

Geneset	stat	num.genes	pval	p.adj	gene.vals
Adenoma, Villous	0.16726084	13	3.681e-02		CDKN2A:419 GNAS:493 PMS2:1183 BRAF:1652.5 TP63:1771 MLH1:2116
Alzheimer Disease, Late Onset	0.04335243	193		9.194e-01	HLA-DPB1:15 SGPL1:40 SIRT1:122.5 ALOX5:170 CNTLN:180 PHF1:200
AMYLOIDOSIS, HEREDITARY, TRANSTHYRETIN-R	-0.10288992	28	5.961e-02		EPO:45 MMP9:100 AGER:463 CTSE:834 NUDT1:977 KRAS:1544
Angina, Unstable	-0.10667684	53	7.273e-03		TNNI3:18 TLR4:94.5 EEF1A2:121.5 SERPINE1:206 OGFOD1:273 CCL2:334
Aortic Aneurysm, Thoracic	-0.06059513	78	6.466e-02	9.194e-01	TLR4:94.5 MMP9:100 SERPINE1:206 PKD2:437 CCL4L2:443 SMARCA4:472
Aphasia, Progressive	-0.28210455	5	2.892e-02	9.194e-01	PLAT:959.5 L1CAM:1944.5 FANCD2:2088 PSEN1:4106 BRCA2:6880.5 NA
Arsenic Poisoning, Inorganic	-0.07509972	51	6.378e-02	9.194e-01	KRT10:91 N4BP2L2:92 CCL20:127 TAF1D:387 CXCL2:534 CD44:612
Bartter syndrome, type 3	0.27052614	5	3.618e-02	9.194e-01	CLCNKB:100 KCNJ1:109 SLC12A2:644 SLC12A3:2049 AP3B1:13802 NA
Cardiomyopathy, Dilated	-0.02874560	350	6.652e-02	9.194e-01	TNNI3:18 ACTC1:59 NKX2-5:83 PPARGC1A:88 TLR4:94.5 MMP9:100
Cardiomyopathy, Familial Idiopathic	-0.03552843	315	3.118e-02	9.194e-01	TACSTD2:14 TNNI3:18 ACTC1:59 NKX2-5:83 TLR4:94.5 MMP9:100
CATARACT, ANTERIOR POLAR	-0.10095812	29	5.998e-02	9.194e-01	SFTPD:72 MMP9:100 SERPINE1:206 CD44:612 BDNF:784 CRYBB3:1249.5
CHARCOT-MARIE-TOOTH DISEASE, AXONAL, TYP	0.28832837	6	1.445e-02	9.194e-01	HSPB8:228.5 HSPB1:1448.5 HSPB3:2061 MAD2L1BP:2687 KIF1B:3844.5 HSPB2:8137
Charcot-Marie-Tooth Disease, Type Ib	-0.20306970	9	3.490e-02	9.194e-01	ACKR1:329 FIG4:388 LRSAM1:1380.5 MPZ:4913.5 HOXD10:5051.5 SLC25A46:5324.5
Cholangitis, Sclerosing	0.05514544	105	5.134e-02	9.194e-01	IL1R1:139 ITGAL:153 DAP:213 HIPK1:304 ERAP2:405 CDKN2A:419
Choledochal Cyst, Type I	0.33212157	5	1.011e-02	9.194e-01	PKHD1:92 AQP1:1089 CFTR:2059.5 SLC4A2:2898 SCT:6012.5 NA
Choledochal Cyst, Type II	0.33212157	5	1.011e-02	9.194e-01	PKHD1:92 AQP1:1089 CFTR:2059.5 SLC4A2:2898 SCT:6012.5 NA
Choledochal Cyst, Type III	0.33212157	5	1.011e-02	9.194e-01	PKHD1:92 AQP1:1089 CFTR:2059.5 SLC4A2:2898 SCT:6012.5 NA
Choledochal Cyst, Type IV	0.33212157	5	1.011e-02	9.194e-01	PKHD1:92 AQP1:1089 CFTR:2059.5 SLC4A2:2898 SCT:6012.5 NA
Choledochal Cyst, Type V	0.33212157	5	1.011e-02	9.194e-01	PKHD1:92 AQP1:1089 CFTR:2059.5 SLC4A2:2898 SCT:6012.5 NA
Chromosome 12, 12p trisomy	-0.28111698	5	2.948e-02	9.194e-01	CD79B:1607 MS4A1:1823.5 BIRC3:2661.5 NOTCH1:4193 SF3B1:5812 NA
Colitis, Ischemic	-0.21470770	8	3.548e-02	9.194e-01	MMP9:100 SERPINE1:206 HSPA5:1807 ABCG2:2164.5 VEGFA:3178.5 MMP2:3253.5
Cone-rod synaptic disorder, congenital n	-0.16685121	10	6.771e-02	9.194e-01	LRIT3:1153 GNAT1:1277.5 GNB3:2607 GPR179:3237.5 SAG:3289.5 GRM6:3836
Congenital secretory diarrhea, sodium ty	-0.21161543	8	3.821e-02	9.194e-01	HGF:873 SLC9A1:1729 SLC9A2:2472 SPINT2:3551 CAV1:3956.5 SLC9A3:4775
Deafness, Acquired	-0.17064870	16	1.813e-02	9.194e-01	POLD1:340 MITF:632.5 BDNF:784 ESPN:1527 GJB3:2174.5 JAG1:2242
Dentin dysplasia, type 1	0.26097395	5	4.328e-02	9.194e-01	CDH11:679 SMOC2:1207 SSUH2:2295 DSPP:6102.5 VPS4B:7014 NA
Dermatitis, Allergic Contact	-0.07167155	82	2.507e-02	9.194e-01	ASRGL1:50 QPCT:54 MMP9:100 CD3D:310 CCL2:334 CXCL2:534
Dermatomyositis, Childhood Type	-0.13072288	28	1.670e-02	9.194e-01	TLR4:94.5 NCAM1:320 WT1:370 SAMHD1:831 RNASEH2B:1340.5 RNASEH2A:1408
Diaphragm, Complete Agenesis Of	-0.31609910	5	1.437e-02	9.194e-01	FREM2:503 FRAS1:1150 ROBO4:3148.5 GLI3:3772.5 FBN1:4947.5 NA
Electron Transport Chain Deficiencies, M	0.17498439	9	6.911e-02	9.194e-01	NUBPL:863 POLG:1817.5 MGME1:1914 FOXRED1:2518 NOS2:3730 COQ9:5346.5
Endometrial stromal sarcoma, high grade	-0.20478542	7	6.062e-02	9.194e-01	CTNNB1:758 JAZF1:1881.5 CCND1:2332 SMARCB1:2874.5 YWHAE:5202 SUZ12:5295.5
Eosinophilia, Tropical	-0.28898113	6	1.423e-02	9.194e-01	TLR4:94.5 HPGDS:720 PTGDS:772 GATA3:2610 RAG2:5583 MYD88:8781.5
Epilepsy, Cryptogenic	0.07347615	56	5.742e-02	9.194e-01	TGFB1:457 FOLR1:481 ADRA2A:582 SLC12A2:644 ABCB1:717 ERN1:728
Familial Partial Lipodystrophy, Type 2	0.14784657	13	6.496e-02	9.194e-01	PLIN1:76 LPL:691 LMNA:752.5 CCND3:1319 HNF4A:2565.5 PPP1R3A:3062
Fatty Liver, Alcoholic	0.09693739	46	2.303e-02	9.194e-01	ACACB:18 HLA-A:88.5 SIRT1:122.5 HLA-B:226 DGAT2:396.5 OPA1:444.5
Fracture, spiral	-0.16996283	11	5.097e-02	9.194e-01	IRX5:501 BMP7:536 FAM210A:600 DKK1:1158 TNFRSF1B:3579 SPTBN1:4813.5
Gait, Scissors	-0.21071550	7	5.353e-02	9.194e-01	TBL1XR1:441 L1CAM:1944.5 KIF1A:2095 TTC19:3867.5 ARL6IP1:3929.5 AMPD2:4165
Hearing Loss, Extreme	-0.17064870	16	1.813e-02	9.194e-01	POLD1:340 MITF:632.5 BDNF:784 ESPN:1527 GJB3:2174.5 JAG1:2242
Hepatitis B, Chronic	0.04195577	160	6.788e-02	9.194e-01	HLA-DPB1:15 CD80:58 TGFA:85 HLA-A:88.5 JMJD6:124 IL1R1:139
Hyperbilirubinemia, Hereditary	0.23453866	8	2.161e-02	9.194e-01	CALB1:349 ABCC3:499.5 HMGB1:2094.5 F7:2227 HMBS:2907.5 BCL2:3517
Hypoxia-Ischemia, Brain	0.19893441	7	6.836e-02	9.194e-01	HIF1A:789 IRAK1:1609 TNF:1996 IRAK4:2085 NOS2:3730 IL1B:8967

