	protein tyrosine phosphatase receptor type S
10653	8,73E-151	1,50E+02	2,13E-152	0,0378	-26,2959943	-0,99418513	11842,58	SPINT2	serine peptidase inhibitor, Kunitz type 2
55004	1,43E-90	8,98E+01	9,65E-92	0,049	-20,3140788	-0,99487423	3972,28	LAMTOR1	late endosomal/lysosomal adaptor, MAPK and MTOR activator 1
1350	2,31E-85	8,46E+01	1,72E-86	0,0505	-19,7115509	-0,99499503	5912,98	COX7C	cytochrome c oxidase subunit 7C
105369893	3,57E-02	1,45E+00	2,72E-02	0,4506	-2,2086901	-0,99518567	14,54	LINC02392	long intergenic non-protein coding RNA 2392
3310	3,64E-02	1,44E+00	2,77E-02	0,4524	-2,2008846	-0,99557338	14,9	HSPA6	heat shock protein family A (Hsp70) member 6
84883	5,12E-71	7,03E+01	5,14E-72	0,0555	-17,9461465	-0,99590449	1699,19	AIFM2	apoptosis inducing factor mitochondria associated 2
2944	2,07E-51	5,07E+01	3,17E-52	0,0655	-15,2070774	-0,99607609	940,42	GSTM1	glutathione S-transferase mu 1
207063	1,45E-29	2,88E+01	3,72E-30	0,0873	-11,4101532	-0,99614595	463,38	DHRSX	dehydrogenase/reductase X-linked
57026	9,65E-62	6,10E+01	1,19E-62	0,0596	-16,7059685	-0,99626564	1258,69	PDXP	pyridoxal phosphatase
7392	5,60E-99	9,83E+01	3,25E-100	0,0469	-21,2506516	-0,99649946	4034,18	USF2	upstream transcription factor 2, c-fos interacting
10960	2,52E-101	1,01E+02	1,40E-102	0,0464	-21,5049145	-0,99682887	7359,27	LMAN2	lectin, mannose binding 2
29901	1,01E-30	3,00E+01	2,52E-31	0,0857	-11,6419026	-0,99785952	679,74	SAC3D1	SAC3 domain containing 1
105372798	2,09E-04	3,68E+00	1,30E-04	0,2608	-3,8265226	-0,99790019	46,42	LOC105372	uncharacterized LOC105372798
51333	6,84E-09	8,16E+00	3,31E-09	0,1688	-5,9153312	-0,99859205	116,56	ZNF771	zinc finger protein 771
994	2,94E-130	1,30E+02	9,52E-132	0,0409	-24,4239471	-0,99880036	7735,54	CDC25B	cell division cycle 25B
9742	1,85E-32	3,17E+01	4,42E-33	0,0834	-11,981997	-0,99901733	550,99	IFT140	intraflagellar transport 140
5118	1,47E-10	9,83E+00	6,65E-11	0,153	-6,528279	-0,99912561	133,01	PCOLCE	procollagen C-endopeptidase enhancer
84967	3,77E-51	5,04E+01	5,81E-52	0,0659	-15,1674107	-0,99965399	1462,34	LSM10	LSM10, U7 small nuclear RNA associated
79633	6,12E-66	6,52E+01	6,83E-67	0,0579	-17,2784994	-0,99984225	1506,91	FAT4	FAT atypical cadherin 4
23144	2,21E-52	5,17E+01	3,33E-53	0,0651	-15,3540413	-1,00008182	1316,89	ZC3H3	zinc finger CCCH-type containing 3
6484	2,92E-94	9,35E+01	1,85E-95	0,0482	-20,7302818	-1,00010657	2697,62	ST3GAL4	ST3 beta-galactoside alpha-2,3-sialyltransferase 4
283643	6,38E-29	2,82E+01	1,66E-29	0,0887	-11,2791733	-1,00024528	613,54	TEDC1	tubulin epsilon and delta complex 1
6364	3,70E-04	3,43E+00	2,35E-04	0,272	-3,6779172	-1,00036444	40,42	CCL20	C-C motif chemokine ligand 20
100505975	5,28E-03	2,28E+00	3,69E-03	0,3445	-2,9038053	-1,00043396	26,14	ENO1-AS1	ENO1 antisense RNA 1
100507589	2,10E-02	1,68E+00	1,55E-02	0,4135	-2,4200858	-1,00062092	17,9	NAGPA-AS1	NAGPA antisense RNA 1
147808	1,04E-18	1,80E+01	3,58E-19	0,1118	-8,9491906	-1,00076987	279,83	ZNF784	zinc finger protein 784
11018	2,56E-54	5,36E+01	3,71E-55	0,064	-15,6429848	-1,00100978	2330,49	TMED1	transmembrane p24 trafficking protein 1
8869	3,71E-32	3,14E+01	8,92E-33	0,084	-11,9235588	-1,00159696	523,66	ST3GAL5	ST3 beta-galactoside alpha-2,3-sialyltransferase 5
79643	1,92E-48	4,77E+01	3,16E-49	0,0679	-14,7482644	-1,00196149	1244,42	CHMP6	charged multivesicular body protein 6
101928045	4,53E-08	7,34E+00	2,28E-08	0,1793	-5,5895829	-1,00198217	99,41	LOC101928(	uncharacterized LOC101928045
95	4,62E-35	3,43E+01	1,04E-35	0,0804	-12,4739402	-1,0024239	741,21	ACY1	aminoacylase 1
79039	2,77E-117	1,17E+02	1,15E-118	0,0433	-23,1600685	-1,00251193	6184,66	DDX54	DEAD-box helicase 54
100506253	8,49E-04	3,07E+00	5,54E-04	0,2903	-3,4531494	-1,0025446	36,06	LOC100506(	uncharacterized LOC100506253
162	2,22E-102	1,02E+02	1,21E-103	0,0464	-21,6181047	-1,00285368	5302,33	AP1B1	adaptor related protein complex 1 subunit beta 1
7071	1,61E-90	8,98E+01	1,08E-91	0,0494	-20,3084184	-1,00312296	3583,31	KLF10	KLF transcription factor 10
124402	4,08E-35	3,44E+01	9,15E-36	0,0804	-12,4837862	-1,00331604	601,49	UBALD1	UBA like domain containing 1
65985	5,20E-53	5,23E+01	7,74E-54	0,065	-15,4483236	-1,00368014	1236,59	AACS	acetoacetyl-CoA synthetase
57801	1,25E-09	8,90E+00	5,85E-10	0,1621	-6,1943422	-1,00400908	124,31	HES4	hes family bHLH transcription factor 4
5986	4,80E-34	3,33E+01	1,10E-34	0,0818	-12,2839515	-1,00422355	770,63	RFNG	RFNG O-fucosylpeptide 3-beta-N-acetylglucosaminyltransferase
5216	7,98E-150	1,49E+02	1,97E-151	0,0383	-26,2114059	-1,00506305	61211,23	PFN1	profilin 1
3613	1,54E-39	3,88E+01	3,12E-40	0,0757	-13,2776184	-1,00536726	1023,89	IMPA2	inositol monophosphatase 2
8665	3,82E-156	1,55E+02	8,57E-158	0,0376	-26,7636099	-1,00561285	9824,89	EIF3F	eukaryotic translation initiation factor 3 subunit F
54498	9,70E-39	3,80E+01	2,00E-39	0,0766	-13,1378499	-1,00576249	697,72	SMOX	spermine oxidase
401565	3,61E-56	5,54E+01	5,02E-57	0,0632	-15,9145241	-1,00586688	1372,59	FAM166A	family with sequence similarity 166 member A
80221	7,26E-56	5,51E+01	1,02E-56	0,0634	-15,8703976	-1,0060747	1169,14	ACSF2	acyl-CoA synthetase family member 2
3110	6,25E-09	8,20E+00	3,02E-09	0,1697	-5,9303513	-1,00609251	124,69	MNX1	motor neuron and pancreas homeobox 1
100302254	5,10E-63	6,23E+01	6,06E-64	0,0596	-16,8823973	-1,00620003	1680,67	MIR1282	microRNA 1282
27013	6,21E-60	5,92E+01	7,97E-61	0,0612	-16,453105	-1,00643761	2053,12	CNPPD1	cyclin Pas1/PHO80 domain containing 1
4830	7,07E-114	1,13E+02	3,13E-115	0,0441	-22,8167584	-1,00718477	5647,19	NME1	NME/NM23 nucleoside diphosphate kinase 1
199990	6,01E-49	4,82E+01	9,76E-50	0,0679	-14,8272598	-1,00747076	895,21	FAAP20	FA core complex associated protein 20
65094	3,58E-32	3,14E+01	8,62E-33	0,0845	-11,9264684	-1,0074931	553,92	JMJD4	jumonji domain containing 4
2869	2,89E-66	6,55E+01	3,20E-67	0,0582	-17,3221147	-1,00765472	1453,27	GRK5	G protein-coupled receptor kinase 5
4066	8,68E-28	2,71E+01	2,34E-28	0,0912	-11,0442877	-1,0076623	479,12	LYL1	LYL1 basic helix-loop-helix family member
2670	9,39E-17	1,60E+01	3,44E-17	0,1195	-8,4306488	-1,00767936	226,74	GFAP	glial fibrillary acidic protein
283149	6,19E-84	8,32E+01	4,74E-85	0,0516	-19,542926	-1,00774285	9405,76	BCL9L	BCL9 like
29781	7,57E-53	5,21E+01	1,13E-53	0,0654	-15,4239114	-1,00809593	2091,4	NCAPH2	non-SMC condensin II complex subunit H2
4358	1,42E-43	4,28E+01	2,63E-44	0,0722	-13,9627973	-1,00821221	902,83	MPV17	mitochondrial inner membrane protein MPV17
8818	5,89E-62	6,12E+01	7,19E-63	0,0602	-16,7358107	-1,00832727	1943,74	DPM2	dolichyl-phosphate mannosyltransferase subunit 2, regulatory
2272	8,06E-20	1,91E+01	2,69E-20	0,1093	-9,2307038	-1,00846245	297,78	FHIT	fragile histidine triad diadenosine triphosphatase
23564	2,56E-68	6,76E+01	2,72E-69	0,0573	-17,594452	-1,00881555	4016,28	DDAH2	dimethylarginine dimethylaminohydrolase 2
3397	1,86E-77	7,67E+01	1,63E-78	0,0538	-18,7589843	-1,0090983	1756,74	ID1	inhibitor of DNA binding 1
79713	8,91E-15	1,41E+01	3,48E-15	0,1283	-7,872299	-1,00962253	194,29	IGFLR1	IGF like family receptor 1
56848	3,62E-26	2,54E+01	1,02E-26	0,0944	-10,699899	-1,0103185	773,74	SPHK2	sphingosine kinase 2
10023	1,01E-10	1,00E+01	4,53E-11	0,1534	-6,585723	-1,01056022	139,28	FRAT1	FRAT regulator of WNT signaling pathway 1
1193	4,81E-04	3,32E+00	3,08E-04	0,2801	-3,6086428	-1,01061235	39,23	CLIC2	chloride intracellular channel 2
23344	5,14E-142	1,41E+02	1,41E-143	0,0396	-25,5132473	-1,01101706	10824,09	ESYT1	extended synaptotagmin 1
2002	4,96E-107	1,06E+02	2,46E-108	0,0457	-22,1113057	-1,01136408	3553	ELK1	ETS transcription factor ELK1
8325	5,11E-44	4,33E+01	9,38E-45	0,0721	-14,0360139	-1,01140119	764,43	FZD8	frizzled class receptor 8
105374382	3,30E-17	1,65E+01	1,19E-17	0,1183	-8,5535134	-1,0116946	243,83	LOC105374	uncharacterized LOC105374382
80235	5,84E-06	5,23E+00	3,28E-06	0,2176	-4,6522602	-1,01218575	77,28	PIGZ	phosphatidylinositol glycan anchor biosynthesis class Z
64419	4,17E-84	8,34E+01	3,18E-85	0,0517	-19,5632965	-1,0122075	2160,35	MTMR14	myotubularin related protein 14
55352	1,90E-71	7,07E+01	1,87E-72	0,0562	-18,0021608	-1,01243658	1959,62	COPRS	coordinator of PRMT5 and differentiation stimulator
8574	2,62E-66	6,56E+01	2,89E-67	0,0584	-17,3279441	-1,01248548	2362,57	AKR7A2	aldo-keto reductase family 7 member A2
4665	2,71E-43	4,26E+01	5,06E-44	0,0728	-13,9160967	-1,01298349	760,39	NAB2	NGFI-A binding protein 2
56100	6,83E-05	4,17E+00	4,10E-05	0,247	-4,1018974	-1,01329919	49,27	PCDHGB6	protocadherin gamma subfamily B, 6
162394	3,67E-66	6,54E+01	4,07E-67	0,0586	-17,3083698	-1,01340545	1683,68	SLFN5	schlafen family member 5
105373581	5,78E-36	3,52E+01	1,27E-36	0,0802	-12,6403409	-1,01377603	581,63	LOC105373	uncharacterized LOC105373581
51114	3,04E-66	6,55E+01	3,36E-67	0,0585	-17,3193009	-1,01383192	2245,86	ZDHHC9	zinc finger DHHC-type palmitoyltransferase 9
10084	3,11E-100	9,95E+01	1,76E-101	0,0474	-21,3872569	-1,01407229	3320,88	PQBP1	polyglutamine binding protein 1
28971	5,28E-23	2,23E+01	1,61E-23	0,1015	-9,9943721	-1,01420198	395,38	AAMDC	adipogenesis associated Mth938 domain containing
83643	6,32E-15	1,42E+01	2,46E-15	0,1282	-7,9157106	-1,01444395	193,27	CCDC3	coiled-coil domain containing 3
128989	2,15E-34	3,37E+01	4,91E-35	0,0822	-12,3493574	-1,01469935	663,29	TANGO2	transport and golgi organization 2 homolog
220972	8,98E-73	7,20E+01	8,62E-74	0,0558	-18,1718488	-1,01484197	1687,92	MARCHF8	membrane associated ring-CH-type finger 8
9540	7,13E-37	3,61E+01	1,53E-37	0,0793	-12,8054459	-1,0149267	823,92	TP53I3	tumor protein p53 inducible protein 3
1757	3,51E-25	2,45E+01	1,01E-25	0,0968	-10,4849578	-1,0152301	477,6	SARDH	sarcosine dehydrogenase
140823	1,23E-39	3,89E+01	2,49E-40	0,0764	-13,2946118	-1,01549939	1974,13	ROMO1	reactive oxygen species modulator 1
347744	1,58E-35	3,48E+01	3,50E-36	0,0809	-12,5599676	-1,01552602	625,34	C6orf52	chromosome 6 open reading frame 52
2597	6,28E-122	1,21E+02	2,41E-123	0,043	-23,6197648	-1,01635221	218968,56	GAPDH	glyceraldehyde-3-phosphate dehydrogenase
7138	1,27E-67	6,69E+01	1,37E-68	0,0581	-17,5023867	-1,01650893	1772,66	TNNT1	troponin T1, slow skeletal type
27089	1,03E-87	8,70E+01	7,36E-89	0,0509	-19,9855236	-1,01664307	3164,95	UQCRQ	ubiquinol-cytochrome c reductase complex III subunit VII

4350	7,82E-45	4,41E+01	1,41E-45	0,0718	-14,1698616	-1,01697025	1032,74	MPG	N-methylpurine DNA glycosylase
10682	9,19E-68	6,70E+01	9,87E-69	0,058	-17,5211916	-1,0169804	1570,35	EBP	EBP cholestenol delta-isomerase
10865	1,10E-20	2,00E+01	3,60E-21	0,1077	-9,4437445	-1,01707425	382,69	ARID5A	AT-rich interaction domain 5A
149603	2,11E-76	7,57E+01	1,88E-77	0,0546	-18,6285713	-1,01764118	3126,02	RNF187	ring finger protein 187
2010	3,81E-95	9,44E+01	2,37E-96	0,0489	-20,8288731	-1,0181778	3126,79	EMD	emerin
107983996	3,54E-03	2,45E+00	2,43E-03	0,3359	-3,0320807	-1,01840814	26,46	LOC107983	replaced by ID 105371856
65263	1,13E-33	3,29E+01	2,62E-34	0,0834	-12,2138577	-1,01842999	990,15	PYCR3	pyrroline-5-carboxylate reductase 3
79990	7,04E-33	3,22E+01	1,67E-33	0,0844	-12,062498	-1,018461	596,24	PLEKHH3	pleckstrin homology, MyTH4 and FERM domain containing H3
4784	1,14E-97	9,69E+01	6,78E-99	0,0483	-21,1075311	-1,01863309	2724,15	NFIX	nuclear factor I X
376693	7,52E-03	2,12E+00	5,33E-03	0,3657	-2,7864214	-1,01894052	22,86	RPS10P7	ribosomal protein S10 pseudogene 7
11219	3,79E-02	1,42E+00	2,89E-02	0,4665	-2,1847757	-1,01921425	13,79	TREX2	three prime repair exonuclease 2
4795	1,85E-54	5,37E+01	2,68E-55	0,0651	-15,6636865	-1,01942657	1154,98	NFKBIL1	NFKB inhibitor like 1
100507567	8,31E-32	3,11E+01	2,02E-32	0,086	-11,8554827	-1,01943239	597,23	RAB11B-AS	RAB11B antisense RNA 1
254295	1,76E-71	7,08E+01	1,74E-72	0,0566	-18,0063201	-1,01950289	1665,23	PHYHD1	phytanoyl-CoA dioxygenase domain containing 1
283927	2,14E-02	1,67E+00	1,58E-02	0,4226	-2,4128187	-1,01970511	17,93	NUDT7	nudix hydrolase 7
114987	3,55E-11	1,04E+01	1,56E-11	0,1513	-6,7419262	-1,01977541	138,87	WDR31	WD repeat domain 31
4723	4,26E-76	7,54E+01	3,83E-77	0,0549	-18,5905627	-1,02021701	4627,33	NDUFV1	NADH:ubiquinone oxidoreductase core subunit V1
84148	4,58E-41	4,03E+01	8,95E-42	0,0754	-13,5410428	-1,0205005	672,13	KAT8	lysine acetyltransferase 8
7580	8,31E-44	4,31E+01	1,53E-44	0,0729	-14,0012912	-1,02086816	751,87	ZNF32	zinc finger protein 32
9823	6,82E-89	8,82E+01	4,76E-90	0,0507	-20,1217604	-1,02116633	2333,77	ARMCX2	armadillo repeat containing X-linked 2
283130	8,78E-08	7,06E+00	4,48E-08	0,1867	-5,4709508	-1,02128584	88,38	SLC25A45	solute carrier family 25 member 45
79024	2,13E-02	1,67E+00	1,58E-02	0,4231	-2,413933	-1,02134474	17,13	SMIM2	small integral membrane protein 2
4881	1,96E-02	1,71E+00	1,45E-02	0,4177	-2,4452936	-1,0214252	17,15	NPR1	natriuretic peptide receptor 1
26025	1,37E-04	3,86E+00	8,40E-05	0,2598	-3,9328191	-1,02190254	44,46	PCDHGA12	protocadherin gamma subfamily A, 12
51295	5,81E-69	6,82E+01	6,08E-70	0,0578	-17,6790776	-1,02191736	1931,47	ECSIT	ECSIT signaling integrator
55187	3,06E-78	7,75E+01	2,62E-79	0,0542	-18,8560404	-1,02194154	1920,28	VPS13D	vacuolar protein sorting 13 homolog D
100422977	1,02E-06	5,99E+00	5,49E-07	0,2041	-5,0081929	-1,02211271	73,99	MIR1184-3	microRNA 1184-3
5223	7,51E-152	1,51E+02	1,82E-153	0,0387	-26,3893433	-1,02222827	19931,12	PGAM1	phosphoglycerate mutase 1
6422	1,77E-04	3,75E+00	1,09E-04	0,2643	-3,8689924	-1,02239449	43,21	SFRP1	secreted frizzled related protein 1
1947	6,12E-21	2,02E+01	1,98E-21	0,1076	-9,5059125	-1,02288627	301,38	EFNB1	ephrin B1
146542	4,36E-14	1,34E+01	1,74E-14	0,1334	-7,6685865	-1,02326568	203,57	ZNF688	zinc finger protein 688
100130283	3,95E-22	2,14E+01	1,24E-22	0,1045	-9,7905957	-1,02351768	310,38	LOC100130	uncharacterized LOC100130283
56927	2,58E-76	7,56E+01	2,31E-77	0,055	-18,6175904	-1,02356053	4215,15	GPR108	G protein-coupled receptor 108
58485	6,04E-69	6,82E+01	6,32E-70	0,0579	-17,6768844	-1,02361753	3825,25	TRAPPC1	trafficking protein particle complex subunit 1
51222	3,33E-32	3,15E+01	8,01E-33	0,0858	-11,9325251	-1,02391291	481,77	ZNF219	zinc finger protein 219
79734	3,07E-34	3,35E+01	7,02E-35	0,0831	-12,3205929	-1,0241873	611,22	KCTD17	potassium channel tetramerization domain containing 17
388722	1,09E-07	6,96E+00	5,58E-08	0,1886	-5,4317638	-1,02424213	92,28	C1orf53	chromosome 1 open reading frame 53
10634	7,64E-73	7,21E+01	7,33E-74	0,0564	-18,1807522	-1,0248478	2921,29	GAS2L1	growth arrest specific 2 like 1
11040	9,59E-51	5,00E+01	1,49E-51	0,0679	-15,1053496	-1,02508807	865,75	PIM2	Pim-2 proto-oncogene, serine/threonine kinase
148932	6,31E-45	4,42E+01	1,13E-45	0,0723	-14,1851942	-1,02523249	805,45	MOB3C	MOB kinase activator 3C
342035	2,04E-02	1,69E+00	1,50E-02	0,4218	-2,4314835	-1,0254918	18,33	GLDN	gliomedin
84548	6,35E-47	4,62E+01	1,08E-47	0,0707	-14,5076698	-1,02552298	833,01	TMEM185A	transmembrane protein 185A
8273	9,02E-47	4,60E+01	1,54E-47	0,0708	-14,4834157	-1,02552407	1729,19	SLC10A3	solute carrier family 10 member 3
100132273	4,41E-03	2,36E+00	3,06E-03	0,3463	-2,9621235	-1,02577796	26,3	NDUFA6-DT	NDUFA6 divergent transcript
9053	5,31E-04	3,27E+00	3,41E-04	0,2865	-3,5820963	-1,02615743	38,42	MAP7	microtubule associated protein 7
124583	1,92E-106	1,06E+02	9,58E-108	0,0466	-22,0498516	-1,02704165	4767,3	CANT1	calcium activated nucleotidase 1
51226	7,71E-07	6,11E+00	4,12E-07	0,2029	-5,0631099	-1,02713139	76,86	COPZ2	COPI coat complex subunit zeta 2
56112	6,94E-05	4,16E+00	4,17E-05	0,2507	-4,0981234	-1,02733293	47,82	PCDHGA3	protocadherin gamma subfamily A, 3
360132	2,72E-09	8,57E+00	1,30E-09	0,1694	-6,0679736	-1,02781128	110,3	FKBP9P1	FKBP prolyl isomerase 9 pseudogene 1
29101	6,05E-127	1,26E+02	2,10E-128	0,0426	-24,1071246	-1,02781484	4821,69	SSU72	SSU72 homolog, RNA polymerase II CTD phosphatase
9641	4,07E-84	8,34E+01	3,10E-85	0,0526	-19,5645892	-1,02824938	2244,86	IKBKE	inhibitor of nuclear factor kappa B kinase subunit epsilon
8357	1,44E-04	3,84E+00	8,86E-05	0,2623	-3,9199512	-1,02833606	46,42	H3C10	H3 clustered histone 10
1534	1,27E-90	8,99E+01	8,57E-92	0,0506	-20,3199302	-1,02856336	2978,35	CYB561	cytochrome b561
1209	6,76E-116	1,15E+02	2,89E-117	0,0447	-23,0207705	-1,02864979	8301,19	CLPTM1	CLPTM1 regulator of GABA type A receptor forward trafficking
107986160	5,36E-08	7,27E+00	2,70E-08	0,1851	-5,559748	-1,02894848	90,58	LOC107986	uncharacterized LOC107986160
81628	4,36E-78	7,74E+01	3,75E-79	0,0546	-18,8370732	-1,0290331	1860,95	TSC22D4	TSC22 domain family member 4
221935	3,55E-29	2,84E+01	9,19E-30	0,0908	-11,3312051	-1,02904667	441,49	SDK1	sidekick cell adhesion molecule 1
63893	9,41E-100	9,90E+01	5,35E-101	0,0482	-21,3351949	-1,02933104	2938,01	UBE2O	ubiquitin conjugating enzyme E2 O
2245	3,08E-43	4,25E+01	5,74E-44	0,0741	-13,9070076	-1,0299638	874,46	FGD1	FYVE, RhoGEF and PH domain containing 1
693224	4,44E-23	2,24E+01	1,35E-23	0,1029	-10,011798	-1,03006391	381,43	MIR639	microRNA 639
1438	1,31E-45	4,49E+01	2,31E-46	0,0721	-14,2961023	-1,03016859	811,6	CSF2RA	colony stimulating factor 2 receptor subunit alpha
112268246	2,71E-59	5,86E+01	3,52E-60	0,063	-16,3629588	-1,03031018	1236,45	LOC112268246	
23303	4,33E-66	6,54E+01	4,81E-67	0,0596	-17,2986921	-1,03036485	1697,02	KIF13B	kinesin family member 13B
53947	2,52E-19	1,86E+01	8,55E-20	0,1132	-9,1059526	-1,03061728	374,93	A4GALT	alpha 1,4-galactosyltransferase (P blood group)
5425	1,70E-95	9,48E+01	1,05E-96	0,0494	-20,867982	-1,03083007	9639,71	POLD2	DNA polymerase delta 2, accessory subunit
100288181	1,66E-07	6,78E+00	8,58E-08	0,1926	-5,3543893	-1,03100113	87,01	LNCOC1	lncRNA associated with ovarian cancer 1
1777	9,12E-81	8,00E+01	7,43E-82	0,0538	-19,1637309	-1,03110196	2344,68	DNASE2	deoxyribonuclease 2, lysosomal
4586	6,41E-30	2,92E+01	1,63E-30	0,0899	-11,4817206	-1,03185671	489,55	MUC5AC	mucin 5AC, oligomeric mucus/gel-forming
780853	8,57E-02	1,07E+00	6,84E-02	0,5665	-1,8220676	-1,03214984	9,51	SNORD3C	small nucleolar RNA, C/D box 3C
10093	1,87E-101	1,01E+02	1,04E-102	0,048	-21,5188394	-1,03246829	4792,71	ARPC4	actin related protein 2/3 complex subunit 4
7316	2,49E-170	1,70E+02	4,54E-172	0,0369	-27,9632859	-1,03316143	73002,66	UBC	ubiquitin C
1436	2,00E-11	1,07E+01	8,75E-12	0,1514	-6,8256755	-1,03362216	145,47	CSF1R	colony stimulating factor 1 receptor
30844	8,66E-123	1,22E+02	3,28E-124	0,0436	-23,7039465	-1,03412327	4731,5	EHD4	EH domain containing 4
339665	2,15E-15	1,47E+01	8,24E-16	0,1285	-8,0506572	-1,03415866	241,32	SLC35E4	solute carrier family 35 member E4
105376114	6,88E-10	9,16E+00	3,19E-10	0,1645	-6,289096	-1,03427965	117,59	UBQLN1-AS	UBQLN1 antisense RNA 1
51608	2,37E-49	4,86E+01	3,80E-50	0,0695	-14,8905138	-1,03441602	1086,76	GET4	guided entry of tail-anchored proteins factor 4
9842	5,39E-66	6,53E+01	6,00E-67	0,0599	-17,2859335	-1,03476442	2068,97	PLEKHM1	pleckstrin homology and RUN domain containing M1
57106	2,54E-42	4,16E+01	4,84E-43	0,0753	-13,7537065	-1,03505002	823,58	NAT14	N-acetyltransferase 14 (putative)
56107	6,38E-05	4,20E+00	3,82E-05	0,2514	-4,1181074	-1,03526887	48,71	PCDHGA9	protocadherin gamma subfamily A, 9
3297	3,03E-61	6,05E+01	3,78E-62	0,0622	-16,6367321	-1,03531666	4009,11	HSF1	heat shock transcription factor 1
27166	1,60E-137	1,37E+02	4,67E-139	0,0413	-25,1024902	-1,03596103	5346,39	PRELID1	PRELI domain containing 1
79035	4,32E-73	7,24E+01	4,12E-74	0,0569	-18,2123718	-1,03630622	1914,04	NABP2	nucleic acid binding protein 2
2906	1,34E-03	2,87E+00	8,85E-04	0,3118	-3,324709	-1,03662978	33,34	GRIN2D	glutamate ionotropic receptor NMDA type subunit 2D
79792	8,41E-74	7,31E+01	7,90E-75	0,0566	-18,3025033	-1,0367934	2294,57	GSDMD	gasdermin D
9399	1,21E-27	2,69E+01	3,27E-28	0,0941	-11,0140224	-1,03690202	538,18	STOML1	stomatin like 1
10999	1,65E-72	7,18E+01	1,59E-73	0,0572	-18,138158	-1,03706583	3039,65	SLC27A4	solute carrier family 27 member 4
81855	4,47E-107	1,06E+02	2,21E-108	0,0469	-22,1160521	-1,03732434	3936,59	SFXN3	sideroflexin 3
83871	7,73E-134	1,33E+02	2,35E-135	0,0419	-24,7611211	-1,03773732	6099,11	RAB34	RAB34, member RAS oncogene family
1277	9,93E-33	3,20E+01	2,36E-33	0,0862	-12,0338799	-1,03776033	524,77	COL1A1	collagen type I alpha 1 chain
1365	1,00E-02	2,00E+00	7,21E-03	0,3862	-2,6870233	-1,03785928	20,19	CLDN3	claudin 3
3155	7,16E-48	4,71E+01	1,19E-48	0,0708	-14,6582981	-1,03789675	784,29	HMGCL	3-hydroxy-3-methylglutaryl-CoA lyase
29998	1,41E-28	2,79E+01	3,72E-29	0,0927	-11,2080735	-1,03848584	460,46	BICRA	BRD4 interacting chromatin remodeling complex associated protein
201254	1,78E-43	4,27E+01	3,30E-44	0,0745	-13,9465378	-1,03855936	1333,87	CENPX	centromere protein X
26001	2,60E-117	1,17E+02	1,08E-118	0,0449	-23,1628338	-1,03909677	4662,87	RNF167	ring finger protein 167
2161	7,49E-08	7,13E+00	3,80E-08	0,1889	-5,4997418	-1,03915905	87,57	F12	coagulation factor XII
101929212	3,66E-04	3,44E+00	2,32E-04	0,2823	-3,6811439	-1,03925737	38,7	SMIM2-AS1	SMIM2 antisense RNA 1
100996246	1,55E-02	1,81E+00	1,13E-02	0,4102	-2,5341595	-1,03951263	17,72	LINC02361	long intergenic non-protein coding RNA 2361
25907	8,03E-59	5,81E+01	1,05E-59	0,0638	-16,2959748	-1,03984351	1067,99	TMEM158	transmembrane protein 158
9919	1,62E-132	1,32E+02	5,03E-134	0,0422	-24,637371	-1,03994423	5499,18	SEC16A	SEC16 homolog A, endoplasmic reticulum export factor
7791	1,50E-81	8,08E+01	1,20E-82	0,054	-19,2583598	-1,04007088	5816,96	ZYX	zyxin
100507290	1,91E-31	3,07E+01	4,67E-32	0,0883	-11,7848301	-1,04036392	590,85	ZNF865	zinc finger protein 865
2323	7,19E-23	2,21E+01	2,21E-23	0,1044	-9,9633363	-1,04048414	363,73	FLT3LG	fms related receptor tyrosine kinase 3 ligand
25987	3,63E-74	7,34E+01	3,38E-75	0,0567	-18,3486547	-1,04069983	1650,46	TSKU	tsukushi, small leucine rich proteoglycan
401944	2,82E-27	2,65E+01	7,69E-28	0,0952	-10,9367809	-1,04106949	400,51	LDLRAD2	low density lipoprotein receptor class A domain containing 2
7167	1,28E-182	1,82E+02	1,96E-184	0,0359	-28,9624459	-1,0411617	31777,05	TPI1	triosephosphate isomerase 1
56098	1,12E-04	3,95E+00	6,83E-05	0,2614	-3,9822848	-1,0411663	44,01	PCDHGC4	protocadherin gamma subfamily C, 4
100507300	3,31E-02	1,48E+00	2,50E-02	0,4647	-2,2406401	-1,04126649	14,1	ALKBH3-AS	ALKBH3 antisense RNA 1
4736	2,38E-166	1,66E+02	4,56E-168	0,0377	-27,6322794	-1,04179878	30314,96	RPL10A	ribosomal protein L10a
51025	1,07E-16	1,60E+01	3,91E-17	0,1239	-8,4155039	-1,04248935	209,75	PAM16	presequence translocase associated motor 16
113878	3,32E-55	5,45E+01	4,73E-56	0,0661	-15,7735901	-1,0427107	1656,28	DTX2	deltex E3 ubiquitin ligase 2
9231	2,25E-124	1,24E+02	8,31E-126	0,0437	-23,8582847	-1,04273977	3950,07	DLG5	discs large MAGUK scaffold protein 5
9260	1,07E-85	8,50E+01	7,87E-87	0,0528	-19,7509747	-1,04314238	4946,99	PDLIM7	PDZ and LIM domain 7
8721	1,18E-114	1,14E+02	5,17E-116	0,0456	-22,8953546	-1,04329107	9812,58	EDF1	endothelial differentiation related factor 1
58190	3,38E-72	7,15E+01	3,30E-73	0,0577	-18,0981265	-1,04368506	2469,72	CTDSP1	CTD small phosphatase 1
441733	1,60E-10	9,80E+00	7,25E-11	0,1602	-6,5154556	-1,04375176	126,23	PRKXP1	PRKX pseudogene 1
79258	1,99E-17	1,67E+01	7,14E-18	0,1212	-8,612631	-1,04392683	222,28	MMEL1	membrane metalloendopeptidase like 1
100302111	2,87E-20	1,95E+01	9,45E-21	0,1118	-9,3420344	-1,04413579	266,85	MIR1184-1	microRNA 1184-1
242	6,67E-02	1,18E+00	5,26E-02	0,5387	-1,9385781	-1,0442388	10,68	ALOX12B	arachidonate 12-lipoxygenase, 12R type
9592	2,15E-91	9,07E+01	1,43E-92	0,0512	-20,4075654	-1,04428498	3250,67	IER2	immediate early response 2
29775	1,12E-56	5,60E+01	1,55E-57	0,0653	-15,9881042	-1,04442907	1319,32	CARD10	caspase recruitment domain family member 10

100129484	1,13E-03	2,95E+00	7,48E-04	0,3098	-3,3714823	-1,04446413	32,2	LINC02983	long intergenic non-protein coding RNA 2983
147645	2,02E-11	1,07E+01	8,83E-12	0,1531	-6,8244203	-1,04449413	139,93	VSIG10L	V-set and immunoglobulin domain containing 10 like
84058	4,85E-71	7,03E+01	4,86E-72	0,0582	-17,9492901	-1,04472648	1869,6	WDR54	WD repeat domain 54
22937	1,41E-115	1,15E+02	6,07E-117	0,0455	-22,9885173	-1,04496154	3937,5	SCAP	SREBF chaperone
728431	1,93E-11	1,07E+01	8,43E-12	0,153	-6,8310021	-1,04529455	136,87	ZC3H12A-D1	ZC3H12A divergent transcript
102723354	6,70E-02	1,17E+00	5,28E-02	0,5399	-1,936391	-1,0455082	10,78	LINC02298	long intergenic non-protein coding RNA 2298
55700	2,07E-131	1,31E+02	6,60E-133	0,0426	-24,5328229	-1,04617267	7865,7	MAP7D1	MAP7 domain containing 1
51296	4,03E-23	2,24E+01	1,23E-23	0,1044	-10,0213725	-1,04638848	340,95	SLC15A3	solute carrier family 15 member 3
548593	2,33E-24	2,36E+01	6,88E-25	0,1016	-10,3022804	-1,0464029	396,19	SLX1A	SLX1 homolog A, structure-specific endonuclease subunit
92799	6,41E-84	8,32E+01	4,91E-85	0,0536	-19,5411555	-1,04646272	2949,21	SHKBP1	SH3KBP1 binding protein 1
1072	6,04E-121	1,20E+02	2,36E-122	0,0445	-23,5232122	-1,04674516	37271,91	CFL1	cofilin 1
10121	4,87E-165	1,64E+02	9,64E-167	0,038	-27,5217773	-1,04678594	9059,33	ACTR1A	actin related protein 1A
105370537	6,50E-02	1,19E+00	5,11E-02	0,5368	-1,9503765	-1,04686569	10,75	LOC105370	replaced by ID 2530
7739	8,58E-130	1,29E+02	2,82E-131	0,0429	-24,3795405	-1,04708673	6725,54	ZNF185	zinc finger protein 185 with LIM domain
3028	1,49E-66	6,58E+01	1,64E-67	0,0603	-17,3605392	-1,04743315	2696,57	HSD17B10	hydroxysteroid 17-beta dehydrogenase 10
105371516	2,97E-04	3,53E+00	1,87E-04	0,2805	-3,7361223	-1,04782141	44,82	LOC105371	516
56101	7,47E-05	4,13E+00	4,49E-05	0,2568	-4,0806115	-1,04789801	45,77	PCDHGB5	protocadherin gamma subfamily B, 5
220	1,49E-38	3,78E+01	3,07E-39	0,08	-13,1052577	-1,04795755	716,55	ALDH1A3	aldehyde dehydrogenase 1 family member A3
5709	1,96E-110	1,10E+02	9,16E-112	0,0467	-22,4648549	-1,04805487	12253,51	PSMD3	proteasome 26S subunit, non-ATPase 3
53635	3,11E-79	7,85E+01	2,62E-80	0,0552	-18,9774621	-1,04831506	2291,7	PTOV1	PTOV1 extended AT-hook containing adaptor protein
715	2,02E-30	2,97E+01	5,09E-31	0,0905	-11,5818713	-1,0483558	492,03	C1R	complement C1r
375757	8,73E-47	4,61E+01	1,49E-47	0,0724	-14,4856889	-1,04840125	808,25	SWI5	SWI5 homologous recombination repair protein
84623	2,72E-06	5,57E+00	1,50E-06	0,218	-4,8111306	-1,04859966	68,97	KIRREL3	kirre like nephrin family adhesion molecule 3
102724297	3,09E-24	2,35E+01	9,15E-25	0,1021	-10,2748286	-1,04861015	334,89	CCR5AS	CCR5 antisense RNA
79654	1,98E-88	8,77E+01	1,39E-89	0,0523	-20,0683934	-1,04908647	2637,41	HECTD3	HECT domain E3 ubiquitin protein ligase 3
10295	6,41E-78	7,72E+01	5,56E-79	0,0558	-18,816273	-1,04921461	2124,66	BCKDK	branched chain keto acid dehydrogenase kinase
401491	4,71E-03	2,33E+00	3,28E-03	0,3568	-2,9406084	-1,04932336	24,32	VLDLR-AS1	VLDLR antisense RNA 1
653513	3,50E-03	2,46E+00	2,40E-03	0,3457	-3,0351048	-1,04936504	25,51	LOC653513	phosphodiesterase 4D interacting protein-like
124936	6,40E-42	4,12E+01	1,23E-42	0,0767	-13,6861601	-1,04958798	631,45	CYB5D2	cytochrome b5 domain containing 2
2621	4,03E-124	1,23E+02	1,50E-125	0,0441	-23,8336426	-1,04993206	10041,85	GAS6	growth arrest specific 6
23094	3,57E-116	1,15E+02	1,51E-117	0,0456	-23,0487481	-1,05036621	4216,01	SIPA1L3	signal induced proliferation associated 1 like 3
113829	3,91E-107	1,06E+02	1,94E-108	0,0475	-22,1220942	-1,05074137	5651,22	SLC35A4	solute carrier family 35 member A4
79856	5,38E-126	1,25E+02	1,91E-127	0,0438	-24,0156553	-1,05081305	4949,63	SNX22	sorting nexin 22
404093	2,00E-90	8,97E+01	1,36E-91	0,0518	-20,2974204	-1,0511274	2049,91	CUEDC1	CUE domain containing 1
57787	8,58E-59	5,81E+01	1,13E-59	0,0645	-16,2919334	-1,05130293	1066,39	MARK4	microtubule affinity regulating kinase 4
64744	1,18E-82	8,19E+01	9,27E-84	0,0542	-19,3905594	-1,05133678	2382,5	SMAP2	small ArfGAP2
632	1,11E-03	2,95E+00	7,34E-04	0,3114	-3,3765978	-1,05135212	32,36	BGLAP	bone gamma-carboxyglutamate protein
6455	1,63E-72	7,18E+01	1,58E-73	0,058	-18,1386713	-1,0514478	3825,8	SH3GL1	SH3 domain containing GRB2 like 1, endophilin A2
389	2,66E-118	1,18E+02	1,09E-119	0,0452	-23,2613931	-1,05152784	9733,91	RHOC	ras homolog family member C
7317	1,27E-130	1,30E+02	4,12E-132	0,043	-24,4581816	-1,0516351	19934,31	UBA1	ubiquitin like modifier activating enzyme 1
9644	5,39E-130	1,29E+02	1,76E-131	0,0431	-24,3987798	-1,05180757	4641,22	SH3PXD2A	SH3 and PX domains 2A
27115	1,19E-50	4,99E+01	1,86E-51	0,0697	-15,0909618	-1,05191807	868,55	PDE7B	phosphodiesterase 7B
25844	1,42E-118	1,18E+02	5,78E-120	0,0452	-23,2886501	-1,05200542	7417,03	YIPF3	Yip1 domain family member 3
8263	3,95E-73	7,24E+01	3,77E-74	0,0578	-18,2172397	-1,05237907	1852,49	F8A1	coagulation factor VIII associated 1
154467	2,44E-59	5,86E+01	3,15E-60	0,0643	-16,3695742	-1,05300486	1144,77	CCDC167	coiled-coil domain containing 167
389541	1,61E-45	4,48E+01	2,85E-46	0,0738	-14,2815988	-1,05347299	861,21	LAMTOR4	late endosomal/lysosomal adaptor, MAPK and MTOR activator 4
57664	4,42E-25	2,44E+01	1,28E-25	0,1007	-10,462825	-1,05349689	365,98	PLEKHA4	pleckstrin homology domain containing A4
25804	4,08E-100	9,94E+01	2,31E-101	0,0493	-21,3744707	-1,05380191	7585,58	LSM4	LSM4 homolog, U6 small nuclear RNA and mRNA degradation associated
6913	6,22E-05	4,21E+00	3,72E-05	0,2555	-4,124453	-1,05394013	46,36	TBX15	T-box transcription factor 15
9075	9,21E-05	4,04E+00	5,57E-05	0,2616	-4,0301225	-1,05415586	51,38	CLDN2	claudin 2
26262	1,18E-82	8,19E+01	9,25E-84	0,0544	-19,3906725	-1,05416587	2518,83	TSPAN17	tetraspanin 17
272	1,60E-70	6,98E+01	1,62E-71	0,059	-17,8824272	-1,05445041	1401,84	AMPD3	adenosine monophosphate deaminase 3
80789	8,56E-65	6,41E+01	9,76E-66	0,0616	-17,1244014	-1,05449228	1693,61	INTS5	integrator complex subunit 5
5833	5,25E-78	7,73E+01	4,54E-79	0,056	-18,8270208	-1,05451726	2282,67	PCYT2	phosphate cytidylyltransferase 2, ethanolamine
116138	3,18E-151	1,50E+02	7,72E-153	0,04	-26,3345466	-1,05453497	9841,29	KLHDC3	kelch domain containing 3
1397	1,30E-28	2,79E+01	3,42E-29	0,094	-11,2154985	-1,05468754	417,92	CRIP2	cysteine rich protein 2
151313	4,16E-38	3,74E+01	8,68E-39	0,081	-13,0261895	-1,05506043	579,14	FAHD2B	fumarylacetoacetate hydrolase domain containing 2B
6919	3,01E-70	6,95E+01	3,06E-71	0,0591	-17,8468439	-1,05510017	1486,21	TCEA2	transcription elongation factor A2
51142	1,96E-127	1,27E+02	6,75E-129	0,0437	-24,154186	-1,05551359	12021,18	CHCHD2	coiled-coil-helix-coiled-coil-helix domain containing 2
100873924	3,84E-02	1,42E+00	2,93E-02	0,4845	-2,1794581	-1,0558591	12,83	HLX-AS1	HLX antisense RNA 1
199745	4,26E-13	1,24E+01	1,75E-13	0,1434	-7,3663456	-1,05602084	181,07	THAP8	THAP domain containing 8
100528022	4,09E-26	2,54E+01	1,15E-26	0,0988	-10,6885155	-1,05616024	356,9	BLOC1S1-RI	BLOC1S1-RDH5 readthrough
79955	3,21E-09	8,49E+00	1,53E-09	0,1748	-6,041031	-1,05617318	105,42	PDZD7	PDZ domain containing 7
7755	2,70E-21	2,06E+01	8,66E-22	0,1101	-9,5917805	-1,05623051	355,79	ZNF205	zinc finger protein 205
57732	6,83E-49	4,82E+01	1,11E-49	0,0713	-14,8185366	-1,05633671	926,49	ZFYVE28	zinc finger FYVE-type containing 28
10360	9,40E-64	6,30E+01	1,10E-64	0,0622	-16,9828086	-1,05660877	1557,57	NPM3	nucleophosmin/nucleoplasmin 3
10522	9,80E-78	7,70E+01	8,53E-79	0,0562	-18,7935504	-1,05679429	2306,93	DEAF1	DEAF1 transcription factor
53827	3,46E-78	7,75E+01	2,97E-79	0,0561	-18,849409	-1,05773666	13522,01	FXYD5	FXYD domain containing ion transport regulator 5
10695	1,70E-107	1,07E+02	8,39E-109	0,0478	-22,1598276	-1,05824506	3925,87	CNPY3	canopy FGF signaling regulator 3
51451	1,10E-66	6,60E+01	1,21E-67	0,0609	-17,3782205	-1,05846421	1242,16	LCMT1	leucine carboxyl methyltransferase 1
374395	1,45E-47	4,68E+01	2,43E-48	0,0725	-14,6099036	-1,05875832	1277,67	TMEM179B	transmembrane protein 179B
8497	2,00E-10	9,70E+00	9,07E-11	0,1634	-6,4816193	-1,05880973	133,41	PPFIA4	PTPRF interacting protein alpha 4
148022	5,29E-34	3,33E+01	1,22E-34	0,0863	-12,2760665	-1,05913442	545,29	TICAM1	TIR domain containing adaptor molecule 1
5827	1,11E-43	4,30E+01	2,05E-44	0,0758	-13,9804434	-1,05952746	678,06	PXMP2	peroxisomal membrane protein 2
51246	2,74E-91	9,06E+01	1,83E-92	0,052	-20,3957047	-1,05957346	6653,19	SHISA5	shisa family member 5
381	3,55E-84	8,34E+01	2,69E-85	0,0541	-19,571756	-1,05978413	2540,12	ARF5	ADP ribosylation factor 5
100500853	4,62E-33	3,23E+01	1,09E-33	0,0876	-12,0975837	-1,06033732	483,98	MIR3605	microRNA 3605
6164	2,00E-102	1,02E+02	1,09E-103	0,049	-21,6231132	-1,06034378	9804,61	RPL34	ribosomal protein L34
10636	3,34E-13	1,25E+01	1,37E-13	0,1433	-7,3990694	-1,06056307	159,15	RGS14	regulator of G protein signaling 14
100131726	1,69E-03	2,77E+00	1,13E-03	0,3257	-3,2568883	-1,06073905	29,79	FAM83A-AS	FAM83A antisense RNA 1
5300	7,03E-103	1,02E+02	3,78E-104	0,049	-21,6719083	-1,061191	2782,06	PIN1	peptidylprolyl cis/trans isomerase, NIMA-interacting 1
3885	7,39E-05	4,13E+00	4,44E-05	0,2599	-4,0832051	-1,06119794	49,27	KRT34	keratin 34
100289279	2,55E-13	1,26E+01	1,04E-13	0,1427	-7,435357	-1,06139641	155,1	CNTNAP3C	contactin associated protein family member 3C
27243	4,36E-130	1,29E+02	1,42E-131	0,0435	-24,4076204	-1,06155195	3802,13	CHMP2A	charged multivesicular body protein 2A
1948	5,09E-113	1,12E+02	2,26E-114	0,0467	-22,7300752	-1,06212336	2746,92	EFNB2	ephrin B2
9862	8,91E-110	1,09E+02	4,21E-111	0,0474	-22,3970278	-1,06258275	5012,84	MED24	mediator complex subunit 24
199699	8,97E-02	1,05E+00	7,19E-02	0,5907	-1,7994901	-1,0629994	8,83	DAND5	DAN domain BMP antagonist family member 5
3321	1,73E-47	4,68E+01	2,91E-48	0,0728	-14,5975484	-1,06300803	738,56	IGSF3	immunoglobulin superfamily member 3
114841035	1,04E-60	6,00E+01	1,31E-61	0,0642	-16,5619343	-1,06345636	1461,78	LOC114841	Uncharacterized protein LOC114841035
23616	1,50E-21	2,08E+01	4,77E-22	0,1102	-9,6531783	-1,06355802	288,86	SH3BP1	SH3 domain binding protein 1
677842	1,12E-02	1,95E+00	8,09E-03	0,4017	-2,6483002	-1,06388701	19,93	SNORA50C	small nucleolar RNA, H/ACA box 50C
2286	4,96E-60	5,93E+01	6,35E-61	0,0646	-16,4668744	-1,06388708	1458,37	FKBP2	FKBP prolyl isomerase 2
101928369	8,27E-02	1,08E+00	6,59E-02	0,5786	-1,8390208	-1,06411598	10,01	LOC101928	uncharacterized LOC101928369
100499467	5,94E-47	4,62E+01	1,01E-47	0,0733	-14,5123598	-1,0642899	883,08	LINC00673	long intergenic non-protein coding RNA 673
90113	6,35E-02	1,20E+00	4,99E-02	0,5428	-1,9609674	-1,06450283	10,39	VWA5B2	von Willebrand factor A domain containing 5B2
6132	3,92E-142	1,41E+02	1,07E-143	0,0417	-25,5239884	-1,06460262	60365,75	RPL8	ribosomal protein L8
8086	7,92E-87	8,61E+01	5,76E-88	0,0536	-19,8825837	-1,06486721	2060,23	AAAS	aladin WD repeat nucleoporin
10046	1,88E-78	7,77E+01	1,61E-79	0,0564	-18,881942	-1,06497348	2139,01	MAMLD1	mastermind like domain containing 1
388341	3,00E-71	7,05E+01	2,99E-72	0,0592	-17,9763038	-1,06498263	2400,92	LRRC75A	leucine rich repeat containing 75A
375704	3,60E-02	1,44E+00	2,74E-02	0,4829	-2,2054193	-1,06505825	13,48	ENHO	energy homeostasis associated
107987299	1,17E-03	2,93E+00	7,73E-04	0,3169	-3,3623628	-1,06537639	31,78	LOC107987	uncharacterized LOC107987299
100616211	5,04E-33	3,23E+01	1,19E-33	0,0881	-12,0903065	-1,06548493	477,1	MIR4709	microRNA 4709
126789	1,82E-42	4,17E+01	3,44E-43	0,0773	-13,7782739	-1,06565233	768,84	PUSL1	pseudouridine synthase like 1
9968	1,40E-112	1,12E+02	6,26E-114	0,047	-22,6852548	-1,06566499	3000,97	MED12	mediator complex subunit 12
7494	1,36E-100	9,99E+01	7,64E-102	0,0497	-21,4260535	-1,06573465	3562,1	XBP1	X-box binding protein 1
100134713	5,40E-24	2,33E+01	1,61E-24	0,1043	-10,2201158	-1,06586966	347,84	NDUFB2-AS	NDUFB2 antisense RNA 1
101928487	3,33E-03	2,48E+00	2,28E-03	0,3496	-3,0510594	-1,06660151	24,56	LOC101928	uncharacterized LOC101928487
9049	1,41E-84	8,39E+01	1,06E-85	0,0544	-19,6191071	-1,06768849	2069,55	AIP	aryl hydrocarbon receptor interacting protein
57479	5,07E-82	8,13E+01	4,02E-83	0,0553	-19,3149146	-1,06825082	1908,09	PRR12	proline rich 12
8612	3,26E-59	5,85E+01	4,24E-60	0,0653	-16,35151	-1,06840838	1367,4	PLPP2	phospholipid phosphatase 2
2319	2,50E-116	1,16E+02	1,06E-117	0,0463	-23,0642669	-1,06862771	5874,98	FLOT2	flotillin 2
3219	1,50E-77	7,68E+01	1,32E-78	0,0569	-18,7704578	-1,06863735	2034,19	HOXB9	homeobox B9
9601	4,07E-187	1,86E+02	5,96E-189	0,0365	-29,3188727	-1,06910722	16610,7	PDIA4	protein disulfide isomerase family A member 4
84836	2,21E-82	8,17E+01	1,75E-83	0,0552	-19,3579238	-1,06916996	2128,41	ABHD14B	abhydrolase domain containing 14B
23423	2,25E-105	1,05E+02	1,15E-106	0,0487	-21,9369636	-1,06931227	2881,64	TMED3	transmembrane p24 trafficking protein 3
100507588	5,21E-13	1,23E+01	2,15E-13	0,1457	-7,3389566	-1,06933875	153,79	TGFBR3L	transforming growth factor beta receptor 3 like
10474	2,67E-138	1,38E+02	7,68E-140	0,0425	-25,1742003	-1,06976747	5458,06	TADA3	transcriptional adaptor 3
84934	8,19E-94	9,31E+01	5,23E-95	0,0517	-20,6801363	-1,06980865	1980,2	RITA1	RBPJ interacting and tubulin associated 1
148398	1,86E-28	2,77E+01	4,91E-29	0,0957	-11,1836056	-1,06986298	473,14	SAMD11	sterile alpha motif domain containing 11
550643	7,83E-66	6,51E+01	8,74E-67	0,062	-17,2642434	-1,06993662	1625,19	NBDY	negative regulator of P-body association

