ESRRA Cluster 1	ESRRA Cluster 2
CEP70	IMPA1
DLG3	CHCHD7
ZNF165	SULT2B1
BCL7A	ACYP1
PLA2G12A	MAT2A
MDH1	TET2
CHCHD3	LPIN1
MUT	HR
ATP5G1	DRAM1
ABHD11	KCNN4
ILVBL	B4GALT5
CKMT1B	CDK5R1
AHCY	DNMT1
NDUFA8	SPP1
CKMT1A	GPR37
SUCLG1	TET3
VDAC3	ELOVL6
STARD7	BAMBI
ATP5G3	CCDC93
NDUFS1	GJB5
UQCRB	CPT1A
COX5A	MPHOSPH9
COX7B	PDSS1
SIRT5	GNE
ATP5C1	RBM38
ATP5O	SOD2
MRPL35	SYNGR3
COQ3	HSPA1B
UQCRFS1	HSPA1A
NDUFA9	UCKL1
NDUFS3	POP1
NDUFA6	DNMT3A
SAMM50	CCNE1

AFG3L2	AURKA
CYCS	GAS2L1
COQ9	NOP16
HSPA9	KCNG1
CISD1	CDR2L
NDUFAF4	STEAP3
DLAT	ATAD3A
PPIF	TBRG4
RAB3A	
SDHA	
IMMT	
GRPEL1	
FH	
IDH3A	
HCCS	
DEFB1	
SLC25A5	
PDHA1	
CS	
AK1	
TACO1	
NRTN	
TMEM223	
GTPBP8	
TIMM17A	
EIF3K	
FASTKD1	
C14orf2	
PHB	
COX6B1	
CIAPIN1	
MRPL2	
MRS2	
CYP27B1	

DHDDS
MAT1A
ISOC2
HSPE1
XPO4
TIMM8A
SMC2
OPA1
MB
C20orf24
TIMM44
SUPV3L1

KEGG 2021 Human Cluster 1

Term	P-value	Adjusted P-	Odds Ratio	Combined S	Genes
Diabetic cardiomyop	2.26E-15	1.90E-13	24.60065	829.6087	NDUFA9;NDUFA8;COX7B;NDUFA6;PDHA1;UQ
Parkinson disease	4.65E-14	1.95E-12	19.71855	605.3334	NDUFA9;NDUFA8;COX7B;NDUFA6;UQCRB;SDI
Prion disease	1.79E-13	4.72E-12	17.86246	524.3103	NDUFA9;NDUFA8;COX7B;NDUFA6;UQCRB;SDI
Citrate cycle (TCA cyc	2.25E-13	4.72E-12	101.9155	2968.252	CS;FH;PDHA1;MDH1;SUCLG1;DLAT;SDHA;IDH
Huntington disease	9.35E-13	1.40E-11	15.81024	437.9144	NDUFA9;NDUFA8;COX7B;NDUFA6;UQCRB;SDI
Non-alcoholic fatty li	9.99E-13	1.40E-11	24.77153	684.4778	NDUFA9;NDUFA8;COX7B;NDUFA6;UQCRB;ND
Oxidative phosphory	4.55E-12	5.46E-11	26.25229	685.6103	NDUFA9;NDUFA8;COX7B;NDUFA6;UQCRB;ND
Alzheimer disease	1.36E-11	1.43E-10	12.95485	324.1448	NDUFA9;NDUFA8;COX7B;NDUFA6;UQCRB;SDI
Thermogenesis	1.15E-10	1.08E-09	16.03881	367.0341	NDUFA9;NDUFA8;COX7B;NDUFA6;UQCRB;ND
Pathways of neurode	4.64E-10	3.90E-09	9.915591	213.1006	NDUFA9;NDUFA8;COX7B;NDUFA6;UQCRB;SDI
Amyotrophic lateral s	1.89E-08	1.44E-07	9.95709	177.0887	NDUFA9;NDUFA8;COX7B;NDUFA6;UQCRB;ND
Spinocerebellar ataxi	2.18E-05	1.52E-04	11.86921	127.4178	AFG3L2;OPA1;VDAC3;PPIF;CYCS;SLC25A5
Cardiac muscle contr	2.43E-05	1.57E-04	16.34723	173.7145	COX7B;UQCRB;UQCRFS1;COX5A;COX6B1
Pyruvate metabolism	3.53E-05	2.12E-04	24.65488	252.7226	FH;PDHA1;MDH1;DLAT
Retrograde endocann	3.01E-04	0.001685	9.345114	75.77628	NDUFA9;NDUFA8;NDUFA6;NDUFS3;NDUFS1
Cysteine and methio	0.001017	0.00534	16.69149	115.0174	AHCY;MDH1;MAT1A
Glyoxylate and dicarb	0.006238	0.030822	18.45362	93.6913	CS;MDH1
Arginine and proline	0.016695	0.077912	10.75379	44.01114	CKMT1A;CKMT1B
cGMP-PKG signaling	0.028489	0.121237	4.755375	16.92081	VDAC3;PPIF;SLC25A5
Glycolysis / Gluconec	0.028866	0.121237	7.934466	28.12843	PDHA1;DLAT
Tuberculosis	0.034454	0.137817	4.403211	14.83055	HSPA9;CYP27B1;CYCS
Neutrophil extracellu	0.038935	0.148659	4.188243	13.59451	VDAC3;PPIF;SLC25A5
Ubiquinone and othe	0.042612	0.155627	25.52692	80.55315	COQ3
Thiamine metabolism	0.057659	0.201806	18.22985	52.01364	AK1
Calcium signaling pat	0.069514	0.233567	3.278481	8.741179	VDAC3;PPIF;SLC25A5
Toxoplasmosis	0.072504	0.234244	4.677922	12.27538	PPIF;CYCS
Steroid biosynthesis	0.076139	0.236877	13.42915	34.58265	CYP27B1
Terpenoid backbone	0.083431	0.250292	12.14896	30.17485	DHDDS
Proximal tubule bicar	0.087055	0.25216	11.59615	28.30869	MDH1
alpha-Linolenic acid r	0.094262	0.263932	10.62874	25.1017	PLA2G12A
Linoleic acid metabol	0.108506	0.294017	9.108516	20.22952	PLA2G12A
Propanoate metabol	0.126002	0.304422	7.726496	16.00512	SUCLG1
Cellular senescence	0.126501	0.304422	3.333952	6.892962	VDAC3;SLC25A5
Ribosome	0.129141	0.304422	3.290876	6.735919	MRPL2;MRPL35
Nicotinate and nicoti	0.12946	0.304422	7.498869	15.33057	SIRT5
Necroptosis	0.130467	0.304422	3.269749	6.659296	VDAC3;SLC25A5
Hepatitis B	0.134461	0.305263	3.207955	6.436697	VDAC3;CYCS
Influenza A	0.14797	0.320928	3.017723	5.766109	CYCS;SLC25A5
Ferroptosis	0.149927	0.320928	6.372115	12.09177	VDAC3
Fat digestion and abs	0.156643	0.320928	6.068071	11.2489	PLA2G12A
Porphyrin and chloro	0.156643	0.320928	6.068071	11.2489	HCCS
ABC transporters	0.163307	0.326614	5.791667	10.49521	DEFB1
Ether lipid metabolis	0.176479	0.34314	5.307959	9.206936	PLA2G12A
Cholesterol metaboli	0.17974	0.34314	5.199372	8.923391	VDAC3
Legionellosis	0.202212	0.375863	4.547848	7.269456	CYCS

Viral myocarditis	0.211656	0.375863	4.31595	6.701781	CYCS
Human T-cell leukem	0.214375	0.375863	2.358489	3.632145	VDAC3;SLC25A5
Arachidonic acid met	0.214779	0.375863	4.243803	6.527586	PLA2G12A
Renal cell carcinoma	0.23933	0.407139	3.743024	5.352199	FH
Central carbon metal	0.242345	0.407139	3.688592	5.228187	PDHA1
p53 signaling pathwa	0.251319	0.413938	3.534366	4.881069	CYCS
Synaptic vesicle cycle	0.266044	0.426268	3.304029	4.374842	RAB3A
RNA degradation	0.268955	0.426268	3.261506	4.28305	HSPA9
Insulin secretion	0.289011	0.441399	2.991855	3.713758	RAB3A
Colorectal cancer	0.289011	0.441399	2.991855	3.713758	CYCS
Small cell lung cancer	0.30577	0.458654	2.793745	3.310373	CYCS
Staphylococcus aureu	0.314002	0.46274	2.704173	3.132396	DEFB1
Glycerophospholipid	0.322138	0.466544	2.620143	2.968034	PLA2G12A
Pancreatic secretion	0.332838	0.473871	2.515867	2.767706	PLA2G12A
Parathyroid hormone	0.343371	0.475769	2.419536	2.58635	CYP27B1
Glucagon signaling pa	0.345978	0.475769	2.396589	2.543691	PDHA1
HIF-1 signaling pathw	0.351163	0.475769	2.351971	2.461351	PDHA1
Purine metabolism	0.400825	0.534434	1.982472	1.812434	AK1
Vascular smooth mus	0.410298	0.538516	1.922009	1.712264	PLA2G12A
Measles	0.42423	0.548235	1.837886	1.57595	CYCS
Apoptosis	0.431074	0.548639	1.798509	1.513403	CYCS
Cushing syndrome	0.459813	0.573307	1.645604	1.278528	FH
Hepatitis C	0.464105	0.573307	1.624343	1.246916	CYCS
Hippo signaling pathv	0.476781	0.58043	1.563707	1.158233	DLG3
Tight junction	0.489161	0.586994	1.507402	1.077888	DLG3
NOD-like receptor sig	0.51306	0.607	1.406054	0.938348	VDAC3
Kaposi sarcoma-asso	0.535854	0.620526	1.317374	0.821902	CYCS
Pathogenic Escherich	0.543215	0.620526	1.290228	0.787361	CYCS
Epstein-Barr virus inf	0.552255	0.620526	1.257813	0.746821	CYCS
Viral carcinogenesis	0.554041	0.620526	1.251523	0.739044	VDAC3
Human immunodefic	0.569808	0.627207	1.197594	0.673594	CYCS
Lipid and atheroscler	0.57494	0.627207	1.180625	0.653464	CYCS
Human cytomegalovi	0.591614	0.637123	1.127347	0.591745	CYCS
Ras signaling pathwa	0.6029	0.641058	1.092796	0.552959	PLA2G12A
Pathways in cancer	0.624082	0.644385	0.952152	0.448915	FH;CYCS
Shigellosis	0.624556	0.644385	1.029618	0.484655	CYCS
Salmonella infection	0.629043	0.644385	1.017008	0.47144	CYCS
Human papillomaviru	0.733128	0.741961	0.761111	0.236276	DLG3
Herpes simplex virus	0.864114	0.864114	0.501058	0.07318	CYCS

CRB;SDHA;COX5A;COX6B1;VDAC3;NDUFS3;PPIF;UQCRFS1;NDUFS1;SLC25A5
HA;COX5A;COX6B1;VDAC3;NDUFS3;PPIF;UQCRFS1;CYCS;NDUFS1;SLC25A5
HA;COX5A;COX6B1;VDAC3;NDUFS3;PPIF;UQCRFS1;CYCS;NDUFS1;SLC25A5

HA;COX5A;COX6B1;VDAC3;NDUFS3;PPIF;UQCRFS1;CYCS;NDUFS1;SLC25A5

HA;COX5A;COX6B1;VDAC3;NDUFS3;PPIF;UQCRFS1;CYCS;NDUFS1;SLC25A5

HA;COX5A;COX6B1;VDAC3;NDUFS3;PPIF;UQCRFS1;CYCS;NDUFS1;SLC25A5

KEGG 2021 Human Cluster 2

Term	P-value	Adjusted P-	Odds Ratio	Combined	Genes
Cysteine and methionine met	1.47E-04	0.010407	33.44681	295.2684	DNMT1;MAT2A;DNMT3A
Longevity regulating pathway	0.001193	0.042337	15.83732	106.6109	SOD2;HSPA1B;HSPA1A
Measles	0.002887	0.068322	11.50716	67.2891	CCNE1;HSPA1B;HSPA1A
Legionellosis	0.006093	0.099035	18.55851	94.65842	HSPA1B;HSPA1A
GnRH secretion	0.007628	0.099035	16.4574	80.24571	SPP1;KCNN4
Lipid and atherosclerosis	0.009671	0.099035	7.353649	34.11109	SOD2;HSPA1B;HSPA1A
p53 signaling pathway	0.009829	0.099035	14.36475	66.40057	STEAP3;CCNE1
Antigen processing and prese	0.011159	0.099035	13.41633	60.31338	HSPA1B;HSPA1A
Toxoplasmosis	0.02211	0.174426	9.253613	35.27209	HSPA1B;HSPA1A
MicroRNAs in cancer	0.025479	0.180903	5.05366	18.54637	DNMT1;CCNE1;DNMT3A
Oocyte meiosis	0.028734	0.185465	8.008076	28.42607	CCNE1;AURKA
Estrogen signaling pathway	0.032093	0.189884	7.530484	25.89819	HSPA1B;HSPA1A
Spliceosome	0.037863	0.206793	6.864518	22.47285	HSPA1B;HSPA1A
Terpenoid backbone biosynth	0.044165	0.223979	23.73571	74.05131	PDSS1
Protein processing in endopla	0.047948	0.225253	6.005159	18.24154	HSPA1B;HSPA1A
Biosynthesis of unsaturated f	0.053934	0.225253	19.16635	55.96572	ELOVL6
Fatty acid elongation	0.053934	0.225253	19.16635	55.96572	ELOVL6
Mucin type O-glycan biosynth	0.071273	0.281132	14.23143	37.58863	B4GALT5
Ferroptosis	0.080771	0.282953	12.44938	31.3243	STEAP3
Fatty acid degradation	0.084544	0.282953	11.85536	29.28845	CPT1A
Pyruvate metabolism	0.092044	0.282953	10.82228	25.81639	ACYP1
Amino sugar and nucleotide s	0.09391	0.282953	10.59149	25.0533	GNE
Endocytosis	0.094167	0.282953	4.042872	9.552029	HSPA1B;HSPA1A
Cocaine addiction	0.095772	0.282953	10.37031	24.32652	CDK5R1
Prion disease	0.107673	0.282953	3.725613	8.303123	HSPA1B;HSPA1A
Pyrimidine metabolism	0.108702	0.282953	9.047273	20.07725	UCKL1
Steroid hormone biosynthesis	0.117826	0.282953	8.29125	17.7312	SULT2B1
Glycerolipid metabolism	0.117826	0.282953	8.29125	17.7312	LPIN1
MAPK signaling pathway	0.121667	0.282953	3.453987	7.275707	HSPA1B;HSPA1A
Adipocytokine signaling path	0.132237	0.282953	7.312868	14.79512	CPT1A
Inositol phosphate metabolis	0.139355	0.282953	6.905208	13.60828	IMPA1
PPAR signaling pathway	0.141126	0.282953	6.810274	13.3352	CPT1A
Human papillomavirus infecti	0.147325	0.282953	3.059777	5.859833	CCNE1;SPP1
Peroxisome	0.155165	0.282953	6.135185	11.43148	SOD2
Insulin secretion	0.1621	0.282953	5.845294	10.63574	KCNN4
PI3K-Akt signaling pathway	0.163802	0.282953	2.856498	5.167674	CCNE1;SPP1
ECM-receptor interaction	0.165547	0.282953	5.710345	10.27005	SPP1
Small cell lung cancer	0.172399	0.282953	5.458242	9.595276	CCNE1
Salivary secretion	0.174104	0.282953	5.398641	9.43739	KCNN4
TGF-beta signaling pathway	0.175805	0.282953	5.340323	9.283521	BAMBI
Phosphatidylinositol signaling	0.180887	0.282953	5.172656	8.844633	IMPA1
Prostate cancer	0.180887	0.282953	5.172656	8.844633	CCNE1
Glycerophospholipid metabo	0.182574	0.282953	5.119072	8.705479	LPIN1
Progesterone-mediated oocy	0.185939	0.282953	5.015152	8.437172	AURKA
Protein digestion and absorpt	0.190961	0.282953	4.866912	8.058089	KCNN4