EnrichmentHsSymbolsFile2 Top pathways by permulation

Geneset	stat	num.genes	pval	p.adj	gene.vals
HOUNKPE_HOUSEKEEPING_GENES	0.07527272	1070	2.282e-16	1.480e-12	RANBP2:39 GPN2:74 PSMB6:87 MRPS2:99 ARNT:103 TNKS2:105
LIU_OVARIAN_CANCER_TUMORS_AND_XENOGRAFTS	-0.06073443	1280	6.736e-13	2.184e-09	RGS4:1 JAM3:6 NCF2:7 SERPINI1:8 SMIM3:20 CARD6:30
DIAZ_CHRONIC_MYELOGENOUS_LEUKEMIA_UP	0.05336500	1320	1.543e-10	3.336e-07	RANBP2:39 SH3GLB2:47 TCEAL9:50 CNOT8:60 VAV3:90 RAP2C:119
NABA_MATRISOME	-0.06294634	714	1.346e-08	1.834e-05	FSTL3:2 SERPINI1:8 CNTF:25 SFRP5:32 EPO:45 ADAM22:47
GRAESSMANN_APOPTOSIS_BY_DOXORUBICIN_DN	0.04298425	1637	1.414e-08	1.834e-05	DHRS11:3 RAD18:12 ACACB:18 GDPD1:27 CHAC2:34 HERC4:38
STARK_PREFRONTAL_CORTEX_22Q11_DELETION_D	0.06783263	478	4.389e-07	4.744e-04	TOMM40L:29 TCEAL9:50 NDUFB10:64 PSMB6:87 SEC61B:122.5 PPP2R5C:228.5
NABA_MATRISOME_ASSOCIATED	-0.06463960	494	1.005e-06	9.314e-04	FSTL3:2 SERPINI1:8 CNTF:25 SFRP5:32 EPO:45 ADAM22:47
MILI_PSEUDOPODIA_HAPTOTAXIS_UP	0.06348093	488	1.800e-06	1.319e-03	AGTPBP1:30 HERC4:38 CCNE2:45 STEEP1:66 CCDC141:69 USP46:75
YAO_TEMPORAL_RESPONSE_TO_PROGESTERONE_CL	0.10817380	164	1.831e-06	1.319e-03	PSAT1:55 PRPSAP2:211 DAP:213 ATP5MK:221 PPP2R5C:228.5 UQCR11:269
ACEVEDO_NORMAL_TISSUE_ADJACENT_TO_LIVER_	0.07913195	306	2.098e-06	1.360e-03	TGDS:51 ARNT:103 DIAPH1:106 FGGY:145 PHGDH:150 LTBR:166
LIM_MAMMARY_STEM_CELL_UP	-0.06581863	429	3.296e-06	1.781e-03	JAM3:6 AGPAT4:27 EPDR1:38 RAB34:52 CCDC85B:53 C19orf12:107
MOOTHA_HUMAN_MITODB_6_2002	0.06945850	387	3.024e-06	1.781e-03	MRPS2:99 AK4:146 GPD2:263 UQCR11:269 FARS2:300 NME4:316
WAKABAYASHI_ADIPOGENESIS_PPARG_RXRA_BOUN	0.04819802	764	7.098e-06	3.298e-03	H2BC17:5 ABHD1:10 ZMYND12:33 RANBP2:39 ZNF559-ZNF177:63 YAP1:68
REACTOME_PROTEIN_LOCALIZATION	0.10782351	146	7.120e-06	3.298e-03	SEC61B:122.5 PEX11B:127 UBE2D1:143 CHCHD2:630.5 BAAT:706 TIMM10:714
REACTOME_METABOLISM_OF_AMINO_ACIDS_AND_D	0.07636698	292	7.666e-06	3.314e-03	PSAT1:55 PSMB6:87 PHGDH:150 AUH:179 SERINC2:329 RPL3:334
GOTZMANN_EPITHELIAL_TO_MESENCHYMAL_TRANS	0.09503867	178	1.271e-05	4.849e-03	PLXNA2:81 HLA-A:88.5 IL1R1:139 KRT19:294 TPD52:412 CDKN2A:419
KIM_BIPOLAR_DISORDER_OLIGODENDROCYTE_DEN	0.05229586	607	1.254e-05	4.849e-03	RAB40B:26 ARL4A:44 FABP7:59 LZTS3:62 PSMB6:87 SEC61B:122.5
LINDGREN_BLADDER_CANCER_CLUSTER_2B	-0.06844254	336	1.748e-05	6.299e-03	JAM3:6 NRN1:12 STMN3:31 RCAN2:151 THBD:169 LIG4:191
SCHUETZ_BREAST_CANCER_DUCTAL_INVASIVE_UP	-0.06833527	311	3.641e-05	1.181e-02	RGS4:1 JAM3:6 ITGBL1:141 RCAN2:151 OLFML1:197 GLS:214
FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_REJECT	0.05445136	498	3.537e-05	1.181e-02	SLC22A2:2 USP2:9 RAB40B:26 ITGA6:86 SULT1C2:114.5 PEX11B:127
REACTOME_CELL_CYCLE_CHECKPOINTS	0.07548541	245	4.953e-05	1.529e-02	H2BC17:5 RANBP2:39 CCNE2:45 PSMB6:87 UBE2D1:143 MCM10:156
BLALOCK_ALZHEIMERS_DISEASE_DN	0.03581912	1156	5.215e-05	1.537e-02	RANBP2:39 SH3GLB2:47 PSAT1:55 FABP7:59 KCNJ3:78 YPEL5:84
PUJANA_CHEK2_PCC_NETWORK	0.04532130	687	5.931e-05	1.672e-02	CD1E:16 CCNE2:45 TGDS:51 FUBP1:133 UBE2I:161 TTC39A:173
ACEVEDO_LIVER_CANCER_DN	0.05489984	455	6.554e-05	1.771e-02	ACACB:18 TGDS:51 MRPS2:99 ARNT:103 DIAPH1:106 PHGDH:150
REACTOME_MITOTIC_METAPHASE_AND_ANAPHASE	0.07899126	210	8.279e-05	1.988e-02	RANBP2:39 PSMB6:87 UBE2D1:143 UBE2I:161 TUBAL3:204 PPP2R5C:228.5
REACTOME_TRANSLATION	0.07613878	227	8.072e-05	1.988e-02	MRPS2:99 SEC61B:122.5 EEF1B2:182 FARS2:300 MRPS23:310 RPL3:334
GARY_CD5_TARGETS_UP	0.05690817	413	7.871e-05	1.988e-02	SESTD1:24 SH3GLB2:47 PSAT1:55 PHGDH:150 MIDN:154 MIF4GD:169
HSIAO_HOUSEKEEPING_GENES	0.06465606	314	8.665e-05	2.007e-02	PSMB6:87 HLA-A:88.5 SEC61B:122.5 EEF1B2:182 HLA-B:226 RPL3:334
REACTOME_NEDDYLATION	0.07532316	227	9.618e-05	2.151e-02	PSMB6:87 UBE2D1:143 FBXO11:302 CCDC22:327 COPS7A:369 FBXO17:391
BOCHKIS_FOXA2_TARGETS	0.06115839	345	1.013e-04	2.189e-02	GDPD1:27 CHAC2:34 HERC4:38 ARHGAP12:46 MRPS2:99 EEF1B2:182
GRAESSMANN_RESPONSE_TO_MC_AND_DOXORUBICI	0.04310923	705	1.103e-04	2.235e-02	GDPD1:27 CHAC2:34 HERC4:38 RUFY3:49 ZNF280C:54 STEAP4:57
REACTOME_EUKARYOTIC_TRANSLATION_INITIATI	0.13694951	67	1.071e-04	2.235e-02	RPL3:334 EIF3G:356 RPS7:521 EIF4A2:655 RPS16:743 EIF3F:759
MOOTHA_PGC	0.05763925	376	1.331e-04	2.615e-02	USP2:9 MRPS2:99 JMJD6:124 CHRNE:222 HSPB8:228.5 DPYSL3:239
MARTENS_TRETINOIN_RESPONSE_UP	-0.04651666	563	1.784e-04	3.201e-02	TACSTD2:14 TNNI3:18 ENO2:28 RRAD:43 PRRT1:75 NKX2-5:83
JAATINEN_HEMATOPOIETIC_STEM_CELL_DN	-0.08136079	179	1.788e-04	3.201e-02	NCF2:7 QPCT:54 MMP9:100 CD86:116 CD247:196 LTF:268
SENGUPTA_NASOPHARYNGEAL_CARCINOMA_DN	-0.06697374	266	1.778e-04	3.201e-02	TMC4:29 FKBP1B:40 RRAD:43 DNAJA4:82 MUC1:104 PACRG:155.5
OUELLET_OVARIAN_CANCER_INVASIVE_VS_LMP_U	0.10386013	109	1.827e-04	3.201e-02	COX7B:424 GNAS:493 CDKN3:536 SNRPD3:748 MEST:787 FH:950.5
WONG_MITOCHONDRIA_GENE_MODULE	0.07697315	197	2.018e-04	3.356e-02	NDUFB10:64 AUH:179 SLC16A5:224 GPD2:263 UQCR11:269 NME4:316
MOOTHA_MITOCHONDRIA	0.05452962	399	1.989e-04	3.356e-02	MRPS2:99 AK4:146 GPD2:263 UQCR11:269 FARS2:300 NME4:316
MID FOTDOOFN CICALALING DATINAVAY	0.00000070		0.400 0.4	0.44000	WENCE AND MARKS AND F. CAMAGE AND FILLY FOR PHYSICAL ADAR CAMACTA AND A

2.103e-04 3.410e-02

IKBKG:452 MAPK9:472.5 GNAS:493 ELK1:707 PIK3CA:1243 GNGT1:1574.5

gene.vals

FSTL3:2 TLR4:94.5 LTF:268 CARTPT:297 FBXW7:940.5 TLR3:1615.5

RANBP3L:3 TACSTD2:14 NKX2-5:83 GDPD5:90 SMYD1:259 LTF:268

CD86:116 FCRLA:339 ZBTB7A:403 BLNK:455.5 RASGRP1:458 HDAC9:669

0.22828876

p.adj

1.979e-04 5.340e-01

1.953e-04 5.340e-01

1.710e-03 5.570e-01

GO\_Biological\_Process\_2023 Top pathways by permulation

WP\_ESTROGEN\_SIGNALING\_PATHWAY

Geneset

Negative Regulation Of Osteoclast Differ

Positive Regulation Of Cell Differentiat

B Cell Activation (GO:0042113)

