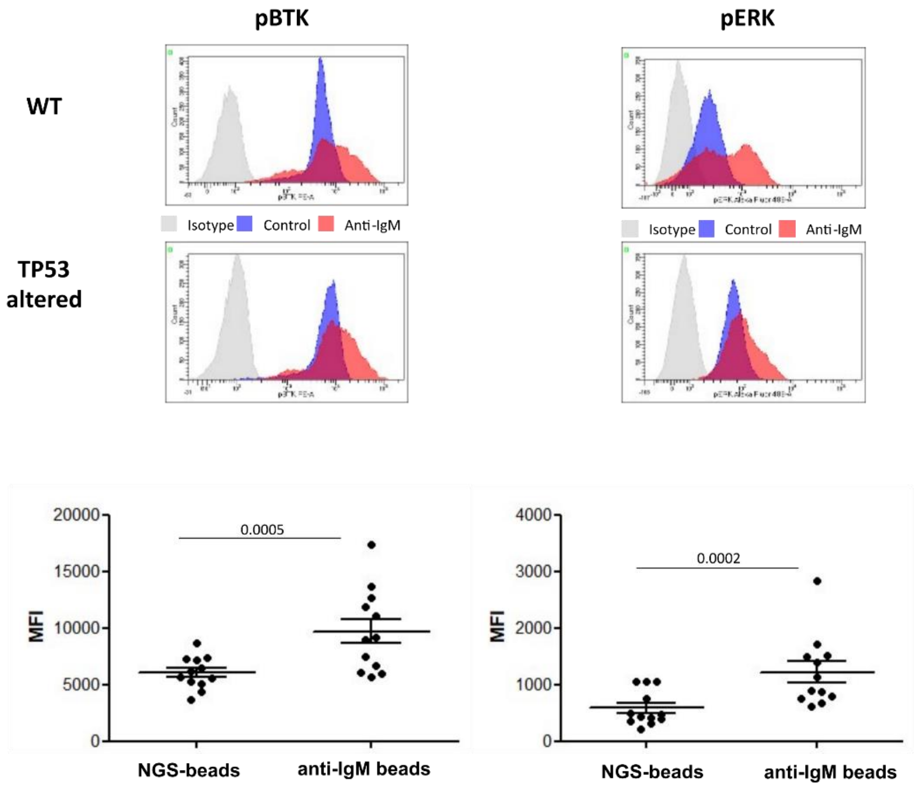
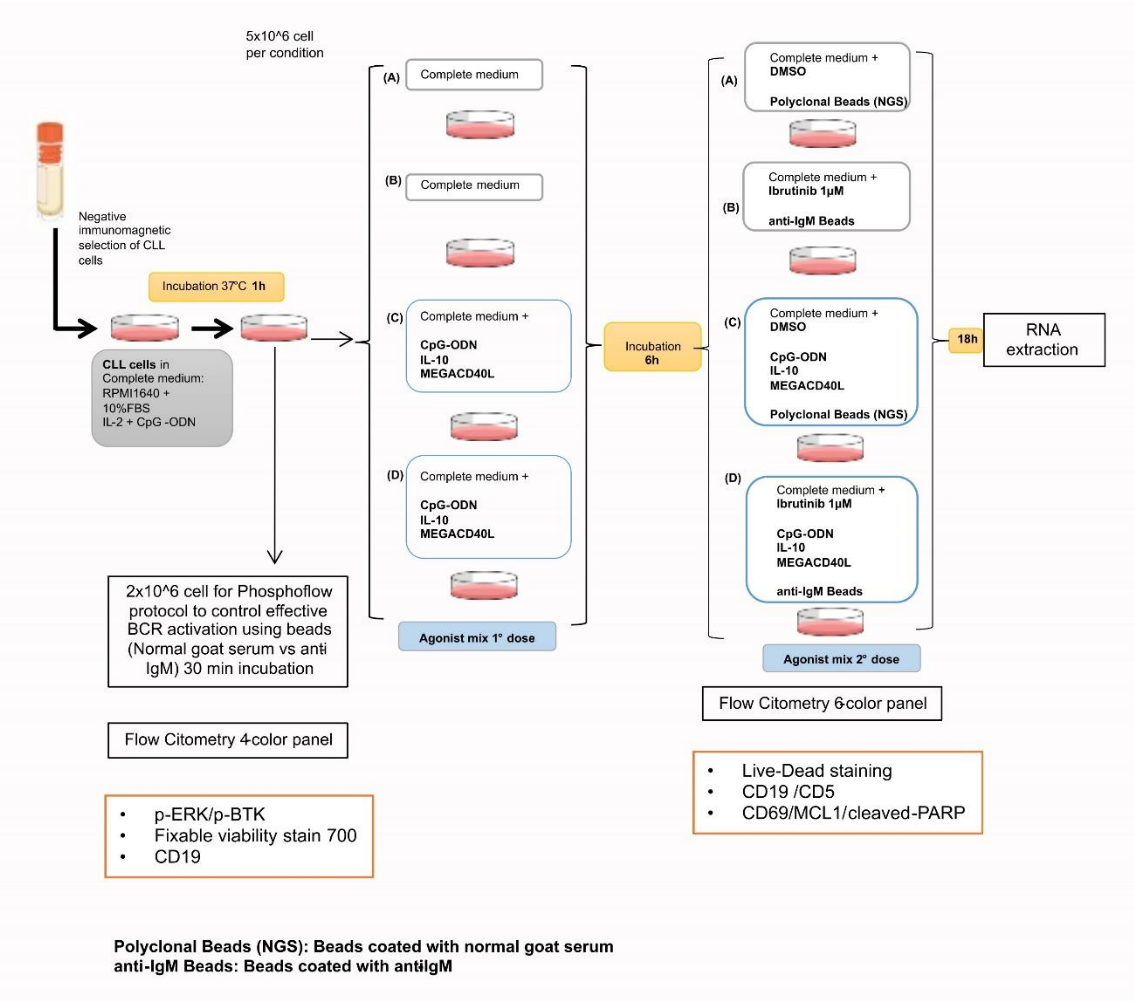
Supplementary Digital Content index:

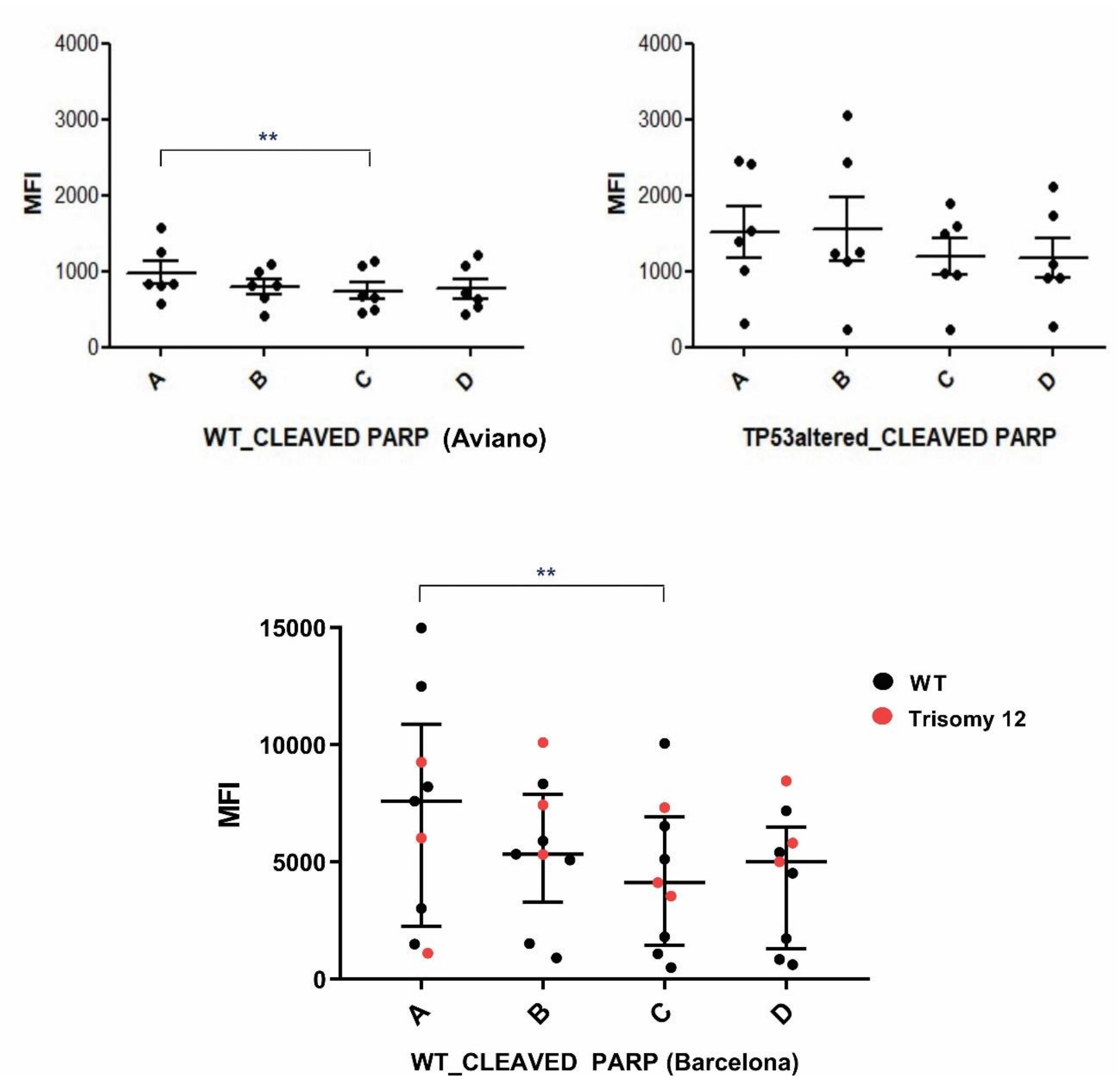


Supplementary Fig.1. Mean fluorescence intensity (MFI) levels of p-ERK and p-BTK measured by flow cytometry (Phosphoflow assay) in primary CLL samples. On the top, a prototypic example of stimulation in WT and *TP53* altered cases. Samples were stimulated for 30 min with beads coated with anti-IgM (anti-IgM beads) compared to beads coated with normal goat serum (NGS beads). Data is shown as mean with SEM.

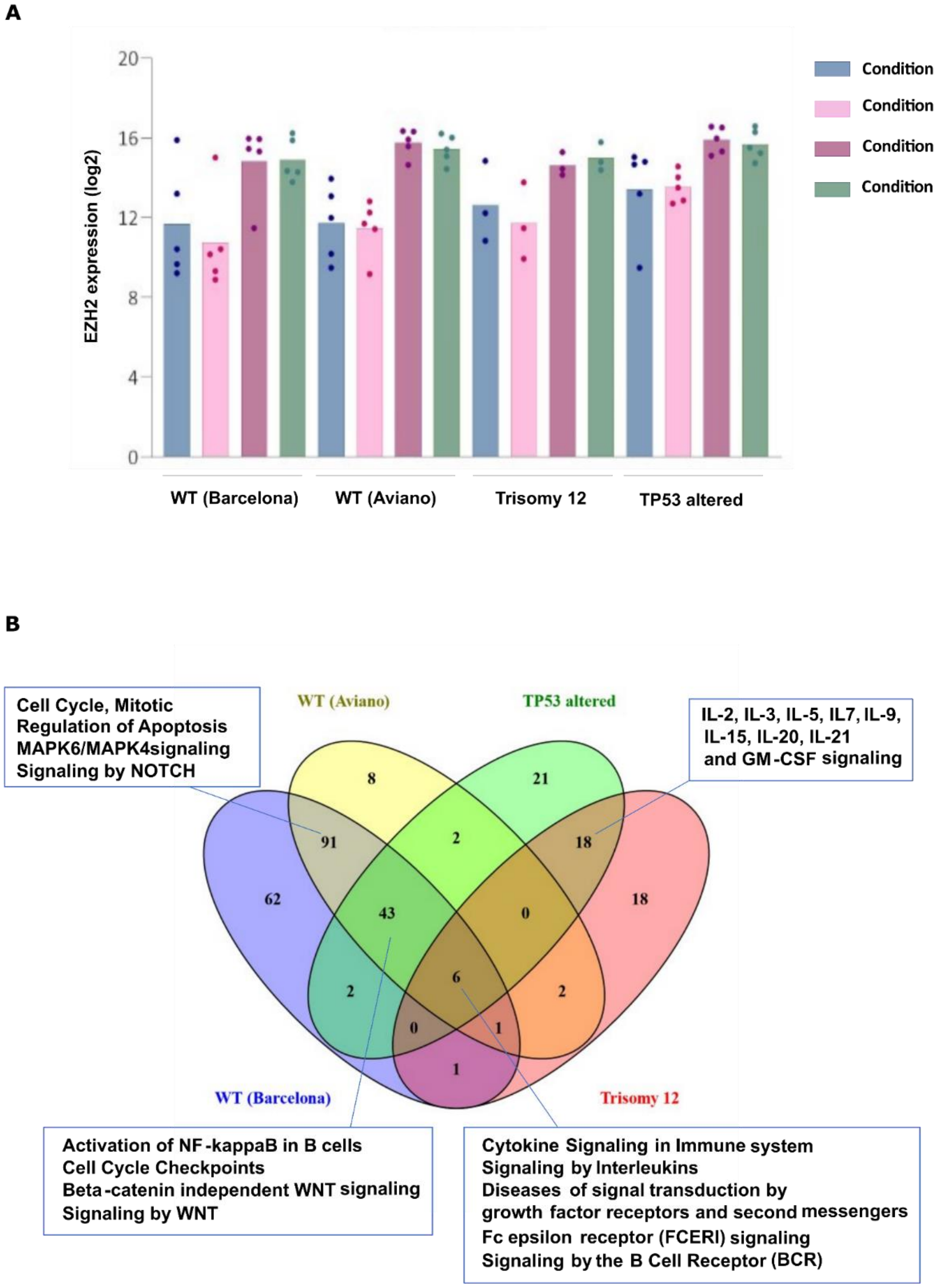


Polyclonal Beads (NGS): Beads coated with normal goat serum
anti-IgM Beads: Beads coated with anti-IgM

Supplementary Fig.2. Depiction of the experimental design with all the stimulations for the screening of the transcriptomic differences associated with microenvironment stimuli agonists in presence or not of ibrutinib.



Supplementary Fig.3. **Cell cytometry analysis of cleaved-PARP expression levels.** Apoptosis measurement by Cleaved-PARP MFI in the different studied cohorts across the different conditions of stimulation. A slight reduction was observed in conditions C and D with agonist mix treatment in the presence or absence of Ibrutinib respect to conditions A and B. In Barcelona cohort reported P-values in red refer to Trisomy 12 cases and black ones to WT cases. Data is shown as mean with standard error of the mean (SEM).



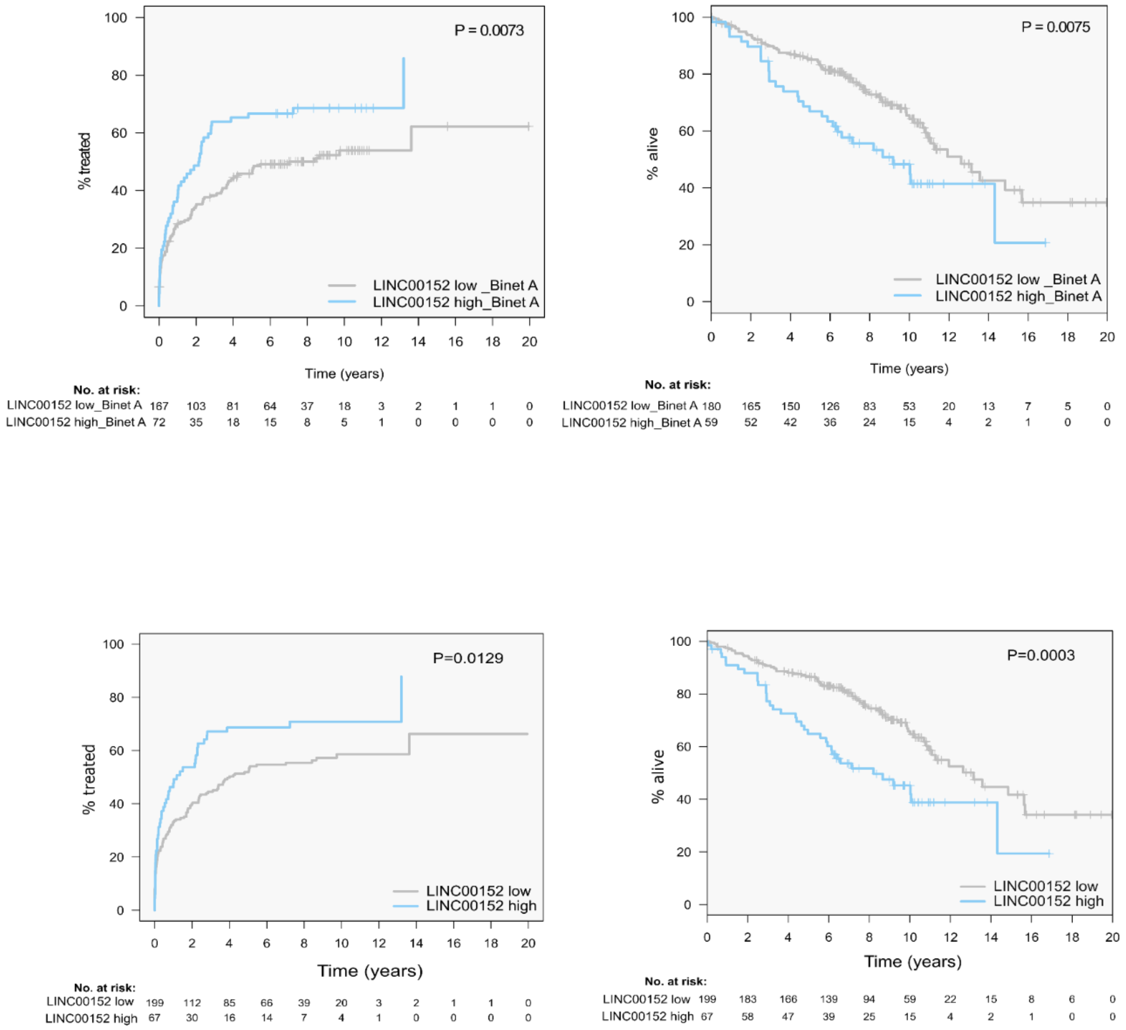
Cell Cycle, Mitotic
Regulation of Apoptosis
MAPK6/MAPK4signaling
Signaling by NOTCH

IL-2, IL-3, IL-5, IL7, IL-9,
IL-15, IL-20, IL-21
and GM-CSF signaling

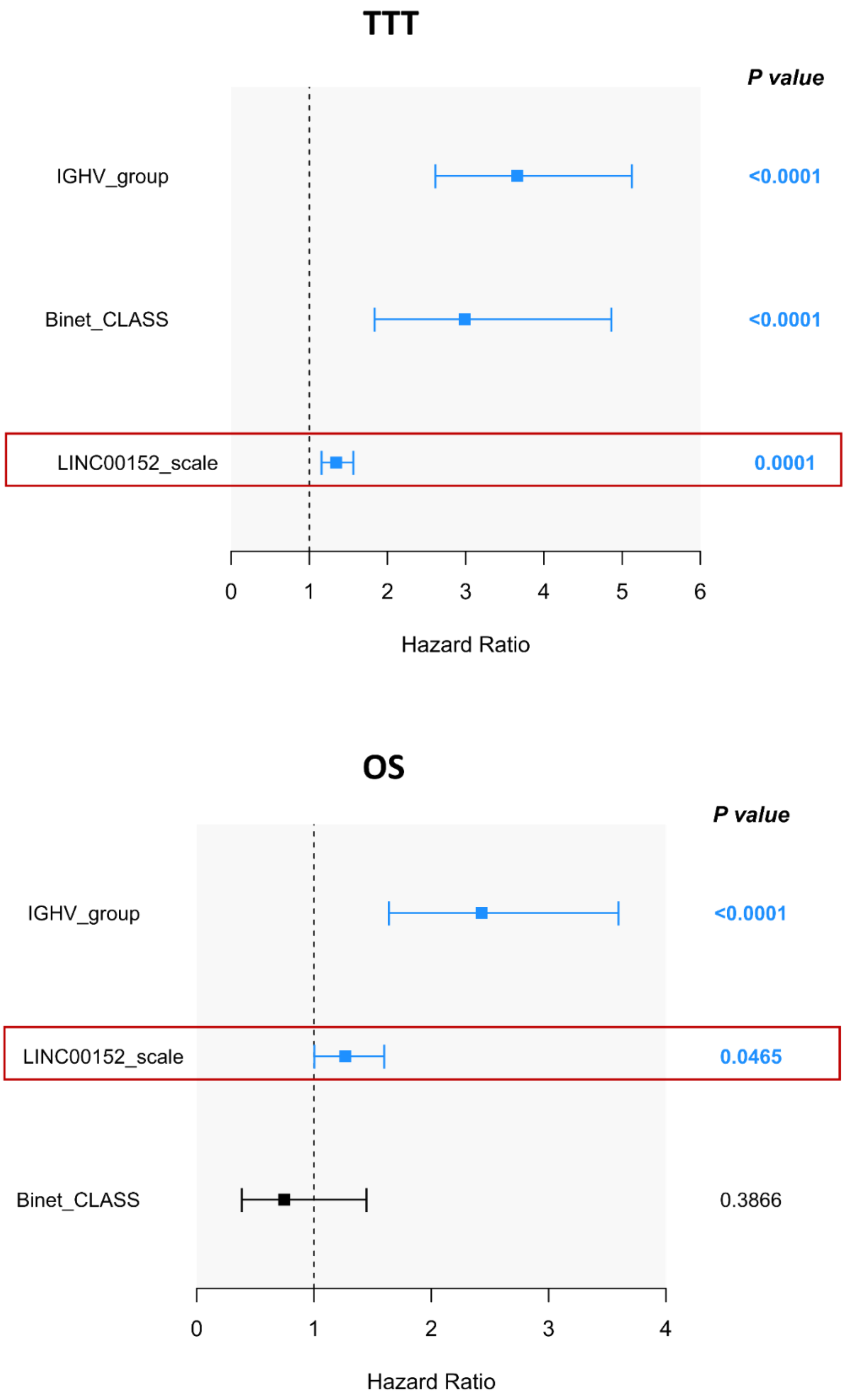
Activation of NF-kappaB in B cells
Cell Cycle Checkpoints
Beta-catenin independent WNT signaling
Signaling by WNT

Cytokine Signaling in Immune system
Signaling by Interleukins
Diseases of signal transduction by
growth factor receptors and second messengers
Fc epsilon receptor (FCERI) signaling
Signaling by the B Cell Receptor (BCR)

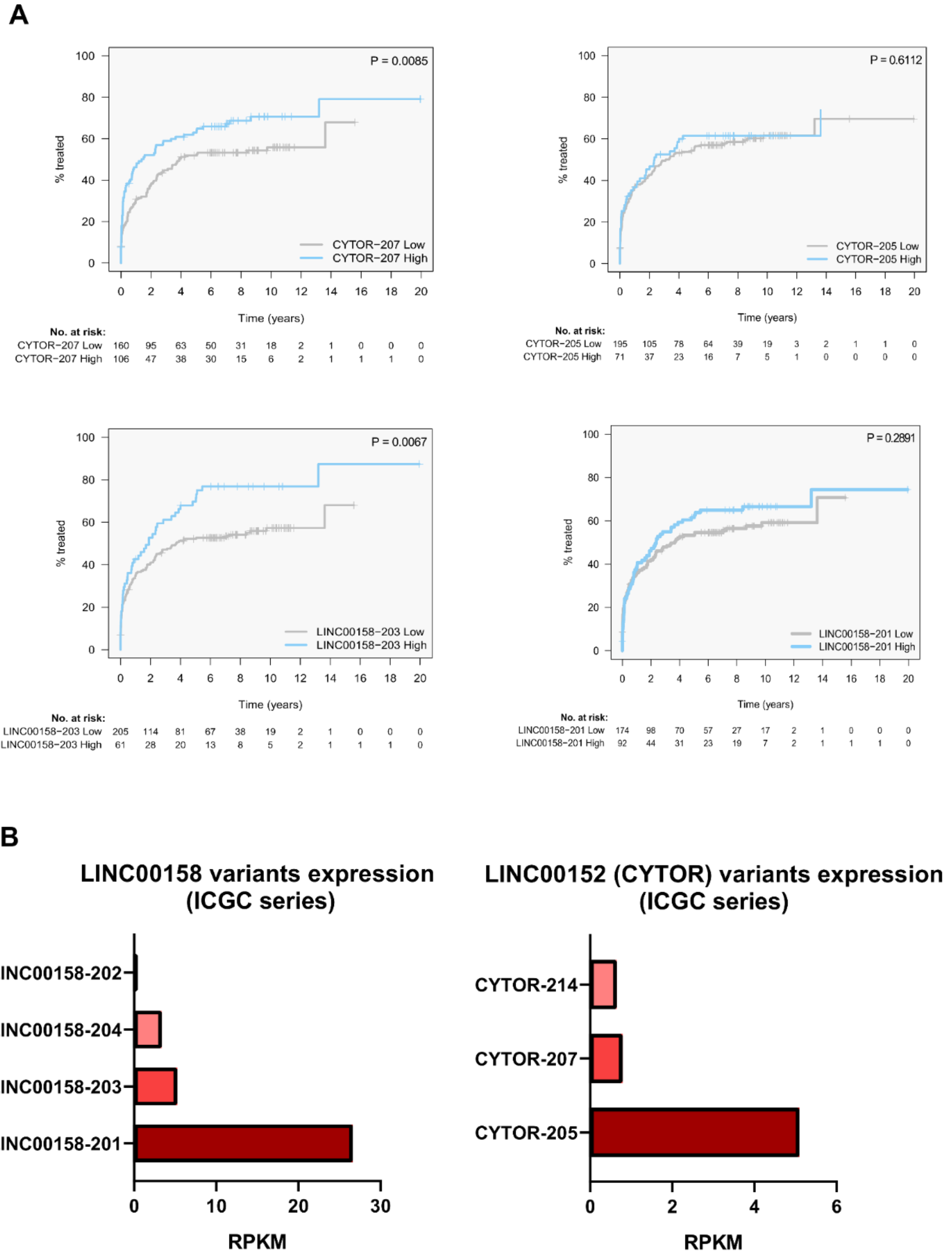
Supplementary Fig.4. **A. *EZH2* expression values were increased in the stimulation of *ex vivo* CLL samples that included the agonist mix (C and D). B. Venn diagram showing numbers of enriched pathways among significantly differentially expressed coding genes modulated by the agonist mix in *ex vivo* experiments (A vs C and B vs D comparisons).** Examples of relevant pathogenetic pathways in CLL are showed in boxes.



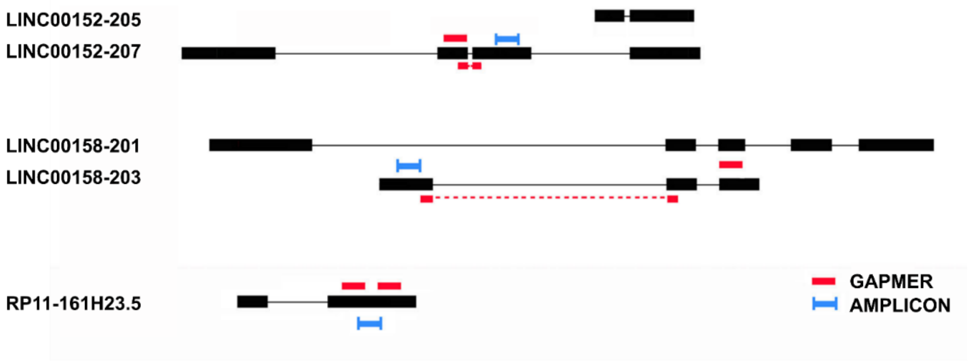
Supplementary Fig.5. CLL cases with high *LINC00152* expression had a significantly shorter TTT and OS than those with low levels, in Binet A alone (top) as including more advanced stages (bottom).



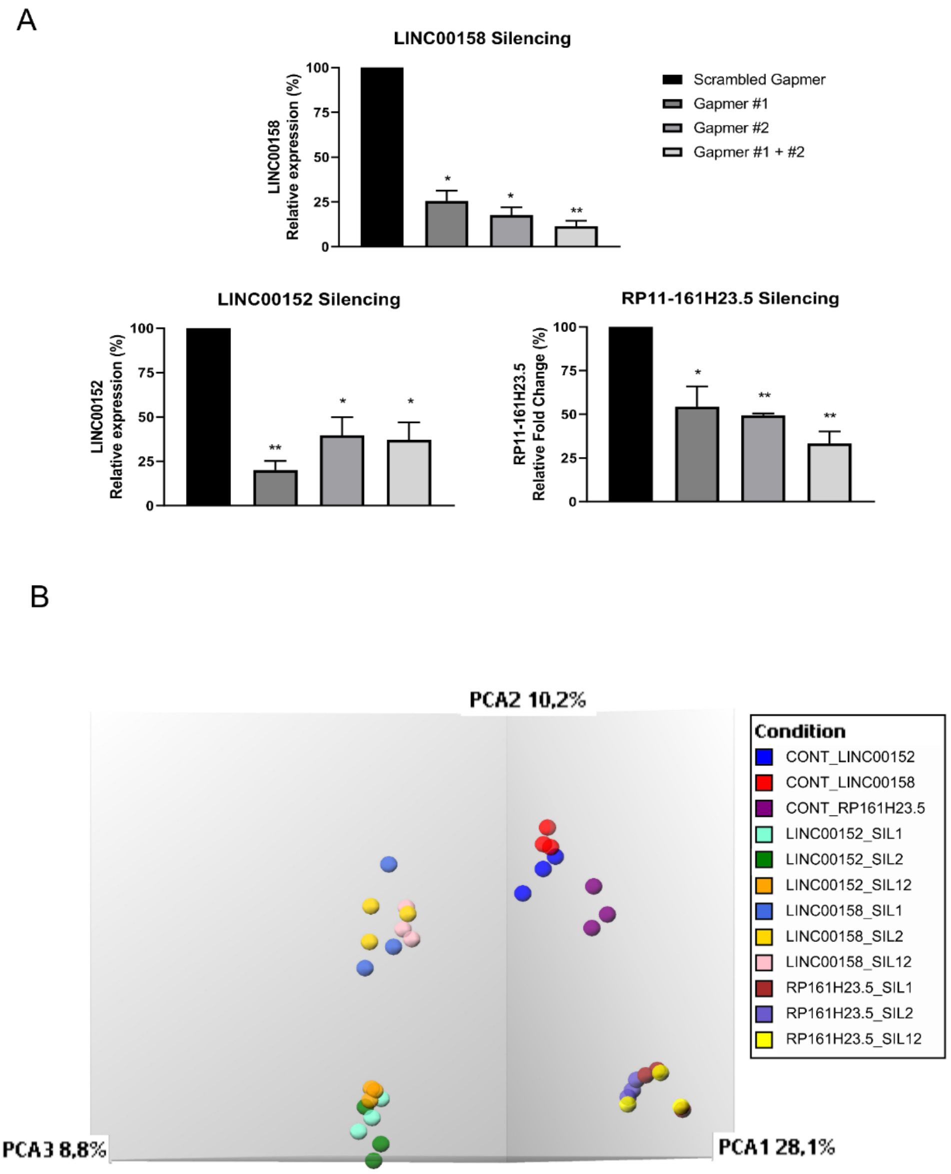
Supplementary Fig.6. *LINC00152* expression as a continuous variable showed independent clinical value in multivariate analyses with other known prognostic factors as Binet stage and IGHV-mutational status groups (ICGC cohort).



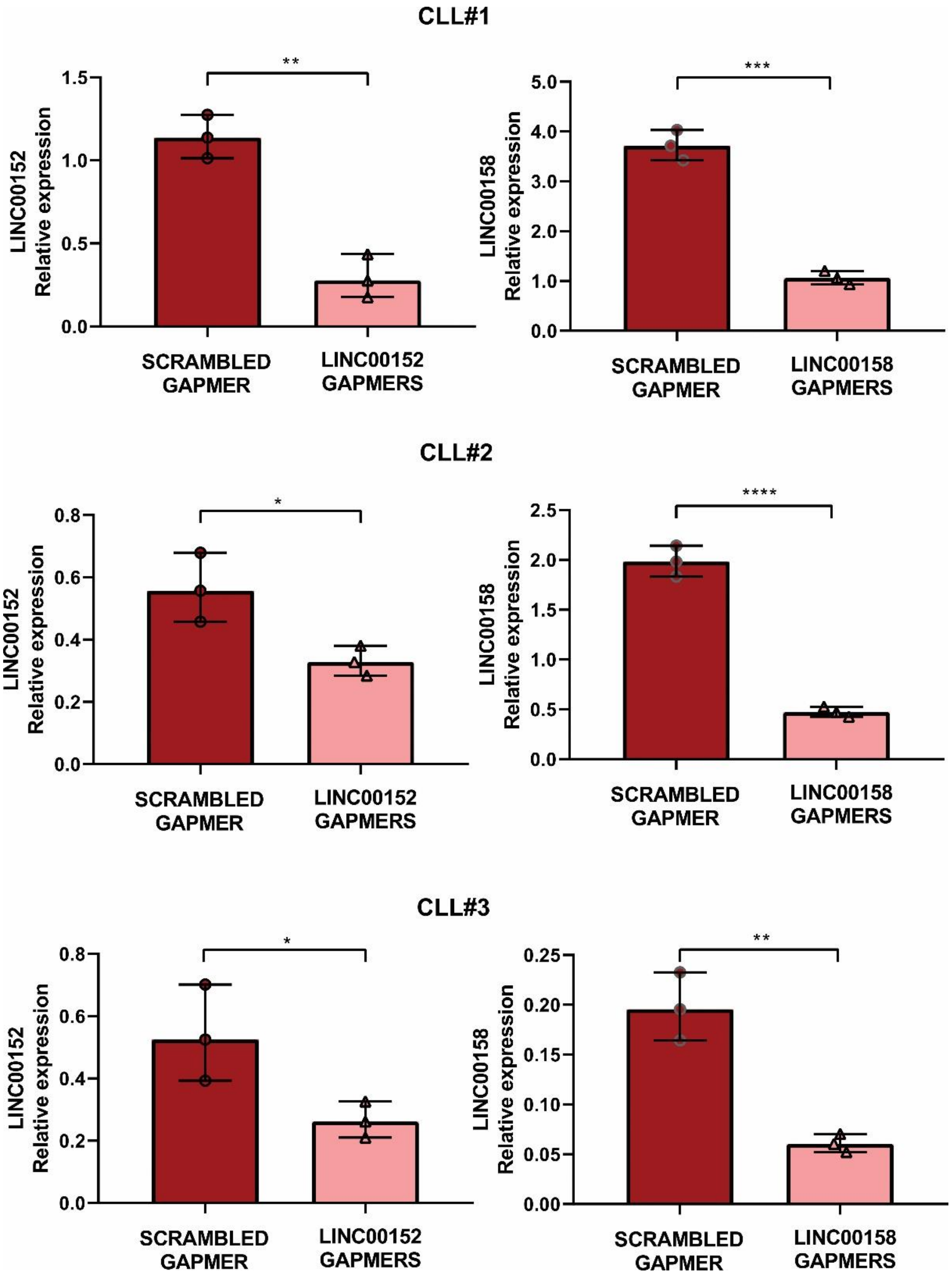
Supplementary Fig.7. A. Kaplan-Meyer curves depicting the shorter TTT associated with high expression of the *LINC00158* transcript variant 203 and *LINC00152* variant 207. These variants showed the most significant clinical impact compared to others from the same lncRNA loci. **B. Levels of the transcript variants of *LINC00158* and *LINC00152* in the ICGC series (266 patients).**



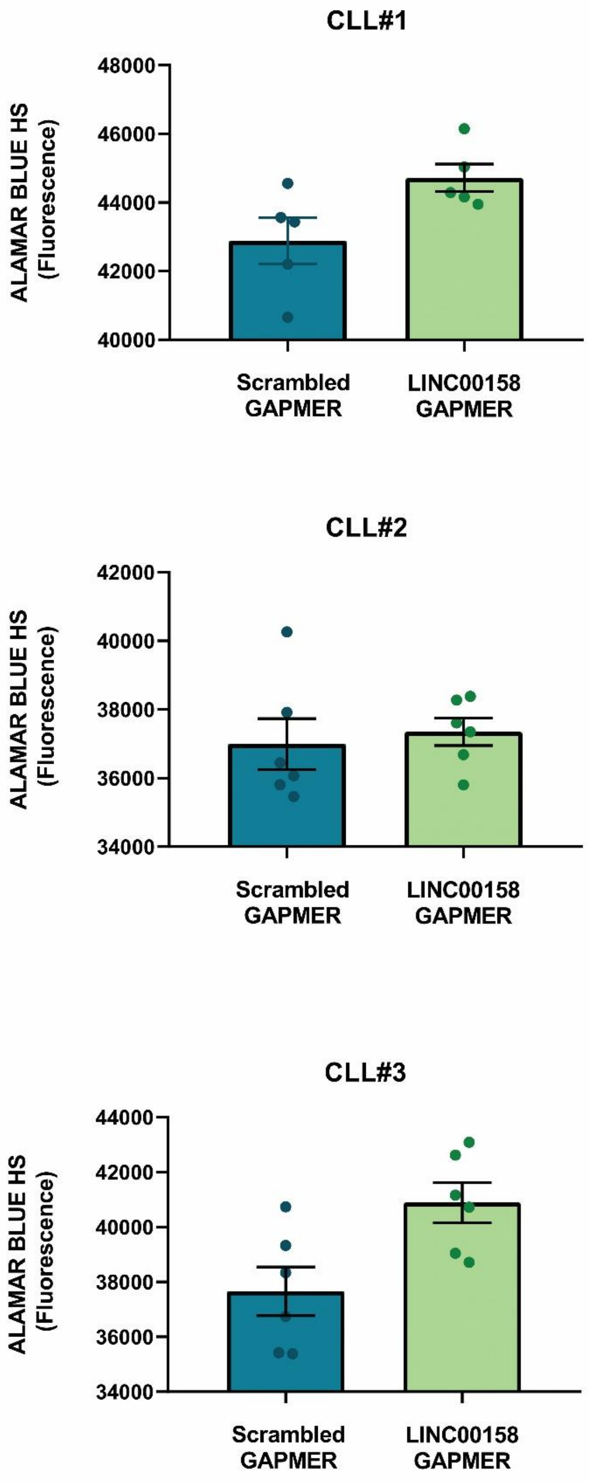
Supplementary Fig.8. Depiction of the Gapmer location to silence the chosen non-coding candidate transcripts and the amplicons to check the expression downregulation upon silencing in MEC-1 cell line.



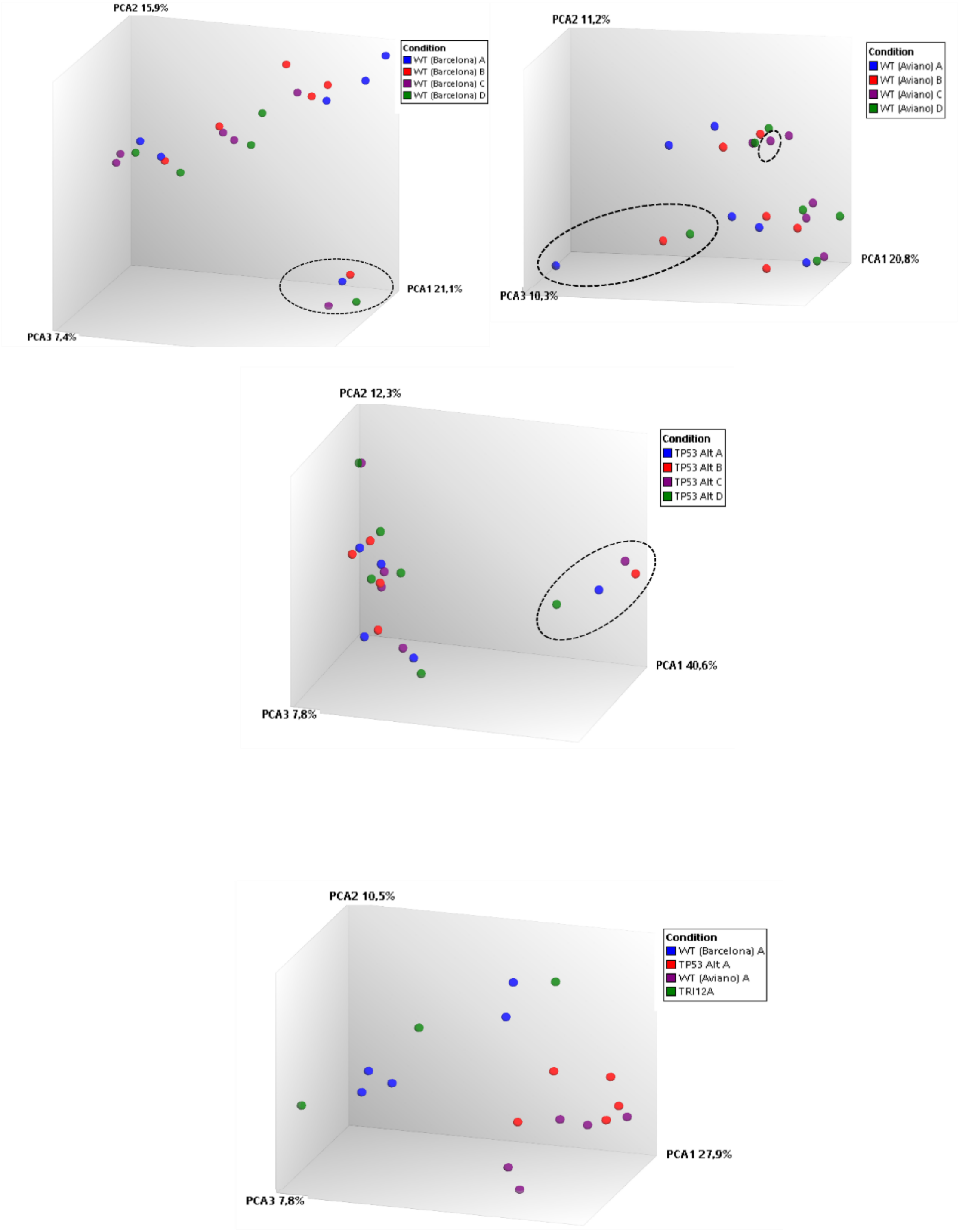
Supplementary Fig.9. A. Silencing degree achieved in MEC-1 cell line of the three lncRNA candidates. Relative expression levels of *LINC00158*, *LINC00152,* and *RP11-161H23.5* upon silencing respect to scrambled Gapmer*.* Data are shown normalized to the median of the corresponding controls and graphics display mean with SEM. **B. Principal Component Analysis (PCA) including all lncRNA/mRNA transcriptomic data showed higher similarity among the negative controls of the different silencing experiments performed for each lncRNA candidate in MEC-1 cell line.** A clear segregation could be observed among the silenced samples by the type of lncRNA assayed by single or combined Gapmer treatments. Abbreviatures: CONT: Control treated with Scrambled Gapmer; SIL: Treated with specific Gapmer #1(1), #2(2) or both (12).



Supplementary Fig.10. Relative expression levels of *LINC00152* and *LINC00158* in silencing experiments in 3 primary CLL samples compared to treatment with scrambled Gapmer. All samples and conditions were treated with the corresponding Gapmers in presence of Ibrutinib together with agonist factors and for all cases the silencing was effective. Significance level (* $p < 0.05$, ** $p < 0.01$, *** $p = 0.001$, **** $p < 0.001$).



Supplementary Fig.11. AlamarBlue HS fluorescence quantification showed the absence of significant variations in cell growth upon LINC00158 silencing in primary CLL samples All samples and conditions were treated with the corresponding Gapmers in presence of Ibrutinib together with agonist factors and for all cases the silencing was effective Significance level (* $p < 0.05$, ** $p < 0.01$, *** $p = 0.001$.



Supplementary Fig.12. Principal Component Analysis (PCA) including all lncRNA/mRNA transcriptomic data from the 4 experimental conditions (top 3 panels) or only control condition A (to see more clearly differences by cohort). Dashed lines marked the samples identified as outliers.

Supplementary Table 1. CLL series analyzed.

CASE CODE	SERIES	ORIGIN	IGHV status	FISH/SNParray*	% CD19	IGHV	TP53 mutations	Number of driver mutations**	CD49d %	CD38 %	ZAP70 %
WT_BCN1	WT	Barcelona	Unmutated	NORM	91***	3-48	wt	0	7	70	10
WT_BCN2	WT	Barcelona	Unmutated	NORM	90	3-33	wt	4	n.a.	6	38
WT_BCN3	WT	Barcelona	Unmutated	NORM	94	1-69	wt	4	n.a.	95	20
WT_BCN4	WT	Barcelona	Unmutated	NORM	91	1-69	wt	1	5	1	14
WT_BCN5	WT †	Barcelona	Unmutated	NORM	86	2-70	wt	5	100	4	79
WT_BCN6	WT	Barcelona	Unmutated	NORM	n.a.	4-39	wt	4	n.a.	45	13
TRI12_1	Trisomy 12	Barcelona	Unmutated	TRIS 12	94	1-18	wt	1	73	88	46
TRI12_2	Trisomy 12	Barcelona	Unmutated	TRIS 12	94	1-3	wt	0	100	68	n.a.
TRI12_3	Trisomy 12	Barcelona	Unmutated	TRIS 12	68	4-39	wt	4	100	98	76
WT_AVI1	WT	Aviano	Unmutated	NORM	95	3-11	wt	2	5	11	49
WT_AVI2	WT †	Aviano	Unmutated	NORM	97.2	3-21	wt	1	2	31.2	12.2
WT_AVI3	WT	Aviano	Unmutated	NORM	96.5	1-69	wt	1	0	11.4	25.1
WT_AVI4	WT	Aviano	Unmutated	DEL13 (95)	95.7	3-49	wt	3	77.3	11.2	21.6
WT_AVI5	WT	Aviano	Unmutated	NORM	97.1	1-69	wt	3	2	1.7	37.2
WT_AVI6	WT †	Aviano	Unmutated	DEL11 (94)	96.7	3-21	wt	3	2.8	69.6	51.9
TP53alt1	TP53 altered	Aviano	Unmutated	DEL17 (95); DEL13 (10)	93.9	1-69	90	1	99.9	19.9	8.7
TP53alt2	TP53 altered	Aviano	Unmutated	DEL17 (68)	92.5	1-2	44.13	1	86.1	42	8.6
TP53alt3	TP53 altered	Aviano	Unmutated	DEL11 (94); DEL17 (5)	95.4	3-30	38.35	2	63.2	0.5	44.9
TP53alt4	TP53 altered	Aviano	Unmutated	TRIS12 (63);DEL13 (80)	90.6	5-51	48	1	99.9	97.8	n.a.
TP53alt5	TP53 altered	Aviano	Unmutated	DEL11 (36);DEL13 (95)	97.7	7-4-1	25	1	64.1	54.6	n.a.
TP53alt6	TP53 altered	Aviano	Unmutated	DEL17 (78)	94.8	3-73	92	1	48	59.4	n.a.

* Only considering alterations with potential impact on Ibrutinib response in CLL. ** Total number of additional mut in drivers. *** From the nearest sample analyzed for this patient. † Outlier in the PCA with Clariom D WT pico. n.a. not analyzed.

Supplementary Table 2. Gapmers, primers and assays used in the functional experiments for lncRNA silencing and monitoring of their expression.

Gene	Transcripts		Gapmers		Primers Sybr Green		Taqman assays
LncRNA	**Variant**	**ENST code**	**Gapmer#1**	**Gapmer#2**	**Forward primer**	**Reverse primer**	**Assay code**
LINC00158	203/201	ENST00000440205.5	GGGTATGGCATGAGTT	GACTAGTTAGAGGTT	CCTGGAAAACTTCCCCCAGT	TGCCTCACGGACTCAAAGAC	Hs00365202_m1 (201)
LINC00152 (CYTOR)	207	ENST00000414584.1	GCATGAGTAGAGAAAA	TCACAGAAGAGTCAAG	TGGAGGCTGGAAGTGCAAA	AAGACTGTGCCAGGAGCTG	Hs03654336_m1
RP11-161H23.5	unique	ENST00000550468.2	GATAGTGCTGACGGAG	CGGGCGCAAAATAGAA	CACAGTGGGAGGCTGGTAAT	TGCCTGTTATACCGTGGTGA	-
U6	-	ENST00000384534 ENST00000383860	-	-	GCTTCGGCAGCACATATACTAA	AACGCTTCACGAATTTGCGT	-
TBP	201-3/206	ENST00000230354 ENST00000392092 ENST00000421512 ENST00000540980	-	-	-	-	Hs00427620_m1
HPRT1	201	ENST00000298556	-	-	-	-	Hs02800695_m1

Supplementary Table 3. Differentially expressed coding genes by agonist mix in absence (C vs A) or presence of Ibrutinib (D vs B).

TP53altered	Fold Change (CvsA)	P-val (CvsA)	Fold Change (DvsB)	P-val (DvsB)
AICDA	8.59	4.43E-02	b.t.	n.s.
NCF2	8.47	9.20E-03	b.t.	n.s.
RFTN1	8.45	1.20E-03	b.t.	n.s.
TNFSF4	7.49	3.18E-02	3.26	4.19E-02
CTH	7.47	8.80E-03	b.t.	n.s.
CLIC2	6.96	7.00E-03	7.86	1.80E-03
ELL2	6.32	8.00E-04	3.8	5.80E-03
PSMB5	6.02	4.21E-02	b.t.	n.s.
TNFRSF9	5.81	2.61E-02	b.t.	n.s.
DDIT4	5.7	2.63E-02	b.t.	n.s.
GPR132	5.37	1.09E-02	9.1	1.00E-03
CDKN1A	5.19	4.08E-02	b.t.	n.s.
PLGRKT	4.73	4.20E-03	b.t.	n.s.
TRAF1	4.59	2.24E-02	6.84	2.15E-02
TRIP10	4.47	9.60E-03	4.12	1.02E-02
KCNN4	4.4	2.40E-03	2.27	4.79E-02
JMY	4.29	3.01E-02	5.39	2.93E-02
TSPAN33	4.23	9.10E-03	2.62	4.65E-02
FLVCR2	4.19	5.80E-03	4.78	3.10E-03
RAB13	4.08	2.01E-02	b.t.	n.s.
LTA	4.03	1.47E-02	3.85	2.61E-02
AIFM2	3.97	1.52E-02	b.t.	n.s.
ETV5	3.87	3.06E-02	b.t.	n.s.
TFEC	3.71	2.72E-02	b.t.	n.s.
TNFAIP3	3.49	4.22E-02	3.68	6.20E-03
CYB5A	3.31	2.20E-03	b.t.	n.s.
SFT2D1	3.25	4.89E-02	b.t.	n.s.

NT5DC2	3.13	2.77E-02	b.t.	n.s.
ARID3A	3.09	2.00E-03	b.t.	n.s.
ARNTL2	3.05	4.84E-02	b.t.	n.s.
CENPW	3.03	3.45E-02	b.t.	n.s.
CARM1	2.96	4.10E-02	b.t.	n.s.
PSMD14	2.96	3.88E-02	b.t.	n.s.
SERF1A	2.87	2.47E-02	1.97	4.36E-02
RAB9A	2.86	1.70E-03	3.44	2.00E-04
ICAM1	2.83	2.50E-03	4.8	2.60E-03
PFN1	2.82	3.47E-02	b.t.	n.s.
KLHL6	2.8	9.60E-03	b.t.	n.s.
HTRA2	2.79	8.00E-04	1.94	1.90E-03
TAGLN2	2.77	3.52E-02	b.t.	n.s.
GLRX2	2.7	4.38E-02	b.t.	n.s.
NFKB2	2.68	1.40E-02	3.77	6.70E-03
HUWE1	2.67	4.25E-02	b.t.	n.s.
SEC11C	2.66	9.00E-04	b.t.	n.s.
TMEM205	2.66	1.16E-02	b.t.	n.s.
TMEM63B	2.66	2.59E-02	4.49	4.12E-02
HELLS	2.62	2.80E-03	b.t.	n.s.
RHOF	2.62	2.60E-03	2.42	1.53E-02
NIT2	2.61	4.24E-02	b.t.	n.s.
COMMD1	2.59	3.50E-02	b.t.	n.s.
HYOU1	2.58	2.24E-02	b.t.	n.s.
MRPS15	2.57	4.89E-02	b.t.	n.s.
RFC2	2.55	7.50E-03	b.t.	n.s.
PDGFA	2.53	4.96E-02	b.t.	n.s.
REEP4	2.48	9.90E-03	b.t.	n.s.
SEC61A2	2.47	1.02E-02	2.34	1.11E-02

MTHFD1	2.46	1.63E-02	b.t.	n.s.
FERMT3	2.44	1.84E-02	b.t.	n.s.
PLAA	2.41	4.60E-02	b.t.	n.s.
ZSWIM4	2.41	5.70E-03	b.t.	n.s.
CYBRD1	2.38	7.30E-03	12.13	4.70E-03
COA1	2.37	3.93E-02	b.t.	n.s.
CSF2RB	2.37	1.47E-02	b.t.	n.s.
CALM3	2.36	2.36E-02	b.t.	n.s.
SLCO5A1	2.35	3.79E-02	3.75	3.63E-02
STAT3	2.33	3.73E-02	b.t.	n.s.
TNFRSF8	2.31	1.50E-02	b.t.	n.s.
PSMD12	2.3	4.49E-02	b.t.	n.s.
POLA2	2.26	7.20E-05	1.82	2.40E-03
LONP1	2.25	3.17E-02	b.t.	n.s.
GTF2H5	2.23	3.21E-02	b.t.	n.s.
OTUD7B	2.23	1.48E-02	b.t.	n.s.
ORC6	2.22	2.34E-02	b.t.	n.s.
VDAC3	2.2	1.50E-02	b.t.	n.s.
EZH2	2.19	1.99E-02	4.41	4.08E-02
STAT5B	2.16	4.70E-03	b.t.	n.s.
ACOT13	2.15	4.99E-02	b.t.	n.s.
CCNB1	2.14	1.71E-02	b.t.	n.s.
NDUFAF5	2.12	3.07E-02	b.t.	n.s.
PPP2R5D	2.1	2.55E-02	b.t.	n.s.
UBL7	2.09	2.63E-02	b.t.	n.s.
CETN3	2.07	4.93E-02	b.t.	n.s.
PSMC4	2.07	4.12E-02	b.t.	n.s.
MORN2	2.06	1.54E-02	b.t.	n.s.
TBCE	2.06	1.87E-02	b.t.	n.s.

FH	2.04	4.41E-02	b.t.	n.s.
NUDT16	2.04	4.18E-02	b.t.	n.s.
SPAG1	2.04	8.20E-03	b.t.	n.s.
ZDHHC18	2.04	6.50E-03	1.67	2.99E-02
COQ3	2.03	3.54E-02	b.t.	n.s.
IL21R	2.03	1.80E-02	1.8	4.82E-02
UNC119	2.03	1.92E-02	b.t.	n.s.
DARS	2.02	1.84E-02	b.t.	n.s.
RDX	2.01	3.09E-02	b.t.	n.s.
IRF4	1.98	4.25E-02	b.t.	n.s.
SPECC1	1.97	2.54E-02	b.t.	n.s.
TP53BP2	1.96	4.00E-02	b.t.	n.s.
ZNF442	1.96	1.26E-02	b.t.	n.s.
FUOM	1.95	3.20E-03	b.t.	n.s.
ULBP1	1.94	1.35E-02	b.t.	n.s.
C15orf65	1.94	3.60E-02	b.t.	n.s.
DCLRE1B	1.94	4.16E-02	b.t.	n.s.
RFFL	1.94	1.93E-02	1.82	2.05E-02
DPCD	1.93	2.23E-02	b.t.	n.s.
GRHPR	1.93	2.94E-02	2.5	3.04E-02
MRPL52	1.93	1.30E-02	b.t.	n.s.
CCDC6	1.91	1.42E-02	2.23	2.05E-02
HMGB3	1.91	3.09E-02	b.t.	n.s.
PCBD2	1.91	3.48E-02	b.t.	n.s.
MCUR1	1.9	4.81E-02	b.t.	n.s.
RBBP9	1.89	9.80E-03	b.t.	n.s.
STAT5A	1.88	9.00E-03	1.8	1.41E-02
ARSB	1.87	2.88E-02	b.t.	n.s.
FAM72A	1.87	4.31E-02	b.t.	n.s.

IL10RB	1.87	4.15E-02	b.t.	n.s.
UQCC3	1.85	2.75E-02	b.t.	n.s.
DNAJC18	1.81	1.37E-02	b.t.	n.s.
FAM72C	1.81	3.21E-02	b.t.	n.s.
MBD2	1.81	2.20E-03	b.t.	n.s.
PLD2	1.81	4.60E-03	b.t.	n.s.
TNIP2	1.81	3.93E-02	b.t.	n.s.
UBQLN2	1.79	2.03E-02	b.t.	n.s.
GLDC	1.79	4.45E-02	b.t.	n.s.
SLC19A1	1.79	2.64E-02	b.t.	n.s.
PCDHB14	1.78	2.21E-02	b.t.	n.s.
MRPL19	1.78	3.38E-02	b.t.	n.s.
UBE4B	1.78	3.06E-02	b.t.	n.s.
GOT2	1.77	1.01E-02	1.83	4.78E-02
CBS	1.76	4.72E-02	b.t.	n.s.
PPP1R7	1.76	4.82E-02	b.t.	n.s.
SUCLG1	1.75	2.71E-02	b.t.	n.s.
RTCA	1.74	2.18E-02	1.54	2.20E-02
POMT1	1.73	1.19E-02	b.t.	n.s.
ARID3B	1.72	3.41E-02	b.t.	n.s.
OLA1	1.72	3.16E-02	b.t.	n.s.
SMG9	1.72	8.80E-03	b.t.	n.s.
TALDO1	1.72	4.70E-02	b.t.	n.s.
AP1AR	1.71	2.27E-02	b.t.	n.s.
SLC27A4	1.71	4.86E-02	b.t.	n.s.
ATOX1	1.7	2.81E-02	b.t.	n.s.
PSMC2	1.7	4.30E-02	b.t.	n.s.
SKA2	1.69	4.46E-02	b.t.	n.s.
SLC12A1	1.69	1.42E-02	b.t.	n.s.

DBI	1.68	4.53E-02	b.t.	n.s.
FAM72B	1.68	1.94E-02	b.t.	n.s.
PGD	1.68	4.14E-02	b.t.	n.s.
BLVRA	1.67	1.30E-03	b.t.	n.s.
HPX	1.67	2.23E-02	b.t.	n.s.
IFT46	1.67	2.20E-02	b.t.	n.s.
SLC26A7	1.67	4.00E-03	b.t.	n.s.
TMEM189-UBE2V1	1.67	3.29E-02	b.t.	n.s.
AIFM1	1.66	3.26E-02	b.t.	n.s.
DTYMK	1.66	3.37E-02	b.t.	n.s.
RHEBL1	1.66	4.76E-02	b.t.	n.s.
RIBC2	1.66	1.62E-02	b.t.	n.s.
TUBE1	1.66	2.88E-02	b.t.	n.s.
NABP2	1.65	3.31E-02	b.t.	n.s.
SCN8A	1.65	4.47E-02	b.t.	n.s.
TFDP2	1.65	4.86E-02	2.08	1.28E-02
GPR3	1.64	8.10E-03	b.t.	n.s.
IER5	1.64	4.50E-02	b.t.	n.s.
PLCB3	1.64	1.18E-02	1.54	2.62E-02
CCDC167	1.62	3.20E-03	b.t.	n.s.
RCAN2	1.62	2.25E-02	b.t.	n.s.
TMEM170B	1.62	1.44E-02	b.t.	n.s.
ACOT7	1.62	2.72E-02	b.t.	n.s.
DECR2	1.62	3.38E-02	b.t.	n.s.
PIGF	1.62	4.74E-02	b.t.	n.s.
SLC6A15	1.62	3.17E-02	b.t.	n.s.
ERICH4	1.61	2.88E-02	b.t.	n.s.
HMBS	1.61	4.98E-02	b.t.	n.s.
MAGEC2	1.61	2.04E-02	b.t.	n.s.

CHRNA9	1.61	3.10E-03	b.t.	n.s.
CLIP2	1.61	2.84E-02	b.t.	n.s.
ELK3	1.61	3.48E-02	b.t.	n.s.
HSPA4L	1.61	2.15E-02	b.t.	n.s.
IPPK	1.61	3.01E-02	b.t.	n.s.
PTDSS2	1.61	2.85E-02	b.t.	n.s.
KRTAP4-7	1.6	4.00E-04	b.t.	n.s.
DES	1.6	9.70E-03	b.t.	n.s.
ERICH2	1.6	2.94E-02	b.t.	n.s.
FBXL2	1.6	2.13E-02	b.t.	n.s.
CYP4F8	1.59	4.00E-04	b.t.	n.s.
MLST8	1.59	3.20E-02	b.t.	n.s.
PIR	1.59	4.38E-02	b.t.	n.s.
MTFR1L	1.58	4.56E-02	b.t.	n.s.
CCL17	1.57	4.32E-02	1.61	2.89E-02
RPS6KA1	1.57	1.39E-02	b.t.	n.s.
GPM6B	1.56	3.15E-02	b.t.	n.s.
RND3	1.56	4.94E-02	b.t.	n.s.
ANKRD7	1.55	2.67E-02	b.t.	n.s.
LRRC49	1.55	2.23E-02	b.t.	n.s.
EPB41L1	1.54	1.50E-03	b.t.	n.s.
RFC3	1.54	4.71E-02	b.t.	n.s.
KIAA0319	1.53	9.10E-03	b.t.	n.s.
ARPC2	1.53	3.60E-03	b.t.	n.s.
GMPS	1.53	4.21E-02	b.t.	n.s.
IRF5	1.53	3.41E-02	b.t.	n.s.
TMEM233	1.53	4.70E-03	b.t.	n.s.
ANP32C	1.52	1.95E-02	b.t.	n.s.
ECT2	1.52	3.36E-02	b.t.	n.s.

GRIN3B	1.52	3.47E-02	b.t.	n.s.
CENPH	1.51	2.78E-02	b.t.	n.s.
CHCHD10	1.51	3.91E-02	b.t.	n.s.
MIA2	1.51	2.21E-02	b.t.	n.s.
STK31	1.51	3.47E-02	b.t.	n.s.
THOP1	1.51	2.14E-02	b.t.	n.s.
FAM98B	1.5	2.91E-02	b.t.	n.s.
SAMD1	1.5	4.67E-02	b.t.	n.s.
ARFGAP3	-1.5	4.68E-02	b.t.	n.s.
NCOA3	-1.5	4.00E-04	b.t.	n.s.
ING5	-1.51	3.88E-02	b.t.	n.s.
LRIG2	-1.51	1.14E-02	b.t.	n.s.
MEX3C	-1.51	4.28E-02	b.t.	n.s.
POLR3GL	-1.51	4.34E-02	b.t.	n.s.
SCML4	-1.51	1.78E-02	b.t.	n.s.
SZT2	-1.51	2.48E-02	b.t.	n.s.
ZNF490	-1.51	7.30E-03	-1.68	3.16E-02
SH3BGRL	-1.52	2.05E-02	b.t.	n.s.
TADA2B	-1.52	1.40E-03	b.t.	n.s.
VPS8	-1.52	4.91E-02	b.t.	n.s.
ZKSCAN8	-1.52	3.30E-03	b.t.	n.s.
ZNF200	-1.52	1.93E-02	b.t.	n.s.
ARL11	-1.53	2.35E-02	b.t.	n.s.
MBNL3	-1.53	5.20E-03	-1.96	2.30E-03
UMAD1	-1.53	3.11E-02	b.t.	n.s.
PNRC2	-1.54	3.08E-02	b.t.	n.s.
SNX16	-1.54	2.48E-02	b.t.	n.s.
EPC1	-1.55	7.90E-03	b.t.	n.s.
ITGB1	-1.55	9.70E-03	b.t.	n.s.

GLRA3	-1.56	2.29E-02	b.t.	n.s.
ZBBX	-1.56	1.25E-02	b.t.	n.s.
ZNF14	-1.56	3.30E-02	b.t.	n.s.
PLEKHA3	-1.57	7.90E-03	b.t.	n.s.
SMAD4	-1.57	3.20E-02	b.t.	n.s.
QRSL1	-1.58	2.32E-02	b.t.	n.s.
TMEM219	-1.58	1.64E-02	b.t.	n.s.
VCPIP1	-1.58	1.49E-02	b.t.	n.s.
DCK	-1.59	3.59E-02	b.t.	n.s.
GRAP2	-1.59	2.18E-02	b.t.	n.s.
HIST4H4	-1.59	4.03E-02	b.t.	n.s.
LHFPL1	-1.59	9.90E-03	b.t.	n.s.
NDRG1	-1.59	2.49E-02	-1.66	3.63E-02
SLC35F5	-1.59	2.39E-02	b.t.	n.s.
C6orf89	-1.6	2.98E-02	b.t.	n.s.
CCDC91	-1.6	3.57E-02	b.t.	n.s.
CHD9	-1.6	2.58E-02	b.t.	n.s.
NFX1	-1.6	4.72E-02	-1.64	1.36E-02
TMEM243	-1.6	2.83E-02	b.t.	n.s.
CD2AP	-1.61	2.20E-02	b.t.	n.s.
RC3H2	-1.61	7.60E-03	b.t.	n.s.
ZNF394	-1.61	4.30E-02	b.t.	n.s.
NOD1	-1.62	2.30E-03	b.t.	n.s.
C5orf56	-1.63	2.04E-02	b.t.	n.s.
DNAJC16	-1.63	3.54E-02	b.t.	n.s.
RASA2	-1.63	3.29E-02	b.t.	n.s.
AMFR	-1.64	4.97E-02	b.t.	n.s.
ZNF597	-1.65	1.40E-02	b.t.	n.s.
AFF4	-1.65	1.90E-02	b.t.	n.s.

MGME1	-1.65	4.37E-02	b.t.	n.s.
PTAR1	-1.65	4.14E-02	b.t.	n.s.
RREB1	-1.65	2.12E-02	b.t.	n.s.
SIRT1	-1.65	9.10E-03	b.t.	n.s.
TBL1X	-1.65	4.34E-02	b.t.	n.s.
ELK4	-1.66	1.13E-02	-1.62	2.28E-02
SENP7	-1.66	2.53E-02	b.t.	n.s.
ZNF611	-1.66	4.19E-02	b.t.	n.s.
C4A	-1.67	3.52E-02	b.t.	n.s.
C4B	-1.67	3.52E-02	b.t.	n.s.
HERPUD2	-1.67	2.97E-02	b.t.	n.s.
CPEB2	-1.68	7.10E-03	b.t.	n.s.
MARCH6	-1.68	3.26E-02	b.t.	n.s.
GRAPL	-1.7	1.20E-02	b.t.	n.s.
ADAM10	-1.7	1.58E-02	b.t.	n.s.
L3HYPDH	-1.7	4.84E-02	b.t.	n.s.
OSBPL11	-1.7	3.84E-02	-1.58	1.86E-02
USP3	-1.7	2.40E-03	b.t.	n.s.
ZNF420	-1.7	1.95E-02	b.t.	n.s.
LCORL	-1.71	5.20E-03	b.t.	n.s.
METTL21A	-1.71	4.90E-03	b.t.	n.s.
TMEM127	-1.73	4.53E-02	b.t.	n.s.
ABCA7	-1.73	4.44E-02	b.t.	n.s.
ANKIB1	-1.73	2.60E-03	-1.63	1.66E-02
IRS1	-1.73	2.80E-03	-1.82	7.70E-03
LIMD1	-1.73	8.00E-03	b.t.	n.s.
ZNF79	-1.73	1.60E-03	b.t.	n.s.
PCF11	-1.74	3.38E-02	b.t.	n.s.
PLEKHG7	-1.75	2.10E-02	b.t.	n.s.

CASP7	-1.75	4.61E-02	b.t.	n.s.
HKR1	-1.75	1.20E-03	-1.83	2.00E-04
P2RY10	-1.75	3.75E-02	b.t.	n.s.
RC3H1	-1.75	8.80E-03	b.t.	n.s.
USPL1	-1.75	3.20E-03	b.t.	n.s.
PIK3AP1	-1.77	4.61E-02	b.t.	n.s.
SYNRG	-1.77	4.50E-03	b.t.	n.s.
ZNF646	-1.78	1.27E-02	b.t.	n.s.
ANKAR	-1.78	2.22E-02	b.t.	n.s.
ARL5B	-1.78	4.39E-02	b.t.	n.s.
GAB3	-1.78	6.80E-03	b.t.	n.s.
TNKS2	-1.78	1.09E-02	b.t.	n.s.
KIAA0513	-1.79	1.81E-02	b.t.	n.s.
RICTOR	-1.79	6.40E-03	b.t.	n.s.
SERGEF	-1.79	2.28E-02	b.t.	n.s.
TMEM64	-1.79	4.39E-02	b.t.	n.s.
TRIM39	-1.8	4.72E-02	b.t.	n.s.
CTDSPL2	-1.8	2.23E-02	b.t.	n.s.
ZNF383	-1.8	2.00E-04	b.t.	n.s.
FNDC3A	-1.81	1.92E-02	-1.63	3.85E-02
LYSMD3	-1.82	3.01E-02	b.t.	n.s.
EFR3A	-1.84	2.99E-02	b.t.	n.s.
TGFBR2	-1.84	1.20E-03	-1.78	3.60E-03
APOL3	-1.85	3.62E-02	b.t.	n.s.
NFATC3	-1.85	1.67E-02	-1.96	5.00E-04
RNF38	-1.85	2.02E-02	b.t.	n.s.
VEZF1	-1.85	2.30E-03	b.t.	n.s.
PARP11	-1.86	1.73E-02	b.t.	n.s.
TULP4	-1.86	5.10E-03	b.t.	n.s.