57529	5,32E-03	2,27E+00	3,71E-03	0,3689	-2,9017074	-1,07052783	22,18	RTL9	retrotransposon Gag like 9
114804	1,89E-02	1,72E+00	1,39E-02	0,4354	-2,4593487	-1,07084222	16,27	RNF157	ring finger protein 157
1491	1,38E-57	5,69E+01	1,86E-58	0,0664	-16,1195629	-1,0710357	922,51	CTH	cystathionine gamma-lyase
3487	1,85E-232	2,32E+02	1,65E-234	0,0328	-32,6983513	-1,07140143	92280,32	IGFBP4	insulin like growth factor binding protein 4
1117	6,47E-04	3,19E+00	4,19E-04	0,3037	-3,5280876	-1,0714879	33,81	CHI3L2	chitinase 3 like 2
822	1,98E-118	1,18E+02	8,08E-120	0,046	-23,2742586	-1,07166072	10959,78	CAPG	capping actin protein, gelsolin like
6133	9,82E-99	9,80E+01	5,73E-100	0,0505	-21,2240525	-1,07169675	21776,04	RPL9	ribosomal protein L9
79590	5,12E-93	9,23E+01	3,32E-94	0,0521	-20,5907792	-1,07180298	4053,44	MRPL24	mitochondrial ribosomal protein L24
292	2,57E-100	9,96E+01	1,45E-101	0,0501	-21,3962226	-1,07219872	18601,65	SLC25A5	solute carrier family 25 member 5
55851	2,09E-93	9,27E+01	1,35E-94	0,052	-20,6344297	-1,07270869	2084,66	PSENEN	presenilin enhancer, gamma-secretase subunit
408	2,54E-102	1,02E+02	1,39E-103	0,0496	-21,6117513	-1,07271927	2756,18	ARRB1	arrestin beta 1
10572	1,55E-47	4,68E+01	2,61E-48	0,0735	-14,6051249	-1,07282094	1138,96	SIVA1	SIVA1 apoptosis inducing factor
80139	8,95E-40	3,90E+01	1,80E-40	0,0806	-13,3186763	-1,07364699	611,86	ZNF703	zinc finger protein 703
6199	1,50E-76	7,58E+01	1,34E-77	0,0576	-18,6468337	-1,07367867	2257,41	RPS6KB2	ribosomal protein S6 kinase B2
6813	4,18E-80	7,94E+01	3,45E-81	0,0563	-19,0837277	-1,07370821	3551,01	STXBP2	syntaxin binding protein 2
653067	1,23E-126	1,26E+02	4,29E-128	0,0446	-24,077618	-1,07395778	5294,11	XAGE1B	X antigen family member 1B
124565	3,15E-68	6,75E+01	3,34E-69	0,0611	-17,5827323	-1,07415291	2445,76	SLC38A10	solute carrier family 38 member 10
50855	2,06E-18	1,77E+01	7,18E-19	0,1212	-8,8720362	-1,0750003	270,56	PARD6A	par-6 family cell polarity regulator alpha
220323	2,15E-95	9,47E+01	1,33E-96	0,0516	-20,8566889	-1,07534338	4314,9	OAF	out at first homolog
358	1,93E-04	3,71E+00	1,20E-04	0,2796	-3,8471093	-1,07568208	40,06	AQP1	aquaporin 1 (Colton blood group)
4939	6,32E-85	8,42E+01	4,73E-86	0,0547	-19,6602127	-1,07571002	2170,6	OAS2	2'-5'-oligoadenylate synthetase 2
55191	2,83E-40	3,95E+01	5,63E-41	0,0803	-13,4052417	-1,07609096	1103,34	NADSYN1	NAD synthetase 1
4716	9,70E-115	1,14E+02	4,24E-116	0,047	-22,9039812	-1,07627708	2757,06	NDUFB10	NADH:ubiquinone oxidoreductase subunit B10
83985	8,69E-34	3,31E+01	2,01E-34	0,088	-12,2353614	-1,07646748	729,53	SPNS1	SPNS lysolipid transporter 1, lysophospholipid
57567	7,85E-40	3,91E+01	1,58E-40	0,0808	-13,3286306	-1,07656917	665,94	ZNF319	zinc finger protein 319
653220	6,62E-124	1,23E+02	2,47E-125	0,0452	-23,8125864	-1,07713075	5265,7	XAGE1A	X antigen family member 1A
25953	6,15E-84	8,32E+01	4,70E-85	0,0552	-19,5433286	-1,07822724	1674,1	PNKD	PNKD metallo-beta-lactamase domain containing
127294	6,27E-02	1,20E+00	4,93E-02	0,5484	-1,9663823	-1,07827381	11,12	MYOM3	myomesin 3
25915	6,65E-57	5,62E+01	9,10E-58	0,0673	-16,0210924	-1,07837361	1104,28	NDUFAF3	NADH:ubiquinone oxidoreductase complex assembly factor 3
6170	1,80E-145	1,45E+02	4,74E-147	0,0418	-25,824258	-1,07841785	24748,85	RPL39	ribosomal protein L39
56926	5,73E-83	8,22E+01	4,45E-84	0,0555	-19,4283002	-1,07864071	3672,16	NCLN	nicalin
105371430	4,38E-03	2,36E+00	3,03E-03	0,3639	-2,9643649	-1,0786588	24,49	LOC105371	uncharacterized LOC105371430
4855	1,80E-09	8,74E+00	8,50E-10	0,1758	-6,1353675	-1,07866979	103,74	NOTCH4	notch receptor 4
4502	1,89E-89	8,87E+01	1,30E-90	0,0535	-20,1858048	-1,0794515	35729,9	MT2A	metallothionein 2A
57655	4,53E-70	6,93E+01	4,64E-71	0,0606	-17,8235335	-1,079587	1709,63	GRAMD1A	GRAM domain containing 1A
51364	1,80E-02	1,74E+00	1,32E-02	0,4357	-2,4781846	-1,07968487	16,81	ZMYND10	zinc finger MYND-type containing 10
23246	3,73E-61	6,04E+01	4,67E-62	0,065	-16,6240244	-1,07995197	5308,09	BOP1	BOP1 ribosomal biogenesis factor
105371490	6,92E-03	2,16E+00	4,89E-03	0,3838	-2,8142367	-1,08001576	23,13	LOC105371	uncharacterized LOC105371490
9907	4,22E-48	4,74E+01	6,99E-49	0,0735	-14,6945113	-1,08029915	983,37	AP5Z1	adaptor related protein complex 5 subunit zeta 1
728635	3,90E-07	6,41E+00	2,06E-07	0,208	-5,1941646	-1,08047388	74,7	DHRS4L1	dehydrogenase/reductase 4 like 1 (pseudogene)
90993	4,59E-101	1,00E+02	2,55E-102	0,0503	-21,477075	-1,08099709	2541,67	CREB3L1	cAMP responsive element binding protein 3 like 1
4043	1,32E-126	1,26E+02	4,61E-128	0,0449	-24,074655	-1,08141691	5713,62	LRPAP1	LDL receptor related protein associated protein 1
399744	1,01E-10	1,00E+01	4,55E-11	0,1643	-6,5850531	-1,08213862	118,57	LINC00999	long intergenic non-protein coding RNA 999
283481	7,65E-03	2,12E+00	5,42E-03	0,3893	-2,7809662	-1,08275073	20,56	FGF14-AS2	FGF14 antisense RNA 2
84629	3,39E-125	1,24E+02	1,23E-126	0,0452	-23,9381923	-1,08286283	3660,31	TNRC18	trinucleotide repeat containing 18
100131655	3,45E-06	5,46E+00	1,91E-06	0,2274	-4,7624063	-1,08297168	63,81	ZNF236-DT	ZNF236 divergent transcript
10430	4,45E-73	7,24E+01	4,25E-74	0,0595	-18,2106633	-1,08394413	2515,01	TMEM147	transmembrane protein 147
23604	6,38E-05	4,20E+00	3,82E-05	0,2632	-4,1181756	-1,08396448	49,4	DAPK2	death associated protein kinase 2
26502	1,21E-99	9,89E+01	6,92E-101	0,0508	-21,3232065	-1,08401912	2371,48	NARF	nuclear prelamin A recognition factor
124220	1,62E-30	2,98E+01	4,05E-31	0,0934	-11,6014501	-1,08407422	406,78	ZG16B	zymogen granule protein 16B
101930593	1,71E-04	3,77E+00	1,05E-04	0,2797	-3,8776552	-1,08447282	39,1	DNAAF3-AS	DNAAF3 antisense RNA 1
54814	4,79E-53	5,23E+01	7,13E-54	0,0702	-15,4536255	-1,08473828	1099,08	QPCTL	glutaminyl-peptide cyclotransferase like
84445	2,32E-72	7,16E+01	2,26E-73	0,0599	-18,1188932	-1,0847497	1993,9	LZTS2	leucine zipper tumor suppressor 2
7802	2,75E-08	7,56E+00	1,37E-08	0,1911	-5,6773509	-1,08485857	85,83	DNALI1	dynein axonemal light intermediate chain 1
51070	3,23E-66	6,55E+01	3,59E-67	0,0627	-17,3156394	-1,08506582	2254,18	NOSIP	nitric oxide synthase interacting protein
81858	4,36E-53	5,24E+01	6,49E-54	0,0702	-15,4597062	-1,08531764	2074,77	SHARPIN	SHANK associated RH domain interactor
26780	7,12E-04	3,15E+00	4,62E-04	0,3101	-3,5016643	-1,08595309	34,73	SNORA68	small nucleolar RNA, H/ACA box 68
3054	3,53E-118	1,17E+02	1,45E-119	0,0467	-23,2491424	-1,08609156	5857,36	HCFC1	host cell factor C1
8792	1,70E-47	4,68E+01	2,85E-48	0,0744	-14,598917	-1,08625582	733,92	TNFRSF11A	TNF receptor superfamily member 11a
8364	8,76E-03	2,06E+00	6,24E-03	0,3973	-2,7347144	-1,08659022	21,56	H4C3	H4 clustered histone 3
107987238	1,45E-03	2,84E+00	9,64E-04	0,3293	-3,300853	-1,08711421	28,07	LOC107987238	
107987128	3,81E-05	4,42E+00	2,25E-05	0,2565	-4,2385825	-1,08732303	49,75	LOC107987128	
83547	8,85E-30	2,91E+01	2,26E-30	0,0949	-11,4535052	-1,0873437	442,15	RILP	Rab interacting lysosomal protein
9185	2,36E-38	3,76E+01	4,91E-39	0,0832	-13,0696698	-1,08772985	572,36	REPS2	RALBP1 associated Eps domain containing 2
101929484	1,13E-08	7,95E+00	5,52E-09	0,1866	-5,8307174	-1,08826402	90,08	LINC01615	long intergenic non-protein coding RNA 1615
83541	8,39E-25	2,41E+01	2,44E-25	0,1046	-10,4015069	-1,08832781	326,16	FAM110A	family with sequence similarity 110 member A
23352	3,36E-172	1,71E+02	5,90E-174	0,0387	-28,1180004	-1,08839446	16949,45	UBR4	ubiquitin protein ligase E3 component n-recognin 4
3996	8,72E-65	6,41E+01	9,96E-66	0,0636	-17,1232368	-1,08865887	2629,55	LLGL1	LLGL scribble cell polarity complex component 1
79008	1,42E-17	1,68E+01	5,08E-18	0,1259	-8,6516459	-1,0888251	216,06	SLX1B	SLX1 homolog B, structure-specific endonuclease subunit
746	3,08E-85	8,45E+01	2,29E-86	0,0553	-19,6969605	-1,08897598	1590,44	TMEM258	transmembrane protein 258
100506797	4,02E-02	1,40E+00	3,07E-02	0,5042	-2,1602961	-1,0892066	12,19	THORLNC	testis associated oncogenic lncRNA
84419	2,84E-88	8,75E+01	2,01E-89	0,0543	-20,0503027	-1,08921824	4045,81	C15orf48	chromosome 15 open reading frame 48
3768	7,97E-02	1,10E+00	6,34E-02	0,5868	-1,8562647	-1,08930283	8,78	KCNJ12	potassium inwardly rectifying channel subfamily J member 12
9168	7,22E-192	1,91E+02	1,00E-193	0,0367	-29,6909547	-1,08949262	57728,43	TMSB10	thymosin beta 10
112268251	6,32E-03	2,20E+00	4,44E-03	0,383	-2,8447893	-1,08957396	20,66	LOC112268	uncharacterized LOC112268251
90480	2,44E-105	1,05E+02	1,25E-106	0,0497	-21,9331656	-1,08961141	5290	GADD45GIP	GADD45G interacting protein 1
64080	1,24E-17	1,69E+01	4,44E-18	0,1257	-8,6669895	-1,08969956	215,07	RBKS	ribokinase
107984500	6,81E-02	1,17E+00	5,37E-02	0,5653	-1,9288679	-1,09035436	9,62	LOC107984	uncharacterized LOC107984500
5371	3,50E-88	8,75E+01	2,48E-89	0,0545	-20,0396938	-1,0911673	3547,23	PML	PML nuclear body scaffold
10549	6,66E-113	1,12E+02	2,97E-114	0,048	-22,718123	-1,0911809	5401,48	PRDX4	peroxiredoxin 4
10458	2,46E-80	7,96E+01	2,01E-81	0,0571	-19,111836	-1,09157221	3036,78	BAIAP2	BAR/IMD domain containing adaptor protein 2
6988	4,39E-77	7,64E+01	3,88E-78	0,0584	-18,712971	-1,09202337	1566,75	TCTA	T cell leukemia translocation altered
7249	3,38E-77	7,65E+01	2,98E-78	0,0583	-18,7270606	-1,09211875	3307,09	TSC2	TSC complex subunit 2
1155	1,21E-115	1,15E+02	5,20E-117	0,0475	-22,9952474	-1,09256382	3811,81	TBCB	tubulin folding cofactor B
79759	2,22E-26	2,57E+01	6,20E-27	0,1017	-10,7458777	-1,09282579	341,36	ZNF668	zinc finger protein 668
55559	5,78E-47	4,62E+01	9,85E-48	0,0753	-14,5142297	-1,09286575	733,49	HAUS7	HAUS augmin like complex subunit 7
333	1,50E-15	1,48E+01	5,72E-16	0,135	-8,0951442	-1,09316741	197,61	APLP1	amyloid beta precursor like protein 1
25771	1,07E-65	6,50E+01	1,19E-66	0,0634	-17,2462561	-1,09322349	1050,6	TBC1D22A	TBC1 domain family member 22A
401010	2,52E-02	1,60E+00	1,88E-02	0,4655	-2,3487956	-1,09324811	13,94	NOC2LP2	NOC2 like nucleolar associated transcriptional repressor pseudogene 2
2063	7,79E-81	8,01E+01	6,34E-82	0,057	-19,1720004	-1,09339395	1404,51	NR2F6	nuclear receptor subfamily 2 group F member 6
63895	1,11E-09	8,95E+00	5,20E-10	0,1761	-6,2130603	-1,0939901	99,77	PIEZO2	piezo type mechanosensitive ion channel component 2
4013	2,24E-07	6,65E+00	1,16E-07	0,2064	-5,299317	-1,09403609	74,75	VWA5A	von Willebrand factor A domain containing 5A
105371099	6,26E-13	1,22E+01	2,59E-13	0,1496	-7,3139734	-1,09413455	148,25	LOC105371	uncharacterized LOC105371099
29965	1,71E-56	5,58E+01	2,36E-57	0,0686	-15,9616913	-1,09462179	976,33	CDIP1	cell death inducing p53 target 1
3726	5,12E-73	7,23E+01	4,91E-74	0,0602	-18,2027663	-1,09507479	1700,14	JUNB	JunB proto-oncogene, AP-1 transcription factor subunit
150356	1,18E-06	5,93E+00	6,39E-07	0,2201	-4,9790525	-1,09578563	65,72	CHADL	chondroadherin like
387254	9,93E-06	5,00E+00	5,66E-06	0,2415	-4,5385729	-1,09622604	62,13	SLC7A5P2	solute carrier family 7 member 5 pseudogene 2
102723817	7,82E-12	1,11E+01	3,36E-12	0,1575	-6,9617965	-1,0964975	140,15	CNIH3-AS2	CNIH3 antisense RNA 2
8677	3,88E-105	1,04E+02	2,00E-106	0,0501	-21,9120012	-1,09676867	3045,54	STX10	syntaxin 10
84264	7,29E-14	1,31E+01	2,93E-14	0,1443	-7,601412	-1,09678806	162,7	HAGHL	hydroxyacylglutathione hydrolase like
64601	2,99E-69	6,85E+01	3,12E-70	0,0619	-17,7166371	-1,09685555	1176,56	VPS16	VPS16 core subunit of CORVET and HOPS complexes
4245	1,14E-139	1,39E+02	3,24E-141	0,0434	-25,2994057	-1,09705631	6799,61	MGAT1	alpha-1,3-mannosyl-glycoprotein 2-beta-N-acetylglucosaminyltransferase
54828	1,30E-58	5,79E+01	1,71E-59	0,0675	-16,266392	-1,09733118	999,42	BCAS3	BCAS3 microtubule associated cell migration factor
5699	2,73E-44	4,36E+01	4,98E-45	0,0779	-14,0808757	-1,09744891	1079,45	PSMB10	proteasome 20S subunit beta 10
55906	4,00E-50	4,94E+01	6,33E-51	0,0731	-15,0098398	-1,09773183	742,37	ZC4H2	zinc finger C4H2-type containing
728130	1,22E-11	1,09E+01	5,28E-12	0,1591	-6,8977579	-1,09774563	131,06	NUTM2D	NUT family member 2D
79155	5,54E-75	7,43E+01	5,09E-76	0,0595	-18,4513355	-1,09781416	1614,4	TNIP2	TNFAIP3 interacting protein 2
112752	1,51E-28	2,78E+01	3,99E-29	0,098	-11,2019839	-1,09787837	372,77	IFT43	intraflagellar transport 43
7086	2,49E-95	9,46E+01	1,54E-96	0,0527	-20,8494811	-1,09824258	16541,05	TKT	transketolase
643	1,51E-74	7,38E+01	1,39E-75	0,0597	-18,3968484	-1,09839363	1576,53	CXCR5	C-X-C motif chemokine receptor 5
7106	4,43E-65	6,44E+01	5,02E-66	0,064	-17,1630067	-1,09891201	3548,33	TSPAN4	tetraspanin 4
55330	1,91E-36	3,57E+01	4,12E-37	0,0864	-12,7281659	-1,10018891	504,11	BLOC1S4	biogenesis of lysosomal organelles complex 1 subunit 4
112398	3,84E-61	6,04E+01	4,81E-62	0,0662	-16,6221982	-1,10047694	1166,14	EGLN2	egl-9 family hypoxia inducible factor 2
84987	5,16E-42	4,13E+01	9,89E-43	0,0803	-13,7018719	-1,10071345	562,37	COX14	cytochrome c oxidase assembly factor COX14
124641	2,51E-51	5,06E+01	3,85E-52	0,0724	-15,1944951	-1,10081143	882,65	OVCA2	OVCA2 serine hydrolase domain containing
254228	2,72E-03	2,57E+00	1,85E-03	0,3536	-3,1135583	-1,10093227	24,51	CALHM5	calcium homeostasis modulator family member 5
241	6,20E-06	5,21E+00	3,49E-06	0,2373	-4,6396471	-1,1009718	58,12	ALOX5AP	arachidonate 5-lipoxygenase activating protein
7490	1,12E-22	2,20E+01	3,47E-23	0,111	-9,9182117	-1,10125529	279,9	WT1	WT1 transcription factor
79180	6,35E-137	1,36E+02	1,87E-138	0,044	-25,0473567	-1,10148237	8482,56	EFHD2	EF-hand domain family member D2
29800	1,59E-20	1,98E+01	5,20E-21	0,1172	-9,4050837	-1,10271015	282,77	ZDHHC1	zinc finger DHHC-type containing 1

283849	1,15E-02	1,94E+00	8,27E-03	0,4176	-2,6408305	-1,10276997	17,88	EXOC3L1	exocyst complex component 3 like 1
100422985	5,26E-10	9,28E+00	2,43E-10	0,1742	-6,3315224	-1,10301394	104,04	MIR1184-2	microRNA 1184-2
100534592	7,76E-103	1,02E+02	4,17E-104	0,051	-21,6673367	-1,1043153	2275,53	URGCP-MRI	URGCP-MRPS24 readthrough
340526	1,26E-27	2,69E+01	3,39E-28	0,1003	-11,0107534	-1,10461808	426,58	RTL5	retrotransposon Gag like 5
100287227	3,16E-12	1,15E+01	1,34E-12	0,1559	-7,0899228	-1,10507868	134,99	TIPARP-AS1	TIPARP antisense RNA 1
4582	1,73E-09	8,76E+00	8,19E-10	0,18	-6,1412495	-1,10556516	110,33	MUC1	mucin 1, cell surface associated
2185	1,49E-21	2,08E+01	4,73E-22	0,1146	-9,6539573	-1,105918	266,99	PTK2B	protein tyrosine kinase 2 beta
30850	6,45E-58	5,72E+01	8,62E-59	0,0684	-16,1669844	-1,10631978	1248,47	CDR2L	cerebellar degeneration related protein 2 like
286262	1,39E-34	3,39E+01	3,15E-35	0,0894	-12,3849704	-1,10671039	642,37	TPRN	taperin
64978	4,66E-75	7,43E+01	4,27E-76	0,06	-18,4607402	-1,10687159	2268,52	MRPL38	mitochondrial ribosomal protein L38
92340	2,77E-19	1,86E+01	9,39E-20	0,1218	-9,0957525	-1,10748689	261,13	PRR29	proline rich 29
148014	2,50E-02	1,60E+00	1,87E-02	0,471	-2,3523067	-1,10799623	14,17	TTC9B	tetratricopeptide repeat domain 9B
284114	8,11E-23	2,21E+01	2,49E-23	0,1113	-9,9511542	-1,1080396	322,41	TMEM102	transmembrane protein 102
441518	1,26E-83	8,29E+01	9,72E-85	0,0568	-19,5062361	-1,10824475	1565,35	RTL8B	retrotransposon Gag like 8B
5518	6,86E-113	1,12E+02	3,06E-114	0,0488	-22,7167461	-1,10891024	11336,28	PPP2R1A	protein phosphatase 2 scaffold subunit Aalpha
284716	7,90E-10	9,10E+00	3,67E-10	0,1769	-6,2673335	-1,10891848	109,5	RIMKLA	ribosomal modification protein rimK like family member A
51548	9,30E-41	4,00E+01	1,83E-41	0,0822	-13,4886083	-1,10895866	627,73	SIRT6	sirtuin 6
81621	9,47E-41	4,00E+01	1,86E-41	0,0823	-13,4872594	-1,11017348	554,96	KAZALD1	Kazal type serine peptidase inhibitor domain 1
7464	4,46E-74	7,34E+01	4,17E-75	0,0606	-18,3372681	-1,11038928	1267,18	CORO2A	coronin 2A
975	8,62E-111	1,10E+02	3,99E-112	0,0493	-22,5017047	-1,11039899	8088,71	CD81	CD81 molecule
9249	3,01E-16	1,55E+01	1,12E-16	0,134	-8,2913192	-1,11067279	191,53	DHRS3	dehydrogenase/reductase 3
644172	4,65E-03	2,33E+00	3,23E-03	0,3771	-2,9450115	-1,11071096	22,88	MAPK8IP1P2	mitogen-activated protein kinase 8 interacting protein 1 pseudogene 2
8409	3,45E-72	7,15E+01	3,36E-73	0,0614	-18,0970008	-1,11137965	1613,01	UXT	ubiquitously expressed prefoldin like chaperone
25829	8,25E-109	1,08E+02	3,95E-110	0,0499	-22,2970174	-1,11156695	4913,16	TMEM184B	transmembrane protein 184B
5970	7,78E-125	1,24E+02	2,84E-126	0,0465	-23,9030963	-1,11168414	5709,24	RELA	RELA proto-oncogene, NF-kB subunit
51684	6,49E-69	6,82E+01	6,80E-70	0,0629	-17,6727741	-1,11175313	1515,77	SUFU	SUFU negative regulator of hedgehog signaling
11156	5,19E-17	1,63E+01	1,89E-17	0,1308	-8,5005883	-1,11195584	203,44	PTP4A3	protein tyrosine phosphatase 4A3
29907	2,65E-53	5,26E+01	3,92E-54	0,0718	-15,4921642	-1,11223794	920,33	SNX15	sorting nexin 15
100506755	9,76E-41	4,00E+01	1,92E-41	0,0825	-13,484972	-1,1129105	590,88	MIR497HG	mir-497-195 cluster host gene
51635	1,02E-46	4,60E+01	1,75E-47	0,0769	-14,4748191	-1,11318185	661,92	DHRS7	dehydrogenase/reductase 7
66005	6,96E-77	7,62E+01	6,18E-78	0,0596	-18,6881584	-1,11350335	2712,1	CHID1	chitinase domain containing 1
101410533	2,02E-02	1,69E+00	1,49E-02	0,4575	-2,43395	-1,113597	14,52	YTHDF3-DT	YTHDF3 divergent transcript
130589	8,14E-64	6,31E+01	9,51E-65	0,0655	-16,9914195	-1,11363623	1091,42	GALM	galactose mutarotase
4267	7,91E-119	1,18E+02	3,22E-120	0,0478	-23,3137456	-1,11368041	6443,93	CD99	CD99 molecule (Xg blood group)
105374836	5,19E-04	3,28E+00	3,33E-04	0,3104	-3,587979	-1,11385612	200,42	LOC105374	uncharacterized LOC105374836
1759	1,05E-43	4,30E+01	1,94E-44	0,0797	-13,9845581	-1,1139375	594,57	DNM1	dynamin 1
11258	1,30E-98	9,79E+01	7,61E-100	0,0526	-21,210702	-1,11506577	2036,22	DCTN3	dynactin subunit 3
79415	2,81E-67	6,66E+01	3,05E-68	0,0639	-17,4568314	-1,11508437	1517,85	CYBC1	cytochrome b-245 chaperone 1
54543	1,43E-75	7,48E+01	1,30E-76	0,0602	-18,5250861	-1,11508848	3053,84	TOMM7	translocase of outer mitochondrial membrane 7
392	7,43E-106	1,05E+02	3,76E-107	0,0507	-21,9879259	-1,11512571	4296,28	ARHGAP1	Rho GTPase activating protein 1
150678	5,79E-50	4,92E+01	9,19E-51	0,0744	-14,9851123	-1,11526184	890,14	COPS9	COP9 signalosome subunit 9
9361	7,19E-105	1,04E+02	3,72E-106	0,051	-21,883578	-1,11563536	4712,48	LONP1	lon peptidase 1, mitochondrial
10948	1,62E-92	9,18E+01	1,06E-93	0,0543	-20,5343422	-1,11583437	2075,24	STARD3	StAR related lipid transfer domain containing 3
10519	7,67E-81	8,01E+01	6,24E-82	0,0582	-19,1728833	-1,11634879	2788,81	CIB1	calcium and integrin binding 1
2197	9,33E-89	8,80E+01	6,51E-90	0,0555	-20,1061922	-1,11647918	8233,17	FAU	FAU ubiquitin like and ribosomal protein S30 fusion
132884	5,29E-02	1,28E+00	4,11E-02	0,5467	-2,0424042	-1,11649282	10,24	EVC2	EvC ciliary complex subunit 2
26063	1,21E-19	1,89E+01	4,05E-20	0,1216	-9,1867513	-1,1170541	250,68	DECR2	2,4-dienoyl-CoA reductase 2
6175	6,71E-150	1,49E+02	1,65E-151	0,0426	-26,2180938	-1,1170921	127919,56	RPLP0	ribosomal protein lateral stalk subunit P0
51092	2,71E-79	7,86E+01	2,28E-80	0,0588	-18,9848012	-1,11719529	1390,7	SIDT2	SID1 transmembrane family member 2
57165	5,27E-02	1,28E+00	4,10E-02	0,5466	-2,0439399	-1,11726685	11,33	GJC2	gap junction protein gamma 2
79058	1,18E-72	7,19E+01	1,14E-73	0,0615	-18,1566543	-1,11746007	1185,82	ASPSCR1	ASPSCR1 tether for SLC2A4, UBX domain containing
389792	7,18E-19	1,81E+01	2,47E-19	0,1243	-8,990263	-1,11753473	220,87	IER5L	immediate early response 5 like
440400	1,08E-77	7,70E+01	9,42E-79	0,0595	-18,7882953	-1,1179219	3197,46	RNASEK	ribonuclease K
2878	1,99E-136	1,36E+02	5,90E-138	0,0447	-25,001444	-1,11798137	5231,35	GPX3	glutathione peroxidase 3
3795	9,24E-32	3,10E+01	2,24E-32	0,0944	-11,846466	-1,11813789	403,34	KHK	ketohexokinase
5355	8,25E-163	1,62E+02	1,67E-164	0,0409	-27,3339685	-1,11852626	16012	PLP2	proteolipid protein 2
79651	4,38E-74	7,34E+01	4,09E-75	0,061	-18,3383154	-1,118606	1850,21	RHBDF2	rhomboid 5 homolog 2
533	4,13E-111	1,10E+02	1,90E-112	0,0497	-22,5346535	-1,11900671	4229,46	ATP6V0B	ATPase H+ transporting V0 subunit b
85456	3,32E-144	1,43E+02	8,89E-146	0,0435	-25,7106317	-1,11911597	5463,04	TNKS1BP1	tankyrase 1 binding protein 1
60678	1,87E-45	4,47E+01	3,31E-46	0,0784	-14,2711092	-1,11932264	623,76	EEFSEC	eukaryotic elongation factor, selenocysteine-tRNA specific
1632	2,70E-46	4,56E+01	4,68E-47	0,0777	-14,4068701	-1,11950337	792,8	ECI1	enoyl-CoA delta isomerase 1
666	9,67E-53	5,20E+01	1,45E-53	0,0727	-15,4080309	-1,11988189	1555,05	BOK	BCL2 family apoptosis regulator BOK
55640	2,89E-07	6,54E+00	1,51E-07	0,2135	-5,2511585	-1,12108475	69,18	FLVCR2	FLVCR heme transporter 2
5438	8,20E-64	6,31E+01	9,59E-65	0,066	-16,990903	-1,12117802	1376,35	POLR2I	RNA polymerase II subunit I
55643	2,06E-64	6,37E+01	2,38E-65	0,0657	-17,072418	-1,12118148	2012,31	BTBD2	BTB domain containing 2
728239	3,14E-24	2,35E+01	9,31E-25	0,1092	-10,2731985	-1,12136753	297,26	MAGED4	MAGE family member D4
51102	3,87E-48	4,74E+01	6,41E-49	0,0763	-14,7003627	-1,12146314	823,31	MECR	mitochondrial trans-2-enoyl-CoA reductase
11054	5,72E-152	1,51E+02	1,38E-153	0,0425	-26,3997974	-1,12151401	4450,76	OGFR	opioid growth factor receptor
10945	3,88E-171	1,70E+02	6,97E-173	0,04	-28,0301633	-1,12187735	11202,01	KDELR1	KDEL endoplasmic reticulum protein retention receptor 1
5605	4,14E-125	1,24E+02	1,50E-126	0,0469	-23,9297161	-1,12192935	6089,96	MAP2K2	mitogen-activated protein kinase kinase 2
6834	1,79E-46	4,57E+01	3,08E-47	0,0777	-14,4357464	-1,12225607	832,82	SURF1	SURF1 cytochrome c oxidase assembly factor
84740	6,08E-147	1,46E+02	1,55E-148	0,0432	-25,9561912	-1,12246321	4045,21	AFAP1-AS1	AFAP1 antisense RNA 1
90362	3,81E-03	2,42E+00	2,62E-03	0,3732	-3,0088326	-1,12291754	23,65	FAM110B	family with sequence similarity 110 member B
9708	2,04E-05	4,69E+00	1,19E-05	0,2564	-4,3799593	-1,12296445	46,2	PCDHGA8	protocadherin gamma subfamily A, 8
4695	2,09E-46	4,57E+01	3,61E-47	0,0779	-14,4248586	-1,12323835	737,77	NDUFA2	NADH:ubiquinone oxidoreductase subunit A2
51294	5,66E-04	3,25E+00	3,64E-04	0,3151	-3,5647146	-1,12331395	31,91	PCDH12	protocadherin 12
2275	2,68E-52	5,16E+01	4,04E-53	0,0732	-15,3415036	-1,123504	1012,7	FHL3	four and a half LIM domains 3
4600	4,57E-18	1,73E+01	1,61E-18	0,1279	-8,7818305	-1,12353588	217,07	MX2	MX dynamin like GTPase 2
6284	9,26E-141	1,40E+02	2,58E-142	0,0442	-25,3991783	-1,12354068	3708,19	S100A13	S100 calcium binding protein A13
200185	3,34E-108	1,07E+02	1,61E-109	0,0506	-22,2340082	-1,12395533	2388,99	KRTCAP2	keratinocyte associated protein 2
102465519	2,34E-02	1,63E+00	1,74E-02	0,4725	-2,3787277	-1,1239737	13,74	MIR6861	microRNA 6861
26255	5,12E-02	1,29E+00	3,98E-02	0,5471	-2,0560174	-1,12481793	10,81	PTTG3P	pituitary tumor-transforming 3, pseudogene
3385	1,63E-43	4,28E+01	3,03E-44	0,0806	-13,9526054	-1,12513289	714,18	ICAM3	intercellular adhesion molecule 3
728024	2,38E-03	2,62E+00	1,61E-03	0,3568	-3,154262	-1,12543501	25,36	LOC728024	STING1 ER exit protein 1 pseudogene
64743	3,94E-72	7,14E+01	3,85E-73	0,0622	-18,0895617	-1,12577088	2013,18	WDR13	WD repeat domain 13
1535	5,47E-78	7,73E+01	4,73E-79	0,0598	-18,8248433	-1,12602301	1864,57	CYBA	cytochrome b-245 alpha chain
197257	2,31E-04	3,64E+00	1,44E-04	0,2963	-3,8010484	-1,12607657	37,99	LDHD	lactate dehydrogenase D
83874	6,93E-45	4,42E+01	1,25E-45	0,0794	-14,1784673	-1,12633899	601,66	TBC1D10A	TBC1 domain family member 10A
7041	5,28E-95	9,43E+01	3,29E-96	0,0541	-20,8130964	-1,126946	1906,13	TGFB1I1	transforming growth factor beta 1 induced transcript 1
105374177	1,52E-04	3,82E+00	9,34E-05	0,2885	-3,9070323	-1,12716257	43,28	LINC02029	long intergenic non-protein coding RNA 2029
64949	9,29E-61	6,00E+01	1,17E-61	0,068	-16,5688109	-1,12748283	1034,9	MRPS26	mitochondrial ribosomal protein S26
100529209	2,74E-94	9,36E+01	1,73E-95	0,0544	-20,7334484	-1,12766357	3981,09	RNASEK-C1	RNASEK-C17orf49 readthrough
55844	1,43E-116	1,16E+02	6,04E-118	0,0489	-23,0885006	-1,12873771	3734,52	PPP2R2D	protein phosphatase 2 regulatory subunit Bdelta
387496	3,18E-11	1,05E+01	1,40E-11	0,1671	-6,7581291	-1,12901152	119,01	RASL11A	RAS like family 11 member A
170961	6,02E-03	2,22E+00	4,23E-03	0,3947	-2,8606453	-1,12902669	19,86	ANKRD24	ankyrin repeat domain 24
100126326	5,16E-02	1,29E+00	4,01E-02	0,5503	-2,0525319	-1,12941995	9,89	MIR936	microRNA 936
3098	1,78E-187	1,87E+02	2,59E-189	0,0385	-29,3472103	-1,12971547	15577,16	HK1	hexokinase 1
94032	1,15E-45	4,49E+01	2,04E-46	0,079	-14,3050222	-1,12988329	672,39	CAMK2N2	calcium/calmodulin dependent protein kinase II inhibitor 2
23223	7,37E-100	9,91E+01	4,18E-101	0,0529	-21,3467291	-1,13012916	2841,99	RRP12	ribosomal RNA processing 12 homolog
5499	2,66E-104	1,04E+02	1,40E-105	0,0518	-21,8232306	-1,13020782	9588,97	PPP1CA	protein phosphatase 1 catalytic subunit alpha
102725231	1,35E-09	8,87E+00	6,35E-10	0,1829	-6,1815283	-1,13056474	92,94	LOC102725	uncharacterized LOC102725231
221395	1,08E-241	2,41E+02	8,82E-244	0,0339	-33,3442762	-1,13085592	37774,76	ADGRF5	adhesion G protein-coupled receptor F5
58506	1,12E-119	1,19E+02	4,44E-121	0,0483	-23,3983658	-1,13094285	4170,02	SCAF1	SR-related CTD associated factor 1
79709	4,09E-87	8,64E+01	2,95E-88	0,0568	-19,9160992	-1,13102174	13740,34	COLGALT1	collagen beta(1-O)galactosyltransferase 1
100532735	4,75E-60	5,93E+01	6,08E-61	0,0687	-16,4695072	-1,13102619	921,36	INO80B-WBI	INO80B-WBP1 readthrough (NMD candidate)
54732	6,34E-147	1,46E+02	1,62E-148	0,0436	-25,9544949	-1,13113652	8642,7	TMED9	transmembrane p24 trafficking protein 9
100130776	5,27E-26	2,53E+01	1,49E-26	0,1061	-10,6648047	-1,13130138	317,22	AGAP2-AS1	AGAP2 antisense RNA 1
100507475	4,18E-02	1,38E+00	3,21E-02	0,5281	-2,1432734	-1,13188328	10,77	IDH1-AS1	IDH1 antisense RNA 1
10809	3,42E-56	5,55E+01	4,76E-57	0,0711	-15,9179719	-1,13227656	789,74	STARD10	StAR related lipid transfer domain containing 10
35	3,14E-24	2,35E+01	9,31E-25	0,1103	-10,2731483	-1,13262205	277,99	ACADS	acyl-CoA dehydrogenase short chain
100616500	1,30E-04	3,89E+00	7,94E-05	0,287	-3,9463091	-1,13268136	39,37	MIR4683	microRNA 4683
388389	1,54E-13	1,28E+01	6,24E-14	0,151	-7,5028539	-1,13274029	140,52	CCDC103	coiled-coil domain containing 103
221927	1,36E-65	6,49E+01	1,53E-66	0,0657	-17,2319902	-1,1327927	1449,11	BRAT1	BRCA1 associated ATM activator 1
55684	3,45E-108	1,07E+02	1,66E-109	0,051	-22,2325497	-1,13307418	4142,27	RABL6	RAB, member RAS oncogene family like 6
100507156	3,95E-84	8,34E+01	3,00E-85	0,0579	-19,5662295	-1,13308841	1733,04	LOC100507	uncharacterized LOC100507156
2785	1,14E-04	3,94E+00	6,95E-05	0,2848	-3,9780493	-1,13309793	37,84	GNG3	G protein subunit gamma 3
10607	1,88E-72	7,17E+01	1,83E-73	0,0625	-18,1306535	-1,13348833	1827,38	TBL3	transducin beta like 3
283234	1,24E-08	7,91E+00	6,04E-09	0,1949	-5,8155172	-1,13373092	87,29	CCDC88B	coiled-coil domain containing 88B
5345	8,02E-03	2,10E+00	5,70E-03	0,4101	-2,7647808	-1,13389144	19,93	SERPINF2	serpin family F member 2
64951	3,29E-103	1,02E+02	1,76E-104	0,0522	-21,7071421	-1,13398372	2134,4	MRPS24	mitochondrial ribosomal protein S24

203	5,21E-80	7,93E+01	4,30E-81	0,0595	-19,0721264	-1,13408582	1759,61	AK1	adenylate kinase 1
10195	2,22E-93	9,27E+01	1,43E-94	0,055	-20,6315853	-1,1349438	3058,13	ALG3	ALG3 alpha-1,3- mannosyltransferase
23295	1,40E-77	7,69E+01	1,23E-78	0,0605	-18,7742753	-1,13509195	1423,83	MGRN1	mahogunin ring finger 1
230	6,10E-20	1,92E+01	2,03E-20	0,1226	-9,2607406	-1,13514686	223,66	ALDOC	aldolase, fructose-bisphosphate C
2946	7,26E-40	3,91E+01	1,46E-40	0,0851	-13,334507	-1,13525545	499,37	GSTM2	glutathione S-transferase mu 2
388552	1,28E-41	4,09E+01	2,48E-42	0,0833	-13,6349321	-1,13564624	539,18	BLOC1S3	biogenesis of lysosomal organelles complex 1 subunit 3
9144	1,09E-104	1,04E+02	5,67E-106	0,0519	-21,8643935	-1,13570068	6329,35	SYNGR2	synaptogyrin 2
9997	1,24E-23	2,29E+01	3,73E-24	0,112	-10,1383847	-1,13584463	314,31	SCO2	synthesis of cytochrome C oxidase 2
606500	6,27E-04	3,20E+00	4,05E-04	0,3213	-3,5365736	-1,13617404	29,36	SNORD68	small nucleolar RNA, C/D box 68
3984	1,11E-87	8,70E+01	7,91E-89	0,0569	-19,9819254	-1,13625204	2679,91	LIMK1	LIM domain kinase 1
10072	3,64E-104	1,03E+02	1,92E-105	0,0521	-21,8087336	-1,1364705	3952,06	DPP3	dipeptidyl peptidase 3
7851	6,00E-35	3,42E+01	1,35E-35	0,0913	-12,4529152	-1,13655767	482,15	MALL	mal, T cell differentiation protein like
11151	1,61E-11	1,08E+01	7,01E-12	0,1657	-6,8573584	-1,1365619	127,02	CORO1A	coronin 1A
1892	2,37E-136	1,36E+02	7,01E-138	0,0455	-24,9945524	-1,1366774	5661,11	ECHS1	enoyl-CoA hydratase, short chain 1
10400	2,54E-75	7,46E+01	2,32E-76	0,0615	-18,4936951	-1,13726494	1215,01	PEMT	phosphatidylethanolamine N-methyltransferase
2101	2,82E-63	6,25E+01	3,33E-64	0,0672	-16,9176846	-1,13763908	1687,22	ESRRA	estrogen related receptor alpha
1847	3,56E-106	1,05E+02	1,79E-107	0,0517	-22,0215877	-1,13770232	2619,38	DUSP5	dual specificity phosphatase 5
7036	1,60E-06	5,80E+00	8,75E-07	0,2315	-4,9177878	-1,13846307	59,21	TFR2	transferrin receptor 2
8495	6,46E-31	3,02E+01	1,60E-31	0,0975	-11,6804459	-1,13886194	439,55	PPFIBP2	PPFIA binding protein 2
6509	6,28E-68	6,72E+01	6,70E-69	0,065	-17,5432569	-1,13948067	1015,8	SLC1A4	solute carrier family 1 member 4
9446	1,71E-144	1,44E+02	4,54E-146	0,0443	-25,7367474	-1,13952507	7227,03	GSTO1	glutathione S-transferase omega 1
6840	4,73E-122	1,21E+02	1,82E-123	0,0482	-23,6318009	-1,1398867	3758,58	SVIL	supervillin
57232	1,16E-02	1,94E+00	8,39E-03	0,4325	-2,6360646	-1,14003885	16,34	ZNF630	zinc finger protein 630
5175	2,24E-30	2,96E+01	5,65E-31	0,0986	-11,5729762	-1,14097091	377,66	PECAM1	platelet and endothelial cell adhesion molecule 1
439	1,41E-86	8,59E+01	1,03E-87	0,0575	-19,853356	-1,14098649	5666,61	GET3	guided entry of tail-anchored proteins factor 3, ATPase
55289	4,26E-15	1,44E+01	1,65E-15	0,1433	-7,9651669	-1,14104424	176,47	ACOXL	acyl-CoA oxidase like
126328	4,58E-67	6,63E+01	5,00E-68	0,0655	-17,4286373	-1,14105542	3175,01	NDUFA11	NADH:ubiquinone oxidoreductase subunit A11
3384	2,57E-36	3,56E+01	5,57E-37	0,0898	-12,7046242	-1,14124733	523,43	ICAM2	intercellular adhesion molecule 2
10534	4,00E-51	5,04E+01	6,17E-52	0,0753	-15,1635233	-1,14195679	990,02	ZNRD2	zinc ribbon domain containing 2
128178	6,44E-08	7,19E+00	3,26E-08	0,2067	-5,5270103	-1,14232203	80	EDARADD	EDAR associated death domain
91319	1,49E-02	1,83E+00	1,09E-02	0,4486	-2,546896	-1,14251208	17,26	DERL3	derlin 3
10459	2,45E-71	7,06E+01	2,43E-72	0,0635	-17,9877918	-1,1425721	1558,87	MAD2L2	mitotic arrest deficient 2 like 2
170463	1,92E-68	6,77E+01	2,03E-69	0,0649	-17,6110794	-1,14266549	1646,23	SSBP4	single stranded DNA binding protein 4
64598	3,03E-31	3,05E+01	7,46E-32	0,0973	-11,7454085	-1,14283671	476,88	MOSPD3	motile sperm domain containing 3
6191	3,08E-205	2,05E+02	3,73E-207	0,0372	-30,7137707	-1,14297293	61171,11	RPS4X	ribosomal protein S4 X-linked
55317	3,09E-73	7,25E+01	2,94E-74	0,0627	-18,2308663	-1,14326879	1165,18	AP5S1	adaptor related protein complex 5 subunit sigma 1
2026	1,30E-134	1,34E+02	3,93E-136	0,046	-24,8331392	-1,14337275	3746,18	ENO2	enolase 2
57468	8,98E-03	2,05E+00	6,41E-03	0,4195	-2,7260898	-1,14361877	18,98	SLC12A5	solute carrier family 12 member 5
55647	1,47E-21	2,08E+01	4,68E-22	0,1185	-9,6550645	-1,14375616	337,25	RAB20	RAB20, member RAS oncogene family
10095	4,91E-100	9,93E+01	2,78E-101	0,0535	-21,3658085	-1,14387033	4190,97	ARPC1B	actin related protein 2/3 complex subunit 1B
100528018	5,05E-98	9,73E+01	2,98E-99	0,0541	-21,1463119	-1,14394429	2670,97	ARL2-SNX15	ARL2-SNX15 readthrough (NMD candidate)
644809	2,91E-03	2,54E+00	1,99E-03	0,37	-3,092323	-1,14423097	22,89	PAK6-AS1	PAK6 antisense RNA 1
64073	1,06E-90	9,00E+01	7,09E-92	0,0563	-20,3292559	-1,1443237	2623,16	C19orf33	chromosome 19 open reading frame 33
8733	1,08E-62	6,20E+01	1,30E-63	0,068	-16,8373923	-1,14455025	3875,25	GPAA1	glycosylphosphatidylinositol anchor attachment 1
100652853	1,35E-05	4,87E+00	7,75E-06	0,2559	-4,4719308	-1,1445757	46,67	LINC01023	long intergenic non-protein coding RNA 1023
56097	1,09E-05	4,96E+00	6,22E-06	0,2533	-4,518718	-1,14477581	47,47	PCDHGC5	protocadherin gamma subfamily C, 5
1289	5,49E-135	1,34E+02	1,65E-136	0,046	-24,8681223	-1,14484843	5150,46	COL5A1	collagen type V alpha 1 chain
110599583	9,41E-12	1,10E+01	4,05E-12	0,1651	-6,9353628	-1,1448896	119,24	EEF1AKMT4	EEF1AKMT4-ECE2 readthrough
114783	1,15E-08	7,94E+00	5,60E-09	0,1964	-5,8283889	-1,14490466	87,15	LMTK3	lemur tyrosine kinase 3
7123	1,21E-04	3,92E+00	7,38E-05	0,289	-3,9635943	-1,14535235	41,93	CLEC3B	C-type lectin domain family 3 member B
1212	3,17E-131	1,30E+02	1,01E-132	0,0467	-24,5153564	-1,1454621	4194,11	CLTB	clathrin light chain B
26115	2,07E-152	1,52E+02	4,92E-154	0,0433	-26,4387164	-1,14580499	4965,64	TANC2	tetratricopeptide repeat, ankyrin repeat and coiled-coil containing 2
80313	2,72E-26	2,56E+01	7,62E-27	0,1068	-10,7268072	-1,1460902	330,54	LRRC27	leucine rich repeat containing 27
10435	1,92E-61	6,07E+01	2,37E-62	0,0688	-16,6645546	-1,14627455	2904,02	CDC42EP2	CDC42 effector protein 2
8659	3,15E-36	3,55E+01	6,85E-37	0,0904	-12,6885243	-1,14700937	626,44	ALDH4A1	aldehyde dehydrogenase 4 family member A1
219699	1,86E-02	1,73E+00	1,36E-02	0,465	-2,4666742	-1,14708958	14,7	UNC5B	unc-5 netrin receptor B
353091	3,50E-12	1,15E+01	1,49E-12	0,1622	-7,075757	-1,14778538	127,13	RAET1G	retinoic acid early transcript 1G
200315	3,23E-06	5,49E+00	1,79E-06	0,2404	-4,7758279	-1,1479095	54,23	APOBEC3A	apolipoprotein B mRNA editing enzyme catalytic subunit 3A
101059906	1,08E-03	2,97E+00	7,12E-04	0,3391	-3,384887	-1,14796092	28,39	LOC101059906	
10237	1,13E-131	1,31E+02	3,56E-133	0,0468	-24,5578697	-1,14820182	2810,52	SLC35B1	solute carrier family 35 member B1
7349	3,40E-03	2,47E+00	2,33E-03	0,3774	-3,0443085	-1,14887849	21,28	UCN	urocortin
5531	1,17E-102	1,02E+02	6,32E-104	0,0531	-21,6482357	-1,14937706	2841,38	PPP4C	protein phosphatase 4 catalytic subunit
11068	5,29E-46	4,53E+01	9,23E-47	0,0801	-14,3599474	-1,14967682	626,3	CYB561D2	cytochrome b561 family member D2
391	3,22E-89	8,85E+01	2,23E-90	0,057	-20,1592064	-1,1496998	2617,99	RHOG	ras homolog family member G
126208	2,96E-59	5,85E+01	3,85E-60	0,0703	-16,3574104	-1,15019072	1067,5	ZNF787	zinc finger protein 787
84988	2,85E-56	5,55E+01	3,96E-57	0,0722	-15,9294514	-1,15038439	1142,47	PPP1R16A	protein phosphatase 1 regulatory subunit 16A
7737	1,26E-64	6,39E+01	1,45E-65	0,0673	-17,1014112	-1,15086942	1149,23	RNF113A	ring finger protein 113A
8705	7,34E-06	5,13E+00	4,15E-06	0,2502	-4,6037678	-1,1516978	49,89	B3GALT4	beta-1,3-galactosyltransferase 4
1938	1,33E-131	1,31E+02	4,21E-133	0,0469	-24,5511016	-1,15221637	44002,48	EEF2	eukaryotic translation elongation factor 2
168544	5,22E-07	6,28E+00	2,77E-07	0,2243	-5,1383853	-1,15239884	70,68	ZNF467	zinc finger protein 467
9679	1,14E-45	4,49E+01	2,02E-46	0,0806	-14,3057262	-1,1525308	623,32	FAM53B	family with sequence similarity 53 member B
115817	1,47E-68	6,78E+01	1,55E-69	0,0654	-17,6260355	-1,15293849	1060,91	DHRS1	dehydrogenase/reductase 1
101927682	9,09E-16	1,50E+01	3,44E-16	0,1414	-8,1568612	-1,15324018	183,59	CD81-AS1	CD81 antisense RNA 1
1508	2,47E-186	1,86E+02	3,63E-188	0,0394	-29,257275	-1,15329787	21862,58	CTSB	cathepsin B
55620	1,88E-50	4,97E+01	2,96E-51	0,0766	-15,0602025	-1,15334178	674,4	STAP2	signal transducing adaptor family member 2
6576	8,14E-83	8,21E+01	6,34E-84	0,0595	-19,4100727	-1,1547245	1538,8	SLC25A1	solute carrier family 25 member 1
10381	6,78E-84	8,32E+01	5,20E-85	0,0591	-19,5382082	-1,15480456	3793,91	TUBB3	tubulin beta 3 class III
10025	1,34E-56	5,59E+01	1,84E-57	0,0723	-15,9772303	-1,15483464	1411,35	MED16	mediator complex subunit 16
65991	2,03E-124	1,24E+02	7,48E-126	0,0484	-23,862691	-1,15493211	2721,51	FUNDC2	FUN14 domain containing 2
112268088	4,00E-03	2,40E+00	2,76E-03	0,3859	-2,9932739	-1,15521437	20,74	LOC112268(	uncharacterized LOC112268088
51093	7,26E-40	3,91E+01	1,46E-40	0,0867	-13,3345049	-1,15552998	635,17	METTL25B	methyltransferase like 25B
221421	2,91E-45	4,45E+01	5,17E-46	0,0812	-14,2400426	-1,1556505	641,43	RSPH9	radial spoke head component 9
6793	1,78E-205	2,05E+02	2,15E-207	0,0376	-30,7316696	-1,15637723	8376,52	STK10	serine/threonine kinase 10
56915	3,91E-62	6,14E+01	4,74E-63	0,069	-16,7605768	-1,1566941	1509,35	EXOSC5	exosome component 5
105374809	1,23E-32	3,19E+01	2,93E-33	0,0963	-12,0158343	-1,15673213	374,64	LOC105374(	uncharacterized LOC105374809
51629	1,31E-82	8,19E+01	1,03E-83	0,0597	-19,3852363	-1,15683689	6325,27	SLC25A39	solute carrier family 25 member 39
6324	2,65E-06	5,58E+00	1,46E-06	0,2402	-4,8168764	-1,15688201	55	SCN1B	sodium voltage-gated channel beta subunit 1
79006	1,02E-26	2,60E+01	2,83E-27	0,107	-10,8178729	-1,15740754	447,29	METRN	meteorin, glial cell differentiation regulator
4696	1,04E-64	6,40E+01	1,20E-65	0,0677	-17,1126086	-1,15780102	1582,67	NDUFA3	NADH:ubiquinone oxidoreductase subunit A3
126321	2,55E-84	8,36E+01	1,93E-85	0,0591	-19,5886078	-1,15821597	2214,17	MFSD12	major facilitator superfamily domain containing 12
81557	3,04E-26	2,55E+01	8,53E-27	0,1081	-10,7163664	-1,15835981	296,03	MAGED4B	MAGE family member D4B
8717	3,28E-25	2,45E+01	9,48E-26	0,1104	-10,4912048	-1,15868016	280,65	TRADD	TNFRSF1A associated via death domain
57333	7,08E-23	2,21E+01	2,17E-23	0,1163	-9,9648746	-1,15878583	281,88	RCN3	reticulocalbin 3
11285	2,36E-51	5,06E+01	3,61E-52	0,0763	-15,198593	-1,15895916	825,15	B4GALT7	beta-1,4-galactosyltransferase 7
90522	2,63E-118	1,18E+02	1,08E-119	0,0498	-23,2619995	-1,15901316	4434,68	YIF1B	Yip1 interacting factor homolog B, membrane trafficking protein
136	4,39E-95	9,44E+01	2,73E-96	0,0557	-20,8220166	-1,15930284	3515,29	ADORA2B	adenosine A2b receptor
2203	7,42E-95	9,41E+01	4,64E-96	0,0557	-20,796685	-1,15936615	1844,13	FBP1	fructose-bisphosphatase 1
6723	2,54E-88	8,76E+01	1,79E-89	0,0578	-20,056006	-1,15943001	6856,69	SRM	spermidine synthase
100506022	5,57E-05	4,25E+00	3,32E-05	0,2794	-4,150358	-1,15970285	44,1	LINC02606	long intergenic non-protein coding RNA 2606
3909	8,91E-99	9,81E+01	5,18E-100	0,0546	-21,2287474	-1,15984939	2432,5	LAMA3	laminin subunit alpha 3
200942	8,87E-26	2,51E+01	2,52E-26	0,1093	-10,6156631	-1,16007045	285,59	KLHDC8B	kelch domain containing 8B
105376517	2,60E-02	1,59E+00	1,95E-02	0,4965	-2,3365493	-1,16016038	14,83	LOC105376(	uncharacterized LOC105376517
124944	7,15E-61	6,01E+01	8,99E-62	0,07	-16,5847155	-1,16034679	835,79	C17orf49	chromosome 17 open reading frame 49
10535	5,11E-113	1,12E+02	2,27E-114	0,0511	-22,7299093	-1,16040577	5241,51	RNASEH2A	ribonuclease H2 subunit A
64374	7,50E-116	1,15E+02	3,21E-117	0,0504	-23,016116	-1,16054904	2854,71	SIL1	SIL1 nucleotide exchange factor
57592	1,72E-64	6,38E+01	1,98E-65	0,0679	-17,0832488	-1,16055202	1240,65	ZNF687	zinc finger protein 687
91966	3,22E-58	5,75E+01	4,27E-59	0,0716	-16,2101858	-1,16072803	799,99	EOLA1	endothelium and lymphocyte associated ASCH domain 1
10164	1,81E-02	1,74E+00	1,33E-02	0,469	-2,4753251	-1,16096825	13,92	CHST4	carbohydrate sulfotransferase 4
27043	7,55E-106	1,05E+02	3,82E-107	0,0528	-21,987129	-1,1613242	1975,15	PELP1	proline, glutamate and leucine rich protein 1
25824	2,04E-152	1,52E+02	4,84E-154	0,0439	-26,4393323	-1,16138633	4976,68	PRDX5	peroxiredoxin 5
116541	6,81E-59	5,82E+01	8,94E-60	0,0712	-16,3060629	-1,16153046	926,48	MRPL54	mitochondrial ribosomal protein L54
6916	4,95E-29	2,83E+01	1,29E-29	0,1028	-11,3018241	-1,16167768	334,43	TBXAS1	thromboxane A synthase 1
54461	8,17E-102	1,01E+02	4,51E-103	0,0539	-21,5574676	-1,16186513	4162,02	FBXW5	F-box and WD repeat domain containing 5
26145	1,09E-68	6,80E+01	1,15E-69	0,0659	-17,6429618	-1,16186858	1230,8	IRF2BP1	interferon regulatory factor 2 binding protein 1
50626	6,61E-67	6,62E+01	7,22E-68	0,0668	-17,4076254	-1,16261773	1580	ZFTRAF1	zinc finger TRAF-type containing 1
6122	8,18E-217	2,16E+02	8,54E-219	0,0368	-31,5734964	-1,16289819	49773,77	RPL3	ribosomal protein L3
57731	1,45E-02	1,84E+00	1,05E-02	0,455	-2,557277	-1,16348058	15,14	SPTBN4	spectrin beta, non-erythrocytic 4
140885	1,99E-03	2,70E+00	1,34E-03	0,3628	-3,208202	-1,16401818	23,19	SIRPA	signal regulatory protein alpha
83696	8,17E-78	7,71E+01	7,10E-79	0,0619	-18,8032981	-1,16447911	1283,53	TRAPPC9	trafficking protein particle complex subunit 9
100529264	3,29E-71	7,05E+01	3,28E-72	0,0648	-17,9711483	-1,16502286	1284,05	RAB4B-EGL	RAB4B-EGLN2 readthrough (NMD candidate)