Toll-like receptor signaling pa	0.192628	0.282953	4.819417	7.937562	SPP1
Glucagon signaling pathway	0.197609	0.282953	4.682311	7.592206	CPT1A
Insulin resistance	0.199263	0.282953	4.638318	7.482216	CPT1A
Drug metabolism	0.199263	0.282953	4.638318	7.482216	UCKL1
Ribosome biogenesis in eukai	0.199263	0.282953	4.638318	7.482216	POP1
AMPK signaling pathway	0.21885	0.304674	4.168067	6.332829	CPT1A
Cell cycle	0.225275	0.307587	4.031707	6.008996	CCNE1
FoxO signaling pathway	0.236394	0.316679	3.813269	5.499707	SOD2
Apelin signaling pathway	0.245801	0.323183	3.643934	5.11329	SPP1
Pathways of neurodegenerat	0.254431	0.328447	2.112647	2.891637	GPR37;CDK5R1
Gastric cancer	0.264277	0.330751	3.346453	4.453323	CCNE1
mTOR signaling pathway	0.271844	0.330751	3.236275	4.215338	LPIN1
Cushing syndrome	0.273348	0.330751	3.215097	4.170011	CCNE1
Cellular senescence	0.274849	0.330751	3.194194	4.125404	CCNE1
Hepatitis B	0.283794	0.335822	3.074224	3.872009	CCNE1
Wnt signaling pathway	0.289697	0.337188	2.999091	3.715638	BAMBI
RNA transport	0.318507	0.364741	2.672162	3.057253	POP1
Focal adhesion	0.339363	0.373674	2.469875	2.669158	SPP1
Epstein-Barr virus infection	0.340731	0.373674	2.457463	2.645857	CCNE1
Viral carcinogenesis	0.342096	0.373674	2.445173	2.622848	CCNE1
Human T-cell leukemia virus 1	0.363569	0.391112	2.263876	2.290557	CCNE1
Thermogenesis	0.380511	0.403228	2.135065	2.062984	CPT1A
Parkinson disease	0.402004	0.419739	1.986996	1.810737	GPR37
Huntington disease	0.468889	0.48248	1.610984	1.22014	SOD2
Alzheimer disease	0.534333	0.541967	1.33091	0.834128	CDK5R1
Pathways in cancer	0.668583	0.668583	0.916462	0.368963	CCNE1

GO BP 2023 Cluster 1

Term	P-value	Adjusted P-	Odds Ratio	Combined	Genes
Aerobic Electron Transport Chain (GC	3.68E-17	1.02E-14	63.53412	2404.278	NDUFA9;NDUFA8;COX
Mitochondrial ATP Synthesis Coupled	5.34E-17	1.02E-14	61.33711	2298.265	NDUFA9;NDUFA8;COX
Cellular Respiration (GO:0045333)	6.30E-16	8.04E-14	48.69679	1704.431	NDUFA9;NDUFA8;COX
Mitochondrial Membrane Organizati	3.55E-11	3.40E-09	77.37333	1861.652	HSPA9;CHCHD3;SAMM
Mitochondrial Respiratory Chain Com	7.99E-11	6.12E-09	31.49206	732.2017	NDUFA9;NDUFA8;TME
Inner Mitochondrial Membrane Orga	3.85E-09	2.46E-07	58.39432	1131.332	HSPA9;TIMM8A;CHCHI
Oxidative Phosphorylation (GO:0006	5.30E-09	2.90E-07	34.48785	657.2067	NDUFA9;NDUFA8;NDU
Energy Derivation By Oxidation Of Or	1.70E-08	8.13E-07	44.17031	790.2417	COX7B;UQCRB;CYCS;N
NADH Dehydrogenase Complex Asse	6.20E-08	2.16E-06	34.75488	576.7971	NDUFA9;NDUFA8;NDU
Proton Motive Force-Driven Mitocho	6.20E-08	2.16E-06	34.75488	576.7971	NDUFA9;NDUFA8;NDU
Mitochondrial Respiratory Chain Com	6.20E-08	2.16E-06	34.75488	576.7971	NDUFA9;NDUFA8;NDU
Aerobic Respiration (GO:0009060)	1.19E-07	3.81E-06	30.81106	491.1477	NDUFA9;NDUFA8;NDU
Proton Motive Force-Driven ATP Synt	1.32E-07	3.90E-06	30.23896	478.9367	NDUFA9;NDUFA8;NDU
Mitochondrial Electron Transport, NA	2.15E-07	5.88E-06	46.34669	711.5186	NDUFA9;NDUFA8;NDU
Mitochondrion Organization (GO:000	2.50E-07	6.37E-06	14.46278	219.8879	SUPV3L1;CHCHD3;SAM
Mitochondrial Electron Transport, Cy	3.96E-07	9.47E-06	88.48444	1304.483	COX7B;CYCS;COX5A;C
Protein Targeting To Mitochondrion (	3.58E-06	8.07E-05	24.85861	311.707	TIMM8A;SAMM50;GRI
Mitochondrial Electron Transport, Ub	1.27E-05	2.56E-04	87.33333	984.4614	UQCRB;CYCS;UQCRFS1
Cristae Formation (GO:0042407)	1.27E-05	2.56E-04	87.33333	984.4614	CHCHD3;SAMM50;IMM
Ubiquinone Biosynthetic Process (GO	1.65E-05	3.16E-04	78.59605	865.5738	NDUFA9;COQ3;COQ9
Protein Import Into Mitochondrial Ma	4.64E-05	8.46E-04	52.38421	522.7293	GRPEL1;TIMM17A;TIM
Mitochondrial Transport (GO:000683	5.70E-05	9.92E-04	21.62939	211.3758	TIMM17A;PPIF;TIMM4
Protein Transmembrane Import Into	2.71E-04	0.004511	27.07623	222.3994	GRPEL1;TIMM17A;TIM
Negative Regulation Of Apoptotic Sig	3.12E-04	0.004893	13.56786	109.52	OPA1;NDUFS3;PPIF;SL
Malate Metabolic Process (GO:00061	3.19E-04	0.004893	103.4597	832.76	FH;MDH1
Negative Regulation Of Mitochondric	4.89E-04	0.007208	21.80373	166.2002	OPA1;PPIF;SLC25A5
Mitochondrial RNA Processing (GO:0	5.45E-04	0.007727	73.89239	555.32	SUPV3L1;FASTKD1
Establishment Of Protein Localization	6.99E-04	0.009562	19.13992	139.066	GRPEL1;TIMM17A;TIM
Intracellular Protein Transmembrane	7.97E-04	0.010522	18.24786	130.1983	GRPEL1;TIMM17A;TIM
Quinone Biosynthetic Process (GO:19	9.91E-04	0.012174	51.71688	357.7157	COQ3;COQ9
acetyl-CoA Biosynthetic Process (GO:	9.91E-04	0.012174	51.71688	357.7157	PDHA1;DLAT
Dicarboxylic Acid Metabolic Process (	0.001017	0.012174	16.69149	115.0174	FH;MDH1;SDHA
Ubiquinone Metabolic Process (GO:0	0.001359	0.014876	43.09307	284.4455	COQ3;COQ9
Respiratory Electron Transport Chain	0.001359	0.014876	43.09307	284.4455	UQCRFS1;SDHA
Electron Transport Chain (GO:00229	0.001359	0.014876	43.09307	284.4455	UQCRFS1;SDHA
Negative Regulation Of Release Of Cy	0.001783	0.01874	36.93321	233.7581	OPA1;PPIF
Negative Regulation Of Intrinsic Apop	0.00181	0.01874	13.51838	85.35787	OPA1;NDUFS3;PPIF
Mitochondrial Fusion (GO:0008053)	0.002262	0.022217	32.31331	196.8328	CHCHD3;OPA1
Regulation Of Mitochondrial Membra	0.002262	0.022217	32.31331	196.8328	PPIF;SLC25A5
Organelle Fusion (GO:0048284)	0.004708	0.045081	21.53355	115.3862	CHCHD3;OPA1
Metallo-Sulfur Cluster Assembly (GO:	0.005072	0.045176	20.67117	109.2271	HSPA9;CIAPIN1
Chaperone Cofactor-Dependent Prot	0.005072	0.045176	20.67117	109.2271	HSPA9;HSPE1
Iron-Sulfur Cluster Assembly (GO:001	0.005072	0.045176	20.67117	109.2271	HSPA9;CIAPIN1
Protein Insertion Into Mitochondrial I	0.005448	0.047424	19.87512	103.5986	TIMM8A;SAMM50
'De Novo' Post-Translational Protein I	0.007076	0.058919	17.22165	85.26422	HSPA9;HSPE1

Purine Ribonucleoside Triphosphate I	0.007076	0.058919	17.22165	85.26422	OPA1;NDUFS1
Mitochondrial Gene Expression (GO:(	0.007903	0.063666	7.824079	37.87282	MRPL2;FASTKD1;MRPL
Protein Transport (GO:0015031)	0.007979	0.063666	4.302606	20.78563	HSPA9;RAB3A;GRPEL1;
Intracellular Protein Transport (GO:0(	0.009297	0.07267	4.138725	19.3611	HSPA9;XPO4;GRPEL1;T
Regulation Of Release Of Cytochrome	0.011434	0.087584	13.24143	59.20461	OPA1;PPIF
Substantia Nigra Development (GO:0	0.011975	0.089931	12.90974	57.12453	NDUFS3;COX6B1
Regulation Of Intrinsic Apoptotic Sign	0.015452	0.113807	11.22247	46.79817	NDUFS3;PPIF
Erythrocyte Differentiation (GO:0030	0.016068	0.115468	10.98314	45.37032	HSPA9;SLC25A5
Pyruvate Metabolic Process (GO:000(	0.016695	0.115468	10.75379	44.01114	PDHA1;DLAT
Negative Regulation Of Programmed	0.017457	0.115468	3.512256	14.21771	SUPV3L1;HSPA9;OPA1;
Negative Regulation Of Erythrocyte D	0.019596	0.115468	63.83654	251.0315	HSPA9
succinyl-CoA Catabolic Process (GO:1	0.019596	0.115468	63.83654	251.0315	SUCLG1
Mitochondrial RNA 3'-End Processing	0.019596	0.115468	63.83654	251.0315	SUPV3L1
Valine Metabolic Process (GO:00065	0.019596	0.115468	63.83654	251.0315	ILVBL
acetyl-CoA Biosynthetic Process From	0.019596	0.115468	63.83654	251.0315	PDHA1
Activation Of Cysteine-Type Endopep	0.019596	0.115468	63.83654	251.0315	CYCS
Response To Bile Acid (GO:1903412)	0.019596	0.115468	63.83654	251.0315	CYP27B1
Isoleucine Metabolic Process (GO:00(	0.019596	0.115468	63.83654	251.0315	ILVBL
Presynaptic Active Zone Organization	0.019596	0.115468	63.83654	251.0315	RAB3A
Regulation Of Plasma Membrane Rep	0.019596	0.115468	63.83654	251.0315	RAB3A
Myeloid Cell Differentiation (GO:003(	0.02137	0.124009	9.381818	36.08043	HSPA9;SLC25A5
Sulfur Amino Acid Catabolic Process (	0.02347	0.128414	51.06667	191.6039	MAT1A
Positive Regulation Of Mitophagy (G(	0.02347	0.128414	51.06667	191.6039	SLC25A5
Regulation Of Ketone Biosynthetic Pr	0.02347	0.128414	51.06667	191.6039	SIRT5
Regulation Of Mitochondrial mRNA S	0.02347	0.128414	51.06667	191.6039	FASTKD1
ADP Transport (GO:0015866)	0.027328	0.129219	42.55342	153.1851	SLC25A5
Regulation Of Chromosome Condens	0.027328	0.129219	42.55342	153.1851	SMC2
Fatty Acid Alpha-Oxidation (GO:0001	0.027328	0.129219	42.55342	153.1851	ILVBL
Negative Regulation Of Keratinocyte	0.027328	0.129219	42.55342	153.1851	CYP27B1
Methionine Metabolic Process (GO:0	0.027328	0.129219	42.55342	153.1851	MAT1A
Negative Regulation Of Monooxygen	0.027328	0.129219	42.55342	153.1851	CYP27B1
NADH Metabolic Process (GO:00067	0.027328	0.129219	42.55342	153.1851	MDH1
Alditol Metabolic Process (GO:00194	0.027328	0.129219	42.55342	153.1851	COQ3
Cytochrome Complex Assembly (GO:	0.027328	0.129219	42.55342	153.1851	HCCS
Regulation Of Mitophagy (GO:190152	0.027328	0.129219	42.55342	153.1851	SLC25A5
Positive Regulation Of Chromosome (	0.027328	0.129219	42.55342	153.1851	SMC2
Nervous System Development (GO:0(	0.028387	0.129769	3.077324	10.96089	TIMM8A;COX7B;TMEM
Activation Of Cysteine-Type Endopep	0.028866	0.129769	7.934466	28.12843	CYCS;HSPE1
succinyl-CoA Metabolic Process (GO:(	0.031172	0.129769	36.47253	126.4956	SUCLG1
Tricarboxylic Acid Metabolic Process	0.031172	0.129769	36.47253	126.4956	IDH3A
Purine Nucleobase Transport (GO:00(	0.031172	0.129769	36.47253	126.4956	VDAC3
Purine Nucleoside Bisphosphate Cata	0.031172	0.129769	36.47253	126.4956	SUCLG1
Regulation Of Vesicle Fusion (GO:003	0.031172	0.129769	36.47253	126.4956	RAB3A
Negative Regulation Of Transporter A	0.031172	0.129769	36.47253	126.4956	PPIF
Response To Vitamin (GO:0033273)	0.031172	0.129769	36.47253	126.4956	CYP27B1
Response To Vitamin D (GO:0033280	0.031172	0.129769	36.47253	126.4956	CYP27B1
Ribonucleoside Bisphosphate Catabo	0.031172	0.129769	36.47253	126.4956	SUCLG1

Positive Regulation Of Mitochondrial	0.035	0.142607	31.91186	106.9814	PPIF
Mitochondrion Morphogenesis (GO:0	0.035	0.142607	31.91186	106.9814	SUPV3L1
Cell Morphogenesis Involved In Neur	0.037251	0.148656	6.873074	22.61298	AFG3L2;RAB3A
Oxygen Transport (GO:0015671)	0.038814	0.148656	28.36467	92.15638	MB
Maintenance Of Synapse Structure (G	0.038814	0.148656	28.36467	92.15638	RAB3A
Negative Regulation Of Mitochondria	0.038814	0.148656	28.36467	92.15638	SLC25A5
Positive Regulation Of Autophagy Of	0.038814	0.148656	28.36467	92.15638	SLC25A5
Alpha-Amino Acid Biosynthetic Proce	0.038814	0.148656	28.36467	92.15638	ILVBL
Negative Regulation Of Apoptotic Pro	0.041985	0.149729	2.754264	8.732232	SUPV3L1;HSPA9;OPA1;
Cell Part Morphogenesis (GO:003299	0.042612	0.149729	25.52692	80.55315	SUPV3L1
Mitochondrial Genome Maintenance	0.042612	0.149729	25.52692	80.55315	OPA1
Mitochondrial Respiratory Chain Com	0.042612	0.149729	25.52692	80.55315	UQCRFS1
Glycerol Metabolic Process (GO:0006	0.042612	0.149729	25.52692	80.55315	COQ3
Vitamin D Metabolic Process (GO:004	0.042612	0.149729	25.52692	80.55315	CYP27B1
Respiratory Chain Complex III Assemb	0.042612	0.149729	25.52692	80.55315	UQCRFS1
Aspartate Family Amino Acid Catabol	0.042612	0.149729	25.52692	80.55315	MAT1A
Programmed Necrotic Cell Death (GO	0.042612	0.149729	25.52692	80.55315	PPIF
Purine Ribonucleotide Metabolic Pro	0.043607	0.151596	6.284131	19.68531	OPA1;NDUFS1
Regulation Of Chromosome Separatio	0.046396	0.151596	23.20513	71.25236	SMC2
Protein Insertion Into Mitochondrial I	0.046396	0.151596	23.20513	71.25236	TIMM8A
Negative Regulation Of Mitochondria	0.046396	0.151596	23.20513	71.25236	SLC25A5
Positive Regulation Of Protein Export	0.046396	0.151596	23.20513	71.25236	XPO4
Positive Regulation Of Regulated Secr	0.046396	0.151596	23.20513	71.25236	RAB3A
Negative Regulation Of Alcohol Biosy	0.046396	0.151596	23.20513	71.25236	CYP27B1
Axonal Transport Of Mitochondrion (	0.046396	0.151596	23.20513	71.25236	OPA1
ATP Transport (GO:0015867)	0.050165	0.151596	21.2703	63.65008	SLC25A5
Outer Mitochondrial Membrane Orga	0.050165	0.151596	21.2703	63.65008	SAMM50
Protein Insertion Into Mitochondrial (	0.050165	0.151596	21.2703	63.65008	SAMM50
GTP Metabolic Process (GO:0046039)	0.050165	0.151596	21.2703	63.65008	OPA1
Regulation Of Short-Term Neuronal S	0.050165	0.151596	21.2703	63.65008	RAB3A
Cellular Response To Arsenic-Contain	0.050165	0.151596	21.2703	63.65008	PPIF
Mitochondrial Fission (GO:0000266)	0.050165	0.151596	21.2703	63.65008	OPA1
Positive Regulation Of Chromosome S	0.050165	0.151596	21.2703	63.65008	SMC2
Regulation Of Cellular Ketone Metabo	0.050165	0.151596	21.2703	63.65008	SIRT5
Protein Localization (GO:0008104)	0.050268	0.151596	3.008492	8.996552	HSPA9;GRPEL1;TIMM1
Protein Maturation By Iron-Sulfur Clu	0.053919	0.158854	19.63314	57.33403	CISD1
Formation Of Cytoplasmic Translation	0.053919	0.158854	19.63314	57.33403	EIF3K
Mitochondrion Transport Along Micro	0.053919	0.158854	19.63314	57.33403	OPA1
Mitochondrial Translation (GO:00325	0.057408	0.161192	5.363907	15.32773	MRPL2;MRPL35
Negative Regulation Of Endoplasmic I	0.057659	0.161192	18.22985	52.01364	OPA1
Gas Transport (GO:0015669)	0.057659	0.161192	18.22985	52.01364	MB
Polyol Biosynthetic Process (GO:0046	0.057659	0.161192	18.22985	52.01364	CYP27B1
Mitotic Chromosome Condensation (	0.057659	0.161192	18.22985	52.01364	SMC2
Dolichol-Linked Oligosaccharide Biosy	0.057659	0.161192	18.22985	52.01364	DHDDS
Negative Regulation Of Cation Transm	0.057659	0.161192	18.22985	52.01364	PPIF
Axon Development (GO:0061564)	0.058446	0.162208	5.308341	15.07387	AFG3L2;RAB3A
Regulation Of Cell Growth (GO:00015	0.06091	0.166738	3.471041	9.713189	SUPV3L1;CYP27B1;NDI