USP28	-1.86	3.00E-04	b.t.	n.s.
KIAA1147	-1.87	4.06E-02	b.t.	n.s.
PKN2	-1.87	1.08E-02	b.t.	n.s.
TESK2	-1.87	4.12E-02	-3.23	9.90E-03
ZNF429	-1.87	7.20E-03	b.t.	n.s.
AKAP11	-1.88	4.90E-03	b.t.	n.s.
CXXC5	-1.88	4.26E-02	b.t.	n.s.
GCNT2	-1.88	4.44E-02	-2.07	3.80E-02
MORC3	-1.88	2.49E-02	b.t.	n.s.
MGAT5	-1.89	6.00E-03	b.t.	n.s.
SIK3	-1.89	4.84E-02	b.t.	n.s.
TRIM23	-1.9	2.70E-03	b.t.	n.s.
TTBK2	-1.9	1.83E-02	b.t.	n.s.
USP33	-1.9	2.08E-02	b.t.	n.s.
RNF168	-1.91	4.71E-02	b.t.	n.s.
ZNF439	-1.91	2.66E-02	b.t.	n.s.
ARHGEF3	-1.92	2.61E-02	b.t.	n.s.
C2CD5	-1.92	2.56E-02	b.t.	n.s.
CREB1	-1.92	4.30E-02	b.t.	n.s.
KLF11	-1.92	3.10E-02	b.t.	n.s.
PHF19	-1.92	1.85E-02	b.t.	n.s.
VPS13C	-1.92	4.01E-02	b.t.	n.s.
RNF111	-1.93	4.40E-02	b.t.	n.s.
UGT8	-1.93	1.08E-02	b.t.	n.s.
ZNF83	-1.93	6.70E-03	b.t.	n.s.
FBXL4	-1.94	4.18E-02	b.t.	n.s.
TGFBI	-1.94	1.02E-02	b.t.	n.s.
TEC	-1.96	2.00E-03	-1.84	9.80E-03
ZNF184	-1.96	4.55E-02	-1.86	8.40E-03

ZNF852	-1.96	2.41E-02	-1.57	1.52E-02
SLC25A26	-1.97	5.00E-04	b.t.	n.s.
CASP8	-1.97	2.23E-02	b.t.	n.s.
FAM3C	-1.97	6.80E-03	b.t.	n.s.
ZNF860	-1.98	2.80E-03	b.t.	n.s.
ATXN7	-1.99	7.90E-03	b.t.	n.s.
C2CD2	-2	9.40E-03	b.t.	n.s.
CUBN	-2	1.56E-02	b.t.	n.s.
KLHL28	-2	4.10E-03	b.t.	n.s.
SFXN3	-2	8.90E-03	-2.36	2.00E-04
CDCA7L	-2.01	2.62E-02	b.t.	n.s.
PRKD3	-2.01	1.50E-02	-1.5	3.00E-02
ACSS1	-2.02	2.64E-02	-1.51	3.30E-02
CTSS	-2.02	2.78E-02	-1.54	2.64E-02
EAF2	-2.02	2.62E-02	b.t.	n.s.
RPRD2	-2.02	2.60E-02	-1.56	1.22E-02
SIDT1	-2.02	1.90E-03	b.t.	n.s.
RSBN1L	-2.04	1.46E-02	-1.88	6.00E-03
SRGAP2B	-2.04	2.89E-02	b.t.	n.s.
ANK1	-2.05	4.84E-02	b.t.	n.s.
BACH2	-2.05	8.30E-03	b.t.	n.s.
FAM122C	-2.05	3.66E-02	b.t.	n.s.
IL1RAP	-2.05	3.60E-03	b.t.	n.s.
KBTBD8	-2.05	3.40E-02	-2.23	6.80E-03
MAPRE2	-2.05	3.91E-02	-2.26	1.06E-02
PARVG	-2.06	2.25E-02	-1.98	3.40E-02
RPS6KC1	-2.06	2.80E-03	b.t.	n.s.
MGAT1	-2.08	4.90E-03	-2.58	6.99E-05
RAB31	-2.08	3.36E-02	-2.17	2.24E-02

SNX30	-2.08	5.20E-03	-3.19	3.45E-05
MILR1	-2.09	4.30E-03	b.t.	n.s.
SETX	-2.09	3.58E-02	-1.85	8.60E-03
SHISA5	-2.09	1.30E-03	-1.91	4.00E-03
SRSF5	-2.09	4.42E-02	b.t.	n.s.
STK17B	-2.09	1.93E-02	-1.61	4.17E-02
FGD2	-2.11	4.63E-02	b.t.	n.s.
RASA3	-2.12	4.82E-02	-1.77	4.13E-02
SLC25A2	-2.12	4.93E-02	b.t.	n.s.
KANSL1	-2.12	7.40E-03	b.t.	n.s.
KMO	-2.12	5.50E-03	b.t.	n.s.
YPEL2	-2.13	3.57E-02	b.t.	n.s.
CLEC17A	-2.14	6.30E-03	b.t.	n.s.
HEATR6	-2.14	4.00E-03	b.t.	n.s.
ANTXR2	-2.15	4.48E-02	-2.34	2.66E-02
SLC35E2B	-2.16	2.82E-02	b.t.	n.s.
SGK3	-2.21	1.50E-03	-1.71	3.47E-02
ZNF92	-2.21	5.00E-03	b.t.	n.s.
MR1	-2.22	2.11E-02	b.t.	n.s.
EGR1	-2.23	1.78E-02	b.t.	n.s.
HIPK3	-2.23	2.71E-02	-2.11	4.20E-03
PYHIN1	-2.24	4.98E-02	b.t.	n.s.
SAMHD1	-2.24	3.68E-02	-2.91	4.36E-02
KAT2B	-2.25	3.20E-03	-1.95	3.39E-02
RIPK1	-2.25	3.70E-03	b.t.	n.s.
CDKL1	-2.26	1.03E-02	-1.73	4.84E-02
MXI1	-2.26	1.14E-02	b.t.	n.s.
ZNF800	-2.27	2.06E-02	b.t.	n.s.
KAT6B	-2.28	5.00E-04	-1.99	4.58E-02

KHDRBS2	-2.28	1.51E-02	b.t.	n.s.
MARCH8	-2.28	1.01E-02	-1.92	1.13E-02
NSUN6	-2.29	6.90E-03	b.t.	n.s.
ZNF763	-2.3	3.24E-02	b.t.	n.s.
CLEC2D	-2.3	1.33E-02	-1.88	4.32E-02
FAM13B	-2.32	8.30E-03	b.t.	n.s.
KANSL1L	-2.32	2.53E-02	b.t.	n.s.
SLFN5	-2.32	2.85E-02	b.t.	n.s.
GAB1	-2.33	2.40E-03	b.t.	n.s.
KIAA0040	-2.33	9.60E-03	-2.63	4.29E-02
PARP8	-2.33	9.50E-03	-2.14	4.73E-02
ZMYM1	-2.35	2.16E-02	b.t.	n.s.
ELF1	-2.36	3.00E-04	-1.93	3.10E-03
LPAR5	-2.36	2.59E-02	-2.06	2.79E-02
B3GALT4	-2.38	2.99E-02	b.t.	n.s.
C16orf74	-2.38	6.40E-03	b.t.	n.s.
AFTPH	-2.39	9.50E-03	-1.56	2.26E-02
NUB1	-2.39	1.51E-02	b.t.	n.s.
OXR1	-2.39	1.00E-04	b.t.	n.s.
STX7	-2.4	1.02E-02	b.t.	n.s.
GTPBP1	-2.41	1.76E-02	b.t.	n.s.
DMXL1	-2.42	1.20E-03	b.t.	n.s.
KCNJ11	-2.42	1.82E-02	b.t.	n.s.
PDP1	-2.42	2.43E-02	-3.05	3.20E-02
STAT2	-2.42	2.70E-03	-3.48	1.58E-02
ZSWIM6	-2.42	7.00E-04	b.t.	n.s.
FMR1	-2.43	1.26E-02	b.t.	n.s.
PCMTD1	-2.46	3.50E-03	b.t.	n.s.
ADD3	-2.48	4.38E-02	-2.88	2.94E-02

TRIM38	-2.49	9.00E-04	-2.38	6.40E-03
CDK14	-2.51	1.27E-02	-2.8	4.52E-02
TCF4	-2.53	1.04E-02	-1.86	2.14E-02
SGPP1	-2.55	1.70E-03	b.t.	n.s.
SPIN4	-2.55	7.00E-04	b.t.	n.s.
HBP1	-2.55	3.02E-02	b.t.	n.s.
IL10RA	-2.55	2.15E-02	b.t.	n.s.
MBP	-2.55	3.61E-02	-3.45	8.10E-03
NFATC1	-2.55	3.00E-04	-2.08	1.50E-03
SOS1	-2.55	7.70E-03	b.t.	n.s.
PARP3	-2.56	1.50E-03	b.t.	n.s.
SLC15A2	-2.56	4.00E-04	b.t.	n.s.
SYK	-2.57	2.22E-02	b.t.	n.s.
OSBPL10	-2.59	9.40E-03	b.t.	n.s.
TBCC	-2.61	2.58E-02	b.t.	n.s.
GPR155	-2.61	4.57E-02	b.t.	n.s.
SESN1	-2.74	1.25E-02	b.t.	n.s.
SETBP1	-2.77	1.11E-02	-3.72	2.40E-03
DCLRE1C	-2.78	1.00E-04	b.t.	n.s.
IRF7	-2.78	2.11E-02	b.t.	n.s.
LCK	-2.78	2.17E-02	b.t.	n.s.
SKIL	-2.78	3.84E-02	b.t.	n.s.
CD37	-2.81	2.91E-02	b.t.	n.s.
BTG2	-2.83	9.00E-04	-1.93	2.05E-02
DNAJC28	-2.88	4.53E-02	b.t.	n.s.
FCGR2C	-2.88	5.00E-03	-2.6	3.20E-02
FIG4	-2.88	3.80E-03	b.t.	n.s.
JAK2	-2.88	2.03E-02	-1.66	4.80E-02
LMBRD1	-2.88	8.70E-03	-1.83	4.12E-02

HSH2D	-2.99	2.21E-02	b.t.	n.s.
ZCCHC2	-3.03	2.00E-04	-1.58	2.22E-02
PYCARD	-3.11	1.33E-02	-2.24	2.77E-02
RNASE6	-3.12	3.93E-02	-3.72	2.69E-02
TMEM140	-3.15	3.30E-03	-2.14	3.08E-02
EGR3	-3.16	1.52E-02	-1.63	4.58E-02
CDKN1B	-3.17	1.12E-02	-2.18	3.69E-02
FAM117B	-3.17	2.90E-02	b.t.	n.s.
TMEM19	-3.19	8.30E-03	-1.81	2.83E-02
ANXA2R	-3.2	1.80E-03	-3.48	4.07E-02
DDAH2	-3.22	3.42E-02	b.t.	n.s.
PPM1K	-3.24	1.80E-03	b.t.	n.s.
ACSF2	-3.26	2.51E-02	-1.89	1.82E-02
SECISBP2L	-3.26	4.40E-03	b.t.	n.s.
SLC12A6	-3.29	3.80E-03	-2.58	9.20E-03
TNFRSF17	-3.3	4.89E-02	b.t.	n.s.
RASGEF1B	-3.31	4.53E-02	b.t.	n.s.
TNFSF13B	-3.36	9.20E-03	-5.57	9.70E-03
EGR2	-3.39	1.37E-02	-11.4	3.70E-03
NAGK	-3.39	4.94E-02	-3.04	3.18E-02
N4BP1	-3.4	2.20E-03	-1.99	2.59E-02
ZBP1	-3.44	2.15E-02	b.t.	n.s.
HMCES	-3.45	1.05E-02	-3.8	4.50E-03
ORAI2	-3.46	3.38E-02	-3.18	3.33E-02
WSB1	-3.46	4.14E-02	b.t.	n.s.
CXorf21	-3.49	5.30E-03	b.t.	n.s.
SLC39A10	-3.49	2.73E-02	-1.72	6.60E-03
PRICKLE1	-3.5	2.00E-04	-1.95	8.00E-03
LRRN1	-3.51	4.03E-02	b.t.	n.s.

PATL2	-3.52	1.05E-02	b.t.	n.s.
PHKB	-3.53	2.60E-03	b.t.	n.s.
CYB561A3	-3.59	1.57E-02	b.t.	n.s.
INPP5F	-3.61	2.80E-02	b.t.	n.s.
CDC25B	-3.62	3.03E-02	b.t.	n.s.
ADRB2	-3.67	7.84E-07	b.t.	n.s.
LPIN2	-3.69	1.47E-02	b.t.	n.s.
CREBRF	-3.7	1.37E-02	b.t.	n.s.
FGD3	-3.7	1.71E-02	b.t.	n.s.
PTPRC	-3.7	3.27E-02	b.t.	n.s.
BCL2L14	-3.76	1.64E-02	b.t.	n.s.
SAT1	-3.86	7.30E-03	b.t.	n.s.
ST6GAL1	-3.89	5.00E-04	-2.37	1.56E-02
SAMD9	-3.91	3.50E-02	b.t.	n.s.
DDX58	-3.94	5.10E-03	b.t.	n.s.
STAP1	-3.95	4.00E-04	b.t.	n.s.
GGA2	-3.98	1.55E-02	b.t.	n.s.
LGALS9B	-4.02	1.32E-02	b.t.	n.s.
EVL	-4.08	4.00E-04	-2.2	1.11E-02
NCF4	-4.08	5.00E-04	-2.42	9.50E-03
HIVEP2	-4.14	6.30E-03	b.t.	n.s.
ADAMTS6	-4.15	4.91E-02	b.t.	n.s.
TRIM22	-4.15	2.54E-02	b.t.	n.s.
GNAZ	-4.18	3.50E-03	b.t.	n.s.
MAP2	-4.18	1.40E-03	-2.34	4.90E-03
FCGR2B	-4.21	1.00E-02	-3.58	3.11E-02
LDLRAP1	-4.21	3.73E-02	-3.23	1.19E-02
NR1D2	-4.21	1.00E-03	b.t.	n.s.
PLEKHA2	-4.25	5.70E-03	-4	4.90E-03

PTPN22	-4.54	5.00E-04	-4.2	1.20E-03
DDX60L	-4.7	3.70E-03	b.t.	n.s.
MAP3K1	-4.93	2.30E-03	-2.71	1.97E-02
ZNF652	-4.98	1.01E-02	b.t.	n.s.
CD79B	-5.06	9.90E-03	-3.66	1.04E-02
RARRES3	-5.11	1.20E-03	b.t.	n.s.
SSBP2	-5.12	1.58E-02	b.t.	n.s.
DNMBP	-5.15	1.20E-03	-2.39	7.10E-03
CHST12	-5.27	2.00E-04	b.t.	n.s.
SMCHD1	-5.3	1.50E-03	b.t.	n.s.
LAX1	-5.31	4.70E-03	b.t.	n.s.
GLIPR1	-5.32	1.79E-02	b.t.	n.s.
TMEM63A	-5.32	7.10E-03	b.t.	n.s.
CD24	-5.34	4.50E-03	b.t.	n.s.
FAM111B	-5.34	2.92E-02	b.t.	n.s.
CD69	-5.43	8.00E-04	b.t.	n.s.
OAS2	-5.45	3.74E-02	b.t.	n.s.
TRIB1	-5.48	7.30E-03	b.t.	n.s.
SLC44A2	-5.49	1.70E-03	b.t.	n.s.
OASL	-5.57	2.36E-02	b.t.	n.s.
PDE7B	-5.82	1.65E-02	b.t.	n.s.
GRK5	-5.84	1.71E-02	b.t.	n.s.
DDX60	-5.9	3.64E-02	b.t.	n.s.
PIK3IP1	-6.2	3.91E-02	b.t.	n.s.
CYSLTR1	-6.24	1.80E-02	-5	4.13E-02
ALOX5	-6.57	4.92E-02	b.t.	n.s.
CLNK	-6.81	2.98E-02	b.t.	n.s.
SELL	-6.81	3.14E-02	b.t.	n.s.
TXNIP	-7.03	3.00E-03	-4.43	4.30E-03

NT5C3A	-7.07	8.00E-04	b.t.	n.s.
FCMR	-7.29	1.77E-02	-8.41	2.92E-02
UTRN	-7.43	2.40E-03	-3.04	3.63E-02
PRKCE	-7.54	5.00E-04	b.t.	n.s.
GNG7	-8.17	2.84E-02	b.t.	n.s.
PECAM1	-8.22	1.60E-03	-5.7	2.90E-03
TNFSF10	-8.23	4.75E-02	b.t.	n.s.
HERC5	-9.17	4.93E-02	b.t.	n.s.
CD27	-9.26	4.33E-02	-6.26	3.35E-02
SCIMP	-9.62	2.50E-03	-8.11	7.50E-03
MX1	-9.81	2.63E-02	b.t.	n.s.
CTLA4	-10.83	2.71E-02	-8.81	1.89E-02
MX2	-13.66	6.40E-03	-8.47	1.99E-02
OAS1	-14.84	1.10E-03	-5.09	4.80E-02
ISG15	-16.75	3.28E-02	b.t.	n.s.
CLMN	-18.03	1.70E-03	-4.98	8.70E-03
IFIT2	-21.84	3.70E-03	b.t.	n.s.
RNASET2	-23.18	8.40E-03	-11.18	3.70E-03
LY86	-23.52	3.77E-05	-7.92	1.50E-03
IFI6	-40.37	1.67E-02	b.t.	n.s.
METTL7A	-45.92	8.60E-03	-8.02	1.77E-02
ID3	-47.42	2.40E-03	-27.39	1.80E-03
IFIT3	-63.03	1.92E-02	b.t.	n.s.
IFIT1	-64.88	2.30E-03	b.t.	n.s.
CCR6	-71.28	4.80E-03	-14.23	1.48E-02
GPR183	b.t.	n.s.	8.77	6.90E-03
ARHGAP31	b.t.	n.s.	4.82	4.67E-02
ADAMDEC1	b.t.	n.s.	4.62	2.06E-02
ST8SIA4	b.t.	n.s.	3.86	1.55E-02

NFKBIA	b.t.	n.s.	3.41	5.30E-03
JUN	b.t.	n.s.	3.3	9.00E-03
EPS15	b.t.	n.s.	3.1	4.28E-02
TCFL5	b.t.	n.s.	3.02	1.02E-02
FANCA	b.t.	n.s.	2.7	7.60E-03
ERO1B	b.t.	n.s.	2.21	1.41E-02
NR6A1	b.t.	n.s.	2.19	2.23E-02
AURKA	b.t.	n.s.	2.02	1.65E-02
PLA2G4C	b.t.	n.s.	1.98	3.60E-02
KIF1C	b.t.	n.s.	1.84	4.78E-02
TMEM161A	b.t.	n.s.	1.82	8.10E-03
IRAK1BP1	b.t.	n.s.	1.79	2.37E-02
SPINK14	b.t.	n.s.	1.78	3.90E-03
ZC3HC1	b.t.	n.s.	1.76	5.00E-04
CNTNAP4	b.t.	n.s.	1.72	4.00E-04
ATP1A4	b.t.	n.s.	1.69	4.70E-03
ORC5	b.t.	n.s.	1.58	4.82E-02
OR10H2	b.t.	n.s.	1.53	1.00E-02
TTC26	b.t.	n.s.	1.53	5.80E-03
GNGT1	b.t.	n.s.	1.51	4.97E-02
PAX6	b.t.	n.s.	1.51	1.48E-02
VCAN	b.t.	n.s.	1.51	1.60E-03
ZFHX2	b.t.	n.s.	1.51	6.83E-05
MARVELD3	b.t.	n.s.	1.5	2.36E-02
OR51I2	b.t.	n.s.	-1.5	1.24E-02
CNPPD1	b.t.	n.s.	-1.5	3.60E-02
EFCAB14	b.t.	n.s.	-1.5	1.01E-02
SRGAP3	b.t.	n.s.	-1.5	3.54E-02
YWHAZ	b.t.	n.s.	-1.5	3.66E-02

TAS2R1	b.t.	n.s.	-1.51	7.30E-03
CALM1	b.t.	n.s.	-1.51	3.88E-02
SIGIRR	b.t.	n.s.	-1.51	4.00E-04
EXOC8	b.t.	n.s.	-1.52	4.10E-02
PPEF2	b.t.	n.s.	-1.52	4.15E-02
SPN	b.t.	n.s.	-1.52	4.34E-02
STK26	b.t.	n.s.	-1.52	3.99E-02
ACADM	b.t.	n.s.	-1.53	3.73E-02
CNST	b.t.	n.s.	-1.53	2.34E-02
GIN1	b.t.	n.s.	-1.53	1.28E-02
HP1BP3	b.t.	n.s.	-1.53	2.03E-02
PITX2	b.t.	n.s.	-1.53	2.99E-02
RNF185	b.t.	n.s.	-1.53	3.48E-02
ZNF468	b.t.	n.s.	-1.53	2.80E-03
HEATR5B	b.t.	n.s.	-1.54	3.97E-02
ITGB7	b.t.	n.s.	-1.54	2.27E-02
ZBTB33	b.t.	n.s.	-1.54	2.44E-02
FLT1	b.t.	n.s.	-1.55	1.00E-03
SEC16A	b.t.	n.s.	-1.55	1.96E-02
STARD3	b.t.	n.s.	-1.55	3.02E-02
CCDC88C	b.t.	n.s.	-1.56	4.07E-02
MIDN	b.t.	n.s.	-1.56	8.60E-03
PQLC2	b.t.	n.s.	-1.57	3.27E-02
PRKCZ	b.t.	n.s.	-1.57	1.75E-02
VPREB3	b.t.	n.s.	-1.58	3.66E-02
DCUN1D3	b.t.	n.s.	-1.58	7.80E-03
KDM3A	b.t.	n.s.	-1.58	2.39E-02
RAB38	b.t.	n.s.	-1.59	8.40E-03
CASP9	b.t.	n.s.	-1.59	3.17E-02

LRCH4	b.t.	n.s.	-1.59	1.56E-02
SHC1	b.t.	n.s.	-1.59	1.55E-02
ZNF699	b.t.	n.s.	-1.59	1.52E-02
ANKS4B	b.t.	n.s.	-1.6	1.30E-02
CD6	b.t.	n.s.	-1.6	3.88E-02
CTSZ	b.t.	n.s.	-1.6	3.73E-02
ITGAE	b.t.	n.s.	-1.6	3.20E-02
TAF4	b.t.	n.s.	-1.6	3.71E-02
LRP10	b.t.	n.s.	-1.61	3.93E-02
TNFSF12	b.t.	n.s.	-1.61	3.54E-02
PTCHD3	b.t.	n.s.	-1.62	3.06E-02
CHAMP1	b.t.	n.s.	-1.62	1.71E-02
FABP3	b.t.	n.s.	-1.62	2.00E-03
RNFT1	b.t.	n.s.	-1.62	1.88E-02
TNFSF12-TNFSF13	b.t.	n.s.	-1.63	2.43E-02
ECI2	b.t.	n.s.	-1.65	4.66E-02
RAP1GAP2	b.t.	n.s.	-1.65	4.20E-02
REPS2	b.t.	n.s.	-1.65	2.71E-02
CH25H	b.t.	n.s.	-1.66	2.01E-02
ZNF768	b.t.	n.s.	-1.66	3.56E-02
TMEM53	b.t.	n.s.	-1.66	4.08E-02
TRIM69	b.t.	n.s.	-1.66	4.31E-02
WIPF1	b.t.	n.s.	-1.66	1.77E-02
DEF6	b.t.	n.s.	-1.67	1.06E-02
GPR82	b.t.	n.s.	-1.67	2.30E-03
SBF1	b.t.	n.s.	-1.67	4.13E-02
SRP68	b.t.	n.s.	-1.67	8.90E-03
DENND2C	b.t.	n.s.	-1.68	1.80E-02
ANKMY2	b.t.	n.s.	-1.69	1.56E-02

FOXN2	b.t.	n.s.	-1.69	1.73E-02
ZNF610	b.t.	n.s.	-1.69	1.88E-02
FAM78A	b.t.	n.s.	-1.7	2.39E-02
CTBP1	b.t.	n.s.	-1.71	2.84E-02
CUL4B	b.t.	n.s.	-1.71	4.74E-02
DENND6A	b.t.	n.s.	-1.71	1.66E-02
MOB3B	b.t.	n.s.	-1.71	6.00E-03
MTM1	b.t.	n.s.	-1.71	4.56E-02
DCLK2	b.t.	n.s.	-1.72	2.02E-02
KIAA1109	b.t.	n.s.	-1.73	1.67E-02
SERTAD1	b.t.	n.s.	-1.73	1.74E-02
PTPRJ	b.t.	n.s.	-1.74	4.80E-02
SMYD2	b.t.	n.s.	-1.74	3.82E-02
FAM102B	b.t.	n.s.	-1.76	4.68E-02
FBXW11	b.t.	n.s.	-1.76	4.20E-03
HPS3	b.t.	n.s.	-1.77	1.30E-03
SAMD3	b.t.	n.s.	-1.77	9.10E-03
IRS2	b.t.	n.s.	-1.78	1.87E-02
ANXA11	b.t.	n.s.	-1.79	4.99E-02
SLC46A3	b.t.	n.s.	-1.79	4.07E-02
BTBD2	b.t.	n.s.	-1.8	4.68E-02
OSBPL3	b.t.	n.s.	-1.8	2.66E-02
FAM81A	b.t.	n.s.	-1.81	2.59E-02
MBNL1	b.t.	n.s.	-1.81	2.18E-02
RAB27B	b.t.	n.s.	-1.81	4.21E-02
TBC1D1	b.t.	n.s.	-1.81	2.54E-02
ABHD17A	b.t.	n.s.	-1.82	2.60E-03
CRTAP	b.t.	n.s.	-1.82	4.36E-02
HCST	b.t.	n.s.	-1.82	3.04E-02

PCYOX1	b.t.	n.s.	-1.82	1.94E-02
JAZF1	b.t.	n.s.	-1.84	4.02E-02
RASGEF1A	b.t.	n.s.	-1.84	2.77E-02
CD5	b.t.	n.s.	-1.85	4.02E-02
TRIM14	b.t.	n.s.	-1.85	1.35E-02
CHML	b.t.	n.s.	-1.86	3.20E-03
HMOX1	b.t.	n.s.	-1.87	3.22E-02
PARP4	b.t.	n.s.	-1.87	3.00E-02
SMURF2	b.t.	n.s.	-1.87	2.02E-02
PPP2R5C	b.t.	n.s.	-1.88	2.24E-02
SIPA1L3	b.t.	n.s.	-1.88	4.44E-02
C16orf72	b.t.	n.s.	-1.9	1.98E-02
CMTM3	b.t.	n.s.	-1.9	1.00E-03
PNPLA8	b.t.	n.s.	-1.92	4.13E-02
S1PR4	b.t.	n.s.	-1.92	6.20E-03
SIPA1	b.t.	n.s.	-1.92	3.49E-02
ATP6V0D1	b.t.	n.s.	-1.95	2.82E-02
GMFG	b.t.	n.s.	-1.97	2.18E-02
KIF16B	b.t.	n.s.	-1.99	3.85E-02
IL12RB1	b.t.	n.s.	-2.02	9.50E-03
IER2	b.t.	n.s.	-2.04	4.00E-02
QPCT	b.t.	n.s.	-2.04	3.51E-02
TMEM117	b.t.	n.s.	-2.05	6.60E-03
SRGAP2	b.t.	n.s.	-2.07	2.81E-02
IL7	b.t.	n.s.	-2.08	4.60E-02
FXYD7	b.t.	n.s.	-2.1	6.50E-03
SIGLEC6	b.t.	n.s.	-2.11	2.00E-04
MARCH3	b.t.	n.s.	-2.13	3.50E-03
SOWAHD	b.t.	n.s.	-2.14	7.00E-04

ELMSAN1	b.t.	n.s.	-2.15	1.33E-02
LCP2	b.t.	n.s.	-2.15	2.59E-02
RPA1	b.t.	n.s.	-2.15	2.56E-02
AKAP6	b.t.	n.s.	-2.18	3.32E-02
MMP14	b.t.	n.s.	-2.18	1.83E-02
PHTF2	b.t.	n.s.	-2.19	1.96E-02
ARHGAP12	b.t.	n.s.	-2.21	1.20E-03
SP4	b.t.	n.s.	-2.21	2.00E-02
DOK3	b.t.	n.s.	-2.22	1.16E-02
COTL1	b.t.	n.s.	-2.26	1.54E-02
DHRS1	b.t.	n.s.	-2.28	4.90E-02
FAM117A	b.t.	n.s.	-2.29	1.15E-02
RAC2	b.t.	n.s.	-2.29	4.73E-02
APBB1IP	b.t.	n.s.	-2.3	4.80E-02
GFOD1	b.t.	n.s.	-2.3	3.45E-02
ITGAL	b.t.	n.s.	-2.3	2.84E-02
MSRA	b.t.	n.s.	-2.31	2.29E-02
ZBTB38	b.t.	n.s.	-2.36	3.13E-02
APAF1	b.t.	n.s.	-2.4	4.91E-02
RBM43	b.t.	n.s.	-2.44	3.40E-03
ASAH1	b.t.	n.s.	-2.47	4.23E-02
EMP1	b.t.	n.s.	-2.47	4.30E-05
VAT1	b.t.	n.s.	-2.53	2.68E-02
ZNF791	b.t.	n.s.	-2.54	4.98E-02
XKRX	b.t.	n.s.	-2.55	3.35E-02
VAMP5	b.t.	n.s.	-2.56	3.70E-02
SIT1	b.t.	n.s.	-2.57	2.65E-02
DDIT3	b.t.	n.s.	-2.59	1.80E-02
SLC37A2	b.t.	n.s.	-2.6	8.00E-03

PHEX	b.t.	n.s.	-2.69	1.22E-02
LY6E	b.t.	n.s.	-2.74	4.98E-02
TSPO	b.t.	n.s.	-2.75	2.65E-02
CTNNA1	b.t.	n.s.	-2.77	2.67E-02
PKIA	b.t.	n.s.	-2.77	1.82E-02
ACP5	b.t.	n.s.	-2.81	7.04E-05
CD52	b.t.	n.s.	-2.81	7.80E-03
STX10	b.t.	n.s.	-2.82	4.26E-02
TMEM156	b.t.	n.s.	-2.82	4.60E-02
IL18BP	b.t.	n.s.	-2.92	1.51E-02
TMC8	b.t.	n.s.	-2.92	2.20E-03
KDM7A	b.t.	n.s.	-2.96	4.51E-02
PDLIM1	b.t.	n.s.	-3.02	1.80E-03
MAP4K1	b.t.	n.s.	-3.22	2.18E-02
ARHGAP18	b.t.	n.s.	-3.59	3.65E-02
PNOC	b.t.	n.s.	-3.88	3.52E-02
RHOC	b.t.	n.s.	-3.89	2.10E-02
CHST11	b.t.	n.s.	-4.36	1.41E-02
GPR34	b.t.	n.s.	-4.63	4.68E-02
PTPN6	b.t.	n.s.	-4.68	2.39E-02
PIK3CG	b.t.	n.s.	-5.27	6.10E-03
FGFBP2	b.t.	n.s.	-5.34	2.94E-02
LRMP	b.t.	n.s.	-5.79	1.79E-02
FAM102A	b.t.	n.s.	-6.58	3.51E-02
RHOBTB2	b.t.	n.s.	-14.06	1.51E-02

Trisomy 12	**Fold Change (CvsA)**	**P-val (CvsA)**	**Fold Change (DvsB)**	**P-val (DvsB)**
CYBRD1	76.54	1.60E-03	52.68	3.00E-04
AICDA	39.29	6.10E-03	26.04	6.10E-03

MGLL	35.25	3.30E-02	33.68	4.50E-03
MYO1G	30.12	1.20E-03	11.4	2.85E-02
FAM129A	22.14	1.95E-02	6.21	3.02E-02
NCF2	15.16	1.11E-02	9.64	1.67E-02
BLK	10.48	1.66E-02	7.64	3.08E-02
TRAF1	10.16	1.60E-02	3.79	1.38E-02
IL2RA	9.32	2.58E-02	14.24	1.09E-02
NR6A1	9.25	6.36E-06	5.73	1.24E-06
ARHGAP31	8.99	2.10E-03	3.24	1.23E-02
ST8SIA4	8.39	2.10E-03	3.78	2.70E-03
PIK3CD	8.2	3.00E-04	b.t.	n.s.
ABCD2	7.98	5.50E-03	4.1	1.32E-02
HELLS	7.59	5.00E-04	3.36	1.40E-03
CORO1A	7.36	1.88E-02	b.t.	n.s.
GPR157	7.24	6.80E-03	5.37	3.24E-02
SOX5	7.2	2.66E-02	3.47	2.30E-02
NLRC5	7.14	1.97E-02	b.t.	n.s.
KCNN4	7.1	5.00E-04	2.29	2.93E-02
IKZF1	6.89	4.00E-04	b.t.	n.s.
BHLHE40	6.87	9.00E-04	2.93	3.70E-03
DNPH1	6.73	2.91E-02	b.t.	n.s.
RNF145	6.63	2.63E-02	b.t.	n.s.
MREG	6.5	4.75E-02	b.t.	n.s.
LCP1	6.39	1.90E-03	3.12	3.60E-03
HLA-DRB1	6.29	4.04E-02	b.t.	n.s.
STARD10	6.24	6.00E-04	3.21	3.20E-03
JADE3	6.18	1.47E-02	b.t.	n.s.
HLA-DPB1	6.17	2.06E-02	b.t.	n.s.
CYB5A	5.76	8.83E-05	4.41	1.00E-04

ATP8A1	5.73	1.30E-03	2.11	2.66E-02
PSMD2	5.62	4.47E-02	b.t.	n.s.
PIK3C2B	5.51	7.60E-03	b.t.	n.s.
BSCL2	5.33	1.71E-02	b.t.	n.s.
NFKB2	5.29	5.00E-04	1.73	2.98E-02
MFSD10	5.07	7.45E-05	4.38	4.80E-03
STAT3	5.07	4.00E-02	2.57	2.66E-02
RPL39L	4.88	2.08E-02	4.42	1.23E-02
ZDHHC18	4.83	2.91E-02	b.t.	n.s.
ZBTB7B	4.78	6.60E-03	b.t.	n.s.
C9orf64	4.75	1.78E-02	b.t.	n.s.
SMIM14	4.73	2.39E-02	4.33	1.90E-02
SLC2A5	4.7	1.67E-02	b.t.	n.s.
PPP1R9B	4.69	1.00E-03	3.4	1.02E-02
IFNGR1	4.65	1.17E-02	6.49	1.66E-02
SFT2D1	4.63	1.76E-02	4.44	8.90E-03
CARM1	4.59	1.40E-03	4.63	3.00E-04
CTSH	4.55	1.04E-02	3.53	3.73E-02
CCND2	4.42	4.92E-02	b.t.	n.s.
NBEAL2	4.41	4.10E-03	3.17	3.30E-02
GPR132	4.4	2.77E-02	2.38	1.12E-02
ALDH2	4.38	2.61E-02	b.t.	n.s.
SLC2A13	4.38	2.02E-02	4.45	3.60E-03
C4orf46	4.32	3.93E-02	2.99	1.34E-02
PARP1	4.32	4.71E-02	b.t.	n.s.
GPX4	4.3	3.76E-02	b.t.	n.s.
NCKAP1L	4.27	1.20E-03	b.t.	n.s.
MYH9	4.25	3.18E-02	b.t.	n.s.
AP1S2	4.24	1.70E-03	2.33	8.20E-03

SLC20A1	4.24	6.10E-03	2.3	3.23E-02
ARNTL2	4.23	1.62E-02	5.68	9.10E-03
KLHL6	4.12	9.00E-04	2.21	2.62E-02
RHOF	4.11	9.00E-03	3.69	6.70E-03
SLX4IP	4.09	2.60E-03	b.t.	n.s.
HTRA2	4.05	2.10E-06	3.56	3.99E-05
RPS6KA1	4.02	4.20E-03	1.88	6.00E-03
SERF1A	3.96	2.32E-02	b.t.	n.s.
ACAD10	3.93	1.48E-02	b.t.	n.s.
EIF2D	3.9	6.50E-03	2.65	2.30E-02
PTPRJ	3.86	5.60E-03	b.t.	n.s.
HTT	3.8	6.10E-03	b.t.	n.s.
TBC1D2B	3.8	2.19E-02	b.t.	n.s.
S1PR2	3.79	3.41E-02	b.t.	n.s.
ARPC4	3.78	4.59E-02	b.t.	n.s.
CSF2RB	3.77	1.38E-02	b.t.	n.s.
BIRC3	3.66	1.47E-02	3.49	3.19E-02
CEPT1	3.65	3.50E-03	b.t.	n.s.
TARBP1	3.58	1.21E-02	1.96	4.50E-02
FGF2	3.57	4.81E-02	b.t.	n.s.
TBC1D9B	3.57	3.30E-02	b.t.	n.s.
IGF2R	3.56	1.37E-02	b.t.	n.s.
IRF4	3.54	1.65E-02	b.t.	n.s.
RMDN1	3.54	1.43E-02	b.t.	n.s.
TP53BP2	3.54	1.15E-02	1.93	1.35E-02
ETFB	3.5	4.17E-02	b.t.	n.s.
CYP2C18	3.47	1.66E-02	3.44	1.10E-03
MKNK2	3.47	4.00E-04	2.77	5.50E-03
SPINT2	3.47	1.15E-02	b.t.	n.s.

FURIN	3.45	1.69E-02	b.t.	n.s.
RBPJ	3.43	1.60E-03	2.5	4.10E-03
COX18	3.42	3.00E-04	b.t.	n.s.
PAX5	3.42	1.73E-02	1.9	3.92E-02
RAP1A	3.41	5.30E-03	2.12	4.70E-03
FAM156A	3.37	5.60E-03	b.t.	n.s.
SENP8	3.34	3.42E-02	b.t.	n.s.
ASXL1	3.33	5.20E-03	3.49	9.10E-03
MBNL2	3.31	1.85E-02	b.t.	n.s.
P2RX4	3.3	2.80E-02	3.07	4.85E-02
TSPAN33	3.28	1.70E-03	3.98	6.60E-03
RAB13	3.27	3.98E-02	b.t.	n.s.
FAN1	3.25	1.85E-02	b.t.	n.s.
SRRD	3.21	1.92E-02	b.t.	n.s.
ADGRE5	3.2	2.90E-03	b.t.	n.s.
GCSAM	3.17	1.62E-02	7	2.80E-03
SLAMF1	3.17	3.44E-02	6.43	1.53E-02
RBM45	3.15	2.38E-02	b.t.	n.s.
TC2N	3.15	4.88E-02	b.t.	n.s.
NLRC4	3.14	5.20E-03	b.t.	n.s.
TIPRL	3.14	3.59E-02	b.t.	n.s.
PHYH	3.13	2.80E-03	1.84	4.78E-02
PTGES2	3.13	1.00E-03	b.t.	n.s.
SLC25A46	3.13	2.18E-02	b.t.	n.s.
TIFA	3.11	2.05E-02	2.5	1.06E-02
PDGFA	3.11	3.01E-02	b.t.	n.s.
NKRF	3.1	3.35E-02	b.t.	n.s.
VDR	3.1	5.00E-04	2.33	3.48E-02
ANAPC16	3.09	2.47E-02	b.t.	n.s.

ICAM1	3.09	4.20E-02	b.t.	n.s.
UBE2D1	3.09	1.56E-02	b.t.	n.s.
MGST3	3.07	3.56E-02	b.t.	n.s.
IFFO2	3.06	4.00E-04	2.68	6.90E-03
NCK2	3.06	8.00E-04	1.64	8.00E-03
PPM1M	3.06	3.69E-02	b.t.	n.s.
AVL9	3.05	1.99E-02	b.t.	n.s.
HMGCL	3.05	3.00E-02	b.t.	n.s.
VCL	3.05	1.50E-03	b.t.	n.s.
WRAP53	3.05	1.53E-02	b.t.	n.s.
HYOU1	3.03	4.20E-02	b.t.	n.s.
APOBEC3G	3.03	2.42E-02	2.89	3.50E-02
NME3	3.02	9.60E-03	b.t.	n.s.
SPIB	3.02	7.00E-03	b.t.	n.s.
TACO1	3.02	2.18E-02	b.t.	n.s.
MAP3K14	3.01	7.00E-03	b.t.	n.s.
BTN2A2	3	2.23E-02	1.97	4.86E-02
TRAPPC3	3	4.91E-02	b.t.	n.s.
PROSER1	2.97	2.23E-02	b.t.	n.s.
RAPGEF1	2.97	4.19E-02	b.t.	n.s.
EIF3F	2.95	1.22E-02	1.51	4.05E-02
RFFL	2.95	8.00E-03	1.75	2.04E-02
NIPAL2	2.94	3.01E-02	b.t.	n.s.
ACLY	2.93	3.57E-02	b.t.	n.s.
IPP	2.93	9.40E-03	b.t.	n.s.
LCLAT1	2.93	1.32E-02	b.t.	n.s.
TIGD2	2.9	4.94E-02	2.72	1.25E-02
PRDX5	2.88	3.60E-03	1.88	4.96E-02
ZKSCAN7	2.88	9.70E-03	1.71	3.10E-03

CAPN1	2.88	6.70E-03	b.t.	n.s.
C17orf99	2.87	3.20E-03	b.t.	n.s.
HINT2	2.87	4.63E-02	2.17	2.59E-02
NCAPD2	2.87	2.16E-02	b.t.	n.s.
NDUFB8	2.87	2.68E-02	b.t.	n.s.
RAB9A	2.86	6.50E-03	4.68	1.60E-03
TMEM260	2.86	1.80E-02	b.t.	n.s.
TRAF3	2.86	5.70E-03	3	3.42E-02
NIT1	2.85	1.70E-03	b.t.	n.s.
GSK3B	2.84	6.90E-03	b.t.	n.s.
HTATIP2	2.84	4.54E-02	b.t.	n.s.
CXorf40B	2.83	2.97E-02	b.t.	n.s.
MRPL55	2.82	1.93E-02	b.t.	n.s.
MTHFD1	2.82	6.30E-03	b.t.	n.s.
NEDD9	2.82	2.60E-02	b.t.	n.s.
TNFAIP3	2.82	4.30E-03	9.84	2.00E-04
PGM2	2.8	1.52E-02	b.t.	n.s.
SQLE	2.8	3.04E-02	b.t.	n.s.
STX6	2.8	3.00E-04	b.t.	n.s.
GPX1	2.79	3.90E-02	b.t.	n.s.
TFDP2	2.76	7.40E-03	3.42	8.00E-04
ZNF425	2.74	4.00E-04	b.t.	n.s.
FXR1	2.73	3.80E-03	1.86	8.00E-03
ANP32A	2.71	2.43E-02	b.t.	n.s.
SUOX	2.71	1.36E-02	b.t.	n.s.
SLC25A23	2.7	4.18E-02	b.t.	n.s.
CARS2	2.69	1.34E-02	b.t.	n.s.
STAT5A	2.69	1.40E-03	2.24	6.00E-04
RCAN3	2.67	2.70E-02	b.t.	n.s.

NUDT19	2.66	3.84E-02	b.t.	n.s.
SDR39U1	2.66	2.62E-02	b.t.	n.s.
ACBD6	2.65	1.90E-02	b.t.	n.s.
MAPKAP1	2.65	2.43E-02	b.t.	n.s.
EMB	2.64	4.19E-02	b.t.	n.s.
TBC1D7	2.62	3.96E-02	b.t.	n.s.
TNFRSF14	2.61	1.52E-02	b.t.	n.s.
ALDH6A1	2.6	2.95E-02	b.t.	n.s.
COQ5	2.6	2.20E-02	b.t.	n.s.
FAS	2.6	4.46E-02	3.43	5.70E-03
RPL18	2.6	2.38E-02	1.99	2.83E-02
HDHD2	2.59	2.51E-02	b.t.	n.s.
NBAS	2.59	3.96E-02	b.t.	n.s.
KIF3B	2.58	9.00E-04	1.54	1.19E-02
SUPT7L	2.58	6.50E-03	b.t.	n.s.
ANP32E	2.57	2.12E-02	b.t.	n.s.
UBXN6	2.57	4.90E-03	b.t.	n.s.
RTTN	2.56	1.62E-02	b.t.	n.s.
CCDC28B	2.53	1.88E-02	b.t.	n.s.
IDH2	2.53	1.48E-02	b.t.	n.s.
RAD17	2.53	9.00E-04	b.t.	n.s.
ANAPC11	2.52	4.94E-02	b.t.	n.s.
IL23A	2.51	1.30E-02	b.t.	n.s.
NKIRAS2	2.51	4.97E-02	b.t.	n.s.
SLC35B3	2.51	2.50E-03	b.t.	n.s.
CFAP20	2.5	2.30E-02	b.t.	n.s.
PIH1D1	2.5	2.86E-02	b.t.	n.s.
CTAGE15	2.49	1.70E-02	1.99	3.97E-02
SAMD1	2.49	3.12E-02	b.t.	n.s.

SSNA1	2.48	2.00E-02	b.t.	n.s.
CASZ1	2.47	4.99E-02	b.t.	n.s.
ADAT2	2.46	3.38E-02	b.t.	n.s.
CXorf40A	2.46	8.60E-03	b.t.	n.s.
ELK3	2.46	7.10E-03	1.98	4.73E-02
NOA1	2.46	6.20E-03	1.55	2.06E-02
CCDC50	2.45	2.50E-02	2.82	2.00E-03
FDPS	2.45	4.91E-02	b.t.	n.s.
GSTP1	2.44	2.00E-03	2.03	8.80E-03
ECH1	2.43	1.16E-02	1.76	2.42E-02
FGGY	2.43	4.70E-03	2.17	2.00E-04
CERS4	2.42	4.93E-02	b.t.	n.s.
TUBGCP2	2.42	2.24E-02	b.t.	n.s.
POLA2	2.41	2.70E-03	2.41	3.35E-02
ALAS1	2.4	1.71E-02	b.t.	n.s.
CAB39	2.4	4.02E-02	b.t.	n.s.
CYP2C8	2.39	2.25E-02	b.t.	n.s.
SEC11C	2.39	2.90E-03	3.08	7.40E-03
SLC30A9	2.39	3.49E-02	b.t.	n.s.
VAV1	2.39	2.00E-03	b.t.	n.s.
ZYG11B	2.39	3.00E-04	b.t.	n.s.
HIBADH	2.38	2.25E-02	b.t.	n.s.
NAGA	2.38	2.05E-02	b.t.	n.s.
PABPC1L	2.38	1.30E-02	b.t.	n.s.
EML3	2.37	2.03E-02	b.t.	n.s.
LIX1L	2.37	1.63E-02	b.t.	n.s.
SEC61B	2.36	4.19E-02	b.t.	n.s.
TMEM218	2.35	3.21E-02	b.t.	n.s.
AGTRAP	2.34	7.10E-03	b.t.	n.s.

ATP6V1A	2.34	1.19E-02	b.t.	n.s.
CUEDC2	2.34	2.58E-02	b.t.	n.s.
ELMOD2	2.34	4.51E-02	b.t.	n.s.
NCOA1	2.33	4.74E-02	b.t.	n.s.
ACSS2	2.32	3.74E-02	b.t.	n.s.
TMEM14C	2.32	2.49E-02	b.t.	n.s.
UBA3	2.32	9.40E-03	b.t.	n.s.
DHTKD1	2.31	2.00E-02	1.55	3.50E-02
FLOT2	2.31	2.71E-02	b.t.	n.s.
LONP2	2.31	8.20E-03	b.t.	n.s.
NDRG3	2.31	2.69E-02	b.t.	n.s.
PLD2	2.31	1.43E-02	2.29	1.61E-02
RASSF2	2.31	2.77E-02	b.t.	n.s.
RFC2	2.31	3.38E-02	1.94	4.53E-02
RPAP1	2.3	4.14E-02	b.t.	n.s.
VPS52	2.3	3.63E-02	b.t.	n.s.
DNMT3A	2.29	4.55E-02	b.t.	n.s.
RAD51B	2.29	2.23E-02	b.t.	n.s.
TAGLN2	2.29	1.09E-02	2.07	1.10E-02
CEP192	2.28	2.41E-02	2.11	2.10E-02
DHX16	2.28	3.23E-02	b.t.	n.s.
STAT5B	2.27	1.30E-03	3.32	7.95E-05
TYK2	2.27	4.30E-03	b.t.	n.s.
H2AFV	2.26	2.36E-02	2.49	2.71E-02
MED16	2.26	5.20E-03	b.t.	n.s.
MLH1	2.26	3.84E-02	b.t.	n.s.
MAP3K11	2.24	2.47E-02	b.t.	n.s.
MAU2	2.24	1.49E-02	b.t.	n.s.
KDM1B	2.21	1.02E-02	b.t.	n.s.

PPM1A	2.21	4.80E-03	3.15	1.00E-04
PPP2R5D	2.21	2.60E-03	b.t.	n.s.
PRMT2	2.21	3.62E-02	b.t.	n.s.
RNF7	2.2	3.35E-02	b.t.	n.s.
ACTR1A	2.19	3.82E-02	b.t.	n.s.
CCDC6	2.18	1.23E-02	1.57	3.90E-03
CPSF2	2.18	3.80E-03	b.t.	n.s.
ZNF284	2.18	4.59E-02	b.t.	n.s.
CD19	2.17	1.70E-03	2.31	9.50E-03
MAPK14	2.15	3.53E-02	b.t.	n.s.
SEMA7A	2.15	3.46E-02	b.t.	n.s.
PCYT1A	2.14	3.16E-02	b.t.	n.s.
SLC9A7	2.14	1.50E-02	b.t.	n.s.
BIRC2	2.13	2.50E-03	2.1	1.50E-02
DUSP22	2.13	4.37E-02	2.86	4.60E-03
ARPC4-TTLL3	2.12	2.62E-02	b.t.	n.s.
ZADH2	2.12	2.98E-02	b.t.	n.s.
C12orf10	2.12	4.71E-02	b.t.	n.s.
CALU	2.12	4.49E-02	b.t.	n.s.
PPID	2.12	1.62E-02	b.t.	n.s.
DHRS7	2.11	9.10E-03	b.t.	n.s.
PPP1R7	2.11	1.35E-02	3.01	2.22E-02
RNF214	2.11	1.50E-03	b.t.	n.s.
TTC5	2.11	4.66E-02	b.t.	n.s.
ATXN2L	2.1	3.80E-02	b.t.	n.s.
CCDC191	2.1	3.69E-02	b.t.	n.s.
DBI	2.1	5.70E-03	4.11	4.40E-03
PIK3R1	2.1	3.24E-02	b.t.	n.s.
ATP11A	2.09	4.68E-02	b.t.	n.s.

BLM	2.09	1.34E-02	2.7	4.22E-02
EIF2AK1	2.09	7.20E-03	b.t.	n.s.
PIGK	2.09	3.40E-02	b.t.	n.s.
POGLUT1	2.09	3.79E-02	b.t.	n.s.
SHKBP1	2.09	6.30E-03	b.t.	n.s.
ETV3	2.07	3.13E-02	1.78	9.10E-03
FASTKD3	2.07	1.34E-02	b.t.	n.s.
FBRS	2.07	2.73E-02	b.t.	n.s.
PIGS	2.07	3.14E-02	b.t.	n.s.
PHTF1	2.06	4.32E-02	b.t.	n.s.
FTO	2.05	4.41E-02	b.t.	n.s.
MAT2B	2.05	3.66E-02	b.t.	n.s.
CALM3	2.04	3.40E-03	1.64	1.37E-02
DCAF8	2.04	2.58E-02	b.t.	n.s.
MAD2L2	2.04	4.26E-02	b.t.	n.s.
NDUFB9	2.04	4.52E-02	b.t.	n.s.
CNTF	2.03	3.00E-03	b.t.	n.s.
HMG20B	2.03	4.20E-02	b.t.	n.s.
MROH8	2.03	7.90E-03	b.t.	n.s.
C15orf41	2.02	2.55E-02	b.t.	n.s.
C1RL	2.02	3.20E-02	b.t.	n.s.
CAPNS1	2.02	3.42E-02	b.t.	n.s.
PAIP1	2.02	2.73E-02	b.t.	n.s.
RYBP	2.02	8.00E-04	1.82	9.60E-03
ACTR3B	2.01	3.63E-02	b.t.	n.s.
TNKS1BP1	2.01	3.50E-02	b.t.	n.s.
WDR83OS	2.01	3.31E-02	b.t.	n.s.
IFNGR2	2	3.49E-02	b.t.	n.s.
PRKACA	2	1.45E-02	b.t.	n.s.

SLC12A4	2	4.20E-02	b.t.	n.s.
ZBTB5	1.99	4.08E-02	b.t.	n.s.
IL21R	1.99	8.10E-03	b.t.	n.s.
POT1	1.99	1.77E-02	b.t.	n.s.
TJAP1	1.99	7.20E-03	b.t.	n.s.
ARID3B	1.98	3.45E-02	b.t.	n.s.
FBXW2	1.98	4.50E-02	b.t.	n.s.
JAK3	1.98	2.12E-02	b.t.	n.s.
MED12	1.98	4.31E-02	b.t.	n.s.
WDR70	1.98	3.70E-03	b.t.	n.s.
HADHA	1.97	1.57E-02	b.t.	n.s.
MAP3K8	1.97	2.20E-02	b.t.	n.s.
P2RY10	1.97	4.66E-02	b.t.	n.s.
PRMT7	1.97	9.00E-03	b.t.	n.s.
SLC25A45	1.97	4.12E-02	b.t.	n.s.
UBA1	1.97	2.78E-02	b.t.	n.s.
BTAF1	1.96	2.20E-03	b.t.	n.s.
ICAM3	1.96	3.42E-02	b.t.	n.s.
PFKFB3	1.96	2.42E-02	b.t.	n.s.
TMOD1	1.96	5.20E-03	2.93	3.00E-04
AP2S1	1.95	3.96E-02	b.t.	n.s.
CSK	1.95	1.51E-02	b.t.	n.s.
EEF2K	1.95	2.17E-02	b.t.	n.s.
ERCC4	1.95	1.46E-02	b.t.	n.s.
LPAR2	1.95	3.94E-02	b.t.	n.s.
CCDC102B	1.94	3.62E-02	b.t.	n.s.
LZTR1	1.94	2.18E-02	b.t.	n.s.
SYNGR2	1.94	1.55E-02	b.t.	n.s.
TMTC2	1.94	8.40E-03	b.t.	n.s.

ZMIZ2	1.94	4.00E-02	b.t.	n.s.
GRN	1.93	4.13E-02	b.t.	n.s.
KLHL23	1.93	1.24E-02	b.t.	n.s.
PLGRKT	1.93	2.69E-02	2.09	2.28E-02
PRIMPOL	1.93	4.58E-02	1.84	3.03E-02
BNIP1	1.92	3.10E-02	b.t.	n.s.
SPRY3	1.92	4.16E-02	b.t.	n.s.
DCAF10	1.92	1.14E-02	b.t.	n.s.
ELMO1	1.92	3.78E-02	b.t.	n.s.
GINM1	1.92	1.10E-03	b.t.	n.s.
FPGT	1.91	4.58E-02	b.t.	n.s.
ACOT13	1.91	4.50E-02	2.04	4.13E-02
EIF4ENIF1	1.91	3.03E-02	b.t.	n.s.
MITD1	1.91	1.80E-02	b.t.	n.s.
ZNF687	1.91	2.32E-02	b.t.	n.s.
GBA3	1.9	3.00E-02	1.58	6.10E-03
MTERF4	1.9	1.73E-02	2.51	2.36E-02
RPL7A	1.89	3.59E-02	1.67	2.94E-02
GLE1	1.89	2.14E-02	b.t.	n.s.
RAC1	1.89	3.92E-02	b.t.	n.s.
TARDBP	1.89	1.74E-02	b.t.	n.s.
TMEM91	1.89	2.39E-02	b.t.	n.s.
ADAT1	1.88	4.30E-03	b.t.	n.s.
IAH1	1.88	3.82E-02	1.5	1.79E-02
KDSR	1.88	1.88E-02	b.t.	n.s.
RPL7	1.88	2.86E-02	b.t.	n.s.
SLC25A35	1.88	3.24E-02	b.t.	n.s.
ASXL3	1.87	4.13E-02	1.53	4.65E-02
BLVRA	1.87	2.10E-03	4.07	7.84E-05

LNPEP	1.87	3.30E-02	b.t.	n.s.
NBR1	1.87	2.79E-02	b.t.	n.s.
AK3	1.86	5.60E-03	b.t.	n.s.
TXNL1	1.86	3.98E-02	b.t.	n.s.
XRCC1	1.86	3.22E-02	b.t.	n.s.
P2RX2	1.85	1.30E-03	b.t.	n.s.
SLC37A4	1.85	3.84E-02	1.61	1.34E-02
AMPD3	1.85	4.15E-02	b.t.	n.s.
MRPL19	1.85	2.83E-02	b.t.	n.s.
RELT	1.85	4.96E-02	b.t.	n.s.
ZNF197	1.84	1.13E-02	b.t.	n.s.
CUTA	1.83	1.52E-02	b.t.	n.s.
ERCC2	1.83	3.34E-02	b.t.	n.s.
PSENEN	1.83	3.04E-02	1.99	2.45E-02
WDSUB1	1.83	1.86E-02	b.t.	n.s.
CBR4	1.82	3.04E-02	2.01	1.78E-02
NDFIP1	1.82	1.91E-02	1.7	1.28E-02
GNG10	1.81	2.58E-02	1.84	2.94E-02
SRGN	1.81	8.60E-03	b.t.	n.s.
CASD1	1.81	4.84E-02	b.t.	n.s.
DNAJC25-GNG10	1.8	4.26E-02	b.t.	n.s.
COL4A3BP	1.8	4.10E-03	b.t.	n.s.
EMC3	1.8	4.99E-02	b.t.	n.s.
GTF2B	1.8	4.34E-02	b.t.	n.s.
IFFO1	1.8	6.90E-03	b.t.	n.s.
ORC3	1.8	3.24E-02	b.t.	n.s.
ABHD17C	1.79	1.44E-02	b.t.	n.s.
NT5DC1	1.79	3.20E-03	1.6	2.32E-02
RASGRP4	1.79	2.02E-02	7.04	2.40E-03

RNF121	1.78	1.37E-02	b.t.	n.s.
IPPK	1.77	4.42E-02	b.t.	n.s.
MFSD13A	1.77	5.80E-03	b.t.	n.s.
ANKLE2	1.76	2.70E-02	2.53	3.51E-02
C6orf163	1.76	1.40E-02	b.t.	n.s.
MBTD1	1.76	3.33E-02	b.t.	n.s.
SLC25A51	1.76	4.89E-02	b.t.	n.s.
ANKRD52	1.75	4.18E-02	b.t.	n.s.
FAM19A2	1.75	3.20E-03	b.t.	n.s.
PAAF1	1.75	1.33E-02	b.t.	n.s.
EDEM1	1.74	1.15E-02	b.t.	n.s.
IL10RB	1.74	3.59E-02	2.76	1.92E-02
LMLN	1.74	2.27E-02	b.t.	n.s.
PRR14	1.74	3.08E-02	b.t.	n.s.
ASL	1.73	1.34E-02	b.t.	n.s.
DDX6	1.73	4.64E-02	b.t.	n.s.
NRAS	1.73	4.12E-02	b.t.	n.s.
QTRT1	1.73	1.44E-02	b.t.	n.s.
TGIF2	1.73	9.60E-03	1.9	4.88E-02
URGCP	1.73	1.22E-02	b.t.	n.s.
UVRAG	1.73	1.69E-02	2.48	1.50E-03
CCDC150	1.72	4.00E-03	b.t.	n.s.
ERGIC3	1.72	9.50E-03	b.t.	n.s.
RPS18	1.72	1.63E-02	b.t.	n.s.
ANKS1A	1.71	1.11E-02	b.t.	n.s.
MFF	1.71	3.98E-02	b.t.	n.s.
NAPEPLD	1.71	2.55E-02	b.t.	n.s.
UBL4A	1.71	3.60E-03	b.t.	n.s.
HPS5	1.7	1.59E-02	b.t.	n.s.

PIGX	1.7	3.92E-02	2.12	7.90E-03
PP2D1	1.7	3.27E-02	b.t.	n.s.
STK25	1.7	3.21E-02	b.t.	n.s.
RANBP6	1.69	1.65E-02	b.t.	n.s.
FAM3A	1.69	3.12E-02	b.t.	n.s.
PBX4	1.69	3.87E-02	b.t.	n.s.
TSTD2	1.69	1.56E-02	b.t.	n.s.
CCDC39	1.68	2.01E-02	b.t.	n.s.
ACBD4	1.68	1.33E-02	b.t.	n.s.
GOT2	1.68	2.63E-02	2.39	8.00E-04
HHEX	1.68	2.94E-02	b.t.	n.s.
ITGAD	1.68	3.00E-02	b.t.	n.s.
NIF3L1	1.67	3.66E-02	b.t.	n.s.
SGSM3	1.67	2.24E-02	b.t.	n.s.
SLMAP	1.67	3.71E-02	b.t.	n.s.
ARID2	1.66	4.97E-02	b.t.	n.s.
MUC1	1.66	3.05E-02	b.t.	n.s.
NECAP2	1.66	8.90E-03	b.t.	n.s.
PIKFYVE	1.66	2.71E-02	b.t.	n.s.
PLLP	1.66	3.96E-02	b.t.	n.s.
TADA3	1.66	3.90E-02	b.t.	n.s.
UNC80	1.66	1.86E-02	b.t.	n.s.
CORO6	1.65	4.04E-02	b.t.	n.s.
DENND1C	1.65	1.79E-02	b.t.	n.s.
FASTK	1.65	2.60E-02	b.t.	n.s.
MTA3	1.65	1.53E-02	b.t.	n.s.
PPP1R16A	1.65	5.30E-03	b.t.	n.s.
TNIP2	1.65	2.26E-02	b.t.	n.s.
DAD1	1.64	2.46E-02	1.61	4.50E-03

PID1	1.64	1.36E-02	b.t.	n.s.
SIRT7	1.64	3.12E-02	b.t.	n.s.
LAGE3	1.63	4.96E-02	b.t.	n.s.
CDC42	1.63	2.36E-02	b.t.	n.s.
CDNF	1.63	2.81E-02	b.t.	n.s.
FLOT1	1.63	3.58E-02	2.47	2.42E-02
RPS21	1.63	3.23E-02	b.t.	n.s.
TBC1D22B	1.63	4.19E-02	b.t.	n.s.
CSTA	1.62	3.94E-02	b.t.	n.s.
TMEM205	1.62	1.58E-02	1.55	1.66E-02
CCDC57	1.61	5.10E-03	b.t.	n.s.
DCAF17	1.61	2.00E-04	b.t.	n.s.
PFKM	1.61	2.40E-03	b.t.	n.s.
INPP5D	1.6	5.90E-03	b.t.	n.s.
ADPRH	1.59	4.70E-02	2.05	3.97E-02
CD58	1.59	4.52E-02	b.t.	n.s.
SMARCAL1	1.58	3.06E-02	b.t.	n.s.
COX8A	1.57	2.86E-02	b.t.	n.s.
HOMEZ	1.57	2.32E-02	b.t.	n.s.
NSUN3	1.57	4.47E-02	b.t.	n.s.
WDR82	1.57	4.20E-03	b.t.	n.s.
MARCH3	1.56	2.20E-02	b.t.	n.s.
PLCB3	1.56	1.60E-03	b.t.	n.s.
TTLL3	1.56	3.92E-02	b.t.	n.s.
ZNF678	1.56	3.17E-02	b.t.	n.s.
MGAM2	1.55	1.33E-02	b.t.	n.s.
NDUFA10	1.54	4.75E-02	b.t.	n.s.
CDH7	1.54	7.10E-03	b.t.	n.s.
HMGB4	1.54	3.88E-02	b.t.	n.s.

RNF4	1.54	1.76E-02	b.t.	n.s.
TCF7	1.54	3.07E-02	1.71	1.30E-03
RNF148	1.53	3.98E-02	b.t.	n.s.
COA1	1.53	4.45E-02	2.99	6.30E-03
MYL1	1.53	2.18E-02	b.t.	n.s.
TMEM120A	1.53	5.20E-03	2.82	1.10E-03
MTMR4	1.52	6.30E-03	b.t.	n.s.
PRG2	1.52	4.38E-02	b.t.	n.s.
DSTYK	1.51	4.59E-02	b.t.	n.s.
GRHPR	1.51	3.24E-02	1.78	8.50E-03
NPR1	1.51	1.52E-02	b.t.	n.s.
WDR7	1.51	3.07E-02	b.t.	n.s.
LRCH3	1.5	6.60E-03	b.t.	n.s.
NIN	1.5	2.50E-02	b.t.	n.s.
RHNO1	1.5	4.05E-02	b.t.	n.s.
GDF2	-1.5	4.00E-04	b.t.	n.s.
TNNC2	-1.5	8.50E-03	b.t.	n.s.
CCDC174	-1.5	4.60E-03	b.t.	n.s.
CXCR2	-1.5	1.65E-02	b.t.	n.s.
HOXA3	-1.5	2.30E-03	b.t.	n.s.
OLFM1	-1.5	8.30E-03	b.t.	n.s.
SPDYE5	-1.51	1.84E-02	b.t.	n.s.
ATP7B	-1.51	2.33E-02	b.t.	n.s.
C1orf185	-1.51	3.57E-02	b.t.	n.s.
DNAJB4	-1.51	2.07E-02	b.t.	n.s.
LEMD3	-1.51	4.15E-02	b.t.	n.s.
LHX8	-1.51	2.32E-02	b.t.	n.s.
TMEM212	-1.51	4.23E-02	b.t.	n.s.
NPHS2	-1.52	1.72E-02	b.t.	n.s.

ABCG2	-1.52	1.82E-02	b.t.	n.s.
ATP1A2	-1.52	4.39E-02	b.t.	n.s.
KEL	-1.52	2.00E-02	b.t.	n.s.
OBSCN	-1.52	2.20E-02	b.t.	n.s.
RTN4	-1.52	1.28E-02	b.t.	n.s.
ADCK5	-1.53	3.26E-02	b.t.	n.s.
ECE2	-1.53	3.34E-02	b.t.	n.s.
TCEAL2	-1.53	1.34E-02	b.t.	n.s.
TSPAN19	-1.53	3.98E-02	b.t.	n.s.
UNC13C	-1.53	2.40E-03	b.t.	n.s.
ESRP1	-1.54	1.65E-02	b.t.	n.s.
PDZD4	-1.54	5.30E-03	b.t.	n.s.
C6orf226	-1.55	7.00E-03	b.t.	n.s.
DPH3P1	-1.55	2.92E-02	b.t.	n.s.
EFHD1	-1.55	3.70E-03	b.t.	n.s.
ETV4	-1.55	4.49E-02	b.t.	n.s.
FAM177A1	-1.55	4.12E-02	b.t.	n.s.
PCDHB12	-1.56	2.80E-02	b.t.	n.s.
NT5C3A	-1.56	3.94E-02	b.t.	n.s.
PTGFRN	-1.56	3.64E-02	b.t.	n.s.
BHMT	-1.57	2.08E-02	b.t.	n.s.
C3orf20	-1.57	8.80E-03	b.t.	n.s.
CCL19	-1.57	4.02E-02	b.t.	n.s.
LRRN2	-1.57	4.30E-03	b.t.	n.s.
PIAS2	-1.57	1.39E-02	b.t.	n.s.
HRASLS	-1.58	3.73E-02	b.t.	n.s.
ACBD3	-1.58	2.68E-02	b.t.	n.s.
CAB39L	-1.58	4.22E-02	b.t.	n.s.
DPEP1	-1.58	1.80E-03	b.t.	n.s.

KIF3C	-1.58	1.85E-02	b.t.	n.s.
MRPL50	-1.58	4.08E-02	b.t.	n.s.
SVEP1	-1.58	3.27E-02	b.t.	n.s.
TTLL6	-1.58	1.34E-02	b.t.	n.s.
H2AFY2	-1.59	3.76E-02	b.t.	n.s.
CHN1	-1.59	2.73E-02	b.t.	n.s.
GPX5	-1.59	1.84E-02	b.t.	n.s.
KCNJ14	-1.59	2.00E-04	b.t.	n.s.
NBPF4	-1.59	3.97E-02	b.t.	n.s.
RLIM	-1.59	3.00E-03	b.t.	n.s.
TRPM3	-1.59	3.17E-02	b.t.	n.s.
SCG5	-1.6	9.20E-03	b.t.	n.s.
TMEM251	-1.6	2.38E-02	b.t.	n.s.
ALKBH4	-1.6	9.30E-03	b.t.	n.s.
EFR3A	-1.6	2.52E-02	b.t.	n.s.
NCAN	-1.6	6.40E-03	b.t.	n.s.
OSBPL6	-1.6	3.10E-03	b.t.	n.s.
ZNF202	-1.6	5.00E-04	b.t.	n.s.
ZNF773	-1.6	2.16E-02	b.t.	n.s.
KCNE1	-1.61	4.37E-02	b.t.	n.s.
SLC26A4	-1.61	2.12E-02	b.t.	n.s.
GMPR	-1.62	3.41E-02	b.t.	n.s.
NCR3LG1	-1.62	8.00E-03	b.t.	n.s.
OTOL1	-1.63	3.46E-02	b.t.	n.s.
ADIG	-1.63	4.50E-03	b.t.	n.s.
ARMC7	-1.63	3.01E-02	b.t.	n.s.
HLX	-1.63	2.65E-02	b.t.	n.s.
OBP2B	-1.64	3.97E-02	b.t.	n.s.
MMP10	-1.64	2.52E-02	b.t.	n.s.

SALL4	-1.64	1.80E-02	b.t.	n.s.
C2CD4C	-1.65	2.12E-02	b.t.	n.s.
FLG2	-1.65	7.20E-03	b.t.	n.s.
HSFY2	-1.65	3.19E-02	b.t.	n.s.
LMNTD2	-1.65	1.31E-02	b.t.	n.s.
MFSD2B	-1.66	9.60E-03	b.t.	n.s.
SMAD5	-1.66	4.74E-02	b.t.	n.s.
ZNF26	-1.66	2.25E-02	b.t.	n.s.
PRAC1	-1.67	1.00E-02	b.t.	n.s.
C5orf67	-1.68	1.74E-02	b.t.	n.s.
CERS3	-1.68	1.38E-02	b.t.	n.s.
CDSN	-1.69	4.00E-03	b.t.	n.s.
CA1	-1.69	1.29E-02	b.t.	n.s.
CST2	-1.7	4.22E-02	b.t.	n.s.
OR5B12	-1.7	2.21E-02	b.t.	n.s.
AKAP10	-1.71	1.79E-02	-1.76	3.52E-02
EPB41L3	-1.71	2.58E-02	b.t.	n.s.
HRK	-1.72	1.21E-02	b.t.	n.s.
KLHDC4	-1.73	3.00E-03	-1.86	3.08E-02
CCR10	-1.74	3.36E-02	b.t.	n.s.
CFAP77	-1.75	3.20E-03	b.t.	n.s.
OR4D11	-1.75	1.48E-02	b.t.	n.s.
ARHGEF2	-1.76	6.80E-03	b.t.	n.s.
DCAF8L2	-1.76	6.00E-03	b.t.	n.s.
DEFB121	-1.76	2.74E-02	b.t.	n.s.
AQP7	-1.78	4.28E-02	b.t.	n.s.
DCK	-1.78	4.02E-02	b.t.	n.s.
KRT81	-1.8	7.28E-05	b.t.	n.s.
DLL1	-1.81	1.50E-02	b.t.	n.s.