-0.28732395

-0.06862267

-0.11262276

251

65

B Cell Differentiation (GO:0030183)         -0.12621521         47           B Cell Homeostasis (GO:0001782)         -0.26001378         9           C-terminal Protein Amino Acid Modificati         0.24916782         11           Golgi Vesicle Transport (GO:0048193)         0.05767787         183           acyl-CoA Metabolic Process (GO:0006637)         0.18305710         27           Amyloid Precursor Protein Metabolic Proc         -0.20576862         15           Axonal Transport (GO:0098930)         0.12757732         37           Axonal Transport Of Mitochondrion (GO:00         0.24968048         12           Axonogenesis (GO:0007409)         -0.07879159         167           Cardiac Cell Development (GO:0055006)         -0.22483346         13           Cardiac Muscle Hypertrophy (GO:0003300)         -0.33679270         7           Cell Communication By Electrical Couplin         -0.21485103         13           Cellular Response To Osmotic Stress (GO:         -0.15576890         26           Cellular Response To Topologically Incor         0.18293546         19           Cholesterol Biosynthetic Process (GO:0000         0.18752836         23           Cholesterol Metabolic Process (GO:000820         0.10906770         53           Cytoplasmic Translation (GO:0007032)         0.1183184	6.914e-03 4.220e-03 7.332e-03 9.981e-04 5.802e-03 7.279e-03 2.749e-03 4.625e-04 5.009e-03 2.031e-03 7.321e-03 5.782e-03 1.857e-03 6.066e-03 5.836e-04 3.584e-03 4.198e-03 6.903e-03 7.001e-03	5.570e-01 5.570e-01	ZBTB7A:403 BLNK:455.5 HDAC9:669 NFAM1:992 NHEJ1:1031.5 KIT:1118 TNFRSF13B:920 TNFAIP3:1160 DOCK10:1293.5 GAPT:1335 PPP2R3C:1936 NCKAP1L:3178.5 AGTPBP1:30 ICMT:411 ATG7:612 GPLD1:2388.5 AGBL4:2685 ATG16L1:2939 STEEP1:66 TMEM115:135 MYO1B:140 RANGRF:408 KIF1C:425 RAB6A:513.5 ACACB:18 ACSL6:413.5 ACOT7:591 GLYAT:604 BAAT:706 OGDH:766 ACHE:215 TMCC2:230 ADAM19:1408 APH1A:1575 ADAM17:2377.5 NSG1:2859 APEX1:389 OPA1:444.5 HIF1A:789 BLOC1S2:1250.5 ARL8B:1350.5 MGARP:1371 APEX1:389 OPA1:444.5 HIF1A:789 MGARP:1371 TRAK2:1386 HDAC6:1463 RAB3A:73 EPHA5:101 FEZ1:150 KIF5C:188 NELL2:303 SLIT2:608.5 NKX2-5:83 CXADR:225 TTN:911 TCAP:1336.5 SLC8A1:1474 MYH11:2177.5 CSRP3:718 TTN:911 TCAP:1336.5 OCRL:1737 RYR2:2794 HDAC4:3260 FKBP1B:40 GJC1:399 ATP1A3:990.5 ATP1A2:1348 SLC8A1:1474 RYR2:2794 EPO:45 DDX3X:390.5 PKD2:437 MTOR:781 SERPINB6:917 ZFP36L1:1833.5 HSPB8:228.5 ERN1:728 STUB1:1055 UBE2W:1186 DNAJB12:1460.5 HDAC6:1463 SC5D:885 LBR:1007 MVD:1073.5 MSMO1:1416 HMGCR:1589 LSS:1807.5 TSKU:468 LBR:1007 MVD:1073.5 SCARF1:1101 ACAA2:1134.5 MSMO1:1416 RPL3:334 RPS7:521 EIF4A2:655 RPS16:743 EIF3I:797 RPL18:802 ZNF365:392 NOL3:1004 DOCK10:1293.5 EPHB3:1973 CTNND2:2034 PAK3:3011 PLEKHA3:130 TMEM9:243 WASHC4:434 TMCC1:528 ARFGEF2:841.5 DNM1:940.5 TOMM40L:29 TOMM34:336 TIMM10:714 RALA:973.5 FBXO7:1366 MGARP:1371 ACACB:18 SGPL1:40 ALOX5:170 THEM4:322 ACSL6:413.5 CYP4F2:570 EZR:385.5 FGD5:1135 SPATA13:1236 SPEF1:1656.5 S1PR2:1702 DNM3:2003
C-terminal Protein Amino Acid Modificati         0.24916782         11           Golgi Vesicle Transport (GO:0048193)         0.05767787         183           acyl-CoA Metabolic Process (GO:0006637)         0.18305710         27           Amyloid Precursor Protein Metabolic Proc         -0.20576862         15           Axonal Transport (GO:0098930)         0.12757732         37           Axonal Transport Of Mitochondrion (GO:00         0.24968048         12           Axonogenesis (GO:0007409)         -0.07879159         167           Cardiac Cell Development (GO:0055006)         -0.22483346         13           Cardiac Muscle Hypertrophy (GO:0003300)         -0.33679270         7           Cell Communication By Electrical Couplin         -0.21485103         13           Cellular Response To Osmotic Stress (GO:         -0.15576890         26           Cellular Response To Topologically Incor         0.18293546         19           Cholesterol Biosynthetic Process (GO:000         0.18752836         23           Cholesterol Metabolic Process (GO:000820         0.10906770         53           Cytoplasmic Translation (GO:0002181)         0.15168617         43           Dendritic Spine Morphogenesis (GO:0006099         -0.23333444         13           Endosome Organization (GO:00070021)	4.220e-03 7.332e-03 9.981e-04 5.802e-03 7.279e-03 2.749e-03 4.625e-04 5.009e-03 2.031e-03 7.321e-03 5.992e-03 5.782e-03 1.857e-03 6.066e-03 5.836e-04 3.584e-03 4.198e-03 6.903e-03 7.001e-03 3.742e-03	5.570e-01 5.570e-01	AGTPBP1:30 ICMT:411 ATG7:612 GPLD1:2388.5 AGBL4:2685 ATG16L1:2939  STEEP1:66 TMEM115:135 MYO1B:140 RANGRF:408 KIF1C:425 RAB6A:513.5  ACACB:18 ACSL6:413.5 ACOT7:591 GLYAT:604 BAAT:706 OGDH:766  ACHE:215 TMCC2:230 ADAM19:1408 APH1A:1575 ADAM17:2377.5 NSG1:2859  APEX1:389 OPA1:444.5 HIF1A:789 BLOC1S2:1250.5 ARL8B:1350.5 MGARP:1371  APEX1:389 OPA1:444.5 HIF1A:789 MGARP:1371 TRAK2:1386 HDAC6:1463  RAB3A:73 EPHA5:101 FEZ1:150 KIF5C:188 NELL2:303 SLIT2:608.5  NKX2-5:83 CXADR:225 TTN:911 TCAP:1336.5 SLC8A1:1474 MYH11:2177.5  CSRP3:718 TTN:911 TCAP:1336.5 OCRL:1737 RYR2:2794 HDAC4:3260  FKBP1B:40 GJC1:399 ATP1A3:990.5 ATP1A2:1348 SLC8A1:1474 RYR2:2794  EPO:45 DDX3X:390.5 PKD2:437 MTOR:781 SERPINB6:917 ZFP36L1:1833.5  HSPB8:228.5 ERN1:728 STUB1:1055 UBE2W:1186 DNAJB12:1460.5 HDAC6:1463  SC5D:885 LBR:1007 MVD:1073.5 MSMO1:1416 HMGCR:1589 LSS:1807.5  TSKU:468 LBR:1007 MVD:1073.5 SCARF1:1101 ACAA2:1134.5 MSMO1:1416  RPL3:334 RPS7:521 EIF4A2:655 RPS16:743 EIF3I:797 RPL18:802  ZNF365:392 NOL3:1004 DOCK10:1293.5 EPHB3:1973 CTNND2:2034 PAK3:3011  PLEKHA3:130 TMEM9:243 WASHC4:434 TMCC1:528 ARFGEF2:841.5 DNM1:940.5  TOMM40L:29 TOMM34:336 TIMM10:714 RALA:973.5 FBXO7:1366 MGARP:1371  ACACB:18 SGPL1:40 ALOX5:170 THEM4:322 ACSL6:413.5 CYP4F2:570
Golgi Vesicle Transport (GO:0048193)         0.05767787         183           acyl-CoA Metabolic Process (GO:0006637)         0.18305710         27           Amyloid Precursor Protein Metabolic Proc         -0.20576862         15           Axonal Transport (GO:0098930)         0.12757732         37           Axonal Transport Of Mitochondrion (GO:00         0.24968048         12           Axonogenesis (GO:0007409)         -0.07879159         167           Cardiac Cell Development (GO:0055006)         -0.22483346         13           Cardiac Muscle Hypertrophy (GO:0003300)         -0.33679270         7           Cell Communication By Electrical Couplin         -0.21485103         13           Cellular Response To Osmotic Stress (GO:         -0.15576890         26           Cellular Response To Topologically Incor         0.18293546         19           Cholesterol Biosynthetic Process (GO:000         0.18752836         23           Cholesterol Metabolic Process (GO:000820         0.10906770         53           Cytoplasmic Translation (GO:0002181)         0.15168617         43           Dendritic Spine Morphogenesis (GO:006099         -0.23333444         13           Endosome Organization (GO:0007032)         0.11831848         49           Establishment Of Protein Localization To         0.	7.332e-03 9.981e-04 5.802e-03 7.279e-03 2.749e-03 4.625e-04 5.009e-03 2.031e-03 7.321e-03 5.992e-03 5.782e-03 1.857e-03 6.066e-03 5.836e-04 3.584e-03 4.198e-03 6.903e-03 7.001e-03 3.742e-03	5.570e-01 5.570e-01 5.570e-01 5.570e-01 5.570e-01 5.570e-01 5.570e-01 5.570e-01 5.570e-01 5.570e-01 5.570e-01 5.570e-01 5.570e-01 5.570e-01 5.570e-01 5.570e-01 5.570e-01 5.570e-01 5.570e-01 5.570e-01	STEEP1:66 TMEM115:135 MYO1B:140 RANGRF:408 KIF1C:425 RAB6A:513.5  ACACB:18 ACSL6:413.5 ACOT7:591 GLYAT:604 BAAT:706 OGDH:766  ACHE:215 TMCC2:230 ADAM19:1408 APH1A:1575 ADAM17:2377.5 NSG1:2859  APEX1:389 OPA1:444.5 HIF1A:789 BLOC1S2:1250.5 ARL8B:1350.5 MGARP:1371  APEX1:389 OPA1:444.5 HIF1A:789 MGARP:1371 TRAK2:1386 HDAC6:1463  RAB3A:73 EPHA5:101 FEZ1:150 KIF5C:188 NELL2:303 SLIT2:608.5  NKX2-5:83 CXADR:225 TTN:911 TCAP:1336.5 SLC8A1:1474 MYH11:2177.5  CSRP3:718 TTN:911 TCAP:1336.5 OCRL:1737 RYR2:2794 HDAC4:3260  FKBP1B:40 GJC1:399 ATP1A3:990.5 ATP1A2:1348 SLC8A1:1474 RYR2:2794  EPO:45 DDX3X:390.5 PKD2:437 MTOR:781 SERPINB6:917 ZFP36L1:1833.5  HSPB8:228.5 ERN1:728 STUB1:1055 UBE2W:1186 DNAJB12:1460.5 HDAC6:1463  SC5D:885 LBR:1007 MVD:1073.5 MSMO1:1416 HMGCR:1589 LSS:1807.5  TSKU:468 LBR:1007 MVD:1073.5 SCARF1:1101 ACAA2:1134.5 MSMO1:1416  RPL3:334 RPS7:521 EIF4A2:655 RPS16:743 EIF3I:797 RPL18:802  ZNF365:392 NOL3:1004 DOCK10:1293.5 EPHB3:1973 CTNND2:2034 PAK3:3011  PLEKHA3:130 TMEM9:243 WASHC4:434 TMCC1:528 ARFGEF2:841.5 DNM1:940.5  TOMM40L:29 TOMM34:336 TIMM10:714 RALA:973.5 FBXO7:1366 MGARP:1371  ACACB:18 SGPL1:40 ALOX5:170 THEM4:322 ACSL6:413.5 CYP4F2:570