Activation Of Cysteine-Type Endopep	0.061384	0.166738	17.01368	47.4785	CYCS
Negative Regulation Of ATP-depende	0.061384	0.166738	17.01368	47.4785	PPIF
Nicotinamide Nucleotide Metabolic P	0.065094	0.174344	15.94952	43.57277	MDH1
Regulation Of Oxidative Phosphorylat	0.065094	0.174344	15.94952	43.57277	PPIF
Vesicle-Mediated Transport In Synaps	0.06879	0.178999	15.01056	40.17863	RAB3A
Regulation Of Mitochondrial Outer M	0.06879	0.178999	15.01056	40.17863	SLC25A5
Positive Regulation Of Chromosome S	0.06879	0.178999	15.01056	40.17863	SMC2
Positive Regulation Of Epidermal Cell	0.06879	0.178999	15.01056	40.17863	CYP27B1
Positive Regulation Of Cysteine-Type	0.069169	0.178999	4.809807	12.84794	CYCS;HSPE1
RNA Metabolic Process (GO:0016070	0.071387	0.183498	4.721077	12.46195	SUPV3L1;FASTKD1
NADP Metabolic Process (GO:000673	0.072472	0.185045	14.17593	37.20551	MDH1
Calcium-Mediated Signaling Using Int	0.076139	0.188137	13.42915	34.58265	DEFB1
Protein Deacylation (GO:0035601)	0.076139	0.188137	13.42915	34.58265	SIRT5
Sulfur Compound Catabolic Process (	0.076139	0.188137	13.42915	34.58265	SUCLG1
Mitochondrial RNA Metabolic Proces	0.076139	0.188137	13.42915	34.58265	FASTKD1
Adenine Nucleotide Transport (GO:0(	0.076139	0.188137	13.42915	34.58265	SLC25A5
Plasma Membrane Repair (GO:00017	0.079792	0.19342	12.75705	32.25405	RAB3A
Negative Regulation Of Reactive Oxyg	0.079792	0.19342	12.75705	32.25405	SIRT5
Innate Immune Response In Mucosa	0.079792	0.19342	12.75705	32.25405	DEFB1
Organelle Fission (GO:0048285)	0.083431	0.194841	12.14896	30.17485	OPA1
Regulation Of Protein Export From Nu	0.083431	0.194841	12.14896	30.17485	XPO4
Protein Peptidyl-Prolyl Isomerization	0.083431	0.194841	12.14896	30.17485	PPIF
Mitochondrial Cytochrome C Oxidase	0.083431	0.194841	12.14896	30.17485	TMEM223
NAD Metabolic Process (GO:0019674	0.083431	0.194841	12.14896	30.17485	MDH1
Negative Regulation Of Myeloid Cell I	0.083431	0.194841	12.14896	30.17485	HSPA9
Negative Regulation Of Growth (GO:(	0.08634	0.200414	4.215244	10.32506	CYP27B1;NDUFS3
Negative Regulation Of Cell Growth (	0.087527	0.201945	4.180762	10.18352	CYP27B1;NDUFS3
Fat-Soluble Vitamin Metabolic Proces	0.090665	0.204777	11.09142	26.62583	CYP27B1
Regulation Of Endoplasmic Reticulum	0.090665	0.204777	11.09142	26.62583	OPA1
Protein Targeting (GO:0006605)	0.092323	0.204777	4.048267	9.644825	TIMM17A;TIMM44
Purine Ribonucleotide Catabolic Proc	0.094262	0.204777	10.62874	25.1017	SUCLG1
Regulation Of Keratinocyte Proliferat	0.094262	0.204777	10.62874	25.1017	CYP27B1
Negative Regulation Of Response To	0.094262	0.204777	10.62874	25.1017	OPA1
Positive Regulation Of Release Of Cyt	0.094262	0.204777	10.62874	25.1017	PPIF
Regulation Of Biomineral Tissue Deve	0.094262	0.204777	10.62874	25.1017	CYP27B1
Calcium-Ion Regulated Exocytosis (GO	0.097844	0.204777	10.20308	23.71587	RAB3A
Protein Export From Nucleus (GO:00(	0.097844	0.204777	10.20308	23.71587	XPO4
Establishment Or Maintenance Of Ap	0.097844	0.204777	10.20308	23.71587	DLG3
Positive Regulation Of Monooxygena	0.097844	0.204777	10.20308	23.71587	CYP27B1
Regulation Of Keratinocyte Differenti	0.097844	0.204777	10.20308	23.71587	CYP27B1
Respiratory Chain Complex IV Assemb	0.097844	0.204777	10.20308	23.71587	TMEM223
Regulation Of Myeloid Cell Differenti	0.097844	0.204777	10.20308	23.71587	HSPA9
Regulation Of Nucleotide-Excision Re	0.097844	0.204777	10.20308	23.71587	BCL7A
cAMP-mediated Signaling (GO:00199	0.097844	0.204777	10.20308	23.71587	DEFB1
Peptidyl-Proline Modification (GO:00	0.101412	0.20995	9.810158	22.45119	PPIF
Phospholipid Biosynthetic Process (G	0.101412	0.20995	9.810158	22.45119	DHDDS
Regulation Of Chromosome Segregat	0.104966	0.214984	9.446344	21.29317	SMC2

Mucosal Immune Response (GO:0002	0.104966	0.214984	9.446344	21.29317	DEFB1
DNA Geometric Change (GO:0032392	0.112033	0.22703	8.793988	19.24971	SUPV3L1
Cytoplasmic Translational Initiation (	0.112033	0.22703	8.793988	19.24971	EIF3K
Neuron Projection Morphogenesis (G	0.113507	0.228806	3.56728	7.762009	AFG3L2;RAB3A
Mesenchymal Cell Migration (GO:009	0.119045	0.235021	8.225806	17.50663	NRTN
Gluconeogenesis (GO:0006094)	0.119045	0.235021	8.225806	17.50663	MDH1
Chromosome Condensation (GO:003	0.119045	0.235021	8.225806	17.50663	SMC2
Regulation Of Metaphase/Anaphase	0.119045	0.235021	8.225806	17.50663	BCL7A
Positive Regulation Of RNA Metabolic	0.12253	0.236562	7.968349	16.72875	SUPV3L1
Regulation Of G0 To G1 Transition (G	0.12253	0.236562	7.968349	16.72875	BCL7A
Positive Regulation Of Chromosome	0.12253	0.236562	7.968349	16.72875	SMC2
ATP Metabolic Process (GO:0046034)	0.126002	0.236562	7.726496	16.00512	NDUFS1
Membrane Protein Proteolysis (GO:0	0.126002	0.236562	7.726496	16.00512	AFG3L2
Cellular Response To Hydrogen Perox	0.126002	0.236562	7.726496	16.00512	PPIF
Purine Nucleotide Metabolic Process	0.126002	0.236562	7.726496	16.00512	MDH1
Response To Estrogen (GO:0043627)	0.126002	0.236562	7.726496	16.00512	CYP27B1
Apoptotic Mitochondrial Changes (G	0.126002	0.236562	7.726496	16.00512	NDUFS1
Regulation Of Neuronal Synaptic Plas	0.126002	0.236562	7.726496	16.00512	RAB3A
Regulation Of Regulated Secretory Pa	0.12946	0.240695	7.498869	15.33057	RAB3A
Hexose Biosynthetic Process (GO:001	0.12946	0.240695	7.498869	15.33057	MDH1
Protein Destabilization (GO:0031648)	0.132905	0.243552	7.284249	14.70052	ISOC2
Regulation Of Erythrocyte Differentia	0.132905	0.243552	7.284249	14.70052	HSPA9
Neural Crest Cell Migration (GO:0001	0.132905	0.243552	7.284249	14.70052	NRTN
Synaptic Vesicle Cycle (GO:0099504)	0.136336	0.246305	7.081553	14.11095	RAB3A
Regulation Of Ossification (GO:00302	0.136336	0.246305	7.081553	14.11095	CYP27B1
Positive Regulation Of Exocytosis (GC	0.136336	0.246305	7.081553	14.11095	RAB3A
mRNA Transcription By RNA Polymer	0.139754	0.246662	6.889813	13.55829	CYP27B1
RNA 3'-End Processing (GO:0031123)	0.139754	0.246662	6.889813	13.55829	SUPV3L1
Positive Regulation Of Protein Tyrosi	0.139754	0.246662	6.889813	13.55829	DLG3
Positive Regulation Of Bone Mineraliz	0.139754	0.246662	6.889813	13.55829	CYP27B1
Signal Release From Synapse (GO:009	0.139754	0.246662	6.889813	13.55829	RAB3A
Regulation Of Protein Tyrosine Kinase	0.143158	0.248452	6.708165	13.03937	DLG3
Regulation Of Mitochondrial Membra	0.143158	0.248452	6.708165	13.03937	NDUFS1
Axonal Transport (GO:0098930)	0.143158	0.248452	6.708165	13.03937	OPA1
Regulation Of Apoptotic Process (GO	0.146157	0.248452	1.855309	3.5679	SUPV3L1;HSPA9;OPA1
Protein Deacetylation (GO:0006476)	0.146549	0.248452	6.535832	12.55138	SIRT5
Establishment Or Maintenance Of Ep	0.146549	0.248452	6.535832	12.55138	DLG3
Cyclic-Nucleotide-Mediated Signaling	0.146549	0.248452	6.535832	12.55138	DEFB1
Positive Regulation Of Stem Cell Popu	0.146549	0.248452	6.535832	12.55138	BCL7A
Metal Ion Transport (GO:0030001)	0.146606	0.248452	3.035733	5.828624	NDUFA9;CYP27B1
DNA Duplex Unwinding (GO:0032508	0.149927	0.250751	6.372115	12.09177	SUPV3L1
Synaptic Vesicle Exocytosis (GO:0016	0.149927	0.250751	6.372115	12.09177	RAB3A
Positive Regulation Of Ossification (G	0.149927	0.250751	6.372115	12.09177	CYP27B1
Lysosome Localization (GO:0032418)	0.153292	0.254159	6.216385	11.65829	RAB3A
DNA Recombination (GO:0006310)	0.153292	0.254159	6.216385	11.65829	SUPV3L1
mRNA Catabolic Process (GO:000640	0.156643	0.255295	6.068071	11.2489	SUPV3L1
mRNA Transcription (GO:0009299)	0.156643	0.255295	6.068071	11.2489	CYP27B1

Positive Regulation Of Biomineral Tis	0.156643	0.255295	6.068071	11.2489	CYP27B1
Neurotransmitter Secretion (GO:000	0.156643	0.255295	6.068071	11.2489	RAB3A
Synaptic Vesicle Recycling (GO:00364	0.159982	0.255304	5.926655	10.86176	RAB3A
Positive Regulation Of Nucleocytopla	0.159982	0.255304	5.926655	10.86176	XPO4
Neural Crest Cell Development (GO:0	0.159982	0.255304	5.926655	10.86176	NRTN
Response To Unfolded Protein (GO:0	0.159982	0.255304	5.926655	10.86176	HSPE1
Nucleobase-Containing Compound C	0.159982	0.255304	5.926655	10.86176	SUPV3L1
Negative Regulation Of Cellular Proce	0.162719	0.257393	1.940013	3.522537	CYP27B1;BCL7A;DLG3;
Establishment Of Protein Localization	0.163307	0.257393	5.791667	10.49521	RAB3A
Zymogen Activation (GO:0031638)	0.163307	0.257393	5.791667	10.49521	CYCS
Response To Hydrogen Peroxide (GO	0.166619	0.26047	5.662678	10.14776	PPIF
Negative Regulation Of Cellular Meta	0.166619	0.26047	5.662678	10.14776	SIRT5
Secondary Alcohol Metabolic Process	0.169919	0.263786	5.539298	9.818041	IDH3A
Axonogenesis (GO:0007409)	0.170118	0.263786	2.7559	4.881429	AFG3L2;RAB3A
Antibacterial Humoral Response (GO	0.176479	0.270366	5.307959	9.206936	DEFB1
Regulation Of Mitotic Metaphase/An	0.176479	0.270366	5.307959	9.206936	BCL7A
Nuclear Export (GO:0051168)	0.176479	0.270366	5.307959	9.206936	XPO4
Regulated Exocytosis (GO:0045055)	0.182988	0.279221	5.095128	8.65323	RAB3A
Fatty Acid Oxidation (GO:0019395)	0.186224	0.28303	4.994972	8.395586	ILVBL
Protein Homotetramerization (GO:00	0.189446	0.28679	4.898669	8.149667	MAT1A
Regulation Of Exocytosis (GO:001715	0.192657	0.290502	4.805999	7.914741	RAB3A
Positive Regulation Of Multicellular C	0.196947	0.295807	2.008326	3.263168	CYP27B1;FH;BCL7A
Regulation Of Reactive Oxygen Specie	0.199039	0.296623	4.630769	7.475233	SIRT5
Regulation Of Stem Cell Population M	0.199039	0.296623	4.630769	7.475233	BCL7A
RNA Catabolic Process (GO:0006401)	0.202212	0.300183	4.547848	7.269456	SUPV3L1
Positive Regulation Of Mitochondrior	0.205372	0.30137	4.467836	7.072277	PPIF
Response To Organic Cyclic Compour	0.205372	0.30137	4.467836	7.072277	CYP27B1
Regulation Of Bone Mineralization (G	0.205372	0.30137	4.467836	7.072277	CYP27B1
Glucose Metabolic Process (GO:0006	0.20852	0.304821	4.390584	6.883204	MDH1
Fatty Acid Catabolic Process (GO:000	0.214779	0.312777	4.243803	6.527586	ILVBL
Inorganic Anion Transmembrane Tra	0.220989	0.320602	4.106493	6.199334	CYP27B1
Regulation Of Secretion By Cell (GO:1	0.224076	0.321427	4.041107	6.044568	RAB3A
Positive Regulation Of Macroautopha	0.224076	0.321427	4.041107	6.044568	SLC25A5
Positive Regulation Of Cysteine-Type	0.224076	0.321427	4.041107	6.044568	CYCS
Antimicrobial Humoral Immune Resp	0.227151	0.324622	3.977764	5.895611	DEFB1
Negative Regulation Of Intracellular S	0.231811	0.330051	2.233539	3.265057	NDUFS3;PPIF
Protein Secretion (GO:0009306)	0.233264	0.330889	3.856838	5.613951	RAB3A
Translation (GO:0006412)	0.236187	0.332735	2.204322	3.181127	MRPL2;MRPL35
B Cell Differentiation (GO:0030183)	0.236303	0.332735	3.799082	5.480711	SLC25A5
Cellular Response To Calcium Ion (GC	0.23933	0.333321	3.743024	5.352199	PPIF
Response To Molecule Of Bacterial O	0.23933	0.333321	3.743024	5.352199	CYP27B1
Regulation Of Monoatomic Ion Trans	0.23933	0.333321	3.743024	5.352199	PPIF
Negative Regulation Of Epithelial Cell	0.242345	0.333878	3.688592	5.228187	CYP27B1
Sulfur Compound Biosynthetic Proces	0.242345	0.333878	3.688592	5.228187	MAT1A
Regulation Of Cellular Biosynthetic Pr	0.242345	0.333878	3.688592	5.228187	SIRT5
Plasma Membrane Organization (GO:	0.24834	0.340911	3.584326	4.992818	RAB3A
Protein Tetramerization (GO:005126	0.251319	0.341331	3.534366	4.881069	MAT1A