5660	3,24E-160	1,59E+02	6,90E-162	0,043	-27,1130944	-1,16507771	27388,45	PSAP	prosaposin
84316	1,55E-77	7,68E+01	1,36E-78	0,0621	-18,7688724	-1,16518156	1716,86	NAA38	N-alpha-acetyltransferase 38, NatC auxiliary subunit
1351	1,44E-111	1,11E+02	6,55E-113	0,0516	-22,5817812	-1,16603733	5307,94	COX8A	cytochrome c oxidase subunit 8A
3665	3,38E-40	3,95E+01	6,73E-41	0,0871	-13,3920088	-1,1661611	633,75	IRF7	interferon regulatory factor 7
90120	1,43E-73	7,28E+01	1,35E-74	0,0638	-18,2732256	-1,16628626	2608,46	TMEM250	transmembrane protein 250
105375489	1,03E-16	1,60E+01	3,76E-17	0,1386	-8,4202622	-1,16672772	186,6	LOC105375	uncharacterized LOC105375489
10209	2,06E-182	1,82E+02	3,17E-184	0,0403	-28,9457687	-1,16696711	28451,69	EIF1	eukaryotic translation initiation factor 1
4851	1,22E-81	8,09E+01	9,80E-83	0,0606	-19,2689141	-1,16701898	1754,82	NOTCH1	notch receptor 1
2747	7,45E-05	4,13E+00	4,48E-05	0,286	-4,0813689	-1,16725977	38,46	GLUD2	glutamate dehydrogenase 2
1175	7,22E-148	1,47E+02	1,82E-149	0,0449	-26,0384436	-1,16820685	8299,22	AP2S1	adaptor related protein complex 2 subunit sigma 1
4862	8,20E-126	1,25E+02	2,92E-127	0,0487	-23,9979631	-1,16845544	6717,2	NPAS2	neuronal PAS domain protein 2
105372506	2,94E-03	2,53E+00	2,00E-03	0,3782	-3,0900899	-1,16870715	21,84	LOC105372	506
51279	1,30E-22	2,19E+01	4,01E-23	0,118	-9,9037274	-1,16882013	237,84	C1RL	complement C1r subcomponent like
122970	1,09E-13	1,30E+01	4,40E-14	0,1549	-7,5485947	-1,16905722	133,97	ACOT4	acyl-CoA thioesterase 4
100507670	1,28E-04	3,89E+00	7,84E-05	0,2961	-3,9491139	-1,16919288	36,27	ZNF687-AS1	ZNF687 antisense RNA 1
2987	6,54E-88	8,72E+01	4,65E-89	0,0584	-20,0084719	-1,16940281	4092,48	GUK1	guanylate kinase 1
313	4,44E-03	2,35E+00	3,08E-03	0,3951	-2,9597037	-1,16943001	22,44	AOAH	acyloxyacyl hydrolase
22933	6,51E-119	1,18E+02	2,64E-120	0,0501	-23,3221596	-1,169522	2226,52	SIRT2	sirtuin 2
107986820	1,01E-03	3,00E+00	6,62E-04	0,3436	-3,4048385	-1,16988448	29,1	LOC107986	uncharacterized LOC107986820
102724360	3,66E-05	4,44E+00	2,16E-05	0,2755	-4,2480502	-1,17027233	42,11	HOMER3-AS	HOMER3 antisense RNA 1
8660	2,06E-72	7,17E+01	1,99E-73	0,0646	-18,125793	-1,17033841	1099,88	IRS2	insulin receptor substrate 2
6286	2,10E-02	1,68E+00	1,55E-02	0,4838	-2,4204891	-1,17091469	15,36	S100P	S100 calcium binding protein P
23241	1,36E-69	6,89E+01	1,40E-70	0,066	-17,7615633	-1,17146059	1720,75	PACS2	phosphofurin acidic cluster sorting protein 2
7454	4,28E-02	1,37E+00	3,29E-02	0,5492	-2,1333786	-1,17156781	10,4	WAS	WASP actin nucleation promoting factor
102466190	6,06E-28	2,72E+01	1,62E-28	0,1058	-11,0769725	-1,17157829	367,07	MIR6721	microRNA 6721
8266	7,03E-108	1,07E+02	3,44E-109	0,0528	-22,1999684	-1,1716132	2391,91	UBL4A	ubiquitin like 4A
5142	2,35E-46	4,56E+01	4,07E-47	0,0814	-14,4166236	-1,17280295	572,32	PDE4B	phosphodiesterase 4B
4435	9,85E-05	4,01E+00	5,98E-05	0,2923	-4,01376	-1,17329499	35,9	CITED1	Cbp/p300 interacting transactivator with Glu/Asp rich carboxy-terminal domain 1
284361	5,15E-106	1,05E+02	2,60E-107	0,0533	-22,0045659	-1,17336063	2570,09	EMC10	ER membrane protein complex subunit 10
1912	2,01E-132	1,32E+02	6,25E-134	0,0476	-24,6285086	-1,17342286	10297,42	PHC2	polyhomeotic homolog 2
22820	2,01E-202	2,02E+02	2,54E-204	0,0385	-30,5008144	-1,17371821	7986,24	COPG1	COPI coat complex subunit gamma 1
84166	7,58E-60	5,91E+01	9,73E-61	0,0714	-16,4409814	-1,1738043	872,02	NLRC5	NLR family CARD domain containing 5
2852	1,92E-10	9,72E+00	8,71E-11	0,181	-6,4877803	-1,17401666	97,97	GPER1	G protein-coupled estrogen receptor 1
91689	4,42E-42	4,14E+01	8,46E-43	0,0856	-13,7132125	-1,17428768	638,2	SMDT1	single-pass membrane protein with aspartate rich tail 1
10755	1,39E-119	1,19E+02	5,53E-121	0,0502	-23,3890363	-1,17433969	9026,14	GIPC1	GIPC PDZ domain containing family member 1
5016	6,28E-07	6,20E+00	3,35E-07	0,2303	-5,1026113	-1,17487997	64,61	OVGP1	oviductal glycoprotein 1
63874	1,12E-92	9,20E+01	7,34E-94	0,0572	-20,5522975	-1,1748967	2313,03	ABHD4	abhydrolase domain containing 4, N-acyl phospholipase B
60	5,66E-161	1,60E+02	1,19E-162	0,0432	-27,1776395	-1,17522281	169317,11	ACTB	actin beta
6883	8,61E-20	1,91E+01	2,88E-20	0,1274	-9,2235012	-1,17551931	222,12	TAF12	TATA-box binding protein associated factor 12
400566	1,28E-08	7,89E+00	6,27E-09	0,2024	-5,8095158	-1,17578354	82,45	C17orf97	chromosome 17 open reading frame 97
6609	4,04E-90	8,94E+01	2,75E-91	0,0581	-20,2626019	-1,17652693	2163,06	SMPD1	sphingomyelin phosphodiesterase 1
26123	5,89E-121	1,20E+02	2,30E-122	0,05	-23,5243312	-1,17723204	2861,28	TCTN3	tectonic family member 3
4585	3,21E-06	5,49E+00	1,78E-06	0,2465	-4,7773015	-1,17740032	57,15	MUC4	mucin 4, cell surface associated
4758	2,35E-119	1,19E+02	9,44E-121	0,0504	-23,3661883	-1,17774317	3688,8	NEU1	neuraminidase 1
8541	1,18E-10	9,93E+00	5,30E-11	0,1795	-6,5623395	-1,17816321	98,9	PPFIA3	PTPRF interacting protein alpha 3
107984661	2,09E-93	9,27E+01	1,34E-94	0,0571	-20,6345819	-1,17857677	1946,72	LOC107984	uncharacterized LOC107984661
4861	6,14E-07	6,21E+00	3,27E-07	0,2308	-5,1070378	-1,1789069	67,89	NPAS1	neuronal PAS domain protein 1
57418	1,76E-64	6,38E+01	2,03E-65	0,069	-17,0817384	-1,17891856	1524,9	WDR18	WD repeat domain 18
9715	2,68E-19	1,86E+01	9,10E-20	0,1296	-9,0991575	-1,17924936	206,13	FAM131B	family with sequence similarity 131 member B
8878	3,26E-111	1,10E+02	1,50E-112	0,0523	-22,5452203	-1,17944988	20124,68	SQSTM1	sequestosome 1
5106	1,89E-66	6,57E+01	2,09E-67	0,068	-17,3467201	-1,17965839	921,8	PCK2	phosphoenolpyruvate carboxykinase 2, mitochondrial
115939	1,13E-79	7,89E+01	9,36E-81	0,062	-19,031484	-1,17972414	1112,16	TSR3	TSR3 ribosome maturation factor
9788	3,48E-26	2,55E+01	9,77E-27	0,1103	-10,7037654	-1,18050422	287,05	MTSS1	MTSS I-BAR domain containing 1
10169	2,70E-144	1,44E+02	7,18E-146	0,0459	-25,7189116	-1,18060468	4007,42	SERF2	small EDRK-rich factor 2
81502	1,65E-122	1,22E+02	6,26E-124	0,0499	-23,6767442	-1,18118912	12909,18	HM13	histocompatibility minor 13
51073	2,96E-121	1,21E+02	1,14E-122	0,0502	-23,553932	-1,18140447	4320,42	MRPL4	mitochondrial ribosomal protein L4
8986	3,86E-92	9,14E+01	2,55E-93	0,0577	-20,4918118	-1,18191303	3725,99	RPS6KA4	ribosomal protein S6 kinase A4
285313	4,99E-04	3,30E+00	3,20E-04	0,3285	-3,5986761	-1,1823313	30,68	IGSF10	immunoglobulin superfamily member 10
160	1,21E-115	1,15E+02	5,20E-117	0,0514	-22,9952463	-1,18243548	6949,11	AP2A1	adaptor related protein complex 2 subunit alpha 1
124221	4,09E-02	1,39E+00	3,13E-02	0,5493	-2,1526916	-1,18248504	10,1	PRSS30P	serine protease 30, pseudogene
390937	3,25E-02	1,49E+00	2,46E-02	0,5267	-2,247435	-1,18372187	10,95	ERFL	ETS repressor factor like
147015	7,51E-54	5,31E+01	1,10E-54	0,0761	-15,5736121	-1,18497389	685,1	DHRS13	dehydrogenase/reductase 13
967	1,72E-164	1,64E+02	3,44E-166	0,0431	-27,4755183	-1,18515487	12149,35	CD63	CD63 molecule
25855	4,05E-108	1,07E+02	1,96E-109	0,0534	-22,225089	-1,1857348	2610,85	BRMS1	BRMS1 transcriptional repressor and anoikis regulator
84315	1,10E-48	4,80E+01	1,80E-49	0,0802	-14,7860296	-1,18596848	734,36	MON1A	MON1 homolog A, secretory trafficking associated
6515	1,38E-87	8,69E+01	9,89E-89	0,0594	-19,9707538	-1,18625813	1427,44	SLC2A3	solute carrier family 2 member 3
10595	2,87E-04	3,54E+00	1,81E-04	0,3169	-3,7442501	-1,18668589	32,07	ERN2	endoplasmic reticulum to nucleus signaling 2
85395	5,42E-72	7,13E+01	5,30E-73	0,0657	-18,0719541	-1,18686298	1113,12	SLX9	SLX9 ribosome biogenesis factor
5526	2,34E-71	7,06E+01	2,31E-72	0,066	-17,9904881	-1,18769944	1026,46	PPP2R5B	protein phosphatase 2 regulatory subunit B'beta
5372	7,40E-51	5,01E+01	1,15E-51	0,0785	-15,1225479	-1,18773419	735,43	PMM1	phosphomannomutase 1
10078	2,19E-62	6,17E+01	2,64E-63	0,0709	-16,795396	-1,19026734	1419,03	TSSC4	tumor suppressing subtransferable candidate 4
4825	1,19E-06	5,92E+00	6,46E-07	0,2392	-4,9770451	-1,19068608	58,77	NKX6-1	NK6 homeobox 1
147746	3,48E-02	1,46E+00	2,64E-02	0,537	-2,2197651	-1,19191768	10,69	HIPK4	homeodomain interacting protein kinase 4
92579	3,35E-161	1,60E+02	7,05E-163	0,0438	-27,1970009	-1,19193645	4488,72	G6PC3	glucose-6-phosphatase catalytic subunit 3
256302	1,18E-25	2,49E+01	3,37E-26	0,1126	-10,5885343	-1,1926853	336,91	NATD1	N-acetyltransferase domain containing 1
5646	2,52E-77	7,66E+01	2,22E-78	0,0637	-18,7428098	-1,19298526	1833,26	PRSS3	serine protease 3
10148	9,05E-09	8,04E+00	4,40E-09	0,2034	-5,868408	-1,19354803	96,44	EBI3	Epstein-Barr virus induced 3
51148	7,62E-83	8,21E+01	5,94E-84	0,0615	-19,4134831	-1,19374168	2256,87	CERCAM	cerebral endothelial cell adhesion molecule
8237	2,65E-164	1,64E+02	5,31E-166	0,0435	-27,4597662	-1,1943458	4840,26	USP11	ubiquitin specific peptidase 11
9246	2,73E-117	1,17E+02	1,13E-118	0,0516	-23,1607387	-1,194761	2275,97	UBE2L6	ubiquitin conjugating enzyme E2 L6
101930010	9,16E-07	6,04E+00	4,92E-07	0,2376	-5,029283	-1,19514908	57,46	DST-AS1	DST antisense RNA 1
114879	1,57E-35	3,48E+01	3,47E-36	0,0952	-12,5607102	-1,1955639	408,58	OSBPL5	oxysterol binding protein like 5
6001	6,86E-125	1,24E+02	2,50E-126	0,05	-23,9084733	-1,19584434	2937,75	RGS10	regulator of G protein signaling 10
80149	6,96E-108	1,07E+02	3,40E-109	0,0539	-22,2004158	-1,19614984	2488,19	ZC3H12A	zinc finger CCCH-type containing 12A
9784	9,26E-164	1,63E+02	1,86E-165	0,0436	-27,4140724	-1,19626257	5910,52	SNX17	sorting nexin 17
254863	9,09E-61	6,00E+01	1,15E-61	0,0722	-16,5701391	-1,19684957	820,05	TMEM256	transmembrane protein 256
6890	1,86E-154	1,54E+02	4,23E-156	0,045	-26,6177251	-1,19698696	3885,03	TAP1	transporter 1, ATP binding cassette subfamily B member
4565	6,44E-17	1,62E+01	2,35E-17	0,1413	-8,4750379	-1,19759225	292,21	TRNI	tRNA-Ile
55741	7,47E-57	5,61E+01	1,02E-57	0,0748	-16,0137652	-1,19768888	674,7	EDEM2	ER degradation enhancing alpha-mannosidase like protein 2
107985334	9,58E-03	2,02E+00	6,86E-03	0,4432	-2,7033287	-1,1981836	15,85	LOC107985	uncharacterized LOC107985334
1408	4,88E-38	3,73E+01	1,02E-38	0,0921	-13,0137569	-1,19875246	466,87	CRY2	cryptochrome circadian regulator 2
2023	3,14E-226	2,26E+02	2,93E-228	0,0372	-32,2557021	-1,19881399	191094,59	ENO1	enolase 1
54976	9,54E-63	6,20E+01	1,14E-63	0,0712	-16,8450684	-1,19918421	2714,5	C20orf27	chromosome 20 open reading frame 27
3911	1,67E-154	1,54E+02	3,79E-156	0,0451	-26,6218561	-1,19956414	7837,68	LAMA5	laminin subunit alpha 5
8192	2,04E-131	1,31E+02	6,50E-133	0,0489	-24,5334072	-1,19980162	3484,02	CLPP	caseinolytic mitochondrial matrix peptidase proteolytic subunit
105376384	6,71E-19	1,82E+01	2,30E-19	0,1334	-8,9978971	-1,20033528	185,79	LOC105376	uncharacterized LOC105376384
4953	3,69E-146	1,45E+02	9,59E-148	0,0464	-25,8859412	-1,2009403	19896,69	ODC1	ornithine decarboxylase 1
375323	1,33E-21	2,09E+01	4,23E-22	0,1243	-9,665468	-1,20104337	274,03	LHFPL4	LHFPL tetraspan subfamily member 4
1891	1,02E-85	8,50E+01	7,51E-87	0,0608	-19,7533173	-1,20112701	3674,98	ECH1	enoyl-CoA hydratase 1
84232	1,01E-141	1,41E+02	2,78E-143	0,0471	-25,4865704	-1,20132548	9022,26	MAF1	MAF1 homolog, negative regulator of RNA polymerase III
5794	4,12E-13	1,24E+01	1,70E-13	0,163	-7,3708819	-1,20165002	121,71	PTPRH	protein tyrosine phosphatase receptor type H
284184	1,13E-42	4,19E+01	2,14E-43	0,087	-13,8127298	-1,20189559	578,14	NDUFAF8	NADH:ubiquinone oxidoreductase complex assembly factor 8
85352	3,19E-05	4,50E+00	1,88E-05	0,2809	-4,27921	-1,20194532	42,45	SHISAL1	shisa like 1
400759	4,00E-02	1,40E+00	3,07E-02	0,5565	-2,1615753	-1,20292948	10,34	GBP1P1	guanylate binding protein 1 pseudogene 1
6275	2,64E-158	1,58E+02	5,78E-160	0,0446	-26,9494853	-1,20311683	6396,26	S100A4	S100 calcium binding protein A4
738	1,98E-96	9,57E+01	1,20E-97	0,0574	-20,9711847	-1,20370165	2074,04	VPS51	VPS51 subunit of GARP complex
112483	2,10E-71	7,07E+01	2,08E-72	0,0669	-17,9964408	-1,20439361	1173,42	SAT2	spermidine/spermine N1-acetyltransferase family member 2
2647	2,62E-36	3,56E+01	5,68E-37	0,0949	-12,7030963	-1,20508273	391,61	BLOC1S1	biogenesis of lysosomal organelles complex 1 subunit 1
7376	5,37E-91	9,03E+01	3,59E-92	0,0592	-20,3625767	-1,20553832	2870,82	NR1H2	nuclear receptor subfamily 1 group H member 2
81926	7,49E-77	7,61E+01	6,66E-78	0,0645	-18,6841649	-1,20565277	1180,58	ABHD17A	abhydrolase domain containing 17A, depalmitoylase
105373372	1,38E-15	1,49E+01	5,24E-16	0,1487	-8,1058957	-1,20566138	154,98	LOC105373	uncharacterized LOC105373372
147912	1,80E-53	5,27E+01	2,66E-54	0,0777	-15,5171553	-1,20582186	682,28	SIX5	SIX homeobox 5
54838	1,17E-110	1,10E+02	5,45E-112	0,0536	-22,4879203	-1,20595137	1841,77	WBP1L	WW domain binding protein 1 like
10245	2,16E-70	6,97E+01	2,18E-71	0,0675	-17,8656195	-1,20606384	1665,53	TIMM17B	translocase of inner mitochondrial membrane 17B
26020	1,85E-208	2,08E+02	2,15E-210	0,039	-30,9553973	-1,2061825	12712,02	LRP10	LDL receptor related protein 10
107987373	7,32E-46	4,51E+01	1,28E-46	0,0842	-14,3370553	-1,20701078	610,81	LOC107987	replaced by ID 6150
283450	1,01E-89	8,90E+01	6,95E-91	0,0597	-20,216904	-1,20754422	1924,57	HECTD4	HECT domain E3 ubiquitin protein ligase 4
7425	1,04E-05	4,98E+00	5,96E-06	0,2667	-4,5278293	-1,20777124	44,69	VGF	VGF nerve growth factor inducible
79414	2,08E-67	6,67E+01	2,25E-68	0,0691	-17,4741692	-1,20784864	924,19	LRFN3	leucine rich repeat and fibronectin type III domain containing 3
105376396	4,43E-03	2,35E+00	3,07E-03	0,408	-2,9605932	-1,20791306	18,31	LOC105376	uncharacterized LOC105376396

3654	1,63E-110	1,10E+02	7,61E-112	0,0538	-22,4730722	-1,20839366	10667,26	IRAK1	interleukin 1 receptor associated kinase 1
84876	1,21E-90	8,99E+01	8,14E-92	0,0595	-20,3224268	-1,20852871	2021,2	ORAI1	ORAI calcium release-activated calcium modulator 1
23558	3,75E-137	1,36E+02	1,10E-138	0,0482	-25,0684543	-1,20939622	5694,91	WBP2	WW domain binding protein 2
55009	2,61E-35	3,46E+01	5,82E-36	0,0966	-12,519751	-1,20943173	604,51	FAM174C	family with sequence similarity 174 member C
255783	3,91E-11	1,04E+01	1,73E-11	0,1798	-6,72754	-1,20947409	105,83	INAFM1	InaF motif containing 1
282974	1,23E-49	4,89E+01	1,96E-50	0,081	-14,9347423	-1,2099541	855,97	STK32C	serine/threonine kinase 32C
2863	1,98E-69	6,87E+01	2,04E-70	0,0683	-17,7404244	-1,21080288	943,68	GPR39	G protein-coupled receptor 39
79001	4,41E-116	1,15E+02	1,87E-117	0,0526	-23,039515	-1,21121522	2106,6	VKORC1	vitamin K epoxide reductase complex subunit 1
113622	7,07E-33	3,22E+01	1,67E-33	0,1004	-12,0622219	-1,21125061	363,18	ADPRHL1	ADP-ribosylhydrolase like 1
105371956	5,48E-03	2,26E+00	3,83E-03	0,4189	-2,8917592	-1,21144633	19,59	LOC105371	uncharacterized LOC105371956
196743	1,27E-23	2,29E+01	3,82E-24	0,1195	-10,1360013	-1,21150982	234,58	PAOX	polyamine oxidase
3727	5,54E-152	1,51E+02	1,33E-153	0,0459	-26,4011488	-1,2115617	3411,99	JUND	JunD proto-oncogene, AP-1 transcription factor subunit
57593	1,28E-30	2,99E+01	3,21E-31	0,1043	-11,6214542	-1,21263299	309,75	EBF4	EBF family member 4
79789	9,81E-50	4,90E+01	1,56E-50	0,0811	-14,9497055	-1,21269939	592,19	CLMN	calmin
25841	7,03E-72	7,12E+01	6,88E-73	0,0672	-18,0575521	-1,21296669	1192,25	ABTB2	ankyrin repeat and BTB domain containing 2
6666	1,29E-95	9,49E+01	7,90E-97	0,0581	-20,8814123	-1,21340974	1482,93	SOX12	SRY-box transcription factor 12
2593	8,39E-66	6,51E+01	9,38E-67	0,0703	-17,2601947	-1,21355947	1194,28	GAMT	guanidinoacetate N-methyltransferase
84299	1,54E-91	9,08E+01	1,02E-92	0,0594	-20,4239945	-1,21391448	1757,39	MIEN1	migration and invasion enhancer 1
4681	5,45E-70	6,93E+01	5,59E-71	0,0682	-17,8130784	-1,21475683	1120,72	NBL1	NBL1, DAN family BMP antagonist
100506076	3,77E-03	2,42E+00	2,60E-03	0,4034	-3,0117582	-1,21503941	18,81	LOC100506	uncharacterized LOC100506076
149345	3,56E-29	2,84E+01	9,20E-30	0,1073	-11,3311481	-1,21530482	314,57	SHISA4	shisa family member 4
10391	7,03E-85	8,42E+01	5,27E-86	0,0618	-19,6547453	-1,21542007	1165,34	CORO2B	coronin 2B
2907	2,67E-96	9,56E+01	1,62E-97	0,058	-20,9569392	-1,21567605	5611,61	GRINA	glutamate ionotropic receptor NMDA type subunit associated protein 1
874	4,84E-59	5,83E+01	6,32E-60	0,0745	-16,327173	-1,21640334	779,15	CBR3	carbonyl reductase 3
1959	2,40E-03	2,62E+00	1,62E-03	0,3864	-3,1514994	-1,21780231	22,48	EGR2	early growth response 2
79873	4,26E-08	7,37E+00	2,14E-08	0,2175	-5,6004642	-1,21787031	66,47	NUDT18	nudix hydrolase 18
51763	1,61E-96	9,58E+01	9,76E-98	0,058	-20,9810951	-1,21792656	1528,17	INPP5K	inositol polyphosphate-5-phosphatase K
7067	6,82E-74	7,32E+01	6,39E-75	0,0665	-18,3140514	-1,21810947	1502,65	THRA	thyroid hormone receptor alpha
7076	7,20E-124	1,23E+02	2,69E-125	0,0512	-23,8090316	-1,21818872	12085,26	TIMP1	TIMP metallopeptidase inhibitor 1
80045	9,26E-85	8,40E+01	6,96E-86	0,062	-19,6406133	-1,21823829	1148,45	GPR157	G protein-coupled receptor 157
4317	3,24E-02	1,49E+00	2,45E-02	0,5418	-2,2484123	-1,2182797	11,55	MMP8	matrix metallopeptidase 8
54929	3,77E-57	5,64E+01	5,13E-58	0,0759	-16,0567329	-1,21839869	949,55	TMEM161A	transmembrane protein 161A
5880	4,13E-96	9,54E+01	2,52E-97	0,0582	-20,9359318	-1,21889663	9577,43	RAC2	Rac family small GTPase 2
84926	1,48E-85	8,48E+01	1,09E-86	0,0618	-19,7343637	-1,2190015	1263,9	SPRYD3	SPRY domain containing 3
71	3,97E-125	1,24E+02	1,44E-126	0,0509	-23,9315851	-1,21911323	151385,67	ACTG1	actin gamma 1
537	5,00E-128	1,27E+02	1,70E-129	0,0504	-24,2111985	-1,21936436	5125,85	ATP6AP1	ATPase H+ transporting accessory protein 1
105378460	7,28E-38	3,71E+01	1,53E-38	0,0939	-12,9830339	-1,21937215	437,72	LOC105378	uncharacterized LOC105378460
3339	1,95E-108	1,08E+02	9,40E-110	0,0548	-22,2581885	-1,21951935	5511,09	HSPG2	heparan sulfate proteoglycan 2
28231	1,07E-183	1,83E+02	1,60E-185	0,042	-29,0485841	-1,2198315	7267,39	SLCO4A1	solute carrier organic anion transporter family member 4A1
107985050	2,11E-38	3,77E+01	4,38E-39	0,0933	-13,0783367	-1,22005476	435,07	LOC107985	050
29085	1,14E-86	8,59E+01	8,28E-88	0,0615	-19,8643903	-1,22100805	2151,01	PHPT1	phosphohistidine phosphatase 1
5164	1,31E-89	8,89E+01	8,98E-91	0,0604	-20,2042839	-1,2210968	1349,38	PDK2	pyruvate dehydrogenase kinase 2
51079	2,72E-79	7,86E+01	2,28E-80	0,0643	-18,9847035	-1,22116358	3328,52	NDUFA13	NADH:ubiquinone oxidoreductase subunit A13
1468	1,68E-60	5,98E+01	2,13E-61	0,0739	-16,5326887	-1,22201819	1733,31	SLC25A10	solute carrier family 25 member 10
122704	1,92E-94	9,37E+01	1,21E-95	0,0589	-20,7506215	-1,22250153	3252,38	MRPL52	mitochondrial ribosomal protein L52
100131733	4,48E-04	3,35E+00	2,86E-04	0,3372	-3,6276086	-1,22316378	27,03	USP30-AS1	USP30 antisense RNA 1
4354	5,89E-78	7,72E+01	5,10E-79	0,065	-18,8207718	-1,22333366	1218,45	MPP1	MAGUK p55 scaffold protein 1
2706	1,05E-71	7,10E+01	1,03E-72	0,0678	-18,0353238	-1,22364718	870,27	GJB2	gap junction protein beta 2
57146	2,05E-61	6,07E+01	2,55E-62	0,0734	-16,6603473	-1,2236864	785,38	LDAF1	lipid droplet assembly factor 1
10011	2,75E-117	1,17E+02	1,14E-118	0,0528	-23,1603087	-1,22387871	2181,86	SRA1	steroid receptor RNA activator 1
100529144	1,73E-50	4,98E+01	2,71E-51	0,0812	-15,066073	-1,22400135	843	CORO7-PAM	CORO7-PAM16 readthrough
115098	2,00E-105	1,05E+02	1,02E-106	0,0558	-21,9423654	-1,22476013	6057,99	CCDC124	coiled-coil domain containing 124
80271	1,01E-40	4,00E+01	1,99E-41	0,0909	-13,4824115	-1,2258252	531,62	ITPKC	inositol-trisphosphate 3-kinase C
83442	1,98E-152	1,52E+02	4,70E-154	0,0464	-26,4404636	-1,22593097	22081,75	SH3BGRL3	SH3 domain binding glutamate rich protein like 3
192286	6,46E-101	1,00E+02	3,60E-102	0,0572	-21,4611049	-1,22666369	2028,16	HIGD2A	HIG1 hypoxia inducible domain family member 2A
100233156	1,78E-12	1,17E+01	7,49E-13	0,1712	-7,1701451	-1,22757084	111,38	LOC100233	tektin 4 pseudogene
56894	3,60E-160	1,59E+02	7,69E-162	0,0453	-27,1090869	-1,22840621	4203,48	AGPAT3	1-acylglycerol-3-phosphate O-acyltransferase 3
51161	3,98E-65	6,44E+01	4,51E-66	0,0716	-17,1692405	-1,22862064	784,29	C3orf18	chromosome 3 open reading frame 18
55630	2,20E-66	6,57E+01	2,43E-67	0,0709	-17,3380613	-1,22876411	827,75	SLC39A4	solute carrier family 39 member 4
442454	4,20E-03	2,38E+00	2,90E-03	0,4127	-2,9777336	-1,22888662	19,81	UQCRBP1	ubiquinol-cytochrome c reductase binding protein pseudogene 1
293	8,41E-88	8,71E+01	5,98E-89	0,0615	-19,9958987	-1,2297735	10629,92	SLC25A6	solute carrier family 25 member 6
101927559	1,56E-21	2,08E+01	4,97E-22	0,1275	-9,6488901	-1,22978952	218,26	CEBPB-AS1	CEBPB antisense RNA 1
89891	2,96E-121	1,21E+02	1,15E-122	0,0522	-23,5538768	-1,2304379	4427,27	DYNC2I2	dynein 2 intermediate chain 2
283152	1,14E-05	4,94E+00	6,52E-06	0,2729	-4,5087928	-1,2306714	44,35	CCDC153	coiled-coil domain containing 153
6176	1,94E-110	1,10E+02	9,07E-112	0,0548	-22,4652772	-1,23075834	28964,91	RPLP1	ribosomal protein lateral stalk subunit P1
197370	8,87E-63	6,21E+01	1,06E-63	0,0731	-16,8494164	-1,2314665	973,95	NSMCE1	NSE1 homolog, SMC5-SMC6 complex component
56005	9,88E-158	1,57E+02	2,18E-159	0,0458	-26,900305	-1,23176543	3797,04	MYDGF	myeloid derived growth factor
84518	4,65E-09	8,33E+00	2,23E-09	0,2061	-5,9797555	-1,23221457	78,02	CNFN	cornifelin
407977	2,74E-39	3,86E+01	5,59E-40	0,0932	-13,2339741	-1,2330749	403,57	TNFSF12-TN	TNFSF12-TNFSF13 readthrough
84866	1,06E-73	7,30E+01	9,97E-75	0,0674	-18,2898549	-1,23346149	943,78	TMEM25	transmembrane protein 25
4569	2,38E-11	1,06E+01	1,05E-11	0,1814	-6,8000911	-1,2335183	103,23	TRNM	tRNA-Met
4519	1,31E-124	1,24E+02	4,82E-126	0,0517	-23,8810137	-1,23352688	65485,5	CYTB	cytochrome b
4627	8,42E-220	2,19E+02	8,50E-222	0,0388	-31,7914387	-1,23403377	72104,99	MYH9	myosin heavy chain 9
1453	1,39E-211	2,11E+02	1,53E-213	0,0396	-31,1883736	-1,2345132	10115,25	CSNK1D	casein kinase 1 delta
283248	1,50E-03	2,82E+00	9,97E-04	0,3752	-3,2914593	-1,23489012	22,97	RCOR2	REST corepressor 2
9524	1,08E-135	1,35E+02	3,23E-137	0,0495	-24,9334557	-1,23505762	10162,85	TECR	trans-2,3-enoyl-CoA reductase
102465513	8,97E-42	4,10E+01	1,73E-42	0,0904	-13,6612131	-1,23519369	455,88	MIR6852	microRNA 6852
79171	1,72E-125	1,25E+02	6,16E-127	0,0516	-23,9668939	-1,23563522	2965,88	RBM42	RNA binding motif protein 42
23130	1,03E-90	9,00E+01	6,92E-92	0,0608	-20,3304457	-1,23582362	2454,13	ATG2A	autophagy related 2A
23640	1,56E-86	8,58E+01	1,14E-87	0,0623	-19,8482722	-1,23631438	2011,85	HSPBP1	HSPA (Hsp70) binding protein 1
100507347	2,97E-240	2,40E+02	2,45E-242	0,0372	-33,2445527	-1,23666336	19001,97	VIM-AS1	VIM antisense RNA 1
54539	1,67E-118	1,18E+02	6,82E-120	0,0531	-23,2815675	-1,23702384	2698,15	NDUFB11	NADH:ubiquinone oxidoreductase subunit B11
90353	1,46E-12	1,18E+01	6,13E-13	0,1719	-7,1975536	-1,23708259	107,43	CTU1	cytosolic thiouridylase subunit 1
100129792	8,99E-03	2,05E+00	6,42E-03	0,4539	-2,7253518	-1,23709513	14,9	CCDC152	coiled-coil domain containing 152
54555	4,40E-73	7,24E+01	4,20E-74	0,0679	-18,2112724	-1,23741	2273,06	DDX49	DEAD-box helicase 49
7784	8,91E-03	2,05E+00	6,36E-03	0,4537	-2,7285123	-1,23783445	15,01	ZP3	zona pellucida glycoprotein 3
6236	1,09E-29	2,90E+01	2,79E-30	0,1083	-11,4352037	-1,23803383	411,34	RRAD	RRAD, Ras related glycolysis inhibitor and calcium channel regulator
6217	3,60E-162	1,61E+02	7,38E-164	0,0454	-27,2797503	-1,23842925	21438,07	RPS16	ribosomal protein S16
147798	1,23E-03	2,91E+00	8,16E-04	0,3701	-3,3473184	-1,23874517	25,68	TMC4	transmembrane channel like 4
6404	1,40E-16	1,59E+01	5,15E-17	0,1478	-8,3831206	-1,23928557	150,6	SELPLG	selectin P ligand
54101	3,63E-75	7,44E+01	3,33E-76	0,0671	-18,4742843	-1,23957574	1028,58	RIPK4	receptor interacting serine/threonine kinase 4
125988	1,56E-63	6,28E+01	1,83E-64	0,0732	-16,9530022	-1,24038882	1449,67	MICOS13	mitochondrial contact site and cristae organizing system subunit 13
4319	1,84E-03	2,74E+00	1,23E-03	0,3839	-3,2313983	-1,24041235	22,28	MMP10	matrix metallopeptidase 10
4923	4,93E-03	2,31E+00	3,43E-03	0,4241	-2,9260266	-1,24097828	17,68	NTSR1	neurotensin receptor 1
84269	1,36E-23	2,29E+01	4,08E-24	0,1225	-10,1296177	-1,24114883	262,4	CHCHD5	coiled-coil-helix-coiled-coil-helix domain containing 5
26470	2,63E-110	1,10E+02	1,23E-111	0,0553	-22,4517615	-1,24198628	1858,98	SEZ6L2	seizure related 6 homolog like 2
23224	1,40E-103	1,03E+02	7,44E-105	0,0572	-21,7465938	-1,24406699	2625,35	SYNE2	spectrin repeat containing nuclear envelope protein 2
105372733	3,18E-02	1,50E+00	2,40E-02	0,5513	-2,2567763	-1,24425576	10	LOC105372	uncharacterized LOC105372733
100616340	6,22E-05	4,21E+00	3,72E-05	0,3018	-4,1243902	-1,24493806	34,98	MIR4758	microRNA 4758
51596	1,20E-139	1,39E+02	3,41E-141	0,0493	-25,2974042	-1,24702106	10375,67	CUTA	cutA divalent cation tolerance homolog
8613	9,99E-111	1,10E+02	4,64E-112	0,0554	-22,4950961	-1,2471608	1749,89	PLPP3	phospholipid phosphatase 3
116372	1,79E-48	4,77E+01	2,95E-49	0,0845	-14,7529321	-1,24723051	527,45	LYPD1	LY6/PLAUR domain containing 1
102465483	2,71E-02	1,57E+00	2,03E-02	0,5374	-2,3213418	-1,24737913	10,82	MIR6805	microRNA 6805
7094	5,04E-255	2,54E+02	3,67E-257	0,0364	-34,2550123	-1,24766124	39632,57	TLN1	talin 1
80256	2,38E-112	1,12E+02	1,07E-113	0,0551	-22,6615804	-1,24773451	2002,58	ATOSB	atos homolog B
116844	1,51E-04	3,82E+00	9,27E-05	0,3195	-3,9088777	-1,24895482	31,71	LRG1	leucine rich alpha-2-glycoprotein 1
1310	7,62E-05	4,12E+00	4,59E-05	0,3065	-4,0757827	-1,24911522	33,23	COL19A1	collagen type XIX alpha 1 chain
79363	1,91E-06	5,72E+00	1,04E-06	0,2558	-4,8834096	-1,24914691	48,23	CPLANE2	ciliogenesis and planar polarity effector complex subunit 2
257236	6,83E-12	1,12E+01	2,93E-12	0,1789	-6,9810274	-1,24917815	111,96	CCDC96	coiled-coil domain containing 96
203413	1,86E-41	4,07E+01	3,62E-42	0,0918	-13,607414	-1,24960922	498,83	CT83	cancer/testis antigen 83
6187	3,75E-249	2,48E+02	2,86E-251	0,0369	-33,8570117	-1,2499936	53288,52	RPS2	ribosomal protein S2
26231	2,55E-03	2,59E+00	1,73E-03	0,3991	-3,1334654	-1,25046665	20,56	FBXL9P	F-box and leucine rich repeat protein, pseudogene
221491	4,57E-78	7,73E+01	3,94E-79	0,0664	-18,8345287	-1,25105694	1916,81	SMIM29	small integral membrane protein 29
11337	4,79E-197	1,96E+02	6,32E-199	0,0416	-30,0911851	-1,25116981	9457,41	GABARAP	GABA type A receptor-associated protein
84304	2,20E-43	4,27E+01	4,08E-44	0,0898	-13,931408	-1,25141364	852,72	NUDT22	nudix hydrolase 22
25791	1,68E-24	2,38E+01	4,93E-25	0,1211	-10,3343221	-1,25144464	262,71	NGEF	neuronal guanine nucleotide exchange factor
54788	4,54E-149	1,48E+02	1,13E-150	0,0479	-26,1448641	-1,25216968	2952,89	DNAJB12	DnaJ heat shock protein family (Hsp40) member B12
6253	3,70E-42	4,14E+01	7,07E-43	0,0912	-13,7262941	-1,25222857	466,02	RTN2	reticulon 2
415116	5,35E-107	1,06E+02	2,66E-108	0,0567	-22,1077786	-1,25262229	1780,75	PIM3	Pim-3 proto-oncogene, serine/threonine kinase
85014	6,55E-60	5,92E+01	8,40E-61	0,0762	-16,4498783	-1,25269328	1061,04	TMEM141	transmembrane protein 141

92002	8,30E-68	6,71E+01	8,90E-69	0,0715	-17,527114	-1,25273015	770,51	CCNQ	cyclin Q
27132	1,23E-07	6,91E+00	6,30E-08	0,2316	-5,4101642	-1,25312486	58,77	CPNE7	copine 7
10609	1,99E-51	5,07E+01	3,05E-52	0,0824	-15,2096845	-1,25339508	565,09	P3H4	prolyl 3-hydroxylase family member 4 (inactive)
100500804	3,93E-75	7,44E+01	3,61E-76	0,0679	-18,4699292	-1,25355726	1992,09	MIR3654	microRNA 3654
3678	3,88E-162	1,61E+02	7,97E-164	0,046	-27,2769089	-1,25435964	12389,01	ITGA5	integrin subunit alpha 5
126299	2,44E-45	4,46E+01	4,33E-46	0,0881	-14,2524591	-1,25513685	537,46	ZNF428	zinc finger protein 428
105371168	1,09E-02	1,96E+00	7,85E-03	0,4722	-2,6584961	-1,25530661	13,67	LOC105371	uncharacterized LOC105371168
10467	1,73E-84	8,38E+01	1,31E-85	0,064	-19,6084083	-1,25542164	1159,93	ZNHIT1	zinc finger HIT-type containing 1
9546	1,30E-38	3,79E+01	2,68E-39	0,0957	-13,1154787	-1,25565757	472,83	APBA3	amyloid beta precursor protein binding family A member 3
445	2,42E-49	4,86E+01	3,88E-50	0,0844	-14,8891039	-1,25601765	505,35	ASS1	argininosuccinate synthase 1
9636	1,50E-65	6,48E+01	1,69E-66	0,0729	-17,226328	-1,25604557	2248,51	ISG15	ISG15 ubiquitin like modifier
26301	8,06E-03	2,09E+00	5,72E-03	0,4546	-2,7632778	-1,25632356	15,61	GBGT1	globoside alpha-1,3-N-acetylgalactosaminyltransferase 1 (FORS blood group)
28958	1,31E-144	1,44E+02	3,46E-146	0,0488	-25,7473093	-1,25639616	2577,34	COA3	cytochrome c oxidase assembly factor 3
8356	4,09E-02	1,39E+00	3,13E-02	0,5837	-2,1526281	-1,25657603	9,53	H3C12	H3 clustered histone 12
84662	7,39E-56	5,51E+01	1,03E-56	0,0792	-15,8692656	-1,2569341	682,16	GLIS2	GLIS family zinc finger 2
10916	1,14E-245	2,45E+02	8,87E-248	0,0374	-33,6189594	-1,25721027	11186,68	MAGED2	MAGE family member D2
105371566	2,20E-10	9,66E+00	9,99E-11	0,1946	-6,4670534	-1,25818515	87,06	LOC105371	uncharacterized LOC105371566
125058	1,47E-110	1,10E+02	6,85E-112	0,056	-22,4777745	-1,25845871	1655,73	TBC1D16	TBC1 domain family member 16
254122	9,24E-124	1,23E+02	3,47E-125	0,0529	-23,7984221	-1,25865973	8396,64	SNX32	sorting nexin 32
23288	5,09E-62	6,13E+01	6,19E-63	0,0752	-16,7446732	-1,25907419	723,03	IQCE	IQ motif containing E
7542	1,52E-108	1,08E+02	7,33E-110	0,0565	-22,2692957	-1,25912994	1805,72	ZFPL1	zinc finger protein like 1
22901	4,20E-78	7,74E+01	3,61E-79	0,0669	-18,8391005	-1,25943119	951,39	ARSG	arylsulfatase G
100996756	2,91E-03	2,54E+00	1,98E-03	0,4074	-3,0929794	-1,26005821	19,47	LOC100996	uncharacterized LOC100996756
388697	1,78E-12	1,17E+01	7,49E-13	0,1758	-7,1702385	-1,26030881	110,43	HRNR	hornerin
11092	1,90E-11	1,07E+01	8,29E-12	0,1845	-6,8334513	-1,26046594	110,11	SPACA9	sperm acrosome associated 9
23521	2,01E-202	2,02E+02	2,56E-204	0,0413	-30,5005664	-1,26063023	51418,58	RPL13A	ribosomal protein L13a
493913	2,73E-26	2,56E+01	7,63E-27	0,1175	-10,7266223	-1,26064743	239,74	PAPPA-AS1	PAPPA antisense RNA 1
51160	3,02E-88	8,75E+01	2,14E-89	0,0629	-20,0471787	-1,2607154	2746,47	VPS28	VPS28 subunit of ESCRT-I
4913	4,16E-46	4,54E+01	7,25E-47	0,0877	-14,376654	-1,26096787	472,88	NTHL1	nth like DNA glycosylase 1
2057	4,61E-26	2,53E+01	1,30E-26	0,1182	-10,6774437	-1,26235665	260,74	EPOR	erythropoietin receptor
107986827	2,46E-72	7,16E+01	2,40E-73	0,0697	-18,1156875	-1,2627886	1141,64	CZ1P-ASNS	CZ1P-ASNS readthrough
54785	1,06E-30	3,00E+01	2,64E-31	0,1085	-11,6380511	-1,26318412	331,31	BORCS6	BLOC-1 related complex subunit 6
26472	6,65E-209	2,08E+02	7,68E-211	0,0408	-30,9885812	-1,26320406	8277,78	PPP1R14B	protein phosphatase 1 regulatory inhibitor subunit 14B
23030	7,02E-86	8,52E+01	5,17E-87	0,0639	-19,7721853	-1,26407121	1181,43	KDM4B	lysine demethylase 4B
84309	5,23E-64	6,33E+01	6,09E-65	0,0743	-17,017536	-1,26519771	829,23	NUDT16L1	nudix hydrolase 16 like 1
107987250	1,85E-17	1,67E+01	6,64E-18	0,1468	-8,6208921	-1,26525248	157,36	LOC107987	250
3892	2,23E-39	3,87E+01	4,55E-40	0,0955	-13,2494489	-1,26540765	455,71	KRT86	keratin 86
51545	6,11E-47	4,62E+01	1,04E-47	0,0873	-14,510375	-1,26633155	656,98	ZNF581	zinc finger protein 581
54512	7,13E-62	6,11E+01	8,72E-63	0,0757	-16,7242785	-1,26642919	859,95	EXOSC4	exosome component 4
155382	5,18E-03	2,29E+00	3,61E-03	0,4355	-2,9103895	-1,26742376	17,59	VPS37D	VPS37D subunit of ESCRT-I
84326	1,44E-54	5,38E+01	2,09E-55	0,0809	-15,6796099	-1,26777307	967,42	METTL26	methyltransferase like 26
8971	2,76E-116	1,16E+02	1,17E-117	0,0551	-23,0598152	-1,26968087	2319,62	H1-10	H1.10 linker histone
10669	2,20E-07	6,66E+00	1,14E-07	0,2395	-5,3026695	-1,26974774	55	CGREF1	cell growth regulator with EF-hand domain 1
1944	4,32E-13	1,24E+01	1,78E-13	0,1725	-7,3644567	-1,27049677	120,12	EFNA3	ephrin A3
80164	5,47E-07	6,26E+00	2,90E-07	0,2478	-5,1296285	-1,2709561	54,93	PRR36	proline rich 36
51181	2,60E-59	5,86E+01	3,38E-60	0,0777	-16,365431	-1,27105254	1031,74	DCXR	dicarbonyl and L-xylulose reductase
347148	7,52E-05	4,12E+00	4,52E-05	0,3117	-4,0789628	-1,27140876	32,7	QRFP	pyroglutamylated RFamide peptide
101930114	6,21E-04	3,21E+00	4,01E-04	0,3593	-3,5394692	-1,27162402	26,56	HSD11B1-AS	HSD11B1 antisense RNA 1
8029	8,88E-12	1,11E+01	3,82E-12	0,1832	-6,9435405	-1,27221644	103,05	CUBN	cubilin
64137	5,37E-04	3,27E+00	3,45E-04	0,3555	-3,5788618	-1,27223646	25,35	ABCG4	ATP binding cassette subfamily G member 4
127833	2,40E-08	7,62E+00	1,19E-08	0,2234	-5,7009561	-1,27351052	68,27	SYT2	synaptotagmin 2
54344	1,40E-32	3,19E+01	3,34E-33	0,1061	-12,0052044	-1,27380256	332,52	DPM3	dolichyl-phosphate mannosyltransferase subunit 3, regulatory
374907	1,39E-10	9,86E+00	6,26E-11	0,1949	-6,5374669	-1,2743131	88	B3GNT8	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 8
11020	4,03E-17	1,64E+01	1,46E-17	0,1495	-8,5300992	-1,27489389	158,85	IFT27	intraflagellar transport 27
25798	1,85E-93	9,27E+01	1,19E-94	0,0618	-20,640557	-1,27507537	2230,79	BRI3	brain protein I3
10891	2,03E-19	1,87E+01	6,87E-20	0,1398	-9,1297185	-1,27590476	182,27	PPARGC1A	PPARG coactivator 1 alpha
2821	6,07E-245	2,44E+02	4,80E-247	0,038	-33,5687171	-1,27657936	20212,39	GPI	glucose-6-phosphate isomerase
100652759	1,44E-22	2,18E+01	4,46E-23	0,1291	-9,8930559	-1,27692395	206,42	PRICKLE2-A	PRICKLE2 antisense RNA 1
5672	6,21E-13	1,22E+01	2,57E-13	0,1746	-7,3149718	-1,27711906	110,87	PSG4	pregnancy specific beta-1-glycoprotein 4
107986809	1,89E-05	4,72E+00	1,10E-05	0,2906	-4,3966935	-1,27774984	37,32	ELN-AS1	ELN antisense RNA 1
111089941	4,26E-67	6,64E+01	4,65E-68	0,0733	-17,4328714	-1,27805443	719,81	MMP24-AS1	MMP24-AS1-EDEM2 readthrough
5360	2,58E-57	5,66E+01	3,49E-58	0,0795	-16,0805971	-1,27834831	701,13	PLTP	phospholipid transfer protein
9023	5,25E-09	8,28E+00	2,53E-09	0,2145	-5,9597888	-1,27851115	70,65	CH25H	cholesterol 25-hydroxylase
100616453	1,42E-07	6,85E+00	7,32E-08	0,2375	-5,3831924	-1,27860201	55,86	MIR4687	microRNA 4687
2041	2,06E-39	3,87E+01	4,18E-40	0,0965	-13,2557178	-1,27910102	434,55	EPHA1	EPH receptor A1
5333	9,10E-42	4,10E+01	1,76E-42	0,0936	-13,6600927	-1,27923459	437,8	PLCD1	phospholipase C delta 1
11118	2,52E-119	1,19E+02	1,01E-120	0,0548	-23,3631314	-1,27979372	2193,58	BTN3A2	butyrophilin subfamily 3 member A2
10444	4,66E-117	1,16E+02	1,95E-118	0,0553	-23,1374051	-1,27989931	2046,93	ZER1	zyg-11 related cell cycle regulator
51337	1,39E-100	9,99E+01	7,81E-102	0,0598	-21,4250079	-1,2803779	2233,45	THEM6	thioesterase superfamily member 6
4017	2,79E-209	2,09E+02	3,19E-211	0,0413	-31,0168626	-1,28041428	31223,36	LOXL2	lysyl oxidase like 2
105371856	1,02E-05	4,99E+00	5,85E-06	0,2826	-4,5316796	-1,28067288	39,24	LOC105371	uncharacterized LOC105371856
64115	2,01E-37	3,67E+01	4,25E-38	0,0993	-12,9043845	-1,28082887	379,2	VSIR	V-set immunoregulatory receptor
8379	3,55E-103	1,02E+02	1,90E-104	0,059	-21,7035439	-1,28083467	1986,16	MAD1L1	mitotic arrest deficient 1 like 1
6203	2,76E-123	1,23E+02	1,04E-124	0,0539	-23,7523006	-1,28119368	16678,87	RPS9	ribosomal protein S9
10938	7,00E-161	1,60E+02	1,48E-162	0,0472	-27,1696258	-1,28128671	7950,37	EHD1	EH domain containing 1
147965	1,99E-30	2,97E+01	5,01E-31	0,1106	-11,5832575	-1,28135595	307,63	FAM98C	family with sequence similarity 98 member C
101927469	4,25E-02	1,37E+00	3,26E-02	0,5999	-2,1364655	-1,28170424	8,68	LOC101927	uncharacterized LOC101927469
57178	2,73E-174	1,74E+02	4,68E-176	0,0453	-28,2892775	-1,28224451	5793,19	ZMIZ1	zinc finger MIZ-type containing 1
6182	1,95E-129	1,29E+02	6,47E-131	0,0527	-24,3454682	-1,28304068	3614,08	MRPL12	mitochondrial ribosomal protein L12
10335	3,47E-02	1,46E+00	2,63E-02	0,5777	-2,2211655	-1,28322286	10,33	IRAG1	inositol 1,4,5-triphosphate receptor associated 1
768213	1,25E-08	7,90E+00	6,13E-09	0,2208	-5,8131046	-1,28351214	66,98	MIR671	microRNA 671
124976	7,04E-42	4,12E+01	1,35E-42	0,0939	-13,6791122	-1,28419902	468,56	SPNS2	SPNS lysolipid transporter 2, sphingosine-1-phosphate
53836	2,86E-05	4,54E+00	1,67E-05	0,2986	-4,3045265	-1,28542892	41,08	GPR87	G protein-coupled receptor 87
10134	2,56E-158	1,58E+02	5,58E-160	0,0477	-26,9508437	-1,28574942	12100,41	BCAP31	B cell receptor associated protein 31
83937	3,21E-57	5,65E+01	4,35E-58	0,08	-16,0669065	-1,28602898	638,98	RASSF4	Ras association domain family member 4
105370966	2,75E-05	4,56E+00	1,61E-05	0,2986	-4,3132729	-1,28778332	34,81	IDH2-DT	IDH2 divergent transcript
322	1,24E-85	8,49E+01	9,15E-87	0,0652	-19,7433713	-1,28816115	1164,9	APBB1	amyloid beta precursor protein binding family B member 1
79033	3,50E-141	1,40E+02	9,71E-143	0,0506	-25,4375052	-1,28825391	2814,06	ERI3	ERI1 exoribonuclease family member 3
51700	9,85E-79	7,80E+01	8,35E-80	0,0681	-18,9164527	-1,28882138	1069,6	CYB5R2	cytochrome b5 reductase 2
51751	5,94E-04	3,23E+00	3,83E-04	0,3629	-3,5515191	-1,28893323	25,39	HIGD1B	HIG1 hypoxia inducible domain family member 1B
23166	4,45E-12	1,14E+01	1,90E-12	0,1831	-7,041643	-1,28901413	102,04	STAB1	stabilin 1
54922	7,78E-03	2,11E+00	5,52E-03	0,4646	-2,7751581	-1,28929457	14,85	RASIP1	Ras interacting protein 1
3257	4,23E-87	8,64E+01	3,05E-88	0,0647	-19,9144324	-1,28945563	1224,38	HPS1	HPS1 biogenesis of lysosomal organelles complex 3 subunit 1
7083	8,81E-132	1,31E+02	2,76E-133	0,0525	-24,5683016	-1,28966931	4599,2	TK1	thymidine kinase 1
79671	8,27E-42	4,11E+01	1,59E-42	0,0944	-13,6671849	-1,29056671	438,19	NLRX1	NLR family member X1
4549	7,79E-128	1,27E+02	2,65E-129	0,0533	-24,192758	-1,29061381	33340,5	RNR1	s-rRNA
2997	3,17E-138	1,37E+02	9,14E-140	0,0513	-25,1672926	-1,29070583	3538,12	GYS1	glycogen synthase 1
645249	4,87E-14	1,33E+01	1,95E-14	0,1687	-7,654148	-1,29105486	117,81	MNX1-AS1	MNX1 antisense RNA 1 (head to head)
100130519	8,98E-03	2,05E+00	6,41E-03	0,4737	-2,7258542	-1,29125204	14,37	TMEM221	transmembrane protein 221
55343	1,79E-74	7,37E+01	1,66E-75	0,0702	-18,3873824	-1,29144031	987,71	SLC35C1	solute carrier family 35 member C1
101927482	1,24E-04	3,91E+00	7,57E-05	0,3265	-3,9575809	-1,29202204	30,14	HECW2-AS1	HECW2 antisense RNA 1
645700	2,22E-02	1,65E+00	1,65E-02	0,5387	-2,39866	-1,29219882	10,65	ZNF890P	zinc finger protein 890, pseudogene
116540	5,44E-77	7,63E+01	4,82E-78	0,0691	-18,7014158	-1,29286894	1022,5	MRPL53	mitochondrial ribosomal protein L53
10591	7,66E-69	6,81E+01	8,05E-70	0,0732	-17,6632574	-1,2932612	953	DNPH1	2'-deoxynucleoside 5'-phosphate N-hydrolase 1
28996	6,14E-170	1,69E+02	1,13E-171	0,0463	-27,930746	-1,29383883	3494,47	HIPK2	homeodomain interacting protein kinase 2
1465	1,59E-216	2,16E+02	1,67E-218	0,041	-31,5522743	-1,29415132	9605,87	CSRP1	cysteine and glycine rich protein 1
51293	4,15E-130	1,29E+02	1,35E-131	0,0531	-24,4097113	-1,29520973	2965,41	CD320	CD320 molecule
124446	2,32E-97	9,66E+01	1,39E-98	0,0615	-21,0736432	-1,29556352	1704,59	TMEM219	transmembrane protein 219
26007	7,16E-90	8,91E+01	4,90E-91	0,0641	-20,2341826	-1,29602095	1339,83	TKFC	triokinase and FMN cyclase
10226	2,48E-157	1,57E+02	5,49E-159	0,0482	-26,8659885	-1,29618175	6041,27	PLIN3	perilipin 3
100505622	6,11E-15	1,42E+01	2,37E-15	0,1637	-7,920018	-1,29636307	132,95	POU2F2-AS	POU2F2 antisense RNA 1
2232	1,75E-40	3,98E+01	3,45E-41	0,0965	-13,4415264	-1,29651623	450,32	FDXR	ferredoxin reductase
4007	5,93E-134	1,33E+02	1,80E-135	0,0523	-24,7719572	-1,29658026	3746,21	PRICKLE3	prickle planar cell polarity protein 3
3675	2,10E-234	2,34E+02	1,82E-236	0,0395	-32,8357753	-1,29697854	70788,96	ITGA3	integrin subunit alpha 3
84222	8,80E-05	4,06E+00	5,32E-05	0,3213	-4,0409952	-1,2983919	31,55	TMEM191A	transmembrane protein 191A (pseudogene)
100131205	3,83E-17	1,64E+01	1,39E-17	0,1523	-8,5362084	-1,30012808	172,7	RPL21P28	ribosomal protein L21 pseudogene 28
29937	3,69E-99	9,84E+01	2,13E-100	0,0611	-21,2704392	-1,30025777	1260,73	NENF	neudesin neurotrophic factor
8085	4,50E-106	1,05E+02	2,27E-107	0,0591	-22,0107636	-1,30055878	2980,51	KMT2D	lysine methyltransferase 2D
1051	5,49E-76	7,53E+01	4,96E-77	0,07	-18,5766998	-1,30076963	847,24	CEBPB	CCAAT enhancer binding protein beta
101928917	2,74E-04	3,56E+00	1,72E-04	0,3464	-3,7567173	-1,30125508	25,7	HSFX3	heat shock transcription factor family, X-linked member 3