acyl-CoA Metabolic Process (GO:0006637)         0.18305710         27           Amyloid Precursor Protein Metabolic Proc         -0.20576862         15           Axonal Transport (GO:0098930)         0.12757732         37           Axonal Transport Of Mitochondrion (GO:00         0.24968048         12           Axonogenesis (GO:0007409)         -0.07879159         167           Cardiac Cell Development (GO:0055006)         -0.22483346         13           Cardiac Muscle Hypertrophy (GO:0003300)         -0.33679270         7           Cell Communication By Electrical Couplin         -0.21485103         13           Cellular Response To Osmotic Stress (GO:         -0.15576890         26           Cellular Response To Topologically Incor         0.18293546         19           Cholesterol Biosynthetic Process (GO:000         0.18752836         23           Cholesterol Metabolic Process (GO:000820         0.10906770         53           Cytoplasmic Translation (GO:0002181)         0.15168617         43           Dendritic Spine Morphogenesis (GO:006099         -0.23333444         13           Establishment Of Protein Localization To         0.12352306         40           Fatty Acid Metabolic Process (GO:0006631         0.07668591         104           Filopodium Assembly (GO:0046847)	9.981e-04 5.802e-03 7.279e-03 2.749e-03 4.625e-04 5.009e-03 2.031e-03 7.321e-03 5.992e-03 5.782e-03 1.857e-03 6.066e-03 5.836e-04 3.584e-03 4.198e-03 6.903e-03 7.001e-03 3.742e-03	5.570e-01 5.570e-01 5.570e-01 5.570e-01 5.570e-01 5.570e-01 5.570e-01 5.570e-01 5.570e-01 5.570e-01 5.570e-01 5.570e-01 5.570e-01 5.570e-01 5.570e-01 5.570e-01 5.570e-01 5.570e-01	ACACB:18 ACSL6:413.5 ACOT7:591 GLYAT:604 BAAT:706 OGDH:766  ACHE:215 TMCC2:230 ADAM19:1408 APH1A:1575 ADAM17:2377.5 NSG1:2859  APEX1:389 OPA1:444.5 HIF1A:789 BLOC1S2:1250.5 ARL8B:1350.5 MGARP:1371  APEX1:389 OPA1:444.5 HIF1A:789 MGARP:1371 TRAK2:1386 HDAC6:1463  RAB3A:73 EPHA5:101 FEZ1:150 KIF5C:188 NELL2:303 SLIT2:608.5  NKX2-5:83 CXADR:225 TTN:911 TCAP:1336.5 SLC8A1:1474 MYH11:2177.5  CSRP3:718 TTN:911 TCAP:1336.5 OCRL:1737 RYR2:2794 HDAC4:3260  FKBP1B:40 GJC1:399 ATP1A3:990.5 ATP1A2:1348 SLC8A1:1474 RYR2:2794  EPO:45 DDX3X:390.5 PKD2:437 MTOR:781 SERPINB6:917 ZFP36L1:1833.5  HSPB8:228.5 ERN1:728 STUB1:1055 UBE2W:1186 DNAJB12:1460.5 HDAC6:1463  SC5D:885 LBR:1007 MVD:1073.5 MSMO1:1416 HMGCR:1589 LSS:1807.5  TSKU:468 LBR:1007 MVD:1073.5 SCARF1:1101 ACAA2:1134.5 MSMO1:1416  RPL3:334 RPS7:521 EIF4A2:655 RPS16:743 EIF3I:797 RPL18:802  ZNF365:392 NOL3:1004 DOCK10:1293.5 EPHB3:1973 CTNND2:2034 PAK3:3011  PLEKHA3:130 TMEM9:243 WASHC4:434 TMCC1:528 ARFGEF2:841.5 DNM1:940.5  TOMM40L:29 TOMM34:336 TIMM10:714 RALA:973.5 FBXO7:1366 MGARP:1371  ACACB:18 SGPL1:40 ALOX5:170 THEM4:322 ACSL6:413.5 CYP4F2:570
Amyloid Precursor Protein Metabolic Proc	5.802e-03 7.279e-03 2.749e-03 4.625e-04 5.009e-03 2.031e-03 7.321e-03 5.992e-03 5.782e-03 1.857e-03 6.066e-03 5.836e-04 3.584e-03 4.198e-03 6.903e-03 7.001e-03 3.742e-03	5.570e-01 5.570e-01 5.570e-01 5.570e-01 5.570e-01 5.570e-01 5.570e-01 5.570e-01 5.570e-01 5.570e-01 5.570e-01 5.570e-01 5.570e-01 5.570e-01 5.570e-01 5.570e-01 5.570e-01	ACHE:215 TMCC2:230 ADAM19:1408 APH1A:1575 ADAM17:2377.5 NSG1:2859  APEX1:389 OPA1:444.5 HIF1A:789 BLOC1S2:1250.5 ARL8B:1350.5 MGARP:1371  APEX1:389 OPA1:444.5 HIF1A:789 MGARP:1371 TRAK2:1386 HDAC6:1463  RAB3A:73 EPHA5:101 FEZ1:150 KIF5C:188 NELL2:303 SLIT2:608.5  NKX2-5:83 CXADR:225 TTN:911 TCAP:1336.5 SLC8A1:1474 MYH11:2177.5  CSRP3:718 TTN:911 TCAP:1336.5 OCRL:1737 RYR2:2794 HDAC4:3260  FKBP1B:40 GJC1:399 ATP1A3:990.5 ATP1A2:1348 SLC8A1:1474 RYR2:2794  EPO:45 DDX3X:390.5 PKD2:437 MTOR:781 SERPINB6:917 ZFP36L1:1833.5  HSPB8:228.5 ERN1:728 STUB1:1055 UBE2W:1186 DNAJB12:1460.5 HDAC6:1463  SC5D:885 LBR:1007 MVD:1073.5 MSMO1:1416 HMGCR:1589 LSS:1807.5  TSKU:468 LBR:1007 MVD:1073.5 SCARF1:1101 ACAA2:1134.5 MSMO1:1416  RPL3:334 RPS7:521 EIF4A2:655 RPS16:743 EIF3I:797 RPL18:802  ZNF365:392 NOL3:1004 DOCK10:1293.5 EPHB3:1973 CTNND2:2034 PAK3:3011  PLEKHA3:130 TMEM9:243 WASHC4:434 TMCC1:528 ARFGEF2:841.5 DNM1:940.5  TOMM40L:29 TOMM34:336 TIMM10:714 RALA:973.5 FBXO7:1366 MGARP:1371  ACACB:18 SGPL1:40 ALOX5:170 THEM4:322 ACSL6:413.5 CYP4F2:570
Axonal Transport (GO:0098930) 0.12757732 37  Axonal Transport Of Mitochondrion (GO:00 0.24968048 12  Axonogenesis (GO:0007409) -0.07879159 167  Cardiac Cell Development (GO:0055006) -0.22483346 13  Cardiac Muscle Hypertrophy (GO:0003300) -0.33679270 7  Cell Communication By Electrical Couplin -0.21485103 13  Cellular Response To Osmotic Stress (GO: -0.15576890 26  Cellular Response To Topologically Incor 0.18293546 19  Cholesterol Biosynthetic Process (GO:000 0.18752836 23  Cholesterol Metabolic Process (GO:000820 0.10906770 53  Cytoplasmic Translation (GO:0002181) 0.15168617 43  Dendritic Spine Morphogenesis (GO:006099 -0.23333444 13  Endosome Organization (GO:0007032) 0.11831848 49  Establishment Of Protein Localization To 0.12352306 40  Fatty Acid Metabolic Process (GO:0006631 0.07668591 104  Filopodium Assembly (GO:0046847) -0.21623718 15  Granulocyte Chemotaxis (GO:0071621) -0.12833695 37  Hematopoietic Progenitor Cell Differenti -0.16304149 25  Lymphocyte Differentiation (GO:0030098) -0.10473537 65	7.279e-03 2.749e-03 4.625e-04 5.009e-03 2.031e-03 7.321e-03 5.992e-03 5.782e-03 1.857e-03 6.066e-03 5.836e-04 3.584e-03 4.198e-03 6.903e-03 7.001e-03 3.742e-03	5.570e-01 5.570e-01 5.570e-01 5.570e-01 5.570e-01 5.570e-01 5.570e-01 5.570e-01 5.570e-01 5.570e-01 5.570e-01 5.570e-01 5.570e-01 5.570e-01 5.570e-01	APEX1:389 OPA1:444.5 HIF1A:789 BLOC1S2:1250.5 ARL8B:1350.5 MGARP:1371  APEX1:389 OPA1:444.5 HIF1A:789 MGARP:1371 TRAK2:1386 HDAC6:1463  RAB3A:73 EPHA5:101 FEZ1:150 KIF5C:188 NELL2:303 SLIT2:608.5  NKX2-5:83 CXADR:225 TTN:911 TCAP:1336.5 SLC8A1:1474 MYH11:2177.5  CSRP3:718 TTN:911 TCAP:1336.5 OCRL:1737 RYR2:2794 HDAC4:3260  FKBP1B:40 GJC1:399 ATP1A3:990.5 ATP1A2:1348 SLC8A1:1474 RYR2:2794  EPO:45 DDX3X:390.5 PKD2:437 MTOR:781 SERPINB6:917 ZFP36L1:1833.5  HSPB8:228.5 ERN1:728 STUB1:1055 UBE2W:1186 DNAJB12:1460.5 HDAC6:1463  SC5D:885 LBR:1007 MVD:1073.5 MSMO1:1416 HMGCR:1589 LSS:1807.5  TSKU:468 LBR:1007 MVD:1073.5 SCARF1:1101 ACAA2:1134.5 MSMO1:1416  RPL3:334 RPS7:521 EIF4A2:655 RPS16:743 EIF3I:797 RPL18:802  ZNF365:392 NOL3:1004 DOCK10:1293.5 EPHB3:1973 CTNND2:2034 PAK3:3011  PLEKHA3:130 TMEM9:243 WASHC4:434 TMCC1:528 ARFGEF2:841.5 DNM1:940.5  TOMM40L:29 TOMM34:336 TIMM10:714 RALA:973.5 FBXO7:1366 MGARP:1371  ACACB:18 SGPL1:40 ALOX5:170 THEM4:322 ACSL6:413.5 CYP4F2:570