Cellular Response To Reactive Oxyge	0.251319	0.341331	3.534366	4.881069	PPIF
Positive Regulation Of Secretion By C	0.251319	0.341331	3.534366	4.881069	RAB3A
Regulation Of mRNA Stability (GO:00	0.254287	0.34293	3.485774	4.773036	FASTKD1
Regulation Of Cell Cycle G1/S Phase T	0.254287	0.34293	3.485774	4.773036	BCL7A
Defense Response To Gram-negative	0.257244	0.3457	3.438496	4.668551	DEFB1
Monoatomic Cation Homeostasis (G	0.263122	0.352363	3.347672	4.469599	CYP27B1
Wound Healing (GO:0042060)	0.271854	0.361528	3.220058	4.194098	RAB3A
Response To Type II Interferon (GO:0	0.271854	0.361528	3.220058	4.194098	CYP27B1
Positive Regulation Of Growth (GO:0	0.274741	0.364104	3.179647	4.107865	SUPV3L1
Regulation Of Cysteine-Type Endope	0.283337	0.372812	3.064257	3.864391	CYCS
Positive Regulation Of Double-Strand	0.283337	0.372812	3.064257	3.864391	BCL7A
Calcium-Mediated Signaling (GO:001	0.28618	0.372812	3.027625	3.787969	DEFB1
Macromolecule Catabolic Process (G	0.28618	0.372812	3.027625	3.787969	SUPV3L1
Defense Response To Gram-positive	0.28618	0.372812	3.027625	3.787969	DEFB1
Exocytosis (GO:0006887)	0.289011	0.373957	2.991855	3.713758	RAB3A
Regulation Of Mitotic Cell Cycle Phas	0.289011	0.373957	2.991855	3.713758	BCL7A
Regulation Of Double-Strand Break R	0.294641	0.379731	2.922782	3.57163	BCL7A
Positive Regulation Of DNA Repair (G	0.29744	0.379731	2.889423	3.503551	BCL7A
Regulation Of Vesicle-Mediated Tran	0.29744	0.379731	2.889423	3.503551	RAB3A
Sodium Ion Transport (GO:0006814)	0.29744	0.379731	2.889423	3.503551	NDUFA9
Lymphocyte Differentiation (GO:003	0.303004	0.38555	2.824929	3.372992	SLC25A5
B Cell Activation (GO:0042113)	0.30577	0.386501	2.793745	3.310373	SLC25A5
Steroid Metabolic Process (GO:00082	0.30577	0.386501	2.793745	3.310373	CYP27B1
Peptidyl-Lysine Modification (GO:001	0.311269	0.392157	2.733388	3.190135	SIRT5
MAPK Cascade (GO:0000165)	0.322138	0.403199	2.620143	2.968034	NRTN
Positive Regulation Of Cold-Induced T	0.322138	0.403199	2.620143	2.968034	FH
Protein Complex Oligomerization (G	0.327509	0.407259	2.566952	2.865335	OPA1
Antimicrobial Humoral Response (G	0.327509	0.407259	2.566952	2.865335	DEFB1
Visual Perception (GO:0007601)	0.330178	0.40925	2.541154	2.815909	OPA1
Calcium Ion Homeostasis (GO:00550	0.332838	0.409893	2.515867	2.767706	CYP27B1
Sensory Perception Of Light Stimulus	0.332838	0.409893	2.515867	2.767706	OPA1
Intrinsic Apoptotic Signaling Pathway	0.340753	0.417495	2.442924	2.630046	CYCS
Regulation Of G1/S Transition Of Mit	0.343371	0.417495	2.419536	2.58635	BCL7A
Response To Calcium Ion (GO:00515	0.343371	0.417495	2.419536	2.58635	PPIF
Positive Regulation Of Cell Growth (G	0.343371	0.417495	2.419536	2.58635	SUPV3L1
Positive Regulation Of Metabolic Pro	0.348575	0.422482	2.374071	2.502035	FH
Negative Regulation Of Development	0.351163	0.422941	2.351971	2.461351	BCL7A
Cellular Response To Salt (GO:19020	0.351163	0.422941	2.351971	2.461351	PPIF
Response To Lipid (GO:0033993)	0.35374	0.424709	2.330275	2.421609	CYP27B1
Mitotic Sister Chromatid Segregation	0.356306	0.426454	2.308974	2.382779	SMC2
Regulation Of Cell Population Prolifer	0.358604	0.426847	1.340962	1.375206	CYP27B1;BCL7A;DLG3;
Calcium Ion Transport (GO:0006816)	0.358863	0.426847	2.288057	2.344834	CYP27B1
Protein Maturation (GO:0051604)	0.371497	0.439147	2.188882	2.16746	AFG3L2
Protein Processing (GO:0016485)	0.371497	0.439147	2.188882	2.16746	AFG3L2
Protein-Containing Complex Assembl	0.372678	0.439186	1.56123	1.540999	SAMM50;OPA1
Positive Regulation Of Cell Cycle Proc	0.373995	0.439386	2.170064	2.134288	SMC2
Response To Cytokine (GO:0034097)	0.391203	0.458198	2.046836	1.921016	CYP27B1

Positive Regulation Of Intracellular Pr	0.393623	0.459626	2.030359	1.893031	XPO4
Protein Homooligomerization (GO:00	0.400825	0.465146	1.982472	1.812434	MAT1A
Regulation Of DNA Repair (GO:00062	0.400825	0.465146	1.982472	1.812434	BCL7A
Positive Regulation Of Peptidyl-Tyros	0.403207	0.465146	1.967005	1.786638	DLG3
Regulation Of Cell Cycle Process (GO:	0.403207	0.465146	1.967005	1.786638	BCL7A
Plasma Membrane Bounded Cell Proj	0.407944	0.469196	1.936778	1.736566	NRTN
Cellular Response To Metal Ion (GO:0	0.414978	0.475858	1.893131	1.665063	PPIF
Positive Regulation Of Cellular Proces	0.417735	0.47759	1.291077	1.126991	SUPV3L1;BCL7A;SLC25
Protein Localization To Plasma Memb	0.419622	0.478319	1.865102	1.619655	RAB3A
Intracellular Calcium Ion Homeostasis	0.42423	0.482137	1.837886	1.57595	AFG3L2
Protein Localization To Cell Periphery	0.431074	0.488465	1.798509	1.513403	RAB3A
Positive Regulation Of Protein Kinase	0.437837	0.494276	1.760773	1.454238	DLG3
Regulation Of Cold-Induced Thermog	0.440074	0.494276	1.748541	1.435226	FH
Positive Regulation Of Cellular Catabo	0.440074	0.494276	1.748541	1.435226	SUPV3L1
Negative Regulation Of Cell Populatio	0.443098	0.496218	1.346516	1.096016	CYP27B1;DLG3
Defense Response To Symbiont (GO:0	0.444521	0.49636	1.724577	1.398215	NDUFAF4
protein-RNA Complex Assembly (GO:	0.448933	0.498381	1.701256	1.362504	EIF3K
Neuron Development (GO:0048666)	0.448933	0.498381	1.701256	1.362504	NRTN
Peptide Biosynthetic Process (GO:004	0.466239	0.516097	1.613915	1.231509	MRPL35
Response To Lipopolysaccharide (GO	0.468364	0.516955	1.603619	1.21636	CYP27B1
Membrane Organization (GO:006102	0.485067	0.533853	1.525718	1.103808	OPA1
Organelle Organization (GO:0006996	0.493993	0.542118	1.217845	0.858865	OPA1;SIRT5
Macromolecule Biosynthetic Process	0.516934	0.564062	1.390462	0.917482	MRPL35
RNA Processing (GO:0006396)	0.516934	0.564062	1.390462	0.917482	FASTKD1
Defense Response To Virus (GO:0051	0.528375	0.574908	1.345676	0.858472	NDUFAF4
Protein Localization To Membrane (G	0.533995	0.576113	1.324339	0.830848	RAB3A
Transcription By RNA Polymerase II (0	0.533995	0.576113	1.324339	0.830848	CYP27B1
Neuron Projection Development (GO	0.533995	0.576113	1.324339	0.830848	NRTN
Regulation Of Cell Differentiation (GO	0.535854	0.576494	1.317374	0.821902	BCL7A
Negative Regulation Of Nucleic Acid-T	0.540731	0.580112	1.113736	0.684762	CYP27B1;BCL7A
Anterograde Trans-Synaptic Signaling	0.546852	0.58504	1.277066	0.770807	DLG3
Organic Substance Transport (GO:007	0.550461	0.587261	1.264167	0.754706	CYP27B1
Defense Response To Bacterium (GO:	0.555821	0.591332	1.245295	0.731373	DEFB1
Negative Regulation Of Cell Different	0.561118	0.595313	1.226973	0.708975	BCL7A
Positive Regulation Of Cell Populatior	0.57212	0.60531	1.049761	0.586193	BCL7A;SLC25A5
Chromatin Remodeling (GO:0006338	0.596489	0.627625	1.112278	0.574708	BCL7A
Apoptotic Process (GO:0006915)	0.596489	0.627625	1.112278	0.574708	NDUFS1
Positive Regulation Of Developmenta	0.604487	0.634297	1.088031	0.547687	BCL7A
Positive Regulation Of Signal Transdu	0.653485	0.683838	0.950943	0.404565	CYP27B1
Chromatin Organization (GO:000632	0.656254	0.684864	0.943724	0.397504	BCL7A
Chemical Synaptic Transmission (GO:	0.663081	0.690109	0.926141	0.380513	DLG3
Central Nervous System Developmen	0.676336	0.701996	0.892844	0.349161	COX7B
DNA Metabolic Process (GO:0006259	0.682769	0.706758	0.877066	0.334688	SUPV3L1
Gene Expression (GO:0010467)	0.6928	0.715208	0.852934	0.313039	MRPL35
Proteolysis (GO:0006508)	0.732052	0.753698	0.763463	0.238127	AFG3L2
Positive Regulation Of Macromolecul	0.766344	0.786889	0.690754	0.183827	CYP27B1
Cellular Response To Oxygen-Contain	0.802772	0.82209	0.61779	0.135719	PPIF

Vesicle-Mediated Transport (GO:001(	0.806717	0.823927	0.6101	0.131039	RAB3A
Positive Regulation Of Gene Expressi(	0.853819	0.869715	0.520368	0.082237	CYP27B1
Negative Regulation Of DNA-templat(	0.917884	0.932492	0.479821	0.041113	CYP27B1;BCL7A
Negative Regulation Of Transcription	0.953992	0.966611	0.322347	0.015183	CYP27B1
Positive Regulation Of Transcription E	0.977681	0.987999	0.259749	0.005863	CYP27B1
Regulation Of DNA-templated Transc	0.985029	0.992449	0.3703	0.005586	ZNF165;CYP27B1;BCL7
Regulation Of Transcription By RNA P	0.989554	0.992449	0.34885	0.003663	ZNF165;CYP27B1;BCL7
Regulation Of Gene Expression (GO:0	0.989857	0.992449	0.213998	0.002182	CYP27B1
Positive Regulation Of DNA-template	0.993773	0.993773	0.192813	0.001204	CYP27B1

7B;NDUFA6;UQCRB;NDUFS3;UQCRFS1;CYCS;NDUFS1;SDHA;COX5A;COX6B1
7B;NDUFA6;UQCRB;NDUFS3;UQCRFS1;CYCS;NDUFS1;SDHA;COX5A;COX6B1
7B;NDUFA6;UQCRB;NDUFS3;UQCRFS1;CYCS;NDUFS1;SDHA;COX5A;COX6B1

GO BP 2023 Cluster 2

Term	P-value	Adjusted P	Odds Ratio	Combined S	Genes
Positive Regulation	2.82E-05	0.005636	60.5253	634.1739	HSPA1B;CDK5R1;HSPA1A
Heat Acclimation ((	4.08E-05	0.005636	341.1282	3447.387	HSPA1B;HSPA1A
Cellular Heat Acclin	4.08E-05	0.005636	341.1282	3447.387	HSPA1B;HSPA1A
Regulation Of Nucl	6.12E-05	0.006332	255.8333	2482.011	HSPA1B;HSPA1A
Positive Regulation	8.55E-05	0.007083	204.6564	1916.914	HSPA1B;HSPA1A
Positive Regulation	1.14E-04	0.00786	170.5385	1548.508	HSPA1B;HSPA1A
Negative Regulatio	1.83E-04	0.008399	127.891	1100.918	HSPA1B;HSPA1A
Regulation Of Inclu	1.83E-04	0.008399	127.891	1100.918	HSPA1B;HSPA1A
Regulation Of Micr	1.83E-04	0.008399	127.891	1100.918	HSPA1B;HSPA1A
Purine Ribonucleot	6.79E-04	0.022932	19.37427	141.3348	SULT2B1;HSPA1B;HSPA1A
mRNA Metabolic P	7.03E-04	0.022932	19.13703	138.9437	HSPA1B;TBRG4;HSPA1A
Regulation Of Mito	7.61E-04	0.022932	56.81197	407.9592	HSPA1B;HSPA1A
Cellular Response T	8.03E-04	0.022932	18.24327	130.0118	SOD2;HSPA1B;HSPA1A
Protein O-linked Gl	9.13E-04	0.022932	17.42895	121.983	TET3;TET2;B4GALT5
Negative Regulatio	9.23E-04	0.022932	51.12564	357.2695	HSPA1B;HSPA1A
Negative Regulatio	9.23E-04	0.022932	51.12564	357.2695	HSPA1B;HSPA1A
Cellular Response T	9.42E-04	0.022932	17.23655	120.1018	GAS2L1;HSPA1B;HSPA1A
Negative Regulatio	0.001009	0.023216	48.68864	335.8734	GPR37;SOD2
Positive Regulation	0.001117	0.02434	7.117874	48.38051	BAMBI;SPP1;ELOVL6;LPIN1;B4GALT5
Cellular Response T	0.001194	0.024712	44.45039	299.1775	HSPA1B;HSPA1A
Positive Regulation	0.001292	0.025077	42.59615	283.3432	HSPA1B;HSPA1A
Regulation Of Extri	0.001393	0.025077	40.89026	268.9018	HSPA1B;HSPA1A
Chaperone Cofacto	0.001393	0.025077	40.89026	268.9018	HSPA1B;HSPA1A
Regulation Of Prote	0.001607	0.025593	37.85755	243.5456	HSPA1B;HSPA1A
Regulation Of Spinc	0.001607	0.025593	37.85755	243.5456	HSPA1B;HSPA1A
Response To Steroi	0.001607	0.025593	37.85755	243.5456	HSPA1B;HSPA1A
Cellular Response T	0.001769	0.027122	13.74307	87.09606	SOD2;HSPA1B;HSPA1A
'De Novo' Post-Tra	0.001956	0.027923	34.06667	212.4695	HSPA1B;HSPA1A
Purine Ribonucleos	0.001956	0.027923	34.06667	212.4695	HSPA1B;HSPA1A
ATP Metabolic Proc	0.002207	0.030451	31.93429	195.3204	HSPA1B;HSPA1A
Regulation Of Eryth	0.002472	0.031976	30.05279	180.4043	HSPA1B;HSPA1A
Positive Regulation	0.002472	0.031976	30.05279	180.4043	HSPA1B;HSPA1A
Regulation Of Vasc	0.002609	0.032736	29.19267	173.6567	DNMT1;SOD2
Regulation Of Mito	0.002896	0.03526	27.61192	161.3783	HSPA1B;HSPA1A
Cellular Response T	0.003044	0.036008	26.88394	155.7795	HSPA1B;HSPA1A
Protein Glycosylati	0.00338	0.038872	10.86349	61.81147	TET3;TET2;B4GALT5
mRNA Catabolic Pr	0.003511	0.039281	24.91307	140.808	HSPA1B;HSPA1A
Positive Regulation	0.003673	0.039416	24.31868	136.3487	HSPA1B;HSPA1A
Cellular Response T	0.003713	0.039416	10.49629	58.73603	SPP1;HSPA1B;HSPA1A
Regulation Of Tum	0.004357	0.044746	22.19955	120.6759	HSPA1B;HSPA1A
Regulation Of Cell F	0.004431	0.044746	4.330602	23.46775	SULT2B1;BAMBI;SOD2;HSPA1B;TBRG4;HSPA1
Negative Regulatio	0.004856	0.047868	6.391078	34.04852	DNMT1;HSPA1B;AURKA;HSPA1A
Regulation Of Cycli	0.005288	0.050459	20.0181	104.9397	CCNE1;CDK5R1
Negative Regulatio	0.005485	0.050459	19.63215	102.2009	HSPA1B;HSPA1A
Negative Regulatio	0.005485	0.050459	19.63215	102.2009	HSPA1B;HSPA1A