89944	2,65E-38	3,76E+01	5,52E-39	0,0996	-13,0607585	-1,30144984	355,35	GLB1L2	galactosidase beta 1 like 2
100128788	1,53E-02	1,82E+00	1,11E-02	0,5128	-2,5385887	-1,30175188	12,15	SRRM2-AS1	SRRM2 antisense RNA 1
112267986	1,43E-02	1,84E+00	1,04E-02	0,5084	-2,5616163	-1,30244414	12,16	LOC112267	uncharacterized LOC112267986
110599564	4,45E-27	2,64E+01	1,22E-27	0,1196	-10,8948196	-1,30276543	263,79	EEF1AKMT4	EEF1A lysine methyltransferase 4
5190	1,16E-116	1,16E+02	4,89E-118	0,0564	-23,0976587	-1,30342515	2343,97	PEX6	peroxisomal biogenesis factor 6
102724344	2,70E-04	3,57E+00	1,69E-04	0,3467	-3,7606623	-1,30372777	27,03	LINC02188	long intergenic non-protein coding RNA 2188
56666	2,62E-07	6,58E+00	1,37E-07	0,2475	-5,2697433	-1,30424996	51,56	PANX2	pannexin 2
5971	1,79E-72	7,17E+01	1,73E-73	0,0719	-18,1336405	-1,30452527	1087,42	RELB	RELB proto-oncogene, NF-kB subunit
9235	1,07E-62	6,20E+01	1,28E-63	0,0775	-16,8381932	-1,30516539	702,2	IL32	interleukin 32
105375019	2,81E-13	1,26E+01	1,15E-13	0,1759	-7,4225859	-1,30582759	114,05	LOC105375(	uncharacterized LOC105375019
320	3,79E-10	9,42E+00	1,74E-10	0,2047	-6,3827857	-1,30625789	77,01	APBA1	amyloid beta precursor protein binding family A member 1
645332	1,61E-10	9,79E+00	7,30E-11	0,2006	-6,5143739	-1,30646886	83,51	FAM86C2P	family with sequence similarity 86, member A pseudogene
6915	1,43E-06	5,84E+00	7,79E-07	0,2645	-4,9405848	-1,306896	46,75	TBXA2R	thromboxane A2 receptor
105373378	2,21E-02	1,66E+00	1,64E-02	0,5444	-2,4006976	-1,30694597	10,64	LOC105373(	uncharacterized LOC105373378
283383	1,15E-37	3,69E+01	2,42E-38	0,101	-12,9475864	-1,30712492	344,71	ADGRD1	adhesion G protein-coupled receptor D1
8309	9,19E-34	3,30E+01	2,13E-34	0,1069	-12,230796	-1,30725469	305,13	ACOX2	acyl-CoA oxidase 2
10801	3,29E-225	2,24E+02	3,08E-227	0,0406	-32,1826898	-1,30748956	15563,83	SEPTIN9	septin 9
90024	7,72E-18	1,71E+01	2,73E-18	0,1499	-8,7220226	-1,30766915	157,77	FLJ20021	uncharacterized LOC90024
8324	7,98E-124	1,23E+02	2,99E-125	0,055	-23,8046302	-1,30875967	1692,19	FZD7	frizzled class receptor 7
105371038	1,20E-03	2,92E+00	7,95E-04	0,3902	-3,3545506	-1,30887408	21,06	LOC105371(	uncharacterized LOC105371038
51761	3,52E-16	1,55E+01	1,31E-16	0,1584	-8,2722116	-1,30995653	144,08	ATP8A2	ATPase phospholipid transporting 8A2
55691	1,91E-131	1,31E+02	6,06E-133	0,0534	-24,5362726	-1,31074008	2338,95	FRMD4A	FERM domain containing 4A
255374	7,80E-05	4,11E+00	4,70E-05	0,3221	-4,0701813	-1,31080977	30,49	MBLAC1	metallo-beta-lactamase domain containing 1
84885	8,91E-65	6,41E+01	1,02E-65	0,0766	-17,1219401	-1,31097359	1291,23	ZDHHC12	zinc finger DHHC-type palmitoyltransferase 12
3265	4,85E-83	8,23E+01	3,76E-84	0,0675	-19,4369568	-1,31120989	2371,07	HRAS	HRas proto-oncogene, GTPase
79847	1,08E-129	1,29E+02	3,54E-131	0,0538	-24,3702058	-1,31133258	1935,52	MFSD13A	major facilitator superfamily domain containing 13A
81543	3,98E-13	1,24E+01	1,64E-13	0,1778	-7,3753691	-1,31167827	110,91	LRRC3	leucine rich repeat containing 3
369	2,00E-131	1,31E+02	6,34E-133	0,0535	-24,534445	-1,31187899	3691,21	ARAF	A-Raf proto-oncogene, serine/threonine kinase
50512	4,22E-89	8,84E+01	2,93E-90	0,0651	-20,1458152	-1,31202765	1016,52	PODXL2	podocalyxin like 2
23149	4,96E-52	5,13E+01	7,52E-53	0,0858	-15,3010987	-1,31209221	664,23	FCHO1	FCH and mu domain containing endocytic adaptor 1
80776	1,29E-18	1,79E+01	4,45E-19	0,1471	-8,9250529	-1,31285504	161,69	B9D2	B9 domain containing 2
84261	1,39E-48	4,79E+01	2,28E-49	0,089	-14,7700955	-1,31479292	650,54	FBXW9	F-box and WD repeat domain containing 9
10233	5,59E-13	1,23E+01	2,31E-13	0,1794	-7,3294087	-1,31480646	109,61	LRRC23	leucine rich repeat containing 23
4814	1,75E-64	6,38E+01	2,02E-65	0,077	-17,0820516	-1,31490288	1156,98	NINJ1	ninjurin 1
59269	1,30E-116	1,16E+02	5,50E-118	0,057	-23,0925895	-1,31516182	1748,95	HIVEP3	HIVEP zinc finger 3
23464	9,53E-34	3,30E+01	2,21E-34	0,1076	-12,2277571	-1,31572639	464,7	GCAT	glycine C-acetyltransferase
6811	3,37E-127	1,26E+02	1,17E-128	0,0546	-24,1315271	-1,31661938	2986,34	STX5	syntaxin 5
11344	1,96E-111	1,11E+02	8,92E-113	0,0584	-22,568096	-1,31686826	3220,87	TWF2	twinfilin actin binding protein 2
10734	4,71E-09	8,33E+00	2,26E-09	0,2204	-5,9776118	-1,31755651	65,88	STAG3	stromal antigen 3
161145	4,02E-17	1,64E+01	1,46E-17	0,1545	-8,5305647	-1,31783801	144,35	TMEM229B	transmembrane protein 229B
2879	1,09E-192	1,92E+02	1,50E-194	0,0443	-29,7547831	-1,31802885	8353,05	GPX4	glutathione peroxidase 4
144195	3,78E-06	5,42E+00	2,10E-06	0,278	-4,7431773	-1,31840631	41,28	SLC2A14	solute carrier family 2 member 14
823	6,83E-165	1,64E+02	1,36E-166	0,0479	-27,5093567	-1,31841716	8606,37	CAPN1	calpain 1
79803	1,07E-68	6,80E+01	1,13E-69	0,0747	-17,6441119	-1,31860999	1078,16	HPS6	HPS6 biogenesis of lysosomal organelles complex 2 subunit 3
10844	1,54E-187	1,87E+02	2,24E-189	0,0449	-29,352166	-1,31893907	6754,17	TUBGCP2	tubulin gamma complex associated protein 2
26173	2,31E-128	1,28E+02	7,77E-130	0,0544	-24,2433496	-1,31916531	3349,46	INTS1	integrator complex subunit 1
54584	3,26E-34	3,35E+01	7,45E-35	0,1073	-12,3157626	-1,3209696	336,66	GNB1L	G protein subunit beta 1 like
26018	8,16E-106	1,05E+02	4,14E-107	0,0601	-21,9834749	-1,32146251	1300,35	LRIG1	leucine rich repeats and immunoglobulin like domains 1
113246	9,00E-91	9,00E+01	6,03E-92	0,065	-20,3371784	-1,32170307	2158,84	C12orf57	chromosome 12 open reading frame 57
101927635	8,65E-03	2,06E+00	6,17E-03	0,4826	-2,7387237	-1,32176948	14,56	PORCN-DT	PORCN divergent transcript
9500	4,77E-176	1,75E+02	8,03E-178	0,0465	-28,4324687	-1,32210515	4743,3	MAGED1	MAGE family member D1
4987	1,53E-06	5,82E+00	8,32E-07	0,2683	-4,9277147	-1,32227987	44,52	OPRL1	opioid related nociceptin receptor 1
8729	7,19E-239	2,38E+02	6,05E-241	0,0399	-33,1479905	-1,32263378	6873,64	GBF1	golgi brefeldin A resistant guanine nucleotide exchange factor 1
57175	4,54E-108	1,07E+02	2,21E-109	0,0595	-22,2198542	-1,32269894	4778,74	CORO1B	coronin 1B
6234	1,44E-29	2,88E+01	3,71E-30	0,1159	-11,4103623	-1,32301147	10364,64	RPS28	ribosomal protein S28
147685	2,43E-02	1,61E+00	1,81E-02	0,5602	-2,3635589	-1,32409915	10,42	C19orf18	chromosome 19 open reading frame 18
57407	1,29E-96	9,59E+01	7,81E-98	0,0631	-20,9916781	-1,32431897	1281,38	NMRAL1	NmrA like redox sensor 1
100506476	1,15E-03	2,94E+00	7,56E-04	0,3932	-3,3684746	-1,32434437	21,15	MIDEAS-AS	MIDEAS antisense RNA 1
4924	1,15E-144	1,44E+02	3,03E-146	0,0514	-25,7523659	-1,32444889	6142,47	NUCB1	nucleobindin 1
131578	1,86E-09	8,73E+00	8,80E-10	0,2161	-6,1297917	-1,32486507	69,91	LRRC15	leucine rich repeat containing 15
11332	5,61E-109	1,08E+02	2,67E-110	0,0594	-22,3144727	-1,32513785	5819,42	ACOT7	acyl-CoA thioesterase 7
7077	1,32E-270	2,70E+02	8,36E-273	0,0376	-35,2900159	-1,32529211	29179,01	TIMP2	TIMP metallopeptidase inhibitor 2
100128292	1,77E-04	3,75E+00	1,09E-04	0,3426	-3,868755	-1,32562068	27,7	DLG5-AS1	DLG5 antisense RNA 1
8538	1,30E-06	5,89E+00	7,05E-07	0,2673	-4,9599755	-1,3259081	45,3	BARX2	BARX homeobox 2
22924	1,59E-27	2,68E+01	4,30E-28	0,1207	-10,9893236	-1,32596871	232,74	MAPRE3	microtubule associated protein RP/EB family member 3
6050	1,50E-111	1,11E+02	6,81E-113	0,0587	-22,5800105	-1,32642748	9695,67	RNH1	ribonuclease/angiogenin inhibitor 1
81603	4,62E-205	2,04E+02	5,62E-207	0,0432	-30,7004207	-1,32646724	7772,84	TRIM8	tripartite motif containing 8
105372261	2,82E-06	5,55E+00	1,56E-06	0,2763	-4,8036278	-1,32706762	42,07	LOC105372(	uncharacterized LOC105372261
142689	1,60E-02	1,80E+00	1,17E-02	0,5262	-2,5222894	-1,32729699	11,91	ASB12	ankyrin repeat and SOCS box containing 12
5989	2,36E-65	6,46E+01	2,67E-66	0,0772	-17,1997549	-1,32798383	692,79	RFX1	regulatory factor X1
7001	2,26E-161	1,61E+02	4,71E-163	0,0488	-27,2118246	-1,32819695	8985,02	PRDX2	peroxiredoxin 2
9518	3,16E-42	4,15E+01	6,01E-43	0,0967	-13,7379734	-1,32829043	412,39	GDF15	growth differentiation factor 15
5209	4,09E-167	1,66E+02	7,79E-169	0,048	-27,6960675	-1,32957039	3994,47	PFKFB3	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3
102724532	8,48E-06	5,07E+00	4,82E-06	0,2908	-4,5726874	-1,32967503	37,87	SP2-DT	SP2 divergent transcript
80772	1,45E-58	5,78E+01	1,91E-59	0,0818	-16,2597063	-1,32989839	982,91	CPTP	ceramide-1-phosphate transfer protein
140686	1,44E-13	1,28E+01	5,86E-14	0,1771	-7,5112646	-1,33061431	109,45	WFDC3	WAP four-disulfide core domain 3
11067	2,34E-28	2,76E+01	6,20E-29	0,1192	-11,1628691	-1,33089365	254,08	DEPP1	DEPP autophagy regulator 1
101927752	4,27E-19	1,84E+01	1,46E-19	0,1471	-9,0479003	-1,33120258	155,54	CLN8-AS1	CLN8 antisense RNA 1
8644	1,30E-78	7,79E+01	1,11E-79	0,0704	-18,9015165	-1,33150174	857,44	AKR1C3	aldo-keto reductase family 1 member C3
6193	1,25E-129	1,29E+02	4,15E-131	0,0547	-24,3637498	-1,33213772	16250,97	RPS5	ribosomal protein S5
4320	3,20E-10	9,49E+00	1,46E-10	0,2079	-6,4089981	-1,33244904	87,26	MMP11	matrix metallopeptidase 11
6907	1,06E-171	1,71E+02	1,88E-173	0,0475	-28,0768775	-1,33317336	2840,07	TBL1X	transducin beta like 1 X-linked
474384	5,19E-14	1,33E+01	2,07E-14	0,1744	-7,6459175	-1,33325058	107,22	F8A3	coagulation factor VIII associated 3
10101	2,66E-64	6,36E+01	3,08E-65	0,0783	-17,0574684	-1,33540283	1385,27	NUBP2	NUBP iron-sulfur cluster assembly factor 2, cytosolic
105378948	4,60E-31	3,03E+01	1,14E-31	0,1141	-11,709646	-1,33603905	270,47	LOC105378(	uncharacterized LOC105378948
2548	1,57E-94	9,38E+01	9,86E-96	0,0644	-20,760476	-1,33623897	1662,96	GAA	alpha glucosidase
83538	3,11E-04	3,51E+00	1,96E-04	0,3589	-3,7237229	-1,33647651	25,03	ODAD4	outer dynein arm docking complex subunit 4
84850	1,60E-02	1,80E+00	1,17E-02	0,53	-2,5217794	-1,33650607	10,89	GLIS3-AS1	GLIS3 antisense RNA 1
4900	1,99E-87	8,67E+01	1,43E-88	0,067	-19,9525055	-1,33671325	1191,88	NRGN	neurogranin
6781	7,18E-157	1,56E+02	1,59E-158	0,0498	-26,8264127	-1,33692926	6523,66	STC1	stanniocalcin 1
10555	3,65E-71	7,04E+01	3,64E-72	0,0744	-17,965338	-1,33728707	1616,17	AGPAT2	1-acylglycerol-3-phosphate O-acyltransferase 2
5187	1,66E-55	5,48E+01	2,35E-56	0,0846	-15,8177952	-1,33749719	573,3	PER1	period circadian regulator 1
8673	4,21E-172	1,71E+02	7,42E-174	0,0476	-28,1098858	-1,33830754	5082,06	VAMP8	vesicle associated membrane protein 8
113178	6,59E-111	1,10E+02	3,05E-112	0,0595	-22,5137231	-1,33913542	3247,47	SCAMP4	secretory carrier membrane protein 4
113179	1,44E-21	2,08E+01	4,58E-22	0,1387	-9,6571964	-1,33954663	169,77	ADAT3	adenosine deaminase tRNA specific 3
23038	1,79E-122	1,22E+02	6,82E-124	0,0566	-23,6731328	-1,33990236	2141,68	WDTC1	WD and tetratricopeptide repeats 1
4296	1,31E-96	9,59E+01	7,89E-98	0,0638	-20,9911901	-1,33995089	2199,86	MAP3K11	mitogen-activated protein kinase kinase kinase 11
84954	1,50E-19	1,88E+01	5,04E-20	0,1463	-9,1631285	-1,34076091	181,7	MPND	MPN domain containing
29916	1,33E-101	1,01E+02	7,33E-103	0,0623	-21,5349348	-1,34100334	1373,92	SNX11	sorting nexin 11
1026	1,30E-170	1,70E+02	2,34E-172	0,0479	-27,9869223	-1,34106268	6341,36	CDKN1A	cyclin dependent kinase inhibitor 1A
9563	1,13E-223	2,23E+02	1,09E-225	0,0418	-32,071679	-1,34121032	6331,62	H6PD	hexose-6-phosphate dehydrogenase/glucose 1-dehydrogenase
166336	5,53E-78	7,73E+01	4,78E-79	0,0713	-18,8242244	-1,34126249	797,85	PRICKLE2	prickle planar cell polarity protein 2
54985	2,19E-114	1,14E+02	9,64E-116	0,0587	-22,8681558	-1,34180784	3091,26	HCFC1R1	host cell factor C1 regulator 1
10331	3,91E-53	5,24E+01	5,80E-54	0,0868	-15,4669595	-1,34183383	552,79	B3GNT3	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 3
84681	7,55E-97	9,61E+01	4,54E-98	0,0639	-21,0174496	-1,34256856	1210,15	HINT2	histidine triad nucleotide binding protein 2
169436	6,38E-05	4,20E+00	3,82E-05	0,3261	-4,1179928	-1,34272293	32,66	STKLD1	serine/threonine kinase like domain containing 1
59335	2,52E-04	3,60E+00	1,58E-04	0,3555	-3,7787611	-1,34330482	25,4	PRDM12	PR/SET domain 12
9398	1,22E-18	1,79E+01	4,20E-19	0,1504	-8,9315307	-1,34333819	148,91	CD101	CD101 molecule
2873	3,26E-131	1,30E+02	1,04E-132	0,0548	-24,5141259	-1,34392556	5253,08	GPS1	G protein pathway suppressor 1
284427	1,37E-05	4,86E+00	7,86E-06	0,3007	-4,4689259	-1,34401155	35,29	SLC25A41	solute carrier family 25 member 41
144501	1,71E-181	1,81E+02	2,66E-183	0,0466	-28,8722666	-1,34448428	5535,65	KRT80	keratin 80
8321	3,88E-105	1,04E+02	2,00E-106	0,0614	-21,9118556	-1,3446007	1458,94	FZD1	frizzled class receptor 1
100287837	3,49E-04	3,46E+00	2,21E-04	0,3641	-3,6936958	-1,34484399	27,32	ARHGEF17-	ARHGEF17 antisense RNA 1
79763	5,97E-90	8,92E+01	4,08E-91	0,0664	-20,2431861	-1,34487791	1819,95	ISOC2	isochorismatase domain containing 2
105370792	7,02E-33	3,22E+01	1,66E-33	0,1115	-12,0628209	-1,34500319	276,42	LOC105370(	uncharacterized LOC105370792
5654	1,92E-130	1,30E+02	6,23E-132	0,0551	-24,4412902	-1,34559173	2557,3	HTRA1	HtrA serine peptidase 1
8260	5,68E-176	1,75E+02	9,59E-178	0,0473	-28,4262288	-1,34570821	3250,51	NAA10	N-alpha-acetyltransferase 10, NatA catalytic subunit
84065	8,96E-90	8,90E+01	6,15E-91	0,0666	-20,222958	-1,3468164	1321,41	TMEM222	transmembrane protein 222
587	6,99E-105	1,04E+02	3,61E-106	0,0615	-21,8849613	-1,34695755	1693,88	BCAT2	branched chain amino acid transaminase 2
92737	4,37E-58	5,74E+01	5,83E-59	0,0832	-16,1910772	-1,34730611	595,12	DNER	delta/notch like EGF repeat containing

84270	5,96E-98	9,72E+01	3,52E-99	0,0638	-21,1384495	-1,34784661	1634,81	CARD19	caspase recruitment domain family member 19
105751187	8,09E-04	3,09E+00	5,27E-04	0,3888	-3,4663938	-1,34789497	21,04	LRP1-AS	LRP1 antisense RNA
79586	3,98E-99	9,84E+01	2,30E-100	0,0634	-21,266885	-1,34816345	2306,57	CHPF	chondroitin polymerizing factor
652968	4,33E-22	2,14E+01	1,36E-22	0,1379	-9,7812605	-1,34875625	227,43	CASTOR1	cytosolic arginine sensor for mTORC1 subunit 1
23625	2,22E-50	4,97E+01	3,49E-51	0,0897	-15,0492701	-1,34920881	694,91	FAM89B	family with sequence similarity 89 member B
118472	4,47E-106	1,05E+02	2,25E-107	0,0613	-22,0111089	-1,34965572	1299,8	ZNF511	zinc finger protein 511
5585	3,85E-179	1,78E+02	6,24E-181	0,0471	-28,6828661	-1,35064688	21301,27	PKN1	protein kinase N1
3159	6,23E-134	1,33E+02	1,89E-135	0,0546	-24,7698534	-1,3512001	100551,12	HMGA1	high mobility group AT-hook 1
114984	1,91E-58	5,77E+01	2,52E-59	0,0833	-16,2425263	-1,35238626	612,08	FLYWCH2	FLYWCH family member 2
107985021	2,83E-11	1,05E+01	1,24E-11	0,1996	-6,7752774	-1,35250942	81,69	LOC107985021	
100507463	3,88E-62	6,14E+01	4,70E-63	0,0807	-16,7610664	-1,35265815	637,77	PSMB8-AS1	PSMB8 antisense RNA 1 (head to head)
415	1,80E-30	2,97E+01	4,52E-31	0,1168	-11,5921219	-1,35404387	249,48	ARSL	arylsulfatase L
3858	4,58E-62	6,13E+01	5,56E-63	0,0808	-16,7510731	-1,35416881	734,67	KRT10	keratin 10
4493	2,81E-125	1,25E+02	1,01E-126	0,0566	-23,9461805	-1,35425166	3125,89	MT1E	metallothionein 1E
10626	5,16E-125	1,24E+02	1,87E-126	0,0566	-23,9204986	-1,35455455	1715,46	TRIM16	tripartite motif containing 16
81490	3,44E-82	8,15E+01	2,72E-83	0,0701	-19,3351083	-1,35578006	2276,74	PTDSS2	phosphatidylserine synthase 2
29926	1,08E-104	1,04E+02	5,62E-106	0,062	-21,8648346	-1,3564754	1561,2	GMPPA	GDP-mannose pyrophosphorylase A
64342	2,57E-74	7,36E+01	2,39E-75	0,0739	-18,3675811	-1,35677918	858,44	HS1BP3	HCLS1 binding protein 3
387841	8,75E-26	2,51E+01	2,48E-26	0,1278	-10,6170225	-1,35715563	228,87	RPL13AP20	ribosomal protein L13a pseudogene 20
93129	8,52E-63	6,21E+01	1,02E-63	0,0806	-16,8519053	-1,3578049	764,1	ORAI3	ORAI calcium release-activated calcium modulator 3
102723996	4,33E-49	4,84E+01	7,01E-50	0,0915	-14,8494702	-1,35839012	470,77	LOC102723	ICOS ligand
100847079	4,46E-03	2,35E+00	3,09E-03	0,4595	-2,9581908	-1,35936061	14,94	MIR5193	microRNA 5193
286122	9,39E-06	5,03E+00	5,34E-06	0,2989	-4,5507856	-1,36032815	35,49	LINC02904	long intergenic non-protein coding RNA 2904
138716	9,45E-67	6,60E+01	1,04E-67	0,0782	-17,386948	-1,36042927	679,77	RPP25L	ribonuclease P/MRP subunit p25 like
84514	2,07E-97	9,67E+01	1,24E-98	0,0645	-21,0790536	-1,36050578	1522,04	GHDC	GH3 domain containing
1201	3,54E-85	8,45E+01	2,64E-86	0,0691	-19,6897038	-1,36063477	967,33	CLN3	CLN3 lysosomal/endosomal transmembrane protein, battenin
105376626	2,25E-04	3,65E+00	1,40E-04	0,3574	-3,8079276	-1,3609583	25,29	LOC105376	uncharacterized LOC105376626
7039	6,87E-180	1,79E+02	1,10E-181	0,0474	-28,7434028	-1,36188333	4937,44	TGFA	transforming growth factor alpha
116412	6,74E-11	1,02E+01	3,00E-11	0,2049	-6,646428	-1,36196266	79,16	ZNF837	zinc finger protein 837
6817	2,58E-09	8,59E+00	1,23E-09	0,2242	-6,076457	-1,3624573	63,61	SULT1A1	sulfotransferase family 1A member 1
51042	1,87E-66	6,57E+01	2,06E-67	0,0786	-17,3473774	-1,36287489	636,34	ZNF593	zinc finger protein 593
79446	6,91E-41	4,02E+01	1,35E-41	0,1009	-13,5106256	-1,36326444	361,98	WDR25	WD repeat domain 25
217	5,26E-94	9,33E+01	3,34E-95	0,0659	-20,7017544	-1,363712	2179,17	ALDH2	aldehyde dehydrogenase 2 family member
10654	5,60E-82	8,13E+01	4,45E-83	0,0706	-19,3097299	-1,36416649	1642,99	PMVK	phosphomevalonate kinase
9545	3,17E-64	6,35E+01	3,68E-65	0,08	-17,0470346	-1,36459989	606,85	RAB3D	RAB3D, member RAS oncogene family
9479	7,17E-65	6,41E+01	8,17E-66	0,0797	-17,134758	-1,36483127	626,6	MAPK8IP1	mitogen-activated protein kinase 8 interacting protein 1
105378691	3,88E-03	2,41E+00	2,67E-03	0,4545	-3,0031312	-1,36498313	15,55	LOC105378	uncharacterized LOC105378691
400752	3,88E-03	2,41E+00	2,67E-03	0,4545	-3,0031312	-1,36498313	15,55	LINC01144	long intergenic non-protein coding RNA 1144
221424	3,13E-03	2,50E+00	2,14E-03	0,4446	-3,0703299	-1,36522079	17,28	LRRC73	leucine rich repeat containing 73
91768	2,69E-126	1,26E+02	9,51E-128	0,0568	-24,0445829	-1,36611376	1630,55	CABLES1	Cdk5 and Abl enzyme substrate 1
57476	2,67E-37	3,66E+01	5,67E-38	0,1061	-12,8822274	-1,36696003	317,1	GRAMD1B	GRAM domain containing 1B
58473	1,28E-17	1,69E+01	4,58E-18	0,1579	-8,663318	-1,3675943	139,34	PLEKHB1	pleckstrin homology domain containing B1
55698	1,12E-06	5,95E+00	6,05E-07	0,2741	-4,9896549	-1,36779653	44,13	RADIL	Rap associating with DIL domain
389333	1,46E-14	1,38E+01	5,76E-15	0,1752	-7,8090034	-1,36804707	107,84	PROB1	proline rich basic protein 1
6276	2,86E-13	1,25E+01	1,17E-13	0,1845	-7,4202058	-1,36869848	119,5	S100A5	S100 calcium binding protein A5
80700	5,73E-114	1,13E+02	2,53E-115	0,06	-22,8260525	-1,37064586	1968,39	UBXN6	UBX domain protein 6
6181	2,81E-139	1,39E+02	8,02E-141	0,0543	-25,2636332	-1,37141983	17340,98	RPLP2	ribosomal protein lateral stalk subunit P2
388	8,80E-75	7,41E+01	8,10E-76	0,0744	-18,4262102	-1,37149251	867,42	RHOB	ras homolog family member B
387885	6,11E-52	5,12E+01	9,29E-53	0,0897	-15,2873248	-1,37187896	468,08	CFAP73	cilia and flagella associated protein 73
6150	1,11E-67	6,70E+01	1,19E-68	0,0784	-17,5105525	-1,37208891	852,9	MRPL23	mitochondrial ribosomal protein L23
158880	7,85E-06	5,11E+00	4,45E-06	0,2991	-4,5892759	-1,3727225	36,87	USP51	ubiquitin specific peptidase 51
1593	4,54E-31	3,03E+01	1,12E-31	0,1173	-11,7106213	-1,37315891	271,86	CYP27A1	cytochrome P450 family 27 subfamily A member 1
170689	1,13E-156	1,56E+02	2,51E-158	0,0512	-26,8093605	-1,373188	4080,53	ADAMTS15	ADAM metallopeptidase with thrombospondin type 1 motif 15
23559	2,95E-57	5,65E+01	4,00E-58	0,0855	-16,0721321	-1,37382457	579,88	WBP1	WW domain binding protein 1
8448	5,20E-23	2,23E+01	1,59E-23	0,1375	-9,9959609	-1,37468835	204,95	DOC2A	double C2 domain alpha
100528020	4,19E-03	2,38E+00	2,90E-03	0,4616	-2,9780328	-1,37469722	14,56	FAM187A	family with sequence similarity 187 member A
2783	1,56E-110	1,10E+02	7,26E-112	0,0612	-22,4751567	-1,37519433	6104,46	GNB2	G protein subunit beta 2
1312	1,71E-99	9,88E+01	9,81E-101	0,0646	-21,3068527	-1,37590897	1882,06	COMT	catechol-O-methyltransferase
8636	1,08E-94	9,40E+01	6,77E-96	0,0663	-20,7785384	-1,37736906	2012,21	SSNA1	SS nuclear autoantigen 1
100616414	4,53E-23	2,23E+01	1,38E-23	0,1377	-10,0096756	-1,37875508	191,68	MIR4761	microRNA 4761
84279	2,67E-69	6,86E+01	2,78E-70	0,0778	-17,723146	-1,37881587	755,96	PRADC1	protease associated domain containing 1
11282	4,84E-203	2,02E+02	6,08E-205	0,0452	-30,5476502	-1,3792909	5682,55	MGAT4B	alpha-1,3-mannosyl-glycoprotein 4-beta-N-acetylglucosaminyltransferase B
283991	2,42E-143	1,43E+02	6,55E-145	0,0538	-25,6329653	-1,3795317	2579,45	UBALD2	UBA like domain containing 2
51537	6,63E-95	9,42E+01	4,14E-96	0,0663	-20,8020809	-1,37959865	1215,37	MTFP1	mitochondrial fission process 1
101927949	3,53E-04	3,45E+00	2,24E-04	0,3739	-3,690814	-1,37981627	25,66	LOC101927	uncharacterized LOC101927949
5214	5,29E-230	2,29E+02	4,77E-232	0,0424	-32,5246955	-1,38064489	17097,17	PFKP	phosphofructokinase, platelet
57172	6,99E-05	4,16E+00	4,20E-05	0,3372	-4,0964453	-1,38119285	30,2	CAMK1G	calcium/calmodulin dependent protein kinase IG
79585	4,20E-54	5,34E+01	6,11E-55	0,0885	-15,611164	-1,38207486	777,33	CORO7	coronin 7
83707	2,64E-46	4,56E+01	4,58E-47	0,0959	-14,4084428	-1,3824331	504,07	TRPT1	tRNA phosphotransferase 1
56731	3,05E-122	1,22E+02	1,17E-123	0,0585	-23,6504073	-1,38335891	2345,01	SLC2A4RG	SLC2A4 regulator
10603	1,60E-12	1,18E+01	6,72E-13	0,1926	-7,1850399	-1,38349328	89,15	SH2B2	SH2B adaptor protein 2
9409	1,07E-55	5,50E+01	1,50E-56	0,0873	-15,8458581	-1,38368944	675,22	PEX16	peroxisomal biogenesis factor 16
440	1,48E-77	7,68E+01	1,29E-78	0,0738	-18,7714738	-1,38466925	1054,41	ASNS	asparagine synthetase (glutamine-hydrolyzing)
5914	2,53E-98	9,76E+01	1,49E-99	0,0654	-21,1790819	-1,38503471	1663,84	RARA	retinoic acid receptor alpha
100507057	3,52E-35	3,45E+01	7,87E-36	0,1109	-12,4957972	-1,38543167	291,93	MELTF-AS1	MELTF antisense RNA 1
23705	2,31E-04	3,64E+00	1,44E-04	0,3648	-3,8007748	-1,38645616	27,52	CADM1	cell adhesion molecule 1
79581	6,94E-108	1,07E+02	3,39E-109	0,0625	-22,2006164	-1,38656316	4091,38	SLC52A2	solute carrier family 52 member 2
8742	1,24E-71	7,09E+01	1,22E-72	0,0769	-18,0258766	-1,38669473	667,64	TNFSF12	TNF superfamily member 12
3430	3,05E-71	7,05E+01	3,03E-72	0,0772	-17,9754718	-1,3872301	739,56	IFI35	interferon induced protein 35
57104	3,22E-144	1,43E+02	8,60E-146	0,054	-25,7119384	-1,38758488	4025,28	PNPLA2	patatin like phospholipase domain containing 2
84221	1,81E-74	7,37E+01	1,68E-75	0,0755	-18,3868238	-1,38827744	742,42	SPATC1L	spermatogenesis and centriole associated 1 like
100507103	9,37E-07	6,03E+00	5,04E-07	0,2764	-5,0247905	-1,38881416	45	LINC02937	long intergenic non-protein coding RNA 2937
101927546	1,37E-06	5,86E+00	7,44E-07	0,2807	-4,9494064	-1,38909195	43,94	ANO7L1	anoctamin 7 like 1 (pseudogene)
57326	6,42E-122	1,21E+02	2,47E-123	0,0589	-23,6187983	-1,3900687	1586,3	PBXIP1	PBX homeobox interacting protein 1
29997	1,37E-163	1,63E+02	2,77E-165	0,0507	-27,3995801	-1,39010327	3318,31	NOP53	NOP53 ribosome biogenesis factor
6923	3,24E-130	1,29E+02	1,05E-131	0,0569	-24,4198074	-1,39032205	3931,75	ELOB	elongin B
80199	6,38E-31	3,02E+01	1,58E-31	0,119	-11,6815982	-1,39043104	263,4	FUZ	fuzzy planar cell polarity protein
3718	1,05E-02	1,98E+00	7,52E-03	0,5204	-2,6728615	-1,39102603	12,84	JAK3	Janus kinase 3
728192	1,62E-06	5,79E+00	8,81E-07	0,2829	-4,9164716	-1,39107031	41,65	LINC00460	long intergenic non-protein coding RNA 460
107985053	1,05E-02	1,98E+00	7,56E-03	0,5212	-2,6711177	-1,39231383	12,71	SPNS2-AS1	SPNS2 antisense RNA 1
54508	2,63E-03	2,58E+00	1,78E-03	0,4457	-3,1239744	-1,39239835	17,44	EPB41L4A-D	EPB41L4A divergent transcript
79094	1,48E-28	2,78E+01	3,89E-29	0,1243	-11,204155	-1,39282014	233,64	CHAC1	ChaC glutathione specific gamma-glutamylcyclotransferase 1
105373247	1,36E-04	3,87E+00	8,35E-05	0,3543	-3,9340913	-1,39376725	26,84	LOC105373	uncharacterized LOC105373247
2876	7,38E-37	3,61E+01	1,58E-37	0,1089	-12,8027407	-1,3941915	10472,63	GPX1	glutathione peroxidase 1
50486	6,40E-162	1,61E+02	1,32E-163	0,0513	-27,2585104	-1,39736004	3969,5	G0S2	G0/G1 switch 2
9158	1,08E-184	1,84E+02	1,61E-186	0,048	-29,1274678	-1,39762889	5454,33	FIBP	FGF1 intracellular binding protein
1978	1,61E-171	1,71E+02	2,87E-173	0,0498	-28,0618069	-1,39847651	3233,08	EIF4EBP1	eukaryotic translation initiation factor 4E binding protein 1
255130	3,33E-80	7,95E+01	2,74E-81	0,0734	-19,0957674	-1,4008394	910,23	IGFBP7-AS1	IGFBP7 antisense RNA 1
6535	1,31E-23	2,29E+01	3,93E-24	0,1383	-10,1332375	-1,40159262	187,49	SLC6A8	solute carrier family 6 member 8
2791	2,37E-94	9,36E+01	1,50E-95	0,0676	-20,7403444	-1,40214284	1521,72	GNG11	G protein subunit gamma 11
79639	2,80E-43	4,26E+01	5,22E-44	0,1008	-13,9138363	-1,4022651	373,18	TMEM53	transmembrane protein 53
968	2,38E-169	1,69E+02	4,41E-171	0,0503	-27,8820033	-1,40244452	8861,46	CD68	CD68 molecule
79176	1,75E-33	3,28E+01	4,09E-34	0,1152	-12,1776011	-1,40346696	268,9	FBXL15	F-box and leucine rich repeat protein 15
1652	6,03E-71	7,02E+01	6,06E-72	0,0783	-17,9370384	-1,40445998	641,08	DDT	D-dopachrome tautomerase
5831	4,73E-116	1,15E+02	2,02E-117	0,061	-23,0363231	-1,4046734	3367,19	PYCR1	pyrroline-5-carboxylate reductase 1
10791	4,33E-03	2,36E+00	3,00E-03	0,4734	-2,9676974	-1,40483028	14,91	VAMP5	vesicle associated membrane protein 5
57537	9,64E-122	1,21E+02	3,72E-123	0,0595	-23,6015404	-1,40530952	1365,24	SORCS2	sortilin related VPS10 domain containing receptor 2
105379444	3,70E-03	2,43E+00	2,55E-03	0,4661	-3,0176047	-1,40664985	14,85	LOC105379	uncharacterized LOC105379444
80194	2,41E-55	5,46E+01	3,42E-56	0,0891	-15,7940296	-1,40708265	490,19	TMEM134	transmembrane protein 134
6137	5,10E-203	2,02E+02	6,44E-205	0,0461	-30,5457494	-1,40757399	21491,09	RPL13	ribosomal protein L13
9751	7,40E-54	5,31E+01	1,08E-54	0,0904	-15,5746569	-1,40844889	567,16	SNPH	syntaphilin
107985694	1,19E-06	5,92E+00	6,45E-07	0,283	-4,977126	-1,40855918	60,77	LOC107985	uncharacterized LOC107985694
5553	7,43E-05	4,13E+00	4,47E-05	0,3452	-4,0817559	-1,40914404	27,18	PRG2	proteoglycan 2, pro eosinophil major basic protein
4713	2,76E-34	3,36E+01	6,30E-35	0,1143	-12,3292525	-1,4093395	4032,48	NDUFB7	NADH:ubiquinone oxidoreductase subunit B7
794	6,09E-204	2,03E+02	7,58E-206	0,046	-30,615623	-1,40960201	3433,12	CALB2	calbindin 2
11279	1,10E-17	1,70E+01	3,90E-18	0,1625	-8,6815278	-1,41046255	123,05	KLF8	KLF transcription factor 8
84818	5,35E-87	8,63E+01	3,88E-88	0,0709	-19,9024355	-1,41096869	1021,94	IL17RC	interleukin 17 receptor C
64840	2,25E-89	8,86E+01	1,55E-90	0,0699	-20,1772465	-1,4109828	1626,37	PORCN	porcupine O-acyltransferase
2116	9,04E-07	6,04E+00	4,86E-07	0,2805	-5,0317922	-1,41117501	44,83	ETV2	ETS variant transcription factor 2
85441	7,16E-138	1,37E+02	2,08E-139	0,0562	-25,1346598	-1,41217479	1698,74	HELZ2	helicase with zinc finger 2

163033	8,95E-40	3,90E+01	1,80E-40	0,1061	-13,3187212	-1,41264819	317,01	ZNF579	zinc finger protein 579
83938	8,16E-03	2,09E+00	5,80E-03	0,5123	-2,7589241	-1,41330901	11,89	LRMDA	leucine rich melanocyte differentiation associated
79026	2,71E-139	1,39E+02	7,71E-141	0,0559	-25,2651996	-1,41353952	64350,19	AHNAK	AHNAK nucleoprotein
474383	6,03E-21	2,02E+01	1,95E-21	0,1488	-9,5074443	-1,41427293	153,21	F8A2	coagulation factor VIII associated 2
5738	2,37E-65	6,46E+01	2,68E-66	0,0822	-17,1993826	-1,41427922	611,83	PTGFRN	prostaglandin F2 receptor inhibitor
55201	7,21E-165	1,64E+02	1,44E-166	0,0514	-27,5073103	-1,41445928	3719,57	MAP1S	microtubule associated protein 1S
409	1,24E-102	1,02E+02	6,72E-104	0,0653	-21,6453807	-1,41451178	1080,13	ARRB2	arrestin beta 2
100528019	8,74E-03	2,06E+00	6,23E-03	0,5171	-2,7354691	-1,41460849	11,94	HSPB2-C11(	HSPB2-C11orf52 readthrough (NMD candidate)
91894	8,74E-03	2,06E+00	6,23E-03	0,5171	-2,7354691	-1,41460849	11,94	C11orf52	chromosome 11 open reading frame 52
101928069	4,11E-18	1,74E+01	1,44E-18	0,1609	-8,7938756	-1,41492084	137,96	DPP3-DT	DPP3 divergent transcript
9935	9,48E-03	2,02E+00	6,79E-03	0,5232	-2,7071939	-1,41642773	14,07	MAFB	MAF bZIP transcription factor B
6142	9,00E-128	1,27E+02	3,07E-129	0,0587	-24,1867116	-1,41948592	43246,81	RPL18A	ribosomal protein L18a
339894	3,58E-08	7,45E+00	1,79E-08	0,2521	-5,6310464	-1,41954462	50,54	LINC00880	long intergenic non-protein coding RNA 880
8517	5,02E-63	6,23E+01	5,96E-64	0,0841	-16,8833611	-1,41993893	839,74	IKBKG	inhibitor of nuclear factor kappa B kinase regulatory subunit gamma
6206	9,81E-229	2,28E+02	9,02E-231	0,0438	-32,43428	-1,42175421	18781,96	RPS12	ribosomal protein S12
10327	7,09E-123	1,22E+02	2,68E-124	0,06	-23,7124471	-1,42221502	2202,24	AKR1A1	aldo-keto reductase family 1 member A1
115704	2,30E-150	1,50E+02	5,63E-152	0,0542	-26,259087	-1,42221976	2635,38	EVI5L	ecotropic viral integration site 5 like
9947	1,64E-106	1,06E+02	8,20E-108	0,0645	-22,0569012	-1,42240208	1186	MAGEC1	MAGE family member C1
50861	1,77E-44	4,38E+01	3,21E-45	0,1009	-14,1117606	-1,42358964	415,02	STMN3	stathmin 3
6252	2,49E-12	1,16E+01	1,05E-12	0,2001	-7,1233886	-1,42547025	85,12	RTN1	reticulon 1
127700	1,01E-24	2,40E+01	2,94E-25	0,1373	-10,383625	-1,42548029	178,42	OSCP1	organic solute carrier partner 1
26471	2,73E-07	6,56E+00	1,43E-07	0,271	-5,2617419	-1,42572991	47,46	NUPR1	nuclear protein 1, transcriptional regulator
100129845	2,35E-02	1,63E+00	1,75E-02	0,5999	-2,3766882	-1,42581872	9,27	PCOLCE-AS	PCOLCE antisense RNA 1
54538	6,82E-154	1,53E+02	1,57E-155	0,0537	-26,5685663	-1,42611358	2634,88	ROBO4	roundabout guidance receptor 4
122622	1,02E-02	1,99E+00	7,34E-03	0,5319	-2,6811624	-1,42613453	12,02	ADSS1	adenylosuccinate synthase 1
3691	9,23E-147	1,46E+02	2,37E-148	0,055	-25,9398542	-1,42631525	5149,79	ITGB4	integrin subunit beta 4
7057	0	#NUM!	0	0,0337	-42,405853	-1,42701514	50062,79	THBS1	thrombospondin 1
374882	2,08E-112	1,12E+02	9,35E-114	0,063	-22,667608	-1,4281456	2257,61	TMEM205	transmembrane protein 205
387755	1,38E-06	5,86E+00	7,49E-07	0,2888	-4,9482145	-1,42906591	38,68	INSC	INSC spindle orientation adaptor protein
752	7,07E-267	2,66E+02	4,68E-269	0,0408	-35,0448045	-1,42958388	7568,21	FMNL1	formin like 1
55850	3,33E-61	6,05E+01	4,16E-62	0,086	-16,6309217	-1,42986573	605,72	USE1	unconventional SNARE in the ER 1
101928465	3,02E-32	3,15E+01	7,24E-33	0,1198	-11,9409709	-1,43013109	239,03	SLCO4A1-A!	SLCO4A1 antisense RNA 2
5351	1,04E-219	2,19E+02	1,06E-221	0,045	-31,784536	-1,43061598	10073,99	PLOD1	procollagen-lysine,2-oxoglutarate 5-dioxygenase 1
29924	5,58E-205	2,04E+02	6,82E-207	0,0466	-30,6940995	-1,43126112	5566,07	EPN1	epsin 1
51084	2,35E-73	7,26E+01	2,23E-74	0,0785	-18,2458416	-1,43215314	621,82	CRYL1	crystallin lambda 1
5211	1,98E-136	1,36E+02	5,85E-138	0,0574	-25,0017721	-1,43401264	5370,34	PFKL	phosphofructokinase, liver type
113218487	5,38E-121	1,20E+02	2,09E-122	0,061	-23,5283034	-1,43407501	4188,01	MIR10394	microRNA 10394
150248	3,09E-05	4,51E+00	1,82E-05	0,3346	-4,2862286	-1,43412043	28,88	C22orf15	chromosome 22 open reading frame 15
22921	2,97E-52	5,15E+01	4,49E-53	0,0936	-15,3346616	-1,43467618	532,13	MSRB2	methionine sulfoxide reductase B2
3959	3,40E-159	1,58E+02	7,37E-161	0,0531	-27,0257266	-1,43507412	25656,64	LGALS3BP	galectin 3 binding protein
56655	3,14E-96	9,55E+01	1,91E-97	0,0685	-20,9492375	-1,43521223	1001,46	POLE4	DNA polymerase epsilon 4, accessory subunit
105375006	2,38E-02	1,62E+00	1,77E-02	0,6052	-2,3716091	-1,43538558	9	LOC105375(	uncharacterized LOC105375006
5329	2,82E-244	2,44E+02	2,27E-246	0,0429	-33,5225039	-1,4373	9074,97	PLAUR	plasminogen activator, urokinase receptor
352909	3,70E-31	3,04E+01	9,13E-32	0,1227	-11,7282392	-1,43915801	224,83	DNAAF3	dynein axonemal assembly factor 3
126308	1,32E-199	1,99E+02	1,71E-201	0,0475	-30,2867948	-1,43985239	3776,17	MOB3A	MOB kinase activator 3A
83443	1,33E-159	1,59E+02	2,86E-161	0,0532	-27,0606897	-1,44046389	2685,35	SF3B5	splicing factor 3b subunit 5
64849	1,63E-07	6,79E+00	8,40E-08	0,2689	-5,358224	-1,44060448	46,99	SLC13A3	solute carrier family 13 member 3
402	1,53E-118	1,18E+02	6,24E-120	0,0619	-23,2853345	-1,44242827	3463,9	ARL2	ADP ribosylation factor like GTPase 2
27124	8,68E-14	1,31E+01	3,50E-14	0,1903	-7,5785199	-1,44243428	89,69	INPP5J	inositol polyphosphate-5-phosphatase J
51117	1,47E-127	1,27E+02	5,04E-129	0,0597	-24,1662237	-1,44250621	1988,81	COQ4	coenzyme Q4
735301	3,18E-15	1,45E+01	1,23E-15	0,1805	-8,0016989	-1,44451406	98,73	SNHG9	small nucleolar RNA host gene 9
54935	3,57E-63	6,24E+01	4,22E-64	0,0855	-16,9037773	-1,4452019	557,06	DUSP23	dual specificity phosphatase 23
64856	1,01E-42	4,20E+01	1,90E-43	0,1046	-13,8209879	-1,44548391	423,96	VWA1	von Willebrand factor A domain containing 1
6618	4,26E-109	1,08E+02	2,03E-110	0,0648	-22,3268354	-1,44653694	1640,71	SNAPC2	small nuclear RNA activating complex polypeptide 2
11135	3,55E-111	1,10E+02	1,63E-112	0,0642	-22,5413832	-1,44698096	3155,52	CDC42EP1	CDC42 effector protein 1
23308	3,69E-53	5,24E+01	5,47E-54	0,0935	-15,4707352	-1,4469853	460,63	ICOSLG	inducible T cell costimulator ligand
340542	1,53E-03	2,82E+00	1,02E-03	0,4405	-3,2849423	-1,44711499	17,36	BEX5	brain expressed X-linked 5
59307	4,14E-25	2,44E+01	1,20E-25	0,1382	-10,4691848	-1,44726466	177,12	SIGIRR	single Ig and TIR domain containing
122618	2,34E-08	7,63E+00	1,16E-08	0,2537	-5,7057838	-1,44732993	50,24	PLD4	phospholipase D family member 4
7108	2,20E-45	4,47E+01	3,90E-46	0,1015	-14,2598034	-1,448005	362,64	TM7SF2	transmembrane 7 superfamily member 2
123920	1,21E-100	9,99E+01	6,79E-102	0,0676	-21,4315642	-1,44824838	1013,03	CMTM3	CKLF like MARVEL transmembrane domain containing 3
138162	1,49E-17	1,68E+01	5,33E-18	0,1676	-8,6461433	-1,44899113	120,72	PIERCE1	piercer of microtubule wall 1
8862	1,07E-35	3,50E+01	2,36E-36	0,1152	-12,5912097	-1,44990501	288,87	APLN	apelin
29948	2,42E-51	5,06E+01	3,72E-52	0,0954	-15,1967542	-1,4504831	488,71	OSGIN1	oxidative stress induced growth inhibitor 1
79365	4,86E-46	4,53E+01	8,48E-47	0,101	-14,3658271	-1,45077747	372,26	BHLHE41	basic helix-loop-helix family member e41
727800	2,32E-35	3,46E+01	5,17E-36	0,1159	-12,5291082	-1,45170515	272,74	RNF208	ring finger protein 208
144717	1,88E-90	8,97E+01	1,27E-91	0,0715	-20,3006232	-1,45202982	921,29	PHETA1	PH domain containing endocytic trafficking adaptor 1
8927	3,05E-05	4,52E+00	1,79E-05	0,3386	-4,2896616	-1,45252188	29,69	BSN	bassoon presynaptic cytomatrix protein
3692	1,46E-182	1,82E+02	2,25E-184	0,0502	-28,9576246	-1,45351121	19216,7	EIF6	eukaryotic translation initiation factor 6
3569	3,34E-153	1,52E+02	7,80E-155	0,0549	-26,508169	-1,45416168	2375,65	IL6	interleukin 6
6853	5,95E-03	2,23E+00	4,18E-03	0,5077	-2,8645618	-1,45435256	12,63	SYN1	synapsin I
1364	2,94E-93	9,25E+01	1,90E-94	0,0705	-20,617821	-1,45441501	1228,28	CLDN4	claudin 4
2678	3,18E-71	7,05E+01	3,17E-72	0,0809	-17,9729966	-1,45444678	611,85	GGT1	gamma-glutamyltransferase 1
26580	3,08E-77	7,65E+01	2,71E-78	0,0778	-18,732073	-1,45655439	860,86	BSCL2	BSCL2 lipid droplet biogenesis associated, seipin
9844	5,77E-16	1,52E+01	2,16E-16	0,1774	-8,2125984	-1,45667971	104,08	ELMO1	engulfment and cell motility 1
3696	1,37E-15	1,49E+01	5,19E-16	0,1797	-8,1068498	-1,45708377	99,9	ITGB8	integrin subunit beta 8
3133	5,19E-303	3,02E+02	2,59E-305	0,039	-37,3494212	-1,4571716	17615,22	HLA-E	major histocompatibility complex, class I, E
396	4,45E-166	1,65E+02	8,63E-168	0,0528	-27,6091759	-1,45751332	29071,14	ARHGDIA	Rho GDP dissociation inhibitor alpha
53373	4,71E-194	1,93E+02	6,36E-196	0,0488	-29,8607743	-1,45827344	4214,99	TPCN1	two pore segment channel 1
54972	1,53E-176	1,76E+02	2,56E-178	0,0512	-28,4726416	-1,45860306	5986,27	TMEM132A	transmembrane protein 132A
10493	1,47E-260	2,60E+02	1,01E-262	0,0421	-34,6265449	-1,45866609	12643,32	VAT1	vesicle amine transport 1
2118	7,38E-136	1,35E+02	2,20E-137	0,0585	-24,9488125	-1,45874208	3473,15	ETV4	ETS variant transcription factor 4
55036	5,56E-08	7,25E+00	2,81E-08	0,2628	-5,553173	-1,45922085	46,51	CCDC40	coiled-coil domain containing 40
64788	9,35E-19	1,80E+01	3,22E-19	0,1629	-8,9608125	-1,4601503	133,2	LMF1	lipase maturation factor 1
374291	5,57E-62	6,13E+01	6,80E-63	0,0872	-16,7391396	-1,46038103	1078,34	NDUFS7	NADH:ubiquinone oxidoreductase core subunit S7
54998	1,24E-139	1,39E+02	3,54E-141	0,0577	-25,2959816	-1,4604719	2617,92	AURKAIP1	aurora kinase A interacting protein 1
6209	2,06E-297	2,97E+02	1,08E-299	0,0395	-37,0014762	-1,46083492	8758,1	RPS15	ribosomal protein S15
1778	0	#NUM!	0	0,0349	-41,8057032	-1,46100704	55243,2	DYNC1H1	dynein cytoplasmic 1 heavy chain 1
11316	2,27E-146	1,46E+02	5,86E-148	0,0564	-25,9049292	-1,46104139	5245,65	COPE	COPI coat complex subunit epsilon
4357	2,17E-84	8,37E+01	1,64E-85	0,0746	-19,5969126	-1,46149944	1079,76	MPST	mercaptopyruvate sulfurtransferase
3590	1,87E-18	1,77E+01	6,50E-19	0,1646	-8,8831072	-1,46228899	120,86	IL11RA	interleukin 11 receptor subunit alpha
9289	2,59E-141	1,41E+02	7,16E-143	0,0575	-25,4494496	-1,46277183	2767,32	ADGRG1	adhesion G protein-coupled receptor G1
3338	7,99E-47	4,61E+01	1,36E-47	0,101	-14,4918091	-1,46359405	367,58	DNAJC4	DnaJ heat shock protein family (Hsp40) member C4
4303	8,54E-54	5,31E+01	1,25E-54	0,0941	-15,565278	-1,46404014	471,68	FOXO4	forkhead box O4
2184	6,33E-140	1,39E+02	1,79E-141	0,0579	-25,3229368	-1,46605634	1949,91	FAH	fumarylacetoacetate hydrolase
126133	3,56E-155	1,54E+02	8,04E-157	0,055	-26,6799637	-1,4662294	1894,18	ALDH16A1	aldehyde dehydrogenase 16 family member A1
376497	1,15E-88	8,79E+01	8,07E-90	0,073	-20,095565	-1,46638261	861,89	SLC27A1	solute carrier family 27 member 1
114794	1,87E-72	7,17E+01	1,81E-73	0,0809	-18,1310807	-1,46690238	671,78	ELFN2	extracellular leucine rich repeat and fibronectin type III domain containing 2
8350	1,24E-02	1,91E+00	9,00E-03	0,5619	-2,612054	-1,46765991	10,06	H3C1	H3 clustered histone 1
728489	9,56E-30	2,90E+01	2,44E-30	0,1283	-11,44673	-1,46856137	244,84	DNLZ	DNL-type zinc finger
102724050	9,09E-21	2,00E+01	2,96E-21	0,1552	-9,4640682	-1,46926574	151,25	GPR84-AS1	GPR84, ZNF385A, ITGA5 and GTSF1 antisense RNA 1
170487	2,39E-03	2,62E+00	1,62E-03	0,4661	-3,152621	-1,46950483	14,82	ACTL10	actin like 10
6223	4,13E-153	1,52E+02	9,67E-155	0,0555	-26,5000693	-1,46992686	19529,07	RPS19	ribosomal protein S19
220004	3,29E-03	2,48E+00	2,25E-03	0,4815	-3,0549579	-1,47098453	13,68	PPP1R32	protein phosphatase 1 regulatory subunit 32
115811	8,86E-18	1,71E+01	3,14E-18	0,169	-8,7061994	-1,47103021	117,5	IQCD	IQ motif containing D
4708	7,20E-94	9,31E+01	4,59E-95	0,0711	-20,6864414	-1,47162649	1039,57	NDUFB2	NADH:ubiquinone oxidoreductase subunit B2
5361	4,00E-251	2,50E+02	3,00E-253	0,0433	-33,9912208	-1,47239616	11577,35	PLXNA1	plexin A1
79004	6,17E-126	1,25E+02	2,19E-127	0,0613	-24,0098926	-1,47283212	1900,31	CUEDC2	CUE domain containing 2
105372632	1,04E-03	2,98E+00	6,80E-04	0,4337	-3,3974545	-1,47341294	16,82	LOC105372	632
51438	1,26E-21	2,09E+01	4,00E-22	0,1525	-9,6710276	-1,47522455	151,05	MAGEC2	MAGE family member C2
2517	6,52E-197	1,96E+02	8,64E-199	0,0491	-30,080814	-1,47630294	4458,88	FUCA1	alpha-L-fucosidase 1
27044	9,24E-290	2,89E+02	4,98E-292	0,0405	-36,5219319	-1,47744484	12399,94	SND1	staphylococcal nuclease and tudor domain containing 1
105378482	1,42E-06	5,85E+00	7,74E-07	0,2992	-4,9418976	-1,4784101	40,62	LOC105378	uncharacterized LOC105378482
221191	1,25E-02	1,90E+00	9,08E-03	0,5667	-2,6092063	-1,47851778	10,28	PRSS54	serine protease 54
101928864	4,56E-05	4,34E+00	2,70E-05	0,3523	-4,1973549	-1,47870597	26,54	LOC101928	uncharacterized LOC101928864
7263	1,20E-74	7,39E+01	1,10E-75	0,0804	-18,4094978	-1,4793062	753,8	TST	thiosulfate sulfurtransferase
60676	1,35E-03	2,87E+00	8,95E-04	0,4454	-3,3214761	-1,47936932	17,65	PAPPA2	pappalysin 2
3956	9,29E-208	2,07E+02	1,09E-209	0,0479	-30,9028257	-1,4800282	24992,95	LGALS1	galectin 1
107985040	4,04E-100	9,94E+01	2,28E-101	0,0693	-21,3749667	-1,48116904	953,25	FMNL1-AS1	FMNL1 antisense RNA 1
284439	9,75E-34	3,30E+01	2,26E-34	0,1212	-12,2259195	-1,48117751	246,17	SLC25A42	solute carrier family 25 member 42