PPEF2	-1.81	5.40E-03	b.t.	n.s.
ACOT9	-1.82	3.32E-02	b.t.	n.s.
C19orf73	-1.83	3.40E-03	b.t.	n.s.
MTSS1L	-1.83	1.38E-02	b.t.	n.s.
TBL1X	-1.83	1.64E-02	b.t.	n.s.
MRGPRX4	-1.84	3.07E-02	b.t.	n.s.
TMEM98	-1.84	5.00E-04	b.t.	n.s.
THRSP	-1.85	3.98E-02	b.t.	n.s.
PCK1	-1.86	3.20E-03	b.t.	n.s.
TRMT13	-1.86	4.10E-02	b.t.	n.s.
TUFT1	-1.86	1.16E-02	b.t.	n.s.
ZNF546	-1.86	3.92E-02	b.t.	n.s.
ALB	-1.87	2.28E-02	b.t.	n.s.
SEC31A	-1.88	1.33E-02	b.t.	n.s.
SLBP	-1.89	2.28E-02	b.t.	n.s.
FAM71A	-1.9	1.60E-02	b.t.	n.s.
PYGO2	-1.9	2.47E-02	b.t.	n.s.
CASC10	-1.91	2.53E-02	b.t.	n.s.
GPX6	-1.91	2.00E-04	b.t.	n.s.
ZCCHC2	-1.94	2.49E-02	-2.91	1.58E-02
LIPN	-1.95	2.00E-04	b.t.	n.s.
TMEM140	-1.95	1.47E-02	-1.93	2.56E-02
PEG10	-1.96	4.58E-02	b.t.	n.s.
AMBP	-1.97	1.34E-02	b.t.	n.s.
SIDT1	-1.97	2.62E-02	b.t.	n.s.
ARHGEF1	-1.99	7.80E-03	b.t.	n.s.
MIS18BP1	-2	2.89E-02	b.t.	n.s.
ST7L	-2	2.61E-02	b.t.	n.s.
TGFBR2	-2	4.15E-02	-2.29	2.40E-03

TMEM255B	-2	4.10E-03	b.t.	n.s.
TNFSF13	-2	8.00E-03	b.t.	n.s.
INO80D	-2.01	2.62E-02	b.t.	n.s.
TRIM23	-2.08	2.87E-02	b.t.	n.s.
ZNF567	-2.1	3.75E-02	b.t.	n.s.
PKP4	-2.11	1.61E-02	b.t.	n.s.
DCAF4	-2.12	3.23E-02	b.t.	n.s.
FAM133B	-2.14	5.00E-03	b.t.	n.s.
ABHD16B	-2.17	4.10E-03	b.t.	n.s.
BHMT2	-2.19	2.00E-04	b.t.	n.s.
F13B	-2.2	3.64E-02	b.t.	n.s.
KLF5	-2.2	3.05E-02	b.t.	n.s.
PHACTR4	-2.2	2.67E-02	b.t.	n.s.
MGAT5	-2.26	6.20E-03	-2.42	1.43E-02
MMP26	-2.28	3.00E-04	b.t.	n.s.
TRIM14	-2.38	5.50E-03	-1.97	4.31E-02
DOCK4	-2.55	2.48E-02	b.t.	n.s.
DNM3	-2.66	8.40E-03	b.t.	n.s.
PARP8	-2.76	1.88E-02	b.t.	n.s.
PLK2	-2.8	4.17E-02	b.t.	n.s.
KAT6B	-2.81	3.28E-02	-2.54	2.20E-02
MTFR1	-3.02	2.93E-02	b.t.	n.s.
RPS6KB1	-3.31	8.50E-03	b.t.	n.s.
CREM	-3.55	4.27E-02	b.t.	n.s.
HMCES	-4.08	1.43E-02	-2.9	1.80E-02
XAF1	-5.68	2.56E-02	-4.88	3.63E-02
BMP6	-6.87	3.06E-07	-2.48	5.95E-05
OAS1	-9.43	3.31E-02	-12.78	2.07E-02
RASGRP3	b.t.	n.s.	10.79	2.94E-02

EZH2	b.t.	n.s.	9.34	1.64E-02
CLIC2	b.t.	n.s.	9.14	7.90E-03
BATF3	b.t.	n.s.	5.54	1.54E-02
RASSF4	b.t.	n.s.	4.59	4.23E-02
S100A8	b.t.	n.s.	4.37	9.60E-03
CHRNA6	b.t.	n.s.	4.24	2.43E-02
TCFL5	b.t.	n.s.	4.21	2.22E-02
UNC119	b.t.	n.s.	4.03	6.80E-03
STPG1	b.t.	n.s.	3.9	2.16E-02
TCTN1	b.t.	n.s.	3.75	7.60E-03
TSPAN5	b.t.	n.s.	3.59	3.12E-02
C4BPB	b.t.	n.s.	3.57	4.00E-04
TNFRSF8	b.t.	n.s.	3.56	1.20E-03
HMSD	b.t.	n.s.	3.54	1.34E-02
USP12	b.t.	n.s.	3.38	2.80E-02
SEC61A2	b.t.	n.s.	3.37	2.33E-02
TMEM63B	b.t.	n.s.	3.36	4.13E-02
FLVCR2	b.t.	n.s.	3.06	1.14E-02
ARID5A	b.t.	n.s.	3.04	8.30E-03
CLIP2	b.t.	n.s.	3	3.66E-02
FNBP1	b.t.	n.s.	2.97	4.80E-02
LACTB	b.t.	n.s.	2.93	3.80E-02
RBBP9	b.t.	n.s.	2.9	7.00E-04
UBL7	b.t.	n.s.	2.89	2.90E-03
NFKBIE	b.t.	n.s.	2.85	2.67E-02
JUN	b.t.	n.s.	2.79	1.96E-02
ERO1B	b.t.	n.s.	2.78	3.30E-03
ETFA	b.t.	n.s.	2.62	1.72E-02
SAMD13	b.t.	n.s.	2.56	1.53E-02

NFKBIA	b.t.	n.s.	2.55	3.70E-03
CFLAR	b.t.	n.s.	2.54	2.91E-02
CCL22	b.t.	n.s.	2.44	8.30E-03
OXCT1	b.t.	n.s.	2.43	4.76E-02
TRIP10	b.t.	n.s.	2.31	1.98E-02
CCR7	b.t.	n.s.	2.26	3.27E-02
GRINA	b.t.	n.s.	2.24	3.91E-02
ARPC5	b.t.	n.s.	2.22	3.91E-02
CTSB	b.t.	n.s.	2.21	3.95E-02
PFDN4	b.t.	n.s.	2.21	4.55E-02
ZNF660	b.t.	n.s.	2.19	1.48E-02
SCARB1	b.t.	n.s.	2.18	4.96E-02
DYRK4	b.t.	n.s.	2.17	1.73E-02
GPR55	b.t.	n.s.	2.14	4.23E-02
NUDT6	b.t.	n.s.	2.14	2.71E-02
SYNPO	b.t.	n.s.	2.14	2.59E-02
C1orf50	b.t.	n.s.	2.13	4.42E-02
TMSB4X	b.t.	n.s.	2.09	2.23E-02
CCDC167	b.t.	n.s.	2.04	4.07E-02
FGD6	b.t.	n.s.	2.02	1.60E-03
CR2	b.t.	n.s.	2.01	2.50E-02
NACAD	b.t.	n.s.	2.01	1.25E-02
RBMX2	b.t.	n.s.	1.98	2.63E-02
ASPM	b.t.	n.s.	1.96	2.00E-03
SMCO2	b.t.	n.s.	1.96	7.90E-03
TIMM17B	b.t.	n.s.	1.95	3.48E-02
BASP1	b.t.	n.s.	1.94	2.64E-02
RAP2A	b.t.	n.s.	1.94	4.50E-02
APOC2	b.t.	n.s.	1.92	1.31E-02

ELP6	b.t.	n.s.	1.92	3.49E-02
GPM6B	b.t.	n.s.	1.92	3.93E-02
OIT3	b.t.	n.s.	1.92	2.20E-03
PGBD4	b.t.	n.s.	1.9	4.98E-02
CRTC2	b.t.	n.s.	1.9	2.59E-02
MRPL40	b.t.	n.s.	1.9	1.56E-02
PARK7	b.t.	n.s.	1.9	9.10E-03
CBLN3	b.t.	n.s.	1.88	1.68E-02
ANGEL2	b.t.	n.s.	1.88	1.96E-02
DPH5	b.t.	n.s.	1.88	4.00E-03
FSIP1	b.t.	n.s.	1.88	4.80E-03
LYN	b.t.	n.s.	1.88	2.11E-02
SLC2A6	b.t.	n.s.	1.87	4.07E-02
PFN1	b.t.	n.s.	1.85	3.79E-02
SUMO2	b.t.	n.s.	1.85	1.62E-02
COMMD1	b.t.	n.s.	1.84	1.44E-02
LYPLAL1	b.t.	n.s.	1.84	3.93E-02
RPL18A	b.t.	n.s.	1.84	3.81E-02
C5orf63	b.t.	n.s.	1.83	3.27E-02
INAFM2	b.t.	n.s.	1.83	1.86E-02
THEMIS2	b.t.	n.s.	1.83	3.35E-02
USP32	b.t.	n.s.	1.82	4.45E-02
DEFB115	b.t.	n.s.	1.81	3.70E-02
SNN	b.t.	n.s.	1.8	1.26E-02
MTFR1L	b.t.	n.s.	1.79	2.04E-02
RPL24	b.t.	n.s.	1.79	4.98E-02
SOCS2	b.t.	n.s.	1.78	1.50E-02
UBLCP1	b.t.	n.s.	1.78	2.92E-02
C6orf99	b.t.	n.s.	1.77	3.03E-02

POMT1	b.t.	n.s.	1.77	3.98E-02
LIPK	b.t.	n.s.	1.76	1.80E-02
RP1L1	b.t.	n.s.	1.76	1.00E-04
TRIM24	b.t.	n.s.	1.74	1.19E-02
SNX10	b.t.	n.s.	1.73	2.32E-02
CFAP54	b.t.	n.s.	1.71	1.08E-02
UBA5	b.t.	n.s.	1.71	3.66E-02
FADD	b.t.	n.s.	1.7	1.36E-02
GABRG2	b.t.	n.s.	1.7	1.30E-02
ANXA13	b.t.	n.s.	1.7	2.57E-02
AZGP1	b.t.	n.s.	1.69	2.79E-02
AHCYL2	b.t.	n.s.	1.68	3.75E-02
SERTAD2	b.t.	n.s.	1.68	1.78E-02
DCBLD2	b.t.	n.s.	1.67	3.25E-02
DLL4	b.t.	n.s.	1.67	3.44E-02
LYG1	b.t.	n.s.	1.67	3.60E-02
P2RY13	b.t.	n.s.	1.66	2.90E-03
PTH	b.t.	n.s.	1.66	1.14E-02
DAB1	b.t.	n.s.	1.66	4.30E-02
KRT79	b.t.	n.s.	1.66	6.00E-04
ROM1	b.t.	n.s.	1.66	1.00E-04
KRTAP19-7	b.t.	n.s.	1.65	4.76E-02
ADGRF1	b.t.	n.s.	1.65	2.54E-02
SPATA31C1	b.t.	n.s.	1.65	1.58E-02
ZNF648	b.t.	n.s.	1.63	6.00E-04
PIM2	b.t.	n.s.	1.63	4.00E-02
CHRNB4	b.t.	n.s.	1.62	2.90E-03
IFNA5	b.t.	n.s.	1.62	1.64E-02
CASQ1	b.t.	n.s.	1.62	5.20E-03

FBXO4	b.t.	n.s.	1.62	5.00E-04
UBE2K	b.t.	n.s.	1.62	4.70E-02
ZCCHC7	b.t.	n.s.	1.62	1.20E-03
DARS	b.t.	n.s.	1.61	3.22E-02
NINJ1	b.t.	n.s.	1.6	3.86E-02
PTPRR	b.t.	n.s.	1.6	2.81E-02
CLIC6	b.t.	n.s.	1.59	3.90E-03
DZIP3	b.t.	n.s.	1.59	2.38E-02
KIAA0391	b.t.	n.s.	1.59	4.41E-02
IGSF9B	b.t.	n.s.	1.58	4.52E-02
MKS1	b.t.	n.s.	1.58	4.21E-02
NENF	b.t.	n.s.	1.58	4.92E-02
IFT52	b.t.	n.s.	1.57	3.58E-02
KBTBD12	b.t.	n.s.	1.57	1.16E-02
ZNF358	b.t.	n.s.	1.57	2.30E-03
MAP3K6	b.t.	n.s.	1.56	4.79E-02
NXF5	b.t.	n.s.	1.56	3.30E-02
PSMG3	b.t.	n.s.	1.56	4.28E-02
ATP1B4	b.t.	n.s.	1.55	8.50E-03
ZNF696	b.t.	n.s.	1.55	2.83E-02
ADCY10	b.t.	n.s.	1.55	3.52E-02
ARHGAP23	b.t.	n.s.	1.55	3.04E-02
GIPC2	b.t.	n.s.	1.54	1.72E-02
LRIG1	b.t.	n.s.	1.54	3.64E-02
SERPINB3	b.t.	n.s.	1.54	2.29E-02
RGR	b.t.	n.s.	1.54	9.90E-03
SLC6A11	b.t.	n.s.	1.54	1.76E-02
TIMP4	b.t.	n.s.	1.54	1.45E-02
MOG	b.t.	n.s.	1.53	4.37E-02

NOXRED1	b.t.	n.s.	1.53	2.19E-02
ZSCAN4	b.t.	n.s.	1.52	7.30E-03
RIMS2	b.t.	n.s.	1.52	2.72E-02
RPS6KL1	b.t.	n.s.	1.52	2.45E-02
VEPH1	b.t.	n.s.	1.52	4.91E-02
HESX1	b.t.	n.s.	1.51	4.28E-02
PENK	b.t.	n.s.	1.51	8.70E-03
STAC	b.t.	n.s.	1.51	1.84E-02
OCM	b.t.	n.s.	1.5	3.92E-02
CLEC18C	b.t.	n.s.	1.5	2.24E-02
LY6H	b.t.	n.s.	1.5	1.60E-02
MALSU1	b.t.	n.s.	1.5	2.07E-02
PRRT3	b.t.	n.s.	1.5	2.00E-02
SASS6	b.t.	n.s.	1.5	3.33E-02
TMEM144	b.t.	n.s.	1.5	4.10E-02
DGKD	b.t.	n.s.	-1.5	1.58E-02
ARHGEF40	b.t.	n.s.	-1.5	9.60E-03
COX4I2	b.t.	n.s.	-1.5	3.51E-02
BACH2	b.t.	n.s.	-1.52	3.41E-02
DAW1	b.t.	n.s.	-1.52	7.40E-03
HARS2	b.t.	n.s.	-1.52	3.71E-02
USP31	b.t.	n.s.	-1.53	3.28E-02
CMYA5	b.t.	n.s.	-1.54	3.44E-02
GPR107	b.t.	n.s.	-1.54	1.45E-02
SHC4	b.t.	n.s.	-1.54	1.00E-02
GAPVD1	b.t.	n.s.	-1.55	3.64E-02
MTMR3	b.t.	n.s.	-1.55	4.92E-02
EIF2AK3	b.t.	n.s.	-1.56	3.19E-02
SEMA4B	b.t.	n.s.	-1.56	3.99E-02

TRAF2	b.t.	n.s.	-1.56	1.23E-02
INSL5	b.t.	n.s.	-1.57	6.60E-03
AQP12A	b.t.	n.s.	-1.57	7.00E-04
LINGO2	b.t.	n.s.	-1.57	1.71E-02
PDPK1	b.t.	n.s.	-1.57	2.48E-02
OR4C12	b.t.	n.s.	-1.59	6.00E-04
CTDP1	b.t.	n.s.	-1.59	3.02E-02
KCNH1	b.t.	n.s.	-1.59	1.36E-02
SULT1A1	b.t.	n.s.	-1.59	2.52E-02
RRN3	b.t.	n.s.	-1.6	3.98E-02
TANC1	b.t.	n.s.	-1.6	5.40E-03
TYW1B	b.t.	n.s.	-1.6	2.79E-02
SIM1	b.t.	n.s.	-1.61	2.15E-02
SMAD3	b.t.	n.s.	-1.61	1.69E-02
SERPINA9	b.t.	n.s.	-1.65	3.04E-02
ANKMY1	b.t.	n.s.	-1.66	1.03E-02
CPEB2	b.t.	n.s.	-1.66	4.36E-02
HSDL1	b.t.	n.s.	-1.67	3.97E-02
SPATA25	b.t.	n.s.	-1.68	4.31E-02
FAM169A	b.t.	n.s.	-1.68	1.32E-02
SLC9B2	b.t.	n.s.	-1.7	1.57E-02
SRD5A1	b.t.	n.s.	-1.71	2.01E-02
GIGYF2	b.t.	n.s.	-1.75	3.63E-02
TOE1	b.t.	n.s.	-1.75	1.56E-02
CNST	b.t.	n.s.	-1.76	3.00E-03
TAF13	b.t.	n.s.	-1.76	2.12E-02
MAD1L1	b.t.	n.s.	-1.77	3.96E-02
ACSS1	b.t.	n.s.	-1.78	3.86E-02
BRD9	b.t.	n.s.	-1.81	2.06E-02

ING5	b.t.	n.s.	-1.82	1.21E-02
CRACR2A	b.t.	n.s.	-1.84	4.09E-02
MECP2	b.t.	n.s.	-1.84	1.99E-02
BRD1	b.t.	n.s.	-1.85	1.17E-02
ZNF776	b.t.	n.s.	-1.85	2.25E-02
CNNM4	b.t.	n.s.	-1.88	3.81E-02
ZNF565	b.t.	n.s.	-1.88	2.07E-02
TOP1MT	b.t.	n.s.	-1.9	4.55E-02
PPIE	b.t.	n.s.	-1.93	3.45E-02
VPS11	b.t.	n.s.	-1.93	1.80E-02
NRF1	b.t.	n.s.	-2.01	1.94E-02
ADRB2	b.t.	n.s.	-2.02	8.00E-03
QPCTL	b.t.	n.s.	-2.05	4.63E-02
CRAMP1	b.t.	n.s.	-2.11	3.80E-03
SLC25A30	b.t.	n.s.	-2.11	2.06E-02
ZNF131	b.t.	n.s.	-2.15	2.20E-03
KDM4B	b.t.	n.s.	-2.17	2.00E-04
C5orf56	b.t.	n.s.	-2.18	1.26E-02
CYFIP2	b.t.	n.s.	-2.18	4.43E-02
NDEL1	b.t.	n.s.	-2.2	1.38E-02
MLXIP	b.t.	n.s.	-2.22	9.00E-04
GFOD1	b.t.	n.s.	-2.22	1.56E-02
ITIH4	b.t.	n.s.	-2.22	4.48E-02
SLC25A26	b.t.	n.s.	-2.33	2.76E-02
ARHGAP9	b.t.	n.s.	-2.34	3.46E-02
ZNF613	b.t.	n.s.	-2.37	1.51E-02
MADD	b.t.	n.s.	-2.39	2.10E-03
SYCP3	b.t.	n.s.	-2.41	1.08E-02
C19orf66	b.t.	n.s.	-2.47	3.96E-02

NF1	b.t.	n.s.	-2.48	1.67E-02
PLEKHA7	b.t.	n.s.	-2.51	1.73E-02
INPP5A	b.t.	n.s.	-2.56	4.98E-02
ZNF331	b.t.	n.s.	-2.58	2.72E-02
BANP	b.t.	n.s.	-2.62	1.58E-02
ZZEF1	b.t.	n.s.	-2.88	4.62E-02
PLEKHA2	b.t.	n.s.	-2.97	3.49E-02
OSBPL3	b.t.	n.s.	-2.98	7.90E-03
SAT1	b.t.	n.s.	-3.05	4.85E-02
PELI1	b.t.	n.s.	-3.09	1.75E-02
HIST1H4A	b.t.	n.s.	-3.17	1.78E-02
PACSIN2	b.t.	n.s.	-3.22	2.30E-02
NFATC1	b.t.	n.s.	-3.29	4.87E-02
SGK3	b.t.	n.s.	-3.48	1.00E-04
IL18R1	b.t.	n.s.	-3.5	2.61E-02
LAX1	b.t.	n.s.	-4.15	2.76E-02
HIST1H2BI	b.t.	n.s.	-4.23	1.12E-02
APBB2	b.t.	n.s.	-5.31	3.33E-02
LY9	b.t.	n.s.	-7.82	1.17E-02
P2RX5	b.t.	n.s.	-8.83	3.68E-02
TBC1D9	b.t.	n.s.	-10.95	1.13E-02

WT (Barcelona)	Fold Change (CvsA)	P-val (CvsA)	Fold Change (DvsB)	P-val (DvsB)
CYBRD1	111.12	4.22E-06	26.75	2.00E-04
GPR160	56.5	7.30E-03	17.29	3.05E-02
MGLL	43.95	5.40E-03	13.54	9.30E-03
BATF	40.95	4.00E-04	28.68	9.00E-04
BATF3	40.79	9.00E-04	37.47	1.80E-03
TNFRSF9	38.59	1.82E-02	b.t.	n.s.

STAT3	34.99	5.79E-07	23.05	7.47E-06
P2RX7	32.12	3.04E-02	b.t.	n.s.
SLC43A3	29.57	3.20E-03	6.14	1.98E-02
SESN2	28.39	3.90E-03	b.t.	n.s.
DGKG	24.85	1.10E-03	63.47	9.36E-05
BASP1	23.64	2.20E-03	7.23	4.20E-03
BCAR3	21.96	8.50E-03	b.t.	n.s.
C4orf46	21.68	1.60E-03	11.17	1.30E-03
TNFAIP3	20.43	6.57E-05	10.91	3.30E-05
TRAF1	19.75	5.00E-04	26.03	4.00E-04
BID	19.33	1.70E-03	4.8	2.92E-02
ELL2	18.89	4.60E-05	18.36	1.22E-05
NAMPT	18.62	2.21E-02	b.t.	n.s.
ATF3	17.45	3.30E-02	12.58	3.80E-03
SLC7A5	17.09	4.30E-03	b.t.	n.s.
NCF2	16	2.30E-03	6.91	9.10E-03
PLGRKT	15.77	9.59E-05	5.43	9.00E-04
MYO1G	15.15	9.00E-04	7.49	1.35E-02
GPR183	13.78	2.29E-02	18.45	2.21E-02
SLAMF1	13.09	3.71E-02	b.t.	n.s.
IL2RB	12.67	7.24E-05	5.29	4.90E-03
GPR132	12.35	5.00E-04	16.94	8.83E-05
LDHA	11.69	1.44E-02	b.t.	n.s.
RAB29	11.01	1.10E-03	6.99	7.00E-03
TUBB	10.85	2.00E-04	b.t.	n.s.
C1QBP	10.68	1.64E-02	b.t.	n.s.
EZH2	10.63	2.20E-03	28.25	2.00E-04
HUWE1	10.54	1.30E-03	6	3.40E-03
RANBP1	10.09	4.61E-02	b.t.	n.s.

WARS	9.98	3.00E-04	3.53	4.99E-02
PSMB5	9.7	5.30E-03	4.35	4.40E-02
CHRNA6	9.68	1.90E-03	18.83	2.00E-04
MREG	9.62	2.78E-02	8.19	2.27E-02
PRMT1	9.56	2.55E-02	b.t.	n.s.
SLC1A5	9.51	1.02E-02	b.t.	n.s.
RHOF	9.43	2.00E-04	6.06	8.00E-04
PKM	9.28	4.00E-04	4.38	9.70E-03
NFKBIA	9.2	1.00E-03	8.5	2.91E-05
VDAC1	8.95	1.35E-02	b.t.	n.s.
TMEM97	8.92	5.40E-03	b.t.	n.s.
GRAMD1B	8.88	2.84E-02	19.96	9.30E-03
BOLA3	8.85	1.08E-02	b.t.	n.s.
SARS	8.72	1.19E-02	b.t.	n.s.
CCND2	8.64	1.20E-03	5.34	8.20E-03
BCAT1	8.5	1.70E-03	6.93	1.51E-02
IFNGR1	8.45	1.40E-03	4.7	4.10E-03
COX17	8.35	8.40E-03	3.22	2.99E-02
RASSF2	8.28	3.30E-03	3.34	2.77E-02
FASN	8.26	8.70E-03	b.t.	n.s.
PTPN1	8.2	2.36E-06	5.6	1.21E-05
NFE2L1	8.16	2.00E-04	2.2	3.42E-02
SERPINB9	8.06	4.41E-02	b.t.	n.s.
SNX11	7.98	1.61E-02	3.17	1.52E-02
PHB	7.89	9.70E-03	b.t.	n.s.
GOT1	7.86	7.00E-03	b.t.	n.s.
POLR3H	7.81	2.61E-02	b.t.	n.s.
PSMB2	7.8	1.24E-02	3.44	2.44E-02
PSMC5	7.8	1.23E-02	b.t.	n.s.

LILRB4	7.71	6.00E-03	b.t.	n.s.
MTX1	7.66	5.90E-03	3.09	4.02E-02
MRPL24	7.64	7.10E-03	b.t.	n.s.
CD80	7.61	4.73E-02	11.17	7.80E-03
RPL26L1	7.6	1.52E-02	b.t.	n.s.
LCP1	7.53	6.00E-04	3.52	1.86E-02
ARPC5L	7.5	1.23E-02	b.t.	n.s.
EIF4EBP1	7.5	3.94E-02	b.t.	n.s.
COX5A	7.48	1.77E-02	b.t.	n.s.
PCK2	7.47	2.83E-02	b.t.	n.s.
DCPS	7.36	3.70E-03	b.t.	n.s.
COLCA2	7.17	1.20E-03	5.52	1.28E-02
ZNF460	7.16	1.00E-04	6.89	4.60E-05
LY96	7	3.70E-03	4.12	2.95E-02
PRDX1	7	9.00E-04	2.91	2.46E-02
PSMA1	6.83	4.80E-03	b.t.	n.s.
CCT3	6.81	2.19E-02	b.t.	n.s.
ARHGAP31	6.8	4.40E-03	6.4	1.40E-03
LRP8	6.79	4.20E-03	b.t.	n.s.
MRPL23	6.7	9.60E-03	b.t.	n.s.
PSMB10	6.69	3.09E-02	b.t.	n.s.
KSR1	6.65	5.60E-03	4.47	9.60E-03
PSMD3	6.58	3.50E-03	b.t.	n.s.
POLD2	6.57	3.30E-03	2.28	4.21E-02
NDUFA11	6.54	1.05E-02	b.t.	n.s.
SFT2D1	6.53	3.20E-03	5.05	1.32E-02
FLVCR2	6.52	1.00E-04	8.53	7.84E-05
GPR157	6.52	5.20E-03	b.t.	n.s.
PSMA6	6.52	3.90E-03	2.89	2.64E-02

MPC1	6.45	2.08E-02	b.t.	n.s.
PSMA3	6.39	9.30E-03	2.45	4.06E-02
SLC6A9	6.38	2.59E-02	b.t.	n.s.
PSMC3	6.37	1.42E-02	3.19	3.91E-02
ANAPC11	6.36	8.00E-04	b.t.	n.s.
LAT2	6.29	5.70E-03	b.t.	n.s.
CPNE5	6.25	2.80E-03	5.97	2.00E-03
JMY	6.23	1.80E-03	11.82	6.00E-04
TUBA1C	6.22	2.10E-03	b.t.	n.s.
DBI	6.19	1.00E-04	1.93	4.19E-02
ABTB2	6.18	1.27E-02	b.t.	n.s.
ENO1	6.14	1.62E-02	b.t.	n.s.
SLIRP	6.1	4.95E-02	b.t.	n.s.
SLC2A5	6.07	2.00E-04	3.81	8.00E-04
COX7B	5.92	1.67E-02	b.t.	n.s.
PHPT1	5.85	6.40E-03	b.t.	n.s.
NAA38	5.81	3.70E-03	b.t.	n.s.
SEC61G	5.8	6.20E-03	b.t.	n.s.
PABPC4	5.77	2.68E-02	b.t.	n.s.
SLC2A13	5.71	4.00E-04	4.4	2.30E-03
PIK3C2B	5.67	4.60E-03	b.t.	n.s.
LARS	5.63	1.58E-02	2.33	2.08E-02
SOD2	5.62	4.32E-02	b.t.	n.s.
JAK3	5.55	4.97E-05	4.08	4.30E-03
CSF2RB	5.54	1.00E-03	3.89	2.44E-02
KLHL6	5.54	6.00E-04	2.56	4.42E-02
POLR2I	5.52	2.00E-03	b.t.	n.s.
PRELID1	5.51	1.47E-02	b.t.	n.s.
DDIT4	5.43	1.70E-03	3.38	4.09E-02

RCN1	5.42	2.70E-02	b.t.	n.s.
TFRC	5.42	2.00E-03	7.74	6.00E-04
XPOT	5.4	3.21E-02	b.t.	n.s.
RASSF4	5.39	1.34E-02	4.76	2.40E-03
BCL6	5.3	1.30E-03	7.31	5.00E-04
TBC1D9B	5.3	1.52E-02	b.t.	n.s.
ST8SIA4	5.28	2.71E-02	9.01	5.00E-04
CBX6	5.24	2.28E-02	4.2	2.48E-02
PPIF	5.23	3.20E-03	b.t.	n.s.
ZDHHC18	5.22	3.00E-04	3.2	4.80E-03
MRPS15	5.07	4.20E-03	b.t.	n.s.
CD274	5.06	2.45E-02	b.t.	n.s.
AIMP2	5.05	3.51E-02	b.t.	n.s.
CHAC1	5.02	8.70E-03	b.t.	n.s.
HSD17B10	5	7.00E-03	b.t.	n.s.
PSMD11	5	1.08E-02	3.66	3.05E-02
AKR1A1	4.97	2.50E-03	b.t.	n.s.
MRPL47	4.97	2.08E-02	b.t.	n.s.
HCCS	4.91	2.88E-02	b.t.	n.s.
MTHFD2	4.91	3.40E-03	2.95	1.05E-02
SLC7A1	4.9	2.50E-03	b.t.	n.s.
EPRS	4.88	1.39E-02	b.t.	n.s.
ZSCAN2	4.86	2.78E-02	b.t.	n.s.
CALR	4.81	2.00E-04	b.t.	n.s.
PTGER4	4.81	3.80E-03	b.t.	n.s.
AGMAT	4.8	1.53E-02	b.t.	n.s.
PSMA7	4.79	2.00E-03	2.57	2.75E-02
HELLS	4.76	8.84E-05	5.68	6.72E-06
MRPS28	4.76	4.31E-02	b.t.	n.s.

RUVBL1	4.76	4.04E-02	b.t.	n.s.
PSMC1	4.73	1.33E-02	b.t.	n.s.
CDKN1A	4.72	1.59E-02	3.18	4.17E-02
BLVRA	4.69	7.37E-08	2.92	7.67E-05
PDGFA	4.69	1.62E-02	b.t.	n.s.
CTH	4.64	4.60E-03	6.36	6.20E-03
RFC2	4.63	3.10E-03	3.24	5.30E-03
SEC11C	4.6	9.24E-06	3.09	5.00E-04
POMP	4.58	2.71E-02	b.t.	n.s.
TUBA1A	4.57	7.70E-03	b.t.	n.s.
TUBA1B	4.5	4.30E-03	b.t.	n.s.
TSPAN5	4.49	1.70E-03	3.68	1.30E-03
RFTN1	4.48	1.56E-02	5.6	1.42E-02
ELL3	4.43	6.90E-03	3.78	6.90E-03
PSMC2	4.43	1.05E-02	3.28	2.34E-02
POU2AF1	4.42	6.20E-03	2.68	4.42E-02
PARP1	4.41	1.21E-02	2.49	4.35E-02
PNP	4.4	4.90E-03	b.t.	n.s.
RSL24D1	4.37	2.37E-02	2.91	4.74E-02
HSPA9	4.35	1.10E-02	b.t.	n.s.
TWISTNB	4.35	4.80E-02	b.t.	n.s.
ZNF267	4.35	2.30E-03	3.11	1.90E-03
MYCN	4.33	4.32E-02	b.t.	n.s.
BANF1	4.32	4.77E-02	b.t.	n.s.
GARS	4.31	8.00E-03	2.94	2.17E-02
CST7	4.28	2.13E-02	b.t.	n.s.
CHAF1B	4.28	1.80E-03	2.89	8.50E-03
NBEAL2	4.28	1.40E-03	2.93	2.49E-02
GHITM	4.25	1.12E-02	b.t.	n.s.

ARNTL2	4.22	4.85E-02	6.3	3.70E-03
NIT2	4.21	3.30E-03	b.t.	n.s.
GTDC1	4.2	9.60E-03	4.03	1.40E-03
PDCD5	4.2	2.12E-02	b.t.	n.s.
RAD23A	4.2	7.10E-03	b.t.	n.s.
TRIP10	4.19	1.52E-02	7.83	1.13E-02
CENPW	4.18	2.77E-02	b.t.	n.s.
NDUFB9	4.18	2.60E-03	2.87	3.20E-02
API5	4.17	2.76E-02	b.t.	n.s.
SLC25A23	4.15	3.20E-03	b.t.	n.s.
SMARCA2	4.15	2.08E-02	4.14	1.62E-02
CYC1	4.13	4.60E-03	b.t.	n.s.
CYB5A	4.12	3.00E-03	3.86	2.80E-03
BUD31	4.11	9.40E-03	2.6	1.44E-02
SNF8	4.1	1.57E-02	b.t.	n.s.
MRPL40	4.09	7.30E-03	3.26	4.03E-02
NDUFB7	4.09	1.81E-02	b.t.	n.s.
F5	4.08	1.30E-03	b.t.	n.s.
SRA1	4.08	1.65E-02	b.t.	n.s.
SSRP1	4.08	1.26E-02	b.t.	n.s.
PSMD2	4.07	1.20E-03	2.77	4.21E-02
SNRPE	4.06	1.99E-02	b.t.	n.s.
CCT7	4.05	3.87E-02	b.t.	n.s.
PSMA4	4.05	4.78E-02	b.t.	n.s.
IRF4	4.04	2.50E-03	b.t.	n.s.
SLC25A19	4.04	3.30E-03	b.t.	n.s.
PARK7	4.03	8.00E-04	2.93	1.15E-02
PSMD14	4.03	1.02E-02	b.t.	n.s.
RAB13	4.02	7.10E-03	4.9	1.60E-03

ARSG	4.01	1.85E-02	b.t.	n.s.
CHCHD2	4	6.50E-03	b.t.	n.s.
IARS	3.98	7.30E-03	b.t.	n.s.
MRPL11	3.98	2.31E-02	b.t.	n.s.
PSMA5	3.97	1.11E-02	2.85	1.46E-02
SRI	3.96	4.70E-03	b.t.	n.s.
AICDA	3.9	4.40E-02	b.t.	n.s.
JUN	3.9	1.50E-03	4.96	4.00E-04
EIF3I	3.89	2.70E-02	b.t.	n.s.
LILRB1	3.89	1.00E-03	3.93	4.00E-03
ABCD2	3.87	4.94E-05	12.77	9.10E-03
TNFSF4	3.87	1.15E-02	10.29	7.00E-03
HTRA2	3.85	1.12E-06	3.34	5.51E-05
TOMM22	3.84	2.89E-02	b.t.	n.s.
EXOSC1	3.81	2.80E-03	b.t.	n.s.
MRPS7	3.81	4.47E-02	b.t.	n.s.
PPP1R9B	3.81	1.90E-03	3.06	8.50E-03
ZDHHC16	3.8	2.30E-03	b.t.	n.s.
HMBS	3.78	2.08E-02	1.95	1.80E-03
CNTNAP1	3.77	3.58E-02	b.t.	n.s.
NDUFAB1	3.77	4.09E-02	b.t.	n.s.
RPS19	3.77	2.30E-03	1.82	2.44E-02
ICAM1	3.75	6.60E-03	3.7	3.30E-03
C5AR1	3.74	2.00E-04	3.08	4.00E-04
CCDC6	3.74	3.00E-04	2.93	7.00E-04
ROMO1	3.74	1.08E-02	b.t.	n.s.
RPLP0	3.74	2.90E-03	2.02	2.38E-02
AGPAT3	3.71	5.00E-03	1.97	8.30E-03
PSMD4	3.71	3.62E-02	b.t.	n.s.

STOML2	3.71	9.80E-03	b.t.	n.s.
BLVRB	3.7	6.50E-03	b.t.	n.s.
COX8A	3.7	1.60E-02	b.t.	n.s.
RAB9A	3.69	1.71E-02	2.92	2.80E-03
PSMB1	3.68	1.77E-02	b.t.	n.s.
MRPL13	3.67	4.05E-02	b.t.	n.s.
CARM1	3.66	8.00E-04	3.05	4.90E-03
H2AFZ	3.66	1.09E-02	b.t.	n.s.
TXN	3.66	2.00E-04	b.t.	n.s.
NAGA	3.65	6.50E-03	b.t.	n.s.
PSMB4	3.65	1.30E-03	2.33	2.13E-02
SQLE	3.64	1.58E-02	b.t.	n.s.
SLC3A2	3.63	3.51E-02	b.t.	n.s.
LYPLA2	3.6	1.81E-02	b.t.	n.s.
PCCB	3.6	1.17E-02	b.t.	n.s.
PSMD8	3.59	2.77E-02	b.t.	n.s.
COX6A1	3.58	2.03E-02	b.t.	n.s.
POLR2K	3.57	4.71E-02	2.28	3.44E-02
MTCH2	3.55	5.70E-03	b.t.	n.s.
STAT5B	3.55	4.61E-05	3.66	7.95E-05
ERAL1	3.54	5.50E-03	b.t.	n.s.
EIF2S2	3.52	1.52E-02	b.t.	n.s.
PLBD2	3.52	4.80E-03	b.t.	n.s.
G6PC3	3.51	4.44E-02	b.t.	n.s.
PDIA6	3.51	2.23E-02	b.t.	n.s.
PPP5C	3.5	1.80E-03	2.4	2.03E-02
AARS	3.49	1.50E-03	b.t.	n.s.
NDUFS5	3.49	9.00E-04	1.82	4.17E-02
FERMT3	3.48	2.50E-03	b.t.	n.s.

LRRC42	3.47	8.00E-04	b.t.	n.s.
MRPS18C	3.47	2.62E-02	2.57	2.57E-02
STPG1	3.46	1.00E-03	4.37	4.00E-04
PSMB7	3.45	1.20E-02	b.t.	n.s.
MIF	3.44	3.01E-02	b.t.	n.s.
TMEM205	3.44	1.00E-04	2.18	1.68E-02
CCDC124	3.43	2.44E-02	b.t.	n.s.
PFN1	3.43	1.60E-03	b.t.	n.s.
ACTG1	3.42	1.09E-02	b.t.	n.s.
ASNA1	3.42	5.70E-03	b.t.	n.s.
CFLAR	3.42	1.00E-03	4.24	1.00E-04
HMSD	3.42	1.88E-02	4.81	1.21E-02
MRPL46	3.42	3.44E-02	b.t.	n.s.
ATF4	3.41	2.94E-02	b.t.	n.s.
LACTB	3.41	1.29E-02	3.74	2.90E-03
NACC1	3.41	1.08E-02	b.t.	n.s.
SLC20A1	3.41	6.00E-04	2.7	5.00E-04
ERH	3.4	4.00E-04	2.68	9.00E-04
TXNL4A	3.39	4.64E-02	b.t.	n.s.
ACOT13	3.38	1.20E-03	1.82	1.49E-02
ANXA2	3.38	4.80E-03	b.t.	n.s.
HSPA5	3.38	2.63E-02	b.t.	n.s.
NTHL1	3.38	4.02E-02	b.t.	n.s.
PSMB3	3.38	6.90E-03	2.81	3.85E-02
TAGLN2	3.38	1.90E-03	5.98	1.00E-04
EFTUD2	3.37	5.90E-03	b.t.	n.s.
NUP155	3.37	3.49E-02	b.t.	n.s.
RFX5	3.35	1.10E-03	2.25	3.60E-03
DSTN	3.34	4.60E-03	4.6	5.00E-04

ZNRF1	3.34	1.86E-02	b.t.	n.s.
ARPC4	3.33	8.30E-03	b.t.	n.s.
IDH2	3.33	3.50E-03	b.t.	n.s.
QDPR	3.33	2.77E-02	b.t.	n.s.
XBP1	3.33	4.00E-04	2.31	1.89E-02
CLIP1	3.32	8.60E-03	3.37	2.18E-02
NRAS	3.32	1.10E-03	2.07	1.24E-02
SNRPB	3.32	3.28E-02	b.t.	n.s.
FSD1L	3.31	4.86E-02	2.83	2.29E-02
COX7A2	3.3	3.15E-02	b.t.	n.s.
NME3	3.3	1.90E-03	b.t.	n.s.
PSMD7	3.29	4.20E-03	b.t.	n.s.
TP53BP2	3.29	2.40E-03	3.11	7.00E-04
GNA12	3.28	1.00E-03	3.08	2.00E-04
ADRM1	3.27	1.60E-02	b.t.	n.s.
SNRPD3	3.27	2.25E-02	b.t.	n.s.
NDUFB3	3.26	2.83E-02	b.t.	n.s.
HAX1	3.26	2.06E-02	b.t.	n.s.
APEX1	3.25	3.13E-02	b.t.	n.s.
KCNN4	3.25	7.80E-03	b.t.	n.s.
LAMTOR2	3.25	1.35E-02	b.t.	n.s.
ARHGDIA	3.24	2.92E-02	b.t.	n.s.
ACBD6	3.23	1.08E-02	b.t.	n.s.
COX6B1	3.23	8.90E-03	b.t.	n.s.
TMED2	3.23	3.19E-02	b.t.	n.s.
ACTN4	3.21	2.40E-02	b.t.	n.s.
MCL1	3.21	2.70E-03	2.92	4.60E-03
MRPL1	3.2	3.58E-02	b.t.	n.s.
GSTP1	3.17	4.70E-03	2.55	3.68E-02

NFKB2	3.17	1.41E-02	3.43	3.20E-03
PSMD1	3.17	1.34E-02	b.t.	n.s.
CRELD2	3.16	8.20E-03	b.t.	n.s.
MANF	3.16	1.01E-02	b.t.	n.s.
PSME1	3.16	1.90E-02	2.82	3.69E-02
UQCRQ	3.16	2.23E-02	b.t.	n.s.
NDUFAF3	3.15	4.50E-02	b.t.	n.s.
TMEM208	3.15	4.12E-02	b.t.	n.s.
TMEM63B	3.15	1.94E-02	2.82	3.12E-02
LDHB	3.14	3.72E-02	b.t.	n.s.
CXCR5	3.13	2.89E-02	4.37	8.30E-03
TNIP2	3.13	1.20E-03	1.9	1.90E-02
DPYSL2	3.11	3.87E-02	b.t.	n.s.
GLRX3	3.1	2.90E-03	b.t.	n.s.
GOT2	3.1	1.70E-03	2.8	3.40E-03
SUB1	3.1	4.58E-02	b.t.	n.s.
SUMO3	3.1	1.40E-02	b.t.	n.s.
TFDP1	3.1	4.96E-02	b.t.	n.s.
ZNF442	3.1	4.00E-04	1.54	8.60E-03
CLPP	3.09	1.50E-03	b.t.	n.s.
HTT	3.09	1.24E-02	b.t.	n.s.
EIF2S1	3.08	3.68E-02	b.t.	n.s.
MAPKAP1	3.08	6.20E-03	b.t.	n.s.
MFSD10	3.08	6.00E-04	b.t.	n.s.
NUDT5	3.08	4.63E-02	b.t.	n.s.
OXCT1	3.08	2.20E-03	b.t.	n.s.
SLC25A43	3.07	7.61E-05	2.15	2.47E-02
IER5	3.06	2.30E-03	1.64	4.31E-02
GPS1	3.06	4.30E-03	b.t.	n.s.

HIGD1A	3.06	3.45E-02	b.t.	n.s.
NHP2	3.06	4.20E-02	b.t.	n.s.
PPP1R7	3.06	3.70E-03	2.23	3.60E-02
OGFOD3	3.05	3.90E-02	b.t.	n.s.
TRAPPC1	3.05	3.93E-02	b.t.	n.s.
EIF4H	3.04	9.50E-03	b.t.	n.s.
COX6C	3.02	1.80E-03	b.t.	n.s.
LSM3	3.02	9.20E-03	2.51	3.44E-02
SLCO5A1	3.02	4.20E-03	4.26	1.00E-04
TUBG1	3.02	9.30E-03	b.t.	n.s.
FDPS	3.01	6.60E-03	b.t.	n.s.
COA3	3	4.00E-02	b.t.	n.s.
GTF3C6	3	4.82E-02	b.t.	n.s.
JADE3	3	8.50E-03	3.76	8.50E-03
TOX2	3	7.70E-03	b.t.	n.s.
YARS	3	2.46E-02	b.t.	n.s.
YARS2	3	4.52E-02	b.t.	n.s.
CTSA	2.99	2.35E-02	b.t.	n.s.
MTHFD1	2.99	3.00E-04	2.49	1.20E-03
ORMDL2	2.99	2.27E-02	b.t.	n.s.
CCDC167	2.98	5.80E-03	2.63	4.50E-03
IMPDH2	2.98	2.90E-03	b.t.	n.s.
INTS9	2.98	5.60E-03	2.27	7.00E-03
MDH2	2.98	4.31E-02	b.t.	n.s.
MRPL22	2.98	1.38E-02	b.t.	n.s.
TACO1	2.98	4.14E-02	b.t.	n.s.
AIFM2	2.97	8.00E-03	b.t.	n.s.
PGK1	2.96	2.57E-02	b.t.	n.s.
SLC35F2	2.96	2.73E-02	b.t.	n.s.

FURIN	2.95	9.40E-03	1.83	2.90E-02
PGAM1	2.94	1.43E-02	b.t.	n.s.
POLE2	2.94	2.29E-02	2.16	2.93E-02
UBL7	2.94	1.00E-04	3.59	3.00E-04
PSMC4	2.93	8.30E-03	3.05	1.15E-02
DEGS1	2.93	6.70E-03	2.64	1.50E-03
NDUFA2	2.93	4.03E-02	b.t.	n.s.
CLIP2	2.92	1.53E-02	b.t.	n.s.
NDUFA12	2.92	1.88E-02	b.t.	n.s.
CHCHD3	2.91	3.75E-02	2.65	3.06E-02
STK38L	2.9	4.10E-03	1.79	4.59E-02
ARPC5	2.89	9.90E-03	b.t.	n.s.
IKZF1	2.89	3.11E-02	4.5	5.10E-03
UBE2L3	2.89	9.60E-03	1.55	4.29E-02
RNASEH2A	2.88	1.75E-02	b.t.	n.s.
SF3B6	2.88	1.09E-02	b.t.	n.s.
APOO	2.87	3.46E-02	b.t.	n.s.
HMGCR	2.87	1.29E-02	b.t.	n.s.
PROSER1	2.87	1.57E-02	b.t.	n.s.
UNC119	2.87	2.18E-02	b.t.	n.s.
GLRX2	2.86	2.76E-02	b.t.	n.s.
NABP2	2.86	1.10E-03	b.t.	n.s.
YIF1B	2.86	2.84E-02	b.t.	n.s.
ALYREF	2.85	2.79E-02	b.t.	n.s.
APRT	2.85	3.49E-02	b.t.	n.s.
CSRP1	2.85	1.43E-02	b.t.	n.s.
TMPRSS6	2.85	1.00E-04	3.06	1.40E-03
MRPS16	2.84	1.14E-02	b.t.	n.s.
NPM3	2.84	4.22E-02	b.t.	n.s.

COX7A2L	2.83	2.74E-02	b.t.	n.s.
KCNC4	2.83	9.00E-04	b.t.	n.s.
MAP4	2.83	2.69E-02	2.35	4.35E-02
NUP93	2.83	2.11E-02	b.t.	n.s.
PCYT2	2.83	8.60E-03	b.t.	n.s.
TIFA	2.82	9.40E-03	5.93	6.03E-05
IL21R	2.82	3.80E-03	4.08	6.00E-04
RPGRIP1L	2.81	2.20E-03	b.t.	n.s.
GGH	2.8	3.27E-02	b.t.	n.s.
MRPL20	2.8	4.93E-02	b.t.	n.s.
ELMO1	2.79	6.70E-03	3.38	1.71E-02
RASGRP4	2.79	1.69E-02	8.74	1.71E-02
DARS	2.78	6.00E-04	2.08	6.70E-03
KIF9	2.78	2.68E-02	b.t.	n.s.
NDUFA13	2.78	7.70E-03	b.t.	n.s.
UBE2N	2.78	4.69E-02	b.t.	n.s.
COMMD7	2.77	5.30E-03	b.t.	n.s.
NR6A1	2.77	3.30E-03	3.05	5.00E-04
NT5C	2.77	1.00E-04	3.03	3.30E-03
PPIB	2.77	7.40E-03	b.t.	n.s.
TARBP1	2.77	2.32E-02	b.t.	n.s.
ADAT2	2.76	3.48E-02	b.t.	n.s.
FNBP1	2.76	8.30E-03	2.92	1.98E-02
KIF21A	2.76	1.23E-02	b.t.	n.s.
STAT5A	2.76	5.00E-04	2.61	3.50E-03
COMMD1	2.75	6.00E-03	3.81	3.90E-03
CPSF3	2.75	4.03E-02	1.73	3.72E-02
HINT2	2.75	3.04E-02	b.t.	n.s.
PEA15	2.75	3.10E-03	b.t.	n.s.

GRB2	2.74	3.80E-03	b.t.	n.s.
PSMB8	2.74	2.02E-02	b.t.	n.s.
ASNS	2.73	2.86E-02	2.35	2.54E-02
MED20	2.71	4.57E-02	b.t.	n.s.
PPID	2.71	1.00E-03	2.3	8.00E-04
AP3M2	2.7	4.13E-02	b.t.	n.s.
DNAJB11	2.7	2.50E-02	b.t.	n.s.
MBD2	2.7	5.32E-05	2.39	3.57E-05
MMAB	2.7	3.15E-02	b.t.	n.s.
POLDIP2	2.7	2.30E-03	b.t.	n.s.
RPS15	2.7	2.78E-02	2.28	4.14E-02
SEC61B	2.7	5.20E-03	b.t.	n.s.
UQCRH	2.7	8.70E-03	b.t.	n.s.
CLTA	2.69	2.36E-02	b.t.	n.s.
EIF2B1	2.69	1.35E-02	b.t.	n.s.
EIF2D	2.69	7.70E-03	1.89	4.88E-02
NDUFA4	2.69	7.20E-03	b.t.	n.s.
PRDX3	2.69	1.69E-02	b.t.	n.s.
ACOT4	2.68	7.50E-03	2.1	2.02E-02
TUBB4B	2.68	2.12E-02	b.t.	n.s.
CALM3	2.67	3.00E-04	1.97	2.39E-02
CARS	2.67	1.31E-02	b.t.	n.s.
IER3IP1	2.67	1.16E-02	b.t.	n.s.
NDUFB11	2.67	1.08E-02	b.t.	n.s.
OSTC	2.67	1.39E-02	b.t.	n.s.
C9orf64	2.66	5.10E-03	1.61	1.21E-02
ALG5	2.65	3.97E-02	b.t.	n.s.
PFDN4	2.65	3.50E-02	2.99	6.30E-03
ARID5A	2.64	3.40E-03	3.76	9.00E-04

CSTF2	2.64	3.40E-03	2.62	3.69E-02
NT5DC2	2.64	2.94E-02	b.t.	n.s.
PSENEN	2.64	9.40E-03	1.74	1.40E-02
ANAPC16	2.63	2.02E-02	b.t.	n.s.
LARP1	2.63	3.66E-02	b.t.	n.s.
SDF2L1	2.63	2.07E-02	b.t.	n.s.
VIM	2.63	1.13E-02	2.33	3.38E-02
AP2S1	2.62	6.70E-03	b.t.	n.s.
CBS	2.62	4.21E-02	b.t.	n.s.
MZT2B	2.62	2.08E-02	b.t.	n.s.
RPS9	2.62	4.61E-02	b.t.	n.s.
ACLY	2.61	9.00E-03	b.t.	n.s.
INTS3	2.61	3.52E-02	b.t.	n.s.
CCZ1B	2.6	8.30E-03	1.98	1.53E-02
CYB5B	2.6	1.88E-02	b.t.	n.s.
MAD2L2	2.6	1.27E-02	1.84	2.45E-02
TFEB	2.6	1.33E-02	b.t.	n.s.
FKBP5	2.59	3.30E-03	1.74	3.11E-02
GRHPR	2.59	7.40E-03	2.94	4.40E-03
RFXANK	2.59	7.80E-03	b.t.	n.s.
CRLS1	2.58	1.97E-02	b.t.	n.s.
MRPS5	2.58	3.81E-02	b.t.	n.s.
PAX5	2.58	3.55E-02	b.t.	n.s.
PLEKHO1	2.58	3.92E-02	b.t.	n.s.
RAB27A	2.58	3.16E-02	b.t.	n.s.
REXO2	2.58	2.46E-02	b.t.	n.s.
GTF2H3	2.57	1.09E-02	2.45	4.70E-02
HNRNPA1	2.57	2.29E-02	b.t.	n.s.
KLF6	2.57	3.97E-02	b.t.	n.s.

MRPL48	2.57	4.71E-02	b.t.	n.s.
THOC7	2.57	8.60E-03	b.t.	n.s.
YWHAE	2.57	9.80E-03	2.4	3.07E-02
UBQLN2	2.56	2.80E-03	2.44	3.10E-03
ASXL1	2.56	6.00E-04	3.8	1.00E-04
GLS	2.56	1.64E-02	1.86	3.69E-02
PPP4C	2.56	3.67E-02	b.t.	n.s.
HMGB2	2.55	2.83E-02	b.t.	n.s.
NDUFB8	2.55	3.10E-03	b.t.	n.s.
PCBD1	2.55	2.50E-02	b.t.	n.s.
DNAJC25-GNG10	2.54	2.40E-03	1.85	5.90E-03
ACOT7	2.54	5.10E-03	1.82	3.12E-02
ZDHHC12	2.54	1.23E-02	b.t.	n.s.
AGPS	2.53	4.99E-02	b.t.	n.s.
CAPZB	2.53	6.60E-03	2.04	2.02E-02
REEP4	2.53	7.90E-03	1.65	4.34E-02
RPS6KA1	2.52	1.80E-03	1.94	2.06E-02
CETN2	2.52	1.12E-02	b.t.	n.s.
SBNO2	2.52	2.05E-02	b.t.	n.s.
COPE	2.51	1.50E-02	b.t.	n.s.
FERMT2	2.51	3.57E-02	b.t.	n.s.
MORN2	2.51	3.40E-03	b.t.	n.s.
POC5	2.51	2.91E-02	2.66	1.89E-02
TMEM167A	2.5	3.33E-02	b.t.	n.s.
VCP	2.5	3.20E-03	b.t.	n.s.
COX5B	2.49	2.99E-02	b.t.	n.s.
S1PR2	2.49	2.16E-02	b.t.	n.s.
COMMD4	2.48	1.16E-02	b.t.	n.s.
MIPEP	2.48	4.00E-03	2.09	4.18E-02

NUDT19	2.48	2.02E-02	b.t.	n.s.
PPME1	2.48	6.90E-03	b.t.	n.s.
SUMO1	2.48	1.47E-02	2.3	1.92E-02
TXNL1	2.47	2.91E-02	b.t.	n.s.
SRGN	2.46	9.10E-03	2.23	3.00E-02
TSPAN17	2.46	3.00E-04	b.t.	n.s.
ATP6V0E1	2.45	2.71E-02	b.t.	n.s.
BABAM1	2.45	1.55E-02	b.t.	n.s.
NENF	2.45	7.47E-05	b.t.	n.s.
TIGD2	2.45	1.72E-02	3.14	3.90E-03
MCTS1	2.44	3.36E-02	b.t.	n.s.
TP53	2.42	4.23E-02	b.t.	n.s.
CEBPG	2.42	2.48E-02	b.t.	n.s.
SF3B5	2.42	4.46E-02	b.t.	n.s.
ACAT1	2.42	3.35E-02	b.t.	n.s.
GMPPB	2.42	3.05E-02	b.t.	n.s.
NANS	2.42	3.22E-02	b.t.	n.s.
NDUFB6	2.41	1.72E-02	b.t.	n.s.
BLM	2.41	4.62E-02	b.t.	n.s.
CFL1	2.41	2.15E-02	b.t.	n.s.
FUCA2	2.41	4.08E-02	b.t.	n.s.
NDUFB10	2.41	4.39E-02	b.t.	n.s.
TUBB8	2.41	4.50E-03	b.t.	n.s.
TSPAN31	2.4	1.86E-02	b.t.	n.s.
VLDLR	2.4	1.20E-03	b.t.	n.s.
UQCRFS1	2.39	1.30E-02	b.t.	n.s.
IMPAD1	2.39	4.56E-02	b.t.	n.s.
KATNA1	2.39	9.60E-03	b.t.	n.s.
USP46	2.39	1.15E-02	b.t.	n.s.

VPS25	2.39	2.96E-02	b.t.	n.s.
MSMO1	2.38	4.06E-02	b.t.	n.s.
CUEDC2	2.37	3.37E-02	b.t.	n.s.
MRPS33	2.37	2.91E-02	b.t.	n.s.
RPA2	2.37	1.66E-02	1.81	3.28E-02
SARNP	2.37	4.47E-02	b.t.	n.s.
SLC39A9	2.37	5.40E-03	b.t.	n.s.
AGA	2.36	4.90E-03	b.t.	n.s.
POMGNT1	2.36	2.10E-02	b.t.	n.s.
PPIH	2.36	3.43E-02	b.t.	n.s.
PPM1M	2.36	4.23E-02	b.t.	n.s.
CCT6A	2.35	2.23E-02	2	4.34E-02
HNRNPL	2.35	1.63E-02	b.t.	n.s.
HSP90AB1	2.35	3.18E-02	b.t.	n.s.
MRPL51	2.35	1.82E-02	b.t.	n.s.
DYNLRB1	2.34	7.40E-03	b.t.	n.s.
LILRB2	2.34	1.48E-02	2.8	6.20E-03
NDUFV1	2.34	4.70E-03	1.91	1.10E-02
PIH1D1	2.34	1.22E-02	b.t.	n.s.
RPL39L	2.33	4.95E-02	2.24	4.59E-02
COPZ1	2.33	3.99E-02	b.t.	n.s.
XRCC6	2.33	3.49E-02	b.t.	n.s.
ANXA5	2.32	2.20E-02	b.t.	n.s.
PGM2	2.32	1.80E-03	b.t.	n.s.
CETN3	2.31	1.38E-02	b.t.	n.s.
NDUFB1	2.31	4.30E-03	b.t.	n.s.
RAB10	2.31	4.85E-02	2.32	4.57E-02
RPS27L	2.31	2.76E-02	b.t.	n.s.
SNRPA	2.31	2.67E-02	b.t.	n.s.

ALDOA	2.3	2.35E-02	b.t.	n.s.
CANX	2.3	9.00E-04	1.68	4.72E-02
FLAD1	2.3	4.93E-02	b.t.	n.s.
HARS	2.3	2.78E-02	b.t.	n.s.
SLC25A11	2.3	3.00E-03	b.t.	n.s.
SSR4	2.3	2.42E-02	b.t.	n.s.
CHMP2A	2.29	9.80E-03	b.t.	n.s.
ELAVL1	2.29	8.30E-03	b.t.	n.s.
HHLA3	2.29	1.03E-02	b.t.	n.s.
STRAP	2.29	2.52E-02	b.t.	n.s.
RPP25L	2.28	2.08E-02	b.t.	n.s.
DAP3	2.28	2.71E-02	b.t.	n.s.
ETFA	2.28	5.70E-03	2.08	5.10E-03
MED8	2.28	2.46E-02	b.t.	n.s.
ANXA7	2.27	7.40E-03	1.79	1.42E-02
EDF1	2.27	1.42E-02	b.t.	n.s.
MOB1A	2.27	3.92E-02	2.03	3.90E-02
SREBF2	2.27	2.14E-02	b.t.	n.s.
COPS6	2.26	1.83E-02	1.92	3.07E-02
NDUFV2	2.26	3.00E-02	2.48	1.00E-02
PLD2	2.26	1.00E-04	1.68	6.30E-03
HSPBP1	2.25	3.80E-02	b.t.	n.s.
SF3B3	2.25	2.07E-02	b.t.	n.s.
ACSL1	2.24	3.89E-02	b.t.	n.s.
ARPC1A	2.24	2.23E-02	b.t.	n.s.
ISY1	2.24	2.22E-02	b.t.	n.s.
MAPK13	2.24	2.77E-02	b.t.	n.s.
SLC25A52	2.23	1.62E-02	1.91	2.20E-02
ACTB	2.23	1.48E-02	b.t.	n.s.

CAPN1	2.23	7.00E-04	b.t.	n.s.
CASZ1	2.23	1.24E-02	1.94	1.20E-03
DDB1	2.23	9.10E-03	b.t.	n.s.
MRFAP1	2.23	2.66E-02	b.t.	n.s.
NAV1	2.23	3.04E-02	b.t.	n.s.
ACTA1	2.22	3.00E-03	b.t.	n.s.
RBX1	2.22	4.64E-02	b.t.	n.s.
LSM7	2.21	4.94E-02	b.t.	n.s.
MECR	2.21	1.42E-02	b.t.	n.s.
RBBP9	2.21	4.22E-02	2.17	1.65E-02
BLMH	2.2	1.83E-02	b.t.	n.s.
RPL12	2.2	3.90E-03	b.t.	n.s.
USP12	2.2	2.60E-02	6.03	1.00E-04
BDH1	2.19	2.63E-02	b.t.	n.s.
CASP6	2.19	1.77E-02	b.t.	n.s.
MAP3K14	2.19	4.75E-02	b.t.	n.s.
MRPL28	2.19	1.97E-02	b.t.	n.s.
PDIA3	2.19	7.20E-03	b.t.	n.s.
ISOC1	2.18	2.10E-02	b.t.	n.s.
RPL10A	2.18	1.16E-02	b.t.	n.s.
SPAG1	2.18	1.84E-02	2.5	1.60E-03
PSMD13	2.17	2.90E-02	b.t.	n.s.
TBCB	2.17	9.30E-03	b.t.	n.s.
UBA5	2.17	1.12E-02	b.t.	n.s.
UQCR10	2.17	4.50E-02	b.t.	n.s.
CDC42	2.16	6.00E-03	1.81	1.30E-02
GBA3	2.16	2.60E-02	2.26	2.18E-02
MPZL1	2.16	2.43E-02	b.t.	n.s.
RALA	2.16	4.98E-02	b.t.	n.s.

TALDO1	2.16	9.20E-03	b.t.	n.s.
TUBE1	2.16	2.83E-02	b.t.	n.s.
ACP2	2.15	4.20E-02	b.t.	n.s.
BSG	2.15	4.53E-02	b.t.	n.s.
LZTR1	2.15	1.10E-03	b.t.	n.s.
RYR3	2.15	8.90E-03	b.t.	n.s.
TAF9B	2.15	7.50E-03	1.98	4.23E-02
UBXN1	2.15	2.60E-03	b.t.	n.s.
GNG10	2.14	2.00E-04	1.52	1.28E-02
SURF4	2.14	3.50E-03	b.t.	n.s.
ASAH2B	2.13	2.03E-02	b.t.	n.s.
FBRS	2.13	5.00E-03	b.t.	n.s.
MAPRE1	2.13	2.89E-02	1.74	4.34E-02
MCAT	2.13	3.64E-02	b.t.	n.s.
MDH1	2.13	2.21E-02	1.64	4.97E-02
SOD1	2.13	2.16E-02	b.t.	n.s.
SRD5A3	2.13	2.35E-02	b.t.	n.s.
VAMP8	2.13	2.71E-02	b.t.	n.s.
GPX1	2.12	3.59E-02	b.t.	n.s.
MRPL19	2.12	1.41E-02	b.t.	n.s.
UQCR11	2.12	2.63E-02	b.t.	n.s.
ALDH18A1	2.11	2.65E-02	b.t.	n.s.
TXN2	2.11	3.24E-02	b.t.	n.s.
ALDH4A1	2.1	7.20E-03	1.86	1.30E-03
ARMT1	2.1	2.80E-03	b.t.	n.s.
CAPNS1	2.1	4.30E-03	b.t.	n.s.
COPG1	2.1	1.50E-02	b.t.	n.s.
H3F3B	2.1	2.20E-02	b.t.	n.s.
RFFL	2.1	1.21E-02	3.65	1.10E-03

RPA3	2.1	3.15E-02	1.84	4.23E-02
FBL	2.09	8.30E-03	1.94	1.15E-02
ALAS1	2.09	6.60E-03	b.t.	n.s.
FKTN	2.09	2.62E-02	b.t.	n.s.
GNAI2	2.09	2.28E-02	b.t.	n.s.
UQCRC1	2.09	2.73E-02	b.t.	n.s.
RFC4	2.08	3.48E-02	b.t.	n.s.
RPS27A	2.08	3.08E-02	b.t.	n.s.
YIF1A	2.08	2.36E-02	b.t.	n.s.
DHPS	2.07	3.63E-02	1.87	1.68E-02
MCM5	2.07	4.70E-02	b.t.	n.s.
RPL26	2.07	3.49E-02	b.t.	n.s.
TIMMDC1	2.07	1.60E-02	b.t.	n.s.
UFC1	2.07	1.28E-02	b.t.	n.s.
DDOST	2.06	3.36E-02	b.t.	n.s.
GSS	2.06	1.44E-02	b.t.	n.s.
SAE1	2.06	2.26E-02	b.t.	n.s.
WDR1	2.06	3.95E-02	b.t.	n.s.
IFFO2	2.05	1.39E-02	b.t.	n.s.
ZNF511	2.05	3.22E-02	b.t.	n.s.
GTF2H4	2.04	1.53E-02	b.t.	n.s.
NUP188	2.04	4.40E-03	b.t.	n.s.
SEC61A2	2.04	1.92E-02	3.07	1.10E-03
ARL13B	2.03	3.85E-02	b.t.	n.s.
ECT2	2.03	2.23E-02	b.t.	n.s.
NEK6	2.03	1.52E-02	b.t.	n.s.
PRG2	2.03	4.79E-02	b.t.	n.s.
SPIN3	2.03	4.30E-03	1.77	2.11E-02
UBA3	2.03	9.40E-03	1.63	3.42E-02

VDAC2	2.03	1.96E-02	b.t.	n.s.
CLP1	2.02	9.00E-03	b.t.	n.s.
ACO2	2.02	1.22E-02	b.t.	n.s.
BRK1	2.02	4.79E-02	b.t.	n.s.
EBP	2.02	4.21E-02	b.t.	n.s.
MALSU1	2.02	2.29E-02	b.t.	n.s.
MON1A	2.02	3.82E-05	b.t.	n.s.
POLA2	2.02	3.00E-04	2.31	2.00E-04
RNF181	2.02	3.94E-02	b.t.	n.s.
TMEM173	2.02	3.62E-02	b.t.	n.s.
HYOU1	2.01	1.58E-05	3.79	3.42E-02
MSRB1	2.01	2.49E-02	b.t.	n.s.
RAP1A	2.01	8.00E-04	2.01	2.00E-03
RBM42	2.01	4.00E-03	b.t.	n.s.
RPLP1	2.01	6.10E-03	b.t.	n.s.
RPS5	2.01	1.83E-02	b.t.	n.s.
UCHL5	2.01	2.04E-02	b.t.	n.s.
FBXW5	2	2.80E-03	b.t.	n.s.
RFC3	2	4.70E-03	1.57	5.30E-03
DUSP22	1.99	7.80E-03	2.95	6.00E-04
PEPD	1.99	4.20E-02	b.t.	n.s.
SLC25A33	1.99	4.41E-02	b.t.	n.s.
TDRKH	1.99	1.03E-02	b.t.	n.s.
CCNB1	1.98	7.70E-03	b.t.	n.s.
CSE1L	1.98	2.01E-02	b.t.	n.s.
CWC27	1.98	2.25E-02	b.t.	n.s.
MRPS36	1.98	2.43E-02	2.23	1.88E-02
NDUFA6	1.98	2.43E-02	b.t.	n.s.
NMT1	1.98	7.40E-03	2.15	3.32E-02

RAD51C	1.98	4.39E-02	b.t.	n.s.
SUMO2	1.98	7.90E-03	1.71	2.88E-02
WDR83OS	1.98	4.23E-02	b.t.	n.s.
RPL36AL	1.97	3.74E-02	1.96	1.83E-02
BIVM	1.97	1.56E-02	b.t.	n.s.
C15orf41	1.97	3.79E-02	1.94	3.19E-02
GTF2I	1.97	2.33E-02	3.05	6.40E-03
PRKAG1	1.97	1.82E-02	b.t.	n.s.
SMCO2	1.97	7.10E-03	1.58	9.60E-03
SSNA1	1.97	4.61E-02	b.t.	n.s.
TIMM17B	1.97	1.95E-02	b.t.	n.s.
ENSA	1.96	9.00E-04	b.t.	n.s.
FBXW7	1.96	2.78E-02	b.t.	n.s.
FXR1	1.96	1.96E-02	2.24	2.17E-02
INTS2	1.96	6.70E-03	b.t.	n.s.
KIAA0391	1.96	3.26E-02	b.t.	n.s.
METTL6	1.96	1.12E-02	b.t.	n.s.
MRPL55	1.96	3.48E-02	b.t.	n.s.
NONO	1.96	5.20E-03	b.t.	n.s.
TCF19	1.96	4.96E-02	b.t.	n.s.
TKT	1.96	2.09E-02	b.t.	n.s.
UBE2A	1.96	4.70E-03	b.t.	n.s.
ASPSCR1	1.95	2.09E-02	b.t.	n.s.
CLTB	1.95	2.02E-02	b.t.	n.s.
EIF3K	1.95	4.26E-02	b.t.	n.s.
RPS24	1.95	4.60E-03	1.58	1.62E-02
TNFRSF8	1.95	1.76E-02	2.88	6.80E-03
TSR3	1.95	2.51E-02	b.t.	n.s.
ZNF281	1.95	4.80E-03	1.79	5.70E-03

CISD3	1.94	1.19E-02	b.t.	n.s.
KCTD17	1.94	2.70E-03	b.t.	n.s.
P4HB	1.94	8.30E-03	b.t.	n.s.
SEPHS1	1.94	2.26E-02	b.t.	n.s.
CNIH4	1.93	4.97E-02	b.t.	n.s.
OAT	1.93	3.95E-02	b.t.	n.s.
SLC25A6	1.93	3.03E-02	b.t.	n.s.
PRDX5	1.92	4.88E-02	b.t.	n.s.
PSMG3	1.92	1.66E-02	2.04	3.32E-02
SEC13	1.92	1.94E-02	b.t.	n.s.
AP1AR	1.91	8.00E-04	b.t.	n.s.
LETM1	1.91	3.43E-02	b.t.	n.s.
PLCB3	1.91	1.00E-04	1.7	5.40E-03
RPL18A	1.91	4.60E-03	1.69	3.49E-02
SAMD10	1.91	1.88E-05	b.t.	n.s.
SDHC	1.91	2.42E-02	b.t.	n.s.
SRRD	1.91	3.23E-02	b.t.	n.s.
VKORC1	1.91	1.88E-02	b.t.	n.s.
GNE	1.9	1.78E-02	b.t.	n.s.
MAP2K1	1.9	2.99E-02	b.t.	n.s.
MED16	1.9	6.30E-03	b.t.	n.s.
MGST3	1.9	4.50E-02	b.t.	n.s.
MRPL45	1.9	2.11E-02	b.t.	n.s.
NARS2	1.9	2.16E-02	b.t.	n.s.
RANGAP1	1.9	1.97E-02	b.t.	n.s.
THEMIS2	1.9	8.00E-04	b.t.	n.s.
TRIM24	1.9	8.70E-03	b.t.	n.s.
VTI1B	1.9	4.03E-02	b.t.	n.s.
ZBTB8OS	1.9	3.99E-02	1.58	1.81E-02

AKR1B1	1.89	2.01E-02	b.t.	n.s.
COG7	1.89	1.80E-02	b.t.	n.s.
DR1	1.89	3.20E-02	b.t.	n.s.
GALNT10	1.89	2.81E-02	1.62	2.07E-02
JTB	1.89	1.83E-02	b.t.	n.s.
NDUFS4	1.89	6.60E-03	b.t.	n.s.
SHKBP1	1.89	3.20E-03	b.t.	n.s.
TPRA1	1.89	3.29E-02	b.t.	n.s.
BNIP1	1.88	2.06E-02	b.t.	n.s.
C15orf65	1.88	1.40E-03	b.t.	n.s.
PAFAH1B3	1.88	4.30E-02	b.t.	n.s.
PNKP	1.88	3.36E-02	b.t.	n.s.
RPUSD3	1.88	1.52E-02	b.t.	n.s.
TPX2	1.88	2.12E-02	b.t.	n.s.
GGCX	1.87	7.20E-03	b.t.	n.s.
MSRB2	1.87	4.90E-02	b.t.	n.s.
MT1F	1.87	2.67E-02	b.t.	n.s.
OCIAD1	1.87	2.04E-02	b.t.	n.s.
TFDP2	1.87	1.86E-02	2.78	1.70E-03
ARCN1	1.86	6.30E-03	b.t.	n.s.
CHMP1A	1.86	6.90E-03	b.t.	n.s.
HLA-F	1.86	3.99E-02	b.t.	n.s.
PHF5A	1.86	3.79E-02	b.t.	n.s.
PLLP	1.86	1.70E-03	b.t.	n.s.
RAB1B	1.86	1.53E-02	b.t.	n.s.
RABEPK	1.86	3.12E-02	b.t.	n.s.
RNF126	1.86	3.60E-02	b.t.	n.s.
ATP13A3	1.85	4.05E-02	b.t.	n.s.
G6PD	1.85	2.43E-02	b.t.	n.s.

NCK2	1.85	1.50E-03	1.89	4.82E-02
PTGES2	1.85	2.31E-02	b.t.	n.s.
SKA3	1.85	1.66E-02	b.t.	n.s.
SLC35B4	1.85	3.60E-02	b.t.	n.s.
STXBP2	1.85	1.04E-02	b.t.	n.s.
UBE2T	1.84	1.54E-02	b.t.	n.s.
KRAS	1.83	4.03E-02	b.t.	n.s.
ADIPOR2	1.83	8.60E-03	b.t.	n.s.
ARSB	1.83	2.61E-02	2.41	1.05E-02
C11orf49	1.83	8.00E-04	b.t.	n.s.
C17orf75	1.83	2.44E-02	b.t.	n.s.
HAAO	1.83	3.30E-03	b.t.	n.s.
MRPS14	1.83	1.17E-02	b.t.	n.s.
TAX1BP3	1.82	6.40E-03	b.t.	n.s.
SNX1	1.82	2.69E-02	b.t.	n.s.
STX8	1.82	2.09E-02	b.t.	n.s.
CDK7	1.81	2.00E-04	b.t.	n.s.
DHTKD1	1.81	4.15E-02	2.15	1.67E-02
FASTK	1.81	1.42E-02	b.t.	n.s.
KLHL4	1.81	2.30E-03	b.t.	n.s.
PEX3	1.81	1.64E-02	b.t.	n.s.
RPL36A	1.81	3.62E-02	b.t.	n.s.
TMEM230	1.81	4.81E-02	b.t.	n.s.
ADH5	1.8	4.86E-02	b.t.	n.s.
HSPB11	1.8	2.56E-02	2.1	3.51E-02
KEAP1	1.8	3.29E-02	b.t.	n.s.
RBM14	1.8	9.50E-03	b.t.	n.s.
RPL7A	1.79	6.64E-05	1.59	3.60E-03
DUSP23	1.79	2.70E-02	b.t.	n.s.

POMK	1.79	2.05E-02	1.62	3.66E-02
PPIE	1.79	3.34E-02	b.t.	n.s.
ANAPC1	1.78	2.67E-02	b.t.	n.s.
AP4B1	1.78	6.90E-03	b.t.	n.s.
ARPC2	1.78	9.00E-04	1.89	1.00E-04
BCL9	1.78	8.70E-03	1.89	1.01E-02
SERPINI2	1.78	4.90E-03	b.t.	n.s.
THUMPD3	1.78	1.12E-02	b.t.	n.s.
FAF2	1.77	4.20E-03	b.t.	n.s.
GLYR1	1.77	2.49E-02	b.t.	n.s.
LRRC41	1.77	3.47E-02	b.t.	n.s.
MFN2	1.77	3.45E-02	b.t.	n.s.
PPP1CA	1.77	4.02E-02	b.t.	n.s.
PPP6R2	1.77	1.94E-02	b.t.	n.s.
PRPF31	1.77	3.76E-02	b.t.	n.s.
RSU1	1.77	4.34E-02	b.t.	n.s.
ZNF829	1.77	4.37E-02	b.t.	n.s.
AKR1B10	1.76	2.00E-04	b.t.	n.s.
CYLC2	1.76	4.51E-02	b.t.	n.s.
NIPSNAP1	1.76	2.57E-02	b.t.	n.s.
PTP4A2	1.76	2.99E-02	1.78	1.17E-02
RNF8	1.76	1.71E-02	b.t.	n.s.
SCAMP3	1.76	1.16E-02	b.t.	n.s.
FAM229B	1.75	6.70E-03	b.t.	n.s.
CALU	1.75	1.79E-02	b.t.	n.s.
DAZAP1	1.75	2.26E-02	b.t.	n.s.
KDELR2	1.75	4.79E-02	b.t.	n.s.
STAP2	1.75	1.84E-02	b.t.	n.s.
TPM3	1.75	2.00E-02	b.t.	n.s.

TRPC6	1.75	2.00E-04	b.t.	n.s.
ZMPSTE24	1.75	4.36E-02	b.t.	n.s.
CDK5R1	1.74	3.20E-02	b.t.	n.s.
IARS2	1.74	3.60E-02	b.t.	n.s.
MIEF1	1.74	4.67E-02	b.t.	n.s.
PEX19	1.74	1.03E-02	b.t.	n.s.
PPP2R5D	1.74	5.00E-04	b.t.	n.s.
SFXN2	1.74	3.48E-02	b.t.	n.s.
TTC1	1.74	4.82E-02	b.t.	n.s.
UHRF1BP1	1.74	2.05E-02	b.t.	n.s.
CENPH	1.73	4.32E-02	b.t.	n.s.
DNAAF5	1.73	4.70E-02	b.t.	n.s.
HDAC3	1.73	7.50E-03	b.t.	n.s.
RMDN3	1.73	2.83E-02	b.t.	n.s.
RPS17	1.73	3.69E-02	1.71	1.55E-02
TMEM189-UBE2V1	1.73	1.74E-02	b.t.	n.s.
VDAC3	1.73	3.84E-02	b.t.	n.s.
TRIM77	1.72	1.90E-02	b.t.	n.s.
FLOT2	1.72	2.43E-02	b.t.	n.s.
LIMK2	1.72	9.30E-03	1.54	2.70E-02
OGFOD1	1.72	4.78E-02	2.63	2.80E-03
RPE	1.72	4.77E-02	b.t.	n.s.
RPL37A	1.72	3.30E-03	1.9	8.00E-04
SLC25A26	1.72	3.80E-02	1.76	2.90E-02
SLC35A2	1.72	9.00E-04	b.t.	n.s.
TMOD1	1.72	8.30E-03	2.02	1.20E-03
COMMD5	1.71	1.71E-02	b.t.	n.s.
AAR2	1.71	4.05E-02	b.t.	n.s.
ARID3A	1.71	4.91E-02	b.t.	n.s.

ARL6IP4	1.71	3.36E-02	b.t.	n.s.
BCKDHB	1.71	1.50E-02	b.t.	n.s.
CXorf40A	1.71	7.10E-03	b.t.	n.s.
DARS2	1.71	2.47E-02	b.t.	n.s.
IL10RB	1.71	4.42E-02	2.34	3.30E-03
RPS21	1.71	2.34E-02	b.t.	n.s.
SLC33A1	1.71	2.60E-03	b.t.	n.s.
STIL	1.71	6.10E-03	b.t.	n.s.
TAF12	1.71	3.68E-02	b.t.	n.s.
ZNF197	1.7	1.00E-02	b.t.	n.s.
ACTR3	1.7	1.38E-02	b.t.	n.s.
ARID3B	1.7	1.03E-02	b.t.	n.s.
BUB1	1.7	4.02E-02	b.t.	n.s.
EIF4EBP2	1.7	4.13E-02	b.t.	n.s.
KATNBL1	1.7	2.66E-02	b.t.	n.s.
MLH1	1.7	2.12E-02	2.06	2.50E-03
MTF1	1.7	3.02E-02	b.t.	n.s.