RNA Catabolic Proc	0.006093	0.054841	18.55851	94.65842	HSPA1B;HSPA1A
Positive Regulation	0.006951	0.059951	17.29683	85.94605	HSPA1B;HSPA1A
Negative Regulatio	0.006951	0.059951	17.29683	85.94605	SOD2;HSPA1A
Negative Regulatio	0.007395	0.062484	5.645838	27.70351	SULT2B1;SOD2;HSPA1B;HSPA1A
Negative Regulatio	0.009067	0.069354	15.00075	70.55036	HSPA1B;HSPA1A
Regulation Of mRN	0.010089	0.069354	14.16453	65.10522	RBM38;TBRG4
DNA Methylation In	0.010209	0.069354	124.7188	571.7716	TET3
tRNA Catabolic Pro	0.010209	0.069354	124.7188	571.7716	POP1
Intracellular Oxyge	0.010209	0.069354	124.7188	571.7716	SOD2
Positive Regulation	0.010209	0.069354	124.7188	571.7716	SOD2
Response To Testo	0.010209	0.069354	124.7188	571.7716	SPP1
Negative Regulatio	0.010887	0.069354	13.5959	61.45628	BAMBI;HSPA1A
Long-Chain Fatty A	0.011159	0.069354	13.41633	60.31338	CPT1A;ELOVL6
Regulation Of Cell	0.0112	0.069354	6.955475	31.2431	ATAD3A;HSPA1B;HSPA1A
Cellular Response T	0.011333	0.069354	6.924211	31.02069	SPP1;HSPA1B;HSPA1A
Regulation Of Cycli	0.011434	0.069354	13.24143	59.20461	CCNE1;CDK5R1
Negative Regulatio	0.011434	0.069354	13.24143	59.20461	HSPA1B;HSPA1A
Regulation Of Inter	0.011993	0.069354	12.9049	57.08384	HSPA1B;HSPA1A
Fatty Acid Elongatio	0.012239	0.069354	99.77	439.3038	ELOVL6
Fatty Acid Elongatio	0.012239	0.069354	99.77	439.3038	ELOVL6
Fatty Acid Elongatio	0.012239	0.069354	99.77	439.3038	ELOVL6
Fatty Acid Elongatio	0.012239	0.069354	99.77	439.3038	ELOVL6
Negative Regulatio	0.012239	0.069354	99.77	439.3038	DNMT1
Amino-Acid Betaine	0.012239	0.069354	99.77	439.3038	CPT1A
Regulation Of Mito	0.012239	0.069354	99.77	439.3038	TBRG4
Mitotic Nuclear Me	0.012239	0.069354	99.77	439.3038	LPIN1
Regulation Of Vasc	0.012239	0.069354	99.77	439.3038	SOD2
Copper Ion Import	0.012239	0.069354	99.77	439.3038	STEAP3
Positive Regulation	0.012564	0.069354	12.585	55.08345	HSPA1B;HSPA1A
Positive Regulation	0.012564	0.069354	12.585	55.08345	HSPA1B;HSPA1A
Aromatic Compour	0.014264	0.077702	83.1375	353.3355	TET2
Positive Regulation	0.014654	0.078398	11.57984	48.90207	HSPA1B;HSPA1A
Negative Regulatio	0.016286	0.078398	71.25714	293.3998	SOD2
Positive Regulation	0.016286	0.078398	71.25714	293.3998	SOD2
Isoprenoid Biosyntl	0.016286	0.078398	71.25714	293.3998	PDSS1
Isoprenoid Metabo	0.016286	0.078398	71.25714	293.3998	PDSS1
Nuclear Membrane	0.016286	0.078398	71.25714	293.3998	LPIN1
Protein Hexamerizi	0.016286	0.078398	71.25714	293.3998	MAT2A
Pyrimidine-Contain	0.016286	0.078398	71.25714	293.3998	TET2
Response To Vitam	0.016286	0.078398	71.25714	293.3998	SPP1
Response To Vitam	0.016286	0.078398	71.25714	293.3998	SPP1
Negative Regulatio	0.016694	0.079441	4.405971	18.0323	SOD2;ATAD3A;HSPA1B;HSPA1A
Positive Regulation	0.017213	0.0807	10.61058	43.10111	ELOVL6;LPIN1
Transferrin Transpo	0.018303	0.0807	62.34688	249.4308	STEAP3
Amino Sugar Metal	0.018303	0.0807	62.34688	249.4308	GNE
Carnitine Metabolic	0.018303	0.0807	62.34688	249.4308	CPT1A
Mitochondrial RNA	0.018303	0.0807	62.34688	249.4308	TBRG4

Positive Regulation	0.018303	0.0807	62.34688	249.4308	SULT2B1
Regulation Of RNA	0.018559	0.0807	10.1841	40.60211	RBM38;HSPA1A
Regulation Of Neur	0.019596	0.0807	9.885985	38.87571	SOD2;CDK5R1
Negative Regulatio	0.020316	0.0807	55.41667	215.9217	HSPA1A
N-acetylneuramina	0.020316	0.0807	55.41667	215.9217	GNE
Regulation Of Gene	0.020316	0.0807	55.41667	215.9217	DNMT3A
Neuron Projection	0.020316	0.0807	55.41667	215.9217	CDK5R1
Removal Of Supero	0.020316	0.0807	55.41667	215.9217	SOD2
Copper Ion Transpo	0.020316	0.0807	55.41667	215.9217	STEAP3
Positive Regulation	0.020316	0.0807	55.41667	215.9217	SPP1
Positive Regulation	0.020658	0.0807	9.604741	37.26302	ELOVL6;LPIN1
Regulation Of Prote	0.021017	0.0807	9.514498	36.74891	HSPA1B;HSPA1A
Negative Regulatio	0.021743	0.0807	9.338979	35.75378	BAMBI;HSPA1A
Regulation Of Trans	0.021743	0.0807	9.338979	35.75378	BAMBI;HSPA1A
Mitotic Cell Cycle P	0.021743	0.0807	9.338979	35.75378	CCNE1;AURKA
Regulation Of Prote	0.02211	0.0807	9.253613	35.27209	CCNE1;CDK5R1
Actin Crosslink Forr	0.022326	0.0807	49.8725	189.6162	GAS2L1
Cellular Response T	0.022326	0.0807	49.8725	189.6162	SOD2
Cellular Response T	0.022326	0.0807	49.8725	189.6162	GAS2L1
Central Nervous Sy	0.022326	0.0807	49.8725	189.6162	B4GALT5
Central Nervous Sy	0.022326	0.0807	49.8725	189.6162	B4GALT5
Regulation Of Prote	0.02248	0.0807	9.169785	34.80058	HSPA1B;HSPA1A
Negative Regulatio	0.023766	0.0807	3.940165	14.73432	SULT2B1;SOD2;HSPA1B;HSPA1A
Steroid Catabolic P	0.024331	0.0807	45.33636	168.4702	SPP1
Fatty Acid Elongatic	0.024331	0.0807	45.33636	168.4702	ELOVL6
Fatty Acid Transme	0.024331	0.0807	45.33636	168.4702	CPT1A
Negative Regulatio	0.024331	0.0807	45.33636	168.4702	HSPA1A
Very Long-Chain Fa	0.024331	0.0807	45.33636	168.4702	ELOVL6
Ionotropic Glutama	0.024331	0.0807	45.33636	168.4702	CDK5R1
Axonal Fasciculatio	0.024331	0.0807	45.33636	168.4702	CDK5R1
Quinone Biosynthe	0.024331	0.0807	45.33636	168.4702	PDSS1
Response To Thyro	0.024331	0.0807	45.33636	168.4702	GAS2L1
Regulation Of Prote	0.024366	0.0807	8.772325	32.58544	BAMBI;AURKA
Fatty Acid Metabol	0.02592	0.083218	8.478205	30.96872	CPT1A;LPIN1
Potassium Ion Tran	0.02592	0.083218	8.478205	30.96872	KCNG1;KCNN4
Organonitrogen Co	0.026315	0.083218	8.407713	30.58417	ELOVL6;B4GALT5
Ubiquinone Biosynt	0.026332	0.083218	41.55625	151.1384	PDSS1
Purine Ribonucleos	0.026332	0.083218	41.55625	151.1384	SULT2B1
Positive Regulation	0.026332	0.083218	41.55625	151.1384	KCNN4
Negative Regulatio	0.026712	0.083778	8.338377	30.20704	HSPA1B;HSPA1A
Negative Regulatio	0.027111	0.084377	8.270169	29.83714	HSPA1B;HSPA1A
tRNA 5'-End Proces	0.02833	0.084377	38.35769	136.701	POP1
RNA Phosphodieste	0.02833	0.084377	38.35769	136.701	POP1
Ubiquinone Metab	0.02833	0.084377	38.35769	136.701	PDSS1
Neuron Cell-Cell Ac	0.02833	0.084377	38.35769	136.701	CDK5R1
Positive Regulation	0.02833	0.084377	38.35769	136.701	SYNGR3
Negative Regulatio	0.02833	0.084377	38.35769	136.701	MPHOSPH9

3'-Phosphoadenosi	0.030323	0.086577	35.61607	124.5085	SULT2B1
Negative Regulatio	0.030323	0.086577	35.61607	124.5085	HSPA1A
DNA Alkylation (GC	0.030323	0.086577	35.61607	124.5085	DNMT3A
Ganglioside Biosynt	0.030323	0.086577	35.61607	124.5085	B4GALT5
Vasodilation (GO:0	0.030323	0.086577	35.61607	124.5085	SOD2
Positive Regulation	0.030323	0.086577	35.61607	124.5085	KCNN4
Potassium Ion Tran	0.032093	0.089868	7.530484	25.89819	KCNG1;KCNN4
Stabilization Of Me	0.032312	0.089868	33.24	114.09	KCNN4
Sulfation (GO:0051	0.032312	0.089868	33.24	114.09	SULT2B1
Regulation Of Delay	0.034298	0.089868	31.16094	105.0959	KCNG1
G Protein-Coupled	0.034298	0.089868	31.16094	105.0959	CDK5R1
Triglyceride Biosynt	0.034298	0.089868	31.16094	105.0959	LPIN1
Negative Regulatio	0.034298	0.089868	31.16094	105.0959	SOD2
Positive Regulation	0.034298	0.089868	31.16094	105.0959	KCNN4
Negative Regulatio	0.034298	0.089868	31.16094	105.0959	SOD2
Neuron Maturatior	0.034298	0.089868	31.16094	105.0959	B4GALT5
Long-Chain fatty-ac	0.034298	0.089868	31.16094	105.0959	ELOVL6
Cellular Response T	0.034298	0.089868	31.16094	105.0959	HSPA1A
Central Nervous Sy	0.034298	0.089868	31.16094	105.0959	B4GALT5
Regulation Of Cold-	0.036048	0.090479	7.056624	23.44849	ELOVL6;LPIN1
Regulation Of Epide	0.036279	0.090479	29.32647	97.26176	SULT2B1
Regulation Of Mito	0.036279	0.090479	29.32647	97.26176	HSPA1A
Intracellular Lipid T	0.036279	0.090479	29.32647	97.26176	CPT1A
Regulation Of Oxida	0.036279	0.090479	29.32647	97.26176	SOD2
Positive Regulation	0.036279	0.090479	29.32647	97.26176	KCNN4
Positive Regulation	0.036279	0.090479	29.32647	97.26176	SULT2B1
Regulation Of Cell (	0.036279	0.090479	29.32647	97.26176	AURKA
Neuron Developme	0.037863	0.092746	6.864518	22.47285	B4GALT5;CDK5R1
tRNA Metabolic Pro	0.038256	0.092746	27.69583	90.38385	POP1
Protein Heterooligo	0.038256	0.092746	27.69583	90.38385	MAT2A
Release Of Cytochr	0.038256	0.092746	27.69583	90.38385	SOD2
Positive Regulation	0.038308	0.092746	4.285902	13.98102	DNMT1;HSPA1B;HSPA1A
Positive Regulation	0.038784	0.093045	6.772308	22.00825	HSPA1B;HSPA1A
Regulation Of Cellu	0.039248	0.093045	6.727118	21.78146	ATAD3A;AURKA
DNA Methylation (	0.04023	0.093045	26.23684	84.30285	DNMT3A
Positive Regulation	0.04023	0.093045	26.23684	84.30285	DNMT1
Mitochondrial RNA	0.04023	0.093045	26.23684	84.30285	TBRG4
Monocarboxylic Ac	0.04023	0.093045	26.23684	84.30285	LPIN1
Positive Regulation	0.04023	0.093045	26.23684	84.30285	KCNN4
Positive Regulation	0.04023	0.093045	26.23684	84.30285	SULT2B1
Peptidyl-Serine Pho	0.041598	0.095675	6.509862	20.69949	AURKA;CDK5R1
Chaperone-Mediat	0.042199	0.096522	24.92375	78.89244	HSPA1A
Negative Regulatio	0.042918	0.097257	4.089599	12.87596	ATAD3A;HSPA1B;HSPA1A
Mitochondrion Org	0.043515	0.097257	6.345833	19.89196	CHCHD7;ATAD3A
Vesicle Transport A	0.044165	0.097257	23.73571	74.05131	CDR2L
Acetylcholine Rece	0.044165	0.097257	23.73571	74.05131	CDK5R1
Acylglycerol Biosyn	0.044165	0.097257	23.73571	74.05131	LPIN1