83692	3,37E-285	2,84E+02	1,85E-287	0,0409	-36,2328195	-1,48205568	9127,29	CD99L2	CD99 molecule like 2
10410	1,91E-193	1,93E+02	2,59E-195	0,0497	-29,8138231	-1,4821941	9037,34	IFITM3	interferon induced transmembrane protein 3
26071	1,32E-185	1,85E+02	1,94E-187	0,0508	-29,1999573	-1,4826654	2743,6	RTL8A	retrotransposon Gag like 8A
79174	1,01E-61	6,10E+01	1,24E-62	0,0889	-16,7033432	-1,48473726	496,54	CRELD2	cysteine rich with EGF like domains 2
54777	5,96E-06	5,22E+00	3,35E-06	0,3195	-4,6479519	-1,48495696	33,81	CFAP46	cilia and flagella associated protein 46
30846	1,21E-276	2,76E+02	7,33E-279	0,0416	-35,6827063	-1,48545896	8811,74	EHD2	EH domain containing 2
100616358	5,29E-10	9,28E+00	2,44E-10	0,2348	-6,3306985	-1,48623396	62,14	MIR4800	microRNA 4800
8519	2,47E-115	1,15E+02	1,07E-116	0,0648	-22,9639702	-1,48737891	1222,97	IFITM1	interferon induced transmembrane protein 1
2896	1,84E-123	1,23E+02	6,91E-125	0,0626	-23,7695116	-1,48756991	17933,41	GRN	granulin precursor
80763	7,25E-03	2,14E+00	5,13E-03	0,5316	-2,7985228	-1,48764952	11,77	SPX	spexin hormone
51157	3,97E-82	8,14E+01	3,14E-83	0,077	-19,3277022	-1,4880105	723,2	ZNF580	zinc finger protein 580
23770	3,05E-140	1,40E+02	8,56E-142	0,0587	-25,3519114	-1,48807912	13175,85	FKBP8	FKBP prolyl isomerase 8
6158	1,07E-134	1,34E+02	3,22E-136	0,0599	-24,8412326	-1,48818124	25347,61	RPL28	ribosomal protein L28
5236	0	#NUM!	0	0,0394	-37,7844676	-1,48879468	8929,56	PGM1	phosphoglucomutase 1
113791	2,23E-13	1,27E+01	9,07E-14	0,2	-7,4538548	-1,49055815	89,38	PIK3IP1	phosphoinositide-3-kinase interacting protein 1
6141	7,11E-225	2,24E+02	6,70E-227	0,0464	-32,1585753	-1,49063668	18527,31	RPL18	ribosomal protein L18
56999	3,28E-144	1,43E+02	8,79E-146	0,058	-25,7110775	-1,49132174	2454,22	ADAMTS9	ADAM metallopeptidase with thrombospondin type 1 motif 9
7760	8,66E-41	4,01E+01	1,70E-41	0,1106	-13,493958	-1,49183188	298,11	ZNF213	zinc finger protein 213
102723722	3,97E-03	2,40E+00	2,74E-03	0,4982	-2,9953232	-1,49241904	12,84	LOC102723	uncharacterized LOC102723722
51268	1,87E-02	1,73E+00	1,38E-02	0,6058	-2,4635333	-1,49253126	9,16	PIPOX	pipecolic acid and sarcosine oxidase
440836	3,26E-08	7,49E+00	1,63E-08	0,2643	-5,6478048	-1,49254378	47,49	ODF3B	outer dense fiber of sperm tails 3B
161882	2,56E-19	1,86E+01	8,69E-20	0,1642	-9,1042462	-1,49507699	127,73	ZFPM1	zinc finger protein, FOG family member 1
3421	2,13E-152	1,52E+02	5,09E-154	0,0566	-26,4374638	-1,49568975	2399,1	IDH3G	isocitrate dehydrogenase (NAD(+)) 3 non-catalytic subunit gamma
25809	3,63E-29	2,84E+01	9,41E-30	0,132	-11,3291881	-1,49593441	225,58	TTLL1	TTL family tubulin polyglutamylase complex subunit L1
57674	1,97E-269	2,69E+02	1,27E-271	0,0425	-35,2128897	-1,49634874	5318,87	RNF213	ring finger protein 213
541472	2,44E-56	5,56E+01	3,39E-57	0,0939	-15,9391997	-1,49661502	431,72	IL6-AS1	IL6 antisense RNA 1
10589	0	#NUM!	0	0,0388	-38,5963631	-1,49684191	8260,63	DRAP1	DR1 associated protein 1
57085	6,88E-101	1,00E+02	3,84E-102	0,0698	-21,4581149	-1,49752118	1552,45	AGTRAP	angiotensin II receptor associated protein
100463486	5,58E-05	4,25E+00	3,32E-05	0,3609	-4,1500998	-1,49784812	25,85	MTRNR2L8	MT-RNR2 like 8 (pseudogene)
107985544	7,53E-11	1,01E+01	3,36E-11	0,226	-6,6299502	-1,49845989	64,5	LOC107985	uncharacterized LOC107985544
4489	6,93E-08	7,16E+00	3,51E-08	0,2719	-5,5138305	-1,49948528	706,61	MT1A	metallothionein 1A
23666	1,95E-06	5,71E+00	1,07E-06	0,3075	-4,8787272	-1,50016765	35,06	UBBP4	ubiquitin B pseudogene 4
4241	3,32E-209	2,08E+02	3,82E-211	0,0484	-31,0111184	-1,50097934	4254,33	MELTF	melanotransferrin
393	3,13E-03	2,50E+00	2,14E-03	0,4892	-3,0698303	-1,50181729	13,41	ARHGAP4	Rho GTPase activating protein 4
83882	1,48E-06	5,83E+00	8,03E-07	0,3046	-4,9346266	-1,50321899	35,2	TSPAN10	tetraspanin 10
755	2,76E-51	5,06E+01	4,24E-52	0,099	-15,1881293	-1,50419156	433,5	CFAP410	cilia and flagella associated protein 410
26229	2,66E-79	7,86E+01	2,23E-80	0,0792	-18,9859504	-1,50420871	1460,89	B3GAT3	beta-1,3-glucuronyltransferase 3
10608	4,91E-150	1,49E+02	1,21E-151	0,0574	-26,2300516	-1,50517905	1961,46	MXD4	MAX dimerization protein 4
3489	8,20E-126	1,25E+02	2,93E-127	0,0627	-23,9978815	-1,50586062	1372,61	IGFBP6	insulin like growth factor binding protein 6
8642	1,07E-09	8,97E+00	5,01E-10	0,2422	-6,2187301	-1,50588199	54,91	DCHS1	dachsous cadherin-related 1
162979	1,06E-22	2,20E+01	3,25E-23	0,1518	-9,9246122	-1,50631514	145,73	ZNF296	zinc finger protein 296
79575	4,36E-76	7,54E+01	3,93E-77	0,0811	-18,5892094	-1,50708954	1041,94	ABHD8	abhydrolase domain containing 8
84331	4,85E-30	2,93E+01	1,23E-30	0,131	-11,5061178	-1,50710479	246,4	MCRIP2	MAPK regulated corepressor interacting protein 2
11117	8,11E-11	1,01E+01	3,62E-11	0,2279	-6,6187092	-1,50835914	65,03	EMILIN1	elastin microfibril interfacer 1
2646	1,68E-57	5,68E+01	2,26E-58	0,0937	-16,1074667	-1,50901128	417,94	GCKR	glucokinase regulator
79156	1,12E-26	2,60E+01	3,09E-27	0,1397	-10,8099305	-1,51013031	175,41	PLEKHF1	pleckstrin homology and FYVE domain containing 1
5698	8,58E-103	1,02E+02	4,63E-104	0,0697	-21,6625732	-1,5109256	1078,41	PSMB9	proteasome 20S subunit beta 9
107985553	5,81E-03	2,24E+00	4,08E-03	0,5262	-2,8721931	-1,51124976	11,47	LOC107985	553
85359	1,83E-77	7,67E+01	1,61E-78	0,0807	-18,759963	-1,51460219	846,1	DGCR6L	DiGeorge syndrome critical region gene 6 like
120224	7,63E-58	5,71E+01	1,02E-58	0,0938	-16,1565057	-1,51532359	415,61	TMEM45B	transmembrane protein 45B
114990	8,91E-47	4,61E+01	1,52E-47	0,1046	-14,4842368	-1,51533616	376,86	VASN	vasorin
83853	2,06E-03	2,69E+00	1,39E-03	0,474	-3,197639	-1,51567433	14,92	ROPN1L	rhophilin associated tail protein 1 like
10507	5,47E-154	1,53E+02	1,25E-155	0,057	-26,5769249	-1,51587684	1646,63	SEMA4D	semaphorin 4D
107984245	2,20E-05	4,66E+00	1,28E-05	0,3474	-4,3635659	-1,51589766	27,58	LOC107984	uncharacterized LOC107984245
100288175	8,34E-49	4,81E+01	1,36E-49	0,1026	-14,8050466	-1,51856245	347,89	LOC100288	uncharacterized LOC100288175
7148	6,82E-22	2,12E+01	2,15E-22	0,156	-9,7346145	-1,5189994	150,55	TNXB	tenascin XB
118881	9,62E-31	3,00E+01	2,40E-31	0,1305	-11,6461769	-1,51967515	200,2	COMTD1	catechol-O-methyltransferase domain containing 1
57761	1,37E-122	1,22E+02	5,21E-124	0,0642	-23,6844617	-1,51986955	1375,08	TRIB3	tribbles pseudokinase 3
7089	4,51E-04	3,35E+00	2,88E-04	0,4192	-3,6260422	-1,5200153	18,31	TLE2	TLE family member 2, transcriptional corepressor
100294362	2,04E-14	1,37E+01	8,04E-15	0,1958	-7,7668839	-1,52103437	86,19	RNF213-AS1	RNF213 antisense RNA 1
84187	1,61E-217	2,17E+02	1,66E-219	0,0481	-31,6252421	-1,52105291	2924,83	TMEM164	transmembrane protein 164
54020	1,01E-75	7,50E+01	9,18E-77	0,082	-18,543614	-1,5210789	626,17	SLC37A1	solute carrier family 37 member 1
379	4,86E-73	7,23E+01	4,64E-74	0,0836	-18,2058239	-1,52127633	609,31	ARL4D	ADP ribosylation factor like GTPase 4D
147807	3,90E-31	3,04E+01	9,64E-32	0,1299	-11,7236321	-1,52347511	268,62	ZNF524	zinc finger protein 524
4572	1,43E-14	1,38E+01	5,63E-15	0,195	-7,8118991	-1,52368794	88,7	TRNQ	tRNA-Gln
10897	1,75E-129	1,29E+02	5,79E-131	0,0626	-24,3500479	-1,52389335	1947,16	YIF1A	Yip1 interacting factor homolog A, membrane trafficking protein
51257	1,42E-82	8,18E+01	1,11E-83	0,0787	-19,3811155	-1,5243873	643,63	MARCHF2	membrane associated ring-CH-type finger 2
475	9,37E-211	2,10E+02	1,06E-212	0,049	-31,1262907	-1,52516314	2779,29	ATOX1	antioxidant 1 copper chaperone
4567	4,52E-89	8,83E+01	3,14E-90	0,0758	-20,1423038	-1,5258569	1654,37	TRNL1	tRNA-Leu
9230	5,66E-182	1,81E+02	8,76E-184	0,0528	-28,9106845	-1,5262323	4920,95	RAB11B	RAB11B, member RAS oncogene family
11030	9,40E-62	6,10E+01	1,15E-62	0,0914	-16,7075853	-1,52735531	464,27	RBPMS	RNA binding protein, mRNA processing factor
54436	1,24E-12	1,19E+01	5,20E-13	0,2116	-7,2199159	-1,52807758	77,42	SH3TC1	SH3 domain and tetratricopeptide repeats 1
131601	1,12E-105	1,05E+02	5,74E-107	0,0696	-21,9686696	-1,52833977	1380,39	TPRA1	transmembrane protein adipocyte associated 1
10365	1,20E-90	8,99E+01	8,10E-92	0,0752	-20,3227217	-1,52876324	800,38	KLF2	KLF transcription factor 2
284889	1,33E-144	1,44E+02	3,53E-146	0,0594	-25,7464984	-1,52903809	4879,64	MIF-AS1	MIF antisense RNA 1
57804	3,95E-94	9,34E+01	2,51E-95	0,0738	-20,7155509	-1,52952874	1184,9	POLD4	DNA polymerase delta 4, accessory subunit
105374940	9,12E-03	2,04E+00	6,52E-03	0,5623	-2,720267	-1,52963009	11,36	LOC105374	uncharacterized LOC105374940
101448202	4,03E-13	1,24E+01	1,66E-13	0,2075	-7,3737192	-1,53027536	75,95	LOC101448	uncharacterized LOC101448202
4282	1,94E-143	1,43E+02	5,23E-145	0,0597	-25,6417307	-1,5302878	4874,99	MIF	macrophage migration inhibitory factor
283385	3,03E-04	3,52E+00	1,91E-04	0,4104	-3,7301625	-1,53075517	18,88	MORN3	MORN repeat containing 3
64748	6,91E-123	1,22E+02	2,61E-124	0,0646	-23,7135886	-1,53107406	1758,71	PLPPR2	phospholipid phosphatase related 2
4521	2,30E-75	7,46E+01	2,10E-76	0,0828	-18,4991598	-1,53154131	799,09	NUDT1	nudix hydrolase 1
1230	3,48E-07	6,46E+00	1,83E-07	0,2937	-5,2161149	-1,53187882	37,62	CCR1	C-C motif chemokine receptor 1
57521	2,77E-195	1,95E+02	3,70E-197	0,0512	-29,9558196	-1,53230394	4191,78	RPTOR	regulatory associated protein of MTOR complex 1
113219467	1,29E-102	1,02E+02	7,02E-104	0,0708	-21,643341	-1,53339125	2934,81	MIR12136	microRNA 12136
5230	0	#NUM!	0	0,035	-43,7943991	-1,5343081	55683,89	PGK1	phosphoglycerate kinase 1
93343	8,14E-156	1,55E+02	1,84E-157	0,0574	-26,7351911	-1,53463412	2538,15	MVB12A	multivesicular body subunit 12A
158960	1,83E-08	7,74E+00	9,05E-09	0,2671	-5,7476204	-1,53531325	50,37	ATP6AP1-DT	ATP6AP1 divergent transcript
4324	1,66E-61	6,08E+01	2,04E-62	0,0921	-16,67348	-1,53602301	548,63	MMP15	matrix metallopeptidase 15
285966	3,21E-32	3,15E+01	7,71E-33	0,1288	-11,9357275	-1,53686014	210,68	TCAF2	TRPM8 channel associated factor 2
717	6,53E-33	3,22E+01	1,54E-33	0,1274	-12,0688875	-1,53751087	230,86	C2	complement C2
4052	7,58E-195	1,94E+02	1,02E-196	0,0514	-29,9219432	-1,53827838	4326,37	LTBP1	latent transforming growth factor beta binding protein 1
2537	2,48E-36	3,56E+01	5,38E-37	0,1211	-12,7073928	-1,53882803	245,02	IFI6	interferon alpha inducible protein 6
5034	0	#NUM!	0	0,0383	-40,1285716	-1,53887247	58625,78	P4HB	prolyl 4-hydroxylase subunit beta
51529	2,24E-128	1,28E+02	7,52E-130	0,0635	-24,2446882	-1,54064126	1995,21	ANAPC11	anaphase promoting complex subunit 11
50651	9,89E-11	1,00E+01	4,43E-11	0,2339	-6,5889037	-1,54127328	60,45	SLC45A1	solute carrier family 45 member 1
8358	9,97E-08	7,00E+00	5,09E-08	0,2829	-5,4480174	-1,54134877	40,69	H3C2	H3 clustered histone 2
9056	9,69E-17	1,60E+01	3,55E-17	0,1829	-8,4269924	-1,54137902	107,28	SLC7A7	solute carrier family 7 member 7
102467073	4,64E-03	2,33E+00	3,22E-03	0,5234	-2,9454441	-1,54175687	11,64	PDCD6-DT	PDCD6 divergent transcript
10840	4,46E-17	1,64E+01	1,62E-17	0,1811	-8,5184324	-1,54230796	101,55	ALDH1L1	aldehyde dehydrogenase 1 family member L1
60370	1,18E-78	7,79E+01	1,00E-79	0,0816	-18,9068802	-1,54291735	642,97	AVPI1	arginine vasopressin induced 1
283212	5,14E-06	5,29E+00	2,88E-06	0,3298	-4,6793598	-1,54317713	29,55	KLHL35	kelch like family member 35
83648	3,25E-153	1,52E+02	7,57E-155	0,0582	-26,5092962	-1,54329583	1440,49	FAM167A	family with sequence similarity 167 member A
311	0	#NUM!	0	0,0403	-38,2747548	-1,54421968	9156,52	ANXA11	annexin A11
9610	2,72E-111	1,11E+02	1,24E-112	0,0687	-22,553462	-1,54859487	1743,69	RIN1	Ras and Rab interactor 1
971	7,44E-03	2,13E+00	5,27E-03	0,5551	-2,7899275	-1,5487822	10,48	CD72	CD72 molecule
101928841	4,33E-41	4,04E+01	8,45E-42	0,1144	-13,5453033	-1,54992157	303,89	LOC101928	replaced by ID 113622
79917	1,29E-07	6,89E+00	6,62E-08	0,2872	-5,4012103	-1,55099169	40,12	MAGIX	MAGI family member, X-linked
6624	2,31E-141	1,41E+02	6,39E-143	0,0609	-25,4539168	-1,55108124	1517,08	FSCN1	fascin actin-bundling protein 1
57140	9,08E-99	9,80E+01	5,29E-100	0,0731	-21,2277902	-1,55165466	1352,21	RNPEPL1	arginyl aminopeptidase like 1
25911	1,32E-41	4,09E+01	2,55E-42	0,1138	-13,6330641	-1,55178105	277,92	DPCD	deleted in primary ciliary dyskinesia homolog (mouse)
51282	5,83E-93	9,22E+01	3,78E-94	0,0754	-20,5844722	-1,55227319	1326,54	SCAND1	SCAN domain containing 1
9454	3,75E-140	1,39E+02	1,05E-141	0,0614	-25,3437585	-1,55568657	1654,26	HOMER3	homer scaffold protein 3
741	2,02E-43	4,27E+01	3,76E-44	0,1116	-13,9372745	-1,55606469	289,4	ZNHIT2	zinc finger HIT-type containing 2
9148	1,56E-02	1,81E+00	1,14E-02	0,615	-2,5304632	-1,55615377	9,11	NEURL1	neuralized E3 ubiquitin protein ligase 1
441531	6,12E-104	1,03E+02	3,24E-105	0,0715	-21,7847602	-1,55734861	857,34	PGAM4	phosphoglycerate mutase family member 4
56998	9,53E-151	1,50E+02	2,33E-152	0,0592	-26,2926073	-1,55772425	2016,84	CTNNBIP1	catenin beta interacting protein 1
201191	2,00E-42	4,17E+01	3,79E-43	0,1131	-13,771344	-1,5578873	303,33	SAMD14	sterile alpha motif domain containing 14
150763	1,17E-127	1,27E+02	3,98E-129	0,0645	-24,1759533	-1,55820668	1830,33	GPAT2	glycerol-3-phosphate acyltransferase 2, mitochondrial
7289	7,44E-141	1,40E+02	2,06E-142	0,0613	-25,4078575	-1,55827803	1320,01	TULP3	TUB like protein 3

23096	4,19E-140	1,39E+02	1,18E-141	0,0615	-25,3392793	-1,55904142	1499,76	IQSEC2	IQ motif and Sec7 domain ArfGEF 2
91851	1,83E-162	1,62E+02	3,72E-164	0,0571	-27,3047564	-1,5591746	2844,9	CHRDL1	chordin like 1
107986762	9,79E-17	1,60E+01	3,58E-17	0,1852	-8,4257468	-1,56045501	98,84	LOC107986762	
84310	1,91E-146	1,46E+02	4,91E-148	0,0602	-25,9117724	-1,56100314	1976,53	C7orf50	chromosome 7 open reading frame 50
55062	6,51E-161	1,60E+02	1,38E-162	0,0575	-27,1723894	-1,56161152	1462,32	WIPI1	WD repeat domain, phosphoinositide interacting 1
147166	2,14E-115	1,15E+02	9,27E-117	0,068	-22,9701242	-1,56280065	1060,43	TRIM16L	tripartite motif containing 16 like
8942	1,69E-231	2,31E+02	1,52E-233	0,0479	-32,630457	-1,56307075	3714,81	KYNU	kynureninase
441054	7,64E-06	5,12E+00	4,33E-06	0,3403	-4,5950562	-1,56348194	28,35	C4orf47	chromosome 4 open reading frame 47
100506123	3,06E-04	3,51E+00	1,93E-04	0,4194	-3,7281825	-1,56354759	18,12	APPAT	atherosclerotic plaque pathogenesis associated transcript
105370399	9,71E-04	3,01E+00	6,36E-04	0,4578	-3,4156496	-1,56356935	16	LOC105370399	uncharacterized LOC105370399
6653	7,91E-105	1,04E+02	4,11E-106	0,0716	-21,8791282	-1,56556834	1046,54	SORL1	sortilin related receptor 1
572	1,23E-163	1,63E+02	2,48E-165	0,0572	-27,4036734	-1,5662915	1851,76	BAD	BCL2 associated agonist of cell death
10014	1,23E-103	1,03E+02	6,54E-105	0,072	-21,7525123	-1,56671801	979,51	HDAC5	histone deacetylase 5
388564	1,44E-04	3,84E+00	8,86E-05	0,4001	-3,9198547	-1,56817591	20,26	TMEM238	transmembrane protein 238
3620	1,09E-16	1,60E+01	3,99E-17	0,1865	-8,4133105	-1,56891646	100,49	IDO1	indoleamine 2,3-dioxygenase 1
146429	8,91E-04	3,05E+00	5,82E-04	0,4562	-3,4396783	-1,56930952	16	SLC22A31	solute carrier family 22 member 31
101929335	2,66E-10	9,58E+00	1,21E-10	0,2438	-6,4376247	-1,56934869	57,27	ADAMTS9-A	ADAMTS9 antisense RNA 1
154761	7,54E-13	1,21E+01	3,14E-13	0,2154	-7,2884664	-1,56959589	71,14	LOC154761	family with sequence similarity 115, member C pseudogene
65990	1,08E-22	2,20E+01	3,34E-23	0,1584	-9,9220298	-1,57141114	160,63	ANTKMT	adenine nucleotide translocase lysine methyltransferase
57594	2,19E-07	6,66E+00	1,14E-07	0,2964	-5,3035318	-1,57188613	36,99	HOMEZ	homeobox and leucine zipper encoding
56944	1,28E-16	1,59E+01	4,69E-17	0,1873	-8,3941583	-1,57197841	95,18	OLFML3	olfactomedin like 3
79890	6,71E-127	1,26E+02	2,34E-128	0,0652	-24,1027519	-1,57266279	1165,44	RIN3	Ras and Rab interactor 3
64855	1,03E-244	2,44E+02	8,18E-247	0,0469	-33,5528629	-1,57317123	34687,01	NIBAN2	niban apoptosis regulator 2
100616345	8,90E-10	9,05E+00	4,15E-10	0,2519	-6,2483277	-1,574163	61,49	MIR4426	microRNA 4426
15	2,57E-03	2,59E+00	1,74E-03	0,5036	-3,1306942	-1,57654682	12,8	AANAT	aralkylamine N-acetyltransferase
6134	0	#NUM!	0	0,0396	-39,8754719	-1,57743301	41935,35	RPL10	ribosomal protein L10
1520	1,40E-149	1,49E+02	3,46E-151	0,0602	-26,1899724	-1,57745212	1637,32	CTSS	cathepsin S
113218486	1,93E-14	1,37E+01	7,61E-15	0,203	-7,7739414	-1,57818866	81,07	MIR10392	microRNA 10392
816	1,56E-10	9,81E+00	7,05E-11	0,2421	-6,5195333	-1,57835049	58,85	CAMK2B	calcium/calmodulin dependent protein kinase II beta
23646	1,24E-205	2,05E+02	1,48E-207	0,0514	-30,7437212	-1,57869032	6143,53	PLD3	phospholipase D family member 3
10318	0	#NUM!	0	0,0386	-40,9605362	-1,57905989	26539,02	TNIP1	TNFAIP3 interacting protein 1
283	1,83E-23	2,27E+01	5,53E-24	0,1564	-10,0999233	-1,57930896	136,85	ANG	angiogenin
107984974	5,39E-189	1,88E+02	7,68E-191	0,0536	-29,4667457	-1,57967579	2079,66	LOC107984	SMAD specific E3 ubiquitin protein ligase 2 (SMURF2) pseudogene
105371934	2,20E-11	1,07E+01	9,64E-12	0,232	-6,811786	-1,58010768	60,57	LOC105371	uncharacterized LOC105371934
55506	3,18E-03	2,50E+00	2,18E-03	0,5158	-3,0650427	-1,58103934	12,47	MACROH2A	macroH2A.2 histone
386618	1,27E-02	1,90E+00	9,23E-03	0,6075	-2,6035985	-1,58178253	9,08	KCTD4	potassium channel tetramerization domain containing 4
29886	4,07E-160	1,59E+02	8,73E-162	0,0584	-27,1044501	-1,58318526	2363,58	SNX8	sorting nexin 8
53353	2,25E-06	5,65E+00	1,23E-06	0,3266	-4,8503686	-1,58388907	30,25	LRP1B	LDL receptor related protein 1B
4535	4,47E-155	1,54E+02	1,01E-156	0,0594	-26,6712848	-1,58437604	83170,95	ND1	NADH dehydrogenase subunit 1
100126311	4,91E-62	6,13E+01	5,96E-63	0,0947	-16,7469752	-1,58523232	636,26	MIR147B	microRNA 147b
10263	5,30E-183	1,82E+02	8,08E-185	0,0547	-28,9929048	-1,58632628	2100,02	CDK2AP2	cyclin dependent kinase 2 associated protein 2
205251	1,61E-59	5,88E+01	2,08E-60	0,0969	-16,3950163	-1,58821899	482,42	MTLN	mitoregulin
10043	1,54E-101	1,01E+02	8,54E-103	0,0739	-21,5278421	-1,59138912	1020,43	TOM1	target of myb1 membrane trafficking protein
10882	2,52E-05	4,60E+00	1,47E-05	0,3674	-4,3328002	-1,59195131	24,39	C1QL1	complement C1q like 1
9542	1,01E-10	1,00E+01	4,54E-11	0,2418	-6,5854393	-1,59212136	60,92	NRG2	neuregulin 2
215	4,53E-91	9,03E+01	3,03E-92	0,0782	-20,370962	-1,59314326	762,16	ABCD1	ATP binding cassette subfamily D member 1
10267	2,15E-47	4,67E+01	3,62E-48	0,1093	-14,5826333	-1,59449276	383,9	RAMP1	receptor activity modifying protein 1
7052	4,46E-298	2,97E+02	2,33E-300	0,043	-37,0429858	-1,59452229	23759,92	TGM2	transglutaminase 2
80270	2,93E-156	1,56E+02	6,56E-158	0,0596	-26,7736162	-1,59497131	1615,7	HSD3B7	hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 7
151306	2,32E-01	6,35E-01	1,98E-01	1,2407	-1,2863482	-1,59592362	16,71	GPBAR1	G protein-coupled bile acid receptor 1
54742	5,89E-27	2,62E+01	1,62E-27	0,1468	-10,868988	-1,59598027	158,62	LY6K	lymphocyte antigen 6 family member K
26298	0	#NUM!	0	0,0397	-40,2512997	-1,59646884	12049,27	EHF	ETS homologous factor
1958	5,35E-81	8,03E+01	4,35E-82	0,0832	-19,1916551	-1,59721772	732,65	EGR1	early growth response 1
23641	7,08E-133	1,32E+02	2,19E-134	0,0648	-24,6710504	-1,59769667	1183,88	LDOC1	LDOC1 regulator of NFKB signaling
4828	8,36E-16	1,51E+01	3,16E-16	0,1958	-8,1671533	-1,59882686	92,39	NMB	neuromedin B
84878	6,48E-79	7,82E+01	5,47E-80	0,0844	-18,9387153	-1,5991682	606,02	ZBTB45	zinc finger and BTB domain containing 45
1052	4,42E-70	6,94E+01	4,53E-71	0,0898	-17,8249225	-1,60002637	635,74	CEBPD	CCAAT enhancer binding protein delta
8875	4,40E-12	1,14E+01	1,88E-12	0,2274	-7,0434627	-1,60150086	64,98	VNN2	vanin 2
5441	3,85E-126	1,25E+02	1,36E-127	0,0667	-24,0296424	-1,602312	5766,11	POLR2L	RNA polymerase II, I and III subunit L
221416	1,42E-03	2,85E+00	9,46E-04	0,485	-3,3061869	-1,60334195	15,16	LINC03040	long intergenic non-protein coding RNA 3040
113146	6,49E-178	1,77E+02	1,07E-179	0,0561	-28,5838436	-1,60444417	2320,17	AHNAK2	AHNAK nucleoprotein 2
5475	6,95E-03	2,16E+00	4,91E-03	0,5711	-2,812819	-1,60640991	9,84	PPEF1	protein phosphatase with EF-hand domain 1
729234	5,68E-34	3,32E+01	1,31E-34	0,1309	-12,2703082	-1,60657033	210,03	FAHD2CP	fumarylacetoacetate hydrolase domain containing 2C, pseudogene
80097	1,97E-107	1,07E+02	9,72E-109	0,0725	-22,1531787	-1,60681032	1123,46	MZT2B	mitotic spindle organizing protein 2B
101928176	1,15E-42	4,19E+01	2,16E-43	0,1164	-13,8117951	-1,6072132	267,86	LINC01411	long intergenic non-protein coding RNA 1411
2950	2,66E-170	1,70E+02	4,87E-172	0,0575	-27,9608504	-1,60721727	3822,69	GSTP1	glutathione S-transferase pi 1
101927825	5,86E-101	1,00E+02	3,26E-102	0,0749	-21,4656419	-1,60788709	807,81	LOC101927	uncharacterized LOC101927825
653691	5,12E-07	6,29E+00	2,72E-07	0,3127	-5,1421507	-1,60800554	34,96	TCAF2P1	TRPM8 channel associated factor 2 pseudogene 1
58191	8,50E-30	2,91E+01	2,17E-30	0,1404	-11,4570365	-1,60848378	177,02	CXCL16	C-X-C motif chemokine ligand 16
55586	1,72E-09	8,76E+00	8,14E-10	0,262	-6,1422133	-1,60947961	47,44	MIOX	myo-inositol oxygenase
140576	3,82E-276	2,75E+02	2,33E-278	0,0452	-35,6502731	-1,60974888	13872,68	S100A16	S100 calcium binding protein A16
7923	1,61E-49	4,88E+01	2,57E-50	0,108	-14,9166194	-1,61119293	310,1	HSD17B8	hydroxysteroid 17-beta dehydrogenase 8
105372716	2,30E-25	2,46E+01	6,61E-26	0,1535	-10,5252414	-1,61538419	142,83	LOC105372	uncharacterized LOC105372716
105371453	2,69E-08	7,57E+00	1,34E-08	0,2847	-5,6812186	-1,61728529	42,03	BCAN-AS1	BCAN antisense RNA 1
101929475	8,45E-49	4,81E+01	1,38E-49	0,1092	-14,8041311	-1,61734476	302,19	ITGB1-DT	ITGB1 divergent transcript
105372989	5,87E-07	6,23E+00	3,12E-07	0,3163	-5,1157644	-1,61786113	32,78	LOC105372989	
10901	2,48E-71	7,06E+01	2,46E-72	0,09	-17,9871378	-1,6186504	495,51	DHRS4	dehydrogenase/reductase 4
9149	1,35E-97	9,69E+01	8,04E-99	0,0768	-21,0994699	-1,62107957	705,11	DYRK1B	dual specificity tyrosine phosphorylation regulated kinase 1B
8722	8,64E-166	1,65E+02	1,70E-167	0,0588	-27,5847233	-1,62238704	1551,68	CTSF	cathepsin F
4550	0	#NUM!	0	0,0399	-40,6906272	-1,62404852	227459,08	RNR2	l-rRNA
1831	5,74E-86	8,52E+01	4,22E-87	0,0821	-19,7824345	-1,62413627	613,55	TSC22D3	TSC22 domain family member 3
114088	5,34E-16	1,53E+01	2,00E-16	0,1978	-8,2219383	-1,62632561	87,73	TRIM9	tripartite motif containing 9
5307	2,41E-159	1,59E+02	5,21E-161	0,0602	-27,0385437	-1,62716516	1530,7	PITX1	paired like homeodomain 1
1482	5,60E-03	2,25E+00	3,92E-03	0,5643	-2,8844053	-1,62759492	10,41	NKX2-5	NK2 homeobox 5
55897	1,08E-11	1,10E+01	4,66E-12	0,2355	-6,9156123	-1,62849076	60,65	MESP1	mesoderm posterior bHLH transcription factor 1
4728	5,24E-154	1,53E+02	1,20E-155	0,0613	-26,5786019	-1,62858798	4180,32	NDUFS8	NADH:ubiquinone oxidoreductase core subunit S8
1545	8,83E-225	2,24E+02	8,37E-227	0,0507	-32,151676	-1,6299857	6553,32	CYP1B1	cytochrome P450 family 1 subfamily B member 1
8269	2,41E-24	2,36E+01	7,11E-25	0,1584	-10,2991739	-1,63139605	136,84	TMEM187	transmembrane protein 187
284131	1,69E-67	6,68E+01	1,83E-68	0,0933	-17,4859192	-1,63209831	487,81	ENDOV	endonuclease V
79629	1,11E-130	1,30E+02	3,58E-132	0,0667	-24,463887	-1,63287493	1060,56	OCEL1	occludin/ELL domain containing 1
112694756	5,56E-279	2,78E+02	3,27E-281	0,0456	-35,8339134	-1,6331611	25827,73	LOC112694	uncharaterized LOC112694756
221	3,62E-147	1,46E+02	9,18E-149	0,0629	-25,9763032	-1,63374956	1409,08	ALDH3B1	aldehyde dehydrogenase 3 family member B1
100271849	2,31E-18	1,76E+01	8,05E-19	0,1849	-8,8593471	-1,63767325	99,17	MEF2B	myocyte enhancer factor 2B
65249	4,15E-99	9,84E+01	2,40E-100	0,077	-21,2648289	-1,63833585	795,88	ZSWIM4	zinc finger SWIM-type containing 4
1731	4,58E-10	9,34E+00	2,11E-10	0,2581	-6,3530848	-1,63971263	53,28	SEPTIN1	septin 1
8714	6,06E-99	9,82E+01	3,52E-100	0,0772	-21,2468874	-1,63994972	752,15	ABCC3	ATP binding cassette subfamily C member 3
29950	4,73E-92	9,13E+01	3,12E-93	0,0801	-20,4819305	-1,64011065	850,68	SERTAD1	SERTA domain containing 1
56654	2,62E-105	1,05E+02	1,35E-106	0,0749	-21,929964	-1,6424459	995,19	NPDC1	neural proliferation, differentiation and control 1
222487	3,93E-66	6,54E+01	4,36E-67	0,095	-17,3043746	-1,643246	441,22	ADGRG3	adhesion G protein-coupled receptor G3
57000	2,44E-18	1,76E+01	8,51E-19	0,1856	-8,8531286	-1,643582	100,22	GSN-AS1	GSN antisense RNA 1
260293	6,23E-05	4,21E+00	3,72E-05	0,399	-4,1240357	-1,64530686	21,03	CYP4X1	cytochrome P450 family 4 subfamily X member 1
102546298	2,38E-05	4,62E+00	1,39E-05	0,3786	-4,34559	-1,64543894	23,82	NDST1-AS1	NDST1 antisense RNA 1
64975	9,02E-110	1,09E+02	4,27E-111	0,0735	-22,396417	-1,64560108	873,27	MRPL41	mitochondrial ribosomal protein L41
100996351	1,32E-31	3,09E+01	3,22E-32	0,1393	-11,8162044	-1,64566779	186,46	GNA15-DT	GNA15 divergent transcript
226	5,32E-278	2,77E+02	3,19E-280	0,046	-35,7703729	-1,64667059	26440,8	ALDOA	aldolase, fructose-bisphosphate A
11230	9,59E-131	1,30E+02	3,08E-132	0,0673	-24,4700072	-1,64736817	1680,74	PRAF2	PRA1 domain family member 2
7008	3,66E-74	7,34E+01	3,42E-75	0,0898	-18,3481399	-1,64795271	481,01	TEF	TEF transcription factor, PAR bZIP family member
85446	1,12E-26	2,60E+01	3,10E-27	0,1526	-10,8094627	-1,64929061	154,89	ZFHX2	zinc finger homeobox 2
126	2,60E-05	4,59E+00	1,52E-05	0,3813	-4,3259155	-1,6494462	22,93	ADH1C	alcohol dehydrogenase 1C (class I), gamma polypeptide
114907	1,09E-268	2,68E+02	7,07E-271	0,0469	-35,1641157	-1,64983909	3415,26	FBXO32	F-box protein 32
7058	1,53E-38	3,78E+01	3,15E-39	0,1261	-13,1032741	-1,65219977	253,7	THBS2	thrombospondin 2
2015	1,08E-30	3,00E+01	2,71E-31	0,1421	-11,6359609	-1,65374733	190,69	ADGRE1	adhesion G protein-coupled receptor E1
8651	1,62E-12	1,18E+01	6,81E-13	0,2303	-7,1832049	-1,65446277	74,79	SOCS1	suppressor of cytokine signaling 1
6640	3,26E-70	6,95E+01	3,32E-71	0,0928	-17,8422213	-1,65496015	492,14	SNTA1	syntrophin alpha 1
4313	5,15E-04	3,29E+00	3,30E-04	0,4612	-3,5902736	-1,65567838	15,82	MMP2	matrix metallopeptidase 2
2316	2,00E-261	2,61E+02	1,36E-263	0,0477	-34,6843054	-1,65600735	124726,64	FLNA	filamin A
64122	1,86E-26	2,57E+01	5,18E-27	0,1541	-10,7624075	-1,65818394	158,86	FN3K	fructosamine 3 kinase
81622	1,01E-130	1,30E+02	3,25E-132	0,0679	-24,4678922	-1,6603318	1003,88	UNC93B1	unc-93 homolog B1, TLR signaling regulator
57291	1,31E-153	1,53E+02	3,04E-155	0,0626	-26,5437027	-1,66037675	2311,36	DANCR	differentiation antagonizing non-protein coding RNA
84330	1,50E-65	6,48E+01	1,69E-66	0,0965	-17,22611	-1,66238062	450,33	ZNF414	zinc finger protein 414

107985278	4,47E-04	3,35E+00	2,85E-04	0,4584	-3,6282091	-1,6633203	15,64	LOC107985	uncharacterized LOC107985278
127687	3,68E-135	1,34E+02	1,10E-136	0,0669	-24,8842648	-1,66394955	1063,13	C1orf122	chromosome 1 open reading frame 122
170394	8,66E-41	4,01E+01	1,70E-41	0,1236	-13,4938656	-1,66806736	273,28	PWWP2B	PWWP domain containing 2B
8366	7,50E-04	3,12E+00	4,88E-04	0,4788	-3,4875128	-1,66971669	16,26	H4C2	H4 clustered histone 2
101928589	5,48E-110	1,09E+02	2,58E-111	0,0745	-22,4188793	-1,66980061	759,88	LOC101928	replaced by ID 84187
639	5,75E-30	2,92E+01	1,46E-30	0,1453	-11,4912856	-1,66995904	202,96	PRDM1	PR/SET domain 1
100616124	3,78E-22	2,14E+01	1,18E-22	0,1706	-9,7952862	-1,67062633	119,59	MIR4647	microRNA 4647
2172	4,13E-07	6,38E+00	2,18E-07	0,3226	-5,1832702	-1,67189877	33,99	FABP6	fatty acid binding protein 6
148523	3,46E-14	1,35E+01	1,38E-14	0,2173	-7,6985193	-1,67273902	73,38	CIART	circadian associated repressor of transcription
105376627	3,80E-03	2,42E+00	2,62E-03	0,5561	-3,0096688	-1,67375843	10,74	LOC105376	uncharacterized LOC105376627
23541	1,18E-148	1,48E+02	2,96E-150	0,0641	-26,1080353	-1,67414448	1129,15	SEC14L2	SEC14 like lipid binding 2
374875	1,29E-19	1,89E+01	4,32E-20	0,1824	-9,1797849	-1,67426864	109,67	HSD11B1L	hydroxysteroid 11-beta dehydrogenase 1 like
27147	2,43E-58	5,76E+01	3,22E-59	0,1032	-16,2276514	-1,67439868	369,62	DENND2A	DENN domain containing 2A
7942	2,94E-31	3,05E+01	7,23E-32	0,1425	-11,7480063	-1,67456159	171,82	TFEB	transcription factor EB
201305	1,53E-03	2,82E+00	1,02E-03	0,5101	-3,2843282	-1,67528946	12,44	SPNS3	SPNS lysolipid transporter 3, sphingosine-1-phosphate (putative)
79924	2,65E-17	1,66E+01	9,54E-18	0,1953	-8,5793585	-1,67592929	87,5	ADM2	adrenomedullin 2
55107	4,96E-04	3,30E+00	3,18E-04	0,4657	-3,6000438	-1,67644494	15,94	ANO1	anoctamin 1
8751	7,14E-206	2,05E+02	8,49E-208	0,0545	-30,7618643	-1,67657596	10509,46	ADAM15	ADAM metallopeptidase domain 15
5339	0	#NUM!	0	0,0429	-39,1656735	-1,67883779	50665,32	PLEC	plectin
25849	3,60E-96	9,54E+01	2,19E-97	0,0803	-20,9426576	-1,68233271	670,83	PARM1	prostate androgen-regulated mucin-like protein 1
8623	4,77E-70	6,93E+01	4,90E-71	0,0944	-17,8205521	-1,68302333	634,32	ASMTL	acetylserotonin O-methyltransferase like
3552	1,75E-107	1,07E+02	8,63E-109	0,076	-22,1585215	-1,68331117	1016,12	IL1A	interleukin 1 alpha
3241	3,15E-212	2,12E+02	3,46E-214	0,0539	-31,2359476	-1,68344001	12092,81	HPCAL1	hippocalcin like 1
2498	3,16E-03	2,50E+00	2,16E-03	0,549	-3,0669095	-1,68361834	10,78	FTH1P3	ferritin heavy chain 1 pseudogene 3
140467	3,52E-134	1,33E+02	1,07E-135	0,068	-24,7929814	-1,68598199	1805,85	ZNF358	zinc finger protein 358
84969	6,29E-146	1,45E+02	1,64E-147	0,0652	-25,8653157	-1,68717222	1235,93	TOX2	TOX high mobility group box family member 2
23452	4,39E-179	1,78E+02	7,17E-181	0,0589	-28,6780228	-1,68781681	1838,09	ANGPTL2	angiopoietin like 2
84557	2,54E-16	1,56E+01	9,42E-17	0,2032	-8,3118364	-1,68936878	86,79	MAP1LC3A	microtubule associated protein 1 light chain 3 alpha
55954	6,09E-59	5,82E+01	7,98E-60	0,1038	-16,3129501	-1,6924787	382,75	ZMAT5	zinc finger matrin-type 5
10610	2,65E-11	1,06E+01	1,16E-11	0,2495	-6,784529	-1,69288391	52,98	ST6GALNAC	ST6 N-acetylgalactosaminide alpha-2,6-sialyltransferase 2
118932	3,00E-07	6,52E+00	1,57E-07	0,3231	-5,2438683	-1,69413948	32	ANKRD22	ankyrin repeat domain 22
5947	4,53E-03	2,34E+00	3,15E-03	0,574	-2,9531382	-1,69500188	10,15	RBP1	retinol binding protein 1
107984263	1,78E-12	1,17E+01	7,51E-13	0,2365	-7,1698765	-1,69602483	60,99	LOC107984	uncharacterized LOC107984263
140606	7,12E-58	5,71E+01	9,53E-59	0,105	-16,1608162	-1,69724887	345,59	SELENOM	selenoprotein M
441150	4,31E-70	6,94E+01	4,40E-71	0,0953	-17,8264994	-1,69843688	426,76	C6orf226	chromosome 6 open reading frame 226
4069	9,84E-11	1,00E+01	4,41E-11	0,2579	-6,5896498	-1,699742	53,62	LYZ	lysozyme
2217	5,87E-121	1,20E+02	2,29E-122	0,0723	-23,5245468	-1,70068163	976,26	FCGRT	Fc gamma receptor and transporter
105377806	2,08E-11	1,07E+01	9,08E-12	0,2499	-6,8203906	-1,70423454	53,35	LOC105377	806
4005	1,24E-46	4,59E+01	2,13E-47	0,1179	-14,4612138	-1,70517785	275,41	LMO2	LIM domain only 2
105373334	8,88E-07	6,05E+00	4,77E-07	0,3387	-5,0353011	-1,70558154	28,71	LOC105373	uncharacterized LOC105373334
2954	6,78E-195	1,94E+02	9,09E-197	0,057	-29,9258065	-1,70580754	2112,85	GSTZ1	glutathione S-transferase zeta 1
6676	2,16E-45	4,47E+01	3,83E-46	0,1196	-14,2610191	-1,7059186	258,35	SPAG4	sperm associated antigen 4
340152	8,94E-05	4,05E+00	5,40E-05	0,4232	-4,0373867	-1,70853328	18,98	ZC3H12D	zinc finger CCCH-type containing 12D
102466658	3,13E-05	4,50E+00	1,84E-05	0,3989	-4,2834763	-1,70858381	20,74	MIR6510	microRNA 6510
27350	1,26E-180	1,80E+02	2,00E-182	0,0594	-28,8025005	-1,71122136	1856,68	APOBEC3C	apolipoprotein B mRNA editing enzyme catalytic subunit 3C
4832	1,51E-41	4,08E+01	2,93E-42	0,1259	-13,6227586	-1,71499531	246,58	NME3	NME/NM23 nucleoside diphosphate kinase 3
55049	1,32E-100	9,99E+01	7,38E-102	0,0801	-21,427642	-1,71597657	793,59	REX1BD	required for excision 1-B domain containing
100379249	6,42E-05	4,19E+00	3,84E-05	0,4168	-4,1166909	-1,71602568	20,07	BOK-AS1	BOK antisense RNA 1
64838	5,93E-111	1,10E+02	2,74E-112	0,0763	-22,5184738	-1,71787729	802,23	FNDC4	fibronectin type III domain containing 4
730755	3,71E-35	3,44E+01	8,30E-36	0,1376	-12,4915889	-1,71906577	255,37	KRTAP2-3	keratin associated protein 2-3
653677	1,85E-03	2,73E+00	1,24E-03	0,5329	-3,2293125	-1,72075608	11,53	SEC1P	secretory blood group 1, pseudogene
3866	1,96E-48	4,77E+01	3,23E-49	0,1167	-14,7466721	-1,7209026	297,21	KRT15	keratin 15
101	2,41E-234	2,34E+02	2,10E-236	0,0524	-32,8314548	-1,72136266	8382,64	ADAM8	ADAM metallopeptidase domain 8
28952	3,92E-90	8,94E+01	2,67E-91	0,0851	-20,2640864	-1,72536613	763,91	CCDC22	coiled-coil domain containing 22
146439	3,52E-06	5,45E+00	1,96E-06	0,3628	-4,7579976	-1,72617609	24,96	BICDL2	BICD family like cargo adaptor 2
201181	2,23E-05	4,65E+00	1,30E-05	0,3959	-4,3607767	-1,72644351	20,95	ZNF385C	zinc finger protein 385C
128344	2,77E-03	2,56E+00	1,89E-03	0,5557	-3,1073522	-1,72661354	11	PIFO	primary cilia formation
91584	2,94E-14	1,35E+01	1,17E-14	0,224	-7,7195309	-1,72946434	67,31	PLXNA4	plexin A4
9572	1,19E-129	1,29E+02	3,92E-131	0,071	-24,3660793	-1,72960949	868,62	NR1D1	nuclear receptor subfamily 1 group D member 1
4323	0	#NUM!	0	0,0371	-46,5854592	-1,73020984	60331,21	MMP14	matrix metallopeptidase 14
11033	1,41E-34	3,39E+01	3,19E-35	0,1398	-12,3839738	-1,73079021	199	ADAP1	ArfGAP with dual PH domains 1
100500847	2,96E-05	4,53E+00	1,73E-05	0,403	-4,2966224	-1,73172498	20,95	MIR3615	microRNA 3615
100505839	6,23E-04	3,21E+00	4,03E-04	0,4899	-3,5384046	-1,73336961	13,9	SH3PXD2A-	SH3PXD2A antisense RNA 1
25803	3,34E-173	1,72E+02	5,81E-175	0,0616	-28,2002186	-1,73658916	3660,35	SPDEF	SAM pointed domain containing ETS transcription factor
4501	5,64E-24	2,32E+01	1,68E-24	0,17	-10,2159932	-1,7367849	1553,95	MT1X	metallothionein 1X
105371483	2,68E-07	6,57E+00	1,40E-07	0,3299	-5,2653436	-1,73693286	33,24	LOC105371	uncharacterized LOC105371483
1240	2,13E-181	1,81E+02	3,34E-183	0,0602	-28,8643775	-1,73827854	1853,95	CMKLR1	chemerin chemokine-like receptor 1
3965	3,20E-26	2,55E+01	8,99E-27	0,1625	-10,7115395	-1,74096081	129,14	LGALS9	galectin 9
3053	2,33E-50	4,96E+01	3,66E-51	0,1157	-15,0461606	-1,74117725	314,8	SERPIND1	serpin family D member 1
2769	8,86E-221	2,20E+02	8,80E-223	0,0547	-31,8626248	-1,74207748	2116,43	GNA15	G protein subunit alpha 15
6649	1,60E-76	7,58E+01	1,42E-77	0,0935	-18,6435392	-1,74227751	444,15	SOD3	superoxide dismutase 3
5916	2,49E-193	1,93E+02	3,39E-195	0,0585	-29,8047757	-1,74276477	1809,03	RARG	retinoic acid receptor gamma
116071	9,99E-14	1,30E+01	4,03E-14	0,2306	-7,5601262	-1,74304429	74,33	BATF2	basic leucine zipper ATF-like transcription factor 2
7466	1,69E-211	2,11E+02	1,88E-213	0,056	-31,181875	-1,74671011	4325,56	WFS1	wolframin ER transmembrane glycoprotein
4130	2,66E-07	6,58E+00	1,39E-07	0,3317	-5,2669457	-1,74693182	30,98	MAP1A	microtubule associated protein 1A
2920	9,74E-162	1,61E+02	2,02E-163	0,0642	-27,2429015	-1,74840907	1194,31	CXCL2	C-X-C motif chemokine ligand 2
527	1,41E-253	2,53E+02	1,05E-255	0,0512	-34,1571378	-1,75035718	3576,15	ATP6V0C	ATPase H+ transporting V0 subunit c
10075	0	#NUM!	0	0,0412	-42,475302	-1,750615	29544,71	HUWE1	HECT, UBA and WWE domain containing E3 ubiquitin protein ligase 1
60343	1,81E-159	1,59E+02	3,91E-161	0,0647	-27,0491775	-1,75096575	1458,6	FAM3A	FAM3 metabolism regulating signaling molecule A
4000	4,35E-264	2,63E+02	2,93E-266	0,0502	-34,8607587	-1,75144665	27783,02	LMNA	lamin A/C
100506696	1,56E-09	8,81E+00	7,36E-10	0,2847	-6,1581201	-1,75350921	49,69	PCAT6	prostate cancer associated transcript 6
169611	5,62E-82	8,13E+01	4,47E-83	0,091	-19,3095282	-1,75732422	527,83	OLFML2A	olfactomedin like 2A
51466	2,16E-66	6,57E+01	2,38E-67	0,1014	-17,3392553	-1,75741411	359,59	EVL	Enah/Vasp-like
51308	1,61E-103	1,03E+02	8,53E-105	0,0809	-21,7403361	-1,75805106	644,68	REEP2	receptor accessory protein 2
56000	8,21E-08	7,09E+00	4,18E-08	0,3208	-5,4831288	-1,75892628	32,42	NXF3	nuclear RNA export factor 3
3315	5,11E-177	1,76E+02	8,44E-179	0,0617	-28,5115062	-1,75996201	2295,77	HSPB1	heat shock protein family B (small) member 1
1028	3,07E-26	2,55E+01	8,60E-27	0,1644	-10,7155933	-1,76191951	138,8	CDKN1C	cyclin dependent kinase inhibitor 1C
593	1,58E-116	1,16E+02	6,68E-118	0,0765	-23,0841545	-1,76650469	861,06	BCKDHA	branched chain keto acid dehydrogenase E1 subunit alpha
8214	2,41E-08	7,62E+00	1,20E-08	0,3101	-5,7001333	-1,76769407	36,13	DGCR6	DiGeorge syndrome critical region gene 6
100507551	6,73E-55	5,42E+01	9,64E-56	0,1125	-15,7285168	-1,7694831	297,32	PGLS-DT	PGLS divergent transcript
83982	2,08E-156	1,56E+02	4,63E-158	0,0661	-26,7866023	-1,76975051	1254,88	IFI27L2	interferon alpha inducible protein 27 like 2
7226	3,56E-05	4,45E+00	2,10E-05	0,4164	-4,2543981	-1,77160049	20,28	TRPM2	transient receptor potential cation channel subfamily M member 2
102464833	1,40E-10	9,85E+00	6,33E-11	0,2712	-6,5357729	-1,77248652	45,77	MIR6084	microRNA 6084
83667	7,65E-74	7,31E+01	7,18E-75	0,0969	-18,3077052	-1,77344409	649,97	SESN2	sestrin 2
7056	4,34E-281	2,80E+02	2,48E-283	0,0493	-35,9697885	-1,77405856	5449,16	THBD	thrombomodulin
80727	0	#NUM!	0	0,0464	-38,3385839	-1,77704067	4644,95	TTYH3	tweety family member 3
1474	9,07E-08	7,04E+00	4,63E-08	0,3264	-5,4651443	-1,78407723	31,61	CST6	cystatin E/M
105371893	1,22E-14	1,39E+01	4,80E-15	0,2278	-7,8319693	-1,78443237	69,01	SLC9A3R1-	SLC9A3R1 antisense RNA 1
55231	2,86E-03	2,54E+00	1,95E-03	0,5761	-3,0982377	-1,78475444	10,13	CCDC87	coiled-coil domain containing 87
4242	2,02E-04	3,69E+00	1,26E-04	0,4657	-3,8346117	-1,78587595	15,6	MFNG	MFNG O-fucosylpeptide 3-beta-N-acetylglucosaminyltransferase
83716	2,68E-121	1,21E+02	1,03E-122	0,0758	-23,5581942	-1,78595917	739,19	CRISPLD2	cysteine rich secretory protein LCCL domain containing 2
706	2,51E-193	1,93E+02	3,44E-195	0,0602	-29,8042984	-1,79449193	2686,44	TSPO	translocator protein
155038	7,02E-09	8,15E+00	3,40E-09	0,3038	-5,9112313	-1,79568303	40,69	GIMAP8	GTPase, IMAP family member 8
102724539	2,36E-03	2,63E+00	1,59E-03	0,5693	-3,1569396	-1,79714139	10,72	LINC01714	long intergenic non-protein coding RNA 1714
400916	3,22E-73	7,25E+01	3,06E-74	0,0986	-18,2285696	-1,79744081	394,42	CHCHD10	coiled-coil-helix-coiled-coil-helix domain containing 10
58504	1,96E-224	2,24E+02	1,87E-226	0,056	-32,1266598	-1,79855943	1924,84	ARHGAP22	Rho GTPase activating protein 22
80201	1,30E-28	2,79E+01	3,41E-29	0,1606	-11,2158028	-1,80100938	134,1	HKDC1	hexokinase domain containing 1
9351	0	#NUM!	0	0,0473	-38,1400823	-1,80353598	6562,73	NHERF2	NHERF family PDZ scaffold protein 2
2934	2,90E-220	2,20E+02	2,91E-222	0,0567	-31,8251127	-1,80447796	2617,32	GSN	gelsolin
105372435	1,98E-04	3,70E+00	1,23E-04	0,4699	-3,8400955	-1,80459258	15,15	LOC105372	uncharacterized LOC105372435
101927947	2,28E-04	3,64E+00	1,42E-04	0,4747	-3,8042818	-1,80585965	15,89	LOC101927	uncharacterized LOC101927947
10893	1,21E-88	8,79E+01	8,49E-90	0,0901	-20,0930456	-1,8099502	585,37	MMP24	matrix metallopeptidase 24
283948	5,52E-03	2,26E+00	3,86E-03	0,6265	-2,8891804	-1,81015302	8,49	NHLRC4	NHL repeat containing 4
81031	1,77E-13	1,28E+01	7,19E-14	0,242	-7,4843764	-1,81136433	60,82	SLC2A10	solute carrier family 2 member 10
4061	1,18E-232	2,32E+02	1,04E-234	0,0554	-32,712278	-1,81242041	3400,39	LY6E	lymphocyte antigen 6 family member E
664	4,80E-279	2,78E+02	2,80E-281	0,0506	-35,8382869	-1,81441721	5272,72	BNIP3	BCL2 interacting protein 3
85442	2,03E-04	3,69E+00	1,26E-04	0,4734	-3,834235	-1,81502294	16,4	KNDC1	kinase non-catalytic C-lobe domain containing 1
23474	2,22E-142	1,42E+02	6,04E-144	0,0711	-25,5462568	-1,81667859	1074,44	ETHE1	ETHE1 persulfide dioxygenase
4579	3,34E-169	1,68E+02	6,22E-171	0,0653	-27,8696667	-1,82113668	5160,61	TRNY	tRNA-Tyr
54894	9,13E-39	3,80E+01	1,88E-39	0,1386	-13,1424536	-1,82156711	194,24	RNF43	ring finger protein 43