WT (Aviano)	**Fold Change (CvsA)**	**P-val (CvsA)**	**Fold Change (DvsB)**	**P-val (DvsB)**
CD80	31.49	5.40E-03	7.89	1.55E-02
IL2RA	31.23	2.20E-03	40.38	2.00E-04
CYBRD1	28.05	1.09E-05	12.76	3.00E-04
RFTN1	22.95	1.14E-05	11.84	5.91E-05
FLVCR2	19.25	5.27E-06	11.79	3.54E-06
TNFRSF9	18.31	2.80E-03	7.24	4.78E-02
EZH2	17.59	2.00E-04	11.2	3.00E-04
MGLL	17.04	3.00E-04	15.16	3.00E-04
NCF2	16.27	1.00E-04	8.69	1.50E-03
TVP23A	16.23	3.60E-03	b.t.	n.s.

GPR132	15.44	2.49E-06	20.35	1.22E-07
TRAF1	14.88	1.56E-05	26.58	2.63E-05
SLAMF7	14.47	7.00E-04	b.t.	n.s.
ELL2	11.96	2.72E-05	9.46	5.27E-05
TNFSF4	10.33	5.00E-04	4.71	1.30E-03
ARHGAP31	10.11	7.00E-04	12.85	6.00E-04
SEMA7A	9.11	3.60E-03	9.69	8.00E-04
KDM2B	8.99	1.10E-03	6.52	4.30E-03
CHAC1	8.9	1.76E-02	b.t.	n.s.
SLC43A3	8.54	1.40E-03	b.t.	n.s.
KCNN4	7.73	1.19E-05	6.81	7.43E-05
PTGER4	7.58	5.00E-04	6.13	7.70E-03
EIF4EBP1	7.56	6.90E-03	b.t.	n.s.
RHOF	7.46	2.37E-05	7.2	4.04E-05
TFRC	7.41	1.00E-04	5.59	6.00E-04
VEGFA	7.21	1.66E-02	b.t.	n.s.
RASSF2	6.75	1.40E-03	4.27	1.10E-02
LTA	6.71	1.90E-03	5.52	1.90E-03
FAM129A	6.49	1.41E-02	4.94	3.20E-02
BID	6.43	1.09E-02	5.05	4.25E-02
HUWE1	6.42	3.00E-04	3.94	1.50E-03
ARNTL2	6.24	8.50E-03	8.02	2.10E-03
NEK6	6.11	3.00E-04	b.t.	n.s.
CDKN1A	6.1	8.00E-04	5.98	4.90E-03
CCND2	6.01	1.60E-03	4.18	1.33E-02
IGSF3	5.87	3.20E-02	b.t.	n.s.
BATF	5.85	2.55E-02	b.t.	n.s.
CLIC2	5.5	1.12E-02	14.03	6.00E-04
TNFAIP3	5.5	3.49E-05	9.87	1.26E-05

GPR183	5.42	7.70E-03	35.31	8.00E-04
C4orf46	5.34	5.00E-03	5.19	6.00E-03
NFKBIA	5.23	3.00E-04	5.78	3.37E-05
LRP8	5.15	1.43E-02	b.t.	n.s.
SLC7A5	5.11	1.27E-02	b.t.	n.s.
SESN2	5.05	4.40E-03	b.t.	n.s.
CAD	5.04	1.56E-02	b.t.	n.s.
CTH	5.03	5.30E-03	4.4	2.33E-02
ADCY3	4.88	1.50E-03	b.t.	n.s.
PAICS	4.82	4.46E-02	b.t.	n.s.
SLC1A5	4.82	1.33E-02	b.t.	n.s.
TSPAN33	4.77	8.00E-04	2.86	8.30E-03
BASP1	4.74	6.60E-03	3.81	2.05E-02
PDGFA	4.68	3.70E-03	b.t.	n.s.
TRIP10	4.61	2.00E-04	6.23	1.00E-04
MTHFD1L	4.51	5.20E-03	b.t.	n.s.
SNX11	4.5	6.80E-03	2.37	4.25E-02
DDIT4	4.47	5.50E-03	b.t.	n.s.
ST8SIA4	4.45	1.00E-03	4.66	5.90E-03
IL2RB	4.42	2.63E-02	b.t.	n.s.
CHAF1B	4.41	4.60E-03	2.31	2.59E-02
PREX1	4.38	1.96E-02	b.t.	n.s.
LCP1	4.17	7.70E-03	b.t.	n.s.
RANBP1	4.1	2.27E-02	b.t.	n.s.
TTK	4.05	6.00E-04	2.92	6.70E-03
AIFM2	4.03	4.20E-03	b.t.	n.s.
HMSD	4.02	1.37E-02	5.12	1.40E-03
ABTB2	4.01	5.00E-03	5.22	9.00E-04
PLGRKT	3.99	3.60E-03	2.97	2.74E-02

SLC7A1	3.99	1.20E-02	b.t.	n.s.
GPR157	3.98	1.46E-02	b.t.	n.s.
ADAT2	3.95	5.80E-03	b.t.	n.s.
FASN	3.92	1.23E-02	b.t.	n.s.
RASSF4	3.88	1.70E-03	4.57	5.30E-03
BCL2L1	3.86	6.40E-03	2.9	6.20E-03
CENPW	3.86	1.76E-02	b.t.	n.s.
PDSS1	3.84	8.20E-03	b.t.	n.s.
GALNT14	3.81	8.20E-03	b.t.	n.s.
NFKB2	3.81	9.23E-05	4.57	4.52E-05
JUNB	3.76	7.40E-03	3.79	9.00E-04
POLA2	3.75	1.92E-07	3.57	4.37E-07
DRAM1	3.74	3.92E-02	b.t.	n.s.
JUN	3.74	3.80E-03	5.44	4.40E-05
MFSD2A	3.74	2.00E-02	2.79	1.95E-02
PYCR1	3.71	5.00E-03	b.t.	n.s.
BCS1L	3.66	7.30E-03	b.t.	n.s.
MRPL23	3.64	2.40E-02	b.t.	n.s.
BOLA3	3.63	3.47E-02	b.t.	n.s.
SOX5	3.63	1.21E-02	5.22	4.00E-04
MYO1G	3.61	5.80E-03	4.2	2.76E-02
BLVRA	3.6	3.87E-05	2.05	8.60E-03
PRMT1	3.57	3.86E-02	b.t.	n.s.
PKM	3.55	5.50E-03	3.21	2.07E-02
ZDHHC18	3.53	2.30E-03	3.64	3.50E-03
PSMC2	3.51	4.00E-04	b.t.	n.s.
SLCO5A1	3.49	7.00E-04	5.47	1.70E-03
HYOU1	3.47	4.00E-04	b.t.	n.s.
ASNS	3.45	9.00E-04	b.t.	n.s.

FNBP1	3.44	3.00E-03	3.76	3.20E-03
MKNK2	3.43	3.10E-03	3.54	1.30E-03
RASGRP4	3.41	3.04E-02	6.64	2.00E-03
CD58	3.37	4.40E-03	b.t.	n.s.
STAP2	3.37	6.00E-04	2.21	1.97E-02
DGAT2	3.36	7.10E-03	3.11	1.19E-02
FERMT2	3.35	9.00E-04	b.t.	n.s.
ZSCAN2	3.34	4.49E-02	b.t.	n.s.
EXOSC8	3.31	8.70E-03	b.t.	n.s.
IL21R	3.31	1.00E-03	4.3	3.00E-04
B4GALT5	3.3	1.72E-02	3.27	2.19E-02
RAB13	3.3	9.70E-03	4.28	1.12E-02
NIFK	3.27	4.14E-02	b.t.	n.s.
PSMB5	3.22	3.38E-02	b.t.	n.s.
CYB5A	3.21	1.40E-03	2.66	1.28E-02
ENPP4	3.19	1.64E-02	b.t.	n.s.
BCL2A1	3.13	4.25E-02	b.t.	n.s.
GOT2	3.13	3.00E-04	2.4	2.60E-03
LDHA	3.13	3.63E-02	b.t.	n.s.
AIMP2	3.11	9.50E-03	b.t.	n.s.
LONP1	3.11	4.80E-03	b.t.	n.s.
TMEM63B	3.11	3.90E-03	2.62	3.30E-03
EPRS	3.1	1.79E-02	b.t.	n.s.
SEC61A2	3.1	7.50E-05	2.21	1.50E-03
GRHPR	3.09	2.30E-03	3.72	1.10E-03
CCL17	3.08	1.17E-02	4.67	7.00E-04
SSRP1	3.05	1.19E-02	b.t.	n.s.
OGFOD3	3.04	2.88E-02	b.t.	n.s.
CHRNA6	3.01	4.38E-02	5.04	3.90E-03

NAMPT	3	2.16E-02	b.t.	n.s.
ACSL4	2.98	9.21E-05	1.78	7.70E-03
RPF2	2.98	2.05E-02	b.t.	n.s.
ACAT1	2.97	2.14E-02	b.t.	n.s.
STAT3	2.97	2.60E-02	b.t.	n.s.
VDAC1	2.97	1.71E-02	b.t.	n.s.
COLCA2	2.95	8.70E-03	6.4	4.60E-03
TAGLN2	2.95	1.83E-02	2.15	2.92E-02
PSMC4	2.94	8.40E-03	b.t.	n.s.
LAT2	2.94	3.92E-02	b.t.	n.s.
NT5DC2	2.94	2.21E-02	b.t.	n.s.
RNF145	2.94	7.70E-03	2.43	2.03E-02
XPO5	2.94	1.08E-02	b.t.	n.s.
JADE3	2.92	8.50E-03	2.6	1.49E-02
PCK2	2.92	1.26E-02	b.t.	n.s.
PPP5C	2.92	5.10E-03	b.t.	n.s.
CSF2RB	2.9	7.00E-04	4.11	2.50E-03
SIK1	2.89	1.20E-02	1.99	3.18E-02
IER5	2.87	4.52E-06	2.4	8.86E-05
BZW2	2.87	1.78E-02	b.t.	n.s.
FKTN	2.87	1.30E-03	b.t.	n.s.
PABPC4	2.87	5.50E-03	b.t.	n.s.
MTHFD2	2.86	1.68E-02	b.t.	n.s.
PPP1R9B	2.85	1.10E-03	3.07	1.40E-03
ARID3A	2.84	1.40E-03	b.t.	n.s.
NKRF	2.84	8.80E-03	b.t.	n.s.
DNMT3A	2.8	3.58E-02	b.t.	n.s.
PRDX1	2.8	1.04E-02	b.t.	n.s.
CCDC28B	2.79	2.00E-03	1.9	7.30E-03

PSMB2	2.79	2.82E-02	b.t.	n.s.
ACY1	2.75	1.04E-02	b.t.	n.s.
FH	2.75	3.00E-03	b.t.	n.s.
LARS	2.74	3.80E-03	b.t.	n.s.
ADAMDEC1	2.73	1.12E-02	1.78	2.26E-02
MRPL3	2.73	2.08E-02	b.t.	n.s.
PPP1R14B	2.73	2.20E-02	b.t.	n.s.
RRM1	2.73	3.40E-03	b.t.	n.s.
TCERG1	2.73	1.34E-02	b.t.	n.s.
DPCD	2.72	1.23E-02	b.t.	n.s.
STAT5A	2.72	3.56E-05	2.64	3.18E-05
TNFRSF8	2.7	6.50E-03	2.77	5.00E-04
HAX1	2.69	4.46E-02	b.t.	n.s.
RABEPK	2.69	1.40E-02	b.t.	n.s.
SPAG1	2.69	1.40E-03	2.34	1.50E-03
MDFIC	2.68	3.36E-02	b.t.	n.s.
SYNPO	2.68	3.00E-03	3.78	1.50E-03
ZNF460	2.68	5.60E-03	2.27	4.80E-03
TNF	2.67	2.57E-02	6.5	2.42E-02
CCL5	2.65	4.88E-02	2.11	1.90E-02
CD44	2.65	9.10E-03	3.26	6.00E-03
PDCD5	2.65	1.15E-02	b.t.	n.s.
PSMC1	2.64	1.77E-02	b.t.	n.s.
ICAM1	2.62	6.10E-03	3.55	1.10E-03
PPIF	2.62	2.43E-02	b.t.	n.s.
PSMD14	2.59	9.80E-03	b.t.	n.s.
BLMH	2.58	6.80E-03	2.04	3.17E-02
DESI1	2.58	8.90E-03	b.t.	n.s.
DSTN	2.58	1.26E-02	b.t.	n.s.

ANXA7	2.57	6.30E-05	2.04	3.00E-04
PFAS	2.57	2.01E-02	b.t.	n.s.
RBPJ	2.57	7.87E-05	1.79	1.68E-02
TMEM54	2.57	1.60E-02	2.54	2.70E-03
STAT5B	2.56	1.40E-03	2.37	2.40E-03
TIPIN	2.55	4.88E-02	b.t.	n.s.
AKR1A1	2.54	3.91E-02	b.t.	n.s.
CTSH	2.54	2.16E-02	3.1	1.72E-02
CXCR5	2.52	8.00E-03	4.06	8.00E-04
PGAM1	2.52	1.86E-02	b.t.	n.s.
RBM3	2.52	4.29E-02	b.t.	n.s.
NOC3L	2.51	2.20E-03	2.33	1.14E-02
PSMD11	2.51	1.69E-02	b.t.	n.s.
RDX	2.51	2.86E-02	2.77	2.58E-02
SARS	2.51	4.54E-02	b.t.	n.s.
NFKB1	2.5	4.40E-03	3.92	6.00E-03
SNRPA	2.5	1.28E-02	b.t.	n.s.
KBTBD6	2.49	4.40E-03	b.t.	n.s.
FERMT3	2.48	9.60E-03	b.t.	n.s.
PEA15	2.48	3.10E-03	b.t.	n.s.
PPA1	2.48	2.76E-02	b.t.	n.s.
PSMD3	2.48	1.99E-02	b.t.	n.s.
RAB9A	2.48	1.30E-03	4.59	2.06E-05
DUSP4	2.47	2.11E-02	b.t.	n.s.
ECE1	2.47	1.03E-02	4.81	2.20E-03
ABCF2	2.46	1.45E-02	b.t.	n.s.
ATXN2L	2.46	3.20E-02	b.t.	n.s.
TMA16	2.46	2.90E-03	b.t.	n.s.
FBRS	2.45	1.01E-02	1.96	4.81E-02

CTTN	2.44	1.70E-03	b.t.	n.s.
KLHL6	2.44	1.95E-02	b.t.	n.s.
PSMC3	2.44	4.65E-02	b.t.	n.s.
FARSB	2.43	4.65E-02	b.t.	n.s.
MORN2	2.42	2.93E-02	b.t.	n.s.
STPG1	2.42	1.94E-02	1.95	2.67E-02
DPP3	2.41	8.00E-04	1.65	4.86E-02
PLAA	2.41	2.70E-03	b.t.	n.s.
VIM	2.41	4.90E-03	1.99	2.10E-02
FAM136A	2.4	1.72E-02	b.t.	n.s.
RPL12	2.4	1.79E-02	b.t.	n.s.
DNAJB11	2.39	3.47E-02	b.t.	n.s.
LARP1	2.39	2.93E-02	b.t.	n.s.
POLD2	2.39	2.31E-02	1.64	4.97E-02
RSL1D1	2.39	3.14E-02	b.t.	n.s.
IARS	2.38	1.50E-03	b.t.	n.s.
CBX6	2.36	5.40E-03	3.7	1.22E-02
CHCHD5	2.36	2.13E-02	b.t.	n.s.
RFC2	2.36	1.94E-02	2.22	2.53E-02
BCAT1	2.35	2.27E-02	b.t.	n.s.
ANP32B	2.34	3.18E-02	b.t.	n.s.
ARPC1A	2.34	3.50E-02	b.t.	n.s.
POMP	2.34	3.91E-02	b.t.	n.s.
S100A2	2.34	4.48E-02	b.t.	n.s.
ARL6	2.33	1.60E-02	b.t.	n.s.
GPR137B	2.33	3.11E-02	b.t.	n.s.
NFAT5	2.33	9.50E-03	1.93	5.60E-03
TRAF3IP1	2.33	1.63E-02	b.t.	n.s.
IGF2R	2.32	5.30E-03	b.t.	n.s.

IL10RB	2.32	3.90E-03	2.38	1.70E-03
LGALS3	2.32	4.10E-03	b.t.	n.s.
IMPDH2	2.31	8.80E-03	b.t.	n.s.
NUDC	2.31	4.80E-02	b.t.	n.s.
CLPP	2.3	2.52E-02	b.t.	n.s.
MRPS15	2.3	2.65E-02	b.t.	n.s.
PSMD12	2.3	2.55E-02	b.t.	n.s.
CBS	2.29	5.30E-03	1.8	4.34E-02
CCDC50	2.29	1.17E-02	2.33	1.29E-02
COMMD1	2.29	3.60E-02	2.46	2.21E-02
DNM1L	2.29	6.90E-03	b.t.	n.s.
ERO1B	2.29	3.01E-02	2.45	9.00E-04
G3BP1	2.29	4.99E-02	2.61	2.91E-02
POLR2H	2.29	2.20E-02	b.t.	n.s.
POLR1A	2.28	3.59E-02	b.t.	n.s.
HSPBP1	2.27	2.60E-03	b.t.	n.s.
TMPRSS6	2.27	3.40E-03	2.21	3.50E-03
NFIX	2.26	9.40E-03	b.t.	n.s.
NPM1	2.26	2.28E-02	b.t.	n.s.
PLTP	2.26	4.04E-02	b.t.	n.s.
HELLS	2.25	4.10E-03	2.97	9.00E-04
USP12	2.25	2.76E-02	2.09	1.14E-02
MCTS1	2.24	2.26E-02	b.t.	n.s.
SLC20A1	2.24	4.30E-03	2.28	5.90E-03
TUBE1	2.24	6.20E-03	b.t.	n.s.
ZDHHC12	2.24	4.55E-02	b.t.	n.s.
ORC3	2.23	5.96E-05	2.06	8.00E-04
DNAAF5	2.22	8.00E-03	b.t.	n.s.
SLC25A11	2.22	1.60E-02	b.t.	n.s.

CHCHD3	2.21	2.64E-02	b.t.	n.s.
ETF1	2.21	1.07E-02	b.t.	n.s.
GADD45B	2.21	3.00E-03	2.37	9.00E-03
MFSD10	2.21	3.69E-02	b.t.	n.s.
NTMT1	2.21	4.82E-02	b.t.	n.s.
TRMT10A	2.21	1.00E-03	2.16	3.82E-05
SEC11C	2.2	1.70E-03	2.53	7.20E-03
TET3	2.2	6.70E-03	1.87	4.40E-03
UBR5	2.2	2.56E-02	b.t.	n.s.
RPL36A-HNRNPH2	2.19	1.97E-02	b.t.	n.s.
CFLAR	2.19	7.50E-03	2.53	9.30E-03
CLRN1	2.19	2.10E-03	b.t.	n.s.
EIF2B3	2.19	1.73E-02	b.t.	n.s.
ELAC2	2.19	3.53E-02	b.t.	n.s.
AVEN	2.18	1.49E-02	b.t.	n.s.
CSTF2	2.18	2.73E-02	b.t.	n.s.
ZSWIM4	2.18	3.00E-03	2.64	1.30E-03
RPS6KA1	2.17	3.30E-03	2.1	2.07E-02
CCT2	2.17	4.72E-02	b.t.	n.s.
CNOT11	2.17	4.20E-03	b.t.	n.s.
MCUR1	2.17	4.45E-02	b.t.	n.s.
TMEM205	2.17	1.33E-02	1.55	1.72E-02
ZBTB7B	2.17	2.78E-02	1.94	3.80E-02
CENPH	2.16	1.47E-02	b.t.	n.s.
PPP1R7	2.16	2.30E-02	b.t.	n.s.
NCBP1	2.15	2.50E-03	2	2.00E-03
RPL36A	2.15	1.82E-02	b.t.	n.s.
TUBB	2.15	2.47E-02	b.t.	n.s.
YWHAE	2.15	3.38E-02	b.t.	n.s.

EIF3I	2.14	4.78E-02	b.t.	n.s.
KPNA2	2.14	3.67E-02	b.t.	n.s.
TARS	2.14	3.60E-03	b.t.	n.s.
WDR4	2.14	1.12E-02	b.t.	n.s.
DNAL1	2.13	4.74E-02	b.t.	n.s.
FASTKD1	2.13	8.00E-04	1.65	7.80E-03
GTDC1	2.13	1.20E-03	2.04	4.10E-03
INTS9	2.12	1.30E-03	1.85	8.70E-03
ZNF442	2.12	1.50E-03	3	6.00E-04
ARID5A	2.11	1.60E-02	2.37	1.00E-02
NUP58	2.11	1.30E-03	1.79	5.50E-03
OTUD7B	2.11	1.50E-03	2.66	3.50E-03
SLC43A1	2.11	4.51E-02	b.t.	n.s.
CCDC6	2.1	9.20E-03	2.03	2.13E-02
COQ3	2.1	3.93E-02	b.t.	n.s.
PARK7	2.1	1.27E-02	b.t.	n.s.
TFDP2	2.1	2.02E-02	2.2	5.80E-03
CTSC	2.09	2.77E-02	b.t.	n.s.
KIF1C	2.09	1.90E-03	2.13	7.70E-03
PPID	2.09	7.60E-03	b.t.	n.s.
PTRH1	2.09	1.89E-02	b.t.	n.s.
HMGA1	2.08	4.81E-02	b.t.	n.s.
VCP	2.08	4.80E-03	b.t.	n.s.
CCT8	2.07	4.79E-02	b.t.	n.s.
HENMT1	2.07	3.10E-03	1.74	4.96E-02
VASP	2.07	4.51E-02	b.t.	n.s.
XPOT	2.07	8.90E-03	b.t.	n.s.
RPL26L1	2.06	2.72E-02	b.t.	n.s.
MRRF	2.06	4.40E-02	b.t.	n.s.

ACBD6	2.05	2.70E-02	b.t.	n.s.
DARS	2.05	4.20E-03	2.13	7.40E-03
GSS	2.05	1.56E-02	b.t.	n.s.
TFDP1	2.05	3.81E-02	b.t.	n.s.
WDR3	2.05	3.36E-02	b.t.	n.s.
GPI	2.04	1.90E-02	b.t.	n.s.
RFC4	2.04	2.04E-02	b.t.	n.s.
XPO1	2.04	7.20E-03	b.t.	n.s.
ZPR1	2.04	5.80E-03	b.t.	n.s.
APRT	2.03	3.65E-02	b.t.	n.s.
S100A14	2.03	8.10E-03	2.11	3.08E-02
ABCB6	2.02	8.70E-03	b.t.	n.s.
CLEC12A	2.02	2.40E-03	b.t.	n.s.
PEX3	2.02	4.00E-02	b.t.	n.s.
RBBP9	2.02	6.30E-03	1.71	3.50E-03
RBM39	2.02	6.60E-03	b.t.	n.s.
CHPF	2.01	2.80E-03	b.t.	n.s.
PRMT5	2.01	4.97E-02	b.t.	n.s.
COA1	2	1.00E-02	b.t.	n.s.
CSE1L	2	1.40E-02	b.t.	n.s.
VBP1	2	2.46E-02	b.t.	n.s.
FAM162A	1.99	4.66E-02	b.t.	n.s.
SMS	1.99	3.35E-02	b.t.	n.s.
WDR18	1.99	4.71E-02	b.t.	n.s.
EFHD2	1.98	1.74E-02	b.t.	n.s.
GARS	1.97	7.80E-03	b.t.	n.s.
NBEAL2	1.97	3.12E-02	2.17	2.47E-02
PARVB	1.97	2.25E-02	b.t.	n.s.
HMMR	1.96	4.10E-03	b.t.	n.s.

TIMM17A	1.96	3.94E-02	b.t.	n.s.
AEN	1.95	2.26E-02	2.08	9.80E-03
CPNE2	1.95	4.06E-02	b.t.	n.s.
MLH1	1.95	1.90E-03	b.t.	n.s.
PSMD7	1.95	2.38E-02	b.t.	n.s.
SEC61A1	1.95	1.96E-02	b.t.	n.s.
ALG10B	1.94	9.10E-03	b.t.	n.s.
WDR77	1.94	4.24E-02	b.t.	n.s.
ACOT7	1.93	9.70E-03	b.t.	n.s.
CHCHD10	1.93	2.55E-02	b.t.	n.s.
OLA1	1.93	8.20E-03	b.t.	n.s.
VPS52	1.93	2.36E-02	b.t.	n.s.
DDX18	1.92	1.33E-02	b.t.	n.s.
EIF4H	1.92	1.15E-02	1.76	1.09E-02
KIAA0391	1.92	2.99E-02	b.t.	n.s.
OSBPL9	1.92	2.30E-03	1.59	1.47E-02
PLLP	1.92	6.85E-05	1.82	1.00E-03
PSMD1	1.92	9.50E-03	b.t.	n.s.
RPS17	1.92	4.62E-02	b.t.	n.s.
SF3B3	1.92	1.87E-02	b.t.	n.s.
TPM4	1.92	3.67E-02	b.t.	n.s.
GSTCD	1.91	2.81E-02	b.t.	n.s.
PSMD2	1.91	7.20E-03	b.t.	n.s.
RAB21	1.91	1.42E-02	b.t.	n.s.
USP46	1.91	1.54E-02	b.t.	n.s.
ZNF805	1.91	3.30E-03	1.72	2.80E-03
EIF2A	1.9	2.38E-02	b.t.	n.s.
HEATR1	1.9	4.39E-02	2.38	2.18E-02
OGFOD1	1.9	1.64E-02	b.t.	n.s.

PGLS	1.9	1.52E-02	b.t.	n.s.
PSMD13	1.9	3.18E-02	b.t.	n.s.
RGS7BP	1.9	7.40E-03	b.t.	n.s.
THOP1	1.9	8.40E-03	1.63	2.72E-02
VARS	1.9	1.70E-03	b.t.	n.s.
VDAC3	1.9	1.23E-02	b.t.	n.s.
BCCIP	1.89	3.30E-02	b.t.	n.s.
IRAK1BP1	1.89	6.00E-03	1.97	1.31E-02
PFN1	1.89	1.70E-02	b.t.	n.s.
PPRC1	1.89	4.92E-02	b.t.	n.s.
RAD18	1.89	1.50E-03	1.75	1.50E-03
TARBP1	1.89	4.51E-02	b.t.	n.s.
HMBS	1.88	2.24E-02	b.t.	n.s.
FPGS	1.88	5.20E-03	b.t.	n.s.
ERCC2	1.87	3.80E-03	b.t.	n.s.
MAGI3	1.87	7.70E-03	b.t.	n.s.
CCDC167	1.86	1.12E-02	b.t.	n.s.
RCAN2	1.86	4.50E-03	1.91	6.00E-04
ARHGEF2	1.86	6.50E-03	2.27	4.00E-04
CLDN7	1.86	9.40E-03	b.t.	n.s.
EXOSC1	1.86	4.70E-02	b.t.	n.s.
TMEM161A	1.85	4.00E-03	b.t.	n.s.
ARPC2	1.84	3.70E-03	b.t.	n.s.
ATF4	1.84	3.66E-02	b.t.	n.s.
IRF5	1.84	3.18E-02	2.28	2.26E-02
RALA	1.84	4.88E-02	b.t.	n.s.
SLC16A6	1.84	2.95E-02	b.t.	n.s.
AMMECR1L	1.83	5.10E-03	1.86	3.50E-03
GALE	1.83	4.75E-02	b.t.	n.s.

KNSTRN	1.83	1.82E-02	b.t.	n.s.
MAPRE3	1.83	9.70E-03	b.t.	n.s.
MED27	1.83	2.45E-02	b.t.	n.s.
RRP12	1.83	4.25E-02	b.t.	n.s.
UQCRC2	1.83	1.65E-02	b.t.	n.s.
DNAJC21	1.82	2.26E-02	b.t.	n.s.
FANCD2	1.82	5.00E-04	2.22	5.00E-04
NAP1L1	1.82	9.50E-03	b.t.	n.s.
NFE2L1	1.82	3.82E-02	b.t.	n.s.
PSMC6	1.82	2.04E-02	b.t.	n.s.
SLC25A17	1.82	2.91E-02	b.t.	n.s.
TMEM165	1.82	2.95E-02	b.t.	n.s.
GPAM	1.81	3.39E-02	1.56	2.28E-02
IFFO2	1.81	9.67E-05	2.32	2.00E-04
TEX10	1.81	6.60E-03	b.t.	n.s.
KDM4D	1.8	3.23E-02	b.t.	n.s.
ALDH1B1	1.8	2.09E-02	b.t.	n.s.
KIAA1143	1.8	3.47E-02	b.t.	n.s.
TXN	1.8	1.58E-02	b.t.	n.s.
DDX20	1.78	5.40E-03	b.t.	n.s.
GEMIN8	1.78	2.71E-02	2.66	4.00E-03
IFT46	1.78	1.96E-02	b.t.	n.s.
IZUMO1	1.78	6.90E-03	b.t.	n.s.
RCN1	1.78	1.58E-02	b.t.	n.s.
C15orf41	1.77	2.71E-02	b.t.	n.s.
NDUFA7	1.77	3.69E-02	b.t.	n.s.
NDUFV3	1.77	2.93E-02	b.t.	n.s.
NUP188	1.77	2.31E-02	b.t.	n.s.
DARS2	1.76	4.31E-02	b.t.	n.s.

MRPL12	1.76	4.65E-02	b.t.	n.s.
SMG9	1.76	8.00E-03	2.05	4.00E-04
KPNA3	1.75	3.51E-02	b.t.	n.s.
MTFR1L	1.75	1.42E-02	1.94	4.20E-03
NONO	1.75	2.47E-02	b.t.	n.s.
PADI6	1.75	3.38E-02	b.t.	n.s.
PMPCB	1.75	2.23E-02	b.t.	n.s.
PPIL1	1.75	2.22E-02	b.t.	n.s.
SAAL1	1.75	2.80E-02	b.t.	n.s.
ALDH4A1	1.74	3.04E-02	1.81	1.52E-02
BUD31	1.74	4.87E-02	b.t.	n.s.
CENPE	1.74	1.80E-03	b.t.	n.s.
GLUD1	1.74	3.40E-03	b.t.	n.s.
LIG3	1.74	1.21E-02	b.t.	n.s.
LMAN1	1.74	1.45E-02	b.t.	n.s.
MRPL35	1.74	1.45E-02	b.t.	n.s.
MRPS31	1.74	1.89E-02	b.t.	n.s.
NUDT19	1.74	4.54E-02	b.t.	n.s.
SCFD2	1.74	3.40E-02	b.t.	n.s.
CLTC	1.73	5.30E-03	b.t.	n.s.
DTX4	1.73	2.65E-02	b.t.	n.s.
EMILIN2	1.73	1.71E-02	b.t.	n.s.
MTHFD1	1.73	1.70E-03	2.24	1.39E-02
POLDIP2	1.73	3.38E-02	b.t.	n.s.
ANP32E	1.72	3.39E-02	b.t.	n.s.
FAM98B	1.72	7.60E-03	b.t.	n.s.
MCCC2	1.72	2.75E-02	1.85	2.30E-02
MRPL52	1.72	2.89E-02	b.t.	n.s.
NT5C	1.72	3.18E-02	1.9	3.99E-02

SNX24	1.72	2.13E-02	b.t.	n.s.
TTLL4	1.72	8.20E-03	b.t.	n.s.
VDAC2	1.72	2.47E-02	b.t.	n.s.
ZYX	1.72	1.04E-02	1.99	2.04E-02
E2F3	1.71	9.10E-03	b.t.	n.s.
MNAT1	1.71	2.35E-02	b.t.	n.s.
NCLN	1.71	2.92E-02	b.t.	n.s.
YIPF1	1.71	9.50E-03	b.t.	n.s.
HK2	1.7	1.86E-02	b.t.	n.s.
HTRA2	1.7	2.72E-02	2.07	3.40E-03
MYO5A	1.7	1.46E-02	b.t.	n.s.
OTULIN	1.7	3.26E-02	1.93	1.37E-02
UBL7	1.7	3.63E-02	1.77	2.43E-02
CANX	1.69	3.59E-02	b.t.	n.s.
NARS	1.69	4.63E-02	b.t.	n.s.
TMED3	1.69	7.60E-03	b.t.	n.s.
CDS1	1.68	1.10E-03	b.t.	n.s.
ERCC1	1.68	3.12E-02	b.t.	n.s.
HNRNPDL	1.68	2.20E-02	b.t.	n.s.
POP1	1.68	1.77E-02	1.56	2.51E-02
RHBDF2	1.68	8.80E-03	1.71	1.81E-02
STK38L	1.68	2.10E-02	1.72	1.88E-02
MPHOSPH6	1.67	3.26E-02	b.t.	n.s.
SMARCAD1	1.67	1.57E-02	b.t.	n.s.
STKLD1	1.67	3.70E-03	b.t.	n.s.
TNIP2	1.67	1.13E-02	b.t.	n.s.
UHRF1BP1	1.67	1.20E-02	b.t.	n.s.
HSPH1	1.66	1.01E-02	b.t.	n.s.
NDUFS4	1.66	4.77E-02	b.t.	n.s.

PPME1	1.66	2.07E-02	b.t.	n.s.
TFG	1.66	3.54E-02	b.t.	n.s.
GMPPB	1.65	2.91E-02	2.17	4.77E-02
MTMR4	1.65	3.50E-02	1.88	3.60E-03
NDUFV1	1.65	6.00E-03	b.t.	n.s.
PLCB3	1.65	1.40E-03	1.53	8.00E-03
CHMP4B	1.64	3.69E-02	b.t.	n.s.
FAN1	1.64	2.81E-02	b.t.	n.s.
SLC39A1	1.64	2.00E-04	b.t.	n.s.
SMAP2	1.64	1.40E-03	1.63	7.80E-03
SPIB	1.64	1.74E-02	b.t.	n.s.
TMEM168	1.64	9.60E-03	b.t.	n.s.
CLPB	1.63	7.10E-03	b.t.	n.s.
FCF1	1.63	4.80E-02	b.t.	n.s.
NUF2	1.63	4.97E-02	b.t.	n.s.
PAFAH2	1.63	5.70E-03	b.t.	n.s.
SLC39A6	1.63	4.68E-02	b.t.	n.s.
SPDL1	1.63	2.16E-02	b.t.	n.s.
FITM2	1.62	9.70E-03	b.t.	n.s.
GCSH	1.62	1.77E-02	b.t.	n.s.
NMD3	1.62	3.73E-02	b.t.	n.s.
WNK3	1.62	3.81E-02	b.t.	n.s.
ZC3HAV1L	1.62	2.55E-02	b.t.	n.s.
DAP	1.61	4.20E-03	b.t.	n.s.
IPPK	1.61	7.30E-03	b.t.	n.s.
MARVELD1	1.61	2.75E-02	b.t.	n.s.
MBD2	1.61	2.34E-02	b.t.	n.s.
PPP2R5D	1.61	2.15E-02	b.t.	n.s.
DDAH1	1.6	4.74E-02	b.t.	n.s.

GTPBP4	1.6	4.96E-02	b.t.	n.s.
TRAF3	1.6	1.71E-02	b.t.	n.s.
H1FOO	1.59	7.00E-04	b.t.	n.s.
SURF2	1.59	4.31E-02	b.t.	n.s.
C3orf33	1.59	2.58E-02	b.t.	n.s.
DYNC2LI1	1.59	4.81E-02	b.t.	n.s.
FSIP1	1.59	4.70E-03	1.63	1.46E-02
PLD2	1.59	3.34E-02	b.t.	n.s.
SRSF7	1.59	3.31E-02	b.t.	n.s.
KNG1	1.58	3.77E-02	b.t.	n.s.
ZBTB5	1.58	2.40E-02	2.63	1.20E-03
MOSPD2	1.58	2.84E-02	b.t.	n.s.
NOC2L	1.58	2.90E-02	b.t.	n.s.
SEC24A	1.58	2.73E-02	b.t.	n.s.
SLC1A3	1.58	4.31E-02	b.t.	n.s.
TMOD1	1.58	3.30E-02	b.t.	n.s.
UBA5	1.58	3.41E-02	b.t.	n.s.
ZMIZ1	1.58	2.62E-02	b.t.	n.s.
CSGALNACT1	1.57	1.97E-02	b.t.	n.s.
FAH	1.57	1.07E-02	b.t.	n.s.
GABRG3	1.57	3.64E-02	b.t.	n.s.
MCAT	1.57	3.91E-02	b.t.	n.s.
PTDSS2	1.57	2.81E-02	b.t.	n.s.
RTCA	1.57	1.64E-02	b.t.	n.s.
IDE	1.56	1.01E-02	b.t.	n.s.
NFATC2	1.56	4.56E-02	1.98	4.54E-02
PGM2	1.56	2.10E-02	b.t.	n.s.
ST20	1.56	1.92E-02	b.t.	n.s.
DDX53	1.55	3.90E-02	b.t.	n.s.

GRPR	1.55	1.60E-02	b.t.	n.s.
ASGR1	1.55	1.74E-02	b.t.	n.s.
IPO5	1.55	4.80E-03	b.t.	n.s.
MLLT11	1.55	1.81E-02	1.82	4.20E-03
NRAS	1.55	4.21E-02	b.t.	n.s.
FMR1NB	1.54	4.50E-03	b.t.	n.s.
AP2A1	1.54	2.34E-02	b.t.	n.s.
FBXO22	1.54	4.46E-02	b.t.	n.s.
OTUD6B	1.54	1.29E-02	b.t.	n.s.
YARS	1.54	1.21E-02	b.t.	n.s.
DLGAP5	1.53	3.35E-02	1.54	1.97E-02
NR1I2	1.53	4.43E-02	b.t.	n.s.
SOCS7	1.53	1.12E-02	b.t.	n.s.
ABCG2	1.52	3.70E-03	b.t.	n.s.
ADGRA3	1.52	3.58E-02	b.t.	n.s.
CNBD1	1.52	1.34E-02	b.t.	n.s.
CYP26A1	1.52	2.32E-02	b.t.	n.s.
FAF2	1.52	1.18E-02	1.5	2.23E-02
FAM19A5	1.52	3.90E-03	b.t.	n.s.
FUOM	1.52	2.32E-02	b.t.	n.s.
HSPA13	1.52	2.96E-02	b.t.	n.s.
MMP7	1.52	2.21E-02	b.t.	n.s.
PRRT3	1.52	9.86E-05	1.6	6.00E-04
FABP12	1.51	4.03E-02	b.t.	n.s.
QRFP	1.51	1.20E-03	b.t.	n.s.
COPB2	1.51	4.29E-02	b.t.	n.s.
GALNT1	1.51	2.49E-02	b.t.	n.s.
METAP1D	1.51	4.88E-02	b.t.	n.s.
PSPH	1.51	4.71E-02	b.t.	n.s.

RPS24	1.51	4.73E-02	b.t.	n.s.
SMAD7	1.51	4.49E-02	b.t.	n.s.
CBFA2T3	1.5	2.49E-02	b.t.	n.s.
PCLO	1.5	4.07E-02	b.t.	n.s.
TNKS1BP1	1.5	4.85E-02	1.63	1.70E-02
UBE2I	1.5	2.25E-02	b.t.	n.s.
ACSS1	-1.5	5.00E-04	-1.66	2.90E-03
ARFIP1	-1.5	3.27E-02	b.t.	n.s.
AVIL	-1.5	3.17E-02	b.t.	n.s.
BNIPL	-1.5	7.40E-03	b.t.	n.s.
ZNF792	-1.5	1.75E-02	b.t.	n.s.
ZNRF2	-1.5	3.36E-02	b.t.	n.s.
CPNE3	-1.51	5.90E-03	-1.74	8.60E-03
KIF18A	-1.51	4.48E-02	b.t.	n.s.
MED13	-1.51	3.96E-02	b.t.	n.s.
PTPRG	-1.51	7.20E-03	b.t.	n.s.
SHC1	-1.51	2.90E-02	-1.96	2.20E-03
ZBTB18	-1.51	4.11E-02	b.t.	n.s.
ZMYM2	-1.51	3.51E-02	b.t.	n.s.
MSL2	-1.52	1.99E-02	b.t.	n.s.
CDC73	-1.52	4.77E-02	b.t.	n.s.
CHODL	-1.52	1.00E-03	b.t.	n.s.
CRY2	-1.52	3.50E-02	b.t.	n.s.
CTDSP1	-1.52	4.40E-03	b.t.	n.s.
MIS18BP1	-1.52	2.98E-02	b.t.	n.s.
RCBTB2	-1.52	3.29E-02	b.t.	n.s.
RIPK3	-1.52	3.25E-02	b.t.	n.s.
TM2D3	-1.52	3.88E-02	b.t.	n.s.
TTBK2	-1.52	2.30E-03	-1.73	6.30E-03

FAM209A	-1.53	2.46E-02	b.t.	n.s.
AGPAT4	-1.53	2.60E-02	b.t.	n.s.
MICU1	-1.53	5.60E-03	b.t.	n.s.
TMEM59	-1.53	2.00E-03	b.t.	n.s.
ZNF236	-1.53	2.15E-02	-2.07	9.00E-04
MLXIP	-1.54	3.26E-02	b.t.	n.s.
DMPK	-1.54	4.79E-02	b.t.	n.s.
HELQ	-1.54	3.90E-03	b.t.	n.s.
LHFPL2	-1.54	3.68E-02	-1.74	1.07E-02
PFDN5	-1.54	2.17E-02	b.t.	n.s.
STXBP3	-1.54	3.92E-02	b.t.	n.s.
TBCEL	-1.54	3.59E-02	b.t.	n.s.
UEVLD	-1.54	3.55E-02	b.t.	n.s.
ACYP2	-1.55	3.81E-02	b.t.	n.s.
CDADC1	-1.55	4.50E-03	b.t.	n.s.
CREB1	-1.55	3.31E-02	b.t.	n.s.
CTSF	-1.55	9.20E-03	b.t.	n.s.
GCLC	-1.55	2.03E-02	b.t.	n.s.
HHEX	-1.55	2.94E-02	b.t.	n.s.
METTL21A	-1.55	2.07E-02	b.t.	n.s.
NAA16	-1.55	2.55E-02	b.t.	n.s.
PNPLA2	-1.55	1.00E-04	b.t.	n.s.
USPL1	-1.55	6.00E-04	-1.71	4.10E-03
ZIK1	-1.55	3.63E-02	b.t.	n.s.
C8orf44	-1.56	4.75E-02	b.t.	n.s.
ERVW-1	-1.56	1.85E-02	b.t.	n.s.
PHGR1	-1.56	4.50E-02	b.t.	n.s.
WHAMM	-1.56	4.40E-02	b.t.	n.s.
CCSAP	-1.57	2.60E-03	b.t.	n.s.

CD47	-1.57	3.67E-02	b.t.	n.s.
IQCF2	-1.57	1.40E-02	b.t.	n.s.
CARD8	-1.58	8.60E-03	b.t.	n.s.
SIN3A	-1.58	2.50E-02	b.t.	n.s.
ST7L	-1.58	2.78E-02	b.t.	n.s.
BTN3A3	-1.59	9.80E-03	b.t.	n.s.
FNDC3A	-1.59	1.37E-02	b.t.	n.s.
HERC3	-1.59	2.40E-03	b.t.	n.s.
NEK1	-1.59	2.37E-02	-1.78	3.08E-02
RREB1	-1.59	3.43E-02	b.t.	n.s.
SFTPB	-1.59	2.00E-04	b.t.	n.s.
WDR91	-1.59	2.81E-02	b.t.	n.s.
LYSMD4	-1.6	1.22E-02	b.t.	n.s.
TSPYL1	-1.6	1.44E-02	b.t.	n.s.
ADSSL1	-1.6	4.20E-02	b.t.	n.s.
ATP6V1G1	-1.6	2.20E-02	b.t.	n.s.
CTDSPL2	-1.6	3.81E-02	b.t.	n.s.
EPC1	-1.6	1.41E-02	b.t.	n.s.
ERF	-1.6	2.73E-02	b.t.	n.s.
ETV6	-1.6	3.72E-02	b.t.	n.s.
GRIA1	-1.6	2.99E-02	b.t.	n.s.
PCCA	-1.6	1.32E-02	-1.68	5.40E-03
RC3H1	-1.6	1.89E-02	b.t.	n.s.
RIC1	-1.6	8.90E-03	-1.95	7.40E-03
STRIP1	-1.6	3.60E-03	b.t.	n.s.
ZNF200	-1.6	4.35E-02	b.t.	n.s.
ZNF836	-1.6	2.66E-02	-1.62	1.71E-02
ATG4C	-1.61	4.60E-02	-1.93	4.26E-02
INPP1	-1.61	1.83E-02	b.t.	n.s.

MAN1B1	-1.61	4.46E-02	b.t.	n.s.
SNRNP48	-1.61	1.00E-02	-1.66	1.11E-02
SYPL1	-1.61	1.20E-02	b.t.	n.s.
WIPF1	-1.61	7.00E-04	-1.6	1.00E-03
BCL2L14	-1.62	1.83E-02	b.t.	n.s.
C12orf76	-1.62	3.17E-02	b.t.	n.s.
C1orf56	-1.62	2.13E-02	b.t.	n.s.
CAMK2G	-1.62	2.03E-02	-1.66	7.50E-03
GORASP1	-1.62	3.74E-02	b.t.	n.s.
KBTBD3	-1.62	4.75E-02	-2.03	2.25E-02
MBD4	-1.62	1.37E-02	b.t.	n.s.
ZNF860	-1.62	1.05E-02	b.t.	n.s.
DGKD	-1.63	7.00E-03	b.t.	n.s.
ADPRM	-1.63	1.57E-02	b.t.	n.s.
CBX7	-1.63	1.01E-02	b.t.	n.s.
ECI2	-1.63	4.51E-02	b.t.	n.s.
FBXL4	-1.63	3.82E-02	b.t.	n.s.
MADD	-1.63	4.20E-03	b.t.	n.s.
NCOA3	-1.63	9.00E-04	-1.52	9.00E-04
RIPK1	-1.63	2.30E-03	b.t.	n.s.
ABHD14A	-1.64	1.10E-03	b.t.	n.s.
ANKAR	-1.64	2.29E-02	b.t.	n.s.
ANKRA2	-1.64	4.05E-02	b.t.	n.s.
DECR1	-1.64	3.10E-02	b.t.	n.s.
RPRD2	-1.64	8.70E-03	b.t.	n.s.
TRABD2A	-1.64	2.36E-02	-1.9	1.70E-03
PRKD3	-1.65	5.80E-03	-2.14	8.00E-03
PTPN2	-1.65	2.65E-02	b.t.	n.s.
TMEM53	-1.65	4.59E-02	b.t.	n.s.

ZNF217	-1.65	1.47E-02	b.t.	n.s.
CLEC4A	-1.66	1.94E-02	b.t.	n.s.
PLEKHF1	-1.66	7.50E-03	-2.48	2.00E-04
ARL11	-1.66	4.26E-02	b.t.	n.s.
CNOT8	-1.66	1.24E-02	b.t.	n.s.
PRKCZ	-1.66	2.09E-02	b.t.	n.s.
SH3BGRL	-1.66	4.69E-02	b.t.	n.s.
SH3GLB2	-1.66	3.03E-02	-2.07	7.50E-03
SLPI	-1.66	2.95E-02	b.t.	n.s.
ZNF610	-1.66	2.23E-02	-1.7	4.31E-02
AMFR	-1.67	4.00E-02	b.t.	n.s.
CDK14	-1.67	8.00E-03	-1.93	4.09E-02
CKAP2	-1.67	3.75E-02	b.t.	n.s.
FBXL14	-1.67	1.40E-02	-1.63	4.70E-02
SAP130	-1.67	1.74E-02	b.t.	n.s.
CCNDBP1	-1.68	6.30E-03	b.t.	n.s.
CD55	-1.68	8.90E-03	b.t.	n.s.
FIP1L1	-1.68	3.13E-02	b.t.	n.s.
FOXO4	-1.68	4.79E-02	b.t.	n.s.
PLEKHA3	-1.68	9.00E-04	-1.73	5.60E-03
ZKSCAN3	-1.68	3.92E-02	b.t.	n.s.
ITCH	-1.69	4.44E-02	b.t.	n.s.
RUNDC1	-1.69	1.46E-02	b.t.	n.s.
TMEM159	-1.69	4.86E-02	b.t.	n.s.
USP33	-1.69	5.00E-04	b.t.	n.s.
ANKIB1	-1.7	6.00E-04	-1.8	1.20E-03
CGGBP1	-1.7	7.20E-03	b.t.	n.s.
HDAC7	-1.7	1.13E-02	b.t.	n.s.
KLHL32	-1.7	1.00E-03	b.t.	n.s.

SLC1A7	-1.7	3.10E-03	b.t.	n.s.
WWC3	-1.7	3.46E-02	b.t.	n.s.
BRWD1	-1.71	3.70E-02	-1.73	3.13E-02
HECTD2	-1.71	3.03E-02	-2.39	1.07E-02
PCIF1	-1.71	9.80E-03	b.t.	n.s.
SNX30	-1.71	4.24E-02	-3.2	1.00E-04
ZBTB49	-1.71	2.00E-04	b.t.	n.s.
ZFP82	-1.71	5.00E-04	b.t.	n.s.
ZNF184	-1.71	6.30E-03	b.t.	n.s.
HS3ST1	-1.72	4.47E-02	b.t.	n.s.
PDCL	-1.72	3.00E-03	b.t.	n.s.
AIDA	-1.72	2.72E-02	-2.77	9.00E-04
C18orf25	-1.72	4.17E-02	b.t.	n.s.
C5orf56	-1.72	1.75E-02	-2.11	3.70E-03
CAPN12	-1.72	3.48E-02	-1.59	1.44E-02
FAM3C	-1.72	2.54E-02	b.t.	n.s.
IL12RB1	-1.72	2.44E-02	-3.01	9.00E-04
MKRN1	-1.72	1.01E-02	b.t.	n.s.
NFX1	-1.72	2.35E-02	-1.5	2.49E-02
SENP7	-1.72	4.86E-02	b.t.	n.s.
SETD2	-1.72	4.44E-02	b.t.	n.s.
TMEM80	-1.72	2.17E-02	b.t.	n.s.
TRIM14	-1.72	2.95E-02	b.t.	n.s.
ZKSCAN8	-1.72	9.30E-03	b.t.	n.s.
CAPN14	-1.73	3.92E-02	b.t.	n.s.
GTPBP1	-1.73	7.30E-03	b.t.	n.s.
KCTD21	-1.73	3.47E-02	b.t.	n.s.
ACP5	-1.73	3.28E-02	-5.17	3.42E-08
KLK2	-1.73	4.85E-02	-1.61	5.00E-03

RNF13	-1.73	3.85E-02	b.t.	n.s.
SDHA	-1.73	1.10E-03	-1.86	1.30E-02
ACADM	-1.74	1.34E-02	-1.94	8.20E-03
ARSD	-1.74	2.23E-02	b.t.	n.s.
EPC2	-1.74	6.10E-03	b.t.	n.s.
L3MBTL3	-1.74	3.38E-02	-2.28	4.20E-03
PARP3	-1.74	2.58E-02	b.t.	n.s.
AS3MT	-1.75	2.12E-02	b.t.	n.s.
ELF1	-1.75	2.70E-03	-1.87	2.80E-03
FAM76B	-1.75	4.57E-02	b.t.	n.s.
METTL23	-1.75	8.90E-03	-1.59	1.12E-02
SRGAP3	-1.75	5.00E-04	b.t.	n.s.
SYNRG	-1.75	1.00E-04	b.t.	n.s.
TBC1D5	-1.75	3.59E-02	b.t.	n.s.
EAF2	-1.76	1.34E-02	b.t.	n.s.
MBOAT1	-1.76	4.64E-02	b.t.	n.s.
S1PR4	-1.76	5.00E-03	b.t.	n.s.
CIITA	-1.77	2.15E-02	b.t.	n.s.
DMTF1	-1.77	7.20E-03	b.t.	n.s.
GNS	-1.77	5.40E-03	-2.03	1.23E-02
NADSYN1	-1.77	2.61E-02	b.t.	n.s.
SNRK	-1.77	4.00E-04	b.t.	n.s.
VPS13B	-1.77	6.20E-03	b.t.	n.s.
ZNF83	-1.77	1.49E-02	b.t.	n.s.
DCLK2	-1.78	1.46E-02	b.t.	n.s.
DNAJC16	-1.78	1.81E-02	b.t.	n.s.
HP1BP3	-1.78	9.80E-03	-1.78	2.60E-02
PPP2R5C	-1.78	1.65E-02	-1.8	1.74E-02
SLC25A30	-1.78	2.87E-02	-1.66	1.94E-02

ZCCHC18	-1.78	1.39E-02	b.t.	n.s.
FBXO31	-1.79	3.83E-02	b.t.	n.s.
GSAP	-1.79	2.47E-02	-1.91	1.53E-02
RAB33B	-1.79	1.50E-03	b.t.	n.s.
RBM5	-1.79	5.43E-05	b.t.	n.s.
RSBN1L	-1.79	3.50E-03	-2.03	5.00E-04
AK9	-1.8	1.41E-02	b.t.	n.s.
FBXL17	-1.8	5.90E-03	-1.64	4.88E-02
GOLGA8G	-1.8	1.54E-02	b.t.	n.s.
BBS9	-1.81	1.85E-02	b.t.	n.s.
CASP12	-1.81	4.40E-03	-2.03	1.20E-03
ELK4	-1.81	9.00E-04	-1.73	1.10E-03
FRS2	-1.81	3.78E-02	b.t.	n.s.
GSTK1	-1.81	2.30E-02	b.t.	n.s.
HIPK3	-1.81	6.80E-03	-1.8	1.34E-02
HIVEP2	-1.81	1.50E-03	b.t.	n.s.
MLKL	-1.81	3.84E-02	-3.87	6.40E-03
NSUN6	-1.81	9.00E-04	-2.14	1.30E-03
USP25	-1.81	2.00E-03	-1.76	1.72E-02
ZNF852	-1.81	6.00E-04	-1.58	1.69E-02
CEACAM21	-1.82	3.60E-03	b.t.	n.s.
CNDP2	-1.82	3.35E-02	b.t.	n.s.
KHDRBS2	-1.82	2.30E-02	b.t.	n.s.
PQLC3	-1.82	2.20E-03	b.t.	n.s.
ZMYND11	-1.82	3.63E-02	-1.63	4.14E-02
ARHGAP15	-1.83	7.50E-03	b.t.	n.s.
ARHGAP5	-1.83	4.40E-03	-2.06	2.90E-03
FIG4	-1.83	2.20E-02	b.t.	n.s.
ACBD5	-1.84	8.20E-05	b.t.	n.s.

DOCK9	-1.84	4.50E-02	b.t.	n.s.
GFOD1	-1.84	4.30E-03	-1.86	6.70E-03
MGAT5	-1.84	2.19E-02	b.t.	n.s.
QPCT	-1.84	5.90E-03	-2.08	4.38E-02
SMYD2	-1.84	1.41E-02	b.t.	n.s.
ZNF225	-1.84	6.40E-03	b.t.	n.s.
ZSWIM6	-1.84	1.73E-02	b.t.	n.s.
BTBD7	-1.85	1.40E-03	b.t.	n.s.
CASP4	-1.85	2.98E-02	b.t.	n.s.
PPP3CA	-1.85	2.46E-02	-1.86	1.82E-02
TBC1D1	-1.85	3.55E-02	-1.92	1.83E-02
ZBTB14	-1.85	1.12E-02	-1.72	1.25E-02
GPR174	-1.86	1.74E-02	b.t.	n.s.
HSDL1	-1.86	2.00E-04	-1.54	1.67E-02
SP140	-1.86	3.66E-02	b.t.	n.s.
VPS13C	-1.86	4.35E-02	b.t.	n.s.
ZNF75D	-1.86	1.22E-02	b.t.	n.s.
ZNF773	-1.86	1.30E-03	b.t.	n.s.
APOBEC3F	-1.87	3.49E-02	b.t.	n.s.
DOCK8	-1.87	2.43E-02	b.t.	n.s.
MAT2B	-1.87	3.63E-02	b.t.	n.s.
NUAK2	-1.87	3.94E-02	b.t.	n.s.
OPN3	-1.87	4.06E-02	-2.71	2.77E-02
PDLIM1	-1.87	2.81E-02	-2.4	1.09E-02
PEG10	-1.87	4.20E-02	-2.34	1.80E-03
RDH5	-1.87	1.90E-03	b.t.	n.s.
FAM117A	-1.88	2.94E-02	-2.16	2.81E-02
METTL4	-1.88	3.30E-03	-1.55	4.21E-02
PPP1R3B	-1.89	2.00E-04	-1.52	3.38E-02

CHD7	-1.89	8.80E-03	b.t.	n.s.
CRLF3	-1.89	1.15E-02	-1.83	3.01E-02
RNF24	-1.89	6.70E-03	b.t.	n.s.
TCF4	-1.89	5.30E-03	-1.74	1.15E-02
CD37	-1.9	1.01E-02	b.t.	n.s.
CTDSP2	-1.9	3.05E-02	b.t.	n.s.
CTRL	-1.9	5.80E-03	b.t.	n.s.
DMXL1	-1.9	1.04E-02	-1.88	1.08E-02
FAM78A	-1.9	8.00E-03	b.t.	n.s.
GIMAP2	-1.9	2.05E-02	-1.84	1.08E-02
LIN7B	-1.9	3.60E-03	-1.61	1.90E-03
MTMR3	-1.9	4.91E-02	b.t.	n.s.
TMEM60	-1.9	2.26E-02	b.t.	n.s.
ZNF224	-1.9	3.00E-03	b.t.	n.s.
RCSD1	-1.91	3.34E-02	b.t.	n.s.
SLC35E2B	-1.91	2.46E-02	b.t.	n.s.
TBC1D10C	-1.91	2.90E-02	b.t.	n.s.
TMEM86A	-1.91	1.60E-03	b.t.	n.s.
GNRH1	-1.92	3.53E-02	b.t.	n.s.
KLHL14	-1.92	2.98E-02	b.t.	n.s.
RAP1GAP2	-1.92	4.14E-02	-1.84	1.38E-02
CDC42SE2	-1.93	1.70E-03	-1.87	1.00E-03
HPS3	-1.93	7.00E-04	-1.68	4.90E-03
TMEM219	-1.93	3.80E-05	b.t.	n.s.
MFSD8	-1.94	6.70E-03	b.t.	n.s.
TRAF5	-1.94	1.59E-02	b.t.	n.s.
GIT2	-1.95	3.00E-03	-1.71	5.80E-03
MBNL3	-1.95	2.00E-03	-2.01	3.60E-03
MSRA	-1.95	5.90E-03	-1.6	4.56E-02

NCF1	-1.95	2.10E-03	-1.74	1.89E-02
PRKD2	-1.95	4.67E-02	-2.69	9.80E-03
PRKX	-1.95	1.62E-02	b.t.	n.s.
PTAR1	-1.95	1.19E-02	-1.55	3.14E-02
RC3H2	-1.95	1.00E-03	b.t.	n.s.
ZNF211	-1.95	8.00E-04	b.t.	n.s.
FBXO5	-1.96	4.83E-02	-1.84	2.92E-02
RNF38	-1.96	3.70E-03	-1.97	1.26E-02
SAMHD1	-1.96	2.35E-02	b.t.	n.s.
SDCBP	-1.96	4.75E-02	b.t.	n.s.
TIPARP	-1.96	4.34E-02	-2.24	1.67E-02
USP28	-1.96	1.10E-03	b.t.	n.s.
ZBTB24	-1.96	3.25E-02	b.t.	n.s.
DTNBP1	-1.98	4.24E-02	b.t.	n.s.
ITM2B	-1.98	5.10E-03	b.t.	n.s.
SETDB2	-1.98	3.03E-02	-2.31	2.58E-02
SETX	-1.98	3.40E-03	-2.19	4.80E-03
TXNDC16	-1.98	7.00E-04	-1.85	3.00E-04
CPEB3	-1.99	4.14E-05	b.t.	n.s.
FBXL20	-1.99	1.93E-02	b.t.	n.s.
OXR1	-1.99	9.00E-04	b.t.	n.s.
USP6NL	-1.99	3.79E-02	b.t.	n.s.
ANKRD13A	-2	7.00E-03	-2.08	8.20E-03
APOL3	-2	5.60E-03	-2.81	7.63E-05
CLCN6	-2	7.50E-03	b.t.	n.s.
FMR1	-2	2.00E-04	-2.21	5.00E-04
HERPUD2	-2	4.50E-03	b.t.	n.s.
SELL	-2	6.40E-03	b.t.	n.s.
SOS1	-2	4.00E-04	-2.55	2.00E-04

SUSD6	-2	2.97E-02	b.t.	n.s.
ZNF528	-2	2.93E-02	b.t.	n.s.
GNB5	-2.01	4.80E-03	-1.89	7.60E-03
TCF3	-2.01	4.50E-03	-1.75	1.12E-02
AFTPH	-2.02	5.00E-04	-1.55	7.00E-03
C11orf68	-2.02	3.39E-02	b.t.	n.s.
CCDC28A	-2.02	4.56E-02	-2.71	4.73E-02
PKN2	-2.02	2.65E-02	b.t.	n.s.
SOAT1	-2.02	3.00E-03	b.t.	n.s.
STK38	-2.02	3.57E-02	-1.7	3.53E-02
CMTM1	-2.03	2.66E-02	-1.65	5.50E-03
CYB561A3	-2.03	4.15E-02	b.t.	n.s.
FBXL3	-2.03	2.52E-02	b.t.	n.s.
PHC3	-2.03	5.20E-03	-1.72	3.39E-02
ZNF283	-2.03	7.40E-03	b.t.	n.s.
RFX7	-2.04	4.90E-03	b.t.	n.s.
NDRG1	-2.05	2.00E-03	-2.02	7.50E-03
STARD7	-2.05	6.00E-04	-2.06	1.40E-03
TTC17	-2.05	4.63E-02	b.t.	n.s.
SOWAHD	-2.06	1.00E-02	-1.52	7.40E-03
LCORL	-2.06	3.00E-04	-2.07	1.00E-03
TMX4	-2.06	1.19E-02	-2.52	6.70E-03
CD6	-2.07	4.73E-02	b.t.	n.s.
PDGFRB	-2.07	3.22E-02	b.t.	n.s.
PHF19	-2.07	4.80E-03	b.t.	n.s.
SRGAP2B	-2.07	2.70E-02	-1.57	3.44E-02
LYSMD2	-2.08	4.09E-02	-2.18	2.38E-02
GAB3	-2.08	3.00E-03	-2.22	1.80E-03
LRP5L	-2.08	4.73E-02	b.t.	n.s.

S100PBP	-2.08	4.59E-02	b.t.	n.s.
ZMYM1	-2.09	7.70E-03	b.t.	n.s.
CASS4	-2.1	1.45E-02	-2.12	4.80E-03
YPEL2	-2.1	3.10E-03	-2.03	1.81E-02
BBX	-2.11	6.70E-03	-1.92	1.04E-02
N4BP1	-2.11	2.61E-02	b.t.	n.s.
NEMP1	-2.11	2.35E-02	b.t.	n.s.
SARAF	-2.11	2.11E-02	-2.23	8.10E-03
SLFN13	-2.11	1.98E-02	b.t.	n.s.
SNX16	-2.11	1.20E-03	-1.76	3.94E-02
ZHX2	-2.12	3.40E-02	-1.92	3.27E-02
RICTOR	-2.12	2.40E-03	b.t.	n.s.
TRIM52	-2.12	5.80E-03	-1.67	2.70E-02
ANTXR2	-2.13	8.10E-03	-3.14	8.60E-03
GCNT2	-2.13	7.80E-03	b.t.	n.s.
OPTN	-2.13	3.95E-02	b.t.	n.s.
SGK3	-2.13	5.00E-04	-2.62	1.40E-03
SGPP1	-2.14	4.60E-03	-1.78	2.17E-02
ABCB4	-2.14	6.00E-03	-2.02	8.70E-03
CDKN1B	-2.14	1.32E-02	-1.68	3.36E-02
BANP	-2.15	2.11E-02	b.t.	n.s.
CAPRIN2	-2.15	3.85E-02	b.t.	n.s.
KDM7A	-2.15	3.89E-02	-1.96	3.17E-02
LRRC37B	-2.15	2.54E-02	b.t.	n.s.
TEC	-2.15	6.70E-03	-2.12	1.90E-03
NFATC1	-2.16	2.80E-03	-2.25	6.00E-03
ATP9B	-2.17	8.60E-03	b.t.	n.s.
HBP1	-2.17	2.20E-03	-2.14	2.58E-02
LRRC37A3	-2.17	1.72E-02	b.t.	n.s.

SLC18B1	-2.17	2.00E-03	b.t.	n.s.
SLC35A1	-2.17	2.80E-03	b.t.	n.s.
IL10RA	-2.18	4.47E-02	b.t.	n.s.
SLC15A2	-2.18	2.00E-03	-2	1.56E-02
TP53INP1	-2.18	7.60E-03	b.t.	n.s.
ABCA7	-2.19	4.69E-02	b.t.	n.s.
FAM13B	-2.19	2.00E-04	b.t.	n.s.
NBPF12	-2.19	4.62E-02	b.t.	n.s.
PITPNM2	-2.19	1.82E-02	b.t.	n.s.
SHISA5	-2.19	1.89E-02	b.t.	n.s.
ATXN1	-2.2	2.46E-02	b.t.	n.s.
IQCG	-2.2	6.60E-03	-2.03	3.97E-02
MBP	-2.2	1.44E-02	-1.98	1.95E-02
RAPGEF2	-2.2	1.82E-02	b.t.	n.s.
RNF149	-2.2	3.40E-03	-2.4	1.35E-02
ACSF2	-2.21	8.80E-03	-2.69	1.36E-02
ARHGAP12	-2.22	1.10E-03	-2.02	3.10E-03
CCDC30	-2.22	1.02E-02	b.t.	n.s.
HDAC5	-2.22	1.14E-02	-1.95	2.89E-02
LPAR5	-2.22	1.37E-02	b.t.	n.s.
MAN2A1	-2.22	7.60E-03	-2.04	1.93E-02
TRIM38	-2.22	2.50E-03	-1.52	4.80E-03
BTBD9	-2.23	1.11E-02	b.t.	n.s.
LCK	-2.23	1.28E-02	-2.47	4.90E-03
C16orf74	-2.24	2.05E-02	b.t.	n.s.
ING4	-2.24	9.70E-03	-1.5	4.01E-02
SYK	-2.24	3.16E-02	-1.96	3.80E-03
CD52	-2.25	1.91E-02	-2.34	1.22E-02
SIK3	-2.25	3.47E-02	b.t.	n.s.

PNPLA8	-2.26	2.70E-03	-1.93	8.20E-03
PTPRC	-2.26	2.74E-02	b.t.	n.s.
ST6GAL1	-2.26	5.00E-04	-1.81	5.70E-03
TNKS2	-2.26	5.23E-05	-2.12	2.00E-04
FAXDC2	-2.27	2.28E-02	-3.04	9.20E-03
PARVG	-2.27	1.50E-02	-2.25	1.98E-02
RNF122	-2.27	2.60E-03	-1.91	2.04E-02
RPA1	-2.27	1.57E-02	-1.93	7.50E-03
DNMBP	-2.29	8.00E-04	-2.32	5.10E-03
FGD3	-2.29	8.90E-03	-2.34	2.84E-02
MGME1	-2.29	4.80E-03	b.t.	n.s.
TULP4	-2.29	1.10E-03	-2.61	2.50E-03
WDFY1	-2.29	2.24E-02	-3.16	4.33E-02
ARRDC5	-2.3	1.95E-02	b.t.	n.s.
NFATC3	-2.3	5.43E-05	-2.58	1.83E-05
C12orf74	-2.31	2.30E-03	-2.16	1.06E-02
KAT6B	-2.31	4.60E-05	-2.24	2.20E-03
KAT2B	-2.31	3.20E-03	-1.91	3.20E-03
SLC39A10	-2.31	2.40E-03	-1.97	3.88E-02
UGT8	-2.31	6.00E-04	-1.89	4.32E-02
ZFP14	-2.31	1.87E-02	b.t.	n.s.
BMPR2	-2.32	2.04E-02	-2.14	4.86E-02
CDKL1	-2.32	4.40E-03	-1.85	7.00E-03
PGBD2	-2.32	7.00E-04	b.t.	n.s.
TRIM23	-2.32	1.00E-03	b.t.	n.s.
CXXC5	-2.33	6.60E-03	b.t.	n.s.
PDE4B	-2.33	2.27E-02	b.t.	n.s.
ZNF862	-2.33	2.95E-02	b.t.	n.s.
SPIN4	-2.34	2.00E-04	-1.98	4.50E-03

GLIPR1	-2.35	3.53E-02	b.t.	n.s.
ITGAE	-2.35	2.20E-03	-2.45	2.40E-03
KLHDC1	-2.35	2.01E-02	b.t.	n.s.
SECISBP2L	-2.35	3.80E-03	-2.26	9.20E-03
BROX	-2.36	2.00E-04	b.t.	n.s.
VEZF1	-2.36	3.00E-04	b.t.	n.s.
STAP1	-2.37	1.24E-02	b.t.	n.s.
SLC44A2	-2.37	6.90E-03	b.t.	n.s.
VCPIP1	-2.37	1.63E-06	-2.16	7.64E-05
GAB1	-2.38	1.08E-05	-2.34	6.00E-04
NIPA1	-2.38	2.07E-02	b.t.	n.s.
NOD1	-2.38	5.84E-05	-1.62	3.00E-03
PCMTD2	-2.38	1.03E-02	b.t.	n.s.
NMT2	-2.39	5.80E-03	b.t.	n.s.
SRGAP2C	-2.4	4.22E-02	-1.85	4.42E-02
CXorf21	-2.41	7.00E-03	b.t.	n.s.
SIPA1L3	-2.41	1.34E-02	-2.34	1.26E-02
ZBTB1	-2.41	2.87E-02	b.t.	n.s.
ZCCHC2	-2.41	3.30E-03	-2.71	1.40E-02
OSBPL10	-2.42	1.10E-02	-2.94	3.90E-02
ZER1	-2.42	3.94E-02	b.t.	n.s.
SLAMF6	-2.43	2.17E-02	b.t.	n.s.
HSD17B11	-2.43	1.85E-02	b.t.	n.s.
RGL2	-2.43	4.06E-02	b.t.	n.s.
HS2ST1	-2.46	1.20E-03	-1.86	2.69E-02
MXI1	-2.47	6.80E-03	-2.8	2.40E-03
SIDT1	-2.48	4.20E-03	-1.63	3.89E-02
TMEM71	-2.48	3.34E-02	-2.13	4.32E-02
SLC12A6	-2.49	7.20E-03	-2.62	4.10E-03

ZNF592	-2.49	4.00E-04	b.t.	n.s.
BTG2	-2.5	1.10E-03	-1.9	3.29E-02
PRDM8	-2.51	4.40E-03	-2.03	4.26E-02
ATP10D	-2.52	4.94E-02	b.t.	n.s.
CTSS	-2.52	5.00E-04	-2.22	1.10E-03
MARCH3	-2.52	8.00E-03	-1.93	2.00E-03
NLRP1	-2.52	3.37E-02	b.t.	n.s.
RPS6KA5	-2.52	2.60E-03	-2.49	4.30E-03
KLHL24	-2.53	6.40E-03	b.t.	n.s.
OTUD1	-2.54	1.60E-03	-2.08	4.10E-03
DDX58	-2.54	2.06E-02	b.t.	n.s.
SIAH1	-2.54	7.50E-03	-2.66	1.14E-02
CASP8	-2.55	2.19E-02	b.t.	n.s.
LPP	-2.55	2.05E-02	b.t.	n.s.
RALGPS2	-2.55	1.68E-02	b.t.	n.s.
SRGAP2	-2.56	1.46E-02	-2.15	1.63E-02
VIPR1	-2.57	1.87E-06	-1.66	2.30E-03
CARD16	-2.58	2.01E-02	b.t.	n.s.
MOB3C	-2.58	2.10E-03	-2.5	1.51E-02
UBR2	-2.58	3.00E-04	b.t.	n.s.
PRDM2	-2.59	2.89E-02	b.t.	n.s.
ZBTB38	-2.59	1.43E-02	-2.56	1.21E-02
YPEL5	-2.6	4.00E-04	-2.13	1.49E-02
SLC25A28	-2.61	4.65E-08	-1.62	7.89E-05
B3GALT4	-2.63	4.50E-03	-1.61	2.17E-02
SLC29A3	-2.63	4.00E-04	b.t.	n.s.
ZNF831	-2.64	2.30E-03	-1.93	6.20E-03
XKRX	-2.64	2.84E-02	-3.76	4.13E-02
CHST11	-2.65	2.30E-03	-2.95	2.40E-02

IGFLR1	-2.65	1.87E-02	-2.85	7.50E-03
FAM214A	-2.7	7.10E-03	b.t.	n.s.
SLC30A4	-2.71	1.20E-03	-2.26	3.41E-02
SUSD3	-2.72	6.60E-03	-2.04	1.80E-02
ZNF652	-2.72	9.00E-03	-2.31	2.91E-02
GMFG	-2.73	8.00E-04	-2.9	1.20E-03
RTP4	-2.74	2.52E-02	-3.63	3.36E-02
CDCA7L	-2.75	1.01E-02	-2.89	6.10E-03
TEP1	-2.75	2.40E-03	-3.04	1.76E-02
BTD	-2.76	6.00E-04	b.t.	n.s.
HLA-DMA	-2.77	9.40E-03	-3.02	2.82E-02
LRRN1	-2.77	1.53E-02	-2.01	4.32E-02
TESK2	-2.77	7.90E-03	-2.97	2.08E-02
ARHGAP9	-2.79	2.34E-02	-2.27	4.25E-02
ATM	-2.8	1.26E-02	-2.25	4.02E-02
VAMP1	-2.8	7.00E-04	-1.63	1.34E-02
SELPLG	-2.82	2.51E-02	b.t.	n.s.
HMCES	-2.82	1.01E-02	-3.56	1.10E-03
PHKB	-2.83	1.18E-02	-3.57	4.74E-02
ADRB2	-2.84	2.26E-06	-1.67	2.40E-03
OR56B1	-2.84	3.79E-02	b.t.	n.s.
MORC3	-2.84	4.00E-04	b.t.	n.s.
ARAP2	-2.85	7.60E-03	-2.76	2.73E-02
SLFN12L	-2.85	3.39E-02	b.t.	n.s.
FCRL1	-2.91	4.00E-03	b.t.	n.s.
PATL2	-2.92	2.00E-04	-2.41	9.00E-04
E2F5	-2.93	7.00E-04	-2.56	1.09E-02
ABLIM1	-2.97	4.70E-02	b.t.	n.s.
CREBRF	-2.97	9.90E-03	-2.25	3.37E-02

DDAH2	-2.98	4.46E-02	-3.42	3.23E-02
HLA-DMB	-2.98	7.20E-03	-3.08	1.39E-02
LRRK2	-2.99	4.39E-05	-3.68	8.01E-05
PLEKHG7	-3.01	3.00E-03	-1.76	2.17E-02
HEATR6	-3.02	6.00E-03	-2.12	2.80E-02
TEAD2	-3.02	3.17E-02	b.t.	n.s.
ZNF266	-3.02	8.90E-03	b.t.	n.s.
PCMTD1	-3.03	6.00E-04	-1.93	5.70E-03
LMBRD1	-3.04	1.00E-04	-1.84	3.10E-03
NT5C2	-3.04	2.12E-02	b.t.	n.s.
SFXN3	-3.05	8.00E-04	-2.55	7.00E-04
ZBTB44	-3.06	8.00E-04	-1.96	1.38E-02
DHRS1	-3.08	1.09E-02	b.t.	n.s.
CDK19	-3.11	1.02E-02	-2.27	2.00E-02
RAB31	-3.11	4.20E-03	-3.29	1.40E-03
RHOC	-3.11	2.09E-02	-3.58	2.32E-02
ATP2A3	-3.14	3.85E-02	b.t.	n.s.
TNFRSF17	-3.15	3.18E-02	b.t.	n.s.
PARP11	-3.16	1.80E-03	-2.75	2.31E-02
TRAM2	-3.2	2.70E-02	b.t.	n.s.
DNAJC1	-3.24	3.39E-05	-2.14	7.00E-04
ILK	-3.24	9.00E-04	-1.84	1.55E-02
IRS1	-3.25	2.63E-05	-1.78	1.39E-02
NR1D2	-3.25	6.53E-05	-2.53	7.20E-03
DCLRE1C	-3.27	6.87E-07	-2.85	1.00E-04
ZC4H2	-3.27	2.00E-04	-2.29	1.70E-03
CCDC88A	-3.28	4.67E-02	b.t.	n.s.
CD69	-3.28	5.80E-03	b.t.	n.s.
SERPINI1	-3.28	2.30E-03	-3.91	2.80E-03

BTN3A2	-3.29	1.64E-02	b.t.	n.s.
MAP3K1	-3.3	6.00E-04	-2.58	6.40E-03
CLK1	-3.34	1.50E-02	b.t.	n.s.
CHPT1	-3.36	1.30E-02	-2.83	8.80E-03
XRN1	-3.36	3.22E-02	b.t.	n.s.
PVRIG	-3.37	5.00E-04	-3.64	9.00E-04
ANXA2R	-3.38	4.97E-05	-4.4	2.00E-04
TNFSF13B	-3.41	1.36E-02	-7.59	3.00E-04
RHOH	-3.43	1.80E-03	-1.91	4.58E-02
SMCHD1	-3.43	1.20E-03	-2.11	2.97E-02
UTRN	-3.44	3.70E-03	-2.55	2.32E-02
LRRC37A	-3.49	2.09E-02	b.t.	n.s.
AIM2	-3.5	1.40E-02	-3.36	4.21E-02
VAV3	-3.5	1.60E-03	-2.69	1.04E-02
MAP2	-3.51	6.00E-04	-2.01	2.29E-02
FAM122C	-3.53	3.00E-04	-1.85	2.15E-02
ORAI2	-3.55	1.10E-03	-2.99	2.40E-03
RERE	-3.56	8.70E-03	-2.15	1.65E-02
PIK3IP1	-3.57	5.70E-03	-2.69	2.20E-02
TCL1A	-3.62	1.00E-02	b.t.	n.s.
CASP10	-3.64	4.62E-02	b.t.	n.s.
IL7	-3.65	2.57E-02	-2.22	1.44E-02
SETBP1	-3.65	8.00E-04	-3.31	1.00E-03
GGA2	-3.68	2.00E-04	-2.27	6.00E-03
TRIM22	-3.68	2.98E-02	b.t.	n.s.
CABLES1	-3.7	3.18E-02	b.t.	n.s.
TMEM63A	-3.72	8.00E-04	-3.36	3.80E-03
SAT1	-3.76	5.00E-04	-3.65	1.60E-03
ANKRD12	-3.77	3.76E-02	b.t.	n.s.