Oxoacid Metabolic	0.044165	0.097257	23.73571	74.05131	SULT2B1
Cellular Response T	0.044165	0.097257	23.73571	74.05131	HSPA1A
Peptidyl-Serine Mo	0.045465	0.098435	6.189806	19.13152	AURKA;CDK5R1
Regulation Of Cent	0.046126	0.098435	22.65568	69.69723	AURKA
Positive Regulation	0.046126	0.098435	22.65568	69.69723	CDK5R1
Long-Chain Fatty A	0.046126	0.098435	22.65568	69.69723	CPT1A
Long-Chain fatty-ac	0.046126	0.098435	22.65568	69.69723	ELOVL6
Cellular Lipid Catab	0.046126	0.098435	22.65568	69.69723	LPIN1
Metal Ion Transpor	0.047948	0.10105	6.005159	18.24154	KCNG1;KCNN4
Regulation Of Endo	0.048084	0.10105	21.66957	65.76286	HSPA1A
Iron Ion Transport (	0.048084	0.10105	21.66957	65.76286	STEAP3
fatty-acyl-CoA Bios	0.050038	0.103063	20.76563	62.19252	ELOVL6
Negative Regulatio	0.050038	0.103063	20.76563	62.19252	HSPA1A
Long-Chain Fatty A	0.050038	0.103063	20.76563	62.19252	ELOVL6
Regulation Of Posts	0.050038	0.103063	20.76563	62.19252	CDK5R1
Positive Regulation	0.051988	0.106024	19.934	58.9398	CDK5R1
Regulation Of Pota	0.051988	0.106024	19.934	58.9398	KCNG1
Positive Regulation	0.053934	0.10892	19.16635	55.96572	AURKA
Regulation Of Micr	0.053934	0.10892	19.16635	55.96572	GAS2L1
Phosphate-Contain	0.054628	0.109786	5.572556	16.20058	IMPA1;ACYP1
Negative Regulatio	0.055684	0.110682	5.511427	15.91737	DNMT1;AURKA
RNA Phosphodieste	0.055876	0.110682	18.45556	53.23735	POP1
Regulation Of Bone	0.055876	0.110682	18.45556	53.23735	SPP1
Axonogenesis (GO:	0.056747	0.111872	5.451613	15.64154	B4GALT5;CDK5R1
Negative Regulatio	0.057814	0.112901	17.79554	50.72663	MPHOSPH9
Carbohydrate Deriv	0.057814	0.112901	17.79554	50.72663	B4GALT5
Regulation Of Denc	0.059748	0.11613	17.18103	48.40956	CDK5R1
Very Long-Chain Fa	0.063605	0.123049	16.07097	44.27649	ELOVL6
Regulation Of Pota	0.065528	0.124443	15.56797	42.42708	KCNN4
Carboxylic Acid Me	0.065528	0.124443	15.56797	42.42708	GNE
Positive Regulation	0.065528	0.124443	15.56797	42.42708	HSPA1A
ncRNA Catabolic Pr	0.065528	0.124443	15.56797	42.42708	POP1
Superoxide Metabc	0.067447	0.125779	15.09545	40.70366	SOD2
Positive Regulation	0.067447	0.125779	15.09545	40.70366	CDK5R1
Apoptotic Mitocho	0.067447	0.125779	15.09545	40.70366	SOD2
Regulation Of T Cel	0.067447	0.125779	15.09545	40.70366	KCNN4
Protein Stabilizatio	0.067759	0.125795	4.917351	13.23652	HSPA1B;HSPA1A
Positive Regulation	0.069362	0.127061	14.65074	39.09433	AURKA
Glutamate Receptc	0.069362	0.127061	14.65074	39.09433	CDK5R1
Liver Development	0.069362	0.127061	14.65074	39.09433	AURKA
Negative Regulatio	0.071273	0.129416	14.23143	37.58863	MPHOSPH9
Positive Regulation	0.071273	0.129416	14.23143	37.58863	HSPA1A
RNA Stabilization ((	0.07318	0.131724	13.83542	36.17728	RBM38
Negative Regulatio	0.07318	0.131724	13.83542	36.17728	SOD2
Positive Regulation	0.074936	0.133985	3.224429	8.3549	DNMT1;HSPA1B;HSPA1A
G2/M Transition Of	0.075084	0.133985	13.46081	34.8521	AURKA
Negative Regulatio	0.076983	0.135622	13.10592	33.60577	HSPA1A

Vesicle Cytoskeleta	0.076983	0.135622	13.10592	33.60577	CDR2L
Organelle Transpor	0.076983	0.135622	13.10592	33.60577	CDR2L
Regulation Of Micr	0.078879	0.136729	12.76923	32.43178	GAS2L1
Regulation Of Micr	0.078879	0.136729	12.76923	32.43178	CDK5R1
Cell Cycle G2/M Ph	0.078879	0.136729	12.76923	32.43178	AURKA
Regulation Of Gene	0.078933	0.136729	2.331774	5.920734	RBM38;DNMT1;HSPA1B;AURKA;HSPA1A
Negative Regulatio	0.080771	0.138179	12.44938	31.3243	RBM38
O-glycan Processing	0.080771	0.138179	12.44938	31.3243	B4GALT5
Regulation Of Micr	0.080771	0.138179	12.44938	31.3243	AURKA
Protein Phosphoryl	0.082414	0.139678	3.091496	7.716392	CCNE1;AURKA;CDK5R1
Positive Regulation	0.082425	0.139678	4.37962	10.93094	AURKA;B4GALT5
Substantia Nigra De	0.08266	0.139678	12.14512	30.27809	SYNGR3
Ephrin Receptor Sig	0.084544	0.142281	11.85536	29.28845	CDK5R1
Cellular Response T	0.086425	0.144274	11.57907	28.35113	SPP1
Response To Unfol	0.086425	0.144274	11.57907	28.35113	HSPA1A
Regulation Of Auto	0.08731	0.145167	4.231306	10.31713	DRAM1;CDK5R1
Establishment Of P	0.088302	0.145645	11.31534	27.46228	STEAP3
Triglyceride Metab	0.088302	0.145645	11.31534	27.46228	LPIN1
Vacuolar Transport	0.090175	0.147129	11.06333	26.61842	HSPA1A
Antiviral Innate Imr	0.090175	0.147129	11.06333	26.61842	ATAD3A
Positive Regulation	0.090408	0.147129	4.143548	9.958718	HSPA1B;HSPA1A
Golgi To Plasma Me	0.092044	0.147129	10.82228	25.81639	CCDC93
Positive Regulation	0.092044	0.147129	10.82228	25.81639	DNMT1
Regulation Of Signa	0.092044	0.147129	10.82228	25.81639	AURKA
Secondary Alcohol	0.092044	0.147129	10.82228	25.81639	SULT2B1
Positive Regulation	0.092044	0.147129	10.82228	25.81639	BAMBI
Myelination (GO:00	0.09391	0.149534	10.59149	25.0533	B4GALT5
tRNA Processing (G	0.09763	0.154271	10.15816	23.63366	POP1
Positive Regulation	0.09763	0.154271	10.15816	23.63366	SYNGR3
Negative Regulatio	0.099485	0.155421	9.9545	22.97251	DNMT1
Microtubule Bundle	0.099485	0.155421	9.9545	22.97251	GAS2L1
Regulated Exocytos	0.099485	0.155421	9.9545	22.97251	SYNGR3
Adenylate Cyclase-	0.101335	0.157127	9.758824	22.34106	GPR37
Cell Cycle G1/S Pha	0.101335	0.157127	9.758824	22.34106	CCNE1
Glycoprotein Metal	0.103183	0.157629	9.570673	21.73745	B4GALT5
mRNA Stabilization	0.103183	0.157629	9.570673	21.73745	RBM38
Protein Homotetra	0.103183	0.157629	9.570673	21.73745	SOD2
Regulation Of Alter	0.103183	0.157629	9.570673	21.73745	RBM38
Organelle Disassem	0.105026	0.15927	9.389623	21.15997	AURKA
Ribosomal Large Su	0.105026	0.15927	9.389623	21.15997	NOP16
Neuron Migration (	0.106866	0.161468	9.215278	20.60705	CDK5R1
Positive Regulation	0.108626	0.161879	2.100274	4.66228	BAMBI;TET3;SPP1;TET2;LPIN1
Regulation Of Mito	0.108702	0.161879	9.047273	20.07725	AURKA
post-Golgi Vesicle-I	0.108702	0.161879	9.047273	20.07725	CCDC93
Regulation Of Catic	0.108702	0.161879	9.047273	20.07725	KCNG1
Membrane Lipid Bi	0.110534	0.163432	8.885268	19.56921	ELOVL6
Myeloid Cell Differe	0.110534	0.163432	8.885268	19.56921	TET2

Positive Regulation	0.112362	0.164375	8.728947	19.0817	AURKA
Peptidyl-Threonine	0.112362	0.164375	8.728947	19.0817	CDK5R1
Response To Organ	0.112362	0.164375	8.728947	19.0817	SPP1
Monoatomic Catio	0.11295	0.164652	3.617315	7.888685	KCNG1;KCNN4
Positive Regulation	0.114187	0.165292	8.578017	18.61356	BAMBI
Regulation Of Cell D	0.114187	0.165292	8.578017	18.61356	HSPA1B
Inorganic Cation Tr	0.114946	0.165811	3.578287	7.740877	KCNG1;KCNN4
Sterol Metabolic Pr	0.116009	0.166452	8.432203	18.16373	SULT2B1
Regulation Of Tran	0.116195	0.166452	1.827371	3.933396	DNMT3A;TET3;TET2;HR;SOD2;LPIN1;HSPA1A
Fatty Acid Catabolic	0.117826	0.168207	8.29125	17.7312	LPIN1
Regulation Of Emb	0.11964	0.17021	8.154918	17.31506	B4GALT5
G1/S Transition Of	0.121451	0.171022	8.022984	16.91444	CCNE1
Phosphatidylinosito	0.121451	0.171022	8.022984	16.91444	IMPA1
Regulation Of Cellu	0.121451	0.171022	8.022984	16.91444	DRAM1
Negative Regulatio	0.123257	0.172394	7.895238	16.52853	HSPA1B
Endocytic Recycling	0.123257	0.172394	7.895238	16.52853	CCDC93
Fatty Acid Biosynth	0.12506	0.173742	7.771484	16.15659	ELOVL6
Positive Regulation	0.12506	0.173742	7.771484	16.15659	AURKA
Peptidyl-Threonine	0.12686	0.175652	7.651538	15.79792	CDK5R1
Protein Secretion (	0.128656	0.176955	7.535227	15.45185	STEAP3
Cholesterol Metab	0.128656	0.176955	7.535227	15.45185	SULT2B1
Neuropeptide Sign	0.130448	0.178826	7.422388	15.11777	GPR37
Sulfur Compound B	0.134022	0.182516	7.206522	14.48333	MAT2A
Positive Regulation	0.134022	0.182516	7.206522	14.48333	CDK5R1
Regulation Of Ciliu	0.135803	0.182541	7.103214	14.18191	MPHOSPH9
Negative Regulatio	0.135803	0.182541	7.103214	14.18191	AURKA
Lipid Biosynthetic P	0.135803	0.182541	7.103214	14.18191	PDSS1
Negative Regulatio	0.135803	0.182541	7.103214	14.18191	BAMBI
Transforming Grow	0.137581	0.184332	7.002817	13.89038	BAMBI
Protein Tetrameriz	0.139355	0.185804	6.905208	13.60828	SOD2
Positive Regulation	0.139577	0.185804	3.167392	6.237024	HSPA1B;HSPA1A
Negative Regulatio	0.141126	0.187264	6.810274	13.3352	SOD2
Regulation Of BMP	0.142894	0.189003	6.717905	13.07073	BAMBI
Protein-Containing	0.145203	0.191445	3.088406	5.959469	CHCHD7;HSPA1A
Sphingolipid Biosyn	0.146417	0.192434	6.540461	12.56615	ELOVL6
Cellular Response T	0.148174	0.194127	6.455195	12.32535	GAS2L1
Regulation Of Neur	0.149927	0.195188	6.372115	12.09177	CDK5R1
Response To Insulin	0.149927	0.195188	6.372115	12.09177	LPIN1
Regulation Of Cytol	0.151677	0.196232	6.291139	11.86512	AURKA
Glycoprotein Biosy	0.151677	0.196232	6.291139	11.86512	B4GALT5
Negative Regulatio	0.155165	0.199872	6.135185	11.43148	HSPA1A
Epigenetic Regulati	0.156904	0.199872	6.060061	11.22396	DNMT3A
Regulation Of Epith	0.156904	0.199872	6.060061	11.22396	BAMBI
Vesicle-Mediated T	0.156904	0.199872	6.060061	11.22396	CCDC93
Regulation Of Cell D	0.156904	0.199872	6.060061	11.22396	AURKA
Epidermis Develop	0.160372	0.201805	5.915179	10.82632	GJB5
Regulation Of Oste	0.160372	0.201805	5.915179	10.82632	BAMBI

Mitotic Spindle Org	0.160372	0.201805	5.915179	10.82632	AURKA
Positive Regulation	0.160372	0.201805	5.915179	10.82632	BAMBI
Exocytosis (GO:000	0.1621	0.202137	5.845294	10.63574	SYNGR3
Regulation Of Mito	0.1621	0.202137	5.845294	10.63574	AURKA
Negative Regulatio	0.1621	0.202137	5.845294	10.63574	AURKA
Negative Regulatio	0.165547	0.205815	5.710345	10.27005	SOD2
Cellular Response T	0.167265	0.207329	5.64517	10.09455	LPIN1
Mitochondrial Resp	0.16898	0.208829	5.581461	9.923695	CHCHD7
Regulation Of RNA	0.170691	0.209692	5.519167	9.757326	RBM38
Positive Regulation	0.170691	0.209692	5.519167	9.757326	BAMBI
Steroid Metabolic P	0.172399	0.211164	5.458242	9.595276	SULT2B1
Regulation Of Apop	0.174883	0.21344	2.165655	3.776122	ATAD3A;HSPA1B;HSPA1A
Sphingolipid Metab	0.175805	0.21344	5.340323	9.283521	ELOVL6
Regulation Of mRN	0.175805	0.21344	5.340323	9.283521	RBM38
Protein Modificatio	0.177941	0.215036	2.146632	3.705735	CCNE1;AURKA;B4GALT5
Regulation Of Macr	0.179196	0.215036	5.227368	8.987274	CDK5R1
Positive Regulation	0.179196	0.215036	5.227368	8.987274	CDK5R1
Cellular Response T	0.179196	0.215036	5.227368	8.987274	BAMBI
Monocarboxylic Ac	0.180887	0.216437	5.172656	8.844633	CPT1A
Phosphatidylinositc	0.182574	0.217827	5.119072	8.705479	IMPA1
Axon Development	0.184258	0.218576	5.066582	8.569697	CDK5R1
Cellular Response T	0.184258	0.218576	5.066582	8.569697	LPIN1
Protein Complex Ol	0.185939	0.219313	5.015152	8.437172	MAT2A
ncRNA Processing (	0.185939	0.219313	5.015152	8.437172	POP1
Hemopoiesis (GO:0	0.187616	0.220662	4.96475	8.307798	TET2
Mitochondrial Gen	0.190961	0.223959	4.866912	8.058089	TBRG4
Lysosomal Transpo	0.194291	0.227222	4.772837	7.819797	HSPA1A
Regulation Of DNA-	0.196818	0.229528	1.614345	2.624083	BAMBI;DNMT3A;SPP1;HR;SOD2;CDK5R1
Glycerophospholipi	0.199263	0.231727	4.638318	7.482216	IMPA1
Positive Regulation	0.200913	0.232992	4.595139	7.37466	BAMBI
Response To Lipid (	0.20256	0.234246	4.552752	7.269462	SPP1
RNA Metabolic Pro	0.204204	0.235489	4.511136	7.166553	TBRG4
Calcium Ion Transp	0.205844	0.236721	4.47027	7.065863	KCNN4
Positive Regulation	0.215618	0.246591	4.239744	6.504808	AURKA
Ribonucleoprotein	0.215618	0.246591	4.239744	6.504808	NOP16
Phosphorylation (G	0.219457	0.25029	2.345764	3.557583	CCNE1;AURKA
Neuron Projection	0.225275	0.256219	4.031707	6.008996	CDK5R1
Regulation Of Mito	0.226873	0.25733	3.998992	5.931967	AURKA
Cellular Response T	0.228468	0.258431	3.9668	5.856426	GAS2L1
Regulation Of Anat	0.230059	0.259522	3.935119	5.782334	CDK5R1
Protein Homooligo	0.233233	0.262387	3.873242	5.638344	SOD2
Transmembrane Re	0.234815	0.262739	3.843023	5.568373	BAMBI
Regulation Of Cell (	0.234815	0.262739	3.843023	5.568373	AURKA
Epithelial Cell Diffe	0.23797	0.264837	3.783969	5.43231	CPT1A
Plasma Membrane	0.23797	0.264837	3.783969	5.43231	CDK5R1
Negative Regulatio	0.239944	0.266318	2.203208	3.144752	DNMT3A;CDK5R1
Actin Filament Orga	0.256633	0.28408	3.464336	4.711876	GAS2L1