113177	3,36E-15	1,45E+01	1,30E-15	0,2281	-7,9948602	-1,82355545	69,36	IZUMO4	IZUMO family member 4
102724463	2,90E-04	3,54E+00	1,83E-04	0,4881	-3,7414926	-1,82613665	14,73	LOC102724	uncharacterized LOC102724463
317749	5,18E-59	5,83E+01	6,77E-60	0,1119	-16,3229922	-1,82705857	377,02	DHRS4L2	dehydrogenase/reductase 4 like 2
8635	1,81E-132	1,32E+02	5,62E-134	0,0742	-24,6328132	-1,82766626	826,38	RNASET2	ribonuclease T2
92840	2,81E-56	5,56E+01	3,90E-57	0,1147	-15,9303173	-1,82771047	289,87	REEP6	receptor accessory protein 6
441502	3,04E-04	3,52E+00	1,92E-04	0,4905	-3,7296067	-1,82938388	14,62	RPS26P11	ribosomal protein S26 pseudogene 11
254552	9,24E-19	1,80E+01	3,18E-19	0,2042	-8,9622173	-1,83024835	86,45	NUDT8	nudix hydrolase 8
100506211	1,36E-42	4,19E+01	2,56E-43	0,1327	-13,7995898	-1,83068026	225,26	MIR210HG	MIR210 host gene
286495	3,52E-10	9,45E+00	1,61E-10	0,2863	-6,3944689	-1,8308729	41,04	TTC3P1	tetratricopeptide repeat domain 3 pseudogene 1
102724770	3,37E-09	8,47E+00	1,61E-09	0,3035	-6,0327587	-1,83107579	37,9	LOC102724	replaced by ID 8214
4553	7,00E-280	2,79E+02	4,05E-282	0,051	-35,8921829	-1,83111592	4408,99	TRNA	tRNA-Ala
130497	1,72E-84	8,38E+01	1,30E-85	0,0935	-19,6089906	-1,83257119	479,89	OSR1	odd-skipped related transcription factor 1
4778	1,30E-05	4,89E+00	7,50E-06	0,4093	-4,4791058	-1,83308453	20,19	NFE2	nuclear factor, erythroid 2
25796	2,01E-240	2,40E+02	1,65E-242	0,0551	-33,2564092	-1,83366903	3711,7	PGLS	6-phosphogluconolactonase
7439	0	#NUM!	0	0,0369	-49,7119078	-1,83418925	21873,49	BEST1	bestrophin 1
5069	1,09E-205	2,05E+02	1,30E-207	0,0597	-30,7479779	-1,83587442	1593,45	PAPPA	pappalysin 1
2109	7,49E-162	1,61E+02	1,55E-163	0,0674	-27,2526345	-1,83789713	1494,45	ETFB	electron transfer flavoprotein subunit beta
105376717	2,82E-14	1,35E+01	1,12E-14	0,2383	-7,7248868	-1,84053128	69,16	LOC105376	uncharacterized LOC105376717
5522	4,46E-152	1,51E+02	1,07E-153	0,0697	-26,4094719	-1,8418143	968,33	PPP2R2C	protein phosphatase 2 regulatory subunit Bgamma
2919	2,66E-259	2,59E+02	1,86E-261	0,0533	-34,5422321	-1,84225224	9086,66	CXCL1	C-X-C motif chemokine ligand 1
105373383	1,31E-04	3,88E+00	7,99E-05	0,4673	-3,9448362	-1,84325389	16,76	LOC105373	uncharacterized LOC105373383
3783	2,00E-164	1,64E+02	4,00E-166	0,0673	-27,4700607	-1,84748655	1400,57	KCNN4	potassium calcium-activated channel subfamily N member 4
113675	3,16E-65	6,45E+01	3,57E-66	0,1076	-17,1827913	-1,84865252	414,73	SDSL	serine dehydratase like
643988	1,94E-99	9,87E+01	1,11E-100	0,0868	-21,3011073	-1,84947686	889,92	FNDC10	fibronectin type III domain containing 10
124044	2,64E-27	2,66E+01	7,19E-28	0,1691	-10,942902	-1,85048204	152,44	SPATA2L	spermatogenesis associated 2 like
126003	6,88E-110	1,09E+02	3,24E-111	0,0826	-22,4086968	-1,85149879	1037,25	TRAPPC5	trafficking protein particle complex subunit 5
100529262	3,61E-37	3,64E+01	7,69E-38	0,1441	-12,8586386	-1,85330249	171,43	MIA-RAB4B	MIA-RAB4B readthrough (NMD candidate)
112464	1,85E-190	1,90E+02	2,60E-192	0,0627	-29,5812899	-1,85520452	1380,52	CAVIN3	caveolae associated protein 3
7483	4,70E-32	3,13E+01	1,13E-32	0,1561	-11,9035586	-1,85813812	149,53	WNT9A	Wnt family member 9A
6567	1,11E-93	9,30E+01	7,09E-95	0,0901	-20,6654253	-1,8619543	488,45	SLC16A2	solute carrier family 16 member 2
274	7,13E-153	1,52E+02	1,68E-154	0,0703	-26,4793512	-1,86225776	1122,84	BIN1	bridging integrator 1
53916	1,03E-37	3,70E+01	2,17E-38	0,1438	-12,956097	-1,86270604	171,68	RAB4B	RAB4B, member RAS oncogene family
2512	5,46E-76	7,53E+01	4,93E-77	0,1003	-18,5770265	-1,86325807	77409,73	FTL	ferritin light chain
91227	4,09E-07	6,39E+00	2,16E-07	0,3595	-5,1849875	-1,86401589	26,32	GGTLC2	gamma-glutamyltransferase light chain 2
6237	6,76E-190	1,89E+02	9,56E-192	0,0631	-29,5372966	-1,8646096	1938,81	RRAS	RAS related
8335	1,71E-04	3,77E+00	1,06E-04	0,4812	-3,8774319	-1,86570155	15,1	H2AC4	H2A clustered histone 4
5210	5,44E-204	2,03E+02	6,74E-206	0,0609	-30,6194617	-1,8659165	1510,14	PFKFB4	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 4
8933	3,23E-188	1,87E+02	4,65E-190	0,0635	-29,4056371	-1,86761695	3651,36	RTL8C	retrotransposon Gag like 8C
100874243	5,26E-06	5,28E+00	2,95E-06	0,3998	-4,6740536	-1,86881597	21,22	PRICKLE2-A	PRICKLE2 antisense RNA 3
1	2,30E-17	1,66E+01	8,27E-18	0,2174	-8,5957877	-1,86899333	74,14	A1BG	alpha-1-B glycoprotein
6948	9,81E-47	4,60E+01	1,68E-47	0,1292	-14,4775898	-1,8710938	246,47	TCN2	transcobalamin 2
6748	0	#NUM!	0	0,0476	-39,3677347	-1,8728574	5052,79	SSR4	signal sequence receptor subunit 4
7262	9,22E-227	2,26E+02	8,54E-229	0,058	-32,2938323	-1,87324632	3502,41	PHLDA2	pleckstrin homology like domain family A member 2
9536	0	#NUM!	0	0,0415	-45,2106344	-1,87600314	8226,07	PTGES	prostaglandin E synthase
9123	2,80E-284	2,84E+02	1,58E-286	0,0519	-36,1735886	-1,87626535	16654,28	SLC16A3	solute carrier family 16 member 3
3426	2,26E-12	1,16E+01	9,57E-13	0,2637	-7,1365597	-1,88163496	51,64	CFI	complement factor I
220002	1,13E-184	1,84E+02	1,69E-186	0,0647	-29,1257863	-1,88322163	1750,91	CYB561A3	cytochrome b561 family member A3
51754	6,61E-48	4,72E+01	1,10E-48	0,1285	-14,6638297	-1,88393183	240,28	TMEM8B	transmembrane protein 8B
7498	1,12E-39	3,90E+01	2,26E-40	0,1416	-13,3017051	-1,88405558	192,68	XDH	xanthine dehydrogenase
2358	3,30E-03	2,48E+00	2,26E-03	0,6187	-3,0536787	-1,88931459	8,95	FPR2	formyl peptide receptor 2
825	1,75E-04	3,76E+00	1,08E-04	0,4883	-3,8716491	-1,89063857	15,35	CAPN3	calpain 3
100128750	2,80E-07	6,55E+00	1,46E-07	0,36	-5,2569348	-1,89260728	26,69	RBPMS-AS1	RBPMS antisense RNA 1
105377731	1,21E-28	2,79E+01	3,16E-29	0,1688	-11,2224543	-1,89385866	139,04	LOC105377	uncharacterized LOC105377731
8626	6,93E-22	2,12E+01	2,18E-22	0,1946	-9,73289	-1,89432464	93,31	TP63	tumor protein p63
80019	4,21E-124	1,23E+02	1,56E-125	0,0797	-23,8317769	-1,89836615	834,15	UBTD1	ubiquitin domain containing 1
2192	7,18E-38	3,71E+01	1,51E-38	0,1463	-12,9840893	-1,89938611	189,97	FBLN1	fibulin 1
389114	9,86E-05	4,01E+00	5,98E-05	0,4748	-4,0134631	-1,90564896	16	ZNF662	zinc finger protein 662
51621	3,30E-214	2,13E+02	3,58E-216	0,0608	-31,3818827	-1,90820189	1586,92	KLF13	KLF transcription factor 13
2584	9,83E-101	1,00E+02	5,49E-102	0,0892	-21,4414092	-1,91264805	881,06	GALK1	galactokinase 1
100506679	1,26E-04	3,90E+00	7,70E-05	0,4841	-3,9536881	-1,91392005	14,77	TTLL1-AS1	TTLL1 antisense RNA 1
1384	1,81E-222	2,22E+02	1,77E-224	0,06	-31,9848475	-1,91768696	1859,64	CRAT	carnitine O-acetyltransferase
125050	7,33E-13	1,21E+01	3,04E-13	0,2631	-7,2924741	-1,91848946	469,99	RN7SK	RNA component of 7SK nuclear ribonucleoprotein
112609	2,72E-11	1,06E+01	1,20E-11	0,2837	-6,7807383	-1,92343952	43,33	MRAP2	melanocortin 2 receptor accessory protein 2
9002	3,98E-27	2,64E+01	1,09E-27	0,1765	-10,9051498	-1,92509879	115,98	F2RL3	F2R like thrombin or trypsin receptor 3
2495	0	#NUM!	0	0,0427	-45,1324498	-1,92554261	28828,17	FTH1	ferritin heavy chain 1
4838	1,13E-03	2,95E+00	7,48E-04	0,5719	-3,3714096	-1,92801503	10,38	NODAL	nodal growth differentiation factor
6865	8,38E-05	4,08E+00	5,06E-05	0,4759	-4,0530151	-1,92875019	16,35	TACR2	tachykinin receptor 2
684	0	#NUM!	0	0,0468	-41,2145691	-1,93064965	6358,73	BST2	bone marrow stromal cell antigen 2
4137	2,26E-18	1,76E+01	7,89E-19	0,2179	-8,8616028	-1,93096404	76,7	MAPT	microtubule associated protein tau
112703	2,90E-27	2,65E+01	7,90E-28	0,1766	-10,9342667	-1,93105048	117,72	GARIN5A	golgi associated RAB2 interactor 5A
79949	5,73E-20	1,92E+01	1,91E-20	0,2093	-9,2674838	-1,93994717	88,1	PLEKHS1	pleckstrin homology domain containing S1
84649	3,53E-214	2,13E+02	3,84E-216	0,0619	-31,3796254	-1,94198834	1415,21	DGAT2	diacylglycerol O-acyltransferase 2
51393	1,91E-30	2,97E+01	4,81E-31	0,1678	-11,586779	-1,94387811	130,11	TRPV2	transient receptor potential cation channel subfamily V member 2
9961	2,59E-274	2,74E+02	1,61E-276	0,0549	-35,5313251	-1,95048283	5603,03	MVP	major vault protein
6277	0	#NUM!	0	0,0474	-41,2080887	-1,95414595	73058,25	S100A6	S100 calcium binding protein A6
28986	2,74E-71	7,06E+01	2,72E-72	0,1092	-17,9815786	-1,96304303	339,17	MAGEH1	MAGE family member H1
4570	0	#NUM!	0	0,0495	-39,6775127	-1,96376016	6203,65	TRNN	tRNA-Asn
513	4,47E-168	1,67E+02	8,47E-170	0,0707	-27,7759389	-1,96388526	1362,43	ATP5F1D	ATP synthase F1 subunit delta
83706	1,45E-23	2,28E+01	4,39E-24	0,1942	-10,1225731	-1,96536624	100,22	FERMT3	FERM domain containing kindlin 3
101928143	1,19E-06	5,92E+00	6,42E-07	0,3952	-4,9782541	-1,96734293	24,57	LOC101928	uncharacterized LOC101928143
388963	4,45E-22	2,14E+01	1,39E-22	0,2015	-9,7783682	-1,97011578	104,68	C2orf81	chromosome 2 open reading frame 81
1608	3,80E-05	4,42E+00	2,24E-05	0,4653	-4,2395084	-1,97277433	16,64	DGKG	diacylglycerol kinase gamma
55890	1,59E-76	7,58E+01	1,42E-77	0,106	-18,6436837	-1,97625683	361,6	GPRC5C	G protein-coupled receptor class C group 5 member C
107986257	2,54E-28	2,76E+01	6,73E-29	0,1773	-11,1554756	-1,97745036	131,49	LOC107986	257
7422	0	#NUM!	0	0,0385	-51,653648	-1,98655638	11400,21	VEGFA	vascular endothelial growth factor A
2539	5,56E-258	2,57E+02	3,96E-260	0,0578	-34,4537085	-1,99160239	4254,3	G6PD	glucose-6-phosphate dehydrogenase
164633	6,27E-33	3,22E+01	1,48E-33	0,1654	-12,0722174	-1,99713498	139,16	CABP7	calcium binding protein 7
4511	7,39E-211	2,10E+02	8,29E-213	0,0642	-31,1342323	-1,99856824	5198,63	TRNC	tRNA-Cys
389813	3,18E-13	1,25E+01	1,30E-13	0,27	-7,4058046	-1,99937196	51,11	AJM1	apical junction component 1 homolog
1628	2,28E-54	5,36E+01	3,30E-55	0,1278	-15,6503436	-2,00054337	238,24	DBP	D-box binding PAR bZIP transcription factor
6469	2,20E-131	1,31E+02	7,02E-133	0,0816	-24,5303232	-2,00229008	793,05	SHH	sonic hedgehog signaling molecule
11094	2,42E-78	7,76E+01	2,07E-79	0,1062	-18,8685384	-2,00382466	429,69	CACFD1	calcium channel flower domain containing 1
56975	0	#NUM!	0	0,0487	-41,2050941	-2,00491597	3881,61	FAM20C	FAM20C golgi associated secretory pathway kinase
23753	1,55E-65	6,48E+01	1,75E-66	0,1167	-17,2241901	-2,009628	302,25	SDF2L1	stromal cell derived factor 2 like 1
84628	1,56E-58	5,78E+01	2,05E-59	0,1236	-16,2551466	-2,00979915	259,92	NTNG2	netrin G2
8522	5,78E-08	7,24E+00	2,92E-08	0,3626	-5,5460857	-2,01088321	27,82	GAS7	growth arrest specific 7
338785	6,88E-06	5,16E+00	3,88E-06	0,4357	-4,6176433	-2,01191501	21,06	KRT79	keratin 79
4576	3,97E-71	7,04E+01	3,97E-72	0,1121	-17,9605353	-2,0126946	348,95	TRNT	tRNA-Thr
92960	3,42E-08	7,47E+00	1,71E-08	0,3569	-5,6393642	-2,01281855	29,28	PEX11G	peroxisomal biogenesis factor 11 gamma
6518	6,70E-09	8,17E+00	3,24E-09	0,3404	-5,9187762	-2,01462725	32,07	SLC2A5	solute carrier family 2 member 5
79144	0	#NUM!	0	0,0518	-38,9173139	-2,0147494	2782,47	PPDPF	pancreatic progenitor cell differentiation and proliferation factor
7022	8,11E-248	2,47E+02	6,23E-250	0,0597	-33,7659695	-2,01510706	1610,5	TFAP2C	transcription factor AP-2 gamma
109864282	1,14E-13	1,29E+01	4,60E-14	0,2673	-7,542738	-2,01610638	84473,68	RNA28SN2	RNA, 28S ribosomal N2
123099	3,69E-07	6,43E+00	1,94E-07	0,3875	-5,2048381	-2,01685022	23,17	DEGS2	delta 4-desaturase, sphingolipid 2
105377073	4,70E-04	3,33E+00	3,00E-04	0,5586	-3,615002	-2,01924806	11,65	LOC105377	uncharacterized LOC105377073
81615	1,66E-103	1,03E+02	8,81E-105	0,0931	-21,7388247	-2,0231082	500,21	TMEM163	transmembrane protein 163
107984844	7,40E-04	3,13E+00	4,81E-04	0,5796	-3,4912346	-2,023636	10,24	SMG1-DT	SMG1 divergent transcript
8338	4,27E-13	1,24E+01	1,76E-13	0,2753	-7,3658779	-2,02799721	48,7	H2AC20	H2A clustered histone 20
150696	1,46E-31	3,08E+01	3,56E-32	0,1721	-11,8076535	-2,03217212	123,38	PROM2	prominin 2
100008589	3,69E-14	1,34E+01	1,47E-14	0,2644	-7,68999	-2,03309248	115496,83	RNA28SN5	RNA, 28S ribosomal N5
101410538	1,87E-260	2,60E+02	1,29E-262	0,0588	-34,6193999	-2,03558091	3448,48	MMP24OS	MMP24 opposite strand
56924	1,84E-50	4,97E+01	2,89E-51	0,1353	-15,0617641	-2,0381523	207,67	PAK6	p21 (RAC1) activated kinase 6
140564	2,83E-77	7,65E+01	2,49E-78	0,1089	-18,7365609	-2,03955756	362,43	APOBEC3D	apolipoprotein B mRNA editing enzyme catalytic subunit 3D
55304	2,15E-284	2,84E+02	1,21E-286	0,0564	-36,1810974	-2,03957137	1975,31	SPTLC3	serine palmitoyltransferase long chain base subunit 3
6196	6,61E-207	2,06E+02	7,82E-209	0,0662	-30,8391971	-2,04029983	1074,72	RPS6KA2	ribosomal protein S6 kinase A2
57580	3,62E-05	4,44E+00	2,14E-05	0,4804	-4,2502522	-2,0419082	16,47	PREX1	phosphatidylinositol-3,4,5-trisphosphate dependent Rac exchange factor 1
5623	2,14E-04	3,67E+00	1,33E-04	0,5355	-3,8207653	-2,04596615	12,44	PSPN	persephin
4102	5,57E-18	1,73E+01	1,96E-18	0,2336	-8,759323	-2,04610489	68,28	MAGEA3	MAGE family member A3
114757	8,09E-21	2,01E+01	2,63E-21	0,2162	-9,4764638	-2,04838269	76,82	CYGB	cytoglobin
51702	7,91E-04	3,10E+00	5,15E-04	0,5899	-3,4727572	-2,04846037	10,5	PADI3	peptidyl arginine deiminase 3

84266	2,08E-156	1,56E+02	4,64E-158	0,0765	-26,786479	-2,0493658	793,71	ALKBH7	alkB homolog 7
4494	2,62E-08	7,58E+00	1,30E-08	0,3604	-5,6858432	-2,04937909	27,7	MT1F	metallothionein 1F
90427	6,02E-51	5,02E+01	9,34E-52	0,1354	-15,1362687	-2,0499686	228,8	BMF	Bcl2 modifying factor
27113	1,09E-39	3,90E+01	2,20E-40	0,1542	-13,3038616	-2,05179365	170,08	BBC3	BCL2 binding component 3
5265	0	#NUM!	0	0,052	-39,5300882	-2,05577083	6067,25	SERPINA1	serpin family A member 1
1471	0	#NUM!	0	0,053	-38,7871162	-2,05689093	11989,64	CST3	cystatin C
112268067	4,39E-07	6,36E+00	2,32E-07	0,3982	-5,1715952	-2,05917695	24,18	LOC112268(	uncharacterized LOC112268067
100507642	6,48E-35	3,42E+01	1,46E-35	0,1658	-12,4466961	-2,06418633	131,82	LINC03014	long intergenic non-protein coding RNA 3014
146562	4,64E-04	3,33E+00	2,96E-04	0,5721	-3,6183487	-2,07010313	11,28	DNAAF8	dynein axonemal assembly factor 8
10567	5,01E-200	1,99E+02	6,44E-202	0,0684	-30,3190294	-2,07419167	1762,12	RABAC1	Rab acceptor 1
23409	2,64E-13	1,26E+01	1,08E-13	0,2801	-7,4310344	-2,08158679	47,13	SIRT4	sirtuin 4
109864272	2,92E-14	1,35E+01	1,16E-14	0,2698	-7,7204618	-2,08287545	191955,71	RNA28SN4	RNA, 28S ribosomal N4
107984690	3,28E-15	1,45E+01	1,26E-15	0,2605	-7,9981491	-2,08317277	53,45	LOC107984(	uncharacterized LOC107984690
8941	4,46E-17	1,64E+01	1,62E-17	0,2446	-8,5183537	-2,08386033	62,83	CDK5R2	cyclin dependent kinase 5 regulatory subunit 2
79090	1,24E-16	1,59E+01	4,54E-17	0,2482	-8,3979908	-2,08445335	57,98	TRAPPC6A	trafficking protein particle complex subunit 6A
266977	0	#NUM!	0	0,0516	-40,3747709	-2,0846651	2613,51	ADGRF1	adhesion G protein-coupled receptor F1
59344	1,79E-08	7,75E+00	8,81E-09	0,3625	-5,7521683	-2,08533893	28,8	ALOXE3	arachidonate lipoxygenase 3
89887	1,91E-65	6,47E+01	2,16E-66	0,1217	-17,2119833	-2,09469107	270,24	ZNF628	zinc finger protein 628
126823	9,33E-10	9,03E+00	4,35E-10	0,3363	-6,2407879	-2,09864777	35,39	KLHDC9	kelch domain containing 9
144110	3,60E-35	3,44E+01	8,05E-36	0,1684	-12,4939735	-2,10405034	137,99	TMEM86A	transmembrane protein 86A
112399	2,14E-113	1,13E+02	9,46E-115	0,0927	-22,7682852	-2,10950024	486,44	EGLN3	egl-9 family hypoxia inducible factor 3
387914	0	#NUM!	0	0,0551	-38,3000791	-2,10978117	2459,67	SHISA2	shisa family member 2
109910382	2,64E-14	1,36E+01	1,05E-14	0,273	-7,7336122	-2,11102409	73940,92	RNA28SN3	RNA, 28S ribosomal N3
89765	7,12E-06	5,15E+00	4,02E-06	0,4582	-4,6103535	-2,11236801	18,01	RSPH1	radial spoke head component 1
101927202	1,35E-09	8,87E+00	6,35E-10	0,3427	-6,1813644	-2,11820995	30,77	LOC1019272	uncharacterized LOC101927202
83988	2,28E-06	5,64E+00	1,25E-06	0,437	-4,8475132	-2,11832629	18,66	NCALD	neurocalcin delta
1509	0	#NUM!	0	0,053	-39,9790969	-2,1185618	37972,93	CTSD	cathepsin D
105375170	4,77E-05	4,32E+00	2,83E-05	0,5063	-4,1868908	-2,1197137	14,41	LOC105375(	uncharacterized LOC105375170
5743	1,41E-257	2,57E+02	1,02E-259	0,0616	-34,4263932	-2,12035921	1907,51	PTGS2	prostaglandin-endoperoxide synthase 2
64077	1,52E-88	8,78E+01	1,07E-89	0,1056	-20,0816474	-2,12074141	362,34	LHPP	phospholysine phosphohistidine inorganic pyrophosphate phosphatase
10326	2,34E-14	1,36E+01	9,24E-15	0,2742	-7,7492979	-2,12520727	48,32	SIRPB1	signal regulatory protein beta 1
105373024	3,75E-04	3,43E+00	2,38E-04	0,5792	-3,6749789	-2,12844576	10,78	LOC105373(	uncharacterized LOC105373024
388931	7,46E-15	1,41E+01	2,91E-15	0,2714	-7,8948408	-2,14254543	56,72	MFSD2B	MFSD2 lysolipid transporter B, sphingolipid
3136	0	#NUM!	0	0,0488	-43,9527874	-2,14456766	5643,77	HLA-H	major histocompatibility complex, class I, H (pseudogene)
344148	7,62E-08	7,12E+00	3,87E-08	0,3904	-5,4967683	-2,1461936	24,18	NCKAP5	NCK associated protein 5
109864271	3,41E-15	1,45E+01	1,32E-15	0,2692	-7,9930123	-2,15151639	200405,54	RNA45SN4	RNA, 45S pre-ribosomal N4
106632264	3,52E-12	1,15E+01	1,50E-12	0,3042	-7,0749487	-2,15205921	5699,23	RNA28SN1	RNA, 28S ribosomal N1
79861	4,98E-06	5,30E+00	2,79E-06	0,4606	-4,6858187	-2,15817355	19,4	TUBAL3	tubulin alpha like 3
54795	1,86E-64	6,37E+01	2,15E-65	0,1265	-17,0784849	-2,16027146	267,4	TRPM4	transient receptor potential cation channel subfamily M member 4
158297	1,05E-12	1,20E+01	4,39E-13	0,2986	-7,243085	-2,16252729	42,06	SAXO1	stabilizer of axonemal microtubules 1
4222	5,09E-05	4,29E+00	3,02E-05	0,5185	-4,1715877	-2,16278386	13,33	MEOX1	mesenchyme homeobox 1
167359	1,54E-15	1,48E+01	5,87E-16	0,2674	-8,0919839	-2,16408707	54,03	NIM1K	NIM1 serine/threonine protein kinase
1890	7,71E-56	5,51E+01	1,08E-56	0,1366	-15,8664823	-2,16671228	205,59	TYMP	thymidine phosphorylase
115330	1,03E-08	7,99E+00	5,02E-09	0,3709	-5,846521	-2,16837739	26,67	GPR146	G protein-coupled receptor 146
109864279	1,86E-15	1,47E+01	7,09E-16	0,2687	-8,0689392	-2,16844007	92756,2	RNA45SN2	RNA, 45S pre-ribosomal N2
563	3,00E-24	2,35E+01	8,89E-25	0,211	-10,2776649	-2,16860021	86,42	AZGP1	alpha-2-glycoprotein 1, zinc-binding
100847070	4,91E-05	4,31E+00	2,92E-05	0,5192	-4,17969	-2,17020412	13,4	MIR5196	microRNA 5196
4261	0	#NUM!	0	0,0547	-39,7011456	-2,17193574	2420,35	CIITA	class II major histocompatibility complex transactivator
105379524	2,79E-10	9,55E+00	1,27E-10	0,3381	-6,4304412	-2,17387881	35,51	LOC105379(	uncharacterized LOC105379524
9047	3,06E-09	8,51E+00	1,46E-09	0,3614	-6,0484203	-2,18569943	27,67	SH2D2A	SH2 domain containing 2A
101929427	4,13E-05	4,38E+00	2,44E-05	0,5188	-4,2200819	-2,18944976	14,13	LOC1019294	uncharacterized LOC101929427
613038	5,49E-15	1,43E+01	2,13E-15	0,2762	-7,9333893	-2,19123002	47,99	LOC613038	SAGA complex associated factor 29 pseudogene
9537	1,25E-14	1,39E+01	4,91E-15	0,2802	-7,8292939	-2,19347364	48,24	TP53I11	tumor protein p53 inducible protein 11
105378586	1,35E-09	8,87E+00	6,34E-10	0,3554	-6,1817613	-2,1968877	29,22	LOC105378(	uncharacterized LOC105378586
56892	1,07E-03	2,97E+00	7,06E-04	0,6487	-3,3870578	-2,19724334	9,87	TCIM	transcriptional and immune response regulator
348262	2,25E-69	6,86E+01	2,34E-70	0,1239	-17,7329225	-2,19780598	2855,98	MCRIP1	MAPK regulated corepressor interacting protein 1
219855	0	#NUM!	0	0,041	-53,7557476	-2,20374833	9815,62	SLC37A2	solute carrier family 37 member 2
23025	1,17E-52	5,19E+01	1,76E-53	0,1433	-15,3953715	-2,20572337	214,08	UNC13A	unc-13 homolog A
54958	1,94E-56	5,57E+01	2,68E-57	0,1383	-15,9538149	-2,20627244	221,75	TMEM160	transmembrane protein 160
654346	8,92E-04	3,05E+00	5,83E-04	0,643	-3,4392571	-2,21141788	9,03	LGALS9C	galectin 9C
1287	2,92E-278	2,78E+02	1,73E-280	0,062	-35,7874057	-2,21747117	1755,86	COL4A5	collagen type IV alpha 5 chain
402415	6,21E-10	9,21E+00	2,87E-10	0,3518	-6,3054289	-2,21800404	31,37	XKRX	XK related X-linked
256933	4,12E-04	3,39E+00	2,63E-04	0,6084	-3,6496488	-2,22031427	9,95	NPB	neuropeptide B
7133	1,31E-133	1,33E+02	4,01E-135	0,0898	-24,7396329	-2,22051037	582,6	TNFRSF1B	TNF receptor superfamily member 1B
4035	0	#NUM!	0	0,0559	-39,7486962	-2,22262355	2442,99	LRP1	LDL receptor related protein 1
283987	1,15E-210	2,10E+02	1,31E-212	0,0715	-31,1194421	-2,22585755	999,68	HID1	HID1 domain containing
29108	5,93E-31	3,02E+01	1,47E-31	0,1905	-11,6877728	-2,22677792	103,24	PYCARD	PYD and CARD domain containing
9214	1,13E-119	1,19E+02	4,47E-121	0,0955	-23,3980614	-2,23397937	520,25	FCMR	Fc mu receptor
100652740	6,51E-11	1,02E+01	2,90E-11	0,3359	-6,6516945	-2,23410551	32,93	PYCARD-AS	PYCARD antisense RNA 1
91978	2,53E-33	3,26E+01	5,92E-34	0,1839	-12,1473726	-2,23439964	123,63	TPGS1	tubulin polyglutamylase complex subunit 1
6414	1,32E-07	6,88E+00	6,80E-08	0,4144	-5,3963451	-2,23626609	21,57	SELENOP	selenoprotein P
2556	8,37E-27	2,61E+01	2,31E-27	0,2066	-10,8365886	-2,23857501	90,63	GABRA3	gamma-aminobutyric acid type A receptor subunit alpha3
1543	4,63E-217	2,16E+02	4,80E-219	0,0709	-31,5916956	-2,23971643	1064,05	CYP1A1	cytochrome P450 family 1 subfamily A member 1
404217	2,58E-69	6,86E+01	2,69E-70	0,1267	-17,7249743	-2,24519704	259,74	CTXN1	cortexin 1
8270	1,86E-126	1,26E+02	6,55E-128	0,0934	-24,0600724	-2,2466948	634,68	LAGE3	L antigen family member 3
100506465	3,43E-14	1,35E+01	1,36E-14	0,2921	-7,6996213	-2,2490122	44,16	LINC01234	long intergenic non-protein coding RNA 1234
107984551	5,31E-07	6,27E+00	2,82E-07	0,4381	-5,135159	-2,2497703	19,35	LOC107984(	uncharacterized LOC107984551
79589	1,15E-29	2,89E+01	2,94E-30	0,1969	-11,4307582	-2,25108932	97,73	RNF128	ring finger protein 128
107986249	9,85E-05	4,01E+00	5,98E-05	0,5617	-4,0137907	-2,25450472	11,67	LOC107986(	uncharacterized LOC107986249
638	2,63E-66	6,56E+01	2,91E-67	0,1307	-17,32757	-2,26556591	235,89	BIK	BCL2 interacting killer
3880	0	#NUM!	0	0,0481	-47,1679685	-2,269954	15819,86	KRT19	keratin 19
101929639	4,46E-17	1,64E+01	1,62E-17	0,2666	-8,518421	-2,27117922	60,03	B4GALT1-AS	B4GALT1 antisense RNA 1
728402	6,28E-07	6,20E+00	3,35E-07	0,4451	-5,1028714	-2,27135537	18,84	TPI1P3	triosephosphate isomerase 1 pseudogene 3
84985	0	#NUM!	0	0,0527	-43,2032512	-2,27609753	2804,86	FAM83A	family with sequence similarity 83 member A
148170	1,57E-07	6,80E+00	8,11E-08	0,4245	-5,3647015	-2,27730331	21,2	CDC42EP5	CDC42 effector protein 5
79812	1,85E-78	7,77E+01	1,58E-79	0,1207	-18,8828448	-2,27905226	287,64	MMRN2	multimerin 2
85235	1,61E-08	7,79E+00	7,91E-09	0,3951	-5,7702958	-2,27962488	27,09	H2AC12	H2A clustered histone 12
113218505	8,12E-05	4,09E+00	4,90E-05	0,5627	-4,0605423	-2,2847054	12,61	MIR10527	microRNA 10527
81796	1,39E-18	1,79E+01	4,80E-19	0,2563	-8,9167062	-2,28501388	787,46	SLCO5A1	solute carrier organic anion transporter family member 5A1
78990	0	#NUM!	0	0,049	-46,6293881	-2,28664178	4437,04	OTUB2	OTU deubiquitinase, ubiquitin aldehyde binding 2
3107	0	#NUM!	0	0,0454	-50,6354995	-2,29811683	19032,77	HLA-C	major histocompatibility complex, class I, C
645	2,95E-188	1,88E+02	4,23E-190	0,0788	-29,4088424	-2,31694227	1454,17	BLVRB	biliverdin reductase B
79095	1,07E-49	4,90E+01	1,71E-50	0,1552	-14,9436149	-2,31986066	1288,32	BBLN	bublin coiled coil protein
202500	5,72E-04	3,24E+00	3,69E-04	0,6517	-3,5615952	-2,32122865	8,88	TCTE1	t-complex-associated-testis-expressed 1
5196	7,90E-07	6,10E+00	4,23E-07	0,4591	-5,0583025	-2,32206391	18,44	PF4	platelet factor 4
440311	1,66E-08	7,78E+00	8,17E-09	0,4028	-5,7648273	-2,32225386	26,65	LOC440311	NOP53 ribosome biogenesis factor pseudogene
2921	2,32E-63	6,26E+01	2,74E-64	0,138	-16,9292538	-2,33670887	1508,53	CXCL3	C-X-C motif chemokine ligand 3
3105	0	#NUM!	0	0,0397	-58,8245077	-2,33802225	32798,43	HLA-A	major histocompatibility complex, class I, A
388242	6,63E-13	1,22E+01	2,75E-13	0,3204	-7,3060564	-2,34096032	36,82	LOC388242	SAGA complex associated factor 29 pseudogene
6289	0	#NUM!	0	0,0526	-44,62557	-2,34543466	2557,74	SAA2	serum amyloid A2
30845	5,83E-124	1,23E+02	2,17E-125	0,0986	-23,8180623	-2,34744543	455,48	EHD3	EH domain containing 3
8514	1,66E-168	1,68E+02	3,11E-170	0,0845	-27,811902	-2,34917915	805,49	KCNAB2	potassium voltage-gated channel subfamily A regulatory beta subunit 2
440044	1,00E-04	4,00E+00	6,08E-05	0,5875	-4,009656	-2,35548202	11,65	SLC22A20P	solute carrier family 22 member 20, pseudogene
7364	7,18E-30	2,91E+01	1,83E-30	0,2054	-11,4718794	-2,35578385	102,53	UGT2B7	UDP glucuronosyltransferase family 2 member B7
1896	4,60E-13	1,23E+01	1,90E-13	0,3203	-7,3558335	-2,3563051	37,12	EDA	ectodysplasin A
100130348	1,64E-05	4,79E+00	9,45E-06	0,533	-4,4294322	-2,36075966	13,98	TMEM262	transmembrane protein 262
400627	2,28E-08	7,64E+00	1,13E-08	0,4141	-5,7096224	-2,36450425	22,4	LOC400627	uncharacterized LOC400627
4577	8,50E-110	1,09E+02	4,01E-111	0,1062	-22,3991779	-2,37806771	486,97	TRNV	tRNA-Val
200316	1,85E-223	2,23E+02	1,80E-225	0,0743	-32,0562163	-2,38103188	1089,87	APOBEC3F	apolipoprotein B mRNA editing enzyme catalytic subunit 3F
3108	0	#NUM!	0	0,0559	-42,5798714	-2,38196455	2318,64	HLA-DMA	major histocompatibility complex, class II, DM alpha
8363	8,68E-20	1,91E+01	2,90E-20	0,2585	-9,2225686	-2,38368625	57,95	H4C11	H4 clustered histone 11
4105	5,96E-87	8,62E+01	4,32E-88	0,12	-19,8969567	-2,38821903	304,5	MAGEA6	MAGE family member A6
7477	0	#NUM!	0	0,0602	-39,6982609	-2,38922174	1913,84	WNT7B	Wnt family member 7B
119385	4,71E-69	6,83E+01	4,92E-70	0,1351	-17,6910112	-2,39016108	236,46	AGAP11	ArfGAP with GTPase domain, ankyrin repeat and PH domain 11
5199	2,59E-126	1,26E+02	9,13E-128	0,0994	-24,0462689	-2,39117124	446,77	CFP	complement factor properdin
10158	4,05E-252	2,51E+02	3,02E-254	0,0703	-34,0586758	-2,39458548	1281,28	PDZK1IP1	PDZK1 interacting protein 1
8362	7,79E-21	2,01E+01	2,53E-21	0,2528	-9,4805163	-2,39666303	60,81	H4C12	H4 clustered histone 12
105373933	6,65E-06	5,18E+00	3,75E-06	0,5187	-4,6248846	-2,39889199	16,7	LOC105373(	uncharacterized LOC105373933
79623	4,22E-189	1,88E+02	6,00E-191	0,0816	-29,4751506	-2,40471115	741,42	GALNT14	polypeptide N-acetylgalactosaminyltransferase 14
84171	0	#NUM!	0	0,0444	-54,1892403	-2,40702005	6459,61	LOXL4	lysyl oxidase like 4

6756	5,42E-125	1,24E+02	1,97E-126	0,1008	-23,9183872	-2,41009263	425,42	SSX1	SSX family member 1
100505592	2,18E-08	7,66E+00	1,08E-08	0,423	-5,7178847	-2,41875642	23	GAPLINC	gastric adenocarcinoma associated, positive CD44 regulator, long intergenic non-coding RNA
112268284	1,47E-14	1,38E+01	5,80E-15	0,3104	-7,8082785	-2,42366314	16925,31	LOC112268284	
3728	0	#NUM!	0	0,0491	-49,3904325	-2,42624332	5717,42	JUP	junction plakoglobin
105373370	1,43E-07	6,84E+00	7,38E-08	0,451	-5,3816664	-2,426914	19,74	MAGEA3-DT	MAGEA3 divergent transcript
64109	9,14E-50	4,90E+01	1,46E-50	0,1623	-14,9544338	-2,42704423	161,63	CRLF2	cytokine receptor like factor 2
109910379	4,27E-19	1,84E+01	1,46E-19	0,2686	-9,0479248	-2,43014669	90449,09	RNA45SN3	RNA, 45S pre-ribosomal N3
8111	0	#NUM!	0	0,0596	-40,8887697	-2,43680674	2894,68	GPR68	G protein-coupled receptor 68
109729184	3,98E-12	1,14E+01	1,70E-12	0,3495	-7,0573459	-2,46626663	32,49	SLC12A5-AS	SLC12A5 and MMP9 antisense RNA 1
114897	2,48E-42	4,16E+01	4,73E-43	0,1795	-13,7554082	-2,46858171	124,92	C1QTNF1	C1q and TNF related 1
105376382	2,72E-62	6,16E+01	3,29E-63	0,1471	-16,7823548	-2,46895651	197,91	LASTR	lncRNA associated with SART3 regulation of splicing
644246	3,53E-06	5,45E+00	1,96E-06	0,5198	-4,7574805	-2,47303689	14,92	KANSL1-AS1	KANSL1 antisense RNA 1
5228	2,95E-115	1,15E+02	1,28E-116	0,108	-22,9561635	-2,47898341	406,69	PGF	placental growth factor
50943	6,57E-08	7,18E+00	3,33E-08	0,4489	-5,5233464	-2,47949152	19,47	FOXP3	forkhead box P3
27128	4,88E-108	1,07E+02	2,37E-109	0,1121	-22,2165873	-2,49013523	351,82	CYTH4	cytohesin 4
3134	0	#NUM!	0	0,0645	-38,8132473	-2,5047819	1451,24	HLA-F	major histocompatibility complex, class I, F
128434	1,24E-220	2,20E+02	1,24E-222	0,0789	-31,8519008	-2,51321007	1138,33	VSTM2L	V-set and transmembrane domain containing 2 like
8605	1,72E-35	3,48E+01	3,81E-36	0,2007	-12,5533032	-2,51940311	107,34	PLA2G4C	phospholipase A2 group IVC
718	0	#NUM!	0	0,041	-61,6785076	-2,52587084	19790,75	C3	complement C3
23551	7,36E-29	2,81E+01	1,92E-29	0,2254	-11,2665684	-2,53928506	81,9	RASD2	RASD family member 2
105374336	3,97E-07	6,40E+00	2,10E-07	0,4892	-5,1905266	-2,53933698	17,41	LOC105374	uncharacterized LOC105374336
5002	2,62E-49	4,86E+01	4,22E-50	0,171	-14,8835485	-2,54571321	146,03	SLC22A18	solute carrier family 22 member 18
6447	5,16E-36	3,53E+01	1,13E-36	0,2018	-12,6491843	-2,55290121	101,84	SCG5	secretogranin V
401115	3,62E-53	5,24E+01	5,37E-54	0,1656	-15,4719092	-2,56254049	155,48	C4orf48	chromosome 4 open reading frame 48
11007	0	#NUM!	0	0,0598	-42,9181874	-2,5648331	2150,95	CCDC85B	coiled-coil domain containing 85B
3934	0	#NUM!	0	0,0643	-39,9719027	-2,56927424	2319,66	LCN2	lipocalin 2
107985563	9,22E-07	6,04E+00	4,96E-07	0,5111	-5,0280358	-2,56996833	15,77	LOC107985	uncharacterized LOC107985563
105376010	2,36E-18	1,76E+01	8,25E-19	0,2904	-8,8565997	-2,57167547	48,41	LOC105376	uncharacterized LOC105376010
10076	0	#NUM!	0	0,0547	-47,1374747	-2,57627211	2485,24	PTPRU	protein tyrosine phosphatase receptor type U
400360	2,93E-09	8,53E+00	1,40E-09	0,4264	-6,0558276	-2,58208908	22,64	LINC02915	long intergenic non-protein coding RNA 2915
54413	1,14E-14	1,39E+01	4,46E-15	0,3312	-7,84128	-2,59728574	37,07	NLGN3	neuroligin 3
933	5,23E-177	1,76E+02	8,65E-179	0,0917	-28,5106357	-2,61511063	574,09	CD22	CD22 molecule
105370401	1,10E-04	3,96E+00	6,67E-05	0,6558	-3,9878941	-2,61514675	9,54	TRD-AS1	TRD antisense RNA 1
3162	2,58E-175	1,75E+02	4,39E-177	0,0924	-28,3727621	-2,62064064	592,9	HMOX1	heme oxygenase 1
6291	4,05E-32	3,14E+01	9,75E-33	0,2207	-11,9161828	-2,62997089	87,21	SAA4	serum amyloid A4, constitutive
280659	2,13E-07	6,67E+00	1,10E-07	0,4957	-5,3086558	-2,63134684	16,49	SSX8P	SSX family member 8, pseudogene
51129	1,06E-242	2,42E+02	8,58E-245	0,0789	-33,414007	-2,63687807	1672,84	ANGPTL4	angiopoietin like 4
27071	1,11E-10	9,95E+00	4,97E-11	0,4016	-6,5719351	-2,6390478	26,33	DAPP1	dual adaptor of phosphotyrosine and 3-phosphoinositides 1
768	1,19E-34	3,39E+01	2,71E-35	0,2133	-12,3972341	-2,64375868	92,95	CA9	carbonic anhydrase 9
100528017	0	#NUM!	0	0,0605	-44,1235359	-2,6710397	1734,6	SAA2-SAA4	SAA2-SAA4 readthrough
9638	6,01E-05	4,22E+00	3,59E-05	0,647	-4,1323253	-2,67370409	10,04	FEZ1	fasciculation and elongation protein zeta 1
9127	4,75E-20	1,93E+01	1,58E-20	0,2898	-9,2877324	-2,69119567	51,35	P2RX6	purinergic receptor P2X 6
105372683	5,41E-05	4,27E+00	3,22E-05	0,6507	-4,1571562	-2,70511687	10,19	LOC105372	uncharacterized LOC105372683
100861532	1,83E-24	2,37E+01	5,39E-25	0,2624	-10,325694	-2,7089501	177174,86	RNA45SN5	RNA, 45S pre-ribosomal N5
55287	1,31E-08	7,88E+00	6,43E-09	0,47	-5,8050848	-2,72853053	19,4	TMEM40	transmembrane protein 40
100506457	6,85E-27	2,62E+01	1,89E-27	0,2521	-10,8550261	-2,73613562	67,01	MIR3681HG	MIR3681 host gene
5003	2,23E-25	2,47E+01	6,40E-26	0,2602	-10,5283252	-2,73993726	69,7	SLC22A18AS	SLC22A18 antisense RNA
105373629	5,65E-10	9,25E+00	2,61E-10	0,4359	-6,3201127	-2,75491084	22,88	LOC105373	uncharacterized LOC105373629
10866	1,23E-217	2,17E+02	1,26E-219	0,0872	-31,6339921	-2,75759957	812,88	HCP5	HLA complex P5
402778	3,50E-85	8,45E+01	2,61E-86	0,1403	-19,690323	-2,76286961	237,99	IFITM10	interferon induced transmembrane protein 10
54541	0	#NUM!	0	0,0457	-60,4430737	-2,76363045	5761,66	DDIT4	DNA damage inducible transcript 4
51655	0	#NUM!	0	0,0691	-40,2197387	-2,77944764	1237,37	RASD1	ras related dexamethasone induced 1
349667	1,93E-142	1,42E+02	5,24E-144	0,1093	-25,5518073	-2,79230628	413,04	RTN4RL2	reticulon 4 receptor like 2
1755	0	#NUM!	0	0,0693	-40,3303123	-2,79333239	1238,85	DMBT1	deleted in malignant brain tumors 1
140862	3,92E-176	1,75E+02	6,57E-178	0,0987	-28,439488	-2,80687009	566,47	ISM1	isthmin 1
5031	1,52E-67	6,68E+01	1,64E-68	0,1608	-17,4923267	-2,81253474	175,87	P2RY6	pyrimidinergic receptor P2Y6
105375267	7,11E-10	9,15E+00	3,30E-10	0,4493	-6,2838958	-2,82325587	21,73	LOC105375	uncharacterized LOC105375267
126119	3,19E-102	1,01E+02	1,75E-103	0,1308	-21,6011512	-2,82637893	325,01	JOSD2	Josephin domain containing 2
8857	3,37E-188	1,87E+02	4,88E-190	0,0962	-29,4040017	-2,8287362	550,42	FCGBP	Fc gamma binding protein
28755	5,07E-115	1,14E+02	2,21E-116	0,1236	-22,9322726	-2,83428126	312,7	TRAC	T cell receptor alpha constant
3748	1,21E-29	2,89E+01	3,11E-30	0,2483	-11,4257307	-2,83740625	71,37	KCNC3	potassium voltage-gated channel subfamily C member 3
4318	1,83E-61	6,07E+01	2,26E-62	0,1712	-16,6674065	-2,85342971	173,34	MMP9	matrix metallopeptidase 9
894	8,20E-76	7,51E+01	7,42E-77	0,1542	-18,5550918	-2,86071954	205,72	CCND2	cyclin D2
100874007	6,63E-31	3,02E+01	1,65E-31	0,2452	-11,6781805	-2,86382216	73,54	VIPR1-AS1	VIPR1 antisense RNA 1
85294	1,15E-15	1,49E+01	4,37E-16	0,3541	-8,1279511	-2,87835302	38,2	KRTAP2-4	keratin associated protein 2-4
51676	1,75E-181	1,81E+02	2,74E-183	0,0999	-28,8712265	-2,88351434	510,91	ASB2	ankyrin repeat and SOCS box containing 2
3109	0	#NUM!	0	0,0709	-40,8693692	-2,89699831	1260,43	HLA-DMB	major histocompatibility complex, class II, DM beta
6023	4,05E-16	1,54E+01	1,51E-16	0,3513	-8,2553658	-2,90018437	151,53	RMRP	RNA component of mitochondrial RNA processing endoribonuclease
10863	6,02E-33	3,22E+01	1,42E-33	0,2403	-12,0756153	-2,9017726	77,74	ADAM28	ADAM metallopeptidase domain 28
79931	7,19E-78	7,71E+01	6,24E-79	0,1543	-18,810139	-2,90234726	195,19	TNIP3	TNFAIP3 interacting protein 3
3106	0	#NUM!	0	0,0437	-66,5188037	-2,90559634	31444,51	HLA-B	major histocompatibility complex, class I, B
107985590	1,88E-31	3,07E+01	4,59E-32	0,2472	-11,7862947	-2,91386464	74,96	LOC107985	uncharacterized LOC107985590
113157	1,91E-08	7,72E+00	9,43E-09	0,5078	-5,7406041	-2,91500047	17,29	RPLP0P2	ribosomal protein lateral stalk subunit P0 pseudogene 2
146227	1,34E-06	5,87E+00	7,26E-07	0,5931	-4,9542966	-2,93849519	12,8	BEAN1	brain expressed associated with NEDD4 1
3137	8,46E-04	3,07E+00	5,52E-04	0,854	-3,4540772	-2,94991872	508,76	HLA-J	major histocompatibility complex, class I, J (pseudogene)
23046	5,14E-98	9,73E+01	3,04E-99	0,1397	-21,1454535	-2,95435331	254,88	KIF21B	kinesin family member 21B
81035	1,23E-67	6,69E+01	1,32E-68	0,1688	-17,5045901	-2,95560749	168,84	COLEC12	collectin subfamily member 12
117195	1,30E-08	7,89E+00	6,35E-09	0,5091	-5,8071488	-2,9566013	17,7	MRGPRX3	MAS related GPR family member X3
105378179	2,57E-18	1,76E+01	9,00E-19	0,3346	-8,8468742	-2,96017729	2037,88	LOC105378	uncharacterized LOC105378179
6352	4,87E-32	3,13E+01	1,17E-32	0,2503	-11,9006855	-2,97844482	80,44	CCL5	C-C motif chemokine ligand 5
105376397	8,41E-05	4,08E+00	5,08E-05	0,7352	-4,0520195	-2,97889872	8,36	LOC105376	uncharacterized LOC105376397
55911	7,56E-15	1,41E+01	2,95E-15	0,3817	-7,8931074	-3,01251207	31,76	APOBR	apolipoprotein B receptor
3008	4,85E-59	5,83E+01	6,33E-60	0,1847	-16,3270839	-3,01558954	161,83	H1-4	H1.4 linker histone, cluster member
389816	1,47E-08	7,83E+00	7,25E-09	0,5229	-5,7850917	-3,02493881	18,43	LRRC26	leucine rich repeat containing 26
3135	4,33E-03	2,36E+00	3,00E-03	1,0238	-2,9679474	-3,03848402	156,04	HLA-G	major histocompatibility complex, class I, G
4593	7,23E-166	1,65E+02	1,41E-167	0,1105	-27,5913754	-3,04918327	460,13	MUSK	muscle associated receptor tyrosine kinase
10974	1,87E-123	1,23E+02	7,02E-125	0,1292	-23,7688022	-3,0699676	327,83	ADIRF	adipogenesis regulatory factor
10397	0	#NUM!	0	0,0388	-79,1037377	-3,07264053	14438,49	NDRG1	N-myc downstream regulated 1
6373	1,33E-179	1,79E+02	2,14E-181	0,1071	-28,7201762	-3,07593394	496,87	CXCL11	C-X-C motif chemokine ligand 11
972	0	#NUM!	0	0,0492	-62,9250008	-3,09377558	40798,07	CD74	CD74 molecule
126961	1,67E-08	7,78E+00	8,23E-09	0,5387	-5,7636045	-3,10512596	16,7	H3C14	H3 clustered histone 14
8530	4,14E-197	1,96E+02	5,43E-199	0,1032	-30,0961936	-3,10650753	589,08	CST7	cystatin F
3059	1,26E-22	2,19E+01	3,87E-23	0,3136	-9,9071689	-3,10715633	50,6	HCLS1	hematopoietic cell-specific Lyn substrate 1
221458	2,53E-08	7,60E+00	1,26E-08	0,5476	-5,6919059	-3,1166344	16,75	KIF6	kinesin family member 6
105376381	2,50E-05	4,60E+00	1,46E-05	0,7199	-4,3347393	-3,12057073	9,14	LOC105376	uncharacterized LOC105376381
7113	4,92E-120	1,19E+02	1,94E-121	0,1343	-23,4337017	-3,14628535	292,38	TMPRSS2	transmembrane serine protease 2
4583	9,81E-08	7,01E+00	5,01E-08	0,5805	-5,4508794	-3,16414902	14,78	MUC2	mucin 2, oligomeric mucus/gel-forming
3834	7,66E-08	7,12E+00	3,89E-08	0,5781	-5,4957453	-3,1771615	14,86	KIF25	kinesin family member 25
107987115	2,74E-100	9,96E+01	1,54E-101	0,1493	-21,393226	-3,19483387	233,71	LOC107987	uncharacterized LOC107987115
6288	0	#NUM!	0	0,0464	-68,9708744	-3,19949386	10591,94	SAA1	serum amyloid A1
23136	1,13E-27	2,69E+01	3,05E-28	0,2916	-11,0203559	-3,21334913	59,29	EPB41L3	erythrocyte membrane protein band 4.1 like 3
107987206	6,83E-16	1,52E+01	2,57E-16	0,3949	-8,1918992	-3,23512527	1616,86	LOC107987	replaced by ID 6029
107984663	5,21E-08	7,28E+00	2,62E-08	0,582	-5,5648957	-3,23899654	15,4	LOC107984	uncharacterized LOC107984663
60489	0	#NUM!	0	0,0854	-37,9552085	-3,24159403	892,95	APOBEC3G	apolipoprotein B mRNA editing enzyme catalytic subunit 3G
924	3,56E-08	7,45E+00	1,78E-08	0,5759	-5,6324529	-3,24358388	15,4	CD7	CD7 molecule
286530	1,85E-06	5,73E+00	1,01E-06	0,667	-4,8897807	-3,26172568	11,46	P2RY8	P2Y receptor family member 8
7433	0	#NUM!	0	0,0646	-50,8274421	-3,28210548	1709,05	VIPR1	vasoactive intestinal peptide receptor 1
333932	1,64E-08	7,79E+00	8,05E-09	0,5695	-5,7673085	-3,28451706	15,83	H3C15	H3 clustered histone 15
6029	1,35E-15	1,49E+01	5,13E-16	0,4055	-8,1083614	-3,28769728	1609,05	RN7SL1	RNA component of signal recognition particle 7SL1
1288	1,77E-185	1,85E+02	2,62E-187	0,1127	-29,1897452	-3,29026085	468,12	COL4A6	collagen type IV alpha 6 chain
1440	0	#NUM!	0	0,0588	-56,0163772	-3,29408145	8990,35	CSF3	colony stimulating factor 3
3071	7,09E-06	5,15E+00	4,00E-06	0,7163	-4,6111861	-3,30314385	10,27	NCKAP1L	NCK associated protein 1 like
7503	1,42E-07	6,85E+00	7,33E-08	0,6145	-5,3828037	-3,30793792	14,77	XIST	X inactive specific transcript
106144526	6,24E-06	5,20E+00	3,51E-06	0,7143	-4,6382724	-3,31304651	10,28	PLA2G4C-AS	PLA2G4C antisense RNA 1
378706	1,52E-15	1,48E+01	5,78E-16	0,41	-8,0939483	-3,3187699	1895,92	RN7SL2	RNA component of signal recognition particle 7SL2
1521	2,82E-95	9,45E+01	1,75E-96	0,1597	-20,8434253	-3,32882921	212,69	CTSW	cathepsin W
929	3,49E-204	2,03E+02	4,31E-206	0,1088	-30,6340806	-3,33256255	495,47	CD14	CD14 molecule
654463	3,09E-13	1,25E+01	1,27E-13	0,4514	-7,4095181	-3,34456193	27,05	FER1L6	fer-1 like family member 6
3429	0	#NUM!	0	0,0788	-42,4483749	-3,34633775	1123,46	IFI27	interferon alpha inducible protein 27
107985449	1,38E-09	8,86E+00	6,52E-10	0,5583	-6,17738	-3,44889761	17,56	LOC107985	uncharacterized LOC107985449