TBC1D9	-3.77	1.00E-03	-4.15	8.80E-03
DNAJC28	-3.78	1.10E-03	-3.87	1.90E-03
CALCOCO1	-3.78	1.85E-02	b.t.	n.s.
RAPGEF3	-3.79	3.10E-03	-2.96	1.46E-02
STIM2	-3.81	2.00E-04	-2.22	1.02E-02
TGFBR2	-3.81	1.33E-06	-2.9	2.83E-05
CYTIP	-3.82	1.49E-02	b.t.	n.s.
NCF4	-3.82	1.88E-05	-2.59	2.30E-03
ADAMTS6	-3.85	1.31E-02	-3.09	3.56E-02
PTPRCAP	-3.87	4.38E-02	b.t.	n.s.
KMO	-3.9	1.50E-03	-3.73	1.50E-03
RAB27B	-3.92	6.60E-03	-5.53	1.80E-03
CEACAM5	-3.97	9.60E-03	-2.05	4.90E-02
PELI1	-3.99	6.00E-04	-2.31	2.30E-02
TNS3	-4.03	3.11E-02	b.t.	n.s.
STAMBPL1	-4.05	7.00E-04	-2.71	4.50E-03
LBH	-4.06	1.71E-02	b.t.	n.s.
BCL11A	-4.14	2.10E-02	-3.74	2.42E-02
IRF1	-4.14	1.78E-02	-7.09	2.09E-02
GNAZ	-4.16	4.50E-03	-2.53	2.47E-02
FCRL5	-4.24	2.32E-02	b.t.	n.s.
NUB1	-4.24	3.00E-04	-2.85	3.30E-03
EVL	-4.26	5.81E-06	-3.01	1.00E-04
LAX1	-4.29	4.30E-03	-2.95	6.40E-03
NAGK	-4.3	5.70E-03	-4.5	7.40E-03
SESN1	-4.32	1.10E-05	-3.27	1.20E-03
NT5C3A	-4.36	1.26E-02	b.t.	n.s.
ATXN7	-4.38	9.87E-07	-2.6	1.64E-05
TMEM140	-4.39	2.52E-05	-3.66	6.00E-04

PDCD1LG2	-4.43	1.96E-02	-2.36	4.29E-02
PECAM1	-4.45	8.60E-03	-6.18	3.50E-03
MARCH8	-4.51	2.09E-05	-2.46	1.20E-03
PRKCE	-4.51	3.00E-04	-6.24	5.00E-04
RASGEF1B	-4.57	9.40E-03	b.t.	n.s.
TMEM19	-4.59	2.70E-05	-2.38	1.40E-03
CHST12	-4.61	1.00E-04	-2.97	1.24E-02
STX7	-4.62	7.56E-06	-2.57	5.20E-03
CDC25B	-4.74	1.08E-02	-3.56	2.46E-02
PDP1	-4.76	9.00E-04	-2.77	8.50E-03
PTPN6	-4.83	1.43E-02	-4.87	8.80E-03
BTN3A1	-4.9	5.00E-04	-2.65	2.46E-02
FAM117B	-4.91	1.00E-03	-5.19	1.20E-03
CEACAM1	-4.95	2.38E-02	-4.24	4.31E-02
KIAA0040	-4.95	6.99E-05	-2.35	4.90E-03
MAPRE2	-5.01	5.38E-05	-3.19	8.00E-04
APBB2	-5.1	7.00E-04	-6.5	2.70E-03
PYCARD	-5.12	2.70E-03	-4.25	1.90E-03
TXNIP	-5.19	3.94E-05	-5.14	9.00E-04
GRK5	-5.22	2.80E-03	-2.75	4.84E-02
LPIN2	-5.27	1.30E-03	-3.34	3.45E-02
L3HYPDH	-5.32	9.40E-03	-2.27	4.56E-02
CLNK	-5.37	1.35E-02	b.t.	n.s.
CCR6	-5.39	2.69E-02	-8.56	1.53E-02
SSBP2	-5.53	2.00E-03	-4.03	3.11E-02
FCGR2C	-5.57	3.60E-03	-4.69	1.47E-02
PRICKLE1	-5.63	1.45E-08	-3.58	7.83E-07
VAMP5	-5.66	2.00E-04	-4.44	7.68E-05
METTL7A	-5.67	2.70E-03	-7.27	1.52E-02

PCDH9	-5.71	1.10E-03	b.t.	n.s.
ARHGEF3	-5.75	5.00E-03	-5.47	2.84E-02
TRIB1	-5.82	5.00E-03	-4.78	4.60E-03
LTB	-5.92	7.70E-03	b.t.	n.s.
STAT2	-6.08	3.00E-04	-7.2	1.30E-03
PIK3CG	-6.14	6.00E-04	-8.88	1.00E-04
DACT1	-6.15	8.89E-09	-4.83	1.83E-06
CD79B	-6.16	6.00E-04	-4.42	2.40E-03
SYNE2	-6.17	1.73E-02	-6.01	3.70E-02
PARP8	-6.19	6.07E-06	-5.26	2.00E-04
IL18BP	-6.32	1.24E-02	-3.26	1.47E-02
FCGR2B	-6.34	4.10E-03	-4.16	2.48E-02
FRY	-6.44	2.62E-02	b.t.	n.s.
ALOX5	-6.53	3.10E-03	-3.65	3.10E-02
PLEKHA2	-6.75	1.15E-05	-4.95	3.00E-04
ANK1	-6.85	8.90E-06	-4.13	4.00E-04
ETV7	-7.18	2.15E-02	-8.44	1.39E-02
COL9A3	-7.88	1.00E-03	-3.97	1.15E-02
CYSLTR1	-8.14	7.60E-03	-5.19	2.17E-02
PTPN22	-8.15	8.00E-07	-4.72	8.26E-05
CLMN	-8.34	2.00E-04	-6.43	1.30E-03
RNASE6	-8.52	4.20E-03	-4.89	1.00E-02
CD24	-8.66	1.30E-05	-4.58	1.20E-03
JAK2	-8.66	3.05E-05	-4.73	2.00E-03
TNFSF10	-8.74	3.68E-02	b.t.	n.s.
OAS1	-8.79	1.76E-02	-4.49	3.64E-02
GPR155	-9.23	1.00E-04	-6.51	5.00E-04
TGFBI	-9.45	1.00E-03	-8.03	9.00E-04
CTLA4	-9.53	2.20E-03	-9.1	2.30E-03

FAM111B	-10	1.90E-03	b.t.	n.s.
GPR18	-10.51	4.00E-04	-5.44	4.30E-03
PDE7B	-10.76	5.00E-03	-11.39	1.69E-02
FCMR	-10.98	3.10E-03	-13.17	1.30E-03
CD27	-12.14	3.50E-03	-15.76	3.20E-03
RNASET2	-12.52	1.70E-03	-12.98	7.00E-04
ID3	-13.57	3.00E-04	-12.99	7.00E-04
SCIMP	-13.77	5.98E-05	-8.87	8.00E-04
LY86	-14.36	1.85E-05	-11.13	8.19E-05
GNG7	-17.08	2.00E-03	-13.38	7.90E-03
ADAM28	-18.71	5.30E-03	b.t.	n.s.
IFIT2	-23.1	1.76E-02	b.t.	n.s.
RARRES3	-33.45	4.59E-08	-36.19	3.61E-07
GRAMD1B	b.t.	n.s.	11.07	2.16E-02
DGKG	b.t.	n.s.	10.14	1.40E-03
MREG	b.t.	n.s.	6.26	1.70E-02
CCL22	b.t.	n.s.	4.58	9.80E-03
JMY	b.t.	n.s.	4.34	9.50E-03
ELL3	b.t.	n.s.	4.07	4.80E-03
CD40	b.t.	n.s.	3.59	7.30E-03
PAX5	b.t.	n.s.	3.39	7.00E-03
TMEM120A	b.t.	n.s.	3.39	1.77E-02
SFT2D1	b.t.	n.s.	3.08	2.67E-02
ATP2B1	b.t.	n.s.	3.02	1.81E-02
MAP3K8	b.t.	n.s.	2.94	1.06E-02
PLA2G4C	b.t.	n.s.	2.93	2.35E-02
CYP27A1	b.t.	n.s.	2.7	7.70E-03
TTC28	b.t.	n.s.	2.69	2.29E-02
TFEB	b.t.	n.s.	2.64	3.62E-02

MYO1C	b.t.	n.s.	2.53	4.00E-04
ETFA	b.t.	n.s.	2.52	3.90E-02
TOP2A	b.t.	n.s.	2.51	1.47E-02
ZNF433	b.t.	n.s.	2.44	2.26E-02
PRKCD	b.t.	n.s.	2.35	2.45E-02
SMARCA2	b.t.	n.s.	2.31	2.19E-02
TLE3	b.t.	n.s.	2.28	1.13E-02
RFFL	b.t.	n.s.	2.27	1.20E-03
SLC2A6	b.t.	n.s.	2.23	3.90E-03
RDH13	b.t.	n.s.	2.21	2.00E-04
TIGD2	b.t.	n.s.	2.21	3.14E-02
SRGN	b.t.	n.s.	2.19	1.44E-02
DUSP22	b.t.	n.s.	2.15	2.90E-03
NFKBIZ	b.t.	n.s.	2.14	2.29E-02
BIRC3	b.t.	n.s.	2.09	4.69E-02
CASZ1	b.t.	n.s.	2.06	1.12E-02
HOXB9	b.t.	n.s.	2.04	4.10E-02
QTRT1	b.t.	n.s.	2.04	2.57E-02
CXCR6	b.t.	n.s.	2.02	1.15E-02
LYN	b.t.	n.s.	1.97	1.93E-02
SDC4	b.t.	n.s.	1.96	4.17E-02
MIPEP	b.t.	n.s.	1.93	4.84E-02
SURF4	b.t.	n.s.	1.92	3.39E-02
HIST1H4G	b.t.	n.s.	1.89	4.52E-02
RAD51B	b.t.	n.s.	1.89	8.50E-03
NR6A1	b.t.	n.s.	1.88	3.61E-02
G0S2	b.t.	n.s.	1.86	4.09E-02
RLN2	b.t.	n.s.	1.85	4.29E-02
CUL1	b.t.	n.s.	1.83	1.69E-02

MSC	b.t.	n.s.	1.81	2.44E-02
IMPAD1	b.t.	n.s.	1.8	4.95E-02
SERF1A	b.t.	n.s.	1.79	3.31E-02
ARID3B	b.t.	n.s.	1.78	1.46E-02
MELK	b.t.	n.s.	1.77	9.90E-03
NUSAP1	b.t.	n.s.	1.77	2.63E-02
TJP2	b.t.	n.s.	1.77	7.90E-03
P4HA2	b.t.	n.s.	1.76	4.79E-02
S100A9	b.t.	n.s.	1.75	4.50E-03
DEPDC4	b.t.	n.s.	1.73	3.49E-02
DOLPP1	b.t.	n.s.	1.73	2.76E-02
KDM4A	b.t.	n.s.	1.73	3.87E-02
NCK2	b.t.	n.s.	1.73	4.84E-02
USP19	b.t.	n.s.	1.73	1.32E-02
FAM229B	b.t.	n.s.	1.72	3.58E-02
TMEM254	b.t.	n.s.	1.72	3.22E-02
PORCN	b.t.	n.s.	1.71	2.66E-02
RPTOR	b.t.	n.s.	1.69	4.94E-02
CAPN1	b.t.	n.s.	1.68	2.28E-02
DCTN4	b.t.	n.s.	1.66	3.41E-02
INAFM2	b.t.	n.s.	1.66	4.03E-02
PARP2	b.t.	n.s.	1.66	3.65E-02
KCNK5	b.t.	n.s.	1.65	3.59E-02
MRPS10	b.t.	n.s.	1.65	2.03E-02
TRIM24	b.t.	n.s.	1.65	1.49E-02
DCUN1D1	b.t.	n.s.	1.64	3.26E-02
GPAT4	b.t.	n.s.	1.64	4.74E-02
UBE4A	b.t.	n.s.	1.64	2.55E-02
MRPL28	b.t.	n.s.	1.63	3.20E-02

ETV3	b.t.	n.s.	1.62	1.10E-02
KLC2	b.t.	n.s.	1.62	2.18E-02
TGIF2	b.t.	n.s.	1.62	8.10E-03
C5orf63	b.t.	n.s.	1.6	4.80E-02
DDX6	b.t.	n.s.	1.6	1.25E-02
STOML1	b.t.	n.s.	1.6	1.00E-03
INTS6	b.t.	n.s.	1.59	5.40E-03
THEMIS2	b.t.	n.s.	1.59	4.78E-02
CNNM1	b.t.	n.s.	1.58	1.40E-02
CRTC2	b.t.	n.s.	1.58	9.20E-03
EIF3L	b.t.	n.s.	1.58	6.10E-03
PTGER2	b.t.	n.s.	1.57	1.94E-02
VN1R3	b.t.	n.s.	1.57	3.55E-02
SLC45A3	b.t.	n.s.	1.56	1.10E-03
NPAT	b.t.	n.s.	1.55	4.16E-02
PIGV	b.t.	n.s.	1.55	3.05E-02
RAB3IL1	b.t.	n.s.	1.55	2.93E-02
ZDHHC11B	b.t.	n.s.	1.55	1.90E-03
ZDHHC3	b.t.	n.s.	1.54	1.88E-02
KIAA1586	b.t.	n.s.	1.54	5.60E-03
PPIC	b.t.	n.s.	1.54	3.88E-02
TAB2	b.t.	n.s.	1.54	4.13E-02
ASXL1	b.t.	n.s.	1.53	2.81E-02
MLIP	b.t.	n.s.	1.52	8.00E-04
ONECUT2	b.t.	n.s.	1.52	1.54E-02
TBC1D21	b.t.	n.s.	1.51	4.00E-03
APOA4	b.t.	n.s.	1.5	4.38E-02
ZDHHC20	b.t.	n.s.	-1.5	2.21E-02
C16orf54	b.t.	n.s.	-1.51	2.78E-02

HEXIM2	b.t.	n.s.	-1.51	1.74E-02
COLEC10	b.t.	n.s.	-1.51	3.38E-02
SEC62	b.t.	n.s.	-1.51	4.24E-02
ST6GALNAC4	b.t.	n.s.	-1.51	2.60E-02
ZNF181	b.t.	n.s.	-1.51	2.75E-02
GSTO2	b.t.	n.s.	-1.52	1.15E-02
KLF9	b.t.	n.s.	-1.52	3.20E-03
PIAS2	b.t.	n.s.	-1.52	4.98E-02
ZNF510	b.t.	n.s.	-1.52	1.52E-02
ARFGEF2	b.t.	n.s.	-1.53	2.72E-02
ARHGEF10L	b.t.	n.s.	-1.53	9.00E-04
RASSF7	b.t.	n.s.	-1.53	3.00E-03
TTC24	b.t.	n.s.	-1.53	8.20E-03
IL20	b.t.	n.s.	-1.54	2.01E-02
BCAS4	b.t.	n.s.	-1.54	3.77E-02
ACTR10	b.t.	n.s.	-1.55	5.00E-03
AUH	b.t.	n.s.	-1.55	1.18E-02
BAK1	b.t.	n.s.	-1.55	3.54E-02
FECH	b.t.	n.s.	-1.55	1.94E-02
U2AF1L4	b.t.	n.s.	-1.55	3.31E-02
GRAPL	b.t.	n.s.	-1.56	1.12E-02
KCTD7	b.t.	n.s.	-1.56	3.12E-02
RGS8	b.t.	n.s.	-1.56	2.22E-02
SLC26A7	b.t.	n.s.	-1.56	3.25E-02
YIPF7	b.t.	n.s.	-1.56	3.02E-02
DENND6A	b.t.	n.s.	-1.57	1.04E-02
DISC1	b.t.	n.s.	-1.57	3.80E-03
LIPT1	b.t.	n.s.	-1.57	2.30E-03
CTBP1	b.t.	n.s.	-1.58	4.32E-02

FNIP1	b.t.	n.s.	-1.58	4.66E-02
NEK5	b.t.	n.s.	-1.58	2.10E-03
RASIP1	b.t.	n.s.	-1.58	4.00E-04
UPF3A	b.t.	n.s.	-1.58	2.80E-03
LNX2	b.t.	n.s.	-1.59	3.49E-02
TMSB10	b.t.	n.s.	-1.59	4.53E-02
ING1	b.t.	n.s.	-1.6	6.30E-03
CUTA	b.t.	n.s.	-1.6	1.29E-02
DMC1	b.t.	n.s.	-1.6	3.82E-02
ZNF174	b.t.	n.s.	-1.6	1.37E-02
NBPF3	b.t.	n.s.	-1.61	4.34E-02
SIMC1	b.t.	n.s.	-1.61	4.31E-02
FOXO3	b.t.	n.s.	-1.62	3.96E-02
OSTM1	b.t.	n.s.	-1.62	2.56E-02
RTP1	b.t.	n.s.	-1.63	1.30E-02
GDPD4	b.t.	n.s.	-1.63	2.04E-02
MEPE	b.t.	n.s.	-1.63	6.70E-03
TSC22D1	b.t.	n.s.	-1.63	9.00E-04
RHOT1	b.t.	n.s.	-1.64	1.93E-02
CMC2	b.t.	n.s.	-1.65	3.51E-02
MAST3	b.t.	n.s.	-1.65	2.50E-02
ABRA	b.t.	n.s.	-1.66	1.44E-02
BARD1	b.t.	n.s.	-1.66	4.00E-03
KIF27	b.t.	n.s.	-1.66	2.85E-02
LSM10	b.t.	n.s.	-1.67	2.98E-02
METTL25	b.t.	n.s.	-1.67	4.31E-02
TBL1X	b.t.	n.s.	-1.67	4.29E-02
CCDC158	b.t.	n.s.	-1.68	1.57E-02
TTLL1	b.t.	n.s.	-1.68	4.06E-02

COL6A5	b.t.	n.s.	-1.69	2.70E-03
HERC4	b.t.	n.s.	-1.69	4.33E-02
PMM1	b.t.	n.s.	-1.69	3.70E-02
ING2	b.t.	n.s.	-1.7	7.20E-03
ZNF705G	b.t.	n.s.	-1.7	2.08E-02
STK25	b.t.	n.s.	-1.7	3.86E-02
PPM1D	b.t.	n.s.	-1.71	1.44E-02
CASP9	b.t.	n.s.	-1.72	5.60E-03
GIN1	b.t.	n.s.	-1.72	1.79E-02
GNA13	b.t.	n.s.	-1.72	3.10E-02
FXYD7	b.t.	n.s.	-1.73	3.29E-02
MGAT1	b.t.	n.s.	-1.73	4.10E-03
MAP3K2	b.t.	n.s.	-1.74	2.96E-02
RASGEF1A	b.t.	n.s.	-1.74	1.22E-02
FABP3	b.t.	n.s.	-1.75	9.20E-03
LIG1	b.t.	n.s.	-1.75	1.61E-02
RAB37	b.t.	n.s.	-1.75	7.20E-03
REEP3	b.t.	n.s.	-1.75	3.30E-03
STRN	b.t.	n.s.	-1.75	2.85E-02
TMOD2	b.t.	n.s.	-1.75	1.42E-02
USP21	b.t.	n.s.	-1.75	2.07E-02
KBTBD8	b.t.	n.s.	-1.76	4.03E-02
SLC12A7	b.t.	n.s.	-1.76	1.73E-02
ABRACL	b.t.	n.s.	-1.77	1.68E-02
CHAMP1	b.t.	n.s.	-1.77	4.40E-03
ESR2	b.t.	n.s.	-1.77	3.80E-03
DENND1A	b.t.	n.s.	-1.79	4.67E-02
PEPD	b.t.	n.s.	-1.79	1.62E-02
SLC35C1	b.t.	n.s.	-1.8	9.30E-03

RFC1	b.t.	n.s.	-1.8	2.10E-02
ZNF846	b.t.	n.s.	-1.8	1.29E-02
EGR3	b.t.	n.s.	-1.81	4.34E-02
MYBL1	b.t.	n.s.	-1.82	4.54E-02
DYRK1B	b.t.	n.s.	-1.84	4.54E-02
C14orf28	b.t.	n.s.	-1.84	2.60E-02
GNAS	b.t.	n.s.	-1.84	3.39E-02
UBE2B	b.t.	n.s.	-1.84	3.08E-02
EGLN2	b.t.	n.s.	-1.85	2.20E-03
TMCC1	b.t.	n.s.	-1.85	4.07E-02
SLF2	b.t.	n.s.	-1.87	3.08E-02
PJA1	b.t.	n.s.	-1.88	1.27E-02
STK26	b.t.	n.s.	-1.88	1.30E-03
TTL	b.t.	n.s.	-1.88	1.40E-03
FLCN	b.t.	n.s.	-1.89	3.11E-02
MNT	b.t.	n.s.	-1.89	2.27E-02
GMCL1	b.t.	n.s.	-1.9	8.70E-03
CKLF-CMTM1	b.t.	n.s.	-1.91	3.66E-02
ITGAL	b.t.	n.s.	-1.91	2.58E-02
SCAMP1	b.t.	n.s.	-1.92	4.50E-03
ARAP1	b.t.	n.s.	-1.93	1.11E-02
METRNL	b.t.	n.s.	-1.93	5.70E-03
ACAP1	b.t.	n.s.	-1.94	4.36E-02
NIN	b.t.	n.s.	-1.94	1.51E-02
VEGFB	b.t.	n.s.	-1.95	3.35E-02
EPB41L4A	b.t.	n.s.	-1.96	4.63E-02
FBXW11	b.t.	n.s.	-1.96	4.63E-02
TNFSF12	b.t.	n.s.	-1.96	1.76E-02
LRRC25	b.t.	n.s.	-1.97	7.90E-03

KANSL1L	b.t.	n.s.	-1.97	4.52E-02
CCDC91	b.t.	n.s.	-1.98	8.40E-03
UMAD1	b.t.	n.s.	-1.98	3.11E-02
TMEM156	b.t.	n.s.	-1.99	2.24E-02
FMO5	b.t.	n.s.	-2.01	1.20E-03
MCOLN1	b.t.	n.s.	-2.02	7.00E-03
TRIM69	b.t.	n.s.	-2.02	5.50E-03
NUDT3	b.t.	n.s.	-2.03	1.15E-02
GRK6	b.t.	n.s.	-2.05	1.20E-03
HEXA	b.t.	n.s.	-2.06	1.97E-02
WNT16	b.t.	n.s.	-2.09	1.73E-02
ACVR1	b.t.	n.s.	-2.1	4.96E-02
KLK1	b.t.	n.s.	-2.1	5.70E-03
MBD5	b.t.	n.s.	-2.1	1.32E-02
HTRA3	b.t.	n.s.	-2.12	4.52E-02
SERTAD1	b.t.	n.s.	-2.14	3.36E-02
ADD3	b.t.	n.s.	-2.15	4.54E-02
CASP3	b.t.	n.s.	-2.15	1.93E-02
CLEC2D	b.t.	n.s.	-2.15	2.04E-02
OSBPL3	b.t.	n.s.	-2.18	2.51E-02
STK24	b.t.	n.s.	-2.18	3.30E-03
KANK1	b.t.	n.s.	-2.19	3.26E-02
RAB20	b.t.	n.s.	-2.22	1.30E-03
MAX	b.t.	n.s.	-2.23	1.50E-03
SLC37A2	b.t.	n.s.	-2.25	2.45E-02
CD5	b.t.	n.s.	-2.29	1.80E-02
ZHX3	b.t.	n.s.	-2.29	4.40E-02
IL12B	b.t.	n.s.	-2.34	8.60E-03
COTL1	b.t.	n.s.	-2.34	1.95E-02

CSRNP2	b.t.	n.s.	-2.34	1.57E-02
PANK1	b.t.	n.s.	-2.36	4.20E-02
RASA3	b.t.	n.s.	-2.38	1.42E-02
LDLRAP1	b.t.	n.s.	-2.39	3.45E-02
MPP7	b.t.	n.s.	-2.41	2.40E-02
ASAH1	b.t.	n.s.	-2.45	1.40E-02
TNFRSF13B	b.t.	n.s.	-2.52	3.80E-02
ACACB	b.t.	n.s.	-2.53	4.13E-02
TTC3	b.t.	n.s.	-2.53	2.92E-02
RNASEH2B	b.t.	n.s.	-2.57	2.49E-02
ARID5B	b.t.	n.s.	-2.59	1.51E-02
CEP68	b.t.	n.s.	-2.62	2.34E-02
TNFRSF18	b.t.	n.s.	-2.68	4.06E-02
SBF2	b.t.	n.s.	-2.68	3.78E-02
CAB39L	b.t.	n.s.	-2.74	4.55E-02
STX10	b.t.	n.s.	-2.75	4.60E-03
TMC8	b.t.	n.s.	-2.77	1.20E-03
LCP2	b.t.	n.s.	-2.9	1.81E-02
ELMSAN1	b.t.	n.s.	-2.98	1.70E-03
CCDC68	b.t.	n.s.	-3.08	2.28E-02
DDIT3	b.t.	n.s.	-3.21	2.60E-03
LRMP	b.t.	n.s.	-3.47	2.31E-02
SLC27A3	b.t.	n.s.	-3.48	4.00E-04
FBXO15	b.t.	n.s.	-4.15	2.87E-02
VAT1	b.t.	n.s.	-4.19	5.40E-03
RHOBTB2	b.t.	n.s.	-4.52	1.54E-02
PNOC	b.t.	n.s.	-4.82	3.10E-03
MRC1	b.t.	n.s.	-4.88	4.17E-02
RGS2	b.t.	n.s.	-6.21	3.84E-02

EGR2	b.t.	n.s.	-7.13	2.90E-03
ARL4C	b.t.	n.s.	-8.22	1.21E-02

n.s. non significant

b.t. below threshold

Supplementary Table 4. Differentially expressed miRNA by agonist mix in absence (C vs A) or presence of Ibrutinib (D vs B).

TP53altered	Fold Change (CvsA)	P-val (CvsA)	Fold Change (DvsB)	P-val (DvsB)
hsa-miR-1260a	1.5	4.12E-02	b.t.	n.s.
hsa-miR-1268b	1.3	2.42E-02	b.t.	n.s.
hsa-miR-155-5p	1.5	3.62E-02	2.5	1.28E-02
hsa-miR-20a-5p	1.8	2.17E-02	3.26	4.19E-02
hsa-miR-29b-1-5p	2.3	2.73E-02	b.t.	n.s.
hsa-miR-3162-5p	1.3	4.44E-02	7.86	1.80E-03
hsa-miR-4286	1.5	3.67E-02	3.8	5.80E-03
hsa-miR-431-3p	9.4	6.10E-03	b.t.	n.s.
hsa-miR-6165	1.4	2.75E-02	b.t.	n.s.
hsa-miR-6829-5p	1.7	3.55E-02	b.t.	n.s.
hsa-miR-7114-5p	1.7	4.80E-02	9.1	1.00E-03
hsa-miR-770-5p	9.0	1.84E-02	b.t.	n.s.
hsa-miR-92a-3p	1.5	4.84E-02	b.t.	n.s.
hsa-miR-150-5p	-1.2	4.23E-02	6.84	2.15E-02
hsa-miR-6716-3p	-9.8	4.49E-02	4.12	1.02E-02
hsa-miR-365a-3p	b.t.	n.s.	8.0	2.08E-02
hsa-miR-4436b-5p	b.t.	n.s.	6.5	4.97E-02
hsa-miR-132-3p	b.t.	n.s.	-24.8	1.79E-02

WT (Aviano)	Fold Change (CvsA)	P-val (CvsA)	Fold Change (DvsB)	P-val (DvsB)
hsa-miR-155-3p	8.0	2.22E-02	5.4	4.31E-03
hsa-miR-18b-5p	7.0	1.44E-02	b.t.	n.s.
hsa-miR-221-5p	5.9	4.97E-02	b.t.	n.s.
hsa-miR-221-3p	5.1	1.33E-02	5.9	2.40E-02
hsa-miR-29b-1-5p	4.7	3.72E-02	b.t.	n.s.
hsa-miR-6840-3p	3.8	4.79E-02	b.t.	n.s.
hsa-miR-17-5p	2.1	4.40E-03	1.9	1.81E-02
hsa-miR-155-5p	2.0	1.43E-02	1.8	2.43E-02
hsa-miR-20b-5p	1.9	2.17E-02	b.t.	n.s.
hsa-miR-20a-5p	1.9	5.99E-03	b.t.	n.s.
hsa-miR-7114-5p	1.9	4.42E-03	b.t.	n.s.
hsa-miR-6826-5p	1.9	1.10E-02	b.t.	n.s.
hsa-miR-212-3p	1.9	3.35E-02	b.t.	n.s.
hsa-miR-92a-3p	1.8	4.96E-03	1.6	3.62E-02
hsa-miR-1233-5p	1.7	2.59E-02	b.t.	n.s.
hsa-miR-34a-5p	1.6	1.98E-02	b.t.	n.s.
hsa-miR-211-3p	1.5	1.70E-02	b.t.	n.s.
hsa-miR-6085	1.5	4.45E-02	b.t.	n.s.
hsa-miR-6829-5p	1.5	4.99E-03	1.3	4.92E-02
hsa-miR-939-5p	1.5	2.51E-03	b.t.	n.s.
hsa-miR-4286	1.5	1.97E-02	b.t.	n.s.
hsa-miR-19b-3p	1.5	3.39E-02	b.t.	n.s.
hsa-miR-7152-3p	1.5	3.07E-02	b.t.	n.s.
hsa-miR-5739	1.5	7.29E-03	1.3	4.50E-02
hsa-miR-6808-5p	1.4	4.07E-02	b.t.	n.s.
hsa-miR-6165	1.4	1.91E-02	b.t.	n.s.
hsa-miR-6763-5p	1.4	2.51E-02	b.t.	n.s.

hsa-miR-7977	1.4	1.68E-02	1.3	2.34E-02
hsa-miR-6807-5p	1.3	2.94E-02	b.t.	n.s.
hsa-miR-6740-5p	1.2	3.69E-02	b.t.	n.s.
hsa-miR-4515	-1.2	7.01E-03	b.t.	n.s.
hsa-miR-6891-5p	-1.2	4.12E-02	b.t.	n.s.
hsa-miR-26a-5p	-1.3	3.80E-02	b.t.	n.s.
hsa-miR-6126	-1.4	4.12E-02	b.t.	n.s.
hsa-miR-3665	-1.5	4.60E-02	b.t.	n.s.
hsa-miR-1290	-1.5	2.00E-02	-1.5	9.86E-03
hsa-miR-1915-3p	-1.5	3.60E-02	b.t.	n.s.
hsa-miR-5787	-1.6	3.32E-02	b.t.	n.s.
hsa-miR-6088	-1.6	3.47E-02	b.t.	n.s.
hsa-miR-4466	-1.7	1.52E-02	b.t.	n.s.
hsa-miR-5703	-1.7	4.23E-02	b.t.	n.s.
hsa-miR-197-3p	-1.7	2.88E-02	b.t.	n.s.
hsa-miR-6727-5p	-1.9	3.30E-02	b.t.	n.s.
hsa-miR-6752-3p	-2.1	3.97E-02	b.t.	n.s.
hsa-miR-1908-3p	-2.8	4.96E-02	b.t.	n.s.
hsa-miR-3934-5p	-3.2	3.50E-02	b.t.	n.s.
hsa-miR-4746-3p	-4.8	8.80E-03	b.t.	n.s.
hsa-miR-564	-6.1	2.40E-02	b.t.	n.s.
hsa-miR-3648	-6.2	3.64E-02	b.t.	n.s.
hsa-miR-584-5p	-7.7	3.73E-02	b.t.	n.s.
hsa-miR-874-3p	-9.6	3.83E-03	-5.7	1.87E-02
hsa-miR-2276-3p	-10.8	2.03E-02	b.t.	n.s.
hsa-miR-770-5p	b.t.	n.s.	7.9	7.20E-03
hsa-miR-202-3p	b.t.	n.s.	7.9	1.63E-02
hsa-miR-4749-3p	b.t.	n.s.	7.6	1.05E-02
hsa-miR-4252	b.t.	n.s.	6.9	4.17E-02

hsa-miR-19a-3p	b.t.	n.s.	1.5	4.87E-02
hsa-miR-8069	b.t.	n.s.	-1.6	1.39E-02
hsa-miR-132-5p	b.t.	n.s.	-5.6	4.25E-02
hsa-miR-6073	b.t.	n.s.	-6.4	8.77E-03
hsa-miR-4745-5p	b.t.	n.s.	-8.0	2.97E-03
hsa-miR-132-3p	b.t.	n.s.	-46.4	1.15E-03

Supplementary Table 5a. Significantly enriched pathways (Reactome) of DE coding genes by agonist mix treatment in TP53 altered CLL cases.

Category	Term	Description	LogP	Log(q-value)	InTerm_InList
Reactome Gene Sets	R-HSA-1280215	Cytokine Signaling in Immune system	-25.06	-20.72	76/715
Reactome Gene Sets	R-HSA-449147	Signaling by Interleukins	-13.58	-9.53	45/462
Reactome Gene Sets	R-HSA-1280218	Adaptive Immune System	-12.45	-8.61	58/769
Reactome Gene Sets	R-HSA-909733	Interferon alpha/beta signaling	-11.54	-8.04	17/72
Reactome Gene Sets	R-HSA-5663202	Diseases of signal transduction by growth factor receptors and second messengers	-10.21	-7.00	38/433
Reactome Gene Sets	R-HSA-2454202	Fc epsilon receptor (FCERI) signaling	-9.58	-6.49	20/134
Reactome Gene Sets	R-HSA-913531	Interferon Signaling	-9.39	-6.38	24/199
Reactome Gene Sets	R-HSA-983705	Signaling by the B Cell Receptor (BCR)	-8.36	-5.64	17/112
Reactome Gene Sets	R-HSA-5607764	CLEC7A (Dectin-1) signaling	-8.18	-5.54	16/101
Reactome Gene Sets	R-HSA-3700989	Transcriptional Regulation by TP53	-8.19	-5.54	31/362
Reactome Gene Sets	R-HSA-9006925	Intracellular signaling by second messengers	-7.99	-5.40	28/309
Reactome Gene Sets	R-HSA-451927	Interleukin-2 family signaling	-7.97	-5.39	11/44
Reactome Gene Sets	R-HSA-9006934	Signaling by Receptor Tyrosine Kinases	-7.96	-5.39	38/521
Reactome Gene Sets	R-HSA-1257604	PIP3 activates AKT signaling	-7.48	-4.98	25/267
Reactome Gene Sets	R-HSA-2586552	Signaling by Leptin	-6.93	-4.59	6/11
Reactome Gene Sets	R-HSA-9006335	Signaling by Erythropoietin	-6.87	-4.56	8/25
Reactome Gene Sets	R-HSA-446652	Interleukin-1 family signaling	-6.84	-4.54	17/141
Reactome Gene Sets	R-HSA-512988	Interleukin-3, Interleukin-5 and GM-CSF signaling	-6.49	-4.25	10/48
Reactome Gene Sets	R-HSA-202403	TCR signaling	-6.31	-4.09	15/120
Reactome Gene Sets	R-HSA-5621481	C-type lectin receptors (CLRs)	-6.07	-3.88	16/142
Reactome Gene Sets	R-HSA-983695	Antigen activates B Cell Receptor (BCR) leading to generation of second messengers	-5.95	-3.78	8/32
Reactome Gene Sets	R-HSA-1433557	Signaling by SCF-KIT	-5.92	-3.76	9/43
Reactome Gene Sets	R-HSA-982772	Growth hormone receptor signaling	-5.77	-3.65	7/24
Reactome Gene Sets	R-HSA-2219528	PI3K/AKT Signaling in Cancer	-5.55	-3.47	13/104
Reactome Gene Sets	R-HSA-877300	Interferon gamma signaling	-5.42	-3.36	12/91
Reactome Gene Sets	R-HSA-9607240	FLT3 Signaling	-5.34	-3.30	8/38
Reactome Gene Sets	R-HSA-3858494	Beta-catenin independent WNT signaling	-5.23	-3.21	15/146

Reactome Gene Sets	R-HSA-9020558	Interleukin-2 signaling	-5.12	-3.11	5/12
Reactome Gene Sets	R-HSA-9669938	Signaling by KIT in disease	-5.09	-3.09	6/20
Reactome Gene Sets	R-HSA-9670439	Signaling by phosphorylated juxtamembrane, extracellular and kinase domain KIT mutants	-5.09	-3.09	6/20
Reactome Gene Sets	R-HSA-1168372	Downstream signaling events of B Cell Receptor (BCR)	-5.04	-3.05	11/83
Reactome Gene Sets	R-HSA-5673001	RAF/MAP kinase cascade	-4.86	-2.92	21/280
Reactome Gene Sets	R-HSA-9020702	Interleukin-1 signaling	-4.86	-2.92	12/103
Reactome Gene Sets	R-HSA-2871796	FCERI mediated MAPK activation	-4.86	-2.92	7/32
Reactome Gene Sets	R-HSA-5683057	MAPK family signaling cascades	-4.85	-2.92	23/325
Reactome Gene Sets	R-HSA-9027283	Erythropoietin activates STAT5	-4.84	-2.92	4/7
Reactome Gene Sets	R-HSA-109581	Apoptosis	-4.73	-2.84	16/180
Reactome Gene Sets	R-HSA-8983432	Interleukin-15 signaling	-4.74	-2.84	5/14
Reactome Gene Sets	R-HSA-5684996	MAPK1/MAPK3 signaling	-4.72	-2.84	21/286
Reactome Gene Sets	R-HSA-69242	S Phase	-4.65	-2.79	15/163
Reactome Gene Sets	R-HSA-453279	Mitotic G1 phase and G1/S transition	-4.48	-2.66	14/149
Reactome Gene Sets	R-HSA-8854691	Interleukin-20 family signaling	-4.48	-2.65	6/25
Reactome Gene Sets	R-HSA-69206	G1/S Transition	-4.45	-2.64	13/131
Reactome Gene Sets	R-HSA-8983711	OAS antiviral response	-4.31	-2.52	4/9
Reactome Gene Sets	R-HSA-195721	Signaling by WNT	-4.24	-2.46	22/332
Reactome Gene Sets	R-HSA-109606	Intrinsic Pathway for Apoptosis	-4.11	-2.36	8/55
Reactome Gene Sets	R-HSA-9020958	Interleukin-21 signaling	-4.09	-2.35	4/10
Reactome Gene Sets	R-HSA-69620	Cell Cycle Checkpoints	-4.08	-2.34	20/293
Reactome Gene Sets	R-HSA-2424491	DAP12 signaling	-4.00	-2.28	6/30
Reactome Gene Sets	R-HSA-9674555	Signaling by CSF3 (G-CSF)	-4.00	-2.28	6/30
Reactome Gene Sets	R-HSA-69481	G2/M Checkpoints	-3.94	-2.23	14/167
Reactome Gene Sets	R-HSA-5357801	Programmed Cell Death	-3.93	-2.21	16/210
Reactome Gene Sets	R-HSA-8878159	Transcriptional regulation by RUNX3	-3.73	-2.06	10/96
Reactome Gene Sets	R-HSA-1169410	Antiviral mechanism by IFN-stimulated genes	-3.67	-2.01	9/80
Reactome Gene Sets	R-HSA-5633007	Regulation of TP53 Activity	-3.57	-1.93	13/160
Reactome Gene Sets	R-HSA-1266695	Interleukin-7 signaling	-3.54	-1.91	6/36

Reactome Gene Sets	R-HSA-69239	Synthesis of DNA	-3.52	-1.89	11/121
Reactome Gene Sets	R-HSA-111459	Activation of caspases through apoptosome-mediated cleavage	-3.49	-1.87	3/6
Reactome Gene Sets	R-HSA-69656	Cyclin A:Cdk2-associated events at S phase entry	-3.47	-1.85	9/85
Reactome Gene Sets	R-HSA-9705462	Inactivation of CSF3 (G-CSF) signaling	-3.41	-1.81	5/25
Reactome Gene Sets	R-HSA-983169	Class I MHC mediated antigen processing & presentation	-3.39	-1.80	22/381
Reactome Gene Sets	R-HSA-6811558	PI5P, PP2A and IER3 Regulate PI3K/AKT Signaling	-3.38	-1.79	10/106
Reactome Gene Sets	R-HSA-4641257	Degradation of AXIN	-3.30	-1.72	7/55
Reactome Gene Sets	R-HSA-111463	SMAC (DIABLO) binds to IAPs	-3.26	-1.69	3/7
Reactome Gene Sets	R-HSA-111464	SMAC(DIABLO)-mediated dissociation of IAP:caspase complexes	-3.26	-1.69	3/7
Reactome Gene Sets	R-HSA-4086400	PCP/CE pathway	-3.21	-1.66	9/92
Reactome Gene Sets	R-HSA-9703648	Signaling by FLT3 ITD and TKD mutants	-3.21	-1.66	4/16
Reactome Gene Sets	R-HSA-199418	Negative regulation of the PI3K/AKT network	-3.16	-1.62	10/113
Reactome Gene Sets	R-HSA-5676590	NIK-->noncanonical NF-kB signaling	-3.11	-1.58	7/59
Reactome Gene Sets	R-HSA-186763	Downstream signal transduction	-3.10	-1.57	5/29
Reactome Gene Sets	R-HSA-187577	SCF(Skp2)-mediated degradation of p27/p21	-3.07	-1.54	7/60
Reactome Gene Sets	R-HSA-5607761	Dectin-1 mediated noncanonical NF-kB signaling	-3.07	-1.54	7/60
Reactome Gene Sets	R-HSA-111469	SMAC, XIAP-regulated apoptotic response	-3.06	-1.54	3/8
Reactome Gene Sets	R-HSA-5619084	ABC transporter disorders	-3.05	-1.53	8/78
Reactome Gene Sets	R-HSA-202424	Downstream TCR signaling	-3.01	-1.50	9/98
Reactome Gene Sets	R-HSA-9759194	Nuclear events mediated by NFE2L2	-3.01	-1.50	8/79
Reactome Gene Sets	R-HSA-2172127	DAP12 interactions	-3.01	-1.50	6/45
Reactome Gene Sets	R-HSA-983168	Antigen processing: Ubiquitination & Proteasome degradation	-2.92	-1.43	18/309
Reactome Gene Sets	R-HSA-2871837	FCERI mediated NF-kB activation	-2.91	-1.42	8/82
Reactome Gene Sets	R-HSA-9013694	Signaling by NOTCH4	-2.91	-1.42	8/82
Reactome Gene Sets	R-HSA-9703465	Signaling by FLT3 fusion proteins	-2.91	-1.42	4/19
Reactome Gene Sets	R-HSA-4608870	Asymmetric localization of PCP proteins	-2.90	-1.42	7/64
Reactome Gene Sets	R-HSA-8985947	Interleukin-9 signaling	-2.90	-1.42	3/9
Reactome Gene Sets	R-HSA-9020933	Interleukin-23 signaling	-2.90	-1.42	3/9
Reactome Gene Sets	R-HSA-9755511	KEAP1-NFE2L2 pathway	-2.89	-1.41	9/102

Reactome Gene Sets	R-HSA-195253	Degradation of beta-catenin by the destruction complex	-2.87	-1.40	8/83
Reactome Gene Sets	R-HSA-69202	Cyclin E associated events during G1/S transition	-2.87	-1.40	8/83
Reactome Gene Sets	R-HSA-69563	p53-Dependent G1 DNA Damage Response	-2.82	-1.36	7/66
Reactome Gene Sets	R-HSA-69580	p53-Dependent G1/S DNA damage checkpoint	-2.82	-1.36	7/66
Reactome Gene Sets	R-HSA-1236975	Antigen processing-Cross presentation	-2.80	-1.34	9/105
Reactome Gene Sets	R-HSA-1169091	Activation of NF-kappaB in B cells	-2.78	-1.32	7/67
Reactome Gene Sets	R-HSA-9702518	STAT5 activation downstream of FLT3 ITD mutants	-2.75	-1.30	3/10

Supplementary Table 5b. Significantly enriched pathways (Reactome) of DE coding genes by agonist mix treatment in Trisomy 12 CLL cases.

Category	Term	Description	LogP	Log(q-value)	InTerm_InList
Reactome Gene Sets	R-HSA-1280215	Cytokine Signaling in Immune system	-13.20	-9.15	63/715
Reactome Gene Sets	R-HSA-1280218	Adaptive Immune System	-9.50	-6.43	58/769
Reactome Gene Sets	R-HSA-449147	Signaling by Interleukins	-8.88	-5.98	41/462
Reactome Gene Sets	R-HSA-556833	Metabolism of lipids	-8.74	-5.89	55/743
Reactome Gene Sets	R-HSA-5663202	Diseases of signal transduction by growth factor receptors and second messengers	-8.14	-5.36	38/433
Reactome Gene Sets	R-HSA-5663202	Diseases of signal transduction by growth factor receptors and second messengers	-8.14	-5.36	38/433
Reactome Gene Sets	R-HSA-512988	Interleukin-3, Interleukin-5 and GM-CSF signaling	-7.81	-5.10	12/48
Reactome Gene Sets	R-HSA-5213460	RIPK1-mediated regulated necrosis	-6.89	-4.40	9/29
Reactome Gene Sets	R-HSA-5675482	Regulation of necroptotic cell death	-6.89	-4.40	9/29
Reactome Gene Sets	R-HSA-451927	Interleukin-2 family signaling	-6.19	-3.83	10/44
Reactome Gene Sets	R-HSA-186763	Downstream signal transduction	-5.75	-3.50	8/29
Reactome Gene Sets	R-HSA-9020958	Interleukin-21 signaling	-5.23	-3.11	5/10
Reactome Gene Sets	R-HSA-9705462	Inactivation of CSF3 (G-CSF) signaling	-5.14	-3.05	7/25
Reactome Gene Sets	R-HSA-5357905	Regulation of TNFR1 signaling	-5.08	-3.00	8/35
Reactome Gene Sets	R-HSA-9669938	Signaling by KIT in disease	-4.67	-2.69	6/20
Reactome Gene Sets	R-HSA-9670439	Signaling by phosphorylated juxtamembrane, extracellular and kinase domain KIT mutants	-4.67	-2.69	6/20
Reactome Gene Sets	R-HSA-9674555	Signaling by CSF3 (G-CSF)	-4.57	-2.61	7/30
Reactome Gene Sets	R-HSA-983705	Signaling by the B Cell Receptor (BCR)	-4.41	-2.48	13/112
Reactome Gene Sets	R-HSA-1433557	Signaling by SCF-KIT	-4.39	-2.46	8/43
Reactome Gene Sets	R-HSA-75893	TNF signaling	-4.31	-2.41	8/44
Reactome Gene Sets	R-HSA-5218859	Regulated Necrosis	-4.27	-2.39	9/57
Reactome Gene Sets	R-HSA-186797	Signaling by PDGF	-4.21	-2.33	9/58
Reactome Gene Sets	R-HSA-8854691	Interleukin-20 family signaling	-4.07	-2.23	6/25
Reactome Gene Sets	R-HSA-8985947	Interleukin-9 signaling	-4.02	-2.19	4/9

Reactome Gene Sets	R-HSA-5655302	Signaling by FGFR1 in disease	-3.87	-2.08	7/38
Reactome Gene Sets	R-HSA-9607240	FLT3 Signaling	-3.87	-2.08	7/38
Reactome Gene Sets	R-HSA-912526	Interleukin receptor SHC signaling	-3.87	-2.07	6/27
Reactome Gene Sets	R-HSA-5676594	TNF receptor superfamily (TNFSF) members mediating non-canonical NF-kB pathway	-3.79	-2.01	5/18
Reactome Gene Sets	R-HSA-1839117	Signaling by cytosolic FGFR1 fusion mutants	-3.79	-2.01	5/18
Reactome Gene Sets	R-HSA-3371378	Regulation by c-FLIP	-3.62	-1.89	4/11
Reactome Gene Sets	R-HSA-5218900	CASP8 activity is inhibited	-3.62	-1.89	4/11
Reactome Gene Sets	R-HSA-69416	Dimerization of procaspase-8	-3.62	-1.89	4/11
Reactome Gene Sets	R-HSA-2454202	Fc epsilon receptor (FCERI) signaling	-3.61	-1.89	13/134
Reactome Gene Sets	R-HSA-9700206	Signaling by ALK in cancer	-3.60	-1.88	8/55
Reactome Gene Sets	R-HSA-9725370	Signaling by ALK fusions and activated point mutants	-3.60	-1.88	8/55
Reactome Gene Sets	R-HSA-5668541	TNFR2 non-canonical NF-kB pathway	-3.54	-1.85	11/102
Reactome Gene Sets	R-HSA-1839124	FGFR1 mutant receptor activation	-3.52	-1.83	6/31
Reactome Gene Sets	R-HSA-9020558	Interleukin-2 signaling	-3.45	-1.79	4/12
Reactome Gene Sets	R-HSA-8983432	Interleukin-15 signaling	-3.17	-1.60	4/14
Reactome Gene Sets	R-HSA-6806834	Signaling by MET	-3.17	-1.60	9/79
Reactome Gene Sets	R-HSA-982772	Growth hormone receptor signaling	-3.16	-1.60	5/24
Reactome Gene Sets	R-HSA-1266695	Interleukin-7 signaling	-3.15	-1.59	6/36
Reactome Gene Sets	R-HSA-166520	Signaling by NTRKs	-3.07	-1.52	12/134
Reactome Gene Sets	R-HSA-9027283	Erythropoietin activates STAT5	-3.04	-1.51	3/7
Reactome Gene Sets	R-HSA-9703648	Signaling by FLT3 ITD and TKD mutants	-2.93	-1.42	4/16
Reactome Gene Sets	R-HSA-2132295	MHC class II antigen presentation	-2.85	-1.36	11/123
Reactome Gene Sets	R-HSA-140534	Caspase activation via Death Receptors in the presence of ligand	-2.83	-1.35	4/17

Supplementary Table 5c. Significantly enriched pathways (Reactome) of DE coding genes by agonist mix treatment in WT (Barcelona) CLL cases.

Category	Term	Description	LogP	Log(q-value)	InTerm_InList
Reactome Gene Sets	R-HSA-8953897	Cellular responses to stimuli	-52.02	-47.67	181/798
Reactome Gene Sets	R-HSA-2262752	Cellular responses to stress	-51.20	-47.15	178/784
Reactome Gene Sets	R-HSA-72766	Translation	-43.09	-39.44	97/291
Reactome Gene Sets	R-HSA-71291	Metabolism of amino acids and derivatives	-41.26	-37.81	108/374
Reactome Gene Sets	R-HSA-9711123	Cellular response to chemical stress	-37.55	-34.31	74/194
Reactome Gene Sets	R-HSA-9675108	Nervous system development	-31.79	-28.67	122/577
Reactome Gene Sets	R-HSA-422475	Axon guidance	-31.22	-28.13	118/552
Reactome Gene Sets	R-HSA-9010553	Regulation of expression of SLITs and ROBOs	-31.02	-27.95	63/171
Reactome Gene Sets	R-HSA-376176	Signaling by ROBO receptors	-30.92	-27.88	71/218
Reactome Gene Sets	R-HSA-8852276	The role of GTSE1 in G2/M progression after G2 checkpoint	-29.36	-26.34	42/77
Reactome Gene Sets	R-HSA-1280218	Adaptive Immune System	-28.69	-25.69	139/769
Reactome Gene Sets	R-HSA-1280215	Cytokine Signaling in Immune system	-28.17	-25.19	132/715
Reactome Gene Sets	R-HSA-449147	Signaling by Interleukins	-26.95	-24.00	100/462
Reactome Gene Sets	R-HSA-611105	Respiratory electron transport	-26.06	-23.14	45/103
Reactome Gene Sets	R-HSA-5658442	Regulation of RAS by GAPs	-25.89	-23.00	37/68
Reactome Gene Sets	R-HSA-162906	HIV Infection	-25.88	-23.00	67/231
Reactome Gene Sets	R-HSA-8953854	Metabolism of RNA	-25.79	-22.93	123/674
Reactome Gene Sets	R-HSA-1168372	Downstream signaling events of B Cell Receptor (BCR)	-25.27	-22.42	40/83
Reactome Gene Sets	R-HSA-9020702	Interleukin-1 signaling	-25.00	-22.18	44/103
Reactome Gene Sets	R-HSA-349425	Autodegradation of the E3 ubiquitin ligase COP1	-24.81	-22.01	32/52
Reactome Gene Sets	R-HSA-1428517	The citric acid (TCA) cycle and respiratory electron transport	-24.52	-21.74	57/178
Reactome Gene Sets	R-HSA-3700989	Transcriptional Regulation by TP53	-24.21	-21.45	83/362
Reactome Gene Sets	R-HSA-9755511	KEAP1-NFE2L2 pathway	-24.16	-21.42	43/102
Reactome Gene Sets	R-HSA-2454202	Fc epsilon receptor (FCERI) signaling	-24.10	-21.36	49/134
Reactome Gene Sets	R-HSA-9604323	Negative regulation of NOTCH4 signaling	-24.08	-21.35	32/54
Reactome Gene Sets	R-HSA-9759194	Nuclear events mediated by NFE2L2	-24.00	-21.28	38/79
Reactome Gene Sets	R-HSA-5676590	NIK-->noncanonical NF-kB signaling	-23.68	-20.99	33/59

Reactome Gene Sets	R-HSA-9762114	GSK3B and BTRC:CUL1-mediated-degradation of NFE2L2	-23.46	-20.77	31/52
Reactome Gene Sets	R-HSA-5607761	Dectin-1 mediated noncanonical NF-kB signaling	-23.36	-20.69	33/60
Reactome Gene Sets	R-HSA-983705	Signaling by the B Cell Receptor (BCR)	-23.20	-20.53	44/112
Reactome Gene Sets	R-HSA-169911	Regulation of Apoptosis	-23.10	-20.44	31/53
Reactome Gene Sets	R-HSA-4641258	Degradation of DVL	-23.05	-20.41	32/57
Reactome Gene Sets	R-HSA-69541	Stabilization of p53	-23.05	-20.41	32/57
Reactome Gene Sets	R-HSA-69275	G2/M Transition	-22.98	-20.35	58/196
Reactome Gene Sets	R-HSA-162909	Host Interactions of HIV factors	-22.90	-20.27	47/130
Reactome Gene Sets	R-HSA-211733	Regulation of activated PAK-2p34 by proteasome mediated degradation	-22.84	-20.22	30/50
Reactome Gene Sets	R-HSA-69563	p53-Dependent G1 DNA Damage Response	-22.80	-20.20	34/66
Reactome Gene Sets	R-HSA-69580	p53-Dependent G1/S DNA damage checkpoint	-22.80	-20.20	34/66
Reactome Gene Sets	R-HSA-180585	Vif-mediated degradation of APOBEC3G	-22.76	-20.18	31/54
Reactome Gene Sets	R-HSA-8854050	FBXL7 down-regulates AURKA during mitotic entry and in early mitosis	-22.76	-20.18	31/54
Reactome Gene Sets	R-HSA-453274	Mitotic G2-G2/M phases	-22.73	-20.16	58/198
Reactome Gene Sets	R-HSA-1236975	Antigen processing-Cross presentation	-22.54	-19.97	42/105
Reactome Gene Sets	R-HSA-1236974	ER-Phagosome pathway	-22.51	-19.96	39/90
Reactome Gene Sets	R-HSA-350562	Regulation of ornithine decarboxylase (ODC)	-22.48	-19.93	30/51
Reactome Gene Sets	R-HSA-163200	Respiratory electron transport, ATP synthesis by chemiosmotic coupling, and heat production by uncoupling proteins.	-22.46	-19.92	46/127
Reactome Gene Sets	R-HSA-4641257	Degradation of AXIN	-22.43	-19.89	31/55
Reactome Gene Sets	R-HSA-351202	Metabolism of polyamines	-22.42	-19.89	32/59
Reactome Gene Sets	R-HSA-5607764	CLEC7A (Dectin-1) signaling	-22.31	-19.79	41/101
Reactome Gene Sets	R-HSA-69615	G1/S DNA Damage Checkpoints	-22.25	-19.74	34/68
Reactome Gene Sets	R-HSA-174084	Autodegradation of Cdh1 by Cdh1:APC/C	-22.17	-19.67	33/64
Reactome Gene Sets	R-HSA-1640170	Cell Cycle	-22.16	-19.67	118/692
Reactome Gene Sets	R-HSA-180534	Vpu mediated degradation of CD4	-22.13	-19.67	30/52
Reactome Gene Sets	R-HSA-69601	Ubiquitin Mediated Degradation of Phosphorylated Cdc25A	-22.13	-19.67	30/52
Reactome Gene Sets	R-HSA-69610	p53-Independent DNA Damage Response	-22.13	-19.67	30/52
Reactome Gene Sets	R-HSA-69613	p53-Independent G1/S DNA damage checkpoint	-22.13	-19.67	30/52
Reactome Gene Sets	R-HSA-75815	Ubiquitin-dependent degradation of Cyclin D	-22.13	-19.67	30/52

Reactome Gene Sets	R-HSA-5610780	Degradation of GLI1 by the proteasome	-22.12	-19.67	32/60
Reactome Gene Sets	R-HSA-5610783	Degradation of GLI2 by the proteasome	-22.12	-19.67	32/60
Reactome Gene Sets	R-HSA-5610785	GLI3 is processed to GLI3R by the proteasome	-22.12	-19.67	32/60
Reactome Gene Sets	R-HSA-5668541	TNFR2 non-canonical NF-kB pathway	-22.11	-19.67	41/102
Reactome Gene Sets	R-HSA-5362768	Hh mutants are degraded by ERAD	-22.10	-19.67	31/56
Reactome Gene Sets	R-HSA-446652	Interleukin-1 family signaling	-22.06	-19.64	48/141
Reactome Gene Sets	R-HSA-5619084	ABC transporter disorders	-21.99	-19.58	36/78
Reactome Gene Sets	R-HSA-382556	ABC-family proteins mediated transport	-21.92	-19.51	41/103
Reactome Gene Sets	R-HSA-1236978	Cross-presentation of soluble exogenous antigens (endosomes)	-21.86	-19.45	29/49
Reactome Gene Sets	R-HSA-69239	Synthesis of DNA	-21.60	-19.20	44/121
Reactome Gene Sets	R-HSA-1169091	Activation of NF-kappaB in B cells	-21.35	-18.97	33/67
Reactome Gene Sets	R-HSA-6798695	Neutrophil degranulation	-21.33	-18.95	93/482
Reactome Gene Sets	R-HSA-3858494	Beta-catenin independent WNT signaling	-21.31	-18.94	48/146
Reactome Gene Sets	R-HSA-9633012	Response of EIF2AK4 (GCN2) to amino acid deficiency	-21.31	-18.94	40/101
Reactome Gene Sets	R-HSA-5387390	Hh mutants abrogate ligand secretion	-21.19	-18.83	31/59
Reactome Gene Sets	R-HSA-174113	SCF-beta-TrCP mediated degradation of Emi1	-21.16	-18.80	30/55
Reactome Gene Sets	R-HSA-8941858	Regulation of RUNX3 expression and activity	-21.16	-18.80	30/55
Reactome Gene Sets	R-HSA-174154	APC/C:Cdc20 mediated degradation of Securin	-21.08	-18.74	33/68
Reactome Gene Sets	R-HSA-8939902	Regulation of RUNX2 expression and activity	-20.97	-18.64	34/73
Reactome Gene Sets	R-HSA-187577	SCF(Skp2)-mediated degradation of p27/p21	-20.90	-18.58	31/60
Reactome Gene Sets	R-HSA-450408	AUF1 (hnRNP D0) binds and destabilizes mRNA	-20.85	-18.53	30/56
Reactome Gene Sets	R-HSA-69278	Cell Cycle, Mitotic	-20.79	-18.48	101/561
Reactome Gene Sets	R-HSA-5358346	Hedgehog ligand biogenesis	-20.71	-18.40	32/65
Reactome Gene Sets	R-HSA-5678895	Defective CFTR causes cystic fibrosis	-20.62	-18.31	31/61
Reactome Gene Sets	R-HSA-1234176	Oxygen-dependent proline hydroxylation of Hypoxia-inducible Factor Alpha	-20.45	-18.15	32/66
Reactome Gene Sets	R-HSA-68949	Orc1 removal from chromatin	-20.34	-18.04	33/71
Reactome Gene Sets	R-HSA-1799339	SRP-dependent cotranslational protein targeting to membrane	-20.30	-18.01	41/112
Reactome Gene Sets	R-HSA-176409	APC/C:Cdc20 mediated degradation of mitotic proteins	-20.26	-17.98	34/76
Reactome Gene Sets	R-HSA-2408522	Selenoamino acid metabolism	-20.23	-17.95	42/118

Reactome Gene Sets	R-HSA-72613	Eukaryotic Translation Initiation	-20.07	-17.80	42/119
Reactome Gene Sets	R-HSA-72737	Cap-dependent Translation Initiation	-20.07	-17.80	42/119
Reactome Gene Sets	R-HSA-68882	Mitotic Anaphase	-20.04	-17.78	60/236
Reactome Gene Sets	R-HSA-176814	Activation of APC/C and APC/C:Cdc20 mediated degradation of mitotic proteins	-20.04	-17.77	34/77
Reactome Gene Sets	R-HSA-4086400	PCP/CE pathway	-20.03	-17.77	37/92
Reactome Gene Sets	R-HSA-2871837	FCERI mediated NF-kB activation	-20.01	-17.76	35/82
Reactome Gene Sets	R-HSA-9013694	Signaling by NOTCH4	-20.01	-17.76	35/82
Reactome Gene Sets	R-HSA-2555396	Mitotic Metaphase and Anaphase	-19.95	-17.70	60/237
Reactome Gene Sets	R-HSA-174184	Cdc20:Phospho-APC/C mediated degradation of Cyclin A	-19.86	-17.63	33/73
Reactome Gene Sets	R-HSA-69017	CDK-mediated phosphorylation and removal of Cdc6	-19.86	-17.63	33/73
Reactome Gene Sets	R-HSA-69242	S Phase	-19.85	-17.61	49/163
Reactome Gene Sets	R-HSA-5619115	Disorders of transmembrane transporters	-19.84	-17.61	51/176
Reactome Gene Sets	R-HSA-4608870	Asymmetric localization of PCP proteins	-19.82	-17.59	31/64
Reactome Gene Sets	R-HSA-69202	Cyclin E associated events during G1/S transition	-19.80	-17.58	35/83
Reactome Gene Sets	R-HSA-8948751	Regulation of PTEN stability and activity	-19.70	-17.49	32/69
Reactome Gene Sets	R-HSA-174178	APC/C:Cdh1 mediated degradation of Cdc20 and other APC/C:Cdh1 targeted proteins in late mitosis/early G1	-19.63	-17.43	33/74
Reactome Gene Sets	R-HSA-179419	APC:Cdc20 mediated degradation of cell cycle proteins prior to satisfation of the cell cycle checkpoint	-19.63	-17.43	33/74
Reactome Gene Sets	R-HSA-156827	L13a-mediated translational silencing of Ceruloplasmin expression	-19.53	-17.33	40/111
Reactome Gene Sets	R-HSA-5663202	Diseases of signal transduction by growth factor receptors and second messengers	-19.47	-17.28	84/433
Reactome Gene Sets	R-HSA-1234174	Cellular response to hypoxia	-19.41	-17.22	33/75
Reactome Gene Sets	R-HSA-69656	Cyclin A:Cdk2-associated events at S phase entry	-19.39	-17.20	35/85
Reactome Gene Sets	R-HSA-72706	GTP hydrolysis and joining of the 60S ribosomal subunit	-19.37	-17.18	40/112
Reactome Gene Sets	R-HSA-382551	Transport of small molecules	-19.30	-17.12	116/729
Reactome Gene Sets	R-HSA-176408	Regulation of APC/C activators between G1/S and early anaphase	-19.18	-17.00	34/81
Reactome Gene Sets	R-HSA-9711097	Cellular response to starvation	-19.11	-16.93	47/156
Reactome Gene Sets	R-HSA-69052	Switching of origins to a post-replicative state	-19.04	-16.86	36/92
Reactome Gene Sets	R-HSA-195253	Degradation of beta-catenin by the destruction complex	-18.77	-16.60	34/83
Reactome Gene Sets	R-HSA-69481	G2/M Checkpoints	-18.55	-16.39	48/167

Reactome Gene Sets	R-HSA-5621481	C-type lectin receptors (CLRs)	-18.46	-16.30	44/142
Reactome Gene Sets	R-HSA-453279	Mitotic G1 phase and G1/S transition	-18.37	-16.21	45/149
Reactome Gene Sets	R-HSA-5357801	Programmed Cell Death	-18.35	-16.19	54/210
Reactome Gene Sets	R-HSA-8878159	Transcriptional regulation by RUNX3	-18.31	-16.16	36/96
Reactome Gene Sets	R-HSA-168255	Influenza Infection	-18.30	-16.15	46/156
Reactome Gene Sets	R-HSA-69206	G1/S Transition	-18.27	-16.13	42/131
Reactome Gene Sets	R-HSA-5673001	RAF/MAP kinase cascade	-18.08	-15.94	63/280
Reactome Gene Sets	R-HSA-174143	APC/C-mediated degradation of cell cycle proteins	-17.81	-15.67	34/88
Reactome Gene Sets	R-HSA-453276	Regulation of mitotic cell cycle	-17.81	-15.67	34/88
Reactome Gene Sets	R-HSA-168273	Influenza Viral RNA Transcription and Replication	-17.73	-15.59	42/135
Reactome Gene Sets	R-HSA-5687128	MAPK6/MAPK4 signaling	-17.63	-15.50	34/89
Reactome Gene Sets	R-HSA-5684996	MAPK1/MAPK3 signaling	-17.59	-15.46	63/286
Reactome Gene Sets	R-HSA-72689	Formation of a pool of free 40S subunits	-17.47	-15.34	36/101
Reactome Gene Sets	R-HSA-5610787	Hedgehog 'off' state	-17.40	-15.27	38/113
Reactome Gene Sets	R-HSA-2467813	Separation of Sister Chromatids	-17.40	-15.27	50/191
Reactome Gene Sets	R-HSA-199991	Membrane Trafficking	-17.36	-15.24	102/634
Reactome Gene Sets	R-HSA-5689603	UCH proteinases	-17.31	-15.19	36/102
Reactome Gene Sets	R-HSA-983169	Class I MHC mediated antigen processing & presentation	-17.25	-15.14	74/381
Reactome Gene Sets	R-HSA-109581	Apoptosis	-17.08	-14.97	48/180
Reactome Gene Sets	R-HSA-5683057	MAPK family signaling cascades	-17.07	-14.96	67/325
Reactome Gene Sets	R-HSA-69620	Cell Cycle Checkpoints	-17.04	-14.93	63/293
Reactome Gene Sets	R-HSA-2408557	Selenocysteine synthesis	-16.93	-14.83	34/93
Reactome Gene Sets	R-HSA-5653656	Vesicle-mediated transport	-16.89	-14.79	105/673
Reactome Gene Sets	R-HSA-450531	Regulation of mRNA stability by proteins that bind AU-rich elements	-16.85	-14.75	33/88
Reactome Gene Sets	R-HSA-156902	Peptide chain elongation	-16.67	-14.58	33/89
Reactome Gene Sets	R-HSA-192823	Viral mRNA Translation	-16.67	-14.58	33/89
Reactome Gene Sets	R-HSA-68886	M Phase	-16.56	-14.47	77/418
Reactome Gene Sets	R-HSA-202403	TCR signaling	-16.40	-14.32	38/120
Reactome Gene Sets	R-HSA-8878166	Transcriptional regulation by RUNX2	-16.26	-14.19	38/121

Reactome Gene Sets	R-HSA-202424	Downstream TCR signaling	-16.12	-14.05	34/98
Reactome Gene Sets	R-HSA-5688426	Deubiquitination	-16.05	-13.98	62/298
Reactome Gene Sets	R-HSA-156842	Eukaryotic Translation Elongation	-16.00	-13.94	33/93
Reactome Gene Sets	R-HSA-72764	Eukaryotic Translation Termination	-16.00	-13.94	33/93
Reactome Gene Sets	R-HSA-9716542	Signaling by Rho GTPases, Miro GTPases and RHOBTB3	-15.99	-13.93	108/723
Reactome Gene Sets	R-HSA-9679506	SARS-CoV Infections	-15.69	-13.64	69/362
Reactome Gene Sets	R-HSA-975956	Nonsense Mediated Decay (NMD) independent of the Exon Junction Complex (EJC)	-15.68	-13.64	33/95
Reactome Gene Sets	R-HSA-6807070	PTEN Regulation	-15.48	-13.44	40/140
Reactome Gene Sets	R-HSA-5632684	Hedgehog 'on' state	-15.47	-13.43	31/85
Reactome Gene Sets	R-HSA-194315	Signaling by Rho GTPases	-15.38	-13.35	105/707
Reactome Gene Sets	R-HSA-8951664	Neddylation	-14.96	-12.93	53/240
Reactome Gene Sets	R-HSA-69306	DNA Replication	-14.85	-12.83	46/188
Reactome Gene Sets	R-HSA-6799198	Complex I biogenesis	-14.83	-12.81	25/57
Reactome Gene Sets	R-HSA-9006925	Intracellular signaling by second messengers	-14.68	-12.67	61/309
Reactome Gene Sets	R-HSA-5358351	Signaling by Hedgehog	-14.46	-12.46	40/149
Reactome Gene Sets	R-HSA-5368286	Mitochondrial translation initiation	-14.22	-12.23	30/87
Reactome Gene Sets	R-HSA-1257604	PIP3 activates AKT signaling	-14.12	-12.13	55/267
Reactome Gene Sets	R-HSA-69002	DNA Replication Pre-Initiation	-14.05	-12.06	41/160
Reactome Gene Sets	R-HSA-73894	DNA Repair	-14.04	-12.05	63/336
Reactome Gene Sets	R-HSA-5689880	Ub-specific processing proteases	-14.03	-12.05	49/220
Reactome Gene Sets	R-HSA-157118	Signaling by NOTCH	-14.02	-12.03	51/236
Reactome Gene Sets	R-HSA-8878171	Transcriptional regulation by RUNX1	-13.78	-11.80	51/239
Reactome Gene Sets	R-HSA-983168	Antigen processing: Ubiquitination & Proteasome degradation	-13.55	-11.57	59/309
Reactome Gene Sets	R-HSA-9694516	SARS-CoV-2 Infection	-13.44	-11.47	56/285
Reactome Gene Sets	R-HSA-5368287	Mitochondrial translation	-13.34	-11.36	30/93
Reactome Gene Sets	R-HSA-5389840	Mitochondrial translation elongation	-13.33	-11.36	29/87
Reactome Gene Sets	R-HSA-5419276	Mitochondrial translation termination	-13.33	-11.36	29/87
Reactome Gene Sets	R-HSA-927802	Nonsense-Mediated Decay (NMD)	-12.96	-11.00	33/115
Reactome Gene Sets	R-HSA-975957	Nonsense Mediated Decay (NMD) enhanced by the Exon Junction Complex (EJC)	-12.96	-11.00	33/115

Reactome Gene Sets	R-HSA-68867	Assembly of the pre-replicative complex	-12.89	-10.94	37/143
Reactome Gene Sets	R-HSA-9012999	RHO GTPase cycle	-12.36	-10.42	72/449
Reactome Gene Sets	R-HSA-195721	Signaling by WNT	-12.15	-10.21	59/332
Reactome Gene Sets	R-HSA-8939236	RUNX1 regulates transcription of genes involved in differentiation of HSCs	-12.05	-10.12	34/130
Reactome Gene Sets	R-HSA-5696399	Global Genome Nucleotide Excision Repair (GG-NER)	-12.03	-10.10	27/84
Reactome Gene Sets	R-HSA-5696398	Nucleotide Excision Repair	-11.87	-9.95	31/111
Reactome Gene Sets	R-HSA-556833	Metabolism of lipids	-11.22	-9.32	98/743
Reactome Gene Sets	R-HSA-9705683	SARS-CoV-2-host interactions	-11.09	-9.20	42/202
Reactome Gene Sets	R-HSA-5696395	Formation of Incision Complex in GG-NER	-10.44	-8.57	18/43
Reactome Gene Sets	R-HSA-446203	Asparagine N-linked glycosylation	-10.15	-8.30	52/304
Reactome Gene Sets	R-HSA-72662	Activation of the mRNA upon binding of the cap-binding complex and eIFs, and subsequent binding to 43S	-9.56	-7.73	20/59
Reactome Gene Sets	R-HSA-72312	rRNA processing	-9.21	-7.40	39/204
Reactome Gene Sets	R-HSA-72695	Formation of the ternary complex, and subsequently, the 43S complex	-8.99	-7.19	18/51
Reactome Gene Sets	R-HSA-72649	Translation initiation complex formation	-8.82	-7.04	19/58
Reactome Gene Sets	R-HSA-72702	Ribosomal scanning and start codon recognition	-8.82	-7.04	19/58
Reactome Gene Sets	R-HSA-8868773	rRNA processing in the nucleus and cytosol	-8.75	-6.97	37/194
Reactome Gene Sets	R-HSA-6804756	Regulation of TP53 Activity through Phosphorylation	-8.69	-6.91	24/92
Reactome Gene Sets	R-HSA-6781827	Transcription-Coupled Nucleotide Excision Repair (TC-NER)	-8.60	-6.83	22/79
Reactome Gene Sets	R-HSA-6782135	Dual incision in TC-NER	-8.58	-6.81	20/66
Reactome Gene Sets	R-HSA-8856688	Golgi-to-ER retrograde transport	-8.37	-6.62	29/133
Reactome Gene Sets	R-HSA-6791226	Major pathway of rRNA processing in the nucleolus and cytosol	-8.28	-6.53	35/184
Reactome Gene Sets	R-HSA-201681	TCF dependent signaling in response to WNT	-8.02	-6.29	40/233
Reactome Gene Sets	R-HSA-6811434	COPI-dependent Golgi-to-ER retrograde traffic	-8.00	-6.27	24/99
Reactome Gene Sets	R-HSA-6782210	Gap-filling DNA repair synthesis and ligation in TC-NER	-7.90	-6.17	19/65
Reactome Gene Sets	R-HSA-5696400	Dual Incision in GG-NER	-7.84	-6.12	15/41
Reactome Gene Sets	R-HSA-5633007	Regulation of TP53 Activity	-7.61	-5.90	31/160
Reactome Gene Sets	R-HSA-199977	ER to Golgi Anterograde Transport	-7.44	-5.75	30/154
Reactome Gene Sets	R-HSA-9754678	SARS-CoV-2 modulates host translation machinery	-7.37	-5.68	16/50
Reactome Gene Sets	R-HSA-6811442	Intra-Golgi and retrograde Golgi-to-ER traffic	-6.71	-5.08	34/202

Reactome Gene Sets	R-HSA-6807878	COPI-mediated anterograde transport	-6.51	-4.89	22/101
Reactome Gene Sets	R-HSA-948021	Transport to the Golgi and subsequent modification	-6.14	-4.55	31/185
Reactome Gene Sets	R-HSA-9705671	SARS-CoV-2 activates/modulates innate and adaptive immune responses	-5.36	-3.84	23/126
Reactome Gene Sets	R-HSA-9013149	RAC1 GTPase cycle	-4.32	-2.92	27/185
Reactome Gene Sets	R-HSA-9013423	RAC3 GTPase cycle	-3.07	-1.88	15/94
Reactome Gene Sets	R-HSA-9013404	RAC2 GTPase cycle	-2.89	-1.75	14/88

Supplementary Table 5d. Significantly enriched pathways (Reactome) of DE coding genes by agonist mix in WT (Aviano) CLL cases.