Positive Regulation	0.260541	0.287637	2.076657	2.793095	BAMBI;TBRG4
Axon Guidance (GC	0.264277	0.290985	3.346453	4.453323	CDK5R1
Epithelium Develop	0.271844	0.298523	3.236275	4.215338	CPT1A
Ribosome Biogenes	0.273348	0.299381	3.215097	4.170011	NOP16
Protein Autophosp	0.283794	0.310001	3.074224	3.872009	AURKA
Adenylate Cyclase-	0.285274	0.310798	3.055093	3.83202	GPR37
Brain Development	0.294093	0.319565	2.945089	3.604379	CDK5R1
Generation Of Neu	0.298462	0.323464	2.892982	3.497941	CDK5R1
Neuron Differentia	0.299913	0.324188	2.876017	3.463484	CDK5R1
Regulation Of Neur	0.30136	0.324607	2.859249	3.429521	CDK5R1
Positive Regulation	0.301869	0.324607	1.606305	1.923973	TET3;TET2;LPIN1
Endosomal Transpo	0.309985	0.332471	2.76257	3.235604	CCDC93
RNA Processing (GO	0.314259	0.335318	2.716621	3.144592	TBRG4
Macromolecule Bio	0.314259	0.335318	2.716621	3.144592	B4GALT5
Positive Regulation	0.317018	0.337392	1.792931	2.059713	BAMBI;SPP1
Defense Response	0.322729	0.342589	2.629122	2.973389	ATAD3A
Neuron Projection	0.326925	0.346156	2.587435	2.892815	CDK5R1
Regulation Of Cell D	0.328318	0.346744	2.573828	2.866657	CDK5R1
Organic Substance	0.339363	0.357497	2.469875	2.669158	KCNN4
Regulation Of MAP	0.343459	0.360893	2.433005	2.600124	GPR37
Positive Regulation	0.344999	0.361593	1.677668	1.785399	BAMBI;TBRG4
Regulation Of Cano	0.34753	0.362411	2.397209	2.533622	BAMBI
Negative Regulation	0.34753	0.362411	2.397209	2.533622	BAMBI
Negative Regulation	0.351389	0.365515	1.462844	1.529933	DNMT3A;CDK5R1;HSPA1A
mRNA Processing (	0.356933	0.370352	2.317606	2.387611	TBRG4
Positive Regulation	0.366205	0.379022	2.243068	2.253302	SOD2
Cilium Organization	0.375346	0.387514	2.173128	2.129464	AURKA
Positive Regulation	0.427551	0.440313	1.829926	1.554856	CDK5R1
Positive Regulation	0.429927	0.441662	1.816236	1.533156	SOD2
Central Nervous Sy	0.442828	0.452669	1.744415	1.420954	CDK5R1
Positive Regulation	0.442828	0.452669	1.744415	1.420954	BAMBI
Transmembrane Re	0.443987	0.452735	1.738163	1.411319	CDK5R1
Regulation Of Intra	0.458836	0.466727	1.660726	1.293808	AURKA
Regulation Of Cell (	0.459963	0.466727	1.655051	1.285329	TBRG4
Negative Regulation	0.46718	0.472891	1.293709	0.984566	DNMT3A;HSPA1A
Positive Regulation	0.473299	0.477916	1.589806	1.18922	GPR37
Protein Transport (	0.476582	0.480061	1.574279	1.166722	STEAP3
Organelle Organiza	0.579729	0.582543	1.171583	0.63874	ATAD3A
Regulation Of Cell M	0.593595	0.595032	1.127367	0.587988	SOD2
Positive Regulation	0.664365	0.664365	0.927242	0.379171	GPR37

Positive Regulation	0.427939	1.90566
Positive Regulation	0.431779	1.876942
Positive Regulation	0.433158	1.862901
Central Nervous Sy	0.444132	1.789234
Positive Regulation	0.444132	1.789234
Transmembrane Re	0.444246	1.782821

Regulation Of Intra	0.458138	1.703396
Regulation Of Cell (	0.458186	1.697574
Positive Regulation	0.470473	1.630653
Protein Transport (	0.472651	1.614727
Protein-Containing	0.487637	1.539481
Organelle Organiza	0.573413	1.201685
Regulation Of Cell M	0.585927	1.156333
Positive Regulation	0.655299	0.951067

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GO CP 2023 Cluster 1

Term	P-value	Adjusted P-	Odds Ratio	Combined S	Genes
Mitochond	2.64E-28	1.56E-26	24.63048	1564.08	MRS2;COX7B;UQCRB;CISD1;MRPL35;COX5A;C
Mitochond	2.14E-24	6.30E-23	26.26946	1431.76	MRS2;COX7B;UQCRB;MRPL35;COX5A;TMEM2
Organelle I	1.30E-23	2.57E-22	24.26273	1278.488	MRS2;COX7B;UQCRB;MRPL35;COX5A;TMEM2
Mitochond	2.05E-15	3.02E-14	17.14803	579.9759	NDUFA9;HSPA9;FH;PDHA1;FASTKD1;SIRT5;TIM
Mitochond	2.95E-10	3.48E-09	21.08376	462.657	NDUFA9;NDUFA8;TIMM8A;NDUFA6;OPA1;ND
Intracellula	4.56E-09	4.49E-08	6.719629	129.0504	NDUFA9;HSPA9;FH;PDHA1;FASTKD1;SIRT5;DE
MIB Compl	1.09E-07	8.03E-07	132.7533	2128.375	HSPA9;CHCHD3;SAMM50;IMMT
SAM Comp	1.09E-07	8.03E-07	132.7533	2128.375	HSPA9;CHCHD3;SAMM50;IMMT
Mitochond	1.61E-07	1.06E-06	29.15607	455.9814	NDUFA8;TIMM8A;OPA1;SIRT5;CYCS;NDUFS1
Organelle E	2.82E-07	1.60E-06	26.32656	397.0368	NDUFA8;TIMM8A;OPA1;SIRT5;CYCS;NDUFS1
TIM23 Mito	2.98E-07	1.60E-06	96.53333	1450.625	HSPA9;GRPEL1;TIMM17A;TIMM44
Mitochond	5.16E-07	2.39E-06	81.67385	1182.412	COX7B;UQCRFS1;COX5A;COX6B1
Respiratory	5.67E-07	2.39E-06	37.3217	536.7956	NDUFA9;NDUFA8;NDUFA6;NDUFS3;NDUFS1
Mitochond	5.67E-07	2.39E-06	37.3217	536.7956	NDUFA9;NDUFA8;NDUFA6;NDUFS3;NDUFS1
Respiratory	8.35E-07	3.29E-06	70.77689	990.5608	COX7B;UQCRFS1;COX5A;COX6B1
Mitochond	1.28E-06	4.73E-06	62.44392	847.1819	HSPA9;CHCHD3;SAMM50;IMMT
Mitochond	2.96E-05	1.03E-04	11.20983	116.8941	CYP27B1;SAMM50;OPA1;STARD7;CISD1;VDAC
Organelle C	5.74E-05	1.88E-04	9.901604	96.68578	CYP27B1;SAMM50;OPA1;STARD7;CISD1;VDAC
MICOS Con	3.19E-04	9.92E-04	103.4597	832.76	CHCHD3;IMMT
Respiratory	8.28E-04	0.002326	57.46609	407.8119	UQCRB;UQCRFS1
Mitochond	8.28E-04	0.002326	57.46609	407.8119	UQCRB;UQCRFS1
Extracellula	0.02352	0.063077	8.895208	33.35604	RAB3A;DEFB1
Clathrin-Sc	0.027328	0.067182	42.55342	153.1851	RAB3A
Clathrin-Sc	0.027328	0.067182	42.55342	153.1851	RAB3A
GBAF Comp	0.050165	0.118389	21.2703	63.65008	BCL7A
Mitochond	0.083431	0.189323	12.14896	30.17485	MRPL35
Condensed	0.104966	0.228639	9.446344	21.29317	SMC2
SWI/SNF C	0.108506	0.228639	9.108516	20.22952	BCL7A
Postsynapt	0.126002	0.256348	7.726496	16.00512	DLG3
Postsynapt	0.139754	0.272462	6.889813	13.55829	DLG3
Neuromusc	0.143158	0.272462	6.708165	13.03937	DLG3
Extracellula	0.202212	0.367285	4.547848	7.269456	RAB3A
Condensed	0.211656	0.367285	4.31595	6.701781	SMC2
Transport V	0.211656	0.367285	4.31595	6.701781	RAB3A
Clathrin-Co	0.300227	0.506097	2.856814	3.437362	RAB3A
Nuclear Ch	0.314002	0.514614	2.704173	3.132396	SMC2
Golgi Lume	0.327509	0.522244	2.566952	2.865335	DEFB1
Nucleolus (	0.363125	0.557793	1.331873	1.349198	PDHA1;CIAPIN1;SDHA;SMC2
Nuclear Lu	0.371262	0.557793	1.315808	1.303764	PDHA1;CIAPIN1;SDHA;SMC2
Neuron Pro	0.378165	0.557793	1.37994	1.341888	RAB3A;OPA1;DLG3
Adherens J	0.448933	0.633725	1.701256	1.362504	DLG3
Postsynapt	0.451126	0.633725	1.689829	1.345118	DLG3
Chromosor	0.478865	0.657047	1.554035	1.144292	SMC2
Microtubul	0.520778	0.698316	1.375209	0.89723	OPA1
Axon (GO:0	0.557594	0.731067	1.239128	0.723805	RAB3A

Vesicle (GC	0.607642	0.779367	1.078622	0.537336	RAB3A
Polymeric (	0.652092	0.808055	0.954594	0.408155	OPA1
Dendrite (G	0.659001	0.808055	0.936612	0.390596	OPA1
Secretory G	0.671097	0.808055	0.905875	0.361301	RAB3A
Cell-Cell Ju	0.69648	0.812458	0.844218	0.305367	DLG3
Intracellula	0.702294	0.812458	0.838735	0.296411	PDHA1;CIAPIN1;SDHA;SMC2
Microtubul	0.744687	0.844934	0.736146	0.217009	OPA1
Focal Adhe	0.787045	0.851544	0.648831	0.155375	HSPA9
Cytoplasmi	0.788757	0.851544	0.64542	0.153156	RAB3A
Cell-Substr	0.793813	0.851544	0.635396	0.146718	HSPA9
Endoplasm	0.830464	0.874953	0.621621	0.115479	ILVBL;DHDDS
Nucleus (G	0.875104	0.90581	0.743855	0.099239	NDUFA9;PDHA1;SIRT5;SMC2;SUPV3L1;CS;CYP
Intracellula	0.940968	0.957192	0.670467	0.040795	NDUFA9;PDHA1;SIRT5;SMC2;SUPV3L1;CS;CYP
Bounding M	0.963473	0.963473	0.299401	0.011141	RAB3A

CYP27B1;TMEM223;MRPL2;CHCHD3;SAMM50;OPA1;TIMM17A;UQCRFS1;NDUFA9;NDUFA8;NDUFA6;ST
223;MRPL2;CHCHD3;OPA1;TIMM17A;UQCRFS1;NDUFA8;NDUFA6;CKMT1A;IMMT;TIMM44;COQ9;SDHA;
223;MRPL2;CHCHD3;OPA1;TIMM17A;UQCRFS1;NDUFA8;NDUFA6;CKMT1A;IMMT;TIMM44;COQ9;SDHA;

ARD7;CKMT1A;IMMT;TIMM44;COQ9;SDHA;COX6B1;AFG3L2;COQ3;NDUFAF4;VDAC3;NDUFS3;CYCS;SLC2

25A5

GO CP 2023 Cluster 2

Term	P-value	Adjusted P-	Odds Ratio	Combined S	Genes
Aggresome	0.002337	0.05581	30.96503	187.6102	HSPA1B;HSPA1A
Neuromusc	0.002896	0.05581	27.61192	161.3783	SYNGR3;CDK5R1
Cyclin-Dep	0.003044	0.05581	26.88394	155.7795	CCNE1;CDK5R1
Intracellula	0.007549	0.096584	3.853916	18.83148	SPP1;PDSS1;SOD2;HSPA1B;TBRG4;HSPA1A
Voltage-Ga	0.009829	0.096584	14.36475	66.40057	KCNG1;KCNN4
Potassium	0.011993	0.096584	12.9049	57.08384	KCNG1;KCNN4
Vesicle (GC	0.012293	0.096584	6.712908	29.5285	KCNN4;HSPA1B;HSPA1A
Ficolin-1-Ri	0.026315	0.175646	8.407713	30.58417	HSPA1B;HSPA1A
Endoribonu	0.034298	0.175646	31.16094	105.0959	POP1
Mitochond	0.035977	0.175646	4.397503	14.62112	PDSS1;SOD2;TBRG4
Connexin C	0.036279	0.175646	29.32647	97.26176	GJB5
Mitochond	0.038323	0.175646	6.818104	22.23869	CPT1A;LPIN1
Gap Junctic	0.042199	0.178535	24.92375	78.89244	GJB5
Organelle (	0.047447	0.1864	6.041209	18.41443	CPT1A;LPIN1
Ficolin-1-Ri	0.054628	0.200303	5.572556	16.20058	HSPA1B;HSPA1A
Euchromat	0.086425	0.288821	11.57907	28.35113	DNMT3A
Multivesicu	0.09763	0.288821	10.15816	23.63366	STEAP3
Mitochond	0.0983	0.288821	2.855337	6.623621	CPT1A;LPIN1;ATAD3A
Exocytic Ve	0.103183	0.288821	9.570673	21.73745	SYNGR3
Synaptic Ve	0.105026	0.288821	9.389623	21.15997	SYNGR3
Serine/Thre	0.116009	0.303832	8.432203	18.16373	CDK5R1
Spindle Mic	0.130448	0.324747	7.422388	15.11777	AURKA
Actin Filam	0.135803	0.324747	7.103214	14.18191	GAS2L1
Focal Adhe	0.187992	0.426659	2.607259	4.357654	HSPA1B;HSPA1A
Cell-Substra	0.193936	0.426659	2.553142	4.187734	HSPA1B;HSPA1A
Asymmetri	0.239542	0.499072	3.755114	5.366152	CDK5R1
Intracellula	0.244999	0.499072	1.330886	1.871894	DNMT1;NOP16;DNMT3A;TET2;AURKA;SULT2E
Mitotic Spi	0.255095	0.501079	3.488908	4.76627	AURKA
Postsynapt	0.267313	0.506972	3.3015	4.35579	CDK5R1
Basolateral	0.297009	0.544516	2.910147	3.532902	AURKA
Neuron Pro	0.317018	0.545005	1.792931	2.059713	KCNN4;CDK5R1
Microtubul	0.317094	0.545005	2.686821	3.08597	AURKA
Axon (GO:(	0.344818	0.552477	2.420956	2.577682	CDK5R1
Late Endos	0.344818	0.552477	2.420956	2.577682	STEAP3
Spindle (GC	0.351576	0.552477	2.36244	2.469526	AURKA
Lytic Vacuc	0.36883	0.556017	2.222635	2.216901	DRAM1
Nuclear Me	0.374048	0.556017	2.182854	2.146556	LPIN1
Polymeric (	0.421566	0.581293	1.865057	1.610995	GAS2L1
Dendrite (G	0.427551	0.581293	1.829926	1.554856	CDK5R1
Nucleus (G	0.44154	0.581293	1.115522	0.911925	DNMT1;CCNE1;DNMT3A;TET3;TET2;LPIN1;HS
Endoplasm	0.443987	0.581293	1.738163	1.411319	SPP1
Intracellula	0.446909	0.581293	1.242957	1.001077	NOP16;POP1;AURKA
Nucleolus (	0.472658	0.581293	1.279717	0.958998	NOP16;POP1
Nuclear Lur	0.478784	0.581293	1.26432	0.93118	NOP16;POP1
Actin Cytos	0.491643	0.581293	1.505598	1.068978	GAS2L1

Endoplasm	0.492915	0.581293	1.229742	0.869942	ELOVL6;LPIN1
Bounding M	0.504845	0.581293	1.201519	0.821244	STEAP3;B4GALT5
Microtubul	0.507311	0.581293	1.43827	0.976055	AURKA
Endosome	0.526481	0.588837	1.361042	0.873162	STEAP3
Mitochond	0.535306	0.588837	1.327236	0.829412	ATAD3A
Cytoplasmi	0.553413	0.594156	1.261018	0.746083	STEAP3
Organelle I	0.561747	0.594156	1.231864	0.71042	ATAD3A
Golgi Mem	0.587584	0.609757	1.146303	0.60953	B4GALT5
Lysosome (	0.648447	0.660455	0.968974	0.419735	DRAM1
Cytoskelet	0.712915	0.712915	0.809406	0.273897	AURKA