Axonal Transport Of Mitochondrion (GO:00 0.24968048 12 Axonogenesis (GO:0007409) -0.07879159 167 Cardiac Cell Development (GO:0055006) -0.22483346 13 Cardiac Muscle Hypertrophy (GO:0003300) -0.33679270 7 Cell Communication By Electrical Couplin -0.21485103 13 Cellular Response To Osmotic Stress (GO: -0.15576890 26 Cellular Response To Topologically Incor 0.18293546 19 Cholesterol Biosynthetic Process (GO:000 0.18752836 23 Cholesterol Metabolic Process (GO:000820 0.10906770 53 Cytoplasmic Translation (GO:0002181) 0.15168617 43 Dendritic Spine Morphogenesis (GO:006099 -0.23333444 13 Endosome Organization (GO:0007032) 0.11831848 49 Establishment Of Protein Localization To 0.12352306 40 Fatty Acid Metabolic Process (GO:0006631 0.07668591 104 Filopodium Assembly (GO:0046847) -0.21623718 15 Granulocyte Chemotaxis (GO:0071621) -0.12833695 37 Hematopoietic Progenitor Cell Differenti -0.16304149 25 Lymphocyte Differentiation (GO:0030098) -0.10473537 65	2.749e-03 4.625e-04 5.009e-03 2.031e-03 7.321e-03 5.992e-03 5.782e-03 1.857e-03 6.066e-03 5.836e-04 3.584e-03 4.198e-03 6.903e-03 7.001e-03 3.742e-03	5.570e-01 5.570e-01 5.570e-01 5.570e-01 5.570e-01 5.570e-01 5.570e-01 5.570e-01 5.570e-01 5.570e-01 5.570e-01 5.570e-01 5.570e-01 5.570e-01 5.570e-01	APEX1:389 OPA1:444.5 HIF1A:789 MGARP:1371 TRAK2:1386 HDAC6:1463 RAB3A:73 EPHA5:101 FEZ1:150 KIF5C:188 NELL2:303 SLIT2:608.5 NKX2-5:83 CXADR:225 TTN:911 TCAP:1336.5 SLC8A1:1474 MYH11:2177.5 CSRP3:718 TTN:911 TCAP:1336.5 OCRL:1737 RYR2:2794 HDAC4:3260 FKBP1B:40 GJC1:399 ATP1A3:990.5 ATP1A2:1348 SLC8A1:1474 RYR2:2794 EPO:45 DDX3X:390.5 PKD2:437 MTOR:781 SERPINB6:917 ZFP36L1:1833.5 HSPB8:228.5 ERN1:728 STUB1:1055 UBE2W:1186 DNAJB12:1460.5 HDAC6:1463 SC5D:885 LBR:1007 MVD:1073.5 MSMO1:1416 HMGCR:1589 LSS:1807.5 TSKU:468 LBR:1007 MVD:1073.5 SCARF1:1101 ACAA2:1134.5 MSMO1:1416 RPL3:334 RPS7:521 EIF4A2:655 RPS16:743 EIF3I:797 RPL18:802 ZNF365:392 NOL3:1004 DOCK10:1293.5 EPHB3:1973 CTNND2:2034 PAK3:3011 PLEKHA3:130 TMEM9:243 WASHC4:434 TMCC1:528 ARFGEF2:841.5 DNM1:940.5 TOMM40L:29 TOMM34:336 TIMM10:714 RALA:973.5 FBXO7:1366 MGARP:1371 ACACB:18 SGPL1:40 ALOX5:170 THEM4:322 ACSL6:413.5 CYP4F2:570
Axonogenesis (GO:0007409)         -0.07879159         167           Cardiac Cell Development (GO:0055006)         -0.22483346         13           Cardiac Muscle Hypertrophy (GO:0003300)         -0.33679270         7           Cell Communication By Electrical Couplin         -0.21485103         13           Cellular Response To Osmotic Stress (GO:         -0.15576890         26           Cellular Response To Topologically Incor         0.18293546         19           Cholesterol Biosynthetic Process (GO:000         0.18752836         23           Cholesterol Metabolic Process (GO:000820         0.10906770         53           Cytoplasmic Translation (GO:0002181)         0.15168617         43           Dendritic Spine Morphogenesis (GO:006099         -0.23333444         13           Endosome Organization (GO:0007032)         0.11831848         49           Establishment Of Protein Localization To         0.12352306         40           Fatty Acid Metabolic Process (GO:0006631         0.07668591         104           Filopodium Assembly (GO:0046847)         -0.21623718         15           Granulocyte Chemotaxis (GO:0071621)         -0.12833695         37           Hematopoietic Progenitor Cell Differenti         -0.16304149         25           Lymphocyte Differentiation (GO:0030098) <t< td=""><td>4.625e-04 5.009e-03 2.031e-03 7.321e-03 5.992e-03 5.782e-03 1.857e-03 6.066e-03 5.836e-04 3.584e-03 4.198e-03 6.903e-03 7.001e-03 3.742e-03</td><td>5.570e-01 5.570e-01 5.570e-01 5.570e-01 5.570e-01 5.570e-01 5.570e-01 5.570e-01 5.570e-01 5.570e-01 5.570e-01 5.570e-01 5.570e-01 5.570e-01</td><td>RAB3A:73 EPHA5:101 FEZ1:150 KIF5C:188 NELL2:303 SLIT2:608.5 NKX2-5:83 CXADR:225 TTN:911 TCAP:1336.5 SLC8A1:1474 MYH11:2177.5 CSRP3:718 TTN:911 TCAP:1336.5 OCRL:1737 RYR2:2794 HDAC4:3260 FKBP1B:40 GJC1:399 ATP1A3:990.5 ATP1A2:1348 SLC8A1:1474 RYR2:2794 EPO:45 DDX3X:390.5 PKD2:437 MTOR:781 SERPINB6:917 ZFP36L1:1833.5 HSPB8:228.5 ERN1:728 STUB1:1055 UBE2W:1186 DNAJB12:1460.5 HDAC6:1463 SC5D:885 LBR:1007 MVD:1073.5 MSMO1:1416 HMGCR:1589 LSS:1807.5 TSKU:468 LBR:1007 MVD:1073.5 SCARF1:1101 ACAA2:1134.5 MSMO1:1416 RPL3:334 RPS7:521 EIF4A2:655 RPS16:743 EIF3I:797 RPL18:802 ZNF365:392 NOL3:1004 DOCK10:1293.5 EPHB3:1973 CTNND2:2034 PAK3:3011 PLEKHA3:130 TMEM9:243 WASHC4:434 TMCC1:528 ARFGEF2:841.5 DNM1:940.5 TOMM40L:29 TOMM34:336 TIMM10:714 RALA:973.5 FBXO7:1366 MGARP:1371 ACACB:18 SGPL1:40 ALOX5:170 THEM4:322 ACSL6:413.5 CYP4F2:570</td></t<>	4.625e-04 5.009e-03 2.031e-03 7.321e-03 5.992e-03 5.782e-03 1.857e-03 6.066e-03 5.836e-04 3.584e-03 4.198e-03 6.903e-03 7.001e-03 3.742e-03	5.570e-01 5.570e-01 5.570e-01 5.570e-01 5.570e-01 5.570e-01 5.570e-01 5.570e-01 5.570e-01 5.570e-01 5.570e-01 5.570e-01 5.570e-01 5.570e-01	RAB3A:73 EPHA5:101 FEZ1:150 KIF5C:188 NELL2:303 SLIT2:608.5 NKX2-5:83 CXADR:225 TTN:911 TCAP:1336.5 SLC8A1:1474 MYH11:2177.5 CSRP3:718 TTN:911 TCAP:1336.5 OCRL:1737 RYR2:2794 HDAC4:3260 FKBP1B:40 GJC1:399 ATP1A3:990.5 ATP1A2:1348 SLC8A1:1474 RYR2:2794 EPO:45 DDX3X:390.5 PKD2:437 MTOR:781 SERPINB6:917 ZFP36L1:1833.5 HSPB8:228.5 ERN1:728 STUB1:1055 UBE2W:1186 DNAJB12:1460.5 HDAC6:1463 SC5D:885 LBR:1007 MVD:1073.5 MSMO1:1416 HMGCR:1589 LSS:1807.5 TSKU:468 LBR:1007 MVD:1073.5 SCARF1:1101 ACAA2:1134.5 MSMO1:1416 RPL3:334 RPS7:521 EIF4A2:655 RPS16:743 EIF3I:797 RPL18:802 ZNF365:392 NOL3:1004 DOCK10:1293.5 EPHB3:1973 CTNND2:2034 PAK3:3011 PLEKHA3:130 TMEM9:243 WASHC4:434 TMCC1:528 ARFGEF2:841.5 DNM1:940.5 TOMM40L:29 TOMM34:336 TIMM10:714 RALA:973.5 FBXO7:1366 MGARP:1371 ACACB:18 SGPL1:40 ALOX5:170 THEM4:322 ACSL6:413.5 CYP4F2:570
Cardiac Cell Development (GO:0055006)         -0.22483346         13           Cardiac Muscle Hypertrophy (GO:0003300)         -0.33679270         7           Cell Communication By Electrical Couplin         -0.21485103         13           Cellular Response To Osmotic Stress (GO:         -0.15576890         26           Cellular Response To Topologically Incor         0.18293546         19           Cholesterol Biosynthetic Process (GO:000         0.18752836         23           Cholesterol Metabolic Process (GO:000820         0.10906770         53           Cytoplasmic Translation (GO:0002181)         0.15168617         43           Dendritic Spine Morphogenesis (GO:006099         -0.23333444         13           Endosome Organization (GO:0007032)         0.11831848         49           Establishment Of Protein Localization To         0.12352306         40           Fatty Acid Metabolic Process (GO:0006631         0.07668591         104           Filopodium Assembly (GO:0046847)         -0.21623718         15           Granulocyte Chemotaxis (GO:0071621)         -0.12833695         37           Hematopoietic Progenitor Cell Differenti         -0.16304149         25           Lymphocyte Differentiation (GO:0030098)         -0.10473537         65	5.009e-03 2.031e-03 7.321e-03 5.992e-03 5.782e-03 1.857e-03 6.066e-03 5.836e-04 3.584e-03 4.198e-03 6.903e-03 7.001e-03 3.742e-03	5.570e-01 5.570e-01 5.570e-01 5.570e-01 5.570e-01 5.570e-01 5.570e-01 5.570e-01 5.570e-01 5.570e-01 5.570e-01 5.570e-01	NKX2-5:83 CXADR:225 TTN:911 TCAP:1336.5 SLC8A1:1474 MYH11:2177.5  CSRP3:718 TTN:911 TCAP:1336.5 OCRL:1737 RYR2:2794 HDAC4:3260  FKBP1B:40 GJC1:399 ATP1A3:990.5 ATP1A2:1348 SLC8A1:1474 RYR2:2794  EPO:45 DDX3X:390.5 PKD2:437 MTOR:781 SERPINB6:917 ZFP36L1:1833.5  HSPB8:228.5 ERN1:728 STUB1:1055 UBE2W:1186 DNAJB12:1460.5 HDAC6:1463  SC5D:885 LBR:1007 MVD:1073.5 MSMO1:1416 HMGCR:1589 LSS:1807.5  TSKU:468 LBR:1007 MVD:1073.5 SCARF1:1101 ACAA2:1134.5 MSMO1:1416  RPL3:334 RPS7:521 EIF4A2:655 RPS16:743 EIF3I:797 RPL18:802  ZNF365:392 NOL3:1004 DOCK10:1293.5 EPHB3:1973 CTNND2:2034 PAK3:3011  PLEKHA3:130 TMEM9:243 WASHC4:434 TMCC1:528 ARFGEF2:841.5 DNM1:940.5  TOMM40L:29 TOMM34:336 TIMM10:714 RALA:973.5 FBXO7:1366 MGARP:1371  ACACB:18 SGPL1:40 ALOX5:170 THEM4:322 ACSL6:413.5 CYP4F2:570