Category	Term	Description	LogP	Log(q-value)	InTerm_InList
Reactome Gene Sets	R-HSA-1280215	Cytokine Signaling in Immune system	-23.39	-19.05	108/715
Reactome Gene Sets	R-HSA-1280218	Adaptive Immune System	-18.88	-15.01	104/769
Reactome Gene Sets	R-HSA-449147	Signaling by Interleukins	-18.17	-14.43	75/462
Reactome Gene Sets	R-HSA-5668541	TNFR2 non-canonical NF-kB pathway	-17.40	-13.79	33/102
Reactome Gene Sets	R-HSA-5663202	Diseases of signal transduction by growth factor receptors and second messengers	-16.90	-13.40	70/433
Reactome Gene Sets	R-HSA-2454202	Fc epsilon receptor (FCERI) signaling	-15.99	-12.72	36/134
Reactome Gene Sets	R-HSA-6798695	Neutrophil degranulation	-15.48	-12.41	72/482
Reactome Gene Sets	R-HSA-5357801	Programmed Cell Death	-14.98	-12.00	44/210
Reactome Gene Sets	R-HSA-5607764	CLEC7A (Dectin-1) signaling	-13.84	-10.97	29/101
Reactome Gene Sets	R-HSA-983705	Signaling by the B Cell Receptor (BCR)	-13.40	-10.56	30/112
Reactome Gene Sets	R-HSA-5621481	C-type lectin receptors (CLRs)	-12.75	-9.98	33/142
Reactome Gene Sets	R-HSA-5688426	Deubiquitination	-12.31	-9.63	49/298
Reactome Gene Sets	R-HSA-69656	Cyclin A:Cdk2-associated events at S phase entry	-12.29	-9.62	25/85
Reactome Gene Sets	R-HSA-453279	Mitotic G1 phase and G1/S transition	-12.12	-9.48	33/149
Reactome Gene Sets	R-HSA-9716542	Signaling by Rho GTPases, Miro GTPases and RHOBTB3	-12.03	-9.42	85/723
Reactome Gene Sets	R-HSA-9012999	RHO GTPase cycle	-11.87	-9.28	62/449
Reactome Gene Sets	R-HSA-109581	Apoptosis	-11.75	-9.20	36/180
Reactome Gene Sets	R-HSA-194315	Signaling by Rho GTPases	-11.73	-9.18	83/707
Reactome Gene Sets	R-HSA-69202	Cyclin E associated events during G1/S transition	-11.65	-9.11	24/83
Reactome Gene Sets	R-HSA-1168372	Downstream signaling events of B Cell Receptor (BCR)	-11.65	-9.11	24/83
Reactome Gene Sets	R-HSA-9006925	Intracellular signaling by second messengers	-11.15	-8.65	48/309
Reactome Gene Sets	R-HSA-69242	S Phase	-10.98	-8.49	33/163
Reactome Gene Sets	R-HSA-446652	Interleukin-1 family signaling	-10.62	-8.14	30/141
Reactome Gene Sets	R-HSA-983169	Class I MHC mediated antigen processing & presentation	-10.36	-7.94	53/381
Reactome Gene Sets	R-HSA-9020702	Interleukin-1 signaling	-10.27	-7.86	25/103
Reactome Gene Sets	R-HSA-2871837	FCERI mediated NF-kB activation	-10.03	-7.65	22/82
Reactome Gene Sets	R-HSA-1257604	PIP3 activates AKT signaling	-10.02	-7.64	42/267

Reactome Gene Sets	R-HSA-69206	G1/S Transition	-10.01	-7.64	28/131
Reactome Gene Sets	R-HSA-9755511	KEAP1-NFE2L2 pathway	-9.58	-7.26	24/102
Reactome Gene Sets	R-HSA-9711123	Cellular response to chemical stress	-9.51	-7.20	34/194
Reactome Gene Sets	R-HSA-202403	TCR signaling	-9.48	-7.18	26/120
Reactome Gene Sets	R-HSA-5676590	NIK-->noncanonical NF-kB signaling	-9.33	-7.05	18/59
Reactome Gene Sets	R-HSA-1169091	Activation of NF-kappaB in B cells	-9.20	-6.94	19/67
Reactome Gene Sets	R-HSA-5607761	Dectin-1 mediated noncanonical NF-kB signaling	-9.19	-6.94	18/60
Reactome Gene Sets	R-HSA-187577	SCF(Skp2)-mediated degradation of p27/p21	-9.19	-6.94	18/60
Reactome Gene Sets	R-HSA-5689880	Ub-specific processing proteases	-9.17	-6.92	36/220
Reactome Gene Sets	R-HSA-174113	SCF-beta-TrCP mediated degradation of Emi1	-8.94	-6.71	17/55
Reactome Gene Sets	R-HSA-1236978	Cross-presentation of soluble exogenous antigens (endosomes)	-8.85	-6.63	16/49
Reactome Gene Sets	R-HSA-2262752	Cellular responses to stress	-8.74	-6.54	81/784
Reactome Gene Sets	R-HSA-1236975	Antigen processing-Cross presentation	-8.56	-6.37	23/105
Reactome Gene Sets	R-HSA-983168	Antigen processing: Ubiquitination & Proteasome degradation	-8.54	-6.36	43/309
Reactome Gene Sets	R-HSA-69563	p53-Dependent G1 DNA Damage Response	-8.45	-6.30	18/66
Reactome Gene Sets	R-HSA-69580	p53-Dependent G1/S DNA damage checkpoint	-8.45	-6.30	18/66
Reactome Gene Sets	R-HSA-349425	Autodegradation of the E3 ubiquitin ligase COP1	-8.42	-6.28	16/52
Reactome Gene Sets	R-HSA-9762114	GSK3B and BTRC:CUL1-mediated-degradation of NFE2L2	-8.42	-6.28	16/52
Reactome Gene Sets	R-HSA-351202	Metabolism of polyamines	-8.42	-6.28	17/59
Reactome Gene Sets	R-HSA-8953897	Cellular responses to stimuli	-8.39	-6.26	81/798
Reactome Gene Sets	R-HSA-5610780	Degradation of GLI1 by the proteasome	-8.30	-6.18	17/60
Reactome Gene Sets	R-HSA-195253	Degradation of beta-catenin by the destruction complex	-8.29	-6.18	20/83
Reactome Gene Sets	R-HSA-69615	G1/S DNA Damage Checkpoints	-8.23	-6.13	18/68
Reactome Gene Sets	R-HSA-8854050	FBXL7 down-regulates AURKA during mitotic entry and in early mitosis	-8.16	-6.07	16/54
Reactome Gene Sets	R-HSA-9604323	Negative regulation of NOTCH4 signaling	-8.16	-6.07	16/54
Reactome Gene Sets	R-HSA-4641257	Degradation of AXIN	-8.03	-5.96	16/55
Reactome Gene Sets	R-HSA-5619084	ABC transporter disorders	-7.99	-5.93	19/78
Reactome Gene Sets	R-HSA-69239	Synthesis of DNA	-7.99	-5.93	24/121
Reactome Gene Sets	R-HSA-5362768	Hh mutants are degraded by ERAD	-7.90	-5.86	16/56

Reactome Gene Sets	R-HSA-9759194	Nuclear events mediated by NFE2L2	-7.89	-5.85	19/79
Reactome Gene Sets	R-HSA-8878159	Transcriptional regulation by RUNX3	-7.86	-5.83	21/96
Reactome Gene Sets	R-HSA-450531	Regulation of mRNA stability by proteins that bind AU-rich elements	-7.82	-5.79	20/88
Reactome Gene Sets	R-HSA-4641258	Degradation of DVL	-7.78	-5.76	16/57
Reactome Gene Sets	R-HSA-69541	Stabilization of p53	-7.78	-5.76	16/57
Reactome Gene Sets	R-HSA-211733	Regulation of activated PAK-2p34 by proteasome mediated degradation	-7.77	-5.75	15/50
Reactome Gene Sets	R-HSA-202424	Downstream TCR signaling	-7.70	-5.69	21/98
Reactome Gene Sets	R-HSA-350562	Regulation of ornithine decarboxylase (ODC)	-7.64	-5.65	15/51
Reactome Gene Sets	R-HSA-5387390	Hh mutants abrogate ligand secretion	-7.55	-5.56	16/59
Reactome Gene Sets	R-HSA-69278	Cell Cycle, Mitotic	-7.53	-5.54	61/561
Reactome Gene Sets	R-HSA-69610	p53-Independent DNA Damage Response	-7.51	-5.53	15/52
Reactome Gene Sets	R-HSA-69613	p53-Independent G1/S DNA damage checkpoint	-7.51	-5.53	15/52
Reactome Gene Sets	R-HSA-69601	Ubiquitin Mediated Degradation of Phosphorylated Cdc25A	-7.51	-5.53	15/52
Reactome Gene Sets	R-HSA-75815	Ubiquitin-dependent degradation of Cyclin D	-7.51	-5.53	15/52
Reactome Gene Sets	R-HSA-180534	Vpu mediated degradation of CD4	-7.51	-5.53	15/52
Reactome Gene Sets	R-HSA-5610783	Degradation of GLI2 by the proteasome	-7.43	-5.47	16/60
Reactome Gene Sets	R-HSA-5610785	GLI3 is processed to GLI3R by the proteasome	-7.43	-5.47	16/60
Reactome Gene Sets	R-HSA-5683057	MAPK family signaling cascades	-7.41	-5.45	42/325
Reactome Gene Sets	R-HSA-5658442	Regulation of RAS by GAPs	-7.40	-5.44	17/68
Reactome Gene Sets	R-HSA-71291	Metabolism of amino acids and derivatives	-7.39	-5.43	46/374
Reactome Gene Sets	R-HSA-169911	Regulation of Apoptosis	-7.39	-5.43	15/53
Reactome Gene Sets	R-HSA-5673001	RAF/MAP kinase cascade	-7.34	-5.39	38/280
Reactome Gene Sets	R-HSA-5678895	Defective CFTR causes cystic fibrosis	-7.32	-5.38	16/61
Reactome Gene Sets	R-HSA-8948751	Regulation of PTEN stability and activity	-7.30	-5.36	17/69
Reactome Gene Sets	R-HSA-1640170	Cell Cycle	-7.28	-5.35	70/692
Reactome Gene Sets	R-HSA-180585	Vif-mediated degradation of APOBEC3G	-7.27	-5.34	15/54
Reactome Gene Sets	R-HSA-8941858	Regulation of RUNX3 expression and activity	-7.15	-5.24	15/55
Reactome Gene Sets	R-HSA-68949	Orc1 removal from chromatin	-7.10	-5.20	17/71
Reactome Gene Sets	R-HSA-5684996	MAPK1/MAPK3 signaling	-7.09	-5.19	38/286

Reactome Gene Sets	R-HSA-450408	AUF1 (hnRNP D0) binds and destabilizes mRNA	-7.04	-5.15	15/56
Reactome Gene Sets	R-HSA-4608870	Asymmetric localization of PCP proteins	-7.00	-5.12	16/64
Reactome Gene Sets	R-HSA-5687128	MAPK6/MAPK4 signaling	-7.00	-5.12	19/89
Reactome Gene Sets	R-HSA-5358346	Hedgehog ligand biogenesis	-6.90	-5.03	16/65
Reactome Gene Sets	R-HSA-9013694	Signaling by NOTCH4	-6.86	-5.00	18/82
Reactome Gene Sets	R-HSA-1234176	Oxygen-dependent proline hydroxylation of Hypoxia-inducible Factor Alpha	-6.80	-4.95	16/66
Reactome Gene Sets	R-HSA-4086400	PCP/CE pathway	-6.76	-4.91	19/92
Reactome Gene Sets	R-HSA-1234174	Cellular response to hypoxia	-6.73	-4.89	17/75
Reactome Gene Sets	R-HSA-162909	Host Interactions of HIV factors	-6.73	-4.89	23/130
Reactome Gene Sets	R-HSA-6807070	PTEN Regulation	-6.73	-4.89	24/140
Reactome Gene Sets	R-HSA-5689603	UCH proteinases	-6.69	-4.86	20/102
Reactome Gene Sets	R-HSA-8878171	Transcriptional regulation by RUNX1	-6.64	-4.81	33/239
Reactome Gene Sets	R-HSA-382556	ABC-family proteins mediated transport	-6.62	-4.79	20/103
Reactome Gene Sets	R-HSA-376176	Signaling by ROBO receptors	-6.56	-4.74	31/218
Reactome Gene Sets	R-HSA-9675108	Nervous system development	-6.39	-4.59	59/577
Reactome Gene Sets	R-HSA-3858494	Beta-catenin independent WNT signaling	-6.38	-4.58	24/146
Reactome Gene Sets	R-HSA-1236974	ER-Phagosome pathway	-6.22	-4.44	18/90
Reactome Gene Sets	R-HSA-176408	Regulation of APC/C activators between G1/S and early anaphase	-6.22	-4.44	17/81
Reactome Gene Sets	R-HSA-174084	Autodegradation of Cdh1 by Cdh1:APC/C	-6.21	-4.43	15/64
Reactome Gene Sets	R-HSA-8939902	Regulation of RUNX2 expression and activity	-6.16	-4.39	16/73
Reactome Gene Sets	R-HSA-8951664	Neddylation	-6.11	-4.35	32/240
Reactome Gene Sets	R-HSA-5357905	Regulation of TNFR1 signaling	-6.08	-4.32	11/35
Reactome Gene Sets	R-HSA-9013149	RAC1 GTPase cycle	-6.03	-4.28	27/185
Reactome Gene Sets	R-HSA-162906	HIV Infection	-6.00	-4.26	31/231
Reactome Gene Sets	R-HSA-422475	Axon guidance	-5.99	-4.25	56/552
Reactome Gene Sets	R-HSA-5619115	Disorders of transmembrane transporters	-5.93	-4.19	26/176
Reactome Gene Sets	R-HSA-5632684	Hedgehog 'on' state	-5.91	-4.18	17/85
Reactome Gene Sets	R-HSA-174154	APC/C:Cdc20 mediated degradation of Securin	-5.85	-4.13	15/68
Reactome Gene Sets	R-HSA-75893	TNF signaling	-5.84	-4.12	12/44

Reactome Gene Sets	R-HSA-8852276	The role of GTSE1 in G2/M progression after G2 checkpoint	-5.83	-4.11	16/77
Reactome Gene Sets	R-HSA-157118	Signaling by NOTCH	-5.80	-4.09	31/236
Reactome Gene Sets	R-HSA-174143	APC/C-mediated degradation of cell cycle proteins	-5.69	-3.99	17/88
Reactome Gene Sets	R-HSA-453276	Regulation of mitotic cell cycle	-5.69	-3.99	17/88
Reactome Gene Sets	R-HSA-453274	Mitotic G2-G2/M phases	-5.45	-3.78	27/198
Reactome Gene Sets	R-HSA-174184	Cdc20:Phospho-APC/C mediated degradation of Cyclin A	-5.44	-3.77	15/73
Reactome Gene Sets	R-HSA-69017	CDK-mediated phosphorylation and removal of Cdc6	-5.44	-3.77	15/73
Reactome Gene Sets	R-HSA-69052	Switching of origins to a post-replicative state	-5.41	-3.75	17/92
Reactome Gene Sets	R-HSA-174178	APC/C:Cdh1 mediated degradation of Cdc20 and other APC/C:Cdh1 targeted proteins in late mitosis/early G1	-5.36	-3.71	15/74
Reactome Gene Sets	R-HSA-179419	APC:Cdc20 mediated degradation of cell cycle proteins prior to satisfaction of the cell cycle checkpoint	-5.36	-3.71	15/74
Reactome Gene Sets	R-HSA-5610787	Hedgehog 'off' state	-5.34	-3.69	19/113
Reactome Gene Sets	R-HSA-176409	APC/C:Cdc20 mediated degradation of mitotic proteins	-5.21	-3.59	15/76
Reactome Gene Sets	R-HSA-176814	Activation of APC/C and APC/C:Cdc20 mediated degradation of mitotic proteins	-5.14	-3.52	15/77
Reactome Gene Sets	R-HSA-9010553	Regulation of expression of SLITs and ROBOs	-5.13	-3.52	24/171
Reactome Gene Sets	R-HSA-69275	G2/M Transition	-5.05	-3.45	26/196
Reactome Gene Sets	R-HSA-8878166	Transcriptional regulation by RUNX2	-4.89	-3.31	19/121
Reactome Gene Sets	R-HSA-2555396	Mitotic Metaphase and Anaphase	-4.87	-3.29	29/237
Reactome Gene Sets	R-HSA-109606	Intrinsic Pathway for Apoptosis	-4.75	-3.20	12/55
Reactome Gene Sets	R-HSA-69620	Cell Cycle Checkpoints	-4.69	-3.14	33/293
Reactome Gene Sets	R-HSA-5357786	TNFR1-induced proapoptotic signaling	-4.65	-3.10	6/13
Reactome Gene Sets	R-HSA-5358351	Signaling by Hedgehog	-4.60	-3.06	21/149
Reactome Gene Sets	R-HSA-68882	Mitotic Anaphase	-4.48	-2.96	28/236
Reactome Gene Sets	R-HSA-69306	DNA Replication	-4.44	-2.93	24/188
Reactome Gene Sets	R-HSA-9013148	CDC42 GTPase cycle	-4.34	-2.85	21/155
Reactome Gene Sets	R-HSA-69481	G2/M Checkpoints	-4.33	-2.84	22/167
Reactome Gene Sets	R-HSA-2467813	Separation of Sister Chromatids	-4.32	-2.83	24/191
Reactome Gene Sets	R-HSA-195721	Signaling by WNT	-4.33	-2.83	35/332
Reactome Gene Sets	R-HSA-2219528	PI3K/AKT Signaling in Cancer	-4.11	-2.65	16/104

Reactome Gene Sets	R-HSA-5357956	TNFR1-induced NFkappaB signaling pathway	-4.00	-2.56	8/30
Reactome Gene Sets	R-HSA-8939236	RUNX1 regulates transcription of genes involved in differentiation of HSCs	-3.93	-2.50	18/130
Reactome Gene Sets	R-HSA-9013423	RAC3 GTPase cycle	-3.52	-2.15	14/94
Reactome Gene Sets	R-HSA-9013406	RHOQ GTPase cycle	-3.11	-1.81	10/59
Reactome Gene Sets	R-HSA-69002	DNA Replication Pre-Initiation	-2.83	-1.59	18/160
Reactome Gene Sets	R-HSA-201681	TCF dependent signaling in response to WNT	-2.68	-1.47	23/233
Reactome Gene Sets	R-HSA-68867	Assembly of the pre-replicative complex	-2.56	-1.38	16/143
Reactome Gene Sets	R-HSA-111471	Apoptotic factor-mediated response	-2.54	-1.37	5/20
Reactome Gene Sets	R-HSA-168928	DDX58/IFIH1-mediated induction of interferon-alpha/beta	-2.51	-1.35	11/82
Reactome Gene Sets	R-HSA-111461	Cytochrome c-mediated apoptotic response	-2.47	-1.31	4/13
Reactome Gene Sets	R-HSA-933543	NF-kB activation through FADD/RIP-1 pathway mediated by caspase-8 and -10	-2.47	-1.31	4/13

Supplementary Table 5e. List of enriched pathways among DE genes by agonist mix treatment and their overlapping in the four CLL studied cohorts.

6 common elements in "WT Aviano", "WT Barcelona", "TP53 altered" and "Trisomy 12":
Cytokine Signaling in Immune system
Adaptive Immune System
Signaling by Interleukins
Diseases of signal transduction by growth factor receptors and second messengers
Fc epsilon receptor (FCERI) signaling
Signaling by the B Cell Receptor (BCR)

43 common elements in "WT Aviano", "WT Barcelona" and "TP53 altered":
Programmed Cell Death
CLEC7A (Dectin-1) signaling
C-type lectin receptors (CLRs)
Cyclin A:Cdk2-associated events at S phase entry
Mitotic G1 phase and G1/S transition
Apoptosis
Cyclin E associated events during G1/S transition
Downstream signaling events of B Cell Receptor (BCR)
Intracellular signaling by second messengers
S Phase
Interleukin-1 family signaling
Class I MHC mediated antigen processing & presentation
Interleukin-1 signaling
FCERI mediated NF-kB activation
PIP3 activates AKT signaling
G1/S Transition
KEAP1-NFE2L2 pathway
TCR signaling

NIK-->noncanonical NF-kB signaling
Activation of NF-kappaB in B cells
Dectin-1 mediated noncanonical NF-kB signaling
SCF(Skp2)-mediated degradation of p27/p21
Antigen processing-Cross presentation
Antigen processing: Ubiquitination & Proteasome degradation
p53-Dependent G1 DNA Damage Response
p53-Dependent G1/S DNA damage checkpoint
Degradation of beta-catenin by the destruction complex
Degradation of AXIN
ABC transporter disorders
Synthesis of DNA
Nuclear events mediated by NFE2L2
Transcriptional regulation by RUNX3
Downstream TCR signaling
MAPK family signaling cascades
RAF/MAP kinase cascade
MAPK1/MAPK3 signaling
Asymmetric localization of PCP proteins
Signaling by NOTCH4
PCP/CE pathway
Beta-catenin independent WNT signaling
Cell Cycle Checkpoints
G2/M Checkpoints
Signaling by WNT

91 common elements in "WT Aviano" and "WT Barcelona":

Neutrophil degranulation
Deubiquitination

Signaling by Rho GTPases, Miro GTPases and RHOBTB3
RHO GTPase cycle
Signaling by Rho GTPases
Cellular response to chemical stress
Ub-specific processing proteases
SCF-beta-TrCP mediated degradation of Emi1
Cross-presentation of soluble exogenous antigens (endosomes)
Cellular responses to stress
Autodegradation of the E3 ubiquitin ligase COP1
GSK3B and BTRC:CUL1-mediated-degradation of NFE2L2
Metabolism of polyamines
Cellular responses to stimuli
Degradation of GLI1 by the proteasome
G1/S DNA Damage Checkpoints
FBXL7 down-regulates AURKA during mitotic entry and in early mitosis
Negative regulation of NOTCH4 signaling
Hh mutants are degraded by ERAD
Regulation of mRNA stability by proteins that bind AU-rich elements
Degradation of DVL
Stabilization of p53
Regulation of activated PAK-2p34 by proteasome mediated degradation
Regulation of ornithine decarboxylase (ODC)
Hh mutants abrogate ligand secretion
Cell Cycle, Mitotic
p53-Independent DNA Damage Response
p53-Independent G1/S DNA damage checkpoint
Ubiquitin Mediated Degradation of Phosphorylated Cdc25A
Ubiquitin-dependent degradation of Cyclin D
Vpu mediated degradation of CD4

Degradation of GLI2 by the proteasome
GLI3 is processed to GLI3R by the proteasome
Regulation of RAS by GAPs
Metabolism of amino acids and derivatives
Regulation of Apoptosis
Defective CFTR causes cystic fibrosis
Regulation of PTEN stability and activity
Cell Cycle
Vif-mediated degradation of APOBEC3G
Regulation of RUNX3 expression and activity
Orc1 removal from chromatin
AUF1 (hnRNP D0) binds and destabilizes mRNA
MAPK6/MAPK4 signaling
Hedgehog ligand biogenesis
Oxygen-dependent proline hydroxylation of Hypoxia-inducible Factor Alpha
Cellular response to hypoxia
Host Interactions of HIV factors
PTEN Regulation
UCH proteinases
Transcriptional regulation by RUNX1
ABC-family proteins mediated transport
Signaling by ROBO receptors
Nervous system development
ER-Phagosome pathway
Regulation of APC/C activators between G1/S and early anaphase
Autodegradation of Cdh1 by Cdh1:APC/C
Regulation of RUNX2 expression and activity
Neddylation
RAC1 GTPase cycle

HIV Infection
Axon guidance
Disorders of transmembrane transporters
Hedgehog 'on' state
APC/C:Cdc20 mediated degradation of Securin
The role of GTSE1 in G2/M progression after G2 checkpoint
Signaling by NOTCH
APC/C-mediated degradation of cell cycle proteins
Regulation of mitotic cell cycle
Mitotic G2-G2/M phases
Cdc20:Phospho-APC/C mediated degradation of Cyclin A
CDK-mediated phosphorylation and removal of Cdc6
Switching of origins to a post-replicative state
APC/C:Cdh1 mediated degradation of Cdc20 and other APC/C:Cdh1 targeted proteins in late mitosis/early G1
APC:Cdc20 mediated degradation of cell cycle proteins prior to satisfation of the cell cycle checkpoint
Hedgehog 'off' state
APC/C:Cdc20 mediated degradation of mitotic proteins
Activation of APC/C and APC/C:Cdc20 mediated degradation of mitotic proteins
Regulation of expression of SLITs and ROBOs
G2/M Transition
Transcriptional regulation by RUNX2
Mitotic Metaphase and Anaphase
Signaling by Hedgehog
Mitotic Anaphase
DNA Replication
Separation of Sister Chromatids
RUNX1 regulates transcription of genes involved in differentiation of HSCs
RAC3 GTPase cycle

DNA Replication Pre-Initiation
TCF dependent signaling in response to WNT
Assembly of the pre-replicative complex

18 common elements in "TP53 altered" and "Trisomy 12":

Interleukin-2 family signaling
Interleukin-3, Interleukin-5 and GM-CSF signaling
Signaling by SCF-KIT
Growth hormone receptor signaling
FLT3 Signaling
Interleukin-2 signaling
Signaling by KIT in disease
Signaling by phosphorylated juxtamembrane, extracellular and kinase domain KIT mutants
Erythropoietin activates STAT5
Interleukin-15 signaling
Interleukin-20 family signaling
Interleukin-21 signaling
Signaling by CSF3 (G-CSF)
Interleukin-7 signaling
Inactivation of CSF3 (G-CSF) signaling
Signaling by FLT3 ITD and TKD mutants
Downstream signal transduction
Interleukin-9 signaling

2 common elements in "WT Barcelona" and "TP53 altered":

Transcriptional Regulation by TP53
Regulation of TP53 Activity

2 common elements in "WT Aviano" and "TP53 altered":

Intrinsic Pathway for Apoptosis
PI3K/AKT Signaling in Cancer

2 common elements in "WT Aviano" and "Trisomy 12":

Regulation of TNFR1 signaling
TNF signaling

1 common element in "WT Aviano", "WT Barcelona" and "Trisomy 12":

TNFR2 non-canonical NF-kB pathway

1 common element in "WT Barcelona" and "Trisomy 12":

Metabolism of lipids

2 common elements in "WT Barcelona" and "TP53 altered":

Transcriptional Regulation by TP53
Regulation of TP53 Activity

8 elements included exclusively in "WT Aviano":

TNFR1-induced proapoptotic signaling
CDC42 GTPase cycle
TNFR1-induced NFkappaB signaling pathway
RHOQ GTPase cycle
Apoptotic factor-mediated response
DDX58/IFIH1-mediated induction of interferon-alpha/beta
Cytochrome c-mediated apoptotic response
NF-kB activation through FADD/RIP-1 pathway mediated by caspase-8 and -10

62 elements included exclusively in "WT Barcelona":

Translation

Respiratory electron transport
Metabolism of RNA
The citric acid (TCA) cycle and respiratory electron transport
Respiratory electron transport, ATP synthesis by chemiosmotic coupling, and heat production by uncoupling proteins.
Response of EIF2AK4 (GCN2) to amino acid deficiency
SRP-dependent cotranslational protein targeting to membrane
Selenoamino acid metabolism
Eukaryotic Translation Initiation
Cap-dependent Translation Initiation
L13a-mediated translational silencing of Ceruloplasmin expression
GTP hydrolysis and joining of the 60S ribosomal subunit
Transport of small molecules
Cellular response to starvation
Influenza Infection
Influenza Viral RNA Transcription and Replication
Formation of a pool of free 40S subunits
Membrane Trafficking
Selenocysteine synthesis
Vesicle-mediated transport
Peptide chain elongation
Viral mRNA Translation
M Phase
Eukaryotic Translation Elongation
Eukaryotic Translation Termination
SARS-CoV Infections
Nonsense Mediated Decay (NMD) independent of the Exon Junction Complex (EJC)
Complex I biogenesis
Mitochondrial translation initiation
DNA Repair

SARS-CoV-2 Infection
Mitochondrial translation
Mitochondrial translation elongation
Mitochondrial translation termination
Nonsense-Mediated Decay (NMD)
Nonsense Mediated Decay (NMD) enhanced by the Exon Junction Complex (EJC)
Global Genome Nucleotide Excision Repair (GG-NER)
Nucleotide Excision Repair
SARS-CoV-2-host interactions
Formation of Incision Complex in GG-NER
Asparagine N-linked glycosylation
Activation of the mRNA upon binding of the cap-binding complex and eIFs, and subsequent binding to 43S
rRNA processing
Formation of the ternary complex, and subsequently, the 43S complex
Translation initiation complex formation
Ribosomal scanning and start codon recognition
rRNA processing in the nucleus and cytosol
Regulation of TP53 Activity through Phosphorylation
Transcription-Coupled Nucleotide Excision Repair (TC-NER)
Dual incision in TC-NER
Golgi-to-ER retrograde transport
Major pathway of rRNA processing in the nucleolus and cytosol
COPI-dependent Golgi-to-ER retrograde traffic
Gap-filling DNA repair synthesis and ligation in TC-NER
Dual Incision in GG-NER
ER to Golgi Anterograde Transport
SARS-CoV-2 modulates host translation machinery
Intra-Golgi and retrograde Golgi-to-ER traffic
COPI-mediated anterograde transport

Transport to the Golgi and subsequent modification
SARS-CoV-2 activates/modulates innate and adaptive immune responses
RAC2 GTPase cycle

21 elements included exclusively in "TP53 altered":

Interferon alpha/beta signaling
Interferon Signaling
Signaling by Receptor Tyrosine Kinases
Signaling by Leptin
Signaling by Erythropoietin
Antigen activates B Cell Receptor (BCR) leading to generation of second messengers
Interferon gamma signaling
FCERI mediated MAPK activation
OAS antiviral response
DAP12 signaling
Antiviral mechanism by IFN-stimulated genes
Activation of caspases through apoptosome-mediated cleavage
PI5P, PP2A and IER3 Regulate PI3K/AKT Signaling
SMAC (DIABLO) binds to IAPs
SMAC(DIABLO)-mediated dissociation of IAP:caspase complexes
Negative regulation of the PI3K/AKT network
SMAC, XIAP-regulated apoptotic response
DAP12 interactions
Signaling by FLT3 fusion proteins
Interleukin-23 signaling
STAT5 activation downstream of FLT3 ITD mutants

18 elements included exclusively in "Trisomy 12":

RIPK1-mediated regulated necrosis

Regulation of necroptotic cell death
Regulated Necrosis
Signaling by PDGF
Signaling by FGFR1 in disease
Interleukin receptor SHC signaling
TNF receptor superfamily (TNFSF) members mediating non-canonical NF-kB pathway
Signaling by cytosolic FGFR1 fusion mutants
Regulation by c-FLIP
CASP8 activity is inhibited
Dimerization of procaspase-8
Signaling by ALK in cancer
Signaling by ALK fusions and activated point mutants
FGFR1 mutant receptor activation
Signaling by MET
Signaling by NTRKs
MHC class II antigen presentation
Caspase activation via Death Receptors in the presence of ligand

Supplementary Table 6. Significant lncRNAs asociated with a shorter Time-To-Treatment (TTT) in 266 CLL (ICGC).

NAME	ENSMBL CODE	HR	CI 95% (min)	CI 95% (max)	P-value	Adjusted P-value
RP11-147L13.2	ENSG00000265100	1.59	1.39	1.82	1.70E-11	7.12E-09
MIR4458HG	ENSG00000247516	1.53	1.37	1.72	1.70E-13	1.58E-10
RNU2-6P	ENSG00000223336	1.52	1.33	1.73	6.80E-10	1.36E-07
RP11-637N19.1	ENSG00000279885	1.51	1.34	1.69	3.30E-12	1.78E-09
ZNF667-AS1	ENSG00000166770	1.48	1.29	1.70	3.10E-08	3.22E-06
RP11-127I20.5	ENSG00000267077	1.47	1.30	1.65	1.60E-10	3.92E-08
ABCA9-AS1	ENSG00000231749	1.46	1.27	1.66	3.40E-08	3.45E-06
DLEU2	ENSG00000231607	1.45	1.26	1.67	2.60E-07	1.79E-05
RP11-114F3.4	ENSG00000277895	1.44	1.31	1.59	2.60E-13	2.19E-10
RP11-311C24.1	ENSG00000260772	1.44	1.28	1.63	4.10E-09	6.05E-07
AC006011.4	ENSG00000244563	1.44	1.30	1.60	2.00E-12	1.18E-09
RP11-289I10.2	ENSG00000223612	1.44	1.29	1.61	5.20E-11	1.61E-08
AGPAT4-IT1	ENSG00000279355	1.44	1.29	1.60	4.50E-11	1.50E-08
KCNJ2-AS1	ENSG00000267365	1.43	1.27	1.61	2.80E-09	4.66E-07
ATP8B5P	ENSG00000179766	1.43	1.27	1.62	6.50E-09	8.79E-07
PTGES3P1	ENSG00000234518	1.43	1.26	1.63	8.20E-08	7.49E-06
RP11-47A8.5	ENSG00000272933	1.43	1.24	1.65	1.00E-06	5.15E-05
EHMT1-IT1	ENSG00000281796	1.43	1.27	1.61	4.40E-09	6.42E-07
SCARNA2	ENSG00000278249	1.43	1.23	1.66	2.70E-06	1.11E-04
RNPS1P1	ENSG00000250896	1.43	1.26	1.62	5.40E-08	5.23E-06
RP11-416N2.4	ENSG00000273108	1.43	1.23	1.65	2.60E-06	1.08E-04
RP5-956O18.2	ENSG00000227006	1.42	1.27	1.59	1.40E-09	2.52E-07
RP11-226M10.3	ENSG00000279281	1.42	1.24	1.62	2.10E-07	1.53E-05
RP11-119F19.5	ENSG00000280355	1.41	1.22	1.63	3.10E-06	1.23E-04
LAMA5-AS1	ENSG00000228812	1.41	1.23	1.62	1.20E-06	5.86E-05
USP3-AS1	ENSG00000259248	1.41	1.26	1.58	3.60E-09	5.56E-07
PPP4R1L	ENSG00000124224	1.41	1.24	1.60	1.40E-07	1.13E-05

BEND3P3	ENSG00000278616	1.41	1.23	1.60	4.30E-07	2.61E-05
ZNRF2P1	ENSG00000237004	1.40	1.22	1.61	1.20E-06	5.86E-05
LLNLR-285B5.1	ENSG00000276578	1.40	1.26	1.57	2.10E-09	3.68E-07
RP11-432I5.8	ENSG00000261513	1.40	1.23	1.60	3.50E-07	2.24E-05
RP11-165D6.1	ENSG00000278462	1.40	1.21	1.63	1.10E-05	3.50E-04
CTC-471C19.1	ENSG00000261037	1.40	1.26	1.55	1.00E-10	2.65E-08
RP1-159A19.4	ENSG00000237429	1.40	1.27	1.53	8.90E-13	6.42E-10
RP11-793H13.8	ENSG00000257379	1.39	1.26	1.53	1.40E-11	6.06E-09
RP11-327F22.6	ENSG00000270120	1.39	1.23	1.57	1.90E-07	1.42E-05
RP11-626G11.3	ENSG00000261759	1.39	1.22	1.57	2.90E-07	1.92E-05
RP13-104F24.3	ENSG00000265298	1.38	1.24	1.54	3.50E-09	5.54E-07
RP11-25L3.3	ENSG00000263655	1.38	1.24	1.55	1.20E-08	1.43E-06
PIK3CD-AS2	ENSG00000231789	1.38	1.21	1.58	1.20E-06	5.86E-05
HNRNPA1P49	ENSG00000233231	1.38	1.20	1.60	8.20E-06	2.75E-04
LOC440461	ENSG00000267472	1.38	1.22	1.56	2.90E-07	1.92E-05
NA	ENSG00000280777	1.38	1.22	1.55	1.90E-07	1.42E-05
CTA-268H5.12	ENSG00000273353	1.38	1.21	1.56	1.20E-06	5.86E-05
AC159540.1	ENSG00000230606	1.37	1.21	1.56	9.00E-07	4.75E-05
CTD-2013N24.2	ENSG00000244513	1.37	1.18	1.60	4.10E-05	1.02E-03
RP11-424C20.2	ENSG00000256663	1.37	1.21	1.55	4.20E-07	2.58E-05
RP11-46H11.3	ENSG00000250790	1.37	1.21	1.55	4.70E-07	2.80E-05
DUSP8P3	ENSG00000215097	1.37	1.16	1.62	2.30E-04	3.92E-03
RP11-797H7.5	ENSG00000189316	1.37	1.24	1.51	1.10E-09	2.07E-07
AC006128.2	ENSG00000279716	1.36	1.21	1.54	6.00E-07	3.39E-05
KLKP1	ENSG00000197588	1.36	1.22	1.53	8.20E-08	7.49E-06
RP11-138C9.1	ENSG00000264558	1.36	1.24	1.50	8.20E-11	2.39E-08
RP11-23P13.6	ENSG00000174171	1.36	1.18	1.58	4.20E-05	1.04E-03
RP11-864I4.4	ENSG00000257058	1.36	1.24	1.49	4.80E-11	1.52E-08
RP11-603J24.7	ENSG00000237493	1.36	1.18	1.57	1.60E-05	4.76E-04

RP11-397P13.7	ENSG00000223505	1.36	1.18	1.57	2.60E-05	7.06E-04
FIRRE	ENSG00000213468	1.36	1.20	1.54	1.40E-06	6.58E-05
LINC00545	ENSG00000236094	1.36	1.21	1.52	1.90E-07	1.42E-05
ABALON	ENSG00000281376	1.36	1.15	1.60	2.30E-04	3.92E-03
LEMD1-AS1	ENSG00000226235	1.36	1.21	1.53	2.40E-07	1.68E-05
AC087491.2	ENSG00000214546	1.36	1.21	1.52	8.40E-08	7.62E-06
CTA-384D8.36	ENSG00000272821	1.36	1.22	1.51	7.70E-09	9.99E-07
RP11-430C7.5	ENSG00000240219	1.36	1.20	1.54	2.30E-06	9.76E-05
RP11-273B20.1	ENSG00000256967	1.36	1.15	1.59	2.10E-04	3.66E-03
UQCRFS1P1	ENSG00000226085	1.35	1.20	1.53	1.60E-06	7.24E-05
RP11-456H18.2	ENSG00000229896	1.35	1.18	1.56	2.10E-05	5.94E-04
CTD-2373N4.5	ENSG00000253112	1.35	1.18	1.55	8.40E-06	2.80E-04
RP11-37N22.1	ENSG00000214803	1.35	1.20	1.52	4.30E-07	2.61E-05
HNRNPA1P4	ENSG00000206228	1.35	1.22	1.50	2.40E-08	2.62E-06
AC092620.2	ENSG00000241772	1.35	1.16	1.58	1.40E-04	2.68E-03
CTC-343N3.1	ENSG00000183562	1.35	1.19	1.54	4.60E-06	1.72E-04
LINC01023	ENSG00000272523	1.35	1.17	1.56	4.30E-05	1.06E-03
AC092171.4	ENSG00000230733	1.35	1.18	1.55	1.50E-05	4.56E-04
RN7SL449P	ENSG00000242889	1.35	1.20	1.51	3.80E-07	2.37E-05
RP1-30M3.6	ENSG00000272402	1.35	1.18	1.53	6.40E-06	2.22E-04
RP11-820K3.3	ENSG00000203437	1.35	1.17	1.55	2.10E-05	5.94E-04
RP11-816J6.3	ENSG00000269889	1.35	1.15	1.58	2.40E-04	4.05E-03
CTD-2339M3.1	ENSG00000242602	1.35	1.19	1.52	2.40E-06	1.00E-04
RP11-331F9.4	ENSG00000227933	1.35	1.17	1.55	3.30E-05	8.50E-04
KRT19P2	ENSG00000216306	1.35	1.18	1.54	1.60E-05	4.76E-04
CASC11	ENSG00000249375	1.34	1.19	1.52	2.10E-06	9.00E-05
RP11-379K17.2	ENSG00000244039	1.34	1.21	1.49	2.50E-08	2.70E-06
CTD-2340D6.2	ENSG00000253562	1.34	1.17	1.55	4.70E-05	1.13E-03
RP11-771K4.3	ENSG00000275769	1.34	1.17	1.54	1.60E-05	4.76E-04

HIST2H2BC	ENSG00000203819	1.34	1.19	1.52	1.80E-06	7.97E-05
RP11-263I1.1	ENSG00000248659	1.34	1.21	1.48	7.90E-09	1.01E-06
RP11-508N22.12	ENSG00000272983	1.34	1.18	1.53	1.30E-05	4.01E-04
LINC01374	ENSG00000280560	1.34	1.20	1.50	2.40E-07	1.68E-05
RP11-946P6.4	ENSG00000279360	1.34	1.23	1.47	1.10E-10	2.80E-08
AP000692.9	ENSG00000228107	1.34	1.16	1.55	7.00E-05	1.56E-03
HIST2H2BD	ENSG00000220323	1.34	1.19	1.51	1.20E-06	5.86E-05
RP13-104F24.2	ENSG00000215769	1.34	1.16	1.54	5.80E-05	1.34E-03
OTUD4P1	ENSG00000118976	1.34	1.19	1.50	6.30E-07	3.48E-05
COX7BP2	ENSG00000234274	1.34	1.22	1.46	9.80E-11	2.65E-08
RP11-126K15.1	ENSG00000265380	1.34	1.18	1.51	4.10E-06	1.57E-04
BIRC6-AS2	ENSG00000279897	1.34	1.18	1.52	9.40E-06	3.07E-04
CERS6-AS1	ENSG00000227617	1.34	1.16	1.53	4.40E-05	1.07E-03
MARCKSL1P1	ENSG00000213277	1.34	1.17	1.53	2.80E-05	7.49E-04
RP11-378A13.2	ENSG00000273361	1.33	1.19	1.49	6.10E-07	3.41E-05
RP11-161H23.5	ENSG00000258232	1.33	1.13	1.57	5.50E-04	7.70E-03
RP11-77H9.6	ENSG00000261481	1.33	1.16	1.53	5.40E-05	1.27E-03
RP11-342K2.1	ENSG00000279133	1.33	1.12	1.59	1.20E-03	1.35E-02
RP11-171I2.1	ENSG00000267784	1.33	1.16	1.53	4.30E-05	1.06E-03
NA	ENSG00000250232	1.33	1.16	1.53	5.40E-05	1.27E-03
RP3-424M6.4	ENSG00000278993	1.33	1.12	1.58	1.00E-03	1.19E-02
STRCP1	ENSG00000166763	1.33	1.22	1.46	6.40E-10	1.30E-07
RP11-327F22.4	ENSG00000260616	1.33	1.16	1.53	6.30E-05	1.42E-03
RP11-572B2.1	ENSG00000268509	1.33	1.20	1.48	9.70E-08	8.45E-06
RP11-386I14.4	ENSG00000273338	1.33	1.21	1.46	5.60E-09	8.08E-07
RP11-188C12.2	ENSG00000255585	1.33	1.12	1.57	9.50E-04	1.17E-02
RP11-505K9.1	ENSG00000260018	1.33	1.16	1.51	2.20E-05	6.14E-04
RP4-565E6.1	ENSG00000227733	1.33	1.17	1.50	5.90E-06	2.08E-04
SNAP47-AS1	ENSG00000230005	1.33	1.14	1.54	1.80E-04	3.24E-03

RP11-513I15.6	ENSG00000225339	1.32	1.16	1.51	3.00E-05	7.90E-04
RPL34P21	ENSG00000244451	1.32	1.22	1.44	4.00E-11	1.37E-08
U91328.21	ENSG00000272558	1.32	1.22	1.43	4.50E-12	2.25E-09
SPG20-AS1	ENSG00000120664	1.32	1.15	1.52	7.20E-05	1.59E-03
RP11-44N21.1	ENSG00000257556	1.32	1.16	1.50	2.00E-05	5.77E-04
FLJ33360	ENSG00000250490	1.32	1.16	1.50	2.40E-05	6.63E-04
RP11-25L3.1	ENSG00000278902	1.32	1.14	1.52	1.50E-04	2.82E-03
RP11-33N14.3	ENSG00000277873	1.32	1.14	1.54	3.00E-04	4.83E-03
AC008277.1	ENSG00000223642	1.32	1.20	1.45	8.60E-09	1.08E-06
MALAT1	ENSG00000251562	1.32	1.18	1.48	1.50E-06	6.88E-05
RP11-350N15.6	ENSG00000272159	1.32	1.16	1.50	2.80E-05	7.49E-04
RP11-118E18.4	ENSG00000263499	1.32	1.18	1.47	6.20E-07	3.44E-05
RP11-211G3.3	ENSG00000228804	1.32	1.14	1.52	1.30E-04	2.53E-03
CTD-2354A18.1	ENSG00000261780	1.32	1.14	1.52	1.80E-04	3.24E-03
ZEB2P1	ENSG00000249506	1.32	1.19	1.46	1.70E-07	1.32E-05
RP5-1057I20.5	ENSG00000276691	1.32	1.15	1.51	7.10E-05	1.58E-03
RP11-386M24.6	ENSG00000260337	1.32	1.12	1.55	1.20E-03	1.35E-02
CH17-437K3.1	ENSG00000227082	1.32	1.20	1.45	1.50E-08	1.74E-06
RP5-849H19.3	ENSG00000278967	1.32	1.13	1.53	4.70E-04	6.79E-03
RP11-106D4.2	ENSG00000276337	1.32	1.16	1.49	1.10E-05	3.50E-04
FLJ46284	ENSG00000248858	1.31	1.20	1.44	3.60E-09	5.56E-07
TBC1D27	ENSG00000128438	1.31	1.13	1.53	3.60E-04	5.54E-03
RP11-268P4.6	ENSG00000274885	1.31	1.15	1.50	3.80E-05	9.65E-04
CTB-96E2.3	ENSG00000258924	1.31	1.13	1.53	4.00E-04	5.97E-03
RP11-36B15.1	ENSG00000248936	1.31	1.21	1.43	4.50E-10	9.90E-08
RP11-519C12.1	ENSG00000259935	1.31	1.18	1.46	5.00E-07	2.94E-05
BTBD9-AS1	ENSG00000226533	1.31	1.17	1.48	6.10E-06	2.15E-04
GAPDHP60	ENSG00000248180	1.31	1.19	1.45	1.20E-07	9.92E-06
ALMS1-IT1	ENSG00000230002	1.31	1.15	1.50	7.90E-05	1.73E-03

RP11-496H1.1	ENSG00000249626	1.31	1.17	1.47	5.80E-06	2.06E-04
DPYD-AS2	ENSG00000235777	1.31	1.11	1.55	1.60E-03	1.66E-02
MTND5P1	ENSG00000227999	1.31	1.20	1.43	1.40E-09	2.52E-07
KRT8P34	ENSG00000264663	1.31	1.14	1.51	1.60E-04	2.97E-03
RP11-44M6.7	ENSG00000274272	1.31	1.14	1.51	2.10E-04	3.66E-03
AMZ2P1	ENSG00000214174	1.31	1.19	1.45	1.10E-07	9.27E-06
RP11-2C24.4	ENSG00000260899	1.31	1.18	1.45	1.90E-07	1.42E-05
RP11-196G18.22	ENSG00000261716	1.31	1.18	1.45	2.80E-07	1.88E-05
RP11-727A23.7	ENSG00000254551	1.31	1.16	1.47	8.50E-06	2.83E-04
AP000295.10	ENSG00000272659	1.31	1.20	1.42	1.10E-09	2.07E-07
HNRNPCP2	ENSG00000204253	1.31	1.16	1.47	1.10E-05	3.50E-04
AC007386.4	ENSG00000232613	1.31	1.14	1.50	1.70E-04	3.10E-03
RP11-820I16.4	ENSG00000273141	1.31	1.19	1.44	3.30E-08	3.40E-06
RN7SL733P	ENSG00000273946	1.31	1.13	1.51	4.30E-04	6.33E-03
ZEB1-AS1	ENSG00000237036	1.31	1.18	1.45	3.20E-07	2.08E-05
RP11-227H4.5	ENSG00000248839	1.30	1.15	1.48	3.60E-05	9.18E-04
AC195454.1	ENSG00000249241	1.30	1.15	1.48	2.20E-05	6.14E-04
RP4-597N16.4	ENSG00000273416	1.30	1.17	1.45	8.20E-07	4.38E-05
CTB-52I2.3	ENSG00000268623	1.30	1.13	1.51	3.10E-04	4.94E-03
RP1-223E5.4	ENSG00000261071	1.30	1.12	1.51	4.60E-04	6.67E-03
RP11-888D10.4	ENSG00000273284	1.30	1.14	1.49	6.90E-05	1.54E-03
RP11-478C6.1	ENSG00000251535	1.30	1.20	1.41	5.50E-11	1.66E-08
METTL15P3	ENSG00000224396	1.30	1.18	1.43	5.70E-08	5.48E-06
L3MBTL4-AS1	ENSG00000264707	1.30	1.15	1.48	3.20E-05	8.34E-04
RP3-510O8.4	ENSG00000232909	1.30	1.18	1.44	5.00E-07	2.94E-05
PCAT6	ENSG00000228288	1.30	1.16	1.46	5.40E-06	1.95E-04
RP11-536C5.7	ENSG00000227741	1.30	1.13	1.50	3.00E-04	4.83E-03
AP003774.1	ENSG00000236935	1.30	1.13	1.49	1.80E-04	3.24E-03
RP11-240G22.5	ENSG00000274554	1.30	1.13	1.50	2.20E-04	3.79E-03

AC061992.2	ENSG00000267737	1.30	1.13	1.50	2.10E-04	3.66E-03
CTC-510F12.2	ENSG00000267082	1.30	1.14	1.48	7.70E-05	1.70E-03
RP11-156E8.1	ENSG00000272195	1.30	1.17	1.44	7.50E-07	4.04E-05
AC025442.3	ENSG00000253744	1.30	1.14	1.48	7.40E-05	1.64E-03
TPM3P7	ENSG00000187536	1.30	1.20	1.41	4.80E-11	1.52E-08
RP1-209B5.2	ENSG00000218857	1.30	1.16	1.46	1.30E-05	4.01E-04
RP11-16E23.5	ENSG00000275638	1.30	1.14	1.48	5.40E-05	1.27E-03
TRERNA1	ENSG00000231265	1.30	1.16	1.46	8.00E-06	2.70E-04
RP11-734K23.9	ENSG00000277701	1.30	1.15	1.47	4.30E-05	1.06E-03
RP11-480D4.7	ENSG00000279075	1.30	1.14	1.48	6.20E-05	1.41E-03
EPB41L4A-AS2	ENSG00000278921	1.30	1.14	1.48	9.70E-05	2.04E-03
RP11-203B7.2	ENSG00000260303	1.30	1.17	1.45	1.90E-06	8.36E-05
RP11-521C22.2	ENSG00000279863	1.30	1.14	1.48	1.20E-04	2.39E-03
LINC01516	ENSG00000231422	1.30	1.15	1.47	4.20E-05	1.04E-03
RP11-426J5.3	ENSG00000278983	1.30	1.15	1.46	2.30E-05	6.38E-04
LINC01063	ENSG00000232065	1.30	1.14	1.48	1.10E-04	2.24E-03
CTD-3065J16.9	ENSG00000255224	1.30	1.11	1.51	7.50E-04	9.75E-03
RP11-927P21.5	ENSG00000263647	1.30	1.12	1.50	4.70E-04	6.79E-03
RP11-525A16.4	ENSG00000273143	1.30	1.17	1.43	2.50E-07	1.73E-05
RP11-460N20.7	ENSG00000270948	1.30	1.16	1.45	5.50E-06	1.98E-04
CH507-254M2.3	ENSG00000280164	1.29	1.14	1.47	8.60E-05	1.86E-03
RP11-266L9.8	ENSG00000275494	1.29	1.17	1.43	5.40E-07	3.11E-05
RP11-85G20.2	ENSG00000241499	1.29	1.17	1.43	9.00E-07	4.75E-05
RP4-730K3.3	ENSG00000232450	1.29	1.13	1.48	1.60E-04	2.97E-03
RP11-333E13.4	ENSG00000205794	1.29	1.10	1.52	1.50E-03	1.60E-02
LINC00552	ENSG00000279770	1.29	1.15	1.45	9.00E-06	2.95E-04
TUBB7P	ENSG00000251297	1.29	1.13	1.48	2.10E-04	3.66E-03
RP11-625L16.3	ENSG00000256482	1.29	1.16	1.45	6.60E-06	2.27E-04
RP11-118E18.2	ENSG00000266100	1.29	1.15	1.45	1.30E-05	4.01E-04

H2AFZP1	ENSG00000213440	1.29	1.17	1.43	8.70E-07	4.63E-05
RP11-317B3.2	ENSG00000237593	1.29	1.13	1.47	1.30E-04	2.53E-03
RP11-103B5.4	ENSG00000277840	1.29	1.14	1.47	7.10E-05	1.58E-03
RP11-16E23.4	ENSG00000259924	1.29	1.13	1.48	1.60E-04	2.97E-03
MIR222HG	ENSG00000270069	1.29	1.11	1.50	8.30E-04	1.06E-02
LINC01353	ENSG00000231507	1.29	1.16	1.44	6.40E-06	2.22E-04
LA16c-390E6.5	ENSG00000261641	1.29	1.15	1.45	1.90E-05	5.54E-04
PRICKLE2-AS3	ENSG00000226017	1.29	1.18	1.41	1.90E-08	2.13E-06
IGKV1OR-2	ENSG00000156755	1.29	1.17	1.43	6.10E-07	3.41E-05
SNHG19	ENSG00000260260	1.29	1.15	1.45	2.60E-05	7.06E-04
ISCA1P1	ENSG00000217416	1.29	1.15	1.44	8.10E-06	2.73E-04
AC006077.3	ENSG00000279799	1.29	1.10	1.51	1.50E-03	1.60E-02
BNIP3P41	ENSG00000248302	1.29	1.13	1.46	9.80E-05	2.06E-03
RP11-759L5.2	ENSG00000235071	1.29	1.15	1.45	1.80E-05	5.29E-04
HYDIN2	ENSG00000276975	1.29	1.16	1.43	4.50E-06	1.68E-04
RP11-177H13.2	ENSG00000253837	1.29	1.10	1.50	1.30E-03	1.43E-02
KB-1732A1.1	ENSG00000253669	1.29	1.15	1.44	1.50E-05	4.56E-04
EIF4HP1	ENSG00000233830	1.29	1.12	1.48	3.80E-04	5.76E-03
CH17-302M23.1	ENSG00000275552	1.29	1.13	1.46	8.40E-05	1.83E-03
CTD-2017C7.3	ENSG00000259161	1.29	1.13	1.46	1.30E-04	2.53E-03
RP11-611O2.3	ENSG00000256664	1.29	1.12	1.48	4.20E-04	6.20E-03
ADAMTSL4-AS1	ENSG00000203804	1.29	1.13	1.46	1.30E-04	2.53E-03
SCGB1B2P	ENSG00000268751	1.29	1.15	1.44	1.30E-05	4.01E-04
PIPSL	ENSG00000180764	1.29	1.12	1.47	3.50E-04	5.42E-03
AP001059.6	ENSG00000278158	1.29	1.11	1.49	8.60E-04	1.09E-02
AP006621.8	ENSG00000255108	1.28	1.15	1.44	1.20E-05	3.76E-04
RP11-361D15.2	ENSG00000259238	1.28	1.14	1.44	2.50E-05	6.85E-04
SRP72P2	ENSG00000188451	1.28	1.15	1.44	1.00E-05	3.23E-04
RN7SL288P	ENSG00000240767	1.28	1.14	1.45	5.50E-05	1.29E-03

SLC7A5P1	ENSG00000260727	1.28	1.09	1.51	2.30E-03	2.19E-02
RP11-281P23.1	ENSG00000251152	1.28	1.13	1.46	1.30E-04	2.53E-03
RPL4P6	ENSG00000230071	1.28	1.10	1.50	2.00E-03	1.95E-02
CTC-436P18.1	ENSG00000251279	1.28	1.15	1.43	4.80E-06	1.77E-04
RP11-401N16.2	ENSG00000275381	1.28	1.18	1.39	1.20E-09	2.22E-07
RP11-386M24.3	ENSG00000258676	1.28	1.13	1.46	1.70E-04	3.10E-03
RP11-54O7.3	ENSG00000223764	1.28	1.19	1.39	6.20E-10	1.30E-07
CTD-2194F4.2	ENSG00000248288	1.28	1.14	1.45	6.00E-05	1.38E-03
RP11-2K6.1	ENSG00000279225	1.28	1.14	1.45	4.70E-05	1.13E-03
MARK3P1	ENSG00000271642	1.28	1.17	1.41	3.70E-07	2.34E-05
CTD-2026K11.6	ENSG00000203392	1.28	1.15	1.42	4.10E-06	1.57E-04
UGT2B29P	ENSG00000250566	1.28	1.14	1.44	4.60E-05	1.12E-03
RP11-680A11.5	ENSG00000257605	1.28	1.10	1.50	1.70E-03	1.74E-02
RP11-673C5.1	ENSG00000259781	1.28	1.10	1.49	1.10E-03	1.27E-02
RP11-655C2.3	ENSG00000255299	1.28	1.11	1.48	8.30E-04	1.06E-02
OR7E102P	ENSG00000168992	1.28	1.15	1.43	1.40E-05	4.30E-04
RN7SL800P	ENSG00000242398	1.28	1.12	1.46	3.10E-04	4.94E-03
RP11-271M24.2	ENSG00000260509	1.28	1.13	1.45	1.30E-04	2.53E-03
ZNF849P	ENSG00000198153	1.28	1.12	1.46	3.20E-04	5.07E-03
RP13-188A5.1	ENSG00000227486	1.28	1.10	1.49	1.80E-03	1.81E-02
CTD-2526A2.4	ENSG00000279273	1.28	1.15	1.43	1.30E-05	4.01E-04
MTCYBP21	ENSG00000224747	1.28	1.16	1.41	1.30E-06	6.20E-05
RP3-522J7.6	ENSG00000260613	1.28	1.16	1.41	7.60E-07	4.08E-05
AC092667.2	ENSG00000230393	1.28	1.11	1.47	7.30E-04	9.55E-03
RP11-817I4.1	ENSG00000274964	1.28	1.11	1.48	9.00E-04	1.12E-02
RP5-1071N3.1	ENSG00000231105	1.28	1.11	1.47	6.00E-04	8.28E-03
RP11-151N17.1	ENSG00000259659	1.28	1.11	1.47	4.40E-04	6.44E-03
RP11-2J18.1	ENSG00000218596	1.28	1.13	1.45	1.50E-04	2.82E-03
TCEB1P19	ENSG00000241975	1.28	1.11	1.48	9.10E-04	1.13E-02

RP11-462G12.1	ENSG00000262185	1.28	1.17	1.39	5.00E-08	4.95E-06
RP5-1009E24.8	ENSG00000275491	1.28	1.14	1.43	1.30E-05	4.01E-04
RPS2P46	ENSG00000189343	1.28	1.17	1.40	1.10E-07	9.27E-06
RP13-36G14.3	ENSG00000203397	1.28	1.11	1.47	9.10E-04	1.13E-02
RP11-561I11.3	ENSG00000224525	1.28	1.16	1.41	1.50E-06	6.88E-05
AP000783.1	ENSG00000254667	1.28	1.13	1.44	9.90E-05	2.06E-03
RN7SKP268	ENSG00000223039	1.28	1.10	1.48	9.80E-04	1.19E-02
RP11-480D4.2	ENSG00000249159	1.28	1.14	1.43	4.00E-05	1.00E-03
PDCL3P5	ENSG00000213089	1.28	1.13	1.44	1.10E-04	2.24E-03
ANXA2P2	ENSG00000231991	1.28	1.13	1.43	5.20E-05	1.24E-03
FTH1P4	ENSG00000242992	1.28	1.13	1.44	5.70E-05	1.33E-03
RP11-1246C19.1	ENSG00000273230	1.27	1.15	1.42	7.00E-06	2.40E-04
NDUFV2P1	ENSG00000267809	1.27	1.11	1.47	7.00E-04	9.25E-03
RP11-757C15.4	ENSG00000255296	1.27	1.16	1.39	1.70E-07	1.32E-05
RP4-568C11.4	ENSG00000274173	1.27	1.17	1.38	9.10E-09	1.12E-06
RP11-701H24.7	ENSG00000271347	1.27	1.11	1.46	5.70E-04	7.91E-03
RP1-111C20.3	ENSG00000226032	1.27	1.15	1.41	2.70E-06	1.11E-04
RP11-455O6.8	ENSG00000276101	1.27	1.09	1.49	2.60E-03	2.38E-02
AC005785.5	ENSG00000279203	1.27	1.10	1.48	1.40E-03	1.51E-02
RPL7AP2	ENSG00000241984	1.27	1.12	1.45	2.20E-04	3.79E-03
RPS18P13	ENSG00000243455	1.27	1.10	1.47	9.40E-04	1.16E-02
RP11-71H17.8	ENSG00000280042	1.27	1.13	1.44	1.10E-04	2.24E-03
RP11-307C12.13	ENSG00000270361	1.27	1.10	1.47	1.10E-03	1.27E-02
RP11-184M15.1	ENSG00000248187	1.27	1.10	1.47	1.30E-03	1.43E-02
RP11-806L2.6	ENSG00000265490	1.27	1.09	1.48	1.70E-03	1.74E-02
ATP8A2P2	ENSG00000229800	1.27	1.11	1.46	6.90E-04	9.18E-03
RP11-1049A21.2	ENSG00000257824	1.27	1.09	1.48	2.00E-03	1.95E-02
CTA-331F8.1	ENSG00000260865	1.27	1.17	1.38	2.80E-09	4.66E-07
AP000704.5	ENSG00000224790	1.27	1.09	1.48	1.60E-03	1.66E-02

RP11-464D20.2	ENSG00000239246	1.27	1.14	1.41	7.90E-06	2.68E-04
HTATSF1P2	ENSG00000271361	1.27	1.12	1.44	2.60E-04	4.33E-03
RP11-544A12.4	ENSG00000236986	1.27	1.14	1.42	3.20E-05	8.34E-04
RP11-723O4.2	ENSG00000231305	1.27	1.15	1.40	1.20E-06	5.86E-05
CH507-24F1.2	ENSG00000275496	1.27	1.15	1.40	1.80E-06	7.97E-05
SMARCA5-AS1	ENSG00000245112	1.27	1.09	1.48	2.40E-03	2.26E-02
ACTG1P14	ENSG00000230581	1.27	1.10	1.46	9.50E-04	1.17E-02
LINC00865	ENSG00000232229	1.27	1.11	1.44	3.10E-04	4.94E-03
CTB-43P18.1	ENSG00000272742	1.27	1.15	1.40	3.30E-06	1.29E-04
RP11-227B21.2	ENSG00000255686	1.27	1.15	1.40	3.70E-06	1.43E-04
XXYLT1-AS2	ENSG00000230266	1.27	1.16	1.38	1.20E-07	9.92E-06
MCRIP2P1	ENSG00000241418	1.27	1.12	1.43	1.30E-04	2.53E-03
RP4-738P15.6	ENSG00000279322	1.27	1.08	1.48	3.10E-03	2.68E-02
RP11-465B22.3	ENSG00000217801	1.27	1.12	1.43	1.40E-04	2.68E-03
AC005785.2	ENSG00000268189	1.27	1.14	1.41	8.20E-06	2.75E-04
KNOP1P2	ENSG00000270429	1.27	1.09	1.47	2.10E-03	2.02E-02
RP11-479O9.4	ENSG00000272693	1.27	1.14	1.41	1.20E-05	3.76E-04
HSPA8P1	ENSG00000234176	1.27	1.11	1.45	6.60E-04	8.89E-03
AC008132.14	ENSG00000239989	1.27	1.15	1.39	1.20E-06	5.86E-05
CTA-972D3.2	ENSG00000262171	1.27	1.11	1.44	4.80E-04	6.90E-03
SAPCD2P3	ENSG00000232491	1.27	1.10	1.46	1.20E-03	1.35E-02
MIR155HG	ENSG00000234883	1.27	1.15	1.39	1.10E-06	5.53E-05
RP11-108K14.12	ENSG00000278518	1.27	1.12	1.42	9.30E-05	1.98E-03
RP11-227G15.12	ENSG00000279762	1.27	1.13	1.41	3.00E-05	7.90E-04
RP11-290F5.1	ENSG00000249096	1.26	1.13	1.41	2.80E-05	7.49E-04
RP11-396B14.2	ENSG00000263033	1.26	1.14	1.40	4.80E-06	1.77E-04
AC006014.7	ENSG00000242073	1.26	1.08	1.47	2.80E-03	2.50E-02
MIR302B	ENSG00000249532	1.26	1.11	1.44	5.70E-04	7.91E-03
AOC4P	ENSG00000260105	1.26	1.11	1.44	3.70E-04	5.64E-03

RP13-890H12.2	ENSG00000267288	1.26	1.11	1.43	3.10E-04	4.94E-03
CTC-444N24.7	ENSG00000279541	1.26	1.10	1.46	1.20E-03	1.35E-02
RP11-886P16.10	ENSG00000279827	1.26	1.07	1.49	4.90E-03	3.75E-02
CTD-3222D19.4	ENSG00000279977	1.26	1.13	1.41	4.00E-05	1.00E-03
RP11-475E11.2	ENSG00000228076	1.26	1.07	1.50	6.80E-03	4.73E-02
PITRM1-AS1	ENSG00000237399	1.26	1.09	1.46	1.60E-03	1.66E-02
FDX1P1	ENSG00000181741	1.26	1.08	1.48	3.60E-03	2.97E-02
RP11-820K3.4	ENSG00000256159	1.26	1.10	1.45	1.10E-03	1.27E-02
RP11-124N14.3	ENSG00000234961	1.26	1.10	1.44	7.00E-04	9.25E-03
SCARNA7	ENSG00000238741	1.26	1.13	1.41	3.40E-05	8.72E-04
RP11-446N19.1	ENSG00000272369	1.26	1.14	1.39	3.00E-06	1.21E-04
RP11-697E2.7	ENSG00000228998	1.26	1.14	1.39	3.00E-06	1.21E-04
SPATA1	ENSG00000122432	1.26	1.10	1.44	7.80E-04	1.01E-02
KB-1592A4.15	ENSG00000197210	1.26	1.17	1.36	5.20E-10	1.11E-07
RP11-302B13.1	ENSG00000239617	1.26	1.11	1.43	3.90E-04	5.87E-03
RP11-427L15.2	ENSG00000277687	1.26	1.11	1.43	3.40E-04	5.30E-03
RP11-626G11.4	ENSG00000260430	1.26	1.08	1.46	2.70E-03	2.44E-02
RP11-812I20.2	ENSG00000216813	1.26	1.13	1.40	4.00E-05	1.00E-03
CTC-205M6.1	ENSG00000280161	1.26	1.13	1.40	1.90E-05	5.54E-04
RP11-567L7.3	ENSG00000278863	1.26	1.14	1.39	3.20E-06	1.27E-04
SEC62-AS1	ENSG00000240373	1.26	1.09	1.45	1.80E-03	1.81E-02
NONOP2	ENSG00000237522	1.26	1.11	1.43	4.20E-04	6.20E-03
AC100830.3	ENSG00000259635	1.26	1.10	1.44	8.80E-04	1.11E-02
RP11-977G19.11	ENSG00000257303	1.26	1.10	1.44	9.90E-04	1.19E-02
RP11-767L7.1	ENSG00000239835	1.26	1.08	1.46	3.00E-03	2.62E-02
RP11-281P23.2	ENSG00000249631	1.26	1.14	1.39	4.40E-06	1.66E-04
LINC01068	ENSG00000227676	1.26	1.13	1.40	4.20E-05	1.04E-03
RP11-20I20.1	ENSG00000251639	1.26	1.12	1.40	5.70E-05	1.33E-03
CTB-193M12.1	ENSG00000257769	1.26	1.07	1.47	4.90E-03	3.75E-02