284194	1,37E-08	7,86E+00	6,74E-09	0,595	-5,7971609	-3,44957885	16,07	LGALS9B	galectin 9B
4151	3,73E-45	4,44E+01	6,66E-46	0,2432	-14,222349	-3,4587816	93,84	MB	myoglobin
2357	1,69E-103	1,03E+02	8,98E-105	0,1593	-21,7379647	-3,46392563	228,73	FPR1	formyl peptide receptor 1
3122	0	#NUM!	0	0,0384	-91,6912676	-3,51875634	15659,79	HLA-DRA	major histocompatibility complex, class II, DR alpha
3782	9,70E-147	1,46E+02	2,49E-148	0,1373	-25,9378771	-3,56199702	317,3	KCNN3	potassium calcium-activated channel subfamily N member 3
50964	5,66E-34	3,32E+01	1,30E-34	0,2903	-12,2705446	-3,56230979	68,87	SOST	sclerostin
64127	2,40E-76	7,56E+01	2,15E-77	0,1927	-18,6215693	-3,58781313	159,36	NOD2	nucleotide binding oligomerization domain containing 2
105379189	1,92E-06	5,72E+00	1,05E-06	0,739	-4,8822964	-3,60806472	10,61	LOC105379	uncharacterized LOC105379189
3113	0	#NUM!	0	0,0453	-81,6619858	-3,69789773	6994,28	HLA-DPA1	major histocompatibility complex, class II, DP alpha 1
2328	5,11E-13	1,23E+01	2,11E-13	0,5147	-7,3415427	-3,77873049	24,01	FMO3	flavin containing dimethylaniline monoxygenase 3
283748	7,50E-24	2,31E+01	2,25E-24	0,3715	-10,1879209	-3,78452988	45,8	PLA2G4D	phospholipase A2 group IVD
109864274	1,32E-56	5,59E+01	1,82E-57	0,2371	-15,9778401	-3,78876196	768,33	RNA5-8SN4	RNA, 5.8S ribosomal N4
109910381	7,65E-56	5,51E+01	1,07E-56	0,2418	-15,8670041	-3,8362594	612,67	RNA5-8SN3	RNA, 5.8S ribosomal N3
3772	1,13E-19	1,89E+01	3,78E-20	0,4234	-9,1942553	-3,89323347	36,29	KCNJ15	potassium inwardly rectifying channel subfamily J member 15
109864281	2,62E-76	7,56E+01	2,35E-77	0,2093	-18,6167609	-3,8963589	207,95	RNA5-8SN2	RNA, 5.8S ribosomal N2
4558	0	#NUM!	0	0,0995	-39,2129682	-3,90107504	768,46	TRNF	tRNA-Phe
6563	2,55E-69	6,86E+01	2,66E-70	0,2279	-17,7256153	-4,04034146	138,41	SLC14A1	solute carrier family 14 member 1 (Kidd blood group)
57477	9,60E-13	1,20E+01	4,00E-13	0,5571	-7,2554836	-4,04212419	23,46	SHROOM4	shroom family member 4
378707	2,29E-30	2,96E+01	5,78E-31	0,3509	-11,5710074	-4,06064041	61,99	RN7SL3	RNA component of signal recognition particle 7SL3
8200	9,30E-11	1,00E+01	4,17E-11	0,6159	-6,5980716	-4,06390322	19,13	GDF5	growth differentiation factor 5
104355287	6,20E-11	1,02E+01	2,76E-11	0,611	-6,6590611	-4,06882741	19,15	LINC01317	long intergenic non-protein coding RNA 1317
6398	0	#NUM!	0	0,0787	-51,7960017	-4,07396293	1703,31	SECTM1	secreted and transmembrane 1
11009	0	#NUM!	0	0,0922	-44,6292328	-4,11368278	1228,34	IL24	interleukin 24
3115	0	#NUM!	0	0,069	-61,0235842	-4,21328659	2446,3	HLA-DPB1	major histocompatibility complex, class II, DP beta 1
3128	0	#NUM!	0	0,1071	-39,6582061	-4,24598533	779,21	HLA-DRB6	major histocompatibility complex, class II, DR beta 6 (pseudogene)
3123	0	#NUM!	0	0,0499	-86,005104	-4,28957788	6641,42	HLA-DRB1	major histocompatibility complex, class II, DR beta 1
27344	3,47E-76	7,55E+01	3,12E-77	0,2308	-18,601562	-4,29303748	152,93	PCSK1N	proprotein convertase subtilisin/kexin type 1 inhibitor
727897	2,04E-43	4,27E+01	3,79E-44	0,3094	-13,9366363	-4,31224034	84,53	MUC5B	mucin 5B, oligomeric mucus/gel-forming
283298	1,92E-16	1,57E+01	7,12E-17	0,5342	-8,3450538	-4,4578328	30,97	OLFML1	olfactomedin like 1
3111	0	#NUM!	0	0,1085	-41,3854131	-4,49063459	901,47	HLA-DOA	major histocompatibility complex, class II, DO alpha
26864	2,24E-14	1,36E+01	8,85E-15	0,5942	-7,7547117	-4,60746501	27,28	RNVU1-7	RNA, variant U1 small nuclear 7
5651	1,10E-06	5,96E+00	5,92E-07	0,9482	-4,9939585	-4,73540068	11,17	TMPRSS15	transmembrane serine protease 15
85495	1,58E-58	5,78E+01	2,08E-59	0,2982	-16,2542891	-4,84734699	132,3	RPPH1	ribonuclease P RNA component H1
3127	0	#NUM!	0	0,0805	-60,3216224	-4,85531137	2243,09	HLA-DRB5	major histocompatibility complex, class II, DR beta 5
3119	3,29E-287	2,86E+02	1,79E-289	0,1336	-36,360551	-4,85930186	630,8	HLA-DQB1	major histocompatibility complex, class II, DQ beta 1
106631777	7,41E-74	7,31E+01	6,95E-75	0,2667	-18,3095386	-4,88282654	50606,56	RNA45SN1	RNA, 45S pre-ribosomal N1
59341	4,55E-112	1,11E+02	2,06E-113	0,2161	-22,6329114	-4,89199571	235,63	TRPV4	transient receptor potential cation channel subfamily V member 4
26871	4,67E-20	1,93E+01	1,55E-20	0,5282	-9,2894264	-4,90710474	41,68	RNU1-1	RNA, U1 small nuclear 1
26869	5,58E-19	1,83E+01	1,91E-19	0,5499	-9,0183869	-4,95956488	38,89	RNU1-3	RNA, U1 small nuclear 3
106480429	4,68E-55	5,43E+01	6,69E-56	0,3156	-15,7516199	-4,9712582	113,3	HLA-DQB1-A	HLA-DQB1 antisense RNA 1
140766	2,13E-65	6,47E+01	2,40E-66	0,2927	-17,2058022	-5,03580318	136,46	ADAMTS14	ADAM metallopeptidase with thrombospondin type 1 motif 14
240	1,14E-102	1,02E+02	6,18E-104	0,2386	-21,649236	-5,16587937	223,63	ALOX5	arachidonate 5-lipoxygenase
106632260	3,94E-21	2,04E+01	1,27E-21	0,5421	-9,5523429	-5,17842632	45,12	RNA5-8SN1	RNA, 5.8S ribosomal N1
124460	3,03E-06	5,52E+00	1,67E-06	1,109	-4,7891531	-5,3113505	10,93	SNX20	sorting nexin 20
3120	5,49E-181	1,80E+02	8,65E-183	0,1848	-28,8314613	-5,32698566	416,1	HLA-DQB2	major histocompatibility complex, class II, DQ beta 2
100008587	2,25E-18	1,76E+01	7,84E-19	0,6037	-8,8622186	-5,34969601	39,41	RNA5-8SN5	RNA, 5.8S ribosomal N5
3904	2,23E-15	1,47E+01	8,53E-16	0,6971	-8,0464027	-5,60925797	33,37	LAIR2	leukocyte associated immunoglobulin like receptor 2
112268313	5,32E-62	6,13E+01	6,47E-63	0,3402	-16,7420282	-5,69562473	390,98	LOC112268313	
692148	2,96E-60	5,95E+01	3,78E-61	0,3615	-16,4982306	-5,96439871	162,61	SCARNA10	small Cajal body-specific RNA 10
109864280	1,72E-97	9,68E+01	1,03E-98	0,2871	-21,0879418	-6,05376026	7451,19	RNA18SN2	RNA, 18S ribosomal N2
109864273	4,29E-112	1,11E+02	1,94E-113	0,2714	-22,6355415	-6,14312023	6970,11	RNA18SN4	RNA, 18S pre-ribosomal N4
106631781	1,88E-112	1,12E+02	8,45E-114	0,2726	-22,672067	-6,1800238	44462,51	RNA18SN1	RNA, 18S ribosomal N1
109910380	2,70E-123	1,23E+02	1,02E-124	0,261	-23,7532493	-6,20032467	14970,87	RNA18SN3	RNA, 18S ribosomal N3
100008588	1,27E-117	1,17E+02	5,26E-119	0,2678	-23,1937941	-6,21026633	61067,26	RNA18SN5	RNA, 18S ribosomal N5
105372577	7,18E-07	6,14E+00	3,84E-07	1,2485	-5,0768831	-6,33850392	11,87	LOC105372	uncharacterized LOC105372577
3117	6,50E-74	7,32E+01	6,08E-75	0,3472	-18,316743	-6,3597465	212,59	HLA-DQA1	major histocompatibility complex, class II, DQ alpha 1
107986589	1,40E-21	2,09E+01	4,45E-22	0,6713	-9,6602942	-6,48528581	60,99	LOC107986589	
10859	1,41E-07	6,85E+00	7,24E-08	1,2371	-5,3850797	-6,66195643	14,85	LILRB1	leukocyte immunoglobulin like receptor B1
11309	3,37E-07	6,47E+00	1,77E-07	1,2851	-5,2223155	-6,71135451	7,79	SLCO2B1	solute carrier organic anion transporter family member 2B1
100288866	1,33E-14	1,39E+01	5,24E-15	0,8615	-7,821132	-6,7379414	43,49	NGFR-AS1	NGFR antisense RNA 1
3118	4,90E-63	6,23E+01	5,82E-64	0,4023	-16,8848146	-6,79219388	211,14	HLA-DQA2	major histocompatibility complex, class II, DQ alpha 2
4804	0	#NUM!	0	0,1419	-49,12536	-6,96847211	1989,66	NGFR	nerve growth factor receptor
779	8,97E-27	2,60E+01	2,48E-27	0,6635	-10,8300879	-7,18536121	98,87	CACNA1S	calcium voltage-gated channel subunit alpha1 S
677766	1,38E-10	9,86E+00	6,21E-11	1,2056	-6,5386157	-7,88290961	34,38	SCARNA2	small Cajal body-specific RNA 2
7012	1,40E-10	9,85E+00	6,30E-11	1,214	-6,5364288	-7,93543883	35,72	TERC	telomerase RNA component
105370065	2,97E-11	1,05E+01	1,30E-11	1,1996	-6,768119	-8,11907737	40,42	LINC02376	long intergenic non-protein coding RNA 2376

Cell_Type	Expression_Type	Regulation	source	native	name	p_value	query_size	intersection_size	term_size	effective_domain_size
Cancer Epithelial	CXCL1-high	Upregulated	GO:MF	GO:0005515	protein binding	2,72E-19	331	313	15082	20208
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0009605	response to external stimulus	3,84E-16	323	97	2427	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0006950	response to stress	7,32E-15	323	128	3984	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0044419	biological process involved in interspecies interaction between organisms	2,11E-14	323	78	1777	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0051707	response to other organism	1,97E-13	323	72	1610	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0043207	response to external biotic stimulus	2,18E-13	323	72	1613	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0009607	response to biotic stimulus	7,68E-13	323	72	1652	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0006952	defense response	6,11E-12	323	76	1883	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0048518	positive regulation of biological process	2,40E-11	323	160	6150	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0030216	keratinocyte differentiation	9,89E-11	323	22	177	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:MF	GO:0048306	calcium-dependent protein binding	1,11E-10	331	16	80	20208
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0050896	response to stimulus	5,11E-10	323	204	9051	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0048522	positive regulation of cellular process	6,23E-10	323	149	5739	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0032101	regulation of response to external stimulus	2,49E-09	323	51	1092	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0140546	defense response to symbiont	3,27E-09	323	51	1100	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0002376	immune system process	3,49E-09	323	93	2913	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0098542	defense response to other organism	6,62E-09	323	51	1121	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0040011	locomotion	6,69E-09	323	54	1236	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0016477	cell migration	1,08E-08	323	61	1532	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0008219	cell death	1,24E-08	323	71	1962	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0009617	response to bacterium	1,81E-08	323	39	719	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0012501	programmed cell death	3,16E-08	323	70	1958	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0048584	positive regulation of response to stimulus	3,34E-08	323	78	2320	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0080134	regulation of response to stress	3,40E-08	323	57	1410	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0008544	epidermis development	5,85E-08	323	28	400	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0071621	granulocyte chemotaxis	1,01E-07	323	16	120	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0045087	innate immune response	1,10E-07	323	46	1018	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0042221	response to chemical	1,23E-07	323	108	3863	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0009913	epidermal cell differentiation	1,47E-07	323	22	254	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0006955	immune response	1,54E-07	323	72	2118	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0048583	regulation of response to stimulus	1,85E-07	323	110	3993	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0006935	chemotaxis	2,54E-07	323	29	456	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0042330	taxis	2,82E-07	323	29	458	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0048870	cell motility	3,18E-07	323	64	1794	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0006954	inflammatory response	4,36E-07	323	41	873	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:MF	GO:0140678	molecular function inhibitor activity	5,17E-07	331	32	559	20208
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0043588	skin development	5,41E-07	323	24	325	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0035556	intracellular signal transduction	8,06E-07	323	88	2963	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:MF	GO:0045296	cadherin binding	9,58E-07	331	24	335	20208
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0006915	apoptotic process	1,20E-06	323	65	1898	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0097530	granulocyte migration	2,42E-06	323	16	148	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0032103	positive regulation of response to external stimulus	3,54E-06	323	33	645	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0019538	protein metabolic process	3,78E-06	323	115	4467	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0008283	cell population proliferation	4,51E-06	323	65	1961	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0051239	regulation of multicellular organismal process	5,07E-06	323	85	2923	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0070887	cellular response to chemical stimulus	5,16E-06	323	70	2199	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0009888	tissue development	5,22E-06	323	66	2014	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:MF	GO:0098772	molecular function regulator activity	5,38E-06	331	73	2266	20208
Cancer Epithelial	CXCL1-high	Upregulated	GO:MF	GO:0004857	enzyme inhibitor activity	6,30E-06	331	26	428	20208
Cancer Epithelial	CXCL1-high	Upregulated	GO:MF	GO:0050839	cell adhesion molecule binding	9,15E-06	331	30	563	20208
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0030593	neutrophil chemotaxis	9,18E-06	323	12	82	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0042127	regulation of cell population proliferation	9,89E-06	323	57	1639	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:MF	GO:0042802	identical protein binding	1,33E-05	331	70	2179	20208
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0031347	regulation of defense response	1,49E-05	323	37	831	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0050789	regulation of biological process	2,53E-05	323	239	12397	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0002682	regulation of immune system process	2,54E-05	323	55	1594	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0030855	epithelial cell differentiation	3,48E-05	323	34	745	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0051246	regulation of protein metabolic process	4,29E-05	323	54	1574	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0060326	cell chemotaxis	4,40E-05	323	21	315	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:MF	GO:0005509	calcium ion binding	5,84E-05	331	33	718	20208
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0043065	positive regulation of apoptotic process	6,16E-05	323	27	512	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0051716	cellular response to stimulus	6,25E-05	323	162	7425	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:MF	GO:0004866	endopeptidase inhibitor activity	6,31E-05	331	15	167	20208
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0141124	intracellular signaling cassette	6,47E-05	323	60	1866	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0007155	cell adhesion	7,56E-05	323	52	1512	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0065007	biological regulation	8,15E-05	323	243	12804	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0030162	regulation of proteolysis	9,26E-05	323	15	166	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:MF	GO:0030414	peptidase inhibitor activity	1,08E-04	331	15	174	20208
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0043068	positive regulation of programmed cell death	1,11E-04	323	27	527	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:1902531	regulation of intracellular signal transduction	1,19E-04	323	61	1945	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0042742	defense response to bacterium	1,20E-04	323	21	334	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0051604	protein maturation	1,25E-04	323	27	530	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0002684	positive regulation of immune system process	1,46E-04	323	42	1111	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0065009	regulation of molecular function	1,47E-04	323	41	1070	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:MF	GO:0050786	RAGE receptor binding	1,53E-04	331	5	10	20208
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0072524	pyridine-containing compound metabolic process	1,60E-04	323	15	173	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:MF	GO:0098641	cadherin binding involved in cell-cell adhesion	1,65E-04	331	6	18	20208
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:1990266	neutrophil migration	1,75E-04	323	12	106	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0097529	myeloid leukocyte migration	1,88E-04	323	17	227	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0030595	leukocyte chemotaxis	1,88E-04	323	17	227	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0097190	apoptotic signaling pathway	1,88E-04	323	29	612	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0043542	endothelial cell migration	2,01E-04	323	17	228	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:MF	GO:0019899	enzyme binding	2,05E-04	331	64	2060	20208
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0002237	response to molecule of bacterial origin	2,08E-04	323	21	345	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0016032	viral process	2,15E-04	323	22	377	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0009185	ribonucleoside diphosphate metabolic process	2,24E-04	323	13	130	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0097193	intrinsic apoptotic signaling pathway	2,49E-04	323	20	318	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0019058	viral life cycle	2,74E-04	323	19	290	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:MF	GO:0005488	binding	2,85E-04	331	324	18447	20208
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0044092	negative regulation of molecular function	3,36E-04	323	21	355	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0060429	epithelium development	3,61E-04	323	44	1234	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0009132	nucleoside diphosphate metabolic process	3,82E-04	323	13	136	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0030334	regulation of cell migration	3,88E-04	323	37	944	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0048519	negative regulation of biological process	3,89E-04	323	131	5753	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0001816	cytokine production	4,00E-04	323	33	786	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:MF	GO:0061135	endopeptidase regulator activity	4,12E-04	331	15	193	20208
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0016485	protein processing	4,92E-04	323	16	215	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0001775	cell activation	5,35E-04	323	41	1123	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0001906	cell killing	5,58E-04	323	16	217	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0009967	positive regulation of signal transduction	6,04E-04	323	51	1569	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0006508	proteolysis	6,14E-04	323	33	801	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:2000145	regulation of cell motility	6,45E-04	323	38	1005	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0098609	cell-cell adhesion	6,66E-04	323	37	965	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0050776	regulation of immune response	7,55E-04	323	37	970	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:MF	GO:0061134	peptidase regulator activity	7,73E-04	331	16	230	20208
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0001817	regulation of cytokine production	1,03E-03	323	32	780	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0050794	regulation of cellular process	1,08E-03	323	227	11962	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0048585	negative regulation of response to stimulus	1,10E-03	323	53	1693	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0031349	positive regulation of defense response	1,11E-03	323	25	519	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0002683	negative regulation of immune system process	1,23E-03	323	25	522	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0072526	pyridine-containing compound catabolic process	1,34E-03	323	11	105	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:MF	GO:0005200	structural constituent of cytoskeleton	1,44E-03	331	11	113	20208
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0009191	ribonucleoside diphosphate catabolic process	1,48E-03	323	11	106	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0050729	positive regulation of inflammatory response	1,50E-03	323	13	153	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0040012	regulation of locomotion	1,72E-03	323	38	1046	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0051248	negative regulation of protein metabolic process	1,77E-03	323	26	569	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0009154	purine ribonucleotide catabolic process	1,79E-03	323	12	131	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0050727	regulation of inflammatory response	1,93E-03	323	21	395	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0009134	nucleoside diphosphate catabolic process	1,96E-03	323	11	109	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:1901292	nucleoside phosphate catabolic process	2,14E-03	323	14	184	20972

Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0023056	positive regulation of signaling	2,19E-03	323	54	1779	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:MF	GO:0043168	anion binding	2,22E-03	331	70	2496	20208
Cancer Epithelial	CXCL1-high	Upregulated	GO:MF	GO:0098632	cell-cell adhesion mediator activity	2,54E-03	331	8	58	20208
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0050790	regulation of catalytic activity	2,59E-03	323	31	774	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0009893	positive regulation of metabolic process	2,60E-03	323	86	3410	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0007165	signal transduction	2,74E-03	323	133	6063	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0009261	ribonucleotide catabolic process	3,13E-03	323	12	138	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0044403	biological process involved in symbiotic interaction	3,14E-03	323	14	190	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0009166	nucleotide catabolic process	3,29E-03	323	13	164	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0006195	purine nucleotide catabolic process	3,64E-03	323	12	140	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0007249	canonical NF-kappaB signal transduction	4,25E-03	323	18	315	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0031639	plasminogen activation	4,52E-03	323	6	26	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0009966	regulation of signal transduction	4,53E-03	323	78	3031	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0009179	purine ribonucleoside diphosphate metabolic process	4,69E-03	323	11	119	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0009135	purine nucleoside diphosphate metabolic process	4,69E-03	323	11	119	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:MF	GO:0032052	bile acid binding	4,74E-03	331	4	9	20208
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0010647	positive regulation of cell communication	4,81E-03	323	53	1778	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0033993	response to lipid	4,87E-03	323	33	880	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0048856	anatomical structure development	4,95E-03	323	130	5948	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:1902532	negative regulation of intracellular signal transduction	5,26E-03	323	28	681	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0010628	positive regulation of gene expression	5,28E-03	323	40	1184	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0006096	glycolytic process	5,52E-03	323	10	98	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:2000147	positive regulation of cell motility	6,19E-03	323	25	571	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0045321	leukocyte activation	6,29E-03	323	35	975	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0043067	regulation of programmed cell death	6,58E-03	323	46	1467	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0046032	ADP catabolic process	6,64E-03	323	10	100	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0032496	response to lipopolysaccharide	6,88E-03	323	18	326	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0019730	antimicrobial humoral response	7,01E-03	323	12	149	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0010466	negative regulation of peptidase activity	7,21E-03	323	6	28	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0042981	regulation of apoptotic process	7,23E-03	323	45	1426	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0050778	positive regulation of immune response	7,67E-03	323	30	775	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0019364	pyridine nucleotide catabolic process	7,96E-03	323	10	102	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0030335	positive regulation of cell migration	8,61E-03	323	24	544	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0009137	purine nucleoside diphosphate catabolic process	8,69E-03	323	10	103	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0009181	purine ribonucleoside diphosphate catabolic process	8,69E-03	323	10	103	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0051247	positive regulation of protein metabolic process	8,81E-03	323	32	863	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:2000026	regulation of multicellular organismal development	9,01E-03	323	44	1392	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0052547	regulation of peptidase activity	9,05E-03	323	7	44	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0031424	keratinization	9,53E-03	323	9	82	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0043122	regulation of canonical NF-kappaB signal transduction	9,54E-03	323	17	301	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0006090	pyruvate metabolic process	9,58E-03	323	11	128	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0042592	homeostatic process	9,66E-03	323	50	1677	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0040017	positive regulation of locomotion	9,74E-03	323	25	586	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:MF	GO:0019834	phospholipase A2 inhibitor activity	9,78E-03	331	3	4	20208
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0042060	wound healing	1,02E-02	323	21	439	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0048523	negative regulation of cellular process	1,15E-02	323	121	5510	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0051241	negative regulation of multicellular organismal process	1,19E-02	323	37	1091	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0072523	purine-containing compound catabolic process	1,21E-02	323	12	157	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:MF	GO:0004859	phospholipase inhibitor activity	1,21E-02	331	4	11	20208
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0046031	ADP metabolic process	1,23E-02	323	10	107	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0009259	ribonucleotide metabolic process	1,23E-02	323	19	374	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0019883	antigen processing and presentation of endogenous antigen	1,36E-02	323	6	31	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0002831	regulation of response to biotic stimulus	1,36E-02	323	24	559	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0032501	multicellular organismal process	1,50E-02	323	151	7337	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0009615	response to virus	1,59E-02	323	20	416	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0019693	ribose phosphate metabolic process	1,60E-02	323	19	381	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0061621	canonical glycolysis	1,64E-02	323	5	19	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0061718	glucose catabolic process to pyruvate	1,64E-02	323	5	19	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:1902533	positive regulation of intracellular signal transduction	1,68E-02	323	37	1108	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0002695	negative regulation of leukocyte activation	1,77E-02	323	13	191	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0051250	negative regulation of lymphocyte activation	1,88E-02	323	12	164	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0009611	response to wounding	1,88E-02	323	24	570	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0048002	antigen processing and presentation of peptide antigen	1,92E-02	323	8	68	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:MF	GO:0042379	chemokine receptor binding	1,94E-02	331	8	76	20208
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0009117	nucleotide metabolic process	1,94E-02	323	22	495	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0009150	purine ribonucleotide metabolic process	1,98E-02	323	18	352	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0046496	nicotinamide nucleotide metabolic process	2,00E-02	323	12	165	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:MF	GO:0033293	monocarboxylic acid binding	2,34E-02	331	8	78	20208
Cancer Epithelial	CXCL1-high	Upregulated	GO:MF	GO:0098631	cell adhesion mediator activity	2,34E-02	331	8	78	20208
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0030155	regulation of cell adhesion	2,40E-02	323	29	780	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:MF	GO:0047086	ketosteroid monooxygenase activity	2,41E-02	331	3	5	20208
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0051240	positive regulation of multicellular organismal process	2,46E-02	323	48	1639	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:MF	GO:0140313	molecular sequestering activity	2,48E-02	331	7	58	20208
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:1903900	regulation of viral life cycle	2,52E-02	323	10	116	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0050792	regulation of viral process	2,59E-02	323	11	142	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0009060	aerobic respiration	2,65E-02	323	16	292	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0023052	signaling	2,77E-02	323	137	6558	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0061620	glycolytic process through glucose-6-phosphate	2,79E-02	323	5	21	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0006163	purine nucleotide metabolic process	2,85E-02	323	20	433	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0045088	regulation of innate immune response	2,86E-02	323	21	470	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0002477	antigen processing and presentation of exogenous peptide antigen via MHC class Ib	2,86E-02	323	3	4	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0009753	response to jasmonic acid	2,86E-02	323	3	4	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0071395	cellular response to jasmonic acid stimulus	2,86E-02	323	3	4	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0001525	angiogenesis	2,88E-02	323	23	546	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0050673	epithelial cell proliferation	3,04E-02	323	20	435	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0035295	tube development	3,08E-02	323	36	1094	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0035239	tube morphogenesis	3,21E-02	323	31	877	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0043086	negative regulation of catalytic activity	3,31E-02	323	14	233	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0044093	positive regulation of molecular function	3,32E-02	323	24	590	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0045333	cellular respiration	3,43E-02	323	17	332	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:MF	GO:0044548	S100 protein binding	3,53E-02	331	4	14	20208
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0045862	positive regulation of proteolysis	3,62E-02	323	8	74	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:2001242	regulation of intrinsic apoptotic signaling pathway	3,63E-02	323	12	175	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0097435	supramolecular fiber organization	3,67E-02	323	29	798	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0010646	regulation of cell communication	3,76E-02	323	83	3480	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0001933	negative regulation of protein phosphorylation	3,83E-02	323	11	148	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0007154	cell communication	3,88E-02	323	137	6598	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0016052	carbohydrate catabolic process	4,30E-02	323	12	178	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0006959	humoral immune response	4,38E-02	323	15	271	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0030154	cell differentiation	4,41E-02	323	100	4443	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0034097	response to cytokine	4,42E-02	323	33	979	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0048869	cellular developmental process	4,46E-02	323	100	4444	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0007010	cytoskeleton organization	4,58E-02	323	45	1534	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0002478	antigen processing and presentation of exogenous peptide antigen	4,64E-02	323	6	38	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0043903	regulation of biological process involved in symbiotic interaction	4,64E-02	323	6	38	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:1901700	response to oxygen-containing compound	4,70E-02	323	47	1632	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:MF	GO:0055102	lipase inhibitor activity	4,75E-02	331	4	15	20208
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0010563	negative regulation of phosphorus metabolic process	4,85E-02	323	13	210	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0045936	negative regulation of phosphate metabolic process	4,85E-02	323	13	210	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0034655	nucleobase-containing compound catabolic process	4,94E-02	323	22	526	20972
Cancer Epithelial	CXCL1-high	Upregulated	GO:BP	GO:0008285	negative regulation of cell population proliferation	4,98E-02	323	26	686	20972
CAFs	CXCL1-high	Upregulated	GO:BP	GO:0033993	response to lipid	1,97E-05	18	9	880	20972
CAFs	CXCL1-high	Upregulated	GO:BP	GO:0070887	cellular response to chemical stimulus	2,56E-05	18	12	2199	20972
CAFs	CXCL1-high	Upregulated	GO:BP	GO:0042221	response to chemical	1,08E-04	18	14	3863	20972
CAFs	CXCL1-high	Upregulated	GO:BP	GO:0006950	response to stress	1,62E-04	18	14	3984	20972
CAFs	CXCL1-high	Upregulated	GO:BP	GO:0006954	inflammatory response	3,87E-04	18	8	873	20972
CAFs	CXCL1-high	Upregulated	GO:BP	GO:0002237	response to molecule of bacterial origin	4,38E-04	18	6	345	20972
CAFs	CXCL1-high	Upregulated	GO:BP	GO:0035556	intracellular signal transduction	7,36E-04	18	12	2963	20972
CAFs	CXCL1-high	Upregulated	GO:BP	GO:0141124	intracellular signaling cassette	1,00E-03	18	10	1866	20972
CAFs	CXCL1-high	Upregulated	GO:BP	GO:0008283	cell population proliferation	1,59E-03	18	10	1961	20972
CAFs	CXCL1-high	Upregulated	GO:MF	GO:0061629	RNA polymerase II-specific DNA-binding transcription factor binding	2,96E-03	18	5	346	20208

CAFs	CXCL1-high	Upregulated	GO:MF	GO:0008009	chemokine activity	3,29E-03	18	3	50	20208
CAFs	CXCL1-high	Upregulated	GO:BP	GO:0007165	signal transduction	3,80E-03	18	15	6063	20972
CAFs	CXCL1-high	Upregulated	GO:BP	GO:0042127	regulation of cell population proliferation	3,97E-03	18	9	1639	20972
CAFs	CXCL1-high	Upregulated	GO:BP	GO:0048545	response to steroid hormone	7,59E-03	18	5	312	20972
CAFs	CXCL1-high	Upregulated	GO:MF	GO:1990841	promoter-specific chromatin binding	8,34E-03	18	3	68	20208
CAFs	CXCL1-high	Upregulated	GO:BP	GO:0032496	response to lipopolysaccharide	9,39E-03	18	5	326	20972
CAFs	CXCL1-high	Upregulated	GO:BP	GO:0050896	response to stimulus	9,73E-03	18	17	9051	20972
CAFs	CXCL1-high	Upregulated	GO:BP	GO:0033554	cellular response to stress	1,12E-02	18	9	1856	20972
CAFs	CXCL1-high	Upregulated	GO:BP	GO:0023052	signaling	1,12E-02	18	15	6558	20972
CAFs	CXCL1-high	Upregulated	GO:BP	GO:0050793	regulation of developmental process	1,15E-02	18	10	2431	20972
CAFs	CXCL1-high	Upregulated	GO:MF	GO:0042379	chemokine receptor binding	1,16E-02	18	3	76	20208
CAFs	CXCL1-high	Upregulated	GO:BP	GO:0007154	cell communication	1,22E-02	18	15	6598	20972
CAFs	CXCL1-high	Upregulated	GO:BP	GO:0030097	hemopoiesis	1,33E-02	18	7	971	20972
CAFs	CXCL1-high	Upregulated	GO:MF	GO:0005125	cytokine activity	1,49E-02	18	4	239	20208
CAFs	CXCL1-high	Upregulated	GO:MF	GO:0140297	DNA-binding transcription factor binding	1,50E-02	18	5	485	20208
CAFs	CXCL1-high	Upregulated	GO:BP	GO:0140467	integrated stress response signaling	1,58E-02	18	3	51	20972
CAFs	CXCL1-high	Upregulated	GO:BP	GO:0009719	response to endogenous stimulus	1,92E-02	18	8	1467	20972
CAFs	CXCL1-high	Upregulated	GO:BP	GO:1902532	negative regulation of intracellular signal transduction	2,24E-02	18	6	681	20972
CAFs	CXCL1-high	Upregulated	GO:BP	GO:0009891	positive regulation of biosynthetic process	2,45E-02	18	10	2645	20972
CAFs	CXCL1-high	Upregulated	GO:BP	GO:0006357	regulation of transcription by RNA polymerase II	2,84E-02	18	10	2688	20972
CAFs	CXCL1-high	Upregulated	GO:BP	GO:0045595	regulation of cell differentiation	2,86E-02	18	8	1549	20972
CAFs	CXCL1-high	Upregulated	GO:MF	GO:0001664	G protein-coupled receptor binding	2,99E-02	18	4	286	20208
CAFs	CXCL1-high	Upregulated	GO:BP	GO:0009617	response to bacterium	3,05E-02	18	6	719	20972
CAFs	CXCL1-high	Upregulated	GO:BP	GO:0071356	cellular response to tumor necrosis factor	3,13E-02	18	4	198	20972
CAFs	CXCL1-high	Upregulated	GO:BP	GO:1903706	regulation of hemopoiesis	3,38E-02	18	5	425	20972
CAFs	CXCL1-high	Upregulated	GO:BP	GO:0070848	response to growth factor	3,43E-02	18	6	734	20972
CAFs	CXCL1-high	Upregulated	GO:MF	GO:0008134	transcription factor binding	4,00E-02	18	5	597	20208
CAFs	CXCL1-high	Upregulated	GO:BP	GO:0034612	response to tumor necrosis factor	4,40E-02	18	4	216	20972
CAFs	CXCL1-high	Upregulated	GO:BP	GO:0006366	transcription by RNA polymerase II	4,45E-02	18	10	2827	20972
Cancer Epithelial	CXCL1-negative	Upregulated	GO:BP	GO:0043069	negative regulation of programmed cell death	1,17E-04	115	20	887	20972
Cancer Epithelial	CXCL1-negative	Upregulated	GO:MF	GO:0005515	protein binding	6,74E-04	115	106	15082	20208
Cancer Epithelial	CXCL1-negative	Upregulated	GO:BP	GO:0043066	negative regulation of apoptotic process	1,58E-03	115	18	856	20972
Cancer Epithelial	CXCL1-negative	Upregulated	GO:BP	GO:0042775	mitochondrial ATP synthesis coupled electron transport	1,89E-03	115	7	98	20972
Cancer Epithelial	CXCL1-negative	Upregulated	GO:BP	GO:0042773	ATP synthesis coupled electron transport	1,89E-03	115	7	98	20972
Cancer Epithelial	CXCL1-negative	Upregulated	GO:BP	GO:0001655	urogenital system development	3,02E-03	115	6	67	20972
Cancer Epithelial	CXCL1-negative	Upregulated	GO:BP	GO:0051248	negative regulation of protein metabolic process	4,79E-03	115	14	569	20972
Cancer Epithelial	CXCL1-negative	Upregulated	GO:BP	GO:0022904	respiratory electron transport chain	5,24E-03	115	7	114	20972
Cancer Epithelial	CXCL1-negative	Upregulated	GO:BP	GO:0051179	localization	5,46E-03	115	53	5493	20972
Cancer Epithelial	CXCL1-negative	Upregulated	GO:BP	GO:0043067	regulation of programmed cell death	6,66E-03	115	23	1467	20972
Cancer Epithelial	CXCL1-negative	Upregulated	GO:MF	GO:0002020	protease binding	7,70E-03	115	7	139	20208
Cancer Epithelial	CXCL1-negative	Upregulated	GO:BP	GO:0012501	programmed cell death	9,24E-03	115	27	1958	20972
Cancer Epithelial	CXCL1-negative	Upregulated	GO:BP	GO:2001242	regulation of intrinsic apoptotic signaling pathway	9,24E-03	115	8	175	20972
Cancer Epithelial	CXCL1-negative	Upregulated	GO:BP	GO:0008219	cell death	9,60E-03	115	27	1962	20972
Cancer Epithelial	CXCL1-negative	Upregulated	GO:BP	GO:0022900	electron transport chain	9,67E-03	115	7	125	20972
Cancer Epithelial	CXCL1-negative	Upregulated	GO:BP	GO:0030850	prostate gland development	1,32E-02	115	5	50	20972
Cancer Epithelial	CXCL1-negative	Upregulated	GO:BP	GO:0097193	intrinsic apoptotic signaling pathway	1,70E-02	115	10	318	20972
Cancer Epithelial	CXCL1-negative	Upregulated	GO:BP	GO:0006120	mitochondrial electron transport, NADH to ubiquinone	1,76E-02	115	5	53	20972
Cancer Epithelial	CXCL1-negative	Upregulated	GO:MF	GO:0015453	oxidoreduction-driven active transmembrane transporter activity	1,79E-02	115	5	65	20208
Cancer Epithelial	CXCL1-negative	Upregulated	GO:BP	GO:0032879	regulation of localization	1,88E-02	115	26	1914	20972
Cancer Epithelial	CXCL1-negative	Upregulated	GO:BP	GO:0019646	aerobic electron transport chain	1,93E-02	115	6	92	20972
Cancer Epithelial	CXCL1-negative	Upregulated	GO:BP	GO:0051049	regulation of transport	1,95E-02	115	23	1566	20972
Cancer Epithelial	CXCL1-negative	Upregulated	GO:BP	GO:0051234	establishment of localization	2,10E-02	115	47	4804	20972
Cancer Epithelial	CXCL1-negative	Upregulated	GO:BP	GO:0046823	negative regulation of nucleocytoplasmic transport	2,28E-02	115	4	27	20972
Cancer Epithelial	CXCL1-negative	Upregulated	GO:BP	GO:0006810	transport	2,28E-02	115	44	4370	20972
Cancer Epithelial	CXCL1-negative	Upregulated	GO:BP	GO:0006119	oxidative phosphorylation	2,68E-02	115	7	146	20972
Cancer Epithelial	CXCL1-negative	Upregulated	GO:BP	GO:0048732	gland development	3,73E-02	115	11	425	20972
Cancer Epithelial	CXCL1-negative	Upregulated	GO:BP	GO:0060736	prostate gland growth	4,28E-02	115	3	11	20972
Cancer Epithelial	CXCL1-negative	Upregulated	GO:MF	GO:0008137	NADH dehydrogenase (ubiquinone) activity	4,46E-02	115	4	41	20208
Cancer Epithelial	CXCL1-negative	Upregulated	GO:BP	GO:0042981	regulation of apoptotic process	4,80E-02	115	21	1426	20972
Cancer Epithelial	CXCL1-negative	Upregulated	GO:BP	GO:0006915	apoptotic process	4,85E-02	115	25	1898	20972
CAFs	CXCL1-negative	Upregulated	GO:MF	GO:0005201	extracellular matrix structural constituent	3,77E-20	21	13	169	20208
CAFs	CXCL1-negative	Upregulated	GO:MF	GO:0005198	structural molecule activity	1,38E-12	21	15	1106	20208
CAFs	CXCL1-negative	Upregulated	GO:MF	GO:0030020	extracellular matrix structural constituent conferring tensile strength	1,27E-09	21	6	44	20208
CAFs	CXCL1-negative	Upregulated	GO:BP	GO:0030199	collagen fibril organization	7,57E-08	21	6	69	20972
CAFs	CXCL1-negative	Upregulated	GO:BP	GO:0030198	extracellular matrix organization	4,74E-07	21	8	307	20972
CAFs	CXCL1-negative	Upregulated	GO:BP	GO:0043062	extracellular structure organization	4,87E-07	21	8	308	20972
CAFs	CXCL1-negative	Upregulated	GO:BP	GO:0045229	external encapsulating structure organization	4,99E-07	21	8	309	20972
CAFs	CXCL1-negative	Upregulated	GO:MF	GO:0005518	collagen binding	3,11E-06	21	5	72	20208
CAFs	CXCL1-negative	Upregulated	GO:MF	GO:0048407	platelet-derived growth factor binding	5,09E-05	21	3	11	20208
CAFs	CXCL1-negative	Upregulated	GO:MF	GO:0002020	protease binding	8,55E-05	21	5	139	20208
CAFs	CXCL1-negative	Upregulated	GO:BP	GO:0007155	cell adhesion	8,88E-04	21	10	1512	20972
CAFs	CXCL1-negative	Upregulated	GO:BP	GO:0071230	cellular response to amino acid stimulus	2,24E-03	21	4	87	20972
CAFs	CXCL1-negative	Upregulated	GO:BP	GO:0071229	cellular response to acid chemical	3,18E-03	21	4	95	20972
CAFs	CXCL1-negative	Upregulated	GO:BP	GO:0001568	blood vessel development	6,35E-03	21	7	727	20972
CAFs	CXCL1-negative	Upregulated	GO:BP	GO:0071560	cellular response to transforming growth factor beta stimulus	6,58E-03	21	5	257	20972
CAFs	CXCL1-negative	Upregulated	GO:BP	GO:0043200	response to amino acid	7,06E-03	21	4	116	20972
CAFs	CXCL1-negative	Upregulated	GO:BP	GO:0071559	response to transforming growth factor beta	7,50E-03	21	5	264	20972
CAFs	CXCL1-negative	Upregulated	GO:BP	GO:1902617	response to fluoride	8,18E-03	21	2	4	20972
CAFs	CXCL1-negative	Upregulated	GO:BP	GO:0001944	vasculature development	8,36E-03	21	7	758	20972
CAFs	CXCL1-negative	Upregulated	GO:BP	GO:0001101	response to acid chemical	1,08E-02	21	4	129	20972
CAFs	CXCL1-negative	Upregulated	GO:BP	GO:0085029	extracellular matrix assembly	1,29E-02	21	3	41	20972
CAFs	CXCL1-negative	Upregulated	GO:MF	GO:0046332	SMAD binding	2,33E-02	21	3	79	20208
CAFs	CXCL1-negative	Upregulated	GO:BP	GO:0031589	cell-substrate adhesion	2,90E-02	21	5	349	20972
CAFs	CXCL1-negative	Upregulated	GO:MF	GO:0046872	metal ion binding	3,00E-02	21	13	4450	20208
CAFs	CXCL1-negative	Upregulated	GO:MF	GO:0005539	glycosaminoglycan binding	3,33E-02	21	4	243	20208
CAFs	CXCL1-negative	Upregulated	GO:MF	GO:0043169	cation binding	3,81E-02	21	13	4548	20208
CAFs	CXCL1-negative	Upregulated	GO:BP	GO:0032502	developmental process	4,04E-02	21	16	6535	20972
Cancer Epithelial	CXCL1-high	Downregulated	GO:BP	GO:0043069	negative regulation of programmed cell death	1,17E-04	115	20	887	20972
Cancer Epithelial	CXCL1-high	Downregulated	GO:MF	GO:0005515	protein binding	6,74E-04	115	106	15082	20208
Cancer Epithelial	CXCL1-high	Downregulated	GO:BP	GO:0043066	negative regulation of apoptotic process	1,58E-03	115	18	856	20972
Cancer Epithelial	CXCL1-high	Downregulated	GO:BP	GO:0042775	mitochondrial ATP synthesis coupled electron transport	1,89E-03	115	7	98	20972
Cancer Epithelial	CXCL1-high	Downregulated	GO:BP	GO:0042773	ATP synthesis coupled electron transport	1,89E-03	115	7	98	20972
Cancer Epithelial	CXCL1-high	Downregulated	GO:BP	GO:0001655	urogenital system development	3,02E-03	115	6	67	20972
Cancer Epithelial	CXCL1-high	Downregulated	GO:BP	GO:0051248	negative regulation of protein metabolic process	4,79E-03	115	14	569	20972
Cancer Epithelial	CXCL1-high	Downregulated	GO:BP	GO:0022904	respiratory electron transport chain	5,24E-03	115	7	114	20972
Cancer Epithelial	CXCL1-high	Downregulated	GO:BP	GO:0051179	localization	5,46E-03	115	53	5493	20972
Cancer Epithelial	CXCL1-high	Downregulated	GO:BP	GO:0043067	regulation of programmed cell death	6,66E-03	115	23	1467	20972
Cancer Epithelial	CXCL1-high	Downregulated	GO:MF	GO:0002020	protease binding	7,70E-03	115	7	139	20208
Cancer Epithelial	CXCL1-high	Downregulated	GO:BP	GO:0012501	programmed cell death	9,24E-03	115	27	1958	20972
Cancer Epithelial	CXCL1-high	Downregulated	GO:BP	GO:2001242	regulation of intrinsic apoptotic signaling pathway	9,24E-03	115	8	175	20972
Cancer Epithelial	CXCL1-high	Downregulated	GO:BP	GO:0008219	cell death	9,60E-03	115	27	1962	20972
Cancer Epithelial	CXCL1-high	Downregulated	GO:BP	GO:0022900	electron transport chain	9,67E-03	115	7	125	20972
Cancer Epithelial	CXCL1-high	Downregulated	GO:BP	GO:0030850	prostate gland development	1,32E-02	115	5	50	20972
Cancer Epithelial	CXCL1-high	Downregulated	GO:BP	GO:0097193	intrinsic apoptotic signaling pathway	1,70E-02	115	10	318	20972
Cancer Epithelial	CXCL1-high	Downregulated	GO:BP	GO:0006120	mitochondrial electron transport, NADH to ubiquinone	1,76E-02	115	5	53	20972
Cancer Epithelial	CXCL1-high	Downregulated	GO:MF	GO:0015453	oxidoreduction-driven active transmembrane transporter activity	1,79E-02	115	5	65	20208
Cancer Epithelial	CXCL1-high	Downregulated	GO:BP	GO:0032879	regulation of localization	1,88E-02	115	26	1914	20972
Cancer Epithelial	CXCL1-high	Downregulated	GO:BP	GO:0019646	aerobic electron transport chain	1,93E-02	115	6	92	20972
Cancer Epithelial	CXCL1-high	Downregulated	GO:BP	GO:0051049	regulation of transport	1,95E-02	115	23	1566	20972
Cancer Epithelial	CXCL1-high	Downregulated	GO:BP	GO:0051234	establishment of localization	2,10E-02	115	47	4804	20972
Cancer Epithelial	CXCL1-high	Downregulated	GO:BP	GO:0046823	negative regulation of nucleocytoplasmic transport	2,28E-02	115	4	27	20972
Cancer Epithelial	CXCL1-high	Downregulated	GO:BP	GO:0006810	transport	2,28E-02	115	44	4370	20972
Cancer Epithelial	CXCL1-high	Downregulated	GO:BP	GO:0006119	oxidative phosphorylation	2,68E-02	115	7	146	20972
Cancer Epithelial	CXCL1-high	Downregulated	GO:BP	GO:0048732	gland development	3,73E-02	115	11	425	20972
Cancer Epithelial	CXCL1-high	Downregulated	GO:BP	GO:0060736	prostate gland growth	4,28E-02	115	3	11	20972
Cancer Epithelial	CXCL1-high	Downregulated	GO:MF	GO:0008137	NADH dehydrogenase (ubiquinone) activity	4,46E-02	115	4	41	20208
Cancer Epithelial	CXCL1-high	Downregulated	GO:BP	GO:0042981	regulation of apoptotic process	4,80E-02	115	21	1426	20972
Cancer Epithelial	CXCL1-high	Downregulated	GO:BP	GO:0006915	apoptotic process	4,85E-02	115	25	1898	20972
CAFs	CXCL1-high	Downregulated	GO:MF	GO:0005201	extracellular matrix structural constituent	3,77E-20	21	13	169	20208
CAFs	CXCL1-high	Downregulated	GO:MF	GO:0005198	structural molecule activity	1,38E-12	21	15	1106	20208
CAFs	CXCL1-high	Downregulated	GO:MF	GO:0030020	extracellular matrix structural constituent conferring tensile strength	1,27E-09	21	6	44	20208