Cardiac Muscle Hypertrophy (GO:0003300)         -0.33679270         7           Cell Communication By Electrical Couplin         -0.21485103         13           Cellular Response To Osmotic Stress (GO:         -0.15576890         26           Cellular Response To Topologically Incor         0.18293546         19           Cholesterol Biosynthetic Process (GO:000         0.18752836         23           Cholesterol Metabolic Process (GO:000820         0.10906770         53           Cytoplasmic Translation (GO:0002181)         0.15168617         43           Dendritic Spine Morphogenesis (GO:006099         -0.23333444         13           Endosome Organization (GO:0007032)         0.11831848         49           Establishment Of Protein Localization To         0.12352306         40           Fatty Acid Metabolic Process (GO:0006631         0.07668591         104           Filopodium Assembly (GO:0046847)         -0.21623718         15           Granulocyte Chemotaxis (GO:0071621)         -0.12833695         37           Hematopoietic Progenitor Cell Differenti         -0.16304149         25           Lymphocyte Differentiation (GO:0030098)         -0.10473537         65	2.031e-03 7.321e-03 5.992e-03 5.782e-03 1.857e-03 6.066e-03 5.836e-04 3.584e-03 4.198e-03 6.903e-03 7.001e-03 3.742e-03	5.570e-01 5.570e-01 5.570e-01 5.570e-01 5.570e-01 5.570e-01 5.570e-01 5.570e-01 5.570e-01 5.570e-01 5.570e-01	CSRP3:718 TTN:911 TCAP:1336.5 OCRL:1737 RYR2:2794 HDAC4:3260 FKBP1B:40 GJC1:399 ATP1A3:990.5 ATP1A2:1348 SLC8A1:1474 RYR2:2794 EPO:45 DDX3X:390.5 PKD2:437 MTOR:781 SERPINB6:917 ZFP36L1:1833.5 HSPB8:228.5 ERN1:728 STUB1:1055 UBE2W:1186 DNAJB12:1460.5 HDAC6:1463 SC5D:885 LBR:1007 MVD:1073.5 MSMO1:1416 HMGCR:1589 LSS:1807.5 TSKU:468 LBR:1007 MVD:1073.5 SCARF1:1101 ACAA2:1134.5 MSMO1:1416 RPL3:334 RPS7:521 EIF4A2:655 RPS16:743 EIF3I:797 RPL18:802 ZNF365:392 NOL3:1004 DOCK10:1293.5 EPHB3:1973 CTNND2:2034 PAK3:3011 PLEKHA3:130 TMEM9:243 WASHC4:434 TMCC1:528 ARFGEF2:841.5 DNM1:940.5 TOMM40L:29 TOMM34:336 TIMM10:714 RALA:973.5 FBXO7:1366 MGARP:1371 ACACB:18 SGPL1:40 ALOX5:170 THEM4:322 ACSL6:413.5 CYP4F2:570
Cell Communication By Electrical Couplin         -0.21485103         13           Cellular Response To Osmotic Stress (GO:         -0.15576890         26           Cellular Response To Topologically Incor         0.18293546         19           Cholesterol Biosynthetic Process (GO:000         0.18752836         23           Cholesterol Metabolic Process (GO:000820         0.10906770         53           Cytoplasmic Translation (GO:0002181)         0.15168617         43           Dendritic Spine Morphogenesis (GO:006099         -0.23333444         13           Endosome Organization (GO:0007032)         0.11831848         49           Establishment Of Protein Localization To         0.12352306         40           Fatty Acid Metabolic Process (GO:0006631         0.07668591         104           Filopodium Assembly (GO:0046847)         -0.21623718         15           Granulocyte Chemotaxis (GO:0071621)         -0.12833695         37           Hematopoietic Progenitor Cell Differenti         -0.16304149         25           Lymphocyte Differentiation (GO:0030098)         -0.10473537         65	7.321e-03 5.992e-03 5.782e-03 1.857e-03 6.066e-03 5.836e-04 3.584e-03 4.198e-03 6.903e-03 7.001e-03 3.742e-03	5.570e-01 5.570e-01 5.570e-01 5.570e-01 5.570e-01 5.570e-01 5.570e-01 5.570e-01 5.570e-01 5.570e-01	FKBP1B:40 GJC1:399 ATP1A3:990.5 ATP1A2:1348 SLC8A1:1474 RYR2:2794 EPO:45 DDX3X:390.5 PKD2:437 MTOR:781 SERPINB6:917 ZFP36L1:1833.5 HSPB8:228.5 ERN1:728 STUB1:1055 UBE2W:1186 DNAJB12:1460.5 HDAC6:1463 SC5D:885 LBR:1007 MVD:1073.5 MSMO1:1416 HMGCR:1589 LSS:1807.5 TSKU:468 LBR:1007 MVD:1073.5 SCARF1:1101 ACAA2:1134.5 MSMO1:1416 RPL3:334 RPS7:521 EIF4A2:655 RPS16:743 EIF3I:797 RPL18:802 ZNF365:392 NOL3:1004 DOCK10:1293.5 EPHB3:1973 CTNND2:2034 PAK3:3011 PLEKHA3:130 TMEM9:243 WASHC4:434 TMCC1:528 ARFGEF2:841.5 DNM1:940.5 TOMM40L:29 TOMM34:336 TIMM10:714 RALA:973.5 FBXO7:1366 MGARP:1371 ACACB:18 SGPL1:40 ALOX5:170 THEM4:322 ACSL6:413.5 CYP4F2:570
Cellular Response To Osmotic Stress (GO:         -0.15576890         26           Cellular Response To Topologically Incor         0.18293546         19           Cholesterol Biosynthetic Process (GO:000         0.18752836         23           Cholesterol Metabolic Process (GO:000820         0.10906770         53           Cytoplasmic Translation (GO:0002181)         0.15168617         43           Dendritic Spine Morphogenesis (GO:006099         -0.23333444         13           Endosome Organization (GO:0007032)         0.11831848         49           Establishment Of Protein Localization To         0.12352306         40           Fatty Acid Metabolic Process (GO:0006631         0.07668591         104           Filopodium Assembly (GO:0046847)         -0.21623718         15           Granulocyte Chemotaxis (GO:0071621)         -0.12833695         37           Hematopoietic Progenitor Cell Differenti         -0.16304149         25           Lymphocyte Differentiation (GO:0030098)         -0.10473537         65	5.992e-03 5.782e-03 1.857e-03 6.066e-03 5.836e-04 3.584e-03 4.198e-03 6.903e-03 7.001e-03 3.742e-03	5.570e-01 5.570e-01 5.570e-01 5.570e-01 5.570e-01 5.570e-01 5.570e-01 5.570e-01 5.570e-01	EPO:45 DDX3X:390.5 PKD2:437 MTOR:781 SERPINB6:917 ZFP36L1:1833.5 HSPB8:228.5 ERN1:728 STUB1:1055 UBE2W:1186 DNAJB12:1460.5 HDAC6:1463 SC5D:885 LBR:1007 MVD:1073.5 MSMO1:1416 HMGCR:1589 LSS:1807.5 TSKU:468 LBR:1007 MVD:1073.5 SCARF1:1101 ACAA2:1134.5 MSMO1:1416 RPL3:334 RPS7:521 EIF4A2:655 RPS16:743 EIF3I:797 RPL18:802 ZNF365:392 NOL3:1004 DOCK10:1293.5 EPHB3:1973 CTNND2:2034 PAK3:3011 PLEKHA3:130 TMEM9:243 WASHC4:434 TMCC1:528 ARFGEF2:841.5 DNM1:940.5 TOMM40L:29 TOMM34:336 TIMM10:714 RALA:973.5 FBXO7:1366 MGARP:1371 ACACB:18 SGPL1:40 ALOX5:170 THEM4:322 ACSL6:413.5 CYP4F2:570
Cellular Response To Osmotic Stress (GO:         -0.15576890         26           Cellular Response To Topologically Incor         0.18293546         19           Cholesterol Biosynthetic Process (GO:000         0.18752836         23           Cholesterol Metabolic Process (GO:000820         0.10906770         53           Cytoplasmic Translation (GO:0002181)         0.15168617         43           Dendritic Spine Morphogenesis (GO:006099         -0.23333444         13           Endosome Organization (GO:0007032)         0.11831848         49           Establishment Of Protein Localization To         0.12352306         40           Fatty Acid Metabolic Process (GO:0006631         0.07668591         104           Filopodium Assembly (GO:0046847)         -0.21623718         15           Granulocyte Chemotaxis (GO:0071621)         -0.12833695         37           Hematopoietic Progenitor Cell Differenti         -0.16304149         25           Lymphocyte Differentiation (GO:0030098)         -0.10473537         65	5.782e-03 1.857e-03 6.066e-03 5.836e-04 3.584e-03 4.198e-03 6.903e-03 7.001e-03 3.742e-03	5.570e-01 5.570e-01 5.570e-01 5.570e-01 5.570e-01 5.570e-01 5.570e-01 5.570e-01	EPO:45 DDX3X:390.5 PKD2:437 MTOR:781 SERPINB6:917 ZFP36L1:1833.5 HSPB8:228.5 ERN1:728 STUB1:1055 UBE2W:1186 DNAJB12:1460.5 HDAC6:1463 SC5D:885 LBR:1007 MVD:1073.5 MSMO1:1416 HMGCR:1589 LSS:1807.5 TSKU:468 LBR:1007 MVD:1073.5 SCARF1:1101 ACAA2:1134.5 MSMO1:1416 RPL3:334 RPS7:521 EIF4A2:655 RPS16:743 EIF3I:797 RPL18:802 ZNF365:392 NOL3:1004 DOCK10:1293.5 EPHB3:1973 CTNND2:2034 PAK3:3011 PLEKHA3:130 TMEM9:243 WASHC4:434 TMCC1:528 ARFGEF2:841.5 DNM1:940.5 TOMM40L:29 TOMM34:336 TIMM10:714 RALA:973.5 FBXO7:1366 MGARP:1371 ACACB:18 SGPL1:40 ALOX5:170 THEM4:322 ACSL6:413.5 CYP4F2:570
Cellular Response To Topologically Incor         0.18293546         19           Cholesterol Biosynthetic Process (GO:000         0.18752836         23           Cholesterol Metabolic Process (GO:000820         0.10906770         53           Cytoplasmic Translation (GO:0002181)         0.15168617         43           Dendritic Spine Morphogenesis (GO:006099         -0.23333444         13           Endosome Organization (GO:0007032)         0.11831848         49           Establishment Of Protein Localization To         0.12352306         40           Fatty Acid Metabolic Process (GO:0006631         0.07668591         104           Filopodium Assembly (GO:0046847)         -0.21623718         15           Granulocyte Chemotaxis (GO:0071621)         -0.12833695         37           Hematopoietic Progenitor Cell Differenti         -0.16304149         25           Lymphocyte Differentiation (GO:0030098)         -0.10473537         65	1.857e-03 6.066e-03 5.836e-04 3.584e-03 4.198e-03 6.903e-03 7.001e-03 3.742e-03	5.570e-01 5.570e-01 5.570e-01 5.570e-01 5.570e-01 5.570e-01 5.570e-01	SC5D:885 LBR:1007 MVD:1073.5 MSMO1:1416 HMGCR:1589 LSS:1807.5 TSKU:468 LBR:1007 MVD:1073.5 SCARF1:1101 ACAA2:1134.5 MSMO1:1416 RPL3:334 RPS7:521 EIF4A2:655 RPS16:743 EIF3I:797 RPL18:802 ZNF365:392 NOL3:1004 DOCK10:1293.5 EPHB3:1973 CTNND2:2034 PAK3:3011 PLEKHA3:130 TMEM9:243 WASHC4:434 TMCC1:528 ARFGEF2:841.5 DNM1:940.5 TOMM40L:29 TOMM34:336 TIMM10:714 RALA:973.5 FBXO7:1366 MGARP:1371 ACACB:18 SGPL1:40 ALOX5:170 THEM4:322 ACSL6:413.5 CYP4F2:570