RP11-326K13.5	ENSG00000274275	1.26	1.11	1.43	4.10E-04	6.10E-03
RP11-296A18.6	ENSG00000236434	1.26	1.11	1.42	2.80E-04	4.55E-03
MTND5P33	ENSG00000261904	1.26	1.09	1.45	1.50E-03	1.60E-02
RP11-93B14.6	ENSG00000167046	1.26	1.11	1.43	4.50E-04	6.56E-03
RP11-332M2.1	ENSG00000203644	1.26	1.11	1.42	2.30E-04	3.92E-03
CTD-2591A1.1	ENSG00000280159	1.26	1.12	1.41	8.90E-05	1.90E-03
RP11-124N2.1	ENSG00000250012	1.25	1.10	1.44	9.80E-04	1.19E-02
RP11-190A12.9	ENSG00000279430	1.25	1.14	1.38	1.30E-06	6.20E-05
TTC41P	ENSG00000214198	1.25	1.15	1.37	1.00E-06	5.15E-05
RP4-622L5.2	ENSG00000250135	1.25	1.11	1.42	2.70E-04	4.42E-03
KRT18P25	ENSG00000249064	1.25	1.11	1.41	1.80E-04	3.24E-03
RPL17P46	ENSG00000239689	1.25	1.13	1.39	1.70E-05	5.03E-04
CTD-2227E11.1	ENSG00000270933	1.25	1.13	1.40	3.90E-05	9.85E-04
RP11-73E17.2	ENSG00000258738	1.25	1.14	1.37	1.50E-06	6.88E-05
LINC01033	ENSG00000249069	1.25	1.15	1.37	9.60E-07	5.02E-05
RP11-197P3.5	ENSG00000229587	1.25	1.10	1.43	6.10E-04	8.37E-03
C6orf99	ENSG00000203711	1.25	1.09	1.44	1.10E-03	1.27E-02
RP11-350N15.4	ENSG00000255201	1.25	1.14	1.38	6.50E-06	2.24E-04
CCDC162P	ENSG00000203799	1.25	1.09	1.44	1.40E-03	1.51E-02
RP11-77K12.3	ENSG00000261476	1.25	1.09	1.44	1.30E-03	1.43E-02
RP5-1063M23.2	ENSG00000236908	1.25	1.07	1.46	4.00E-03	3.22E-02
HAR1A	ENSG00000225978	1.25	1.15	1.37	3.80E-07	2.37E-05
JMJD1C-AS1	ENSG00000272767	1.25	1.07	1.47	5.20E-03	3.91E-02
LINC01422	ENSG00000223704	1.25	1.09	1.45	2.00E-03	1.95E-02
YBX2P1	ENSG00000213438	1.25	1.12	1.41	1.50E-04	2.82E-03
ATP1B1P1	ENSG00000249212	1.25	1.11	1.42	3.00E-04	4.83E-03
PPP1R14BP3	ENSG00000179967	1.25	1.09	1.44	1.60E-03	1.66E-02
LINC00467	ENSG00000153363	1.25	1.09	1.44	1.70E-03	1.74E-02
CTA-246H3.11	ENSG00000231466	1.25	1.07	1.46	4.80E-03	3.69E-02

RP11-1348G14.8	ENSG00000275807	1.25	1.08	1.45	3.00E-03	2.62E-02
PDCD4-AS1	ENSG00000203497	1.25	1.08	1.45	3.10E-03	2.68E-02
RPL17P40	ENSG00000241067	1.25	1.13	1.39	1.80E-05	5.29E-04
RP5-1000K24.2	ENSG00000248503	1.25	1.09	1.43	1.10E-03	1.27E-02
CTD-3076O17.1	ENSG00000254744	1.25	1.11	1.41	1.50E-04	2.82E-03
RP11-91I20.4	ENSG00000255321	1.25	1.11	1.41	1.80E-04	3.24E-03
RP11-485M7.2	ENSG00000279691	1.25	1.07	1.46	4.50E-03	3.52E-02
XXbac-B135H6.15	ENSG00000237476	1.25	1.10	1.42	5.20E-04	7.38E-03
CNN2P9	ENSG00000213149	1.25	1.09	1.44	1.90E-03	1.88E-02
RP11-352G9.1	ENSG00000273009	1.25	1.08	1.45	3.20E-03	2.75E-02
RP11-779O18.2	ENSG00000213386	1.25	1.12	1.39	4.70E-05	1.13E-03
NA	ENSG00000280413	1.25	1.07	1.46	4.00E-03	3.22E-02
CTC-506B8.1	ENSG00000249180	1.25	1.10	1.42	7.40E-04	9.65E-03
AC073842.19	ENSG00000235077	1.25	1.11	1.41	2.60E-04	4.33E-03
CTD-2647L4.5	ENSG00000259607	1.25	1.09	1.43	1.40E-03	1.51E-02
SLC9A9-AS2	ENSG00000244493	1.25	1.08	1.45	2.70E-03	2.44E-02
SNRPGP2	ENSG00000264350	1.25	1.14	1.36	6.40E-07	3.50E-05
RPL7P19	ENSG00000241458	1.25	1.15	1.36	8.80E-08	7.77E-06
BTF3L4P2	ENSG00000213189	1.25	1.11	1.40	1.90E-04	3.38E-03
NUDT4P1	ENSG00000177144	1.25	1.09	1.43	1.20E-03	1.35E-02
NUDT4P2	ENSG00000271121	1.25	1.09	1.43	1.20E-03	1.35E-02
KIF9-AS1	ENSG00000227398	1.25	1.13	1.38	2.10E-05	5.94E-04
LINC01484	ENSG00000253686	1.25	1.10	1.41	4.00E-04	5.97E-03
RP11-85E16.1	ENSG00000272984	1.25	1.13	1.38	8.90E-06	2.94E-04
RP11-152P23.2	ENSG00000260350	1.25	1.10	1.42	6.30E-04	8.58E-03
RP11-264F23.1	ENSG00000213970	1.25	1.09	1.43	1.00E-03	1.19E-02
URAHP	ENSG00000222019	1.25	1.10	1.42	5.10E-04	7.26E-03
DDX3P1	ENSG00000232928	1.25	1.11	1.41	3.50E-04	5.42E-03
RP1-47A17.1	ENSG00000274717	1.25	1.16	1.34	2.10E-09	3.68E-07

RP4-647C14.2	ENSG00000258376	1.25	1.10	1.41	5.10E-04	7.26E-03
PDXDC2P	ENSG00000255185	1.25	1.10	1.41	5.30E-04	7.49E-03
AC005498.3	ENSG00000267421	1.25	1.11	1.40	2.30E-04	3.92E-03
RN7SL809P	ENSG00000241217	1.25	1.10	1.41	3.80E-04	5.76E-03
TATDN1P1	ENSG00000234369	1.25	1.07	1.46	6.00E-03	4.35E-02
RP11-756J15.2	ENSG00000279275	1.25	1.11	1.41	3.20E-04	5.07E-03
RP11-430L17.1	ENSG00000226457	1.25	1.08	1.44	3.00E-03	2.62E-02
MDC1-AS1	ENSG00000224328	1.25	1.09	1.43	1.80E-03	1.81E-02
CTB-113P19.4	ENSG00000260581	1.25	1.14	1.36	5.70E-07	3.26E-05
AC006942.4	ENSG00000269194	1.25	1.10	1.41	6.00E-04	8.28E-03
DUTP1	ENSG00000229048	1.25	1.08	1.45	3.40E-03	2.86E-02
AC007679.4	ENSG00000237041	1.25	1.08	1.43	2.00E-03	1.95E-02
RBMY2EP	ENSG00000223637	1.25	1.13	1.38	1.10E-05	3.50E-04
TSSC1-IT1	ENSG00000224885	1.25	1.14	1.36	1.70E-06	7.63E-05
RN7SL846P	ENSG00000242818	1.25	1.07	1.46	6.00E-03	4.35E-02
RP11-666F17.1	ENSG00000234428	1.25	1.11	1.40	2.10E-04	3.66E-03
RP11-46H11.11	ENSG00000278949	1.25	1.12	1.39	6.20E-05	1.41E-03
RP11-298P3.4	ENSG00000270008	1.25	1.16	1.34	8.80E-10	1.73E-07
SNORA14	ENSG00000251922	1.25	1.14	1.36	6.40E-07	3.50E-05
NA	ENSG00000279188	1.25	1.09	1.42	9.50E-04	1.17E-02
RP11-35O15.2	ENSG00000278022	1.25	1.11	1.39	1.20E-04	2.39E-03
FLNB-AS1	ENSG00000244161	1.25	1.13	1.37	5.60E-06	2.00E-04
AL133243.4	ENSG00000279544	1.25	1.09	1.43	1.50E-03	1.60E-02
RP11-203B9.4	ENSG00000226803	1.25	1.09	1.42	1.20E-03	1.35E-02
RP5-1181K21.4	ENSG00000279960	1.25	1.14	1.36	1.60E-06	7.24E-05
RP11-769O8.3	ENSG00000264635	1.25	1.11	1.39	1.20E-04	2.39E-03
RP11-793A3.2	ENSG00000266846	1.25	1.09	1.42	1.00E-03	1.19E-02
RP11-405L18.4	ENSG00000230188	1.25	1.10	1.41	7.00E-04	9.25E-03
AL133243.2	ENSG00000276517	1.25	1.07	1.45	5.00E-03	3.80E-02

RP11-407N17.5	ENSG00000258940	1.25	1.07	1.46	5.80E-03	4.24E-02
RP11-21M24.3	ENSG00000260635	1.25	1.08	1.44	2.80E-03	2.50E-02
RP11-247L20.3	ENSG00000258857	1.24	1.12	1.38	3.20E-05	8.34E-04
ERICH6-AS1	ENSG00000240137	1.24	1.10	1.41	7.00E-04	9.25E-03
MTCYBP3	ENSG00000232373	1.24	1.08	1.43	2.00E-03	1.95E-02
RP11-480I12.5	ENSG00000214796	1.24	1.09	1.42	1.40E-03	1.51E-02
RP11-490H24.5	ENSG00000216285	1.24	1.12	1.39	8.90E-05	1.90E-03
UNC93B2	ENSG00000155070	1.24	1.11	1.39	1.10E-04	2.24E-03
RP11-428K3.1	ENSG00000273062	1.24	1.08	1.43	2.10E-03	2.02E-02
BACH1-IT2	ENSG00000228817	1.24	1.10	1.41	6.90E-04	9.18E-03
HMGN1P8	ENSG00000241120	1.24	1.08	1.43	1.80E-03	1.81E-02
LINC00987	ENSG00000237248	1.24	1.11	1.39	1.50E-04	2.82E-03
CTA-212A2.1	ENSG00000279805	1.24	1.10	1.40	4.00E-04	5.97E-03
OSTCP8	ENSG00000226801	1.24	1.16	1.34	6.00E-09	8.37E-07
RP11-379F4.7	ENSG00000272087	1.24	1.12	1.39	8.90E-05	1.90E-03
RP11-225B17.2	ENSG00000273014	1.24	1.12	1.38	4.10E-05	1.02E-03
AC002116.8	ENSG00000248101	1.24	1.06	1.46	6.80E-03	4.73E-02
RPSAP36	ENSG00000243175	1.24	1.12	1.37	2.10E-05	5.94E-04
RP3-430N8.11	ENSG00000269987	1.24	1.12	1.37	2.20E-05	6.14E-04
CTC-507E2.2	ENSG00000267592	1.24	1.10	1.41	5.60E-04	7.81E-03
CTD-2373J6.2	ENSG00000255647	1.24	1.09	1.42	1.30E-03	1.43E-02
CTD-2231E14.2	ENSG00000279198	1.24	1.14	1.36	1.10E-06	5.53E-05
RP11-324I22.3	ENSG00000269952	1.24	1.14	1.36	1.40E-06	6.58E-05
GS1-393G12.14	ENSG00000272115	1.24	1.07	1.44	3.60E-03	2.97E-02
EEF1B2P1	ENSG00000231169	1.24	1.11	1.39	1.70E-04	3.10E-03
RPL13AP6	ENSG00000234118	1.24	1.10	1.41	6.30E-04	8.58E-03
RP11-464D20.6	ENSG00000264546	1.24	1.07	1.44	3.70E-03	3.03E-02
RP11-290F5.2	ENSG00000180712	1.24	1.09	1.41	1.10E-03	1.27E-02
AC005037.3	ENSG00000183308	1.24	1.07	1.44	5.00E-03	3.80E-02

ESRRAP1	ENSG00000215572	1.24	1.07	1.45	5.50E-03	4.07E-02
MIR92B	ENSG00000231064	1.24	1.17	1.32	1.80E-11	7.30E-09
NA	ENSG00000279978	1.24	1.08	1.43	2.60E-03	2.38E-02
RP11-138I1.4	ENSG00000265401	1.24	1.09	1.41	7.70E-04	9.96E-03
AGAP2-AS1	ENSG00000255737	1.24	1.10	1.39	2.90E-04	4.71E-03
OR7M1P	ENSG00000273336	1.24	1.06	1.45	6.70E-03	4.70E-02
RP11-815J4.7	ENSG00000267533	1.24	1.10	1.40	6.30E-04	8.58E-03
CYP21A1P	ENSG00000204338	1.24	1.08	1.43	2.70E-03	2.44E-02
RP11-598F7.3	ENSG00000256948	1.24	1.16	1.33	2.00E-10	4.64E-08
RP11-778J15.1	ENSG00000250062	1.24	1.13	1.36	5.60E-06	2.00E-04
CTD-2024I7.13	ENSG00000246422	1.24	1.09	1.41	1.10E-03	1.27E-02
LINC00271	ENSG00000231028	1.24	1.12	1.38	5.60E-05	1.31E-03
RP11-63M22.1	ENSG00000260558	1.24	1.06	1.45	7.30E-03	4.98E-02
NPM1P18	ENSG00000225739	1.24	1.12	1.37	3.30E-05	8.50E-04
RP1-86C11.7	ENSG00000272468	1.24	1.11	1.39	1.60E-04	2.97E-03
TVP23CP1	ENSG00000223584	1.24	1.12	1.37	3.00E-05	7.90E-04
HMGB1P7	ENSG00000231148	1.24	1.12	1.38	5.90E-05	1.36E-03
RP1-102G20.2	ENSG00000237249	1.24	1.10	1.39	3.30E-04	5.18E-03
RP6-99M1.3	ENSG00000269902	1.24	1.07	1.43	3.70E-03	3.03E-02
H2AFZP3	ENSG00000218502	1.24	1.10	1.40	5.60E-04	7.81E-03
RP11-626G11.6	ENSG00000278389	1.24	1.11	1.38	1.20E-04	2.39E-03
RP11-142L4.3	ENSG00000226723	1.24	1.09	1.40	8.10E-04	1.04E-02
SETP5	ENSG00000233998	1.24	1.06	1.45	7.20E-03	4.94E-02
NME2P1	ENSG00000123009	1.24	1.09	1.40	8.00E-04	1.03E-02
KRR1P1	ENSG00000237672	1.24	1.07	1.44	5.10E-03	3.86E-02
AC083843.1	ENSG00000259820	1.24	1.08	1.42	2.20E-03	2.11E-02
LINC00158	ENSG00000185433	1.24	1.10	1.40	5.70E-04	7.91E-03
RP11-1090M7.3	ENSG00000280168	1.24	1.08	1.41	1.70E-03	1.74E-02
RP11-409I10.2	ENSG00000259039	1.24	1.09	1.40	9.00E-04	1.12E-02

QRSL1P3	ENSG00000257957	1.24	1.08	1.42	2.10E-03	2.02E-02
RP11-476C8.2	ENSG00000248196	1.24	1.06	1.44	6.60E-03	4.66E-02
RP11-264L1.1	ENSG00000279887	1.24	1.07	1.42	3.00E-03	2.62E-02
MYLK-AS2	ENSG00000250174	1.24	1.08	1.42	2.00E-03	1.95E-02
C2orf48	ENSG00000163009	1.24	1.09	1.41	1.20E-03	1.35E-02
AC009506.1	ENSG00000224152	1.24	1.07	1.43	4.90E-03	3.75E-02
CTD-2357A8.2	ENSG00000279570	1.24	1.07	1.43	3.40E-03	2.86E-02
RP11-391L3.3	ENSG00000279476	1.24	1.07	1.42	3.30E-03	2.81E-02
RP11-798K23.5	ENSG00000253520	1.24	1.09	1.40	8.60E-04	1.09E-02
PRELID1P1	ENSG00000217325	1.24	1.08	1.41	1.70E-03	1.74E-02
TLE1P1	ENSG00000228158	1.24	1.07	1.42	3.40E-03	2.86E-02
RP11-1174L13.2	ENSG00000253536	1.24	1.12	1.36	1.80E-05	5.29E-04
CTB-111H14.1	ENSG00000243797	1.24	1.09	1.40	1.10E-03	1.27E-02
CYP2D7	ENSG00000205702	1.24	1.06	1.44	6.90E-03	4.78E-02
RP11-380M21.3	ENSG00000279366	1.24	1.08	1.41	1.40E-03	1.51E-02
SMCR5	ENSG00000226746	1.24	1.06	1.44	5.60E-03	4.13E-02
RP5-1165K10.2	ENSG00000273432	1.24	1.08	1.41	1.90E-03	1.88E-02
LINC01136	ENSG00000233791	1.24	1.14	1.34	1.70E-07	1.32E-05
RP11-87G24.2	ENSG00000280122	1.24	1.16	1.31	2.00E-11	7.87E-09
AP001437.1	ENSG00000273210	1.24	1.14	1.34	2.90E-07	1.92E-05
RP1-111C20.4	ENSG00000271913	1.24	1.09	1.40	8.30E-04	1.06E-02
CDY4P	ENSG00000228411	1.24	1.12	1.36	3.30E-05	8.50E-04
PTTG3P	ENSG00000213005	1.23	1.08	1.41	2.00E-03	1.95E-02
WI2-1896O14.1	ENSG00000215861	1.23	1.09	1.40	1.30E-03	1.43E-02
RP11-303E16.9	ENSG00000278985	1.23	1.06	1.43	5.30E-03	3.96E-02
RP11-477I4.4	ENSG00000279140	1.23	1.07	1.43	4.10E-03	3.28E-02
RP1-178F15.5	ENSG00000271853	1.23	1.10	1.39	4.60E-04	6.67E-03
RP5-1057I20.2	ENSG00000257488	1.23	1.10	1.39	3.60E-04	5.54E-03
CTB-52I2.4	ENSG00000273654	1.23	1.15	1.33	2.20E-08	2.44E-06

FAM204CP	ENSG00000230902	1.23	1.11	1.37	1.40E-04	2.68E-03
CLSTN2-AS1	ENSG00000250433	1.23	1.10	1.38	3.60E-04	5.54E-03
RP11-43D4.2	ENSG00000258111	1.23	1.09	1.40	9.80E-04	1.19E-02
RP11-313D6.3	ENSG00000232470	1.23	1.08	1.41	2.40E-03	2.26E-02
CTD-2231E14.8	ENSG00000269243	1.23	1.07	1.43	5.00E-03	3.80E-02
KB-68A7.1	ENSG00000274225	1.23	1.11	1.37	1.00E-04	2.06E-03
RP11-49C9.2	ENSG00000183171	1.23	1.11	1.37	1.30E-04	2.53E-03
RP11-48B3.4	ENSG00000260317	1.23	1.14	1.33	2.10E-07	1.53E-05
RP11-146E23.2	ENSG00000253283	1.23	1.08	1.41	2.70E-03	2.44E-02
CTD-2095E4.4	ENSG00000280020	1.23	1.08	1.41	1.70E-03	1.74E-02
RP5-940J5.6	ENSG00000247853	1.23	1.06	1.43	6.10E-03	4.41E-02
CHCHD4P5	ENSG00000225222	1.23	1.06	1.43	5.70E-03	4.18E-02
AP000692.10	ENSG00000273199	1.23	1.07	1.42	3.40E-03	2.86E-02
RP11-686G8.1	ENSG00000238168	1.23	1.13	1.34	1.10E-06	5.53E-05
RP11-227D13.1	ENSG00000259705	1.23	1.09	1.40	1.00E-03	1.19E-02
RP11-1191J2.2	ENSG00000242686	1.23	1.10	1.38	3.50E-04	5.42E-03
OFD1P17	ENSG00000228212	1.23	1.08	1.40	1.70E-03	1.74E-02
C4B-AS1	ENSG00000229776	1.23	1.09	1.39	5.50E-04	7.70E-03
C4A-AS1	ENSG00000233627	1.23	1.09	1.39	5.50E-04	7.70E-03
RP4-646N3.1	ENSG00000235806	1.23	1.09	1.39	6.10E-04	8.37E-03
KB-1254G8.1	ENSG00000253385	1.23	1.07	1.42	3.50E-03	2.92E-02
RP11-196G18.24	ENSG00000272993	1.23	1.13	1.35	5.90E-06	2.08E-04
LSM12P1	ENSG00000232024	1.23	1.06	1.43	6.20E-03	4.46E-02
AHCYP7	ENSG00000259465	1.23	1.11	1.37	1.00E-04	2.06E-03
HNRNPRP1	ENSG00000223984	1.23	1.07	1.42	4.00E-03	3.22E-02
CH507-338C24.1	ENSG00000277991	1.23	1.07	1.41	3.30E-03	2.81E-02
RP11-386G11.10	ENSG00000258017	1.23	1.12	1.36	3.00E-05	7.90E-04
CTB-31O20.3	ENSG00000267007	1.23	1.10	1.38	3.90E-04	5.87E-03
CTD-3030D20.1	ENSG00000268747	1.23	1.08	1.40	1.80E-03	1.81E-02

MTND5P12	ENSG00000251544	1.23	1.12	1.34	6.40E-06	2.22E-04
RP5-1142A6.2	ENSG00000224888	1.23	1.10	1.37	1.50E-04	2.82E-03
Metazoa_SRP	ENSG00000277794	1.23	1.10	1.37	1.70E-04	3.10E-03
RP11-21K12.2	ENSG00000279500	1.23	1.09	1.38	6.60E-04	8.89E-03
RPL5P24	ENSG00000244052	1.23	1.09	1.39	8.30E-04	1.06E-02
RP11-297C4.3	ENSG00000260487	1.23	1.10	1.37	1.70E-04	3.10E-03
RP11-416I2.1	ENSG00000260328	1.23	1.08	1.40	2.40E-03	2.26E-02
HIST1H2BPS2	ENSG00000217646	1.23	1.11	1.36	8.90E-05	1.90E-03
RP11-140H17.2	ENSG00000274093	1.23	1.06	1.42	5.50E-03	4.07E-02
Metazoa_SRP	ENSG00000275586	1.23	1.10	1.38	4.00E-04	5.97E-03
TAGLN2P1	ENSG00000253676	1.23	1.09	1.39	9.70E-04	1.19E-02
RAI1-AS1	ENSG00000237328	1.23	1.07	1.41	3.30E-03	2.81E-02
RP11-34P13.15	ENSG00000268903	1.23	1.08	1.40	1.80E-03	1.81E-02
LINC00426	ENSG00000238121	1.23	1.08	1.40	1.80E-03	1.81E-02
RP11-307L3.4	ENSG00000233367	1.23	1.08	1.40	1.90E-03	1.88E-02
RP11-707G18.1	ENSG00000278743	1.23	1.12	1.35	1.60E-05	4.76E-04
RP1-40E16.12	ENSG00000272277	1.23	1.06	1.42	6.40E-03	4.55E-02
UNC93B6	ENSG00000255562	1.23	1.11	1.36	4.90E-05	1.17E-03
RP11-563N4.1	ENSG00000272716	1.23	1.07	1.41	3.40E-03	2.86E-02
GAPLINC	ENSG00000266835	1.23	1.09	1.39	9.30E-04	1.15E-02
RP11-109G23.3	ENSG00000260278	1.23	1.08	1.39	1.60E-03	1.66E-02
SRSF10P1	ENSG00000267717	1.23	1.08	1.40	2.20E-03	2.11E-02
RP11-471L13.3	ENSG00000263648	1.23	1.07	1.41	3.40E-03	2.86E-02
PRR34-AS1	ENSG00000241990	1.23	1.07	1.40	2.60E-03	2.38E-02
AC008132.15	ENSG00000182824	1.23	1.13	1.34	2.40E-06	1.00E-04
RPS3AP43	ENSG00000242661	1.23	1.09	1.38	7.10E-04	9.34E-03
RP11-364B14.3	ENSG00000230707	1.23	1.08	1.39	1.80E-03	1.81E-02
RP11-153M3.1	ENSG00000257576	1.23	1.14	1.32	5.10E-08	5.01E-06
RP5-1139B12.4	ENSG00000270110	1.23	1.09	1.38	7.30E-04	9.55E-03

RP1-117O3.2	ENSG00000236065	1.23	1.09	1.39	1.10E-03	1.27E-02
RP11-375N15.2	ENSG00000272267	1.23	1.07	1.40	2.60E-03	2.38E-02
AC002456.2	ENSG00000223969	1.23	1.16	1.30	1.40E-11	6.06E-09
RP11-537E18.1	ENSG00000237916	1.23	1.11	1.36	1.10E-04	2.24E-03
RP11-272L13.4	ENSG00000270911	1.23	1.09	1.38	6.50E-04	8.80E-03
RP11-779O18.1	ENSG00000253295	1.23	1.10	1.37	2.20E-04	3.79E-03
CTD-2184C24.2	ENSG00000254718	1.23	1.15	1.31	3.00E-10	6.71E-08
RP11-417O11.5	ENSG00000225761	1.23	1.11	1.36	9.70E-05	2.04E-03
RP11-454H13.1	ENSG00000243396	1.23	1.12	1.35	2.10E-05	5.94E-04
ARSD-AS1	ENSG00000229851	1.23	1.07	1.40	3.20E-03	2.75E-02
RPL7P60	ENSG00000214142	1.23	1.12	1.34	6.20E-06	2.17E-04
NEPNP	ENSG00000218233	1.23	1.06	1.41	5.80E-03	4.24E-02
RP11-71H17.1	ENSG00000242199	1.22	1.07	1.41	4.00E-03	3.22E-02
CH507-513H4.5	ENSG00000281383	1.22	1.12	1.33	3.30E-06	1.29E-04
SMCR2	ENSG00000223979	1.22	1.12	1.34	1.70E-05	5.03E-04
RP11-87G24.6	ENSG00000267521	1.22	1.14	1.31	6.40E-09	8.74E-07
RP11-234G16.5	ENSG00000275005	1.22	1.07	1.40	3.60E-03	2.97E-02
RP11-69H7.2	ENSG00000260660	1.22	1.11	1.35	4.90E-05	1.17E-03
PSMA6P1	ENSG00000215414	1.22	1.06	1.41	6.00E-03	4.35E-02
RP11-338N10.3	ENSG00000269978	1.22	1.11	1.35	3.40E-05	8.72E-04
RP11-673E1.1	ENSG00000251600	1.22	1.07	1.40	3.60E-03	2.97E-02
RP11-754B17.1	ENSG00000255158	1.22	1.06	1.41	5.70E-03	4.18E-02
RP4-641G12.3	ENSG00000238015	1.22	1.12	1.34	1.40E-05	4.30E-04
CTD-2349P21.3	ENSG00000280069	1.22	1.08	1.38	1.20E-03	1.35E-02
RP11-506H20.2	ENSG00000271410	1.22	1.10	1.36	3.10E-04	4.94E-03
RP11-521B24.3	ENSG00000251602	1.22	1.06	1.41	6.20E-03	4.46E-02
RP11-523O18.7	ENSG00000241577	1.22	1.12	1.33	3.80E-06	1.47E-04
RP11-131L23.1	ENSG00000223653	1.22	1.07	1.40	4.10E-03	3.28E-02
LINC00384	ENSG00000232117	1.22	1.06	1.41	5.70E-03	4.18E-02

RP11-56M3.1	ENSG00000234043	1.22	1.11	1.34	4.60E-05	1.12E-03
KRT18P57	ENSG00000215867	1.22	1.10	1.36	2.60E-04	4.33E-03
RP11-290L1.2	ENSG00000257839	1.22	1.09	1.36	3.30E-04	5.18E-03
TECRP1	ENSG00000235043	1.22	1.07	1.39	2.40E-03	2.26E-02
AC005822.1	ENSG00000235554	1.22	1.12	1.33	6.20E-06	2.17E-04
AC139099.5	ENSG00000262094	1.22	1.07	1.39	2.50E-03	2.34E-02
RP13-16H11.5	ENSG00000235843	1.22	1.06	1.40	4.50E-03	3.52E-02
RP1-27K12.4	ENSG00000249379	1.22	1.06	1.41	5.60E-03	4.13E-02
RPS2P35	ENSG00000238172	1.22	1.07	1.39	2.70E-03	2.44E-02
AC008132.13	ENSG00000161103	1.22	1.10	1.36	2.70E-04	4.42E-03
AC006427.2	ENSG00000248851	1.22	1.10	1.35	1.40E-04	2.68E-03
IGKV1OR1-1	ENSG00000276674	1.22	1.09	1.37	5.30E-04	7.49E-03
RP11-709D24.6	ENSG00000261442	1.22	1.05	1.41	7.30E-03	4.98E-02
PTPN2P1	ENSG00000228196	1.22	1.07	1.39	3.30E-03	2.81E-02
RP3-468O1.6	ENSG00000277558	1.22	1.06	1.40	4.80E-03	3.69E-02
Z69890.1	ENSG00000206168	1.22	1.06	1.41	6.70E-03	4.70E-02
RP11-769O8.1	ENSG00000266171	1.22	1.09	1.37	7.10E-04	9.34E-03
RP5-1042K10.10	ENSG00000229999	1.22	1.14	1.31	4.50E-08	4.49E-06
RP4-669L17.8	ENSG00000250575	1.22	1.07	1.39	2.90E-03	2.56E-02
MIR24-2	ENSG00000267519	1.22	1.10	1.35	9.60E-05	2.03E-03
NA	ENSG00000279866	1.22	1.06	1.40	5.00E-03	3.80E-02
RP11-488L18.1	ENSG00000214144	1.22	1.07	1.39	2.60E-03	2.38E-02
RPL12P29	ENSG00000233189	1.22	1.06	1.41	6.60E-03	4.66E-02
TUBBP5	ENSG00000159247	1.22	1.12	1.33	1.10E-05	3.50E-04
RP11-774O3.3	ENSG00000251615	1.22	1.06	1.40	5.70E-03	4.18E-02
RP11-1070N10.3	ENSG00000258572	1.22	1.07	1.39	3.40E-03	2.86E-02
MIR17HG	ENSG00000215417	1.22	1.13	1.31	4.10E-07	2.55E-05
RP11-10J21.4	ENSG00000253307	1.22	1.08	1.38	1.90E-03	1.88E-02
RP11-775J23.2	ENSG00000243508	1.22	1.12	1.32	4.40E-06	1.66E-04

PCAT1	ENSG00000253438	1.22	1.11	1.34	3.90E-05	9.85E-04
LINC01422	ENSG00000235271	1.22	1.08	1.37	1.50E-03	1.60E-02
RP13-93L13.1	ENSG00000225460	1.22	1.05	1.40	7.10E-03	4.89E-02
SEPT14P9	ENSG00000250210	1.22	1.07	1.38	2.10E-03	2.02E-02
MESTIT1	ENSG00000272701	1.22	1.09	1.36	4.20E-04	6.20E-03
AL133243.3	ENSG00000274159	1.22	1.09	1.36	4.90E-04	7.03E-03
PA2G4P2	ENSG00000235698	1.22	1.08	1.37	1.20E-03	1.35E-02
RPS17P13	ENSG00000224706	1.22	1.09	1.36	5.50E-04	7.70E-03
GS1-184P14.2	ENSG00000225071	1.22	1.13	1.31	2.00E-07	1.48E-05
RP11-480I12.10	ENSG00000260021	1.22	1.07	1.39	3.50E-03	2.92E-02
RP11-2C24.5	ENSG00000260082	1.22	1.10	1.34	6.10E-05	1.39E-03
MRPS31P2	ENSG00000232894	1.22	1.07	1.38	2.60E-03	2.38E-02
RP1-224A6.3	ENSG00000228397	1.21	1.07	1.38	3.30E-03	2.81E-02
RP11-946P6.6	ENSG00000277595	1.21	1.07	1.38	3.60E-03	2.97E-02
RP11-113D19.9	ENSG00000275980	1.21	1.09	1.36	6.80E-04	9.08E-03
DLEU2_6	ENSG00000275559	1.21	1.08	1.37	1.60E-03	1.66E-02
RP11-727F15.13	ENSG00000269463	1.21	1.05	1.40	7.10E-03	4.89E-02
PAICSP4	ENSG00000254244	1.21	1.08	1.36	1.10E-03	1.27E-02
RP11-1070N10.7	ENSG00000270038	1.21	1.06	1.40	6.40E-03	4.55E-02
RP11-303E16.2	ENSG00000261061	1.21	1.06	1.39	5.70E-03	4.18E-02
AF186192.6	ENSG00000263612	1.21	1.12	1.31	1.10E-06	5.53E-05
RP13-270P17.1	ENSG00000264235	1.21	1.08	1.36	7.70E-04	9.96E-03
AP004290.1	ENSG00000236583	1.21	1.08	1.36	1.20E-03	1.35E-02
RN7SL390P	ENSG00000241785	1.21	1.08	1.37	1.40E-03	1.51E-02
KARSP2	ENSG00000230371	1.21	1.12	1.32	5.60E-06	2.00E-04
CH507-254M2.2	ENSG00000276077	1.21	1.09	1.35	4.40E-04	6.44E-03
RP11-583F2.5	ENSG00000266598	1.21	1.06	1.38	3.70E-03	3.03E-02
RP11-554A11.9	ENSG00000259799	1.21	1.08	1.36	9.80E-04	1.19E-02
CTD-2270L9.4	ENSG00000260136	1.21	1.08	1.36	1.20E-03	1.35E-02

RP11-113C12.4	ENSG00000256552	1.21	1.09	1.34	2.40E-04	4.05E-03
RPL26P35	ENSG00000244229	1.21	1.10	1.34	1.70E-04	3.10E-03
RP11-75C10.6	ENSG00000279801	1.21	1.06	1.39	5.90E-03	4.30E-02
RP11-419L20.2	ENSG00000254185	1.21	1.07	1.38	3.20E-03	2.75E-02
RP11-48B3.3	ENSG00000254162	1.21	1.13	1.30	1.10E-07	9.27E-06
GAS8-AS1	ENSG00000221819	1.21	1.08	1.36	1.50E-03	1.60E-02
AGGF1P1	ENSG00000214273	1.21	1.07	1.38	3.00E-03	2.62E-02
RPS2P41	ENSG00000244060	1.21	1.11	1.32	1.10E-05	3.50E-04
RP11-99A14.1	ENSG00000253273	1.21	1.06	1.38	3.90E-03	3.16E-02
RP13-452N2.1	ENSG00000242048	1.21	1.10	1.34	1.40E-04	2.68E-03
HCG17	ENSG00000270604	1.21	1.12	1.32	5.40E-06	1.95E-04
RP11-138A9.1	ENSG00000271204	1.21	1.07	1.37	2.60E-03	2.38E-02
CTA-246H3.12	ENSG00000272942	1.21	1.12	1.30	5.00E-07	2.94E-05
RP11-40E6.2	ENSG00000275248	1.21	1.09	1.34	3.30E-04	5.18E-03
RP5-1050D4.3	ENSG00000262429	1.21	1.09	1.35	4.20E-04	6.20E-03
AC011406.2	ENSG00000248696	1.21	1.08	1.36	1.00E-03	1.19E-02
RN7SL395P	ENSG00000244307	1.21	1.10	1.34	1.30E-04	2.53E-03
RP11-191L17.1	ENSG00000272663	1.21	1.06	1.38	3.60E-03	2.97E-02
RP11-380L11.4	ENSG00000270028	1.21	1.07	1.36	1.70E-03	1.74E-02
DPYD-AS1	ENSG00000232878	1.21	1.08	1.36	1.00E-03	1.19E-02
CTC-421K24.1	ENSG00000275839	1.21	1.05	1.39	7.30E-03	4.98E-02
CTC-463A16.1	ENSG00000280047	1.21	1.08	1.35	7.90E-04	1.02E-02
GGT3P	ENSG00000197421	1.21	1.12	1.31	1.50E-06	6.88E-05
MGC45922	ENSG00000180279	1.21	1.06	1.38	3.60E-03	2.97E-02
IQSEC3P1	ENSG00000256902	1.21	1.06	1.38	4.90E-03	3.75E-02
RP11-247I13.3	ENSG00000214093	1.21	1.07	1.36	1.90E-03	1.88E-02
RPS7P4	ENSG00000229133	1.21	1.07	1.36	1.60E-03	1.66E-02
SMPD5	ENSG00000204791	1.21	1.12	1.30	3.50E-07	2.24E-05
RP11-474P2.2	ENSG00000258096	1.21	1.06	1.38	5.00E-03	3.80E-02

RP5-827C21.1	ENSG00000235605	1.21	1.12	1.30	5.10E-07	2.98E-05
AP001610.5	ENSG00000228318	1.21	1.11	1.31	5.10E-06	1.86E-04
RP11-282I1.1	ENSG00000230131	1.21	1.05	1.39	7.30E-03	4.98E-02
RUNDC3A-AS1	ENSG00000267750	1.21	1.12	1.31	1.50E-06	6.88E-05
RP11-58H15.3	ENSG00000250540	1.21	1.08	1.35	1.10E-03	1.27E-02
RP11-274B18.4	ENSG00000226337	1.21	1.06	1.37	3.70E-03	3.03E-02
RP11-463J10.4	ENSG00000258854	1.21	1.07	1.36	2.20E-03	2.11E-02
RP11-354E23.3	ENSG00000280166	1.21	1.07	1.36	2.20E-03	2.11E-02
RP11-109P14.8	ENSG00000235673	1.21	1.08	1.35	1.20E-03	1.35E-02
PCDH9-AS3	ENSG00000225263	1.21	1.06	1.38	5.80E-03	4.24E-02
RP11-54O7.18	ENSG00000273443	1.21	1.08	1.36	1.30E-03	1.43E-02
RP11-687E1.2	ENSG00000276174	1.21	1.07	1.37	2.70E-03	2.44E-02
EFCAB14-AS1	ENSG00000228237	1.21	1.06	1.38	5.30E-03	3.96E-02
AP001631.10	ENSG00000228120	1.21	1.07	1.37	2.90E-03	2.56E-02
CH507-152C13.6	ENSG00000278927	1.21	1.07	1.37	2.90E-03	2.56E-02
RP11-127L20.3	ENSG00000228261	1.21	1.06	1.38	5.50E-03	4.07E-02
RP11-61L19.3	ENSG00000273352	1.21	1.07	1.36	2.00E-03	1.95E-02
HAR1B	ENSG00000231133	1.21	1.10	1.33	1.30E-04	2.53E-03
RP11-388B24.4	ENSG00000235377	1.21	1.13	1.29	1.70E-08	1.94E-06
RP11-377G16.2	ENSG00000248719	1.21	1.10	1.33	1.50E-04	2.82E-03
RN7SL344P	ENSG00000241395	1.21	1.06	1.38	5.20E-03	3.91E-02
AC074183.3	ENSG00000280325	1.21	1.10	1.33	1.20E-04	2.39E-03
RP11-231I16.1	ENSG00000257279	1.21	1.09	1.34	3.50E-04	5.42E-03
RP11-15M15.1	ENSG00000223492	1.21	1.06	1.37	4.50E-03	3.52E-02
LINC00152	ENSG00000222041	1.21	1.07	1.36	2.10E-03	2.02E-02
VN1R80P	ENSG00000268598	1.21	1.08	1.35	1.30E-03	1.43E-02
LOH12CR2	ENSG00000205791	1.21	1.09	1.33	2.50E-04	4.18E-03
RP11-282O18.3	ENSG00000235423	1.21	1.06	1.37	5.30E-03	3.96E-02
RP11-640N11.2	ENSG00000250493	1.21	1.09	1.33	2.30E-04	3.92E-03

NA	ENSG00000279424	1.21	1.05	1.38	6.90E-03	4.78E-02
RP11-397P13.6	ENSG00000227417	1.21	1.10	1.33	1.30E-04	2.53E-03
IGLC5	ENSG00000254030	1.21	1.07	1.36	3.00E-03	2.62E-02
RP11-759F5.1	ENSG00000236327	1.21	1.11	1.30	2.70E-06	1.11E-04
RP11-53I6.2	ENSG00000263917	1.20	1.08	1.35	1.30E-03	1.43E-02
TBL1XR1-AS1	ENSG00000231310	1.20	1.06	1.37	5.20E-03	3.91E-02
CTD-2207P18.2	ENSG00000258976	1.20	1.08	1.34	8.70E-04	1.10E-02
COL6A4P2	ENSG00000228252	1.20	1.08	1.34	9.20E-04	1.14E-02
RN7SKP23	ENSG00000280039	1.20	1.07	1.35	1.70E-03	1.74E-02
AC068657.2	ENSG00000223908	1.20	1.07	1.36	2.60E-03	2.38E-02
GRK5-IT1	ENSG00000228485	1.20	1.10	1.31	2.60E-05	7.06E-04
CTD-2538C1.2	ENSG00000267475	1.20	1.10	1.32	9.10E-05	1.94E-03
RP11-14I17.3	ENSG00000254362	1.20	1.08	1.34	9.60E-04	1.18E-02
RP11-265N6.2	ENSG00000261822	1.20	1.06	1.36	3.70E-03	3.03E-02
RP11-543B16.2	ENSG00000226986	1.20	1.06	1.36	3.00E-03	2.62E-02
LINC00658	ENSG00000226995	1.20	1.14	1.27	2.90E-11	1.08E-08
RP4-584D14.7	ENSG00000261305	1.20	1.06	1.36	3.60E-03	2.97E-02
LINC00891	ENSG00000281852	1.20	1.08	1.34	1.00E-03	1.19E-02
RP4-635E18.6	ENSG00000230337	1.20	1.07	1.36	2.90E-03	2.56E-02
AC006372.4	ENSG00000234210	1.20	1.05	1.37	6.30E-03	4.52E-02
GGTLC5P	ENSG00000276160	1.20	1.10	1.31	2.50E-05	6.85E-04
RP11-563J2.3	ENSG00000212743	1.20	1.09	1.32	2.00E-04	3.52E-03
RP11-96D1.8	ENSG00000279649	1.20	1.06	1.36	3.10E-03	2.68E-02
KYNUP2	ENSG00000265746	1.20	1.08	1.33	4.60E-04	6.67E-03
RP11-618G20.1	ENSG00000258964	1.20	1.12	1.29	3.00E-07	1.98E-05
MTND1P32	ENSG00000232282	1.20	1.08	1.34	9.60E-04	1.18E-02
CFLAR-AS1	ENSG00000226312	1.20	1.07	1.35	2.30E-03	2.19E-02
AC064852.4	ENSG00000241409	1.20	1.07	1.35	1.60E-03	1.66E-02
RNASEH1P1	ENSG00000265790	1.20	1.08	1.34	9.90E-04	1.19E-02

RP11-723O4.9	ENSG00000261159	1.20	1.09	1.32	2.70E-04	4.42E-03
RP11-20E24.1	ENSG00000257526	1.20	1.07	1.34	1.50E-03	1.60E-02
HK2P1	ENSG00000228612	1.20	1.06	1.36	3.20E-03	2.75E-02
RP3-508I15.14	ENSG00000225450	1.20	1.05	1.37	7.30E-03	4.98E-02
RP11-697N18.2	ENSG00000254065	1.20	1.07	1.34	1.20E-03	1.35E-02
TTC4P1	ENSG00000221971	1.20	1.09	1.33	3.60E-04	5.54E-03
CTD-2201I18.1	ENSG00000249825	1.20	1.08	1.33	7.20E-04	9.46E-03
RP1-137D17.1	ENSG00000226194	1.20	1.11	1.30	5.60E-06	2.00E-04
BRWD1-AS2	ENSG00000255568	1.20	1.07	1.34	1.30E-03	1.43E-02
RABGAP1L-IT1	ENSG00000223525	1.20	1.10	1.31	3.50E-05	8.94E-04
RP11-338N10.2	ENSG00000270035	1.20	1.12	1.29	3.40E-07	2.20E-05
AL590762.10	ENSG00000229601	1.20	1.05	1.37	7.20E-03	4.94E-02
ZFY-AS1	ENSG00000233070	1.20	1.08	1.33	6.10E-04	8.37E-03
AC009506.2	ENSG00000225369	1.20	1.08	1.33	5.00E-04	7.14E-03
RP11-380G5.2	ENSG00000224745	1.20	1.05	1.36	6.00E-03	4.35E-02
CTD-2102P23.1	ENSG00000255875	1.20	1.05	1.36	5.40E-03	4.01E-02
MGAT4EP	ENSG00000184774	1.20	1.10	1.31	5.80E-05	1.34E-03
RP11-119H12.4	ENSG00000234841	1.20	1.07	1.34	1.50E-03	1.60E-02
CTA-246H3.8	ENSG00000230637	1.20	1.07	1.34	1.70E-03	1.74E-02
INGX	ENSG00000243468	1.20	1.05	1.36	5.60E-03	4.13E-02
FAUP1	ENSG00000235297	1.20	1.14	1.26	1.20E-12	8.20E-10
CTC-246B18.8	ENSG00000268262	1.20	1.07	1.34	1.90E-03	1.88E-02
OR7E36P	ENSG00000205240	1.20	1.13	1.26	8.30E-11	2.39E-08
RP11-44N11.2	ENSG00000272384	1.20	1.11	1.29	3.00E-06	1.21E-04
RP11-211C9.1	ENSG00000254367	1.20	1.06	1.35	4.00E-03	3.22E-02
AC003989.4	ENSG00000227948	1.20	1.05	1.36	5.90E-03	4.30E-02
RP11-354P11.8	ENSG00000266987	1.20	1.05	1.36	6.50E-03	4.60E-02
FAM103A2P	ENSG00000235272	1.20	1.11	1.28	5.80E-07	3.30E-05
RP11-503N18.5	ENSG00000251229	1.20	1.09	1.31	1.80E-04	3.24E-03

CTB-61M7.2	ENSG00000268734	1.20	1.08	1.33	9.60E-04	1.18E-02
RP11-330C7.3	ENSG00000225505	1.20	1.05	1.36	7.20E-03	4.94E-02
CTA-992D9.11	ENSG00000279440	1.20	1.11	1.29	2.60E-06	1.08E-04
RP1-102E24.8	ENSG00000256433	1.20	1.08	1.33	7.10E-04	9.34E-03
WDR86-AS1	ENSG00000243836	1.20	1.14	1.26	7.40E-12	3.56E-09
RP11-392A14.8	ENSG00000279489	1.19	1.06	1.35	4.80E-03	3.69E-02
RP11-2E11.6	ENSG00000270823	1.19	1.05	1.35	5.40E-03	4.01E-02
RP11-440D17.3	ENSG00000272913	1.19	1.06	1.34	3.00E-03	2.62E-02
DNM1P35	ENSG00000246877	1.19	1.09	1.31	2.00E-04	3.52E-03
CTC-250I14.6	ENSG00000267598	1.19	1.06	1.35	5.00E-03	3.80E-02
MYL12BP2	ENSG00000227765	1.19	1.10	1.29	1.30E-05	4.01E-04
CTD-2003C8.2	ENSG00000250041	1.19	1.09	1.31	1.20E-04	2.39E-03
LINC00506	ENSG00000281392	1.19	1.08	1.32	6.60E-04	8.89E-03
AC007349.5	ENSG00000235728	1.19	1.07	1.33	1.60E-03	1.66E-02
RP11-843B15.4	ENSG00000277342	1.19	1.06	1.34	3.50E-03	2.92E-02
RP11-12M9.3	ENSG00000237214	1.19	1.08	1.32	6.50E-04	8.80E-03
ADAMTS7P4	ENSG00000218052	1.19	1.05	1.35	5.30E-03	3.96E-02
RP11-6O2.4	ENSG00000261054	1.19	1.09	1.30	1.00E-04	2.06E-03
TCAM1P	ENSG00000240280	1.19	1.09	1.31	2.70E-04	4.42E-03
RPS15AP12	ENSG00000232134	1.19	1.06	1.34	3.20E-03	2.75E-02
NA	ENSG00000280874	1.19	1.12	1.27	8.60E-08	7.65E-06
NA	ENSG00000281134	1.19	1.12	1.27	8.60E-08	7.65E-06
KB-173C10.1	ENSG00000253842	1.19	1.10	1.29	1.00E-05	3.23E-04
ATP1B3-AS1	ENSG00000244124	1.19	1.08	1.32	6.30E-04	8.58E-03
RP11-818O24.2	ENSG00000280408	1.19	1.05	1.35	5.50E-03	4.07E-02
MIR9-3HG	ENSG00000255571	1.19	1.07	1.33	1.90E-03	1.88E-02
RN7SL600P	ENSG00000274963	1.19	1.09	1.31	2.40E-04	4.05E-03
POM121L7	ENSG00000239511	1.19	1.10	1.29	2.00E-05	5.77E-04
AD000864.6	ENSG00000280194	1.19	1.09	1.31	2.40E-04	4.05E-03

HSPD1P1	ENSG00000213430	1.19	1.06	1.34	3.50E-03	2.92E-02
RP11-451H23.1	ENSG00000250749	1.19	1.07	1.32	9.60E-04	1.18E-02
RP1-212P9.3	ENSG00000233427	1.19	1.05	1.35	5.10E-03	3.86E-02
CTB-139P11.2	ENSG00000279996	1.19	1.08	1.32	8.10E-04	1.04E-02
RP11-357P18.2	ENSG00000274245	1.19	1.08	1.31	4.40E-04	6.44E-03
RP11-820K3.2	ENSG00000225349	1.19	1.06	1.34	3.10E-03	2.68E-02
RP11-713D19.1	ENSG00000273233	1.19	1.06	1.33	2.80E-03	2.50E-02
AP000487.4	ENSG00000254495	1.19	1.06	1.33	2.60E-03	2.38E-02
RP11-530A18.1	ENSG00000220685	1.19	1.06	1.34	3.00E-03	2.62E-02
RP11-533E19.2	ENSG00000261831	1.19	1.05	1.35	6.00E-03	4.35E-02
ATP2A1-AS1	ENSG00000260442	1.19	1.07	1.32	9.70E-04	1.19E-02
RP11-138A9.2	ENSG00000273319	1.19	1.05	1.34	4.70E-03	3.64E-02
CTB-55O6.4	ENSG00000267670	1.19	1.06	1.33	2.40E-03	2.26E-02
RP11-497H17.1	ENSG00000262663	1.19	1.14	1.24	0.00E+00	0.00E+00
RMRP	ENSG00000277027	1.19	1.05	1.35	5.80E-03	4.24E-02
CDIPT-AS1	ENSG00000214725	1.19	1.09	1.30	1.40E-04	2.68E-03
RN7SL8P	ENSG00000243352	1.19	1.09	1.30	1.10E-04	2.24E-03
RP11-295B17.6	ENSG00000271437	1.19	1.07	1.32	8.90E-04	1.12E-02
RP5-1073O3.2	ENSG00000231128	1.19	1.12	1.27	8.60E-08	7.65E-06
TUBB8P7	ENSG00000261812	1.19	1.05	1.34	4.70E-03	3.64E-02
RP11-709D24.8	ENSG00000278434	1.19	1.06	1.33	2.50E-03	2.34E-02
DENND5B-AS1	ENSG00000255867	1.19	1.05	1.34	4.80E-03	3.69E-02
RP11-1100L3.8	ENSG00000259884	1.19	1.05	1.34	4.70E-03	3.64E-02
AC055764.1	ENSG00000234136	1.19	1.06	1.33	2.70E-03	2.44E-02
RP5-965G21.4	ENSG00000274414	1.19	1.10	1.28	3.30E-06	1.29E-04
POM121L9P	ENSG00000128262	1.19	1.08	1.30	3.60E-04	5.54E-03
MIR3945HG	ENSG00000251230	1.19	1.09	1.30	1.70E-04	3.10E-03
AC067945.4	ENSG00000231858	1.19	1.07	1.31	8.40E-04	1.07E-02
AC004987.9	ENSG00000233225	1.19	1.06	1.33	3.80E-03	3.10E-02

RP11-354B3.1	ENSG00000258632	1.19	1.06	1.33	3.80E-03	3.10E-02
HNRNPA3P2	ENSG00000227688	1.18	1.06	1.33	3.40E-03	2.86E-02
SRP9P1	ENSG00000180581	1.18	1.09	1.29	5.80E-05	1.34E-03
RP11-388M20.6	ENSG00000260304	1.18	1.08	1.30	2.70E-04	4.42E-03
RN7SL417P	ENSG00000244056	1.18	1.08	1.30	4.30E-04	6.33E-03
RP11-303E16.5	ENSG00000261141	1.18	1.10	1.27	2.00E-06	8.71E-05
RP5-1033E15.3	ENSG00000279642	1.18	1.06	1.32	2.10E-03	2.02E-02
MAFA-AS1	ENSG00000254338	1.18	1.06	1.32	2.40E-03	2.26E-02
RP11-603B24.2	ENSG00000259098	1.18	1.08	1.30	3.80E-04	5.76E-03
RP11-350N15.5	ENSG00000272092	1.18	1.07	1.31	1.20E-03	1.35E-02
LINC00452	ENSG00000229373	1.18	1.11	1.26	2.20E-07	1.60E-05
RP11-611O2.1	ENSG00000256325	1.18	1.09	1.29	7.50E-05	1.66E-03
AC019186.1	ENSG00000234584	1.18	1.07	1.31	1.10E-03	1.27E-02
RP11-266J6.2	ENSG00000269886	1.18	1.05	1.34	6.90E-03	4.78E-02
RP11-532F6.3	ENSG00000272463	1.18	1.05	1.34	6.70E-03	4.70E-02
LINC00942	ENSG00000249628	1.18	1.09	1.28	6.50E-05	1.46E-03
RP11-426D19.1	ENSG00000279555	1.18	1.05	1.33	6.60E-03	4.66E-02
CITF22-92A6.2	ENSG00000280424	1.18	1.05	1.33	5.00E-03	3.80E-02
AMZ2P2	ENSG00000219249	1.18	1.06	1.32	3.10E-03	2.68E-02
RP11-452J21.2	ENSG00000249234	1.18	1.05	1.33	5.20E-03	3.91E-02
RP11-290F24.6	ENSG00000267940	1.18	1.06	1.31	2.10E-03	2.02E-02
RP4-794I6.4	ENSG00000277287	1.18	1.06	1.31	2.10E-03	2.02E-02
NUDT16P1	ENSG00000246082	1.18	1.06	1.31	2.00E-03	1.95E-02
CTA-384D8.34	ENSG00000273272	1.18	1.06	1.32	3.40E-03	2.86E-02
RP11-12A20.7	ENSG00000274911	1.18	1.06	1.31	1.80E-03	1.81E-02
RP11-571M6.18	ENSG00000269903	1.18	1.05	1.32	4.40E-03	3.47E-02
CTB-31O20.9	ENSG00000267232	1.18	1.08	1.29	1.30E-04	2.53E-03
RP11-219B4.7	ENSG00000260493	1.18	1.09	1.27	1.60E-05	4.76E-04
CCNJP2	ENSG00000223896	1.18	1.06	1.32	3.60E-03	2.97E-02

ZNF847P	ENSG00000215812	1.18	1.06	1.32	3.30E-03	2.81E-02
RP4-752I6.1	ENSG00000241169	1.18	1.06	1.31	2.40E-03	2.26E-02
LINC00540	ENSG00000276476	1.18	1.09	1.28	5.70E-05	1.33E-03
RP11-94H18.1	ENSG00000248964	1.18	1.08	1.29	2.80E-04	4.55E-03
AP001442.2	ENSG00000233783	1.18	1.06	1.31	1.60E-03	1.66E-02
RP5-937E21.8	ENSG00000225261	1.18	1.12	1.24	3.70E-11	1.30E-08
RP11-401P9.1	ENSG00000260029	1.18	1.06	1.31	2.90E-03	2.56E-02
UBE2R2-AS1	ENSG00000235481	1.18	1.05	1.32	4.50E-03	3.52E-02
RP13-228J13.5	ENSG00000230578	1.18	1.07	1.30	1.40E-03	1.51E-02
SNORA46	ENSG00000207493	1.18	1.07	1.30	7.10E-04	9.34E-03
LINC01284	ENSG00000230317	1.18	1.05	1.32	4.90E-03	3.75E-02
RN7SL209P	ENSG00000240927	1.18	1.05	1.32	3.80E-03	3.10E-02
RP13-1056D16.2	ENSG00000244730	1.18	1.10	1.26	4.10E-06	1.57E-04
RP11-13P5.1	ENSG00000224478	1.18	1.05	1.32	5.10E-03	3.86E-02
CTD-2236F14.1	ENSG00000249713	1.18	1.08	1.29	2.80E-04	4.55E-03
DRAIC	ENSG00000245750	1.18	1.09	1.27	2.50E-05	6.85E-04
MIR3142HG	ENSG00000253522	1.18	1.06	1.31	2.70E-03	2.44E-02
IGKV2-29	ENSG00000253998	1.18	1.14	1.21	0.00E+00	0.00E+00
YBX1P3	ENSG00000240002	1.18	1.05	1.32	6.50E-03	4.60E-02
RP11-862L9.3	ENSG00000266844	1.18	1.07	1.29	6.80E-04	9.08E-03
VN1R82P	ENSG00000268995	1.18	1.05	1.31	4.50E-03	3.52E-02
CTC-205M6.5	ENSG00000260841	1.18	1.05	1.31	3.70E-03	3.03E-02
IFNWP9	ENSG00000226597	1.18	1.07	1.30	1.20E-03	1.35E-02
RP11-656D10.7	ENSG00000279667	1.18	1.10	1.25	3.60E-07	2.29E-05
RP11-567M16.1	ENSG00000267287	1.17	1.05	1.32	5.40E-03	4.01E-02
MTCYBP28	ENSG00000260161	1.17	1.07	1.28	3.90E-04	5.87E-03
AC073115.7	ENSG00000229628	1.17	1.06	1.30	1.50E-03	1.60E-02
LINC01128	ENSG00000228794	1.17	1.11	1.24	3.50E-09	5.54E-07
RP11-216N14.7	ENSG00000223599	1.17	1.05	1.32	5.70E-03	4.18E-02

PDPK2P	ENSG00000205918	1.17	1.06	1.30	1.40E-03	1.51E-02
RP11-167N4.4	ENSG00000256723	1.17	1.07	1.28	3.30E-04	5.18E-03
RP11-807E13.3	ENSG00000267656	1.17	1.07	1.29	8.60E-04	1.09E-02
RP11-63A11.1	ENSG00000250781	1.17	1.10	1.25	1.10E-06	5.53E-05
RP11-12A20.4	ENSG00000278134	1.17	1.05	1.31	6.00E-03	4.35E-02
RP11-890B15.2	ENSG00000254842	1.17	1.07	1.28	7.00E-04	9.25E-03
AC007283.4	ENSG00000235579	1.17	1.07	1.29	1.10E-03	1.27E-02
LINC00640	ENSG00000258479	1.17	1.11	1.23	3.80E-09	5.67E-07
RNVU1-3	ENSG00000201183	1.17	1.08	1.27	6.30E-05	1.42E-03
RP13-870H17.3	ENSG00000254872	1.17	1.10	1.25	1.30E-06	6.20E-05
RP11-30K9.5	ENSG00000259353	1.17	1.09	1.26	9.40E-06	3.07E-04
RP11-182J1.14	ENSG00000259683	1.17	1.06	1.30	2.30E-03	2.19E-02
RP11-665C16.6	ENSG00000258413	1.17	1.06	1.29	1.60E-03	1.66E-02
LINC01307	ENSG00000231671	1.17	1.09	1.26	5.00E-05	1.19E-03
RP5-891H21.5	ENSG00000271329	1.17	1.08	1.27	1.00E-04	2.06E-03
RP11-255G12.2	ENSG00000258942	1.17	1.05	1.31	4.60E-03	3.59E-02
RPL35P1	ENSG00000237991	1.17	1.07	1.29	9.40E-04	1.16E-02
RP11-218E20.3	ENSG00000258711	1.17	1.08	1.27	8.30E-05	1.81E-03
RP11-641D5.1	ENSG00000213178	1.17	1.05	1.31	6.20E-03	4.46E-02
RP11-260E18.1	ENSG00000246214	1.17	1.07	1.29	1.00E-03	1.19E-02
RP11-67L14.1	ENSG00000280228	1.17	1.12	1.22	2.70E-13	2.19E-10
LETM1P2	ENSG00000268660	1.17	1.05	1.30	4.50E-03	3.52E-02
RN7SL692P	ENSG00000239710	1.17	1.05	1.30	3.50E-03	2.92E-02
RNU5E-1	ENSG00000199347	1.17	1.07	1.28	8.70E-04	1.10E-02
RP4-693M11.3	ENSG00000258660	1.17	1.07	1.28	8.20E-04	1.05E-02
AP000240.9	ENSG00000273017	1.17	1.05	1.30	3.80E-03	3.10E-02
RP11-56B16.4	ENSG00000259185	1.17	1.10	1.24	3.80E-07	2.37E-05
RP11-29H23.6	ENSG00000223503	1.17	1.09	1.25	3.60E-06	1.40E-04
LINC01251	ENSG00000233776	1.17	1.06	1.29	1.30E-03	1.43E-02

LA16c-444G7.2	ENSG00000260420	1.17	1.06	1.29	2.80E-03	2.50E-02
HLA-U	ENSG00000228078	1.17	1.08	1.27	1.20E-04	2.39E-03
DLEU2_6	ENSG00000276884	1.17	1.06	1.28	1.20E-03	1.35E-02
LDHAL6DP	ENSG00000250257	1.17	1.05	1.29	2.80E-03	2.50E-02
RN7SL42P	ENSG00000263999	1.17	1.06	1.29	2.40E-03	2.26E-02
CTC-510F12.7	ENSG00000273733	1.17	1.05	1.29	2.80E-03	2.50E-02
RP11-394O4.3	ENSG00000253865	1.17	1.06	1.29	1.60E-03	1.66E-02
AC011515.2	ENSG00000225370	1.17	1.05	1.30	5.30E-03	3.96E-02
RP11-324H9.1	ENSG00000280049	1.17	1.06	1.28	1.00E-03	1.19E-02
CTC-137K3.1	ENSG00000270137	1.17	1.06	1.29	2.50E-03	2.34E-02
RPS20P22	ENSG00000239218	1.17	1.05	1.29	2.60E-03	2.38E-02
RP11-566K11.7	ENSG00000267048	1.17	1.05	1.30	4.80E-03	3.69E-02
AC007389.3	ENSG00000235725	1.17	1.09	1.24	2.80E-06	1.14E-04
RP11-638I2.10	ENSG00000258581	1.17	1.08	1.26	6.10E-05	1.39E-03
RP11-506K6.4	ENSG00000272320	1.16	1.06	1.28	1.30E-03	1.43E-02
RP1-228H13.5	ENSG00000260920	1.16	1.09	1.25	1.60E-05	4.76E-04
CTD-2369P2.8	ENSG00000267607	1.16	1.06	1.27	9.60E-04	1.18E-02
LINC00880	ENSG00000243629	1.16	1.06	1.28	1.90E-03	1.88E-02
RP1-34B20.4	ENSG00000217275	1.16	1.09	1.25	9.80E-06	3.19E-04
NA	ENSG00000226958	1.16	1.10	1.23	2.90E-08	3.09E-06
LINC00671	ENSG00000213373	1.16	1.04	1.30	6.60E-03	4.66E-02
RP1-149L1.1	ENSG00000253809	1.16	1.04	1.30	6.10E-03	4.41E-02
YWHAEP1	ENSG00000232727	1.16	1.07	1.27	6.60E-04	8.89E-03
RNVU1-4	ENSG00000277610	1.16	1.06	1.28	1.30E-03	1.43E-02
XPOTP1	ENSG00000214185	1.16	1.06	1.28	1.90E-03	1.88E-02
RP11-342M1.7	ENSG00000233708	1.16	1.10	1.23	4.50E-07	2.70E-05
RP11-401P9.4	ENSG00000261685	1.16	1.06	1.28	1.70E-03	1.74E-02
RP11-89H19.1	ENSG00000205537	1.16	1.05	1.29	4.50E-03	3.52E-02
HNRNPLP1	ENSG00000233503	1.16	1.07	1.26	2.70E-04	4.42E-03

RP11-163F15.1	ENSG00000203434	1.16	1.04	1.29	6.00E-03	4.35E-02
KRT8P20	ENSG00000227404	1.16	1.09	1.24	2.00E-06	8.71E-05
RP11-723O4.3	ENSG00000250796	1.16	1.10	1.23	5.40E-07	3.11E-05
USP8P1	ENSG00000214892	1.16	1.09	1.24	2.10E-06	9.00E-05
AC018693.6	ENSG00000225284	1.16	1.04	1.29	7.10E-03	4.89E-02
RP11-713P17.3	ENSG00000204241	1.16	1.04	1.29	5.80E-03	4.24E-02
RP11-87C12.5	ENSG00000255856	1.16	1.07	1.26	2.00E-04	3.52E-03
RP11-425A6.5	ENSG00000273312	1.16	1.07	1.26	2.70E-04	4.42E-03
MTND5P32	ENSG00000259379	1.16	1.09	1.24	8.90E-06	2.94E-04
RP11-145E17.2	ENSG00000223729	1.16	1.06	1.27	1.10E-03	1.27E-02
RP11-212P7.1	ENSG00000213280	1.16	1.05	1.28	3.30E-03	2.81E-02
EIF4BP8	ENSG00000243918	1.16	1.09	1.23	1.00E-06	5.15E-05
NIPA2P1	ENSG00000225843	1.16	1.10	1.23	1.20E-07	9.92E-06
LHFPL3-AS2	ENSG00000225329	1.16	1.11	1.21	1.90E-10	4.48E-08
AC024560.2	ENSG00000236833	1.16	1.08	1.24	2.20E-05	6.14E-04
ATP6V1E1P1	ENSG00000225099	1.16	1.09	1.23	4.70E-06	1.74E-04
RP11-973H7.1	ENSG00000260302	1.16	1.11	1.21	2.90E-10	6.60E-08
RP11-82O18.2	ENSG00000261523	1.16	1.05	1.28	2.60E-03	2.38E-02
RP11-719K4.6	ENSG00000261695	1.16	1.05	1.28	2.60E-03	2.38E-02
AC097495.3	ENSG00000228329	1.16	1.08	1.25	8.40E-05	1.83E-03
ZNF680P1	ENSG00000228014	1.16	1.06	1.26	7.80E-04	1.01E-02
RP11-554A11.8	ENSG00000261070	1.16	1.06	1.27	1.30E-03	1.43E-02
RP11-862G15.2	ENSG00000258499	1.16	1.06	1.27	1.30E-03	1.43E-02
LINC00567	ENSG00000259831	1.16	1.07	1.25	1.20E-04	2.39E-03
RP11-23F23.2	ENSG00000254480	1.16	1.09	1.23	4.60E-07	2.75E-05
RP1-68D18.4	ENSG00000255443	1.16	1.09	1.23	2.30E-06	9.76E-05
AC007050.17	ENSG00000236003	1.16	1.05	1.27	2.70E-03	2.44E-02
RP11-252C15.1	ENSG00000254813	1.16	1.04	1.28	6.50E-03	4.60E-02
RP11-186F10.2	ENSG00000257761	1.16	1.09	1.23	4.50E-06	1.68E-04

AP000223.42	ENSG00000260583	1.16	1.11	1.21	8.80E-11	2.48E-08
OR2B7P	ENSG00000187763	1.16	1.07	1.25	3.40E-04	5.30E-03
IGKV1OR2-1	ENSG00000235235	1.16	1.07	1.25	2.70E-04	4.42E-03
RP11-973H7.4	ENSG00000267654	1.15	1.11	1.20	2.70E-12	1.52E-09
RP11-568N6.1	ENSG00000260101	1.15	1.04	1.28	5.20E-03	3.91E-02
RP5-1009E24.9	ENSG00000274949	1.15	1.05	1.26	1.70E-03	1.74E-02
RP1-137D17.2	ENSG00000272848	1.15	1.09	1.22	1.80E-06	7.97E-05
LINC00868	ENSG00000267535	1.15	1.12	1.19	0.00E+00	0.00E+00
RP6-91H8.3	ENSG00000269927	1.15	1.07	1.24	2.70E-04	4.42E-03
RP11-345P4.10	ENSG00000272004	1.15	1.05	1.26	1.80E-03	1.81E-02
CTC-559E9.9	ENSG00000271499	1.15	1.09	1.22	5.20E-07	3.03E-05
RP11-701H16.4	ENSG00000266954	1.15	1.05	1.26	1.90E-03	1.88E-02
RP11-338E21.1	ENSG00000256670	1.15	1.05	1.27	3.80E-03	3.10E-02
FIGNL2	ENSG00000261308	1.15	1.08	1.24	6.20E-05	1.41E-03
RP1-225E12.3	ENSG00000272446	1.15	1.04	1.27	5.20E-03	3.91E-02
RP11-92G12.3	ENSG00000260088	1.15	1.04	1.28	6.90E-03	4.78E-02
RP11-618L22.1	ENSG00000274723	1.15	1.05	1.26	2.90E-03	2.56E-02
RP1-78O14.1	ENSG00000257894	1.15	1.07	1.24	2.10E-04	3.66E-03
RP11-650K20.3	ENSG00000257327	1.15	1.10	1.20	5.20E-10	1.11E-07
CASC4P1	ENSG00000238132	1.15	1.09	1.21	2.70E-07	1.84E-05
RP11-539G18.1	ENSG00000249019	1.15	1.09	1.21	2.10E-07	1.53E-05
RP11-634H22.1	ENSG00000273391	1.15	1.06	1.25	5.30E-04	7.49E-03
RP11-54F2.1	ENSG00000251196	1.15	1.05	1.26	2.80E-03	2.50E-02
FLJ31104	ENSG00000227908	1.15	1.09	1.21	2.80E-07	1.88E-05
CTD-2525P14.5	ENSG00000280073	1.15	1.05	1.26	3.50E-03	2.92E-02
OR2W2P	ENSG00000217315	1.15	1.07	1.24	3.30E-04	5.18E-03
DBH-AS1	ENSG00000225756	1.15	1.08	1.22	3.50E-06	1.36E-04
RPS26P15	ENSG00000223416	1.15	1.10	1.20	8.70E-12	4.03E-09
RP11-63L7.5	ENSG00000271931	1.15	1.09	1.21	1.60E-07	1.27E-05

CH507-39O4.3	ENSG00000279186	1.15	1.07	1.23	1.20E-04	2.39E-03
CH507-236L23.3	ENSG00000279303	1.15	1.07	1.23	1.20E-04	2.39E-03
CH507-338C24.3	ENSG00000279967	1.15	1.07	1.23	1.20E-04	2.39E-03
OR1F2P	ENSG00000203581	1.15	1.05	1.25	2.30E-03	2.19E-02
RP4-568B10.1	ENSG00000280439	1.15	1.06	1.25	1.10E-03	1.27E-02
ACTG1P15	ENSG00000259904	1.15	1.04	1.27	6.80E-03	4.73E-02
LA16c-380F5.1	ENSG00000280062	1.15	1.07	1.23	1.70E-04	3.10E-03
ZBTB20-AS1	ENSG00000241560	1.15	1.04	1.26	5.00E-03	3.80E-02
AC007204.2	ENSG00000267268	1.15	1.07	1.23	6.60E-05	1.48E-03
ABCF2P1	ENSG00000242159	1.15	1.09	1.21	1.60E-07	1.27E-05
U1	ENSG00000206828	1.15	1.06	1.24	6.80E-04	9.08E-03
RNVU1-7	ENSG00000206585	1.15	1.05	1.25	2.60E-03	2.38E-02
LINC01234	ENSG00000249550	1.15	1.08	1.21	1.20E-06	5.86E-05
RP6-218J18.2	ENSG00000214019	1.15	1.07	1.22	4.00E-05	1.00E-03
RP11-608O8.2	ENSG00000270739	1.15	1.04	1.26	4.30E-03	3.41E-02
RP11-364L4.3	ENSG00000250969	1.15	1.09	1.20	8.20E-08	7.49E-06
ELK2BP	ENSG00000234402	1.15	1.09	1.20	7.20E-09	9.54E-07
OR7E1P	ENSG00000255554	1.15	1.04	1.26	6.80E-03	4.73E-02
PPIL1P1	ENSG00000237951	1.15	1.09	1.20	7.10E-08	6.63E-06
VN1R40P	ENSG00000223845	1.14	1.04	1.26	6.00E-03	4.35E-02
RP11-196G18.3	ENSG00000233030	1.14	1.11	1.18	0.00E+00	0.00E+00
UBE2SP1	ENSG00000233966	1.14	1.04	1.26	4.40E-03	3.47E-02
AC005786.6	ENSG00000279590	1.14	1.06	1.24	9.20E-04	1.14E-02
TPTE2P2	ENSG00000272281	1.14	1.04	1.26	5.90E-03	4.30E-02
RP11-779O18.3	ENSG00000253736	1.14	1.05	1.24	1.90E-03	1.88E-02
RP11-465L8.1	ENSG00000256071	1.14	1.04	1.25	4.40E-03	3.47E-02
RP11-236J17.7	ENSG00000279391	1.14	1.06	1.23	3.70E-04	5.64E-03
NA	ENSG00000279216	1.14	1.05	1.24	1.10E-03	1.27E-02
CTD-2231H16.1; lerpor	ENSG00000249430	1.14	1.05	1.24	1.30E-03	1.43E-02