CAFs	CXCL1-high	Downregulated GO:BP	GO:0030199	collagen fibril organization	7,57E-08	21	6	69	20972
CAFs	CXCL1-high	Downregulated GO:BP	GO:0030198	extracellular matrix organization	4,74E-07	21	8	307	20972
CAFs	CXCL1-high	Downregulated GO:BP	GO:0043062	extracellular structure organization	4,87E-07	21	8	308	20972
CAFs	CXCL1-high	Downregulated GO:BP	GO:0045229	external encapsulating structure organization	4,99E-07	21	8	309	20972
CAFs	CXCL1-high	Downregulated GO:MF	GO:0005518	collagen binding	3,11E-06	21	5	72	20208
CAFs	CXCL1-high	Downregulated GO:MF	GO:0048407	platelet-derived growth factor binding	5,09E-05	21	3	11	20208
CAFs	CXCL1-high	Downregulated GO:MF	GO:0002020	protease binding	8,55E-05	21	5	139	20208
CAFs	CXCL1-high	Downregulated GO:BP	GO:0007155	cell adhesion	8,88E-04	21	10	1512	20972
CAFs	CXCL1-high	Downregulated GO:BP	GO:0071230	cellular response to amino acid stimulus	2,24E-03	21	4	87	20972
CAFs	CXCL1-high	Downregulated GO:BP	GO:0071229	cellular response to acid chemical	3,18E-03	21	4	95	20972
CAFs	CXCL1-high	Downregulated GO:BP	GO:0001568	blood vessel development	6,35E-03	21	7	727	20972
CAFs	CXCL1-high	Downregulated GO:BP	GO:0071560	cellular response to transforming growth factor beta stimulus	6,58E-03	21	5	257	20972
CAFs	CXCL1-high	Downregulated GO:BP	GO:0043200	response to amino acid	7,06E-03	21	4	116	20972
CAFs	CXCL1-high	Downregulated GO:BP	GO:0071559	response to transforming growth factor beta	7,50E-03	21	5	264	20972
CAFs	CXCL1-high	Downregulated GO:BP	GO:1902617	response to fluoride	8,18E-03	21	2	4	20972
CAFs	CXCL1-high	Downregulated GO:BP	GO:0001944	vasculature development	8,36E-03	21	7	758	20972
CAFs	CXCL1-high	Downregulated GO:BP	GO:0001101	response to acid chemical	1,08E-02	21	4	129	20972
CAFs	CXCL1-high	Downregulated GO:BP	GO:0085029	extracellular matrix assembly	1,29E-02	21	3	41	20972
CAFs	CXCL1-high	Downregulated GO:MF	GO:0046332	SMAD binding	2,33E-02	21	3	79	20208
CAFs	CXCL1-high	Downregulated GO:BP	GO:0031589	cell-substrate adhesion	2,90E-02	21	5	349	20972
CAFs	CXCL1-high	Downregulated GO:MF	GO:0046872	metal ion binding	3,00E-02	21	13	4450	20208
CAFs	CXCL1-high	Downregulated GO:MF	GO:0005539	glycosaminoglycan binding	3,33E-02	21	4	243	20208
CAFs	CXCL1-high	Downregulated GO:MF	GO:0043169	cation binding	3,81E-02	21	13	4548	20208
CAFs	CXCL1-high	Downregulated GO:BP	GO:0032502	developmental process	4,04E-02	21	16	6535	20972
Cancer Epithelial	CXCL1-negative	Downregulated GO:MF	GO:0005515	protein binding	2,72E-19	331	313	15082	20208
Cancer Epithelial	CXCL1-negative	Downregulated GO:BP	GO:0009605	response to external stimulus	3,84E-16	323	97	2427	20972
Cancer Epithelial	CXCL1-negative	Downregulated GO:BP	GO:0006950	response to stress	7,32E-15	323	128	3984	20972
Cancer Epithelial	CXCL1-negative	Downregulated GO:BP	GO:0044419	biological process involved in interspecies interaction between organisms	2,11E-14	323	78	1777	20972
Cancer Epithelial	CXCL1-negative	Downregulated GO:BP	GO:0051707	response to other organism	1,97E-13	323	72	1610	20972
Cancer Epithelial	CXCL1-negative	Downregulated GO:BP	GO:0043207	response to external biotic stimulus	2,18E-13	323	72	1613	20972
Cancer Epithelial	CXCL1-negative	Downregulated GO:BP	GO:0009607	response to biotic stimulus	7,68E-13	323	72	1652	20972
Cancer Epithelial	CXCL1-negative	Downregulated GO:BP	GO:0006952	defense response	6,11E-12	323	76	1883	20972
Cancer Epithelial	CXCL1-negative	Downregulated GO:BP	GO:0048518	positive regulation of biological process	2,40E-11	323	160	6150	20972
Cancer Epithelial	CXCL1-negative	Downregulated GO:BP	GO:0030216	keratinocyte differentiation	9,89E-11	323	22	177	20972
Cancer Epithelial	CXCL1-negative	Downregulated GO:MF	GO:0048306	calcium-dependent protein binding	1,11E-10	331	16	80	20208
Cancer Epithelial	CXCL1-negative	Downregulated GO:BP	GO:0050896	response to stimulus	5,11E-10	323	204	9051	20972
Cancer Epithelial	CXCL1-negative	Downregulated GO:BP	GO:0048522	positive regulation of cellular process	6,23E-10	323	149	5739	20972
Cancer Epithelial	CXCL1-negative	Downregulated GO:BP	GO:0032101	regulation of response to external stimulus	2,49E-09	323	51	1092	20972
Cancer Epithelial	CXCL1-negative	Downregulated GO:BP	GO:0140546	defense response to symbiont	3,27E-09	323	51	1100	20972
Cancer Epithelial	CXCL1-negative	Downregulated GO:BP	GO:0002376	immune system process	3,49E-09	323	93	2913	20972
Cancer Epithelial	CXCL1-negative	Downregulated GO:BP	GO:0098542	defense response to other organism	6,62E-09	323	51	1121	20972
Cancer Epithelial	CXCL1-negative	Downregulated GO:BP	GO:0040011	locomotion	6,69E-09	323	54	1236	20972
Cancer Epithelial	CXCL1-negative	Downregulated GO:BP	GO:0016477	cell migration	1,08E-08	323	61	1532	20972
Cancer Epithelial	CXCL1-negative	Downregulated GO:BP	GO:0008219	cell death	1,24E-08	323	71	1962	20972
Cancer Epithelial	CXCL1-negative	Downregulated GO:BP	GO:0009617	response to bacterium	1,81E-08	323	39	719	20972
Cancer Epithelial	CXCL1-negative	Downregulated GO:BP	GO:0012501	programmed cell death	3,16E-08	323	70	1958	20972
Cancer Epithelial	CXCL1-negative	Downregulated GO:BP	GO:0048584	positive regulation of response to stimulus	3,34E-08	323	78	2320	20972
Cancer Epithelial	CXCL1-negative	Downregulated GO:BP	GO:0080134	regulation of response to stress	3,40E-08	323	57	1410	20972
Cancer Epithelial	CXCL1-negative	Downregulated GO:BP	GO:0008544	epidermis development	5,85E-08	323	28	400	20972
Cancer Epithelial	CXCL1-negative	Downregulated GO:BP	GO:0071621	granulocyte chemotaxis	1,01E-07	323	16	120	20972
Cancer Epithelial	CXCL1-negative	Downregulated GO:BP	GO:0045087	innate immune response	1,10E-07	323	46	1018	20972
Cancer Epithelial	CXCL1-negative	Downregulated GO:BP	GO:0042221	response to chemical	1,23E-07	323	108	3863	20972
Cancer Epithelial	CXCL1-negative	Downregulated GO:BP	GO:0009913	epidermal cell differentiation	1,47E-07	323	22	254	20972
Cancer Epithelial	CXCL1-negative	Downregulated GO:BP	GO:0006955	immune response	1,54E-07	323	72	2118	20972
Cancer Epithelial	CXCL1-negative	Downregulated GO:BP	GO:0048583	regulation of response to stimulus	1,85E-07	323	110	3993	20972
Cancer Epithelial	CXCL1-negative	Downregulated GO:BP	GO:0006935	chemotaxis	2,54E-07	323	29	456	20972
Cancer Epithelial	CXCL1-negative	Downregulated GO:BP	GO:0042330	taxis	2,82E-07	323	29	458	20972
Cancer Epithelial	CXCL1-negative	Downregulated GO:BP	GO:0048870	cell motility	3,18E-07	323	64	1794	20972
Cancer Epithelial	CXCL1-negative	Downregulated GO:BP	GO:0006954	inflammatory response	4,36E-07	323	41	873	20972
Cancer Epithelial	CXCL1-negative	Downregulated GO:MF	GO:0140678	molecular function inhibitor activity	5,17E-07	331	32	559	20208
Cancer Epithelial	CXCL1-negative	Downregulated GO:BP	GO:0043588	skin development	5,41E-07	323	24	325	20972
Cancer Epithelial	CXCL1-negative	Downregulated GO:BP	GO:0035556	intracellular signal transduction	8,06E-07	323	88	2963	20972
Cancer Epithelial	CXCL1-negative	Downregulated GO:MF	GO:0045296	cadherin binding	9,58E-07	331	24	335	20208
Cancer Epithelial	CXCL1-negative	Downregulated GO:BP	GO:0006915	apoptotic process	1,20E-06	323	65	1898	20972
Cancer Epithelial	CXCL1-negative	Downregulated GO:BP	GO:0097530	granulocyte migration	2,42E-06	323	16	148	20972
Cancer Epithelial	CXCL1-negative	Downregulated GO:BP	GO:0032103	positive regulation of response to external stimulus	3,54E-06	323	33	645	20972
Cancer Epithelial	CXCL1-negative	Downregulated GO:BP	GO:0019538	protein metabolic process	3,78E-06	323	115	4467	20972
Cancer Epithelial	CXCL1-negative	Downregulated GO:BP	GO:0008283	cell population proliferation	4,51E-06	323	65	1961	20972
Cancer Epithelial	CXCL1-negative	Downregulated GO:BP	GO:0051239	regulation of multicellular organismal process	5,07E-06	323	85	2923	20972
Cancer Epithelial	CXCL1-negative	Downregulated GO:BP	GO:0070887	cellular response to chemical stimulus	5,16E-06	323	70	2199	20972
Cancer Epithelial	CXCL1-negative	Downregulated GO:BP	GO:0009888	tissue development	5,22E-06	323	66	2014	20972
Cancer Epithelial	CXCL1-negative	Downregulated GO:MF	GO:0098772	molecular function regulator activity	5,38E-06	331	73	2266	20208
Cancer Epithelial	CXCL1-negative	Downregulated GO:MF	GO:0004857	enzyme inhibitor activity	6,30E-06	331	26	428	20208
Cancer Epithelial	CXCL1-negative	Downregulated GO:MF	GO:0050839	cell adhesion molecule binding	9,15E-06	331	30	563	20208
Cancer Epithelial	CXCL1-negative	Downregulated GO:BP	GO:0030593	neutrophil chemotaxis	9,18E-06	323	12	82	20972
Cancer Epithelial	CXCL1-negative	Downregulated GO:BP	GO:0042127	regulation of cell population proliferation	9,89E-06	323	57	1639	20972
Cancer Epithelial	CXCL1-negative	Downregulated GO:MF	GO:0042802	identical protein binding	1,33E-05	331	70	2179	20208
Cancer Epithelial	CXCL1-negative	Downregulated GO:BP	GO:0031347	regulation of defense response	1,49E-05	323	37	831	20972
Cancer Epithelial	CXCL1-negative	Downregulated GO:BP	GO:0050789	regulation of biological process	2,53E-05	323	239	12397	20972
Cancer Epithelial	CXCL1-negative	Downregulated GO:BP	GO:0002682	regulation of immune system process	2,54E-05	323	55	1594	20972
Cancer Epithelial	CXCL1-negative	Downregulated GO:BP	GO:0030855	epithelial cell differentiation	3,48E-05	323	34	745	20972
Cancer Epithelial	CXCL1-negative	Downregulated GO:BP	GO:0051246	regulation of protein metabolic process	4,29E-05	323	54	1574	20972
Cancer Epithelial	CXCL1-negative	Downregulated GO:BP	GO:0060326	cell chemotaxis	4,40E-05	323	21	315	20972
Cancer Epithelial	CXCL1-negative	Downregulated GO:MF	GO:0005509	calcium ion binding	5,84E-05	331	33	718	20208
Cancer Epithelial	CXCL1-negative	Downregulated GO:BP	GO:0043065	positive regulation of apoptotic process	6,16E-05	323	27	512	20972
Cancer Epithelial	CXCL1-negative	Downregulated GO:BP	GO:0051716	cellular response to stimulus	6,25E-05	323	162	7425	20972
Cancer Epithelial	CXCL1-negative	Downregulated GO:MF	GO:0004866	endopeptidase inhibitor activity	6,31E-05	331	15	167	20208
Cancer Epithelial	CXCL1-negative	Downregulated GO:BP	GO:0141124	intracellular signaling cassette	6,47E-05	323	60	1866	20972
Cancer Epithelial	CXCL1-negative	Downregulated GO:BP	GO:0007155	cell adhesion	7,56E-05	323	52	1512	20972
Cancer Epithelial	CXCL1-negative	Downregulated GO:BP	GO:0065007	biological regulation	8,15E-05	323	243	12804	20972
Cancer Epithelial	CXCL1-negative	Downregulated GO:BP	GO:0030162	regulation of proteolysis	9,26E-05	323	15	166	20972
Cancer Epithelial	CXCL1-negative	Downregulated GO:MF	GO:0030414	peptidase inhibitor activity	1,08E-04	331	15	174	20208
Cancer Epithelial	CXCL1-negative	Downregulated GO:BP	GO:0043068	positive regulation of programmed cell death	1,11E-04	323	27	527	20972
Cancer Epithelial	CXCL1-negative	Downregulated GO:BP	GO:1902531	regulation of intracellular signal transduction	1,19E-04	323	61	1945	20972
Cancer Epithelial	CXCL1-negative	Downregulated GO:BP	GO:0042742	defense response to bacterium	1,20E-04	323	21	334	20972
Cancer Epithelial	CXCL1-negative	Downregulated GO:BP	GO:0051604	protein maturation	1,25E-04	323	27	530	20972
Cancer Epithelial	CXCL1-negative	Downregulated GO:BP	GO:0002684	positive regulation of immune system process	1,46E-04	323	42	1111	20972
Cancer Epithelial	CXCL1-negative	Downregulated GO:BP	GO:0065009	regulation of molecular function	1,47E-04	323	41	1070	20972
Cancer Epithelial	CXCL1-negative	Downregulated GO:MF	GO:0050786	RAGE receptor binding	1,53E-04	331	5	10	20208
Cancer Epithelial	CXCL1-negative	Downregulated GO:BP	GO:0072524	pyridine-containing compound metabolic process	1,60E-04	323	15	173	20972
Cancer Epithelial	CXCL1-negative	Downregulated GO:MF	GO:0098641	cadherin binding involved in cell-cell adhesion	1,65E-04	331	6	18	20208
Cancer Epithelial	CXCL1-negative	Downregulated GO:BP	GO:1990266	neutrophil migration	1,75E-04	323	12	106	20972
Cancer Epithelial	CXCL1-negative	Downregulated GO:BP	GO:0097529	myeloid leukocyte migration	1,88E-04	323	17	227	20972
Cancer Epithelial	CXCL1-negative	Downregulated GO:BP	GO:0030595	leukocyte chemotaxis	1,88E-04	323	17	227	20972
Cancer Epithelial	CXCL1-negative	Downregulated GO:BP	GO:0097190	apoptotic signaling pathway	1,88E-04	323	29	612	20972
Cancer Epithelial	CXCL1-negative	Downregulated GO:BP	GO:0043542	endothelial cell migration	2,01E-04	323	17	228	20972
Cancer Epithelial	CXCL1-negative	Downregulated GO:MF	GO:0019899	enzyme binding	2,05E-04	331	64	2060	20208
Cancer Epithelial	CXCL1-negative	Downregulated GO:BP	GO:0002237	response to molecule of bacterial origin	2,08E-04	323	21	345	20972
Cancer Epithelial	CXCL1-negative	Downregulated GO:BP	GO:0016032	viral process	2,15E-04	323	22	377	20972
Cancer Epithelial	CXCL1-negative	Downregulated GO:BP	GO:0009185	ribonucleoside diphosphate metabolic process	2,24E-04	323	13	130	20972
Cancer Epithelial	CXCL1-negative	Downregulated GO:BP	GO:0097193	intrinsic apoptotic signaling pathway	2,49E-04	323	20	318	20972
Cancer Epithelial	CXCL1-negative	Downregulated GO:BP	GO:0019058	viral life cycle	2,74E-04	323	19	290	20972
Cancer Epithelial	CXCL1-negative	Downregulated GO:MF	GO:0005488	binding	2,85E-04	331	324	18447	20208
Cancer Epithelial	CXCL1-negative	Downregulated GO:BP	GO:0044092	negative regulation of molecular function	3,36E-04	323	21	355	20972
Cancer Epithelial	CXCL1-negative	Downregulated GO:BP	GO:0060429	epithelium development	3,61E-04	323	44	1234	20972
Cancer Epithelial	CXCL1-negative	Downregulated GO:BP	GO:0009132	nucleoside diphosphate metabolic process	3,82E-04	323	13	136	20972
Cancer Epithelial	CXCL1-negative	Downregulated GO:BP	GO:0030334	regulation of cell migration	3,88E-04	323	37	944	20972
Cancer Epithelial	CXCL1-negative	Downregulated GO:BP	GO:0048519	negative regulation of biological process	3,89E-04	323	131	5753	20972
Cancer Epithelial	CXCL1-negative	Downregulated GO:BP	GO:0001816	cytokine production	4,00E-04	323	33	786	20972
Cancer Epithelial	CXCL1-negative	Downregulated GO:MF	GO:0061135	endopeptidase regulator activity	4,12E-04	331	15	193	20208
Cancer Epithelial	CXCL1-negative	Downregulated GO:BP	GO:0016485	protein processing	4,92E-04	323	16	215	20972

Cancer Epithelial	CXCL1-negative	Downregulated	GO:BP	GO:0001775	cell activation	5,35E-04	323	41	1123	20972
Cancer Epithelial	CXCL1-negative	Downregulated	GO:BP	GO:0001906	cell killing	5,58E-04	323	16	217	20972
Cancer Epithelial	CXCL1-negative	Downregulated	GO:BP	GO:0009967	positive regulation of signal transduction	6,04E-04	323	51	1569	20972
Cancer Epithelial	CXCL1-negative	Downregulated	GO:BP	GO:0006508	proteolysis	6,14E-04	323	33	801	20972
Cancer Epithelial	CXCL1-negative	Downregulated	GO:BP	GO:2000145	regulation of cell motility	6,45E-04	323	38	1005	20972
Cancer Epithelial	CXCL1-negative	Downregulated	GO:BP	GO:0098609	cell-cell adhesion	6,66E-04	323	37	965	20972
Cancer Epithelial	CXCL1-negative	Downregulated	GO:BP	GO:0050776	regulation of immune response	7,55E-04	323	37	970	20972
Cancer Epithelial	CXCL1-negative	Downregulated	GO:MF	GO:0061134	peptidase regulator activity	7,73E-04	331	16	230	20208
Cancer Epithelial	CXCL1-negative	Downregulated	GO:BP	GO:0001817	regulation of cytokine production	1,03E-03	323	32	780	20972
Cancer Epithelial	CXCL1-negative	Downregulated	GO:BP	GO:0050794	regulation of cellular process	1,08E-03	323	227	11962	20972
Cancer Epithelial	CXCL1-negative	Downregulated	GO:BP	GO:0048585	negative regulation of response to stimulus	1,10E-03	323	53	1693	20972
Cancer Epithelial	CXCL1-negative	Downregulated	GO:BP	GO:0031349	positive regulation of defense response	1,11E-03	323	25	519	20972
Cancer Epithelial	CXCL1-negative	Downregulated	GO:BP	GO:0002683	negative regulation of immune system process	1,23E-03	323	25	522	20972
Cancer Epithelial	CXCL1-negative	Downregulated	GO:BP	GO:0072526	pyridine-containing compound catabolic process	1,34E-03	323	11	105	20972
Cancer Epithelial	CXCL1-negative	Downregulated	GO:MF	GO:0005200	structural constituent of cytoskeleton	1,44E-03	331	11	113	20208
Cancer Epithelial	CXCL1-negative	Downregulated	GO:BP	GO:0009191	ribonucleoside diphosphate catabolic process	1,48E-03	323	11	106	20972
Cancer Epithelial	CXCL1-negative	Downregulated	GO:BP	GO:0050729	positive regulation of inflammatory response	1,50E-03	323	13	153	20972
Cancer Epithelial	CXCL1-negative	Downregulated	GO:BP	GO:0040012	regulation of locomotion	1,72E-03	323	38	1046	20972
Cancer Epithelial	CXCL1-negative	Downregulated	GO:BP	GO:0051248	negative regulation of protein metabolic process	1,77E-03	323	26	569	20972
Cancer Epithelial	CXCL1-negative	Downregulated	GO:BP	GO:0009154	purine ribonucleotide catabolic process	1,79E-03	323	12	131	20972
Cancer Epithelial	CXCL1-negative	Downregulated	GO:BP	GO:0050727	regulation of inflammatory response	1,93E-03	323	21	395	20972
Cancer Epithelial	CXCL1-negative	Downregulated	GO:BP	GO:0009134	nucleoside diphosphate catabolic process	1,96E-03	323	11	109	20972
Cancer Epithelial	CXCL1-negative	Downregulated	GO:BP	GO:1901292	nucleoside phosphate catabolic process	2,14E-03	323	14	184	20972
Cancer Epithelial	CXCL1-negative	Downregulated	GO:BP	GO:0023056	positive regulation of signaling	2,19E-03	323	54	1779	20972
Cancer Epithelial	CXCL1-negative	Downregulated	GO:MF	GO:0043168	anion binding	2,22E-03	331	70	2496	20208
Cancer Epithelial	CXCL1-negative	Downregulated	GO:MF	GO:0098632	cell-cell adhesion mediator activity	2,54E-03	331	8	58	20208
Cancer Epithelial	CXCL1-negative	Downregulated	GO:BP	GO:0050790	regulation of catalytic activity	2,59E-03	323	31	774	20972
Cancer Epithelial	CXCL1-negative	Downregulated	GO:BP	GO:0009893	positive regulation of metabolic process	2,60E-03	323	86	3410	20972
Cancer Epithelial	CXCL1-negative	Downregulated	GO:BP	GO:0007165	signal transduction	2,74E-03	323	133	6063	20972
Cancer Epithelial	CXCL1-negative	Downregulated	GO:BP	GO:0009261	ribonucleotide catabolic process	3,13E-03	323	12	138	20972
Cancer Epithelial	CXCL1-negative	Downregulated	GO:BP	GO:0044403	biological process involved in symbiotic interaction	3,14E-03	323	14	190	20972
Cancer Epithelial	CXCL1-negative	Downregulated	GO:BP	GO:0009166	nucleotide catabolic process	3,29E-03	323	13	164	20972
Cancer Epithelial	CXCL1-negative	Downregulated	GO:BP	GO:0006195	purine nucleotide catabolic process	3,64E-03	323	12	140	20972
Cancer Epithelial	CXCL1-negative	Downregulated	GO:BP	GO:0007249	canonical NF-kappaB signal transduction	4,25E-03	323	18	315	20972
Cancer Epithelial	CXCL1-negative	Downregulated	GO:BP	GO:0031639	plasminogen activation	4,52E-03	323	6	26	20972
Cancer Epithelial	CXCL1-negative	Downregulated	GO:BP	GO:0009966	regulation of signal transduction	4,53E-03	323	78	3031	20972
Cancer Epithelial	CXCL1-negative	Downregulated	GO:BP	GO:0009179	purine ribonucleoside diphosphate metabolic process	4,69E-03	323	11	119	20972
Cancer Epithelial	CXCL1-negative	Downregulated	GO:BP	GO:0009135	purine nucleoside diphosphate metabolic process	4,69E-03	323	11	119	20972
Cancer Epithelial	CXCL1-negative	Downregulated	GO:MF	GO:0032052	bile acid binding	4,74E-03	331	4	9	20208
Cancer Epithelial	CXCL1-negative	Downregulated	GO:BP	GO:0010647	positive regulation of cell communication	4,81E-03	323	53	1778	20972
Cancer Epithelial	CXCL1-negative	Downregulated	GO:BP	GO:0033993	response to lipid	4,87E-03	323	33	880	20972
Cancer Epithelial	CXCL1-negative	Downregulated	GO:BP	GO:0048856	anatomical structure development	4,95E-03	323	130	5948	20972
Cancer Epithelial	CXCL1-negative	Downregulated	GO:BP	GO:1902532	negative regulation of intracellular signal transduction	5,26E-03	323	28	681	20972
Cancer Epithelial	CXCL1-negative	Downregulated	GO:BP	GO:0010628	positive regulation of gene expression	5,28E-03	323	40	1184	20972
Cancer Epithelial	CXCL1-negative	Downregulated	GO:BP	GO:0006096	glycolytic process	5,52E-03	323	10	98	20972
Cancer Epithelial	CXCL1-negative	Downregulated	GO:BP	GO:2000147	positive regulation of cell motility	6,19E-03	323	25	571	20972
Cancer Epithelial	CXCL1-negative	Downregulated	GO:BP	GO:0045321	leukocyte activation	6,29E-03	323	35	975	20972
Cancer Epithelial	CXCL1-negative	Downregulated	GO:BP	GO:0043067	regulation of programmed cell death	6,58E-03	323	46	1467	20972
Cancer Epithelial	CXCL1-negative	Downregulated	GO:BP	GO:0046032	ADP catabolic process	6,64E-03	323	10	100	20972
Cancer Epithelial	CXCL1-negative	Downregulated	GO:BP	GO:0032496	response to lipopolysaccharide	6,88E-03	323	18	326	20972
Cancer Epithelial	CXCL1-negative	Downregulated	GO:BP	GO:0019730	antimicrobial humoral response	7,01E-03	323	12	149	20972
Cancer Epithelial	CXCL1-negative	Downregulated	GO:BP	GO:0010466	negative regulation of peptidase activity	7,21E-03	323	6	28	20972
Cancer Epithelial	CXCL1-negative	Downregulated	GO:BP	GO:0042981	regulation of apoptotic process	7,23E-03	323	45	1426	20972
Cancer Epithelial	CXCL1-negative	Downregulated	GO:BP	GO:0050778	positive regulation of immune response	7,67E-03	323	30	775	20972
Cancer Epithelial	CXCL1-negative	Downregulated	GO:BP	GO:0019364	pyridine nucleotide catabolic process	7,96E-03	323	10	102	20972
Cancer Epithelial	CXCL1-negative	Downregulated	GO:BP	GO:0030335	positive regulation of cell migration	8,61E-03	323	24	544	20972
Cancer Epithelial	CXCL1-negative	Downregulated	GO:BP	GO:0009137	purine nucleoside diphosphate catabolic process	8,69E-03	323	10	103	20972
Cancer Epithelial	CXCL1-negative	Downregulated	GO:BP	GO:0009181	purine ribonucleoside diphosphate catabolic process	8,69E-03	323	10	103	20972
Cancer Epithelial	CXCL1-negative	Downregulated	GO:BP	GO:0051247	positive regulation of protein metabolic process	8,81E-03	323	32	863	20972
Cancer Epithelial	CXCL1-negative	Downregulated	GO:BP	GO:2000026	regulation of multicellular organismal development	9,01E-03	323	44	1392	20972
Cancer Epithelial	CXCL1-negative	Downregulated	GO:BP	GO:0052547	regulation of peptidase activity	9,05E-03	323	7	44	20972
Cancer Epithelial	CXCL1-negative	Downregulated	GO:BP	GO:0031424	keratinization	9,53E-03	323	9	82	20972
Cancer Epithelial	CXCL1-negative	Downregulated	GO:BP	GO:0043122	regulation of canonical NF-kappaB signal transduction	9,54E-03	323	17	301	20972
Cancer Epithelial	CXCL1-negative	Downregulated	GO:BP	GO:0006090	pyruvate metabolic process	9,58E-03	323	11	128	20972
Cancer Epithelial	CXCL1-negative	Downregulated	GO:BP	GO:0042592	homeostatic process	9,66E-03	323	50	1677	20972
Cancer Epithelial	CXCL1-negative	Downregulated	GO:BP	GO:0040017	positive regulation of locomotion	9,74E-03	323	25	586	20972
Cancer Epithelial	CXCL1-negative	Downregulated	GO:MF	GO:0019834	phospholipase A2 inhibitor activity	9,78E-03	331	3	4	20208
Cancer Epithelial	CXCL1-negative	Downregulated	GO:BP	GO:0042060	wound healing	1,02E-02	323	21	439	20972
Cancer Epithelial	CXCL1-negative	Downregulated	GO:BP	GO:0048523	negative regulation of cellular process	1,15E-02	323	121	5510	20972
Cancer Epithelial	CXCL1-negative	Downregulated	GO:BP	GO:0051241	negative regulation of multicellular organismal process	1,19E-02	323	37	1091	20972
Cancer Epithelial	CXCL1-negative	Downregulated	GO:BP	GO:0072523	purine-containing compound catabolic process	1,21E-02	323	12	157	20972
Cancer Epithelial	CXCL1-negative	Downregulated	GO:MF	GO:0004859	phospholipase inhibitor activity	1,21E-02	331	4	11	20208
Cancer Epithelial	CXCL1-negative	Downregulated	GO:BP	GO:0046031	ADP metabolic process	1,23E-02	323	10	107	20972
Cancer Epithelial	CXCL1-negative	Downregulated	GO:BP	GO:0009259	ribonucleotide metabolic process	1,23E-02	323	19	374	20972
Cancer Epithelial	CXCL1-negative	Downregulated	GO:BP	GO:0019883	antigen processing and presentation of endogenous antigen	1,36E-02	323	6	31	20972
Cancer Epithelial	CXCL1-negative	Downregulated	GO:BP	GO:0002831	regulation of response to biotic stimulus	1,36E-02	323	24	559	20972
Cancer Epithelial	CXCL1-negative	Downregulated	GO:BP	GO:0032501	multicellular organismal process	1,50E-02	323	151	7337	20972
Cancer Epithelial	CXCL1-negative	Downregulated	GO:BP	GO:0009615	response to virus	1,59E-02	323	20	416	20972
Cancer Epithelial	CXCL1-negative	Downregulated	GO:BP	GO:0019693	ribose phosphate metabolic process	1,60E-02	323	19	381	20972
Cancer Epithelial	CXCL1-negative	Downregulated	GO:BP	GO:0061621	canonical glycolysis	1,64E-02	323	5	19	20972
Cancer Epithelial	CXCL1-negative	Downregulated	GO:BP	GO:0061718	glucose catabolic process to pyruvate	1,64E-02	323	5	19	20972
Cancer Epithelial	CXCL1-negative	Downregulated	GO:BP	GO:1902533	positive regulation of intracellular signal transduction	1,68E-02	323	37	1108	20972
Cancer Epithelial	CXCL1-negative	Downregulated	GO:BP	GO:0002695	negative regulation of leukocyte activation	1,77E-02	323	13	191	20972
Cancer Epithelial	CXCL1-negative	Downregulated	GO:BP	GO:0051250	negative regulation of lymphocyte activation	1,88E-02	323	12	164	20972
Cancer Epithelial	CXCL1-negative	Downregulated	GO:BP	GO:0009611	response to wounding	1,88E-02	323	24	570	20972
Cancer Epithelial	CXCL1-negative	Downregulated	GO:BP	GO:0048002	antigen processing and presentation of peptide antigen	1,92E-02	323	8	68	20972
Cancer Epithelial	CXCL1-negative	Downregulated	GO:MF	GO:0042379	chemokine receptor binding	1,94E-02	331	8	76	20208
Cancer Epithelial	CXCL1-negative	Downregulated	GO:BP	GO:0009117	nucleotide metabolic process	1,94E-02	323	22	495	20972
Cancer Epithelial	CXCL1-negative	Downregulated	GO:BP	GO:0009150	purine ribonucleotide metabolic process	1,98E-02	323	18	352	20972
Cancer Epithelial	CXCL1-negative	Downregulated	GO:BP	GO:0046496	nicotinamide nucleotide metabolic process	2,00E-02	323	12	165	20972
Cancer Epithelial	CXCL1-negative	Downregulated	GO:MF	GO:0033293	monocarboxylic acid binding	2,34E-02	331	8	78	20208
Cancer Epithelial	CXCL1-negative	Downregulated	GO:MF	GO:0098631	cell adhesion mediator activity	2,34E-02	331	8	78	20208
Cancer Epithelial	CXCL1-negative	Downregulated	GO:BP	GO:0030155	regulation of cell adhesion	2,40E-02	323	29	780	20972
Cancer Epithelial	CXCL1-negative	Downregulated	GO:MF	GO:0047086	ketosteroid monooxygenase activity	2,41E-02	331	3	5	20208
Cancer Epithelial	CXCL1-negative	Downregulated	GO:BP	GO:0051240	positive regulation of multicellular organismal process	2,46E-02	323	48	1639	20972
Cancer Epithelial	CXCL1-negative	Downregulated	GO:MF	GO:0140313	molecular sequestering activity	2,48E-02	331	7	58	20208
Cancer Epithelial	CXCL1-negative	Downregulated	GO:BP	GO:1903900	regulation of viral life cycle	2,52E-02	323	10	116	20972
Cancer Epithelial	CXCL1-negative	Downregulated	GO:BP	GO:0050792	regulation of viral process	2,59E-02	323	11	142	20972
Cancer Epithelial	CXCL1-negative	Downregulated	GO:BP	GO:0009060	aerobic respiration	2,65E-02	323	16	292	20972
Cancer Epithelial	CXCL1-negative	Downregulated	GO:BP	GO:0023052	signaling	2,77E-02	323	137	6558	20972
Cancer Epithelial	CXCL1-negative	Downregulated	GO:BP	GO:0061620	glycolytic process through glucose-6-phosphate	2,79E-02	323	5	21	20972
Cancer Epithelial	CXCL1-negative	Downregulated	GO:BP	GO:0006163	purine nucleotide metabolic process	2,85E-02	323	20	433	20972
Cancer Epithelial	CXCL1-negative	Downregulated	GO:BP	GO:0045088	regulation of innate immune response	2,86E-02	323	21	470	20972
Cancer Epithelial	CXCL1-negative	Downregulated	GO:BP	GO:0002477	antigen processing and presentation of exogenous peptide antigen via MHC class Ib	2,86E-02	323	3	4	20972
Cancer Epithelial	CXCL1-negative	Downregulated	GO:BP	GO:0009753	response to jasmonic acid	2,86E-02	323	3	4	20972
Cancer Epithelial	CXCL1-negative	Downregulated	GO:BP	GO:0071395	cellular response to jasmonic acid stimulus	2,86E-02	323	3	4	20972
Cancer Epithelial	CXCL1-negative	Downregulated	GO:BP	GO:0001525	angiogenesis	2,88E-02	323	23	546	20972
Cancer Epithelial	CXCL1-negative	Downregulated	GO:BP	GO:0050673	epithelial cell proliferation	3,04E-02	323	20	435	20972
Cancer Epithelial	CXCL1-negative	Downregulated	GO:BP	GO:0035295	tube development	3,08E-02	323	36	1094	20972
Cancer Epithelial	CXCL1-negative	Downregulated	GO:BP	GO:0035239	tube morphogenesis	3,21E-02	323	31	877	20972
Cancer Epithelial	CXCL1-negative	Downregulated	GO:BP	GO:0043086	negative regulation of catalytic activity	3,31E-02	323	14	233	20972
Cancer Epithelial	CXCL1-negative	Downregulated	GO:BP	GO:0044093	positive regulation of molecular function	3,32E-02	323	24	590	20972
Cancer Epithelial	CXCL1-negative	Downregulated	GO:BP	GO:0045333	cellular respiration	3,43E-02	323	17	332	20972
Cancer Epithelial	CXCL1-negative	Downregulated	GO:MF	GO:0044548	S100 protein binding	3,53E-02	331	4	14	20208
Cancer Epithelial	CXCL1-negative	Downregulated	GO:BP	GO:0045862	positive regulation of proteolysis	3,62E-02	323	8	74	20972
Cancer Epithelial	CXCL1-negative	Downregulated	GO:BP	GO:2001242	regulation of intrinsic apoptotic signaling pathway	3,63E-02	323	12	175	20972
Cancer Epithelial	CXCL1-negative	Downregulated	GO:BP	GO:0097435	supramolecular fiber organization	3,67E-02	323	29	798	20972
Cancer Epithelial	CXCL1-negative	Downregulated	GO:BP	GO:0010646	regulation of cell communication	3,76E-02	323	83	3480	20972
Cancer Epithelial	CXCL1-negative	Downregulated	GO:BP	GO:0001933	negative regulation of protein phosphorylation	3,83E-02	323	11	148	20972
Cancer Epithelial	CXCL1-negative	Downregulated	GO:BP	GO:0007154	cell communication	3,88E-02	323	137	6598	20972
Cancer Epithelial	CXCL1-negative	Downregulated	GO:BP	GO:0016052	carbohydrate catabolic process	4,30E-02	323	12	178	20972

Cancer Epithelial	CXCL1-negative	Downregulated GO:BP	GO:0006959	humoral immune response	4,38E-02	323	15	271	20972
Cancer Epithelial	CXCL1-negative	Downregulated GO:BP	GO:0030154	cell differentiation	4,41E-02	323	100	4443	20972
Cancer Epithelial	CXCL1-negative	Downregulated GO:BP	GO:0034097	response to cytokine	4,42E-02	323	33	979	20972
Cancer Epithelial	CXCL1-negative	Downregulated GO:BP	GO:0048869	cellular developmental process	4,46E-02	323	100	4444	20972
Cancer Epithelial	CXCL1-negative	Downregulated GO:BP	GO:0007010	cytoskeleton organization	4,58E-02	323	45	1534	20972
Cancer Epithelial	CXCL1-negative	Downregulated GO:BP	GO:0002478	antigen processing and presentation of exogenous peptide antigen	4,64E-02	323	6	38	20972
Cancer Epithelial	CXCL1-negative	Downregulated GO:BP	GO:0043903	regulation of biological process involved in symbiotic interaction	4,64E-02	323	6	38	20972
Cancer Epithelial	CXCL1-negative	Downregulated GO:BP	GO:1901700	response to oxygen-containing compound	4,70E-02	323	47	1632	20972
Cancer Epithelial	CXCL1-negative	Downregulated GO:MF	GO:0055102	lipase inhibitor activity	4,75E-02	331	4	15	20208
Cancer Epithelial	CXCL1-negative	Downregulated GO:BP	GO:0010563	negative regulation of phosphorus metabolic process	4,85E-02	323	13	210	20972
Cancer Epithelial	CXCL1-negative	Downregulated GO:BP	GO:0045936	negative regulation of phosphate metabolic process	4,85E-02	323	13	210	20972
Cancer Epithelial	CXCL1-negative	Downregulated GO:BP	GO:0034655	nucleobase-containing compound catabolic process	4,94E-02	323	22	526	20972
Cancer Epithelial	CXCL1-negative	Downregulated GO:BP	GO:0008285	negative regulation of cell population proliferation	4,98E-02	323	26	686	20972
CAFs	CXCL1-negative	Downregulated GO:BP	GO:0033993	response to lipid	1,97E-05	18	9	880	20972
CAFs	CXCL1-negative	Downregulated GO:BP	GO:0070887	cellular response to chemical stimulus	2,56E-05	18	12	2199	20972
CAFs	CXCL1-negative	Downregulated GO:BP	GO:0042221	response to chemical	1,08E-04	18	14	3863	20972
CAFs	CXCL1-negative	Downregulated GO:BP	GO:0006950	response to stress	1,62E-04	18	14	3984	20972
CAFs	CXCL1-negative	Downregulated GO:BP	GO:0006954	inflammatory response	3,87E-04	18	8	873	20972
CAFs	CXCL1-negative	Downregulated GO:BP	GO:0002237	response to molecule of bacterial origin	4,38E-04	18	6	345	20972
CAFs	CXCL1-negative	Downregulated GO:BP	GO:0035556	intracellular signal transduction	7,36E-04	18	12	2963	20972
CAFs	CXCL1-negative	Downregulated GO:BP	GO:0141124	intracellular signaling cassette	1,00E-03	18	10	1866	20972
CAFs	CXCL1-negative	Downregulated GO:BP	GO:0008283	cell population proliferation	1,59E-03	18	10	1961	20972
CAFs	CXCL1-negative	Downregulated GO:MF	GO:0061629	RNA polymerase II-specific DNA-binding transcription factor binding	2,96E-03	18	5	346	20208
CAFs	CXCL1-negative	Downregulated GO:MF	GO:0008009	chemokine activity	3,29E-03	18	3	50	20208
CAFs	CXCL1-negative	Downregulated GO:BP	GO:0007165	signal transduction	3,80E-03	18	15	6063	20972
CAFs	CXCL1-negative	Downregulated GO:BP	GO:0042127	regulation of cell population proliferation	3,97E-03	18	9	1639	20972
CAFs	CXCL1-negative	Downregulated GO:BP	GO:0048545	response to steroid hormone	7,59E-03	18	5	312	20972
CAFs	CXCL1-negative	Downregulated GO:MF	GO:1990841	promoter-specific chromatin binding	8,34E-03	18	3	68	20208
CAFs	CXCL1-negative	Downregulated GO:BP	GO:0032496	response to lipopolysaccharide	9,39E-03	18	5	326	20972
CAFs	CXCL1-negative	Downregulated GO:BP	GO:0050896	response to stimulus	9,73E-03	18	17	9051	20972
CAFs	CXCL1-negative	Downregulated GO:BP	GO:0033554	cellular response to stress	1,12E-02	18	9	1856	20972
CAFs	CXCL1-negative	Downregulated GO:BP	GO:0023052	signaling	1,12E-02	18	15	6558	20972
CAFs	CXCL1-negative	Downregulated GO:BP	GO:0050793	regulation of developmental process	1,15E-02	18	10	2431	20972
CAFs	CXCL1-negative	Downregulated GO:MF	GO:0042379	chemokine receptor binding	1,16E-02	18	3	76	20208
CAFs	CXCL1-negative	Downregulated GO:BP	GO:0007154	cell communication	1,22E-02	18	15	6598	20972
CAFs	CXCL1-negative	Downregulated GO:BP	GO:0030097	hemopoiesis	1,33E-02	18	7	971	20972
CAFs	CXCL1-negative	Downregulated GO:MF	GO:0005125	cytokine activity	1,49E-02	18	4	239	20208
CAFs	CXCL1-negative	Downregulated GO:MF	GO:0140297	DNA-binding transcription factor binding	1,50E-02	18	5	485	20208
CAFs	CXCL1-negative	Downregulated GO:BP	GO:0140467	integrated stress response signaling	1,58E-02	18	3	51	20972
CAFs	CXCL1-negative	Downregulated GO:BP	GO:0009719	response to endogenous stimulus	1,92E-02	18	8	1467	20972
CAFs	CXCL1-negative	Downregulated GO:BP	GO:1902532	negative regulation of intracellular signal transduction	2,24E-02	18	6	681	20972
CAFs	CXCL1-negative	Downregulated GO:BP	GO:0009891	positive regulation of biosynthetic process	2,45E-02	18	10	2645	20972
CAFs	CXCL1-negative	Downregulated GO:BP	GO:0006357	regulation of transcription by RNA polymerase II	2,84E-02	18	10	2688	20972
CAFs	CXCL1-negative	Downregulated GO:BP	GO:0045595	regulation of cell differentiation	2,86E-02	18	8	1549	20972
CAFs	CXCL1-negative	Downregulated GO:MF	GO:0001664	G protein-coupled receptor binding	2,99E-02	18	4	286	20208
CAFs	CXCL1-negative	Downregulated GO:BP	GO:0009617	response to bacterium	3,05E-02	18	6	719	20972
CAFs	CXCL1-negative	Downregulated GO:BP	GO:0071356	cellular response to tumor necrosis factor	3,13E-02	18	4	198	20972
CAFs	CXCL1-negative	Downregulated GO:BP	GO:1903706	regulation of hemopoiesis	3,38E-02	18	5	425	20972
CAFs	CXCL1-negative	Downregulated GO:BP	GO:0070848	response to growth factor	3,43E-02	18	6	734	20972
CAFs	CXCL1-negative	Downregulated GO:MF	GO:0008134	transcription factor binding	4,00E-02	18	5	597	20208
CAFs	CXCL1-negative	Downregulated GO:BP	GO:0034612	response to tumor necrosis factor	4,40E-02	18	4	216	20972
CAFs	CXCL1-negative	Downregulated GO:BP	GO:0006366	transcription by RNA polymerase II	4,45E-02	18	10	2827	20972

names	logfoldchanges	pvals_adj
CXCL8	6,08702374	4,72E-29
ANXA1	3,77461982	1,97E-23
CSTB	1,74470472	6,52E-15
S100A6	2,57706451	8,79E-15
CXCL2	4,74733162	2,19E-13
CYBA	2,10248232	2,37E-13
NMB	2,84431982	3,03E-13
KRT17	4,22196770	3,72E-13
S100A2	3,60426402	3,72E-13
TMSB4X	1,66672289	3,72E-13
S100A8	5,21472406	4,42E-13
S100A9	4,63733006	7,22E-13
MT1X	2,53099680	7,22E-13
ANXA2	1,44036829	2,33E-12
ARPC1B	1,86564863	5,14E-12
FABP5	3,08207941	3,58E-11
RARRES1	2,67152858	1,44E-10
B2M	1,46244669	1,53E-10
SLPI	2,01763821	1,65E-10
SOD2	2,05108714	3,18E-10
CXCL3	4,31773376	4,19E-10
PCBP1	1,32842505	5,61E-10
ID3	2,18984151	1,39E-09
CTSC	2,50853276	3,90E-09
S100A16	1,60918164	4,67E-09
S100A11	1,04877245	5,75E-09
MYL12A	1,13605833	9,98E-09
S100A4	2,30949593	1,06E-08
TMEM45A	2,24114227	1,54E-08
TYMP	1,60893762	2,43E-08
ETS2	1,88135278	5,53E-08
YBX1	1,33127081	5,95E-08
PLAUR	2,12144089	6,54E-08
TACSTD2	1,43032062	9,15E-08
S100A7	4,09319353	9,81E-08
SERPINB1	1,72672200	1,42E-07
PFKP	1,87034202	1,49E-07
RNF145	2,40147996	1,80E-07
MYL12B	0,97397977	2,00E-07
NDFIP2	1,58277762	2,05E-07
SERPINB4	5,27355146	3,43E-07
SERPINB3	4,57798624	3,72E-07
ENO1	1,16309428	4,09E-07
S100P	2,04299927	4,64E-07
CPE	2,49504638	5,00E-07
SLC16A3	2,12147450	5,35E-07
KRT81	3,09671879	1,12E-06

S100A14	1,56257081	1,60E-06
NFKBIA	1,20967650	1,60E-06
CD58	2,41015863	2,03E-06
NCOA7	1,76609802	2,48E-06
LDHA	0,88904780	2,65E-06
HLA-E	1,36317790	2,90E-06
HIF1A	1,62246227	3,46E-06
KLF5	1,94000185	4,08E-06
CDKN2A	2,22398686	4,22E-06
STEAP4	2,28724170	5,27E-06
BTG3	1,75743496	7,87E-06
GSN	1,29547596	8,66E-06
S100A10	1,18337953	9,71E-06
TMSB10	0,90126508	1,12E-05
TNFAIP3	1,78176415	1,17E-05
KRT16	3,10627961	1,17E-05
HMGB3	1,64930141	1,45E-05
TUBA4A	1,68618119	1,68E-05
CXCL6	8,46184158	1,90E-05
DEFB1	3,04847288	2,27E-05
PDZK1IP1	1,72428071	2,30E-05
GJB2	3,63671756	2,97E-05
PABPC1	0,64865118	3,05E-05
RDH10	3,09768367	3,20E-05
CLIC4	1,48805976	3,74E-05
RGS2	3,52573681	4,09E-05
PRNP	1,93460095	4,14E-05
NUDT5	1,20529819	4,28E-05
SEC61G	0,82126939	4,94E-05
CASP14	3,19202185	5,34E-05
RAB38	2,50826383	5,56E-05
CCL20	6,80965185	5,83E-05
TFDP1	1,41035903	6,80E-05
ERRFI1	1,34197974	8,84E-05
COX4I1	0,50831175	9,39E-05
FAM83A	3,20718217	9,67E-05
C5orf66-AS1	3,29688811	9,74E-05
KCNK1	1,54633176	1,24E-04
PLK2	1,54171956	1,35E-04
FSCN1	1,43508053	1,35E-04
GDI2	1,10633779	1,37E-04
CAV2	1,56841433	1,79E-04
LY6D	2,78780890	2,06E-04
KRT6A	4,51759148	2,21E-04
CMPK1	1,06070852	2,25E-04
IL32	2,10028148	2,25E-04
CHMP1B	1,37995553	2,29E-04
SFN	1,21928942	2,54E-04

LCN2	3,27916694	2,75E-04
OPN3	1,20005536	2,85E-04
LAMP1	0,94419682	3,06E-04
KRT6B	2,57272863	3,08E-04
PITX1	1,70547652	3,35E-04
UQCRB	0,70942289	3,41E-04
LAD1	1,33693182	3,41E-04
CSTA	2,55902719	3,43E-04
TCEB1	0,76280224	3,89E-04
AKR1C2	3,29123116	4,31E-04
ERO1A	1,29609394	4,67E-04
HLA-DRA	1,71919882	4,84E-04
ATP5C1	0,86922842	4,96E-04
STOM	1,65906692	5,20E-04
CXCL17	1,97660148	5,20E-04
PI3	3,45545769	5,44E-04
PERP	0,82811731	5,92E-04
C1orf106	2,55275655	6,03E-04
CASP4	1,46177864	7,15E-04
PSMA2	1,45301414	7,29E-04
AQP3	1,62720120	7,85E-04
RHOV	1,25500476	8,07E-04
PMAIP1	1,33184826	8,53E-04
SVIL	1,50764287	8,68E-04
B3GNT5	2,03058457	8,77E-04
PLSCR1	1,11488378	8,78E-04
NAMPT	0,92202967	9,51E-04
EFHD2	1,65035367	9,99E-04
MPHOSPH6	1,14506984	1,01E-03
FAM3C	1,31924284	1,08E-03
MAPK6	1,34312952	1,12E-03
GUK1	0,48810625	1,12E-03
GJB3	2,91352868	1,18E-03
GBP2	1,66048539	1,18E-03
PTP4A1	1,00601149	1,23E-03
RIOK3	1,15659297	1,25E-03
KIAA0101	1,94831169	1,41E-03
SDCBP2	2,25614977	1,43E-03
CD74	1,52142000	1,49E-03
SERPINB5	2,42015076	1,50E-03
SGK1	1,93875241	1,59E-03
RSU1	1,11380565	1,59E-03
TMEM208	0,89097244	1,65E-03
TES	1,18034565	1,76E-03
CP	3,18854260	1,88E-03
TRIM29	1,04456472	1,88E-03
PHLDA1	1,04187071	1,96E-03
PHLDA2	0,99095172	1,97E-03

DYNC1LI2	1,10140300	2,08E-03
TUBA1C	0,97328299	2,08E-03
USB1	1,09390664	2,19E-03
DNAJA1	0,88200462	2,35E-03
RND3	1,37779081	2,51E-03
GEM	1,68631101	2,75E-03
TPI1	0,59914500	2,82E-03
TMEM165	0,93754059	2,98E-03
DDIT4	1,08604217	3,13E-03
PPIB	0,73344952	3,15E-03
GRN	0,93642890	3,27E-03
DSC2	0,93674719	3,27E-03
LPCAT2	2,34099865	3,45E-03
C8orf4	1,41382563	3,45E-03
KRT7	0,92978877	3,55E-03
EVA1C	1,29063809	3,58E-03
DNAJB4	1,29756594	4,08E-03
NT5C2	1,80510628	4,10E-03
PDIA3	0,70934296	4,13E-03
CTNNBIP1	0,95771527	4,24E-03
NCCRP1	2,05265212	4,28E-03
CARHSP1	0,90905482	4,46E-03
PCSK1	4,10894251	4,56E-03
GTF2F2	1,22874463	4,56E-03
CKS2	0,99257624	4,63E-03
ARPC5	0,83120066	4,64E-03
UBC	0,71821749	4,78E-03
PLOD2	1,33956730	4,82E-03
HLA-B	1,21592116	4,90E-03
ATAD3A	1,74032950	4,98E-03
CD14	3,31519675	4,99E-03
POLE4	0,83390051	5,12E-03
UBA52	0,52501291	5,20E-03
MXD1	1,29230165	5,26E-03
F3	3,06007242	5,26E-03
TRIM16	1,78322864	5,26E-03
C20orf24	0,73183447	5,26E-03
ZC3H12A	1,25442338	5,37E-03
TPT1	0,47964305	5,64E-03
COMMD6	0,54561865	5,66E-03
AKR1C3	2,09807968	5,73E-03
AKR1C1	2,51477337	6,24E-03
BIRC3	2,05479503	6,24E-03
KARS	1,03715801	6,24E-03
CA9	2,95778656	6,26E-03
PLP2	0,81703675	6,28E-03
TUBB6	1,36516142	6,35E-03
COTL1	1,28103018	6,37E-03

CEBPD	0,89249861	6,42E-03
CASC15	2,03143597	6,44E-03
BACE2	0,66430044	6,47E-03
PPA1	0,68356287	6,47E-03
BIK	1,17385304	6,47E-03
ANXA3	1,29850590	6,77E-03
UBE2V2	0,68160123	6,94E-03
TAX1BP3	1,15420341	7,18E-03
FGG	2,90149045	7,45E-03
PNRC1	0,78787905	7,48E-03
TMEM105	2,83130217	7,57E-03
UQCRH	0,55600375	7,96E-03
MTHFD2	0,85921341	7,98E-03
ISG20	0,83960134	7,98E-03
SPTSSA	0,96878773	8,25E-03
AREG	1,97377229	8,71E-03
TAF12	0,95657218	8,71E-03
CEBPB	0,96616888	8,71E-03
SAR1A	0,84520417	8,74E-03
NME1	1,10629034	9,26E-03
SNRPG	0,72796983	9,55E-03
PSMD7	0,86778516	9,82E-03
UBE2Q2	1,06866026	9,88E-03
TUBA1B	0,77845418	9,88E-03
BST2	0,99086571	9,90E-03
GAPDH	0,51430005	1,01E-02
CDH3	1,42403209	1,01E-02
GPX1	0,72705662	1,03E-02
DUSP1	0,89667392	1,05E-02
ECHDC3	1,10962045	1,11E-02
PHLDB2	1,43179703	1,14E-02
TNFAIP1	1,41619730	1,14E-02
MIR4435-2HG	0,83927751	1,18E-02
CXCL5	9,50144958	1,18E-02
MINOS1	0,78189611	1,20E-02
NDUFA11	0,86349100	1,28E-02
SLC34A2	1,75396049	1,30E-02
FAM96B	0,73637223	1,31E-02
SERBP1	0,69657236	1,31E-02
ARL5B	1,08801806	1,36E-02
GBP1	1,69364595	1,37E-02
TNFAIP2	1,78122818	1,39E-02
LGALS7B	3,45571208	1,39E-02
ADAM9	1,09937251	1,46E-02
RAB10	0,73086929	1,49E-02
CAST	0,78275222	1,52E-02
TMOD3	0,84540391	1,56E-02
NCK1	0,99511647	1,60E-02

PKM	0,63358539	1,60E-02
ATP1A1	0,78544497	1,62E-02
TICAM1	1,50168014	1,62E-02
CTSD	0,68588364	1,62E-02
EMC4	0,69395196	1,63E-02
IFT172	1,13159370	1,65E-02
S100A12	6,07681131	1,65E-02
GIPC1	0,76335210	1,70E-02
C12orf29	0,96558428	1,75E-02
C19orf33	1,14319086	1,78E-02
TNFAIP8	2,00322819	1,88E-02
PSMA4	0,71867126	1,89E-02
PITPNC1	1,15524209	1,93E-02
NUTF2	0,73815864	1,93E-02
HSBP1	0,57532287	1,95E-02
LGALS1	0,97059810	1,96E-02
RP11-783K16.5	0,81722516	1,99E-02
DEF8	1,17671132	1,99E-02
MET	1,58427012	2,02E-02
TMEM170A	1,51211226	2,02E-02
ELP5	0,89544219	2,02E-02
EREG	5,14094448	2,07E-02
PRDX4	0,69317222	2,08E-02
BAG3	1,20300496	2,08E-02
ATAD3B	1,32601082	2,10E-02
FAM46A	1,18420851	2,14E-02
GLRX3	0,76648045	2,22E-02
PSMB9	1,41115141	2,22E-02
PPP3CA	1,17333674	2,23E-02
KDELR2	0,64897746	2,26E-02
MSLN	2,32066655	2,33E-02
LBR	0,95804769	2,33E-02
DEDD2	0,89744192	2,35E-02
SOX15	2,29162478	2,35E-02
SAA1	2,29564905	2,35E-02
RHBDL2	1,50497329	2,36E-02
TRIP6	0,72004884	2,45E-02
CXADR	0,82652026	2,46E-02
NAA50	0,70059937	2,46E-02
ITGB6	1,21471989	2,46E-02
PGK1	0,68038607	2,48E-02
TINAGL1	1,50241590	2,54E-02
WNT7B	1,55783868	2,63E-02
RBM17	0,79031807	2,63E-02
CTA-384D8.35	2,16137958	2,70E-02
TMEM39A	0,46681827	2,71E-02
HOPX	3,05744147	2,74E-02
ADGRG1	0,81422210	2,75E-02

AVPI1	1,81236279	2,75E-02
OPTN	1,10766196	2,77E-02
C1S	1,69720638	2,81E-02
PDXK	0,97240710	2,86E-02
RHCG	4,15635061	2,92E-02
FBXW5	0,79493368	2,92E-02
AHNAK2	1,80816364	2,95E-02
LINC00152	0,88886261	2,96E-02
HES2	3,29408312	2,98E-02
SDR16C5	1,48407161	3,02E-02
PSMC1	0,62179351	3,10E-02
RMDN1	1,09162784	3,10E-02
FUT3	1,93259275	3,12E-02
NDRG1	1,25708985	3,12E-02
TAF1D	0,82132661	3,12E-02
B3GNT3	1,89002919	3,13E-02
FAM207A	1,01108754	3,13E-02
PDIA4	0,65804982	3,21E-02
MAP2K1	1,05387783	3,36E-02
CHP1	0,83101618	3,41E-02
USP6NL	1,36134863	3,45E-02
MTFR1	1,11721003	3,48E-02
C3	1,95086658	3,50E-02
NOB1	0,99384654	3,52E-02
ECHDC1	0,97947621	3,60E-02
ATP2A2	0,55587125	3,60E-02
SNAPC1	1,78520358	3,62E-02
LEMD1	1,88031816	3,68E-02
EIF3D	0,61157668	3,68E-02
EIF4A1	0,83891892	3,68E-02
TNFRSF21	0,91714960	3,81E-02
ANXA5	0,68679523	3,82E-02
TUBB3	1,92697883	3,82E-02
TRIB3	0,82880574	3,83E-02
HSPA6	1,67173040	3,83E-02
PYGL	1,38120043	3,83E-02
SF3B3	0,92556643	3,88E-02
DUSP11	0,93086857	3,89E-02
PPP4R1	0,80004215	3,89E-02
ID1	2,03090167	4,05E-02
PSMA3	0,69785136	4,14E-02
CKMT1A	2,21428275	4,17E-02
RBMS1	0,71141499	4,20E-02
SMOC1	1,55761862	4,23E-02
CYCS	0,64234704	4,23E-02
LYAR	1,03327048	4,26E-02
TPST2	1,14527011	4,28E-02
PNP	0,69938445	4,28E-02

CHIC2	1,05512762	4,34E-02
PFKFB3	1,59824133	4,34E-02
RSRC2	0,69093138	4,44E-02
RCC1	0,96957493	4,44E-02
SOCS1	0,85636801	4,44E-02
TAP2	2,22755933	4,44E-02
GSDMC	1,95673704	4,45E-02
RP11-49I11.1	1,43927872	4,45E-02
CALU	0,71564811	4,51E-02
CMTR2	1,02814555	4,55E-02
TP53I3	0,95938796	4,56E-02
ZDHHC12	0,68230939	4,57E-02
TUBB4B	0,62024057	4,63E-02
AKTIP	0,76377422	4,64E-02
MRPL13	0,65822744	4,64E-02
FHL2	0,46196702	4,66E-02
ARID5B	0,82509917	4,78E-02
VKORC1	0,85193175	4,78E-02
NNMT	1,12615013	4,78E-02
CAPN1	0,86168468	4,80E-02
FOSL2	0,74861747	4,92E-02
INO80C	1,03028607	4,98E-02

Index	CXCL1_compare	gene	mean_expression	fraction_expressed	panel
0	CXCL1_negative	CD68	3,13E-01	3,43E-01	Immune_cells
1	CXCL1_negative	CD163	1,85E-01	2,33E-01	Immune_cells
2	CXCL1_negative	S100A8	6,56E-01	5,35E-01	Immune_cells
3	CXCL1_negative	S100A9	3,37E-01	3,71E-01	Immune_cells
4	CXCL1_negative	CD8A	2,08E-01	2,56E-01	Immune_cells
5	CXCL1_negative	GZMB	9,14E-02	1,16E-01	Immune_cells
6	CXCL1_10high	CD68	2,09E-01	1,43E-01	Immune_cells
7	CXCL1_10high	CD163	2,33E-01	1,43E-01	Immune_cells
8	CXCL1_10high	S100A8	7,16E-01	5,00E-01	Immune_cells
9	CXCL1_10high	S100A9	1,52E-01	1,43E-01	Immune_cells
10	CXCL1_10high	CD8A	6,10E-02	7,14E-02	Immune_cells
11	CXCL1_10high	GZMB	0,00E+00	0,00E+00	Immune_cells
12	CXCL1_negative	CD44	1,09E+00	7,94E-01	Stemness_markers
13	CXCL1_negative	ALDH1A1	1,27E-01	1,69E-01	Stemness_markers
14	CXCL1_negative	VIM	2,88E+00	9,74E-01	Stemness_markers
15	CXCL1_negative	ITGA6	3,10E-01	3,86E-01	Stemness_markers
16	CXCL1_negative	KRT14	1,12E+00	7,78E-01	Stemness_markers
17	CXCL1_10high	CD44	6,32E-01	4,29E-01	Stemness_markers
18	CXCL1_10high	ALDH1A1	0,00E+00	0,00E+00	Stemness_markers
19	CXCL1_10high	VIM	2,68E+00	9,29E-01	Stemness_markers
20	CXCL1_10high	ITGA6	4,85E-01	3,57E-01	Stemness_markers
21	CXCL1_10high	KRT14	5,66E-01	4,29E-01	Stemness_markers
22	CXCL1_negative	EPCAM	9,65E-01	7,20E-01	EMT
23	CXCL1_negative	CDH1	7,13E-01	6,31E-01	EMT
24	CXCL1_negative	VIM	2,88E+00	9,74E-01	EMT