Cholesterol Metabolic Process (GO:000820         0.10906770         53           Cytoplasmic Translation (GO:0002181)         0.15168617         43           Dendritic Spine Morphogenesis (GO:006099         -0.23333444         13           Endosome Organization (GO:0007032)         0.11831848         49           Establishment Of Protein Localization To         0.12352306         40           Fatty Acid Metabolic Process (GO:0006631         0.07668591         104           Filopodium Assembly (GO:0046847)         -0.21623718         15           Granulocyte Chemotaxis (GO:0071621)         -0.12833695         37           Hematopoietic Progenitor Cell Differenti         -0.16304149         25           Lymphocyte Differentiation (GO:0030098)         -0.10473537         65	6.066e-03 5.836e-04 3.584e-03 4.198e-03 6.903e-03 7.001e-03 3.742e-03	5.570e-01 5.570e-01 5.570e-01 5.570e-01 5.570e-01 5.570e-01	TSKU:468 LBR:1007 MVD:1073.5 SCARF1:1101 ACAA2:1134.5 MSMO1:1416  RPL3:334 RPS7:521 EIF4A2:655 RPS16:743 EIF3I:797 RPL18:802  ZNF365:392 NOL3:1004 DOCK10:1293.5 EPHB3:1973 CTNND2:2034 PAK3:3011  PLEKHA3:130 TMEM9:243 WASHC4:434 TMCC1:528 ARFGEF2:841.5 DNM1:940.5  TOMM40L:29 TOMM34:336 TIMM10:714 RALA:973.5 FBXO7:1366 MGARP:1371  ACACB:18 SGPL1:40 ALOX5:170 THEM4:322 ACSL6:413.5 CYP4F2:570
Cholesterol Metabolic Process (GO:000820         0.10906770         53           Cytoplasmic Translation (GO:0002181)         0.15168617         43           Dendritic Spine Morphogenesis (GO:006099         -0.233333444         13           Endosome Organization (GO:0007032)         0.11831848         49           Establishment Of Protein Localization To         0.12352306         40           Fatty Acid Metabolic Process (GO:0006631         0.07668591         104           Filopodium Assembly (GO:0046847)         -0.21623718         15           Granulocyte Chemotaxis (GO:0071621)         -0.12833695         37           Hematopoietic Progenitor Cell Differenti         -0.16304149         25           Lymphocyte Differentiation (GO:0030098)         -0.10473537         65	6.066e-03 5.836e-04 3.584e-03 4.198e-03 6.903e-03 7.001e-03 3.742e-03	5.570e-01 5.570e-01 5.570e-01 5.570e-01 5.570e-01 5.570e-01	RPL3:334 RPS7:521 EIF4A2:655 RPS16:743 EIF3I:797 RPL18:802 ZNF365:392 NOL3:1004 DOCK10:1293.5 EPHB3:1973 CTNND2:2034 PAK3:3011 PLEKHA3:130 TMEM9:243 WASHC4:434 TMCC1:528 ARFGEF2:841.5 DNM1:940.5 TOMM40L:29 TOMM34:336 TIMM10:714 RALA:973.5 FBXO7:1366 MGARP:1371 ACACB:18 SGPL1:40 ALOX5:170 THEM4:322 ACSL6:413.5 CYP4F2:570
Cytoplasmic Translation (GO:0002181)       0.15168617       43         Dendritic Spine Morphogenesis (GO:006099       -0.23333444       13         Endosome Organization (GO:0007032)       0.11831848       49         Establishment Of Protein Localization To       0.12352306       40         Fatty Acid Metabolic Process (GO:0006631       0.07668591       104         Filopodium Assembly (GO:0046847)       -0.21623718       15         Granulocyte Chemotaxis (GO:0071621)       -0.12833695       37         Hematopoietic Progenitor Cell Differenti       -0.16304149       25         Lymphocyte Differentiation (GO:0030098)       -0.10473537       65	3.584e-03 4.198e-03 6.903e-03 7.001e-03 3.742e-03	5.570e-01 5.570e-01 5.570e-01 5.570e-01 5.570e-01	RPL3:334 RPS7:521 EIF4A2:655 RPS16:743 EIF3I:797 RPL18:802 ZNF365:392 NOL3:1004 DOCK10:1293.5 EPHB3:1973 CTNND2:2034 PAK3:3011 PLEKHA3:130 TMEM9:243 WASHC4:434 TMCC1:528 ARFGEF2:841.5 DNM1:940.5 TOMM40L:29 TOMM34:336 TIMM10:714 RALA:973.5 FBXO7:1366 MGARP:1371 ACACB:18 SGPL1:40 ALOX5:170 THEM4:322 ACSL6:413.5 CYP4F2:570
Dendritic Spine Morphogenesis (GO:006099       -0.23333444       13         Endosome Organization (GO:0007032)       0.11831848       49         Establishment Of Protein Localization To       0.12352306       40         Fatty Acid Metabolic Process (GO:0006631       0.07668591       104         Filopodium Assembly (GO:0046847)       -0.21623718       15         Granulocyte Chemotaxis (GO:0071621)       -0.12833695       37         Hematopoietic Progenitor Cell Differenti       -0.16304149       25         Lymphocyte Differentiation (GO:0030098)       -0.10473537       65	4.198e-03 6.903e-03 7.001e-03 3.742e-03	5.570e-01 5.570e-01 5.570e-01 5.570e-01	PLEKHA3:130 TMEM9:243 WASHC4:434 TMCC1:528 ARFGEF2:841.5 DNM1:940.5 TOMM40L:29 TOMM34:336 TIMM10:714 RALA:973.5 FBXO7:1366 MGARP:1371 ACACB:18 SGPL1:40 ALOX5:170 THEM4:322 ACSL6:413.5 CYP4F2:570
Endosome Organization (GO:0007032)       0.11831848       49         Establishment Of Protein Localization To       0.12352306       40         Fatty Acid Metabolic Process (GO:0006631       0.07668591       104         Filopodium Assembly (GO:0046847)       -0.21623718       15         Granulocyte Chemotaxis (GO:0071621)       -0.12833695       37         Hematopoietic Progenitor Cell Differenti       -0.16304149       25         Lymphocyte Differentiation (GO:0030098)       -0.10473537       65	6.903e-03 7.001e-03 3.742e-03	5.570e-01 5.570e-01 5.570e-01	TOMM40L:29 TOMM34:336 TIMM10:714 RALA:973.5 FBXO7:1366 MGARP:1371 ACACB:18 SGPL1:40 ALOX5:170 THEM4:322 ACSL6:413.5 CYP4F2:570
Fatty Acid Metabolic Process (GO:0006631       0.07668591       104         Filopodium Assembly (GO:0046847)       -0.21623718       15         Granulocyte Chemotaxis (GO:0071621)       -0.12833695       37         Hematopoietic Progenitor Cell Differenti       -0.16304149       25         Lymphocyte Differentiation (GO:0030098)       -0.10473537       65	7.001e-03 3.742e-03	5.570e-01 5.570e-01	ACACB:18 SGPL1:40 ALOX5:170 THEM4:322 ACSL6:413.5 CYP4F2:570
Filopodium Assembly (GO:0046847)	7.001e-03 3.742e-03	5.570e-01 5.570e-01	
Filopodium Assembly (GO:0046847)			EZR:385.5 FGD5:1135 SPATA13:1236 SPEF1:1656.5 S1PR2:1702 DNM3:2003
Hematopoietic Progenitor Cell Differenti -0.16304149 25 Lymphocyte Differentiation (GO:0030098) -0.10473537 65	6.938e-03		
Hematopoietic Progenitor Cell Differenti -0.16304149 25 Lymphocyte Differentiation (GO:0030098) -0.10473537 65		5.570e-01	CCL20:127 CXADR:225 CCL2:334 CXCL2:534 PIKFYVE:574 SYK:1194
Lymphocyte Differentiation (GO:0030098) -0.10473537 65	4.790e-03	5.570e-01	FSTL3:2 HOXB4:473 BATF:581 BMP4:822 INHBA:852.5 TNFRSF13B:920
	3.537e-03	5.570e-01	RELB:24 ZBTB7A:403 BLNK:455.5 HDAC9:669 NFAM1:992 NHEJ1:1031.5
	7.533e-03	5.570e-01	COA8:535 SURF1:560 COA5:977.5 SMIM20:1453 COX17:2084 COX16:2668
Mitochondrial Transport (GO:0006839) 0.10807961 51	7.636e-03	5.570e-01	SLC25A31:330 TOMM34:336 TIMM10:714 BCL2L1:884 SLC25A4:991.5 FBXO7:1366
Negative Regulation Of BMP Signaling Pat -0.14077404 35	3.970e-03	5.570e-01	FSTL3:2 SPART:255 GREM1:345 CHRDL2:483 DLX1:524.5 GPR155:595
Negative Regulation Of Bone Remodeling ( -0.28970107 10	1.514e-03	5.570e-01	CARTPT:297 GREM1:345 UBASH3B:361 TNFAIP3:1160 INPP5D:1175.5 SFRP1:1990
Negative Regulation Of Fibrinolysis (GO: -0.31111111 8	2.311e-03	5.570e-01	THBD:169 SERPINE1:206 PLAT:959.5 SERPINF2:1997.5 NRG1:3798 PLAU:3988.5
Negative Regulation Of Intracellular Tra 0.34071755 7	1.798e-03	5.570e-01	ARHGAP8:104 MRLN:518 CRYAA:947 PLN:1843.5 CRYAB:2565.5 INSIG1:3863
Negative Regulation Of Leukocyte Chemota -0.28617165 9	2.952e-03	5.570e-01	GREM1:345 SLIT2:608.5 NBL1:736.5 C5:2855.5 UXT:2861.5 DUSP1:3119
Negative Regulation Of Monocyte Chemotax -0.36409197 5	4.810e-03	5.570e-01	GREM1:345 SLIT2:608.5 NBL1:736.5 DUSP1:3119 SLAMF8:5313.5 NA
Negative Regulation Of Myeloid Leukocyte -0.17357670 22	4.840e-03	5.570e-01	FSTL3:2 TLR4:94.5 CARTPT:297 INHBA:852.5 TLR3:1615.5 PTPN2:2765
Negative Regulation Of Nuclear–Transcrib 0.26190308 11	2.634e-03	5.570e-01	PAIP1:299 TENT4A:649 SYNCRIP:1504 HNRNPU:1512 PABPC1:2241.5 YBX1:2454
Negative Regulation Of Protein Metabolic 0.07134718 124	6.194e-03	5.570e-01	GRB7:53 TM4SF20:149 CPEB3:171 MAD2L2:247 CD84:266 SNX12:730
Neuron Projection Extension (GO:1990138) -0.14398691 38	2.144e-03	5.570e-01	NRN1:12 NELL2:303 CTNNB1:758 IMPACT:1048 SEMA3A:1221 SLC9A6:1632