RAET1K	ENSG00000218358	1.14	1.08	1.20	4.30E-07	2.61E-05
AC083843.4	ENSG00000279518	1.14	1.04	1.26	7.00E-03	4.84E-02
AC024937.4	ENSG00000231464	1.14	1.06	1.23	6.20E-04	8.49E-03
NUTM2HP	ENSG00000232706	1.14	1.04	1.25	4.30E-03	3.41E-02
GAS6-AS2	ENSG00000272695	1.14	1.05	1.24	3.10E-03	2.68E-02
LINC01191	ENSG00000234199	1.14	1.06	1.23	5.40E-04	7.62E-03
RP4-798P15.3	ENSG00000254154	1.14	1.04	1.25	4.40E-03	3.47E-02
RP11-325P15.2	ENSG00000230832	1.14	1.06	1.23	4.80E-04	6.90E-03
AC159540.3	ENSG00000237837	1.14	1.09	1.19	6.90E-08	6.49E-06
LINC00565	ENSG00000260910	1.14	1.08	1.19	1.50E-07	1.20E-05
MTUS2-AS1	ENSG00000179141	1.14	1.09	1.19	5.80E-08	5.54E-06
RP11-87G24.3	ENSG00000267568	1.14	1.04	1.25	7.30E-03	4.98E-02
IFNWP15	ENSG00000232281	1.14	1.05	1.24	2.50E-03	2.34E-02
HSP90AB2P	ENSG00000205940	1.14	1.04	1.25	5.60E-03	4.13E-02
RP11-46C24.3	ENSG00000205015	1.14	1.11	1.17	0.00E+00	0.00E+00
RP11-338N10.1	ENSG00000270171	1.14	1.05	1.23	1.40E-03	1.51E-02
AC007787.3	ENSG00000279044	1.14	1.08	1.19	2.50E-07	1.73E-05
OR2L1P	ENSG00000224227	1.14	1.09	1.19	7.80E-09	1.00E-06
AC115617.2	ENSG00000233585	1.14	1.05	1.23	2.30E-03	2.19E-02
PGAM1P5	ENSG00000257150	1.14	1.05	1.23	1.40E-03	1.51E-02
RP11-472N13.3	ENSG00000237797	1.14	1.04	1.24	4.80E-03	3.69E-02
KARSP3	ENSG00000262962	1.14	1.09	1.19	7.50E-09	9.83E-07
AK3P5	ENSG00000228816	1.14	1.04	1.24	6.20E-03	4.46E-02
CTC-539A10.7	ENSG00000271010	1.13	1.04	1.24	4.10E-03	3.28E-02
RP13-128O4.3	ENSG00000250995	1.13	1.04	1.24	4.60E-03	3.59E-02
AC016894.1	ENSG00000234624	1.13	1.04	1.24	6.20E-03	4.46E-02
CTD-2012K14.8	ENSG00000276075	1.13	1.05	1.22	1.30E-03	1.43E-02
ZNF300P1	ENSG00000197083	1.13	1.07	1.19	3.10E-06	1.23E-04
AC097495.2	ENSG00000237576	1.13	1.04	1.23	3.00E-03	2.62E-02

RP11-107F6.4	ENSG00000270702	1.13	1.08	1.19	2.10E-06	9.00E-05
RP11-589M4.4	ENSG00000271075	1.13	1.08	1.18	9.70E-08	8.45E-06
RPL13AP	ENSG00000231301	1.13	1.05	1.22	1.60E-03	1.66E-02
OR2B8P	ENSG00000182477	1.13	1.05	1.22	2.00E-03	1.95E-02
TTLL13P	ENSG00000213471	1.13	1.09	1.17	1.70E-10	4.09E-08
TPMTP1	ENSG00000267156	1.13	1.09	1.18	3.70E-09	5.58E-07
FAM167A-AS1	ENSG00000184608	1.13	1.05	1.22	1.50E-03	1.60E-02
RP11-15B24.1	ENSG00000225085	1.13	1.06	1.20	1.10E-04	2.24E-03
RPS3AP2	ENSG00000219027	1.13	1.08	1.18	7.20E-09	9.54E-07
RP11-145P16.2	ENSG00000280234	1.13	1.09	1.17	1.20E-10	3.00E-08
AP001626.1	ENSG00000225431	1.13	1.07	1.19	4.30E-06	1.64E-04
RP11-470C13.4	ENSG00000280229	1.13	1.04	1.22	4.20E-03	3.35E-02
RP11-115N4.1	ENSG00000243144	1.13	1.09	1.17	4.30E-12	2.23E-09
RP11-395I6.2	ENSG00000250338	1.13	1.05	1.21	1.60E-03	1.66E-02
AC015849.2	ENSG00000270240	1.13	1.03	1.23	6.90E-03	4.78E-02
NA	ENSG00000280566	1.13	1.05	1.21	1.60E-03	1.66E-02
AC084082.3	ENSG00000253190	1.13	1.04	1.22	2.60E-03	2.38E-02
IFNL4	ENSG00000272395	1.13	1.07	1.18	3.40E-06	1.33E-04
RP11-15B24.4	ENSG00000232749	1.12	1.06	1.19	3.00E-05	7.90E-04
RNU1-13P	ENSG00000238825	1.12	1.05	1.20	3.40E-04	5.30E-03
Metazoa_SRP; RN7SL3	ENSG00000278771	1.12	1.03	1.22	5.90E-03	4.30E-02
AC007750.5	ENSG00000236841	1.12	1.07	1.18	1.90E-06	8.36E-05
ZNF90P2	ENSG00000233366	1.12	1.08	1.17	3.40E-08	3.45E-06
NA	ENSG00000278309	1.12	1.04	1.21	4.10E-03	3.28E-02
GMCL1P1	ENSG00000244234	1.12	1.08	1.17	3.10E-08	3.22E-06
AC016907.3	ENSG00000233862	1.12	1.07	1.17	2.40E-07	1.68E-05
RP11-443B7.3	ENSG00000258082	1.12	1.04	1.21	4.20E-03	3.35E-02
DNM1P51	ENSG00000235370	1.12	1.04	1.21	4.70E-03	3.64E-02
ZNF192P2	ENSG00000218016	1.12	1.06	1.18	1.20E-05	3.76E-04

FGF14-AS2	ENSG00000272143	1.12	1.03	1.21	6.30E-03	4.52E-02
RP11-107N7.1	ENSG00000253572	1.12	1.08	1.15	1.70E-12	1.05E-09
RFPL1S	ENSG00000225465	1.12	1.06	1.18	1.20E-05	3.76E-04
LINC01187	ENSG00000249601	1.12	1.04	1.21	3.40E-03	2.86E-02
RPF2P1	ENSG00000225357	1.12	1.08	1.16	1.30E-08	1.53E-06
AC067945.2	ENSG00000230686	1.12	1.08	1.15	6.70E-13	5.12E-10
U1	ENSG00000274428	1.12	1.04	1.20	3.10E-03	2.68E-02
U91328.2	ENSG00000234816	1.12	1.04	1.20	1.90E-03	1.88E-02
RNU1-120P	ENSG00000199879	1.12	1.05	1.19	4.00E-04	5.97E-03
AC004125.3	ENSG00000260264	1.12	1.09	1.14	0.00E+00	0.00E+00
AC011738.4	ENSG00000231638	1.12	1.08	1.15	1.50E-12	9.73E-10
RP11-89F3.2	ENSG00000236140	1.12	1.04	1.19	1.30E-03	1.43E-02
CTD-2583P5.3	ENSG00000261158	1.11	1.03	1.21	6.70E-03	4.70E-02
GAPDHP65	ENSG00000235587	1.11	1.03	1.21	6.60E-03	4.66E-02
LINC00240	ENSG00000224843	1.11	1.09	1.14	4.40E-16	4.76E-13
RP11-177H2.1	ENSG00000280294	1.11	1.07	1.15	6.30E-09	8.70E-07
RP11-133K1.6	ENSG00000259198	1.11	1.04	1.19	9.80E-04	1.19E-02
RPL22P18	ENSG00000230171	1.11	1.04	1.20	3.60E-03	2.97E-02
RPL7AP34	ENSG00000213312	1.11	1.08	1.14	4.40E-16	4.76E-13
RP13-49I15.6	ENSG00000273980	1.11	1.04	1.20	3.60E-03	2.97E-02
COL11A2P1	ENSG00000228688	1.11	1.07	1.15	3.30E-09	5.35E-07
RP11-184A2.3	ENSG00000229672	1.11	1.09	1.13	0.00E+00	0.00E+00
AP000593.5	ENSG00000228286	1.11	1.08	1.14	4.40E-16	4.76E-13
RP11-126O22.1	ENSG00000232111	1.11	1.08	1.14	1.70E-14	1.70E-11
AC011239.2	ENSG00000279526	1.11	1.08	1.14	2.20E-11	8.40E-09
HTATSF1P1	ENSG00000223457	1.11	1.03	1.19	4.40E-03	3.47E-02
SALL4P6	ENSG00000231280	1.11	1.09	1.13	0.00E+00	0.00E+00
CTC-308K20.3	ENSG00000253785	1.11	1.06	1.16	5.10E-06	1.86E-04
TTLL10-AS1	ENSG00000205231	1.11	1.03	1.19	6.40E-03	4.55E-02

RP1-37N7.1	ENSG00000264177	1.11	1.04	1.18	2.40E-03	2.26E-02
Z95704.3	ENSG00000250238	1.11	1.03	1.19	3.30E-03	2.81E-02
RP11-342M1.6	ENSG00000237090	1.11	1.06	1.15	2.80E-07	1.88E-05
CSPG4P5	ENSG00000272887	1.11	1.04	1.18	1.60E-03	1.66E-02
RP11-222G7.2	ENSG00000272748	1.11	1.05	1.16	1.20E-04	2.39E-03
OR2H5P	ENSG00000232173	1.10	1.07	1.14	3.70E-09	5.58E-07
CHIAP2	ENSG00000203878	1.10	1.08	1.13	0.00E+00	0.00E+00
LINC00208	ENSG00000170983	1.10	1.05	1.16	5.30E-05	1.26E-03
GUCY1B2	ENSG00000123201	1.10	1.07	1.14	1.00E-10	2.65E-08
AC010983.1	ENSG00000235056	1.10	1.03	1.18	4.60E-03	3.59E-02
RP4-555D20.2	ENSG00000261786	1.10	1.04	1.17	9.90E-04	1.19E-02
AC006196.1	ENSG00000230173	1.10	1.04	1.17	2.10E-03	2.02E-02
RP11-544P1.3	ENSG00000280086	1.10	1.05	1.16	1.70E-04	3.10E-03
RP11-881M11.1	ENSG00000256944	1.10	1.05	1.15	4.60E-05	1.12E-03
HNRNPA1P60	ENSG00000233497	1.10	1.03	1.18	7.30E-03	4.98E-02
ABHD15-AS1	ENSG00000264031	1.10	1.03	1.18	5.50E-03	4.07E-02
PNMA6B	ENSG00000268883	1.10	1.04	1.17	1.40E-03	1.51E-02
CTD-2008P7.1	ENSG00000260777	1.10	1.06	1.14	1.30E-07	1.07E-05
RP11-814P5.1	ENSG00000250007	1.10	1.05	1.15	1.60E-04	2.97E-03
RP4-555D20.1	ENSG00000280435	1.10	1.03	1.17	2.50E-03	2.34E-02
BICD1P1	ENSG00000224346	1.10	1.06	1.13	1.00E-08	1.21E-06
AC104699.1	ENSG00000224220	1.09	1.03	1.17	6.30E-03	4.52E-02
RP11-402G3.4	ENSG00000230284	1.09	1.04	1.15	5.40E-04	7.62E-03
RP11-144L1.8	ENSG00000231434	1.09	1.02	1.17	6.80E-03	4.73E-02
FAM187B2P	ENSG00000262497	1.09	1.05	1.13	2.40E-06	1.00E-04
RP4-738P15.1	ENSG00000230725	1.09	1.04	1.15	7.40E-04	9.65E-03
BCRP3	ENSG00000215481	1.09	1.04	1.14	5.00E-04	7.14E-03
RP11-414J4.2	ENSG00000261606	1.09	1.05	1.13	9.40E-07	4.94E-05
RP11-881M11.4	ENSG00000256196	1.09	1.05	1.13	8.00E-06	2.70E-04

MIR4697HG	ENSG00000280237	1.09	1.04	1.14	3.40E-04	5.30E-03
DNAJC8P1	ENSG00000259022	1.08	1.02	1.15	5.60E-03	4.13E-02
KB-1980E6.3	ENSG00000253633	1.08	1.04	1.13	3.70E-04	5.64E-03
SNORA24	ENSG00000275994	1.08	1.03	1.14	4.10E-03	3.28E-02
AC069513.4	ENSG00000229178	1.08	1.04	1.12	5.50E-05	1.29E-03
RP11-162G10.5	ENSG00000236514	1.08	1.02	1.13	4.00E-03	3.22E-02
RPL29P11	ENSG00000224858	1.07	1.05	1.10	1.60E-08	1.84E-06
RP11-417P24.1	ENSG00000270371	1.06	1.03	1.10	9.10E-04	1.13E-02
RP11-490G8.1	ENSG00000241556	1.06	1.02	1.09	2.30E-03	2.19E-02
LINC01013	ENSG00000228495	1.05	1.03	1.08	2.50E-05	6.85E-04
RP11-481J2.2	ENSG00000260186	1.05	1.02	1.08	4.80E-04	6.90E-03
TMED11P	ENSG00000215367	1.05	1.02	1.07	1.50E-04	2.82E-03
RP11-74E22.6	ENSG00000272911	1.04	1.02	1.06	4.60E-04	6.67E-03

Supplementary Table 7. Overexpressed lncRNAs by the agonist mix treatment in the different assayed CLL cohorts that were found also associated with a shorter TTT in 266 CLL (ICGC).

TP53 altered	Fold Change (CvsA)	P-value (CvsA)	Fold Change (DvsB)	P-value (DvsB)
RP11-603J24.7	3.65	1.16E-02	b.t	n.s.
Z69890.1	2.29	8.80E-03	2	2.21E-02
RPS2P35	2.02	2.07E-02	b.t	n.s.
RP11-144L1.8	1.83	3.89E-02	b.t	n.s.
DNAJC8P1	1.76	2.53E-02	b.t	n.s.
CTD-2194F4.2	1.64	8.20E-03	b.t	n.s.
RPL5P24	1.63	2.17E-02	b.t	n.s.
GAPLINC	1.56	4.63E-02	b.t	n.s.
YWHAEP1	1.55	1.50E-03	b.t	n.s.
H2AFZP3	1.54	4.46E-02	b.t	n.s.
LINC00158	b.t	n.s.	3.06	1.37E-02
SRSF10P1	b.t	n.s.	1.97	4.40E-02
RP11-443B7.3	b.t	n.s.	1.86	1.21E-02
KB-1980E6.3	b.t	n.s.	1.8	2.25E-02
LINC01187	b.t	n.s.	1.78	3.90E-03
CTD-2227E11.1	b.t	n.s.	1.76	1.64E-02
RP11-554A11.9	b.t	n.s.	1.61	4.42E-02
SNORA46	b.t	n.s.	1.57	4.27E-02
RP11-330C7.3	b.t	n.s.	1.54	1.60E-03
RP11-126O22.1	-1.5	1.95E-02	b.t	n.s.
RP11-428K3.1	-1.5	3.18E-02	b.t	n.s.
CTD-3222D19.4	-1.69	1.72E-02	b.t	n.s.
BNIP3P41	-1.7	3.25E-02	b.t	n.s.
DLEU2	-1.72	1.73E-02	b.t	n.s.
RP11-103B5.4	-1.75	1.65E-02	b.t	n.s.
MIR302B	-1.77	6.80E-03	b.t	n.s.

CTA-331F8.1	-1.98	4.15E-02	b.t	n.s.
RP11-430C7.5	-2.16	2.03E-02	b.t	n.s.
RP1-102G20.2	-2.22	1.31E-02	b.t	n.s.
RP11-568N6.1	-2.38	4.90E-03	-2.23	2.63E-02
RP11-196G18.24	-3.15	4.80E-02	-2.57	1.79E-02
RP11-686G8.1	b.t	n.s.	-2.08	1.80E-02
LINC00426	b.t	n.s.	-4.57	8.50E-03

Trisomy 12	**Fold Change (CvsA)**	**P-value (CvsA)**	**Fold Change (DvsB)**	**P-value (DvsB)**
SNORA14	12.42	7.40E-03	17.07	3.20E-03
MALAT1	5.18	6.90E-03	b.t	n.s.
CTD-2357A8.2	3.33	1.79E-02	b.t	n.s.
OR7E102P	2.12	3.01E-02	b.t	n.s.
RPS2P46	1.8	3.10E-02	b.t	n.s.
RP11-719K4.6	1.66	7.70E-03	b.t	n.s.
RP11-82O18.2	1.66	7.70E-03	b.t	n.s.
AC055764.1	1.53	8.10E-03	b.t	n.s.
EIF4BP8	1.53	4.20E-02	b.t	n.s.
GAPLINC	b.t	n.s.	2.88	1.97E-02
RP11-46H11.3	b.t	n.s.	2.25	1.10E-02
TAGLN2P1	b.t	n.s.	2.13	4.70E-03
RP11-16E23.5	b.t	n.s.	1.92	4.06E-02
XPOTP1	b.t	n.s.	1.75	2.12E-02
RP11-15M15.1	b.t	n.s.	1.63	4.40E-03
RP11-401N16.2	b.t	n.s.	1.5	2.35E-02
RP11-475E11.2	b.t	n.s.	-1.68	4.60E-03
ALMS1-IT1	b.t	n.s.	-1.7	3.86E-02
CTD-2340D6.2	b.t	n.s.	-1.7	1.50E-03
KYNUP2	b.t	n.s.	-1.7	1.60E-03

RP11-480I12.10	b.t	n.s.	-1.71	4.21E-02
BIRC6-AS2	b.t	n.s.	-1.83	6.30E-03
RN7SL390P	b.t	n.s.	-1.96	9.00E-03
RP4-752I6.1	b.t	n.s.	-1.97	3.58E-02
PDXDC2P	b.t	n.s.	-2.34	3.62E-02
DLEU2	b.t	n.s.	-2.79	2.49E-02
LINC00426	b.t	n.s.	-3.49	5.60E-03
TVP23CP1	-1.5	3.12E-02	-1.6	9.00E-04
RP11-271M24.2	-1.51	7.00E-04	b.t	n.s.
STRCP1	-1.52	4.26E-02	b.t	n.s.
PCAT1	-1.59	3.10E-02	b.t	n.s.
AP000704.5	-1.64	2.20E-03	b.t	n.s.
OR1F2P	-1.7	1.47E-02	b.t	n.s.
LINC00565	-1.75	2.10E-03	b.t	n.s.
RP11-395I6.2	-1.79	7.30E-03	b.t	n.s.
AC097495.2	-1.81	4.22E-02	b.t	n.s.
RP11-272L13.4	-1.81	2.06E-02	b.t	n.s.
LETM1P2	-1.82	7.00E-04	b.t	n.s.
RP1-111C20.4	-1.83	1.84E-02	b.t	n.s.
RP11-428K3.1	-1.87	2.68E-02	b.t	n.s.
RP11-1174L13.2	-1.91	1.02E-02	b.t	n.s.
RP11-307C12.13	-1.93	2.13E-02	b.t	n.s.
RN7SL417P	-1.96	1.27E-02	b.t	n.s.
RP11-326K13.5	-2.01	2.19E-02	b.t	n.s.
LINC00540	-2.05	4.38E-02	b.t	n.s.
AC067945.4	-2.13	6.60E-03	b.t	n.s.
RN7SL692P	-2.32	1.49E-02	b.t	n.s.

WT (Barcelona)	**Fold Change (CvsA)**	**P-value (CvsA)**	**Fold Change (DvsB)**	**P-value (DvsB)**
LINC00152	24.07	1.27E-02	b.t	n.s.
NME2P1	11.88	6.40E-03	b.t	n.s.
PSMA6P1	6.15	5.60E-03	2.45	3.85E-02
SNORA14	4.87	2.71E-02	3.95	6.80E-03
RP11-12M9.3	3.37	4.23E-02	b.t	n.s.
ANXA2P2	2.91	4.40E-03	b.t	n.s.
RPS2P46	2.72	4.00E-04	1.91	1.17E-02
RP11-603J24.7	2.64	4.26E-02	b.t	n.s.
TAGLN2P1	2.38	4.80E-03	4.05	3.00E-04
RP11-503N18.5	2.35	4.00E-04	b.t	n.s.
RP11-638I2.10	2.22	1.92E-02	b.t	n.s.
GAPLINC	2.2	8.00E-04	b.t	n.s.
RP5-827C21.1	2.02	2.08E-02	b.t	n.s.
RN7SL288P	1.92	2.78E-02	b.t	n.s.
HNRNPLP1	1.87	6.90E-03	b.t	n.s.
EIF4HP1	1.86	4.29E-02	b.t	n.s.
RP11-124N14.3	1.82	5.30E-03	1.59	2.40E-02
LETM1P2	1.74	3.80E-03	b.t	n.s.
MALAT1	1.68	1.83E-02	b.t	n.s.
RP11-138I1.4	1.68	2.68E-02	b.t	n.s.
CTB-52I2.4	1.65	3.42E-02	b.t	n.s.
RP11-409I10.2	1.61	3.69E-02	b.t	n.s.
RP11-161H23.5	1.58	8.00E-03	b.t	n.s.
RNU1-120P	b.t	n.s.	6.47	3.17E-02
RP11-138A9.1	b.t	n.s.	3.89	2.40E-02
RNU1-13P	b.t	n.s.	2.93	3.89E-02
EEF1B2P1	b.t	n.s.	2.17	3.07E-02
RPL4P6	b.t	n.s.	2.13	3.98E-02

HNRNPA1P60	b.t	n.s.	2.11	1.44E-02
RPL35P1	b.t	n.s.	1.99	2.89E-02
CTC-444N24.7	b.t	n.s.	1.96	3.33E-02
OR7E102P	b.t	n.s.	1.89	3.50E-03
RPL7AP34	b.t	n.s.	1.85	1.10E-03
Z69890.1	b.t	n.s.	1.83	3.43E-02
RP11-490G8.1	b.t	n.s.	1.78	3.16E-02
RPL7P19	b.t	n.s.	1.78	1.70E-03
LLNLR-285B5.1	b.t	n.s.	1.66	2.55E-02
RPL7P60	b.t	n.s.	1.66	3.86E-02
RP11-313D6.3	b.t	n.s.	1.65	8.30E-03
RPL34P21	b.t	n.s.	1.64	1.30E-02
RP1-34B20.4	b.t	n.s.	1.58	2.56E-02
RP3-468O1.6	-1.52	2.30E-03	b.t	n.s.
CTC-463A16.1	-1.55	3.24E-02	b.t	n.s.
LINC01284	-1.63	1.90E-03	b.t	n.s.
CTA-212A2.1	-1.72	1.92E-02	-1.78	1.07E-02
RN7SL390P	-1.73	4.40E-02	b.t	n.s.
RNU2-6P	-1.85	2.76E-02	b.t	n.s.
RP11-96D1.8	-1.86	3.88E-02	-1.78	2.24E-02
RP11-13P5.1	-2.08	5.50E-03	b.t	n.s.
RP11-145P16.2	-2.08	3.20E-03	b.t	n.s.
SCARNA7	-2.19	4.93E-02	b.t	n.s.
LINC00426	-2.8	4.01E-02	-8.78	2.10E-05
RP11-430C7.5	-2.99	4.10E-03	-2.1	4.79E-02
RP11-126K15.1	-5.19	4.97E-02	-3.72	2.70E-02
BNIP3P41	-25.26	5.55E-05	-6.13	8.00E-04
AC007386.4	-41.84	3.81E-07	-18.78	4.00E-04
AC007386.4	-41.84	3.81E-07	-18.78	4.00E-04

RP1-159A19.4	b.t	n.s.	-1.65	3.04E-02
TRERNA1	b.t	n.s.	-1.69	2.90E-03
LOC440461	b.t	n.s.	-1.74	5.23E-05
RP11-626G11.3	b.t	n.s.	-1.74	3.75E-02
PRICKLE2-AS3	b.t	n.s.	-1.75	6.00E-04
RP11-167N4.4	b.t	n.s.	-1.76	3.00E-03
DLEU2	b.t	n.s.	-2.05	4.01E-02
RP11-391L3.3	b.t	n.s.	-2.24	4.90E-03
RP11-196G18.22	b.t	n.s.	-2.25	8.20E-03
RP11-43D4.2	b.t	n.s.	-2.48	1.10E-02
LINC00891	b.t	n.s.	-2.77	6.40E-03
TBC1D27	b.t	n.s.	-2.84	1.90E-02
CTA-246H3.11	b.t	n.s.	-3.89	3.72E-02
RP11-568N6.1	b.t	n.s.	-4.02	1.13E-02
RP11-196G18.24	b.t	n.s.	-4.2	1.40E-03
MYL12BP2	b.t	n.s.	-4.92	1.06E-02
RP11-862L9.3	b.t	n.s.	-8.97	2.88E-02

WT (Aviano)	**Fold Change (CvsA)**	**P-value (CvsA)**	**Fold Change (DvsB)**	**P-value (DvsB)**
SNORA14	7.86	6.40E-03	7.3	3.30E-03
HSPD1P1	3.62	2.63E-02	b.t	n.s.
TAGLN2P1	3.5	1.34E-02	2.23	9.30E-03
RP11-603J24.7	2.81	2.97E-02	3.93	7.80E-03
RN7SL288P	2.39	3.20E-03	2.09	2.60E-02
NME2P1	2.34	4.22E-02	b.t	n.s.
RP11-490H24.5	2.34	2.78E-02	1.67	3.16E-02
Z69890.1	2.17	2.60E-03	2.73	2.70E-03
RP11-140H17.2	1.95	2.91E-02	2.31	1.10E-02
TATDN1P1	1.92	7.00E-04	b.t	n.s.

CTC-308K20.3	1.82	2.10E-02	b.t	n.s.
RP1-228H13.5	1.81	4.65E-02	b.t	n.s.
LINC01033	1.8	9.00E-04	1.72	8.40E-03
LLNLR-285B5.1	1.78	1.92E-02	b.t	n.s.
HSP90AB2P	1.74	1.89E-02	b.t	n.s.
SLC7A5P1	1.74	1.61E-02	b.t	n.s.
RP11-419L20.2	1.71	1.19E-02	b.t	n.s.
RP11-554A11.9	1.71	1.39E-02	b.t	n.s.
DNAJC8P1	1.69	4.47E-02	b.t	n.s.
RPS2P35	1.64	2.31E-02	b.t	n.s.
RP11-454H13.1	1.59	5.60E-03	b.t	n.s.
RP5-827C21.1	1.56	2.02E-02	1.7	4.16E-02
HNRNPLP1	1.52	2.48E-02	b.t	n.s.
LINC00158	2.54	7.70E-02	5.41	1.90E-03
ABALON	b.t	n.s.	2.7	4.00E-04
RP11-289I10.2	b.t	n.s.	2.22	4.25E-02
RP11-138A9.1	b.t	n.s.	2.04	4.22E-02
RP11-124N14.3	b.t	n.s.	1.98	2.30E-03
RP11-56B16.4	b.t	n.s.	1.98	1.91E-02
RP11-161H23.5	b.t	n.s.	1.75	1.75E-02
SNORA24	b.t	n.s.	1.69	3.58E-02
RP11-144L1.8	b.t	n.s.	1.58	6.50E-03
KB-173C10.1	b.t	n.s.	1.56	1.82E-02
RPL7P60	b.t	n.s.	1.51	2.23E-02
HIST2H2BC	-1.61	4.60E-02	b.t	n.s.
RP11-977G19.11	-1.67	1.20E-02	b.t	n.s.
HIST2H2BD	-1.71	4.90E-03	b.t	n.s.
RP11-391L3.3	-1.93	2.24E-02	b.t	n.s.
TBC1D27	-1.94	4.58E-02	b.t	n.s.

RP11-428K3.1	-2.09	3.00E-04	b.t	n.s.
RP11-567L7.3	-2.09	2.30E-02	b.t	n.s.
RP11-519C12.1	-2.11	8.50E-03	b.t	n.s.
RP11-327F22.6	-2.14	5.90E-03	b.t	n.s.
RP11-196G18.22	-2.21	2.02E-02	b.t	n.s.
RP11-2J18.1	-2.22	9.50E-03	b.t	n.s.
RP11-357P18.2	-2.27	2.29E-02	b.t	n.s.
DLEU2	-2.33	1.12E-02	-2.2	3.30E-02
U91328.2	-2.39	9.90E-03	b.t	n.s.
RP11-430C7.5	-2.49	1.30E-03	-2.16	4.07E-02
RP11-46H11.11	-2.51	3.12E-02	b.t	n.s.
RP11-888D10.4	-2.65	4.10E-02	b.t	n.s.
RP1-102G20.2	-2.67	2.50E-03	b.t	n.s.
RP11-568N6.1	-2.83	2.50E-02	b.t	n.s.
RP11-196G18.24	-2.97	3.00E-04	-2.08	1.59E-02
RP11-126K15.1	-3.31	3.97E-02	b.t	n.s.
LINC00426	-4.13	1.00E-04	-6.08	4.58E-05
AC007386.4	-4.29	4.50E-03	-2.5	3.53E-02
AC007386.4	-4.29	4.50E-03	-2.5	3.53E-02
CTA-212A2.1	-4.62	2.22E-05	-2.85	1.60E-03
RP11-862L9.3	-4.74	2.06E-02	-6.16	3.38E-02
RP11-25L3.1	-5.15	8.10E-03	b.t	n.s.
RP11-25L3.3	-5.5	6.80E-03	b.t	n.s.
BNIP3P41	-12.01	1.84E-05	-5.96	1.50E-03
RP3-468O1.6	b.t	n.s.	-1.59	2.66E-02
PTPN2P1	b.t	n.s.	-1.62	7.70E-03
LINC00891	b.t	n.s.	-2.16	3.80E-03
MYL12BP2	b.t	n.s.	-6.32	9.80E-03

b.t : below threshold (Fold Change [2]).
n.s: non significant P-val

Supplementary Table 8. Expression levels in MEC-1 cell line of lncRNAs found significantly upregulated by agonist mix treatment and associated with shorter TTT.

Venny upregulated (FC ONLY) upon agonist mix	ENSG Code	MEC1 expression
10 elements included exclusively in "Trisomy12":		
AC055764.1	ENSG00000234136	0
CTD-2357A8.2	ENSG00000279570	0.11
EIF4BP8	ENSG00000243918	0.05
RP11-15M15.1	ENSG00000223492	0.01
RP11-16E23.5	ENSG00000275638	0.47
RP11-401N16.2	ENSG00000275381	0.28
RP11-46H11.3	ENSG00000250790	0.03
RP11-719K4.6	ENSG00000261695	0
RP11-82O18.2	ENSG00000261523	0
XPOTP1	ENSG00000214185	0.08
11 elements included exclusively in "TP53 Altered":		
CTD-2194F4.2	ENSG00000248288	0.02
CTD-2227E11.1	ENSG00000270933	3.75
H2AFZP3	ENSG00000218502	0.42
KB-1980E6.3	ENSG00000253633	10.36
LINC01187	ENSG00000249601	0
RP11-330C7.3	ENSG00000225505	0
RP11-443B7.3	ENSG00000258082	0.7
RPL5P24	ENSG00000244052	0.01
SNORA46	ENSG00000207493	0

SRSF10P1	ENSG00000267717	0.03
YWHAEP1	ENSG00000232727	0.02

16 elements included exclusively in "WT (Aviano)":

ABALON	ENSG00000281376	0.32
CTC-308K20.3	ENSG00000253785	0.61
HSP90AB2P	ENSG00000205940	0.06
HSPD1P1	ENSG00000213430	1.07
KB-173C10.1	ENSG00000253842	0.19
LINC01033	ENSG00000249069	0.33
RP11-140H17.2	ENSG00000274093	0.16
RP11-289I10.2	ENSG00000223612	2.62
RP11-419L20.2	ENSG00000241556	0.31
RP11-454H13.1	ENSG00000243396	0
RP11-490H24.5	ENSG00000216285	3.44
RP11-56B16.4	ENSG00000259185	0
RP1-228H13.5	ENSG00000260920	1.17
SLC7A5P1	ENSG00000260727	0.6
SNORA24	ENSG00000275994	0
TATDN1P1	ENSG00000234369	0.06

24 elements included exclusively in "WT (Barcelona)":

ANXA2P2	ENSG00000231991	0.92
CTB-52I2.4	ENSG00000273654	2.8
CTC-444N24.7	ENSG00000279541	0.38
EEF1B2P1	ENSG00000231169	0
EIF4HP1	ENSG00000233830	1.75
HNRNPA1P60	ENSG00000233497	0
LETM1P2	ENSG00000268660	0

LINC00152	ENSG00000222041	11.92
PSMA6P1	ENSG00000215414	0.18
RNU1-120P	ENSG00000199879	0
RNU1-13P	ENSG00000238825	0
RP11-12M9.3	ENSG00000237214	2.46
RP11-138I1.4	ENSG00000265401	68
RP11-313D6.3	ENSG00000232470	0.4
RP11-409I10.2	ENSG00000259039	0.59
RP11-490G8.1	ENSG00000241556	0.31
RP11-503N18.5	ENSG00000251229	0.2
RP11-638I2.10	ENSG00000258581	0.32
RP1-34B20.4	ENSG00000217275	0.12
RPL34P21	ENSG00000244451	0
RPL35P1	ENSG00000237991	1.32
RPL4P6	ENSG00000230071	0.43
RPL7AP34	ENSG00000213312	0
RPL7P19	ENSG00000241458	0.14

3 common elements in "WT (Barcelona)" and "Trisomy 12":

MALAT1	ENSG00000251562	66.74
OR7E102P	ENSG00000168992	0
RPS2P46	ENSG00000189343	24.59

9 common elements in "WT (Barcelona)" and "WT (Aviano)":

HNRNPLP1	ENSG00000233503	0
LLNLR-285B5.1	ENSG00000276578	0
NME2P1	ENSG00000123009	0.42
RN7SL288P	ENSG00000240767	0
RP11-124N14.3	ENSG00000234961	0.64

RP11-138A9.1	ENSG00000271204	0.04
RP11-161H23.5	ENSG00000258232	150.89
RP5-827C21.1	ENSG00000235605	0.95
RPL7P60	ENSG00000214142	0.05

5 common elements in "WT (Aviano)" and "TP53 Altered":

DNAJC8P1	ENSG00000259022	0
LINC00158	ENSG00000185433	6.61
RP11-144L1.8	ENSG00000218276	0
RP11-554A11.9	ENSG00000259799	2.81
RPS2P35	ENSG00000238172	0.01

2 common elements in "WT (Barcelona)", "WT (Aviano)" and "TP53 Altered":

RP11-603J24.7	ENSG00000237493	0.42
Z69890.1	ENSG00000206168	0.53

1 common element in "WT (Barcelona)", "TP53 Altered" and "Trisomy 12":

GAPLINC	ENSG00000266835	0

2 common elements in "WT (Barcelona)", "WT (Aviano)" and "Trisomy 12":

SNORA14	ENSG00000251922	0
TAGLN2P1	ENSG00000253676	0.54

Supplementary Table 9a. Significantly enriched pathways among genes signficantly decreased upon Rp11-161H23.5 silencing in MEC-1 compared to controls.

Category	Term	Description	LogP	Log(q-value)
Reactome Gene Sets	R-HSA-1280215	Cytokine Signaling in Immune system	-11.48	-7.16
Reactome Gene Sets	R-HSA-372790	Signaling by GPCR	-10.54	-6.80
Reactome Gene Sets	R-HSA-388396	GPCR downstream signalling	-10.15	-6.50
Reactome Gene Sets	R-HSA-909733	Interferon alpha/beta signaling	-7.39	-4.12
Reactome Gene Sets	R-HSA-76002	Platelet activation, signaling and aggregation	-7.22	-4.07
Reactome Gene Sets	R-HSA-418594	G alpha (i) signalling events	-6.59	-3.72
Reactome Gene Sets	R-HSA-109582	Hemostasis	-6.46	-3.66
WikiPathways	WP3929	Chemokine signaling pathway	-6.29	-3.53
Reactome Gene Sets	R-HSA-373076	Class A/1 (Rhodopsin-like receptors)	-6.23	-3.49
Reactome Gene Sets	R-HSA-913531	Interferon Signaling	-5.72	-3.06
Reactome Gene Sets	R-HSA-500792	GPCR ligand binding	-5.61	-2.99
Reactome Gene Sets	R-HSA-456926	Thrombin signalling through proteinase activated receptors (PARs)	-4.98	-2.50
Reactome Gene Sets	R-HSA-392518	Signal amplification	-4.90	-2.44
Reactome Gene Sets	R-HSA-9009391	Extra-nuclear estrogen signaling	-4.49	-2.12
Reactome Gene Sets	R-HSA-163685	Integration of energy metabolism	-4.21	-1.93
Reactome Gene Sets	R-HSA-449147	Signaling by Interleukins	-4.04	-1.82
WikiPathways	WP455	GPCRs class A rhodopsin like	-4.04	-1.82
Reactome Gene Sets	R-HSA-375276	Peptide ligand-binding receptors	-3.98	-1.78
Reactome Gene Sets	R-HSA-418597	G alpha (z) signalling events	-3.95	-1.77
Reactome Gene Sets	R-HSA-111885	Opioid Signalling	-3.93	-1.76
WikiPathways	WP4172	PI3K Akt signaling pathway	-3.88	-1.72
WikiPathways	WP58	Monoamine GPCRs	-3.77	-1.63
WikiPathways	WP536	Calcium regulation in cardiac cells	-3.75	-1.62
Reactome Gene Sets	R-HSA-422356	Regulation of insulin secretion	-3.59	-1.51
Reactome Gene Sets	R-HSA-8939211	ESR-mediated signaling	-3.58	-1.50
Reactome Gene Sets	R-HSA-112040	G-protein mediated events	-3.57	-1.50

Reactome Gene Sets	R-HSA-9662851	Anti-inflammatory response favouring Leishmania parasite infection	-3.56	-1.49
Reactome Gene Sets	R-HSA-9664433	Leishmania parasite growth and survival	-3.56	-1.49
Reactome Gene Sets	R-HSA-9658195	Leishmania infection	-3.48	-1.45
Reactome Gene Sets	R-HSA-9824443	Parasitic Infection Pathways	-3.48	-1.45
Reactome Gene Sets	R-HSA-6814122	Cooperation of PDCL (PhLP1) and TRiC/CCT in G-protein beta folding	-3.48	-1.45
Reactome Gene Sets	R-HSA-9006931	Signaling by Nuclear Receptors	-3.45	-1.42
Reactome Gene Sets	R-HSA-380108	Chemokine receptors bind chemokines	-3.45	-1.42
Reactome Gene Sets	R-HSA-392170	ADP signalling through P2Y purinoceptor 12	-3.42	-1.40

Supplementary Table 9b. Significantly enriched pathways among genes significantly decreased upon LINC00152 silencing in MEC-1 compared to controls.

Category	Term	Description	LogP	Log(q-value)
WikiPathways	WP5095	**Overview of proinflammatory and profibrotic mediators**	-7.02	-3.52
Reactome Gene Sets	R-HSA-1474244	**Extracellular matrix organization**	-6.93	-3.49
Reactome Gene Sets	R-HSA-1474290	**Collagen formation**	-6.39	-3.12
WikiPathways	WP5115	Network map of SARS CoV 2 signaling pathway	-6.02	-2.83
Reactome Gene Sets	R-HSA-8978868	**Fatty acid metabolism**	-5.94	-2.77
Reactome Gene Sets	R-HSA-556833	**Metabolism of lipids**	-5.80	-2.69
Reactome Gene Sets	R-HSA-211945	Phase I - Functionalization of compounds	-5.62	-2.58
Reactome Gene Sets	R-HSA-380108	**Chemokine receptors bind chemokines**	-5.43	-2.51
WikiPathways	WP2118	**Arrhythmogenic right ventricular cardiomyopathy**	-5.42	-2.51
WikiPathways	WP43	**Oxidation by cytochrome P450**	-5.13	-2.29
Reactome Gene Sets	R-HSA-211897	**Cytochrome P450 - arranged by substrate type**	-5.02	-2.27
Reactome Gene Sets	R-HSA-1650814	**Collagen biosynthesis and modifying enzymes**	-4.97	-2.26
WikiPathways	WP4721	**Eicosanoid metabolism via lipooxygenases LOX**	-4.67	-2.01
Reactome Gene Sets	R-HSA-2142753	**Arachidonic acid metabolism**	-4.51	-1.91
Reactome Gene Sets	R-HSA-8948216	Collagen chain trimerization	-4.47	-1.91
Reactome Gene Sets	R-HSA-2022090	**Assembly of collagen fibrils and other multimeric structures**	-4.40	-1.87
Reactome Gene Sets	R-HSA-372790	**Signaling by GPCR**	-4.30	-1.81
WikiPathways	WP4541	Hippo Merlin signaling dysregulation	-4.29	-1.81
Reactome Gene Sets	R-HSA-216083	**Integrin cell surface interactions**	-4.13	-1.68
Reactome Gene Sets	R-HSA-388396	GPCR downstream signalling	-4.05	-1.62
Reactome Gene Sets	R-HSA-5617833	Cilium Assembly	-4.01	-1.60
WikiPathways	WP5285	Immune infiltration in pancreatic cancer	-3.82	-1.48
WikiPathways	WP5087	Pleural mesothelioma	-3.75	-1.44
Reactome Gene Sets	R-HSA-211859	Biological oxidations	-3.56	-1.32

Supplementary Table 9c. Significantly enriched pathways among genes significantly decreased upon LINC00158 silencing in MEC-1 compared to controls.

Term	Description	LogP	Log(q-value)
R-HSA-2262752	Cellular responses to stress	-53.62	-49.27
R-HSA-1280218	Adaptive Immune System	-47.45	-43.71
R-HSA-9824446	Viral Infection Pathways	-45.16	-41.51
R-HSA-1280215	**Cytokine Signaling in Immune system**	-41.65	-38.26
R-HSA-983169	Class I MHC mediated antigen processing & presentation	-41.13	-37.79
R-HSA-1640170	**Cell Cycle**	-40.95	-37.65
R-HSA-8953854	Metabolism of RNA	-40.12	-36.86
R-HSA-69278	**Cell Cycle, Mitotic**	-37.23	-34.00
R-HSA-199991	Membrane Trafficking	-34.49	-31.35
R-HSA-983168	Antigen processing: Ubiquitination & Proteasome degradation	-34.03	-30.91
R-HSA-5653656	Vesicle-mediated transport	-32.87	-29.78
R-HSA-68886	M Phase	-29.48	-26.48
R-HSA-5663202	Diseases of signal transduction by growth factor receptors and second messengers	-26.59	-23.63
R-HSA-194315	Signaling by Rho GTPases	-26.27	-23.32
R-HSA-9716542	Signaling by Rho GTPases, Miro GTPases and RHOBTB3	-26.15	-23.24
R-HSA-157118	Signaling by NOTCH	-25.77	-22.87
R-HSA-8878171	Transcriptional regulation by RUNX1	-25.63	-22.75
R-HSA-162906	HIV Infection	-25.58	-22.72
R-HSA-9711123	Cellular response to chemical stress	-24.85	-22.01
R-HSA-449147	Signaling by Interleukins	-24.20	-21.38
R-HSA-3247509	Chromatin modifying enzymes	-22.78	-20.07
R-HSA-4839726	Chromatin organization	-22.78	-20.07
R-HSA-8939236	RUNX1 regulates transcription of genes involved in differentiation of HSCs	-21.81	-19.15
R-HSA-195721	**Signaling by WNT**	-21.42	-18.79
R-HSA-69242	**S Phase**	-21.19	-18.58
R-HSA-1257604	**PIP3 activates AKT signaling**	-21.04	-18.46

R-HSA-446203	Asparagine N-linked glycosylation	-21.05	-18.46
R-HSA-69002	DNA Replication Pre-Initiation	-21.02	-18.45
R-HSA-68867	Assembly of the pre-replicative complex	-20.55	-18.03
R-HSA-69306	**DNA Replication**	-20.00	-17.52
R-HSA-162909	Host Interactions of HIV factors	-19.94	-17.47
R-HSA-9006925	Intracellular signaling by second messengers	-19.86	-17.39
R-HSA-69620	**Cell Cycle Checkpoints**	-19.80	-17.35
R-HSA-983705	**Signaling by the B Cell Receptor (BCR)**	-19.78	-17.33
R-HSA-69275	**G2/M Transition**	-19.28	-16.86
R-HSA-5607764	CLEC7A (Dectin-1) signaling	-19.26	-16.84
R-HSA-201681	TCF dependent signaling in response to WNT	-19.18	-16.77
R-HSA-453274	Mitotic G2-G2/M phases	-19.03	-16.63
R-HSA-69656	Cyclin A:Cdk2-associated events at S phase entry	-18.95	-16.55
R-HSA-948021	Transport to the Golgi and subsequent modification	-18.70	-16.31
R-HSA-9013694	Signaling by NOTCH4	-18.67	-16.29
R-HSA-9675108	Nervous system development	-18.63	-16.26
R-HSA-199977	ER to Golgi Anterograde Transport	-18.53	-16.17
R-HSA-69202	Cyclin E associated events during G1/S transition	-18.44	-16.08
R-HSA-195258	RHO GTPase Effectors	-18.39	-16.03
R-HSA-6807070	PTEN Regulation	-18.31	-15.96
R-HSA-9679506	SARS-CoV Infections	-18.24	-15.90
R-HSA-202424	Downstream TCR signaling	-18.06	-15.74
R-HSA-422475	Axon guidance	-17.91	-15.60
R-HSA-1236975	Antigen processing-Cross presentation	-17.61	-15.32
R-HSA-5357801	Programmed Cell Death	-17.39	-15.10
R-HSA-5676590	**NIK-->noncanonical NF-kB signaling**	-17.37	-15.08
R-HSA-450531	Regulation of mRNA stability by proteins that bind AU-rich elements	-17.36	-15.08
R-HSA-1169091	**Activation of NF-kappaB in B cells**	-17.32	-15.04
R-HSA-176408	Regulation of APC/C activators between G1/S and early anaphase	-17.20	-14.94

R-HSA-176814	Activation of APC/C and APC/C:Cdc20 mediated degradation of mitotic proteins	-17.14	-14.88
R-HSA-5607761	Dectin-1 mediated noncanonical NF-kB signaling	-17.09	-14.84
R-HSA-174178	APC/C:Cdh1 mediated degradation of Cdc20 and other APC/C:Cdh1 targeted proteins in late mitosis/early G1	-16.86	-14.62
R-HSA-202403	TCR signaling	-16.70	-14.47
R-HSA-174143	APC/C-mediated degradation of cell cycle proteins	-16.65	-14.42
R-HSA-453276	**Regulation of mitotic cell cycle**	-16.65	-14.42
R-HSA-69563	**p53-Dependent G1 DNA Damage Response**	-16.56	-14.33
R-HSA-69580	**p53-Dependent G1/S DNA damage checkpoint**	-16.56	-14.33
R-HSA-8878166	Transcriptional regulation by RUNX2	-16.54	-14.32
R-HSA-5668541	**TNFR2 non-canonical NF-kB pathway**	-16.44	-14.23
R-HSA-5688426	Deubiquitination	-16.42	-14.21
R-HSA-176409	**APC/C:Cdc20 mediated degradation of mitotic proteins**	-16.41	-14.20
R-HSA-5621481	C-type lectin receptors (CLRs)	-16.35	-14.16
R-HSA-68882	**Mitotic Anaphase**	-16.33	-14.14
R-HSA-174154	**APC/C:Cdc20 mediated degradation of Securin**	-16.31	-14.13
R-HSA-351202	Metabolism of polyamines	-16.31	-14.12
R-HSA-174084	Autodegradation of Cdh1 by Cdh1:APC/C	-16.30	-14.12
R-HSA-2555396	**Mitotic Metaphase and Anaphase**	-16.23	-14.05
R-HSA-174184	Cdc20:Phospho-APC/C mediated degradation of Cyclin A	-16.12	-13.96
R-HSA-69017	CDK-mediated phosphorylation and removal of Cdc6	-16.12	-13.96
R-HSA-5689880	Ub-specific processing proteases	-16.11	-13.95
R-HSA-69615	**G1/S DNA Damage Checkpoints**	-16.07	-13.92
R-HSA-1236974	ER-Phagosome pathway	-16.06	-13.92
R-HSA-8852276	The role of GTSE1 in G2/M progression after G2 checkpoint	-15.97	-13.83
R-HSA-179419	APC:Cdc20 mediated degradation of cell cycle proteins prior to satisfation of the cell cycle checkpoint	-15.90	-13.76
R-HSA-8939902	Regulation of RUNX2 expression and activity	-15.90	-13.76
R-HSA-8951664	Neddylation	-15.86	-13.73
R-HSA-8948751	Regulation of PTEN stability and activity	-15.84	-13.71
R-HSA-5358346	**Hedgehog ligand biogenesis**	-15.80	-13.68

R-HSA-9755511	KEAP1-NFE2L2 pathway	-15.78	-13.66
R-HSA-1168372	**Downstream signaling events of B Cell Receptor (BCR)**	-15.65	-13.54
R-HSA-180585	Vif-mediated degradation of APOBEC3G	-15.55	-13.45
R-HSA-453279	Mitotic G1 phase and G1/S transition	-15.54	-13.45
R-HSA-72203	Processing of Capped Intron-Containing Pre-mRNA	-15.22	-13.13
R-HSA-109581	Apoptosis	-15.20	-13.12
R-HSA-9020702	Interleukin-1 signaling	-15.12	-13.04
R-HSA-69206	G1/S Transition	-15.06	-12.99
R-HSA-75815	Ubiquitin-dependent degradation of Cyclin D	-15.04	-12.97
R-HSA-187577	SCF(Skp2)-mediated degradation of p27/p21	-15.02	-12.96
R-HSA-5610780	Degradation of GLI1 by the proteasome	-15.02	-12.96
R-HSA-5610783	Degradation of GLI2 by the proteasome	-15.02	-12.96
R-HSA-5610785	GLI3 is processed to GLI3R by the proteasome	-15.02	-12.96
R-HSA-69052	Switching of origins to a post-replicative state	-15.01	-12.96
R-HSA-2871837	**FCERI mediated NF-kB activation**	-14.96	-12.90
R-HSA-69541	Stabilization of p53	-14.76	-12.72
R-HSA-2467813	Separation of Sister Chromatids	-14.75	-12.71
R-HSA-69481	G2/M Checkpoints	-14.71	-12.67
R-HSA-2454202	Fc epsilon receptor (FCERI) signaling	-14.65	-12.63
R-HSA-9694516	SARS-CoV-2 Infection	-14.61	-12.60
R-HSA-211733	Regulation of activated PAK-2p34 by proteasome mediated degradation	-14.53	-12.51
R-HSA-69239	Synthesis of DNA	-14.38	-12.37
R-HSA-446652	**Interleukin-1 family signaling**	-14.34	-12.34
R-HSA-5387390	Hh mutants abrogate ligand secretion	-14.27	-12.28
R-HSA-350562	Regulation of ornithine decarboxylase (ODC)	-14.26	-12.26
R-HSA-4641257	Degradation of AXIN	-14.25	-12.26
R-HSA-8941858	Regulation of RUNX3 expression and activity	-14.25	-12.26
R-HSA-5658442	Regulation of RAS by GAPs	-14.16	-12.18
R-HSA-8878159	Transcriptional regulation by RUNX3	-14.15	-12.17

R-HSA-5358351	Signaling by Hedgehog	-14.14	-12.17
R-HSA-450408	AUF1 (hnRNP D0) binds and destabilizes mRNA	-14.00	-12.03
R-HSA-5362768	Hh mutants are degraded by ERAD	-14.00	-12.03
R-HSA-349425	Autodegradation of the E3 ubiquitin ligase COP1	-13.99	-12.02
R-HSA-9762114	GSK3B and BTRC:CUL1-mediated-degradation of NFE2L2	-13.99	-12.02
R-HSA-9012999	RHO GTPase cycle	-13.96	-11.99
R-HSA-5678895	Defective CFTR causes cystic fibrosis	-13.80	-11.85
R-HSA-4641258	Degradation of DVL	-13.76	-11.80
R-HSA-169911	Regulation of Apoptosis	-13.74	-11.78
R-HSA-376176	Signaling by ROBO receptors	-13.69	-11.74
R-HSA-72163	mRNA Splicing - Major Pathway	-13.64	-11.69
R-HSA-9010553	**Regulation of expression of SLITs and ROBOs**	-13.50	-11.55
R-HSA-9604323	Negative regulation of NOTCH4 signaling	-13.49	-11.55
R-HSA-8854050	FBXL7 down-regulates AURKA during mitotic entry and in early mitosis	-13.25	-11.32
R-HSA-5683057	**MAPK family signaling cascades**	-13.17	-11.25
R-HSA-5610787	Hedgehog 'off' state	-13.13	-11.21
R-HSA-195253	Degradation of beta-catenin by the destruction complex	-13.05	-11.14
R-HSA-5684996	**MAPK1/MAPK3 signaling**	-13.01	-11.09
R-HSA-180534	Vpu mediated degradation of CD4	-12.98	-11.07
R-HSA-69601	Ubiquitin Mediated Degradation of Phosphorylated Cdc25A	-12.98	-11.07
R-HSA-69610	p53-Independent DNA Damage Response	-12.98	-11.07
R-HSA-69613	p53-Independent G1/S DNA damage checkpoint	-12.98	-11.07
R-HSA-72172	mRNA Splicing	-12.90	-11.00
R-HSA-1234176	Oxygen-dependent proline hydroxylation of Hypoxia-inducible Factor Alpha	-12.74	-10.86
R-HSA-68949	Orc1 removal from chromatin	-12.66	-10.78
R-HSA-6807878	COPI-mediated anterograde transport	-12.59	-10.72
R-HSA-3858494	**Beta-catenin independent WNT signaling**	-12.48	-10.61
R-HSA-5689603	UCH proteinases	-12.44	-10.58
R-HSA-5673001	**RAF/MAP kinase cascade**	-12.43	-10.57

R-HSA-9759194	Nuclear events mediated by NFE2L2	-12.41	-10.56
R-HSA-174113	SCF-beta-TrCP mediated degradation of Emi1	-12.28	-10.42
R-HSA-5619084	ABC transporter disorders	-12.25	-10.40
R-HSA-9793380	Formation of paraxial mesoderm	-12.16	-10.31
R-HSA-1234174	**Cellular response to hypoxia**	-11.93	-10.10
R-HSA-5632684	Hedgehog 'on' state	-11.91	-10.08
R-HSA-1236978	Cross-presentation of soluble exogenous antigens (endosomes)	-11.71	-9.89
R-HSA-71291	Metabolism of amino acids and derivatives	-11.71	-9.89
R-HSA-4086400	PCP/CE pathway	-11.62	-9.81
R-HSA-382556	ABC-family proteins mediated transport	-11.56	-9.76
R-HSA-4608870	Asymmetric localization of PCP proteins	-11.35	-9.56
R-HSA-9824272	Somitogenesis	-11.34	-9.55
R-HSA-5687128	**MAPK6/MAPK4 signaling**	-11.30	-9.51
R-HSA-6811442	Intra-Golgi and retrograde Golgi-to-ER traffic	-11.21	-9.43
R-HSA-3214847	HATs acetylate histones	-11.09	-9.31
R-HSA-3214858	RMTs methylate histone arginines	-10.63	-8.88
R-HSA-9705683	SARS-CoV-2-host interactions	-10.58	-8.83
R-HSA-5619115	Disorders of transmembrane transporters	-10.11	-8.39
R-HSA-8856688	Golgi-to-ER retrograde transport	-10.04	-8.33
R-HSA-9705671	SARS-CoV-2 activates/modulates innate and adaptive immune responses	-8.30	-6.72
R-HSA-9758941	Gastrulation	-7.67	-6.13
R-HSA-6811434	COPI-dependent Golgi-to-ER retrograde traffic	-5.58	-4.24
R-HSA-9833482	PKR-mediated signaling	-3.25	-2.21
R-HSA-5693571	Nonhomologous End-Joining (NHEJ)	-3.24	-2.20
R-HSA-73856	RNA Polymerase II Transcription Termination	-3.24	-2.20
R-HSA-156902	Peptide chain elongation	-3.22	-2.18
R-HSA-192823	Viral mRNA Translation	-3.22	-2.18
R-HSA-6791312	TP53 Regulates Transcription of Cell Cycle Genes	-3.22	-2.18
R-HSA-202040	G-protein activation	-3.20	-2.16

R-HSA-982772	Growth hormone receptor signaling	-3.20	-2.16
R-HSA-180897	Vpr-mediated induction of apoptosis by mitochondrial outer membrane permeabilization	-3.19	-2.16
R-HSA-6806664	Metabolism of vitamin K	-3.19	-2.16
R-HSA-9013409	RHOJ GTPase cycle	-3.18	-2.15
R-HSA-9821993	Replacement of protamines by nucleosomes in the male pronucleus	-3.18	-2.15
R-HSA-877312	Regulation of IFNG signaling	-3.17	-2.15
R-HSA-9005891	Loss of function of MECP2 in Rett syndrome	-3.17	-2.15
R-HSA-9005895	Pervasive developmental disorders	-3.17	-2.15
R-HSA-9675151	Disorders of Developmental Biology	-3.17	-2.15
R-HSA-9697154	Disorders of Nervous System Development	-3.17	-2.15
R-HSA-6811558	PI5P, PP2A and IER3 Regulate PI3K/AKT Signaling	-3.17	-2.15
R-HSA-8856825	Cargo recognition for clathrin-mediated endocytosis	-3.17	-2.15
R-HSA-425407	SLC-mediated transmembrane transport	-3.16	-2.14
R-HSA-176407	Conversion from APC/C:Cdc20 to APC/C:Cdh1 in late anaphase	-3.16	-2.13
R-HSA-392851	Prostacyclin signalling through prostacyclin receptor	-3.16	-2.13
R-HSA-9703465	Signaling by FLT3 fusion proteins	-3.16	-2.13
R-HSA-6802957	**Oncogenic MAPK signaling**	-3.14	-2.12
R-HSA-72306	tRNA processing	-3.12	-2.10
R-HSA-9646399	Aggrephagy	-3.08	-2.07
R-HSA-9660821	ADORA2B mediated anti-inflammatory cytokines production	-3.08	-2.07
R-HSA-381183	ATF6 (ATF6-alpha) activates chaperone genes	-3.08	-2.07
R-HSA-9701898	**STAT3 nuclear events downstream of ALK signaling**	-3.08	-2.07
R-HSA-400685	Sema4D in semaphorin signaling	-3.07	-2.06
R-HSA-418592	ADP signalling through P2Y purinoceptor 1	-3.07	-2.06
R-HSA-5357786	TNFR1-induced proapoptotic signaling	-3.07	-2.06
R-HSA-8854691	Interleukin-20 family signaling	-3.07	-2.06
R-HSA-9013508	NOTCH3 Intracellular Domain Regulates Transcription	-3.07	-2.06
R-HSA-5689901	Metalloprotease DUBs	-3.05	-2.05
R-HSA-6784531	tRNA processing in the nucleus	-3.03	-2.03

R-HSA-5625900	RHO GTPases activate CIT	-3.00	-2.00
R-HSA-451927	**Interleukin-2 family signaling**	-2.99	-2.00
R-HSA-5633008	TP53 Regulates Transcription of Cell Death Genes	-2.99	-2.00
R-HSA-6811438	Intra-Golgi traffic	-2.99	-2.00
R-HSA-380320	Recruitment of NuMA to mitotic centrosomes	-2.99	-1.99
R-HSA-8875360	InlB-mediated entry of Listeria monocytogenes into host cell	-2.99	-1.99
R-HSA-9694631	Maturation of nucleoprotein	-2.99	-1.99
R-HSA-9694676	Translation of Replicase and Assembly of the Replication Transcription Complex	-2.99	-1.99
R-HSA-448424	Interleukin-17 signaling	-2.97	-1.98
R-HSA-3928665	EPH-ephrin mediated repulsion of cells	-2.96	-1.97
R-HSA-3232142	SUMOylation of ubiquitinylation proteins	-2.95	-1.96
R-HSA-9013407	RHOH GTPase cycle	-2.95	-1.96
R-HSA-174411	Polymerase switching on the C-strand of the telomere	-2.94	-1.95
R-HSA-912694	Regulation of IFNA/IFNB signaling	-2.94	-1.95
R-HSA-397795	G-protein beta:gamma signalling	-2.93	-1.95
R-HSA-416482	G alpha (12/13) signalling events	-2.93	-1.94
R-HSA-373760	L1CAM interactions	-2.91	-1.92
R-HSA-70171	Glycolysis	-2.90	-1.92
R-HSA-75153	Apoptotic execution phase	-2.88	-1.90
R-HSA-9013406	RHOQ GTPase cycle	-2.88	-1.90
R-HSA-983712	Ion channel transport	-2.88	-1.90
R-HSA-9840310	Glycosphingolipid catabolism	-2.86	-1.88
R-HSA-416572	Sema4D induced cell migration and growth-cone collapse	-2.86	-1.88
R-HSA-5621575	CD209 (DC-SIGN) signaling	-2.86	-1.88
R-HSA-1236977	Endosomal/Vacuolar pathway	-2.85	-1.88
R-HSA-193692	Regulated proteolysis of p75NTR	-2.85	-1.88
R-HSA-9020956	Interleukin-27 signaling	-2.85	-1.88
R-HSA-190236	Signaling by FGFR	-2.84	-1.87
R-HSA-9022692	Regulation of MECP2 expression and activity	-2.83	-1.86

R-HSA-167160	RNA Pol II CTD phosphorylation and interaction with CE during HIV infection	-2.82	-1.85
R-HSA-191273	Cholesterol biosynthesis	-2.82	-1.85
R-HSA-380994	ATF4 activates genes in response to endoplasmic reticulum stress	-2.82	-1.85
R-HSA-77075	RNA Pol II CTD phosphorylation and interaction with CE	-2.82	-1.85
R-HSA-912526	Interleukin receptor SHC signaling	-2.82	-1.85
R-HSA-1295596	Spry regulation of FGF signaling	-2.81	-1.85
R-HSA-205043	NRIF signals cell death from the nucleus	-2.81	-1.85
R-HSA-399954	Sema3A PAK dependent Axon repulsion	-2.81	-1.85
R-HSA-429958	mRNA decay by 3' to 5' exoribonuclease	-2.81	-1.85
R-HSA-5684264	**MAP3K8 (TPL2)-dependent MAPK1/3 activation**	-2.81	-1.85
R-HSA-844456	The NLRP3 inflammasome	-2.81	-1.85
R-HSA-8949664	Processing of SMDT1	-2.81	-1.85
R-HSA-5603029	IkBA variant leads to EDA-ID	-2.81	-1.85
R-HSA-5649702	APEX1-Independent Resolution of AP Sites via the Single Nucleotide Replacement Pathway	-2.81	-1.85
R-HSA-9635465	**Suppression of apoptosis**	-2.81	-1.85
R-HSA-9652817	Signaling by MAPK mutants	-2.81	-1.85
R-HSA-168276	NS1 Mediated Effects on Host Pathways	-2.77	-1.81
R-HSA-5674135	**MAP2K and MAPK activation**	-2.77	-1.81
R-HSA-9013148	CDC42 GTPase cycle	-2.77	-1.81
R-HSA-6802946	Signaling by moderate kinase activity BRAF mutants	-2.74	-1.78
R-HSA-6802949	Signaling by RAS mutants	-2.74	-1.78
R-HSA-6802955	Paradoxical activation of RAF signaling by kinase inactive BRAF	-2.74	-1.78
R-HSA-9649948	Signaling downstream of RAS mutants	-2.74	-1.78
R-HSA-389357	CD28 dependent PI3K/Akt signaling	-2.73	-1.77
R-HSA-9609523	Insertion of tail-anchored proteins into the endoplasmic reticulum membrane	-2.73	-1.77
R-HSA-159231	Transport of Mature mRNA Derived from an Intronless Transcript	-2.68	-1.73
R-HSA-9772755	Formation of WDR5-containing histone-modifying complexes	-2.68	-1.73
R-HSA-418597	G alpha (z) signalling events	-2.66	-1.72
R-HSA-109606	Intrinsic Pathway for Apoptosis	-2.66	-1.71

R-HSA-381033	ATF6 (ATF6-alpha) activates chaperones	-2.65	-1.71
R-HSA-5689877	Josephin domain DUBs	-2.65	-1.71
R-HSA-6803207	TP53 Regulates Transcription of Caspase Activators and Caspases	-2.65	-1.71
R-HSA-114604	GPVI-mediated activation cascade	-2.63	-1.69
R-HSA-9706574	RHOBTB GTPase Cycle	-2.63	-1.69
R-HSA-380259	Loss of Nlp from mitotic centrosomes	-2.63	-1.69
R-HSA-380284	Loss of proteins required for interphase microtubule organization from the centrosome	-2.63	-1.69
R-HSA-110381	Resolution of AP sites via the single-nucleotide replacement pathway	-2.62	-1.69
R-HSA-75944	Transcription from mitochondrial promoters	-2.62	-1.69
R-HSA-9652169	Signaling by MAP2K mutants	-2.62	-1.69
R-HSA-1226099	Signaling by FGFR in disease	-2.61	-1.68
R-HSA-422356	Regulation of insulin secretion	-2.60	-1.67
R-HSA-76005	Response to elevated platelet cytosolic Ca2+	-2.60	-1.67
R-HSA-72086	mRNA Capping	-2.60	-1.67
R-HSA-8863795	Downregulation of ERBB2 signaling	-2.60	-1.67
R-HSA-159234	Transport of Mature mRNAs Derived from Intronless Transcripts	-2.60	-1.67
R-HSA-4551638	SUMOylation of chromatin organization proteins	-2.57	-1.65
R-HSA-196849	Metabolism of water-soluble vitamins and cofactors	-2.55	-1.62
R-HSA-6802948	Signaling by high-kinase activity BRAF mutants	-2.54	-1.62
R-HSA-1236973	Cross-presentation of particulate exogenous antigens (phagosomes)	-2.54	-1.62
R-HSA-9017802	Noncanonical activation of NOTCH3	-2.54	-1.62
R-HSA-9732724	IFNG signaling activates MAPKs	-2.54	-1.62
R-HSA-5696395	Formation of Incision Complex in GG-NER	-2.52	-1.60
R-HSA-1660514	Synthesis of PIPs at the Golgi membrane	-2.51	-1.60
R-HSA-1839117	Signaling by cytosolic FGFR1 fusion mutants	-2.51	-1.60
R-HSA-8964315	**G beta:gamma signalling through BTK**	-2.51	-1.60
R-HSA-9758274	**Regulation of NF-kappa B signaling**	-2.51	-1.60
R-HSA-177929	**Signaling by EGFR**	-2.51	-1.60
R-HSA-110314	Recognition of DNA damage by PCNA-containing replication complex	-2.50	-1.59

R-HSA-114452	Activation of BH3-only proteins	-2.50	-1.59
R-HSA-3928663	EPHA-mediated growth cone collapse	-2.50	-1.59
R-HSA-203927	MicroRNA (miRNA) biogenesis	-2.48	-1.58
R-HSA-429947	Deadenylation of mRNA	-2.48	-1.58
R-HSA-6783589	**Interleukin-6 family signaling**	-2.48	-1.58
R-HSA-9820841	M-decay: degradation of maternal mRNAs by maternally stored factors	-2.48	-1.58
R-HSA-1268020	Mitochondrial protein import	-2.48	-1.58
R-HSA-141424	Amplification of signal from the kinetochores	-2.48	-1.57
R-HSA-141444	Amplification of signal from unattached kinetochores via a MAD2 inhibitory signal	-2.48	-1.57
R-HSA-1358803	Downregulation of ERBB2:ERBB3 signaling	-2.47	-1.57
R-HSA-174430	Telomere C-strand synthesis initiation	-2.47	-1.57
R-HSA-879415	Advanced glycosylation endproduct receptor signaling	-2.47	-1.57
R-HSA-9637687	Suppression of phagosomal maturation	-2.47	-1.57
R-HSA-114608	Platelet degranulation	-2.47	-1.56
R-HSA-8854518	AURKA Activation by TPX2	-2.46	-1.56
R-HSA-180786	Extension of Telomeres	-2.44	-1.54
R-HSA-9754678	SARS-CoV-2 modulates host translation machinery	-2.44	-1.54
R-HSA-8980692	RHOA GTPase cycle	-2.42	-1.52
R-HSA-168271	Transport of Ribonucleoproteins into the Host Nucleus	-2.41	-1.51
R-HSA-168333	NEP/NS2 Interacts with the Cellular Export Machinery	-2.41	-1.51
R-HSA-170822	Regulation of Glucokinase by Glucokinase Regulatory Protein	-2.41	-1.51
R-HSA-182971	EGFR downregulation	-2.41	-1.51
R-HSA-5619107	Defective TPR may confer susceptibility towards thyroid papillary carcinoma (TPC)	-2.41	-1.51
R-HSA-5620912	Anchoring of the basal body to the plasma membrane	-2.38	-1.49
R-HSA-110320	Translesion Synthesis by POLH	-2.38	-1.49
R-HSA-8851708	Signaling by FGFR2 IIIa TM	-2.38	-1.49
R-HSA-1643713	Signaling by EGFR in Cancer	-2.38	-1.48
R-HSA-210991	Basigin interactions	-2.38	-1.48
R-HSA-5696397	Gap-filling DNA repair synthesis and ligation in GG-NER	-2.38	-1.48

R-HSA-9006335	Signaling by Erythropoietin	-2.38	-1.48
R-HSA-390471	Association of TriC/CCT with target proteins during biosynthesis	-2.37	-1.48
R-HSA-9607240	FLT3 Signaling	-2.37	-1.48
R-HSA-9772572	Early SARS-CoV-2 Infection Events	-2.37	-1.48
R-HSA-9634597	GPER1 signaling	-2.36	-1.48
R-HSA-6802952	Signaling by BRAF and RAF1 fusions	-2.36	-1.48
R-HSA-110357	Displacement of DNA glycosylase by APEX1	-2.31	-1.43
R-HSA-1253288	Downregulation of ERBB4 signaling	-2.31	-1.43
R-HSA-8849469	PTK6 Regulates RTKs and Their Effectors AKT1 and DOK1	-2.31	-1.43
R-HSA-8948747	Regulation of PTEN localization	-2.31	-1.43
R-HSA-8985947	**Interleukin-9 signaling**	-2.31	-1.43
R-HSA-9029558	NR1H2 & NR1H3 regulate gene expression linked to lipogenesis	-2.31	-1.43
R-HSA-156581	Methylation	-2.31	-1.43
R-HSA-174490	Membrane binding and targetting of GAG proteins	-2.31	-1.43
R-HSA-174495	Synthesis And Processing Of GAG, GAGPOL Polyproteins	-2.31	-1.43
R-HSA-189451	Heme biosynthesis	-2.31	-1.43
R-HSA-8941856	RUNX3 regulates NOTCH signaling	-2.31	-1.43
R-HSA-8983432	**Interleukin-15 signaling**	-2.31	-1.43
R-HSA-9679504	Translation of Replicase and Assembly of the Replication Transcription Complex	-2.31	-1.43
R-HSA-975110	**TRAF6 mediated IRF7 activation in TLR7/8 or 9 signaling**	-2.31	-1.43
R-HSA-196854	Metabolism of vitamins and cofactors	-2.31	-1.43
R-HSA-8854214	TBC/RABGAPs	-2.29	-1.42
R-HSA-6804756	Regulation of TP53 Activity through Phosphorylation	-2.29	-1.41
R-HSA-2173788	Downregulation of TGF-beta receptor signaling	-2.27	-1.40
R-HSA-198725	Nuclear Events (kinase and transcription factor activation)	-2.27	-1.40
R-HSA-6790901	rRNA modification in the nucleus and cytosol	-2.27	-1.40
R-HSA-168927	TICAM1, RIP1-mediated IKK complex recruitment	-2.26	-1.39
R-HSA-418217	G beta:gamma signalling through PLC beta	-2.26	-1.39
R-HSA-8876384	Listeria monocytogenes entry into host cells	-2.26	-1.39

R-HSA-8964616	G beta:gamma signalling through CDC42	-2.26	-1.39
R-HSA-9013695	NOTCH4 Intracellular Domain Regulates Transcription	-2.26	-1.39
R-HSA-9669938	Signaling by KIT in disease	-2.26	-1.39
R-HSA-9670439	Signaling by phosphorylated juxtamembrane, extracellular and kinase domain KIT mutants	-2.26	-1.39
R-HSA-180689	APOBEC3G mediated resistance to HIV-1 infection	-2.25	-1.39
R-HSA-69478	G2/M DNA replication checkpoint	-2.25	-1.39
R-HSA-9032759	NTRK2 activates RAC1	-2.25	-1.39
R-HSA-163359	Glucagon signaling in metabolic regulation	-2.23	-1.37
R-HSA-168274	Export of Viral Ribonucleoproteins from Nucleus	-2.23	-1.37
R-HSA-180746	Nuclear import of Rev protein	-2.23	-1.37
R-HSA-352230	Amino acid transport across the plasma membrane	-2.23	-1.37
R-HSA-420092	Glucagon-type ligand receptors	-2.23	-1.37
R-HSA-6783783	**Interleukin-10 signaling**	-2.22	-1.37
R-HSA-73762	RNA Polymerase I Transcription Initiation	-2.22	-1.37
R-HSA-9024446	NR1H2 and NR1H3-mediated signaling	-2.22	-1.37
R-HSA-9707616	Heme signaling	-2.22	-1.37
R-HSA-1483166	Synthesis of PA	-2.22	-1.36
R-HSA-2219530	Constitutive Signaling by Aberrant PI3K in Cancer	-2.19	-1.34
R-HSA-446193	Biosynthesis of the N-glycan precursor (dolichol lipid-linked oligosaccharide, LLO) and transfer to a nascent protein	-2.19	-1.34
R-HSA-71406	Pyruvate metabolism and Citric Acid (TCA) cycle	-2.18	-1.33
R-HSA-1368108	BMAL1:CLOCK,NPAS2 activates circadian gene expression	-2.17	-1.32
R-HSA-189445	Metabolism of porphyrins	-2.17	-1.32
R-HSA-2691230	Signaling by NOTCH1 HD Domain Mutants in Cancer	-2.16	-1.32
R-HSA-2691232	Constitutive Signaling by NOTCH1 HD Domain Mutants	-2.16	-1.32
R-HSA-71336	Pentose phosphate pathway	-2.16	-1.32
R-HSA-937039	IRAK1 recruits IKK complex	-2.16	-1.32
R-HSA-9648895	Response of EIF2AK1 (HRI) to heme deficiency	-2.16	-1.32
R-HSA-9706369	Negative regulation of FLT3	-2.16	-1.32
R-HSA-975144	IRAK1 recruits IKK complex upon TLR7/8 or 9 stimulation	-2.16	-1.32

R-HSA-446219	Synthesis of substrates in N-glycan biosythesis	-2.16	-1.31