31;CCNE1;TET3;LPIN1;CCDC93;HSPA1B;CDK5R1;HSPA1A

GO MF 2023 Cluster 1

Term	P-value	Adjusted P-	Odds Ratio	Combined S	Genes
Oxidoredu	6.74E-13	5.73E-11	56.78857	1591.536	NDUFA9;NDUFA8;COX7B;NDUFA6;UQCRB;ND
NADH Deh	1.84E-07	6.09E-06	48.00434	744.4548	NDUFA9;NDUFA8;NDUFA6;NDUFS3;NDUFS1
NADH Deh	2.15E-07	6.09E-06	46.34669	711.5186	NDUFA9;NDUFA8;NDUFA6;NDUFS3;NDUFS1
Active Mor	2.26E-06	4.79E-05	53.06933	690.0091	COX7B;UQCRB;COX5A;COX6B1
Cytochrom	1.27E-05	2.16E-04	87.33333	984.4614	COX7B;COX5A;COX6B1
Proton Tra	2.97E-05	4.21E-04	25.86016	269.5751	COX7B;UQCRB;COX5A;COX6B1
NADH Deh	3.19E-04	0.003878	103.4597	832.76	NDUFA9;NDUFS3
2 Iron, 2 Su	9.91E-04	0.010529	51.71688	357.7157	CISD1;CIAPIN1
3'-5' RNA H	0.019596	0.137465	63.83654	251.0315	SUPV3L1
Flavin Ader	0.019984	0.137465	9.736829	38.09834	ILVBL;SDHA
NAD-deper	0.02347	0.137465	51.06667	191.6039	SIRT5
Oxidoredu	0.027328	0.137465	42.55342	153.1851	PDHA1
Purine Nuc	0.027328	0.137465	42.55342	153.1851	SLC25A5
Mitochond	0.027328	0.137465	42.55342	153.1851	TMEM223
Bile Acid Bi	0.031172	0.137465	36.47253	126.4956	CYP27B1
Prenyltrans	0.031172	0.137465	36.47253	126.4956	DHDDS
Cardiolipin	0.035	0.137465	31.91186	106.9814	OPA1
ADP Transr	0.035	0.137465	31.91186	106.9814	SLC25A5
Purine Nuc	0.035	0.137465	31.91186	106.9814	SLC25A5
O-methyltr	0.035	0.137465	31.91186	106.9814	COQ3
CCR6 Chem	0.035	0.137465	31.91186	106.9814	DEFB1
Magnesium	0.038814	0.137465	28.36467	92.15638	MRS2
ATP Transn	0.038814	0.137465	28.36467	92.15638	SLC25A5
Nuclear Re	0.038814	0.137465	28.36467	92.15638	CYP27B1
NAD+ Bind	0.046396	0.151842	23.20513	71.25236	SIRT5
Heme Bind	0.046446	0.151842	6.061421	18.60534	CYCS;HCCS
Phosphatid	0.050165	0.152771	21.2703	63.65008	OPA1
Adenine Nu	0.053919	0.152771	19.63314	57.33403	SLC25A5
Transamina	0.053919	0.152771	19.63314	57.33403	CISD1
Myosin V B	0.053919	0.152771	19.63314	57.33403	RAB3A
Voltage-Ga	0.057659	0.158097	18.22985	52.01364	VDAC3
Calcium-De	0.061384	0.163051	17.01368	47.4785	PLA2G12A
Nuclear Re	0.065094	0.167667	15.94952	43.57277	CYP27B1
Phosphatas	0.072504	0.179773	4.677922	12.27538	CHCHD3;DLG3
Phosphatid	0.076139	0.179773	13.42915	34.58265	OPA1
Pyridoxal P	0.076139	0.179773	13.42915	34.58265	CISD1
Cyclosporin	0.087055	0.199991	11.59615	28.30869	PPIF
NAD Bindir	0.097844	0.209885	10.20308	23.71587	SIRT5
NAD+ ADP-	0.097844	0.209885	10.20308	23.71587	SIRT5
Oxidoredu	0.101412	0.209885	9.810158	22.45119	CYP27B1
Voltage-Ga	0.101412	0.209885	9.810158	22.45119	VDAC3
RNA Bindin	0.103708	0.209885	1.698298	3.848646	SUPV3L1;HSPA9;CS;MRPL2;FASTKD1;IMMT;SL
Metal Ion T	0.108506	0.214489	9.108516	20.22952	MRS2
Phospholip	0.115546	0.223213	8.500427	18.34468	PLA2G12A
Magnesium	0.125186	0.236462	3.355912	6.97344	OPA1;IDH3A

Methyltran	0.136336	0.251925	7.081553	14.11095	COQ3
Pentosyltra	0.143158	0.258903	6.708165	13.03937	SIRT5
Translation	0.149927	0.261577	6.372115	12.09177	EIF3K
Metal Ion E	0.150792	0.261577	2.001702	3.786932	OPA1;MB;HSPE1;IDH3A
CCR Chemo	0.159982	0.271969	5.926655	10.86176	DEFB1
Hydro-Lyas	0.166619	0.277699	5.662678	10.14776	FH
S-adenosyl	0.17974	0.293806	5.199372	8.923391	COQ3
Antiporter	0.189446	0.296813	4.898669	8.149667	SLC25A5
Monoatom	0.189446	0.296813	4.898669	8.149667	VDAC3
Myosin Bin	0.192657	0.296813	4.805999	7.914741	RAB3A
Hydrolase /	0.199039	0.296813	4.630769	7.475233	SIRT5
Iron Ion Bir	0.199039	0.296813	4.630769	7.475233	CIAPIN1
Double-Str	0.227151	0.332893	3.977764	5.895611	SUPV3L1
Phospholip	0.263122	0.379074	3.347672	4.469599	PLA2G12A
GTPase Act	0.281567	0.385621	1.941435	2.460549	RAB3A;OPA1
Growth Fac	0.28618	0.385621	3.027625	3.787969	NRTN
Ribosome I	0.28618	0.385621	3.027625	3.787969	TMEM223
Ribonucleo	0.288886	0.385621	1.90473	2.365144	RAB3A;OPA1
Ubiquitin P	0.29035	0.385621	1.897552	2.346645	HSPA9;SLC25A5
Oxidoreduc	0.314002	0.407762	2.704173	3.132396	MDH1
Ubiquitin-L	0.316615	0.407762	1.776913	2.043573	HSPA9;SLC25A5
Metalloenc	0.330178	0.418883	2.541154	2.815909	AFG3L2
Carboxylic	0.338125	0.422656	2.466766	2.674813	PLA2G12A
Kinase Acti	0.343371	0.422993	2.419536	2.58635	CKMT1A
Metallopep	0.388773	0.472082	2.063581	1.949587	AFG3L2
Protein Ho	0.488185	0.584447	1.153782	0.827332	SUPV3L1;CISD1;COQ9
Transition I	0.540731	0.636746	1.113736	0.684762	SIRT5;CIAPIN1
Small GTPa	0.546852	0.636746	1.277066	0.770807	XPO4
GTPase Bin	0.591614	0.679557	1.127347	0.591745	XPO4
Microtubul	0.613878	0.695728	1.060278	0.517372	OPA1
Receptor Li	0.719928	0.795565	0.790316	0.259702	NRTN
Tubulin Bin	0.723287	0.795565	0.78281	0.253591	OPA1
Endopeptic	0.73739	0.795565	0.751842	0.22904	AFG3L2
Zinc Ion Bir	0.743657	0.795565	0.738348	0.21868	SIRT5
Calcium Ior	0.748767	0.795565	0.727462	0.210474	MB
Kinase Binc	0.841476	0.88303	0.543601	0.093824	DLG3
DNA Bindir	0.852861	0.884063	0.587093	0.093441	SUPV3L1;CYP27B1
Cis-Regulat	0.93578	0.952019	0.446132	0.029612	ZNF165;CYP27B1
RNA Polym	0.940819	0.952019	0.436016	0.026599	ZNF165;CYP27B1
RNA Polym	0.958524	0.958524	0.397107	0.016822	ZNF165;CYP27B1

UFS3;NDUFS1;COX5A;COX6B1

GO MF 2023 Cluster 2

Term	P-value	Adjusted P-	Odds Ratio	Combined S	Genes
C3HC4-typ	4.08E-05	0.003716	341.1282	3447.387	HSPA1B;HSPA1A
Potassium	0.001836	0.061353	35.24315	222.036	KCNG1;KCNN4
G Protein-(	0.002946	0.061353	11.42259	66.5633	BAMBI;HSPA1B;HSPA1A
2-Oxogluta	0.003196	0.061353	26.19329	150.5015	TET3;TET2
Cyclin-Dep	0.004008	0.061353	23.21096	128.111	CCNE1;CDK5R1
Manganese	0.004357	0.061353	22.19955	120.6759	IMPA1;SOD2
S-adenosyl	0.004719	0.061353	21.27244	113.9363	DNMT1;DNMT3A
DNA-meth	0.010209	0.081265	124.7188	571.7716	DNMT3A
Potassium	0.011434	0.081265	13.24143	59.20461	KCNG1;KCNN4
Fatty Acid I	0.012239	0.081265	99.77	439.3038	ELOVL6
Nucleoside	0.012239	0.081265	99.77	439.3038	UCKL1
Transition I	0.013882	0.081265	4.66563	19.95578	IMPA1;TET3;TET2;SOD2
S-methyltra	0.014264	0.081265	83.1375	353.3355	DNMT3A
Type II Tra	0.016286	0.081265	71.25714	293.3998	BAMBI
Prenyltrans	0.016286	0.081265	71.25714	293.3998	PDSS1
Histone De	0.017545	0.081265	10.50066	42.4538	HSPA1B;HSPA1A
Ubiquitin P	0.017953	0.081265	5.80057	23.31839	GPR37;HSPA1B;HSPA1A
Protein Kin	0.018902	0.081265	10.08276	40.01332	CCNE1;CDK5R1
Monoatom	0.019596	0.081265	9.885985	38.87571	KCNG1;KCNN4
Galactosylt	0.020316	0.081265	55.41667	215.9217	B4GALT5
Racemase /	0.020316	0.081265	55.41667	215.9217	GNE
Fatty Acid S	0.020316	0.081265	55.41667	215.9217	ELOVL6
Ubiquitin-L	0.021245	0.081265	5.43053	20.91642	GPR37;HSPA1B;HSPA1A
Calcium-Ac	0.022326	0.081265	49.8725	189.6162	KCNN4
Carbohydra	0.022326	0.081265	49.8725	189.6162	GNE
Alkali Meta	0.02833	0.095481	38.35769	136.701	IMPA1
Cyclin-Dep	0.02833	0.095481	38.35769	136.701	CDK5R1
tRNA-speci	0.030323	0.098549	35.61607	124.5085	POP1
Transformi	0.036279	0.110046	29.32647	97.26176	BAMBI
Calcium Ac	0.036279	0.110046	29.32647	97.26176	KCNN4
UDP-galact	0.038256	0.112301	27.69583	90.38385	B4GALT5
Gap Junctio	0.04023	0.114403	26.23684	84.30285	GJB5
Disordered	0.046126	0.125263	22.65568	69.69723	HSPA1A
Wide Pore	0.050038	0.125263	20.76563	62.19252	GJB5
Ferrous Iro	0.050038	0.125263	20.76563	62.19252	TET2
Protein Ser	0.051988	0.125263	19.934	58.9398	AURKA
Nuclear Th	0.053934	0.125263	19.16635	55.96572	GAS2L1
RNA Endon	0.055876	0.125263	18.45556	53.23735	POP1
Delayed Re	0.055876	0.125263	18.45556	53.23735	KCNG1
Neuropept	0.055876	0.125263	18.45556	53.23735	GPR37
methyl-CpG	0.057814	0.125263	17.79554	50.72663	TET3
Histone De	0.057814	0.125263	17.79554	50.72663	HR
Beta-Tubul	0.063605	0.134606	16.07097	44.27649	CDK5R1
RNA Bindin	0.066038	0.136392	2.263833	6.152012	RBM38;NOP16;POP1;HSPA1B;TBRG4;HSPA1A
Hsp70 Prot	0.067447	0.136392	15.09545	40.70366	GPR37

Neuropept	0.071273	0.139441	14.23143	37.58863	GPR37
Methyltran	0.07318	0.139441	13.83542	36.17728	DNMT1
Sulfotransf	0.075084	0.139441	13.46081	34.8521	SULT2B1
Alpha-Tubu	0.075084	0.139441	13.46081	34.8521	CDK5R1
Promoter-S	0.08266	0.15044	12.14512	30.27809	DNMT1
Kinase Acti	0.086425	0.154209	11.57907	28.35113	CDK5R1
Pyrophospl	0.095772	0.167601	10.37031	24.32652	ACYP1
Cholestero	0.09763	0.167629	10.15816	23.63366	SULT2B1
Protein Ser	0.108702	0.179852	9.047273	20.07725	CDK5R1
Iron Ion Bir	0.108702	0.179852	9.047273	20.07725	TET2
ATP Bindin	0.111624	0.181389	3.643803	7.989472	HSPA1B;HSPA1A
Sterol Bind	0.114187	0.182299	8.578017	18.61356	SULT2B1
Adenyl Ribo	0.131928	0.20699	3.282719	6.649156	HSPA1B;HSPA1A
Cadherin B	0.138878	0.213818	3.177546	6.272984	CDK5R1;HSPA1A
Tubulin Bin	0.140979	0.213818	3.147276	6.165966	GAS2L1;CDK5R1
G Protein-C	0.146417	0.214903	6.540461	12.56615	GPR37
Phosphotra	0.146417	0.214903	6.540461	12.56615	GNE
Voltage-Ga	0.151677	0.216338	6.291139	11.86512	KCNG1
Zinc Ion Bir	0.154445	0.216338	2.968005	5.54399	TET3;TET2
Chromatin	0.156904	0.216338	6.060061	11.22396	HR
Phosphatas	0.156904	0.216338	6.060061	11.22396	LPIN1
Protein Kin	0.165547	0.224848	5.710345	10.27005	CDK5R1
Hexosyltran	0.179196	0.239807	5.227368	8.987274	B4GALT5
Kinase Acti	0.195952	0.258429	4.727143	7.704706	CDK5R1
Phosphatas	0.205844	0.26636	4.47027	7.065863	KCNN4
Protein Pho	0.210746	0.26636	4.351974	6.776462	KCNN4
Nuclear Re	0.210746	0.26636	4.351974	6.776462	GAS2L1
Kinase Binc	0.24299	0.302905	2.183518	3.089101	AURKA;CDK5R1
DNA Bindir	0.250182	0.307657	1.790223	2.480471	DNMT1;DNMT3A;HR
Purine Ribo	0.255194	0.309636	2.108082	2.879072	HSPA1B;HSPA1A
Magnesium	0.273348	0.327298	3.215097	4.170011	IMPA1
Protein Kin	0.281943	0.333205	1.959599	2.480951	AURKA;CDK5R1
Metal Ion E	0.289584	0.337848	1.920854	2.380535	IMPA1;CDK5R1
Protein Hef	0.32413	0.373365	2.615079	2.946174	AURKA
RNA Polym	0.375346	0.426956	2.173128	2.129464	DNMT3A
Microtubul	0.389451	0.437531	2.071534	1.953492	GAS2L1
G Protein-C	0.403245	0.447504	1.978916	1.797273	GPR37
DNA-bindir	0.441667	0.484238	1.750712	1.430679	DNMT3A
Receptor Li	0.48309	0.523347	1.544104	1.123418	HSPA1A
Protein Ser	0.507311	0.541142	1.43827	0.976055	AURKA
Calcium Ior	0.511408	0.541142	1.421304	0.953108	CDK5R1
Protein Hor	0.748791	0.783218	0.729879	0.211151	IMPA1
Sequence-S	0.776505	0.802977	0.671892	0.169957	TET3
Cis-Regulat	0.901472	0.91655	0.429854	0.044587	DNMT3A
RNA Polym	0.906478	0.91655	0.420116	0.04125	DNMT3A
RNA Polym	0.925287	0.925287	0.382659	0.029714	DNMT3A