p.adj

9.691e-05 2.306e-02

6.093e-05 2.306e-02

8.663e-04 1.032e-01

8.669e-04 1.032e-01

PLIN1:76 FOXP3:83 PKHD1:92 STX2:98 GAB1:102 JMJD6:124

PAK4:20 RANBP2:39 IPMK:48 YAP1:68 PKHD1:92 PRPF31:95

PKHD1:92 NF2:333 RTN4RL1:337 CYS1:407 ONECUT1:606.5 MAP3K7:846

MMP9:100 HOXD9:532 BMP7:536 FGF9:638.5 CTNNB1:758 BMP4:822

stat

0.05665037

0.03782547

0.17909474

-0.10066807

93

MP0000598 abnormal liver morphology

MP0002080 prenatal lethality

MP0002928 abnormal bile duct

MP0002932 abnormal joint morphology

MGI\_Mammalian\_Phenotype\_Level\_4 Top pathways by permulation

MP0005384 cellular phenotype  MP0003724 increased susceptibility to	-0.11921042	1110	2.218e-03	1.7606-01	ACACB:18 GAS6:35 SGPL1:40 PLIN1:76 FOXP3:83 VAV3:90
MP0003724 increased susceptibility to -	0.11921042	57	1.940e-03	1.760e-01	CBL:62 MMP9:100 LIG4:191 HIP1:194 CSF3R:271 GIMAP5:336
	0.04207303	410	4.736e-03	3.021e-01	PAK4:20 SGPL1:40 GAB1:102 SIRT1:122.5 PEX11B:127 XPC:249.5
MP0001175 abnormal lung morphology	-0.22407513	13	5.195e-03	3.021e-01	TLR4:94.5 CD200:732 IL1RN:1290 LGALS9:1556.5 FPR2:2898 DUSP1:3119
wir ooo'i 175 abriofffiai fung morphology —	-0.04634341	317	5.713e-03	3.021e-01	RELB:24 SFTPD:72 PPARGC1A:88 TLR4:94.5 MMP9:100 PTPRD:160.5
MP0005332 abnormal amino acid	0.07705908	105	6.820e-03	3.077e-01	GPD2:263 CYS1:407 CLCN5:453 FOLR1:481 ATG7:612 RRM2B:642
MP0008961 abnormal basal metabolism	0.18243863	17	9.297e-03	3.077e-01	ATE1:562 HTR6:1064 NCOR1:1477 HIF1AN:2009 DECR1:2212 VGF:2853
MP0003122 maternal imprinting (	0.18764103	16	9.445e-03	3.077e-01	DLK1:142 IGF2R:490.5 GNAS:493 MEST:787 IGF2:1548 PEG10:2199
MP0002118 abnormal lipid homeostasis	0.04253752	350	7.907e-03	3.077e-01	ACACB:18 FABP7:59 PLIN1:76 GAB1:102 PLTP:131 DLK1:142
MP0002152 abnormal brain morphology (	0.02874660	888	7.268e-03	3.077e-01	PAK4:20 AGTPBP1:30 IPMK:48 FABP7:59 EFNB1:71 PLXNA2:81
	0.09543985	62	9.697e-03	3.077e-01	GAB1:102 RYK:598.5 LMNA:752.5 SIM2:1168 KRT5:1601 PTH1R:1785.5
	0.06433589	135	1.067e-02		PLIN1:76 SIRT1:122.5 DLK1:142 ALOX5:170 GPD2:263 GNAS:493
	-0.04308321	290	1.371e-02		RELB:24 MMP9:100 CD86:116 TRAF5:154 LIG4:191 NFKBIE:237
	0.23921207	9	1.301e-02		SIRT1:122.5 GABPA:1092.5 CDC7:2674 LIG1:3833 FEN1:4114 ATR:4743
	0.03644658	399	1.566e-02		RAD18:12 AGTPBP1:30 HERC4:38 SGPL1:40 ARL4A:44 CCNE2:45
	0.02676899	837	1.460e-02		PAK4:20 EFNB1:71 FOXP3:83 PRPF31:95 TNKS2:105 SIRT1:122.5
	0.02676899	837	1.460e-02		PAK4:20 EFNB1:71 FOXP3:83 PRPF31:95 TNKS2:105 SIRT1:122.5
1 1	0.03622149	403	1.584e-02		RAD18:12 AGTPBP1:30 SGPL1:40 ARL4A:44 CCNE2:45 FOXP3:83
·	0.06534285	125	1.249e-02		VAV3:90 EXOC6:248 ANGPTL4:260 IKBKG:452 MAPK9:472.5 GNAS:493
	0.04132594	307	1.518e-02		PAK4:20 SGPL1:40 GAB1:102 SIRT1:122.5 PEX11B:127 XPC:249.5
	0.04040710	303	1.829e-02		RAD18:12 SGPL1:40 ARL4A:44 CCNE2:45 FOXP3:83 STX2:98
	-0.03069503	556	1.827e-02		RELB:24 CBL:62 SFTPD:72 TLR4:94.5 MMP9:100 CD86:116
	0.05422774	155	2.138e-02		ACACB:18 VAV3:90 GSTA4:241 GPD2:263 PRDX1:379 ENTPD5:413.5
	-0.02355813	902	2.688e-02		JAM3:6 RELB:24 CNTF:25 CBL:62 SFTPD:72 TLR4:94.5
	-0.02470162	724	3.359e-02		RELB:24 CBL:62 TLR4:94.5 MMP9:100 CD86:116 TRAF5:154
MP0003453 abnormal keratinocyte physiol (	0.08338973	55	3.317e-02	4.726e-01	ARNT:103 CDKN2A:419 IKBKG:452 DSC3:619 CDKN1A:709 FERMT1:872
	0.05376381	139	3.045e-02		RANBP2:39 SIRT1:122.5 CHEK1:178 PRDX1:379 CDKN2A:419 PLK2:499.5
	0.11616139	28	3.376e-02	4.726e-01	NPAS2:259 NPY2R:919 PRNP:1048.5 GABBR1:1390 TNF:1996 CACNA1G:2271
	0.19594345	10	3.203e-02	4.726e-01	CDKN2A:419 KRT1:442 GNAQ:800 BRAF:1652.5 TERF2IP:2778 GNA11:2962
11 1	0.09461826	43	3.239e-02	4.726e-01	EFNB1:71 CNP:159 IL12RB2:332 RRM2B:642 CTNND1:1201 DCN:1350.5
MP0002115 abnormal skeleton extremities –	-0.03793803	273	3.488e-02	4.744e-01	MMP9:100 HOXA10:200 TTC21B:252 FMOD:262.5 FUZ:267 GREM1:345
MP0003953 abnormal hormone level	0.02863726	486	3.796e-02	4.882e-01	ACACB:18 SGPL1:40 PLIN1:76 VAV3:90 GAB1:102 SIRT1:122.5
MP0003698 abnormal male reproductive (	0.02947645	456	3.788e-02	4.882e-01	RAD18:12 AGTPBP1:30 HERC4:38 SGPL1:40 CCNE2:45 FOXP3:83
MP0010768 mortality/aging	0.02161194	942	3.897e-02	4.882e-01	PAK4:20 EFNB1:71 FOXP3:83 PRPF31:95 TNKS2:105 SIRT1:122.5
MP0000609 abnormal liver physiology	0.03326440	336	4.153e-02	5.069e-01	FOXP3:83 ARNT:103 DLK1:142 KRT8:192 GPD2:263 RGN:296
MP0003252 abnormal bile duct	0.11913996	24	4.373e-02	5.204e-01	PKHD1:92 NF2:333 CYS1:407 ATXN2:566 PCTP:752.5 P2RY13:845

tissue\_specific Top pathways by permulation

Geneset	stat	num.genes	pval	p.adj	gene.vals
liver	0.072422680	277	4.519e-05	2.441e-03	SLC17A4:114.5 MOGAT1:196 C2orf72:219 TM4SF5:275 PROX1:538 CYP4F2:570
adrenal.gland	0.081381761	98	5.639e-03	1.523e-01	C2CD2:113 DLK1:142 GSTA4:241 RGN:296 SLC16A9:345 ABCC3:499.5
transformed.skin.fibroblast	-0.049791114	241	8.691e-03	1.564e-01	TRNP1:33 ITGBL1:141 OPN3:190 SERPINE1:206 MPP4:254 MXRA5:286
cerebellum	-0.037986633	326	2.081e-02	2.810e-01	TMEM145:44 PRRT1:75 CAMK2N2:125 KCNC3:146 PTPRD:160.5 ACHE:215
blood	-0.042415536	236	2.690e-02	2.842e-01	NCF2:7 SLC43A2:65 MMP9:100 CD247:196 DENND3:243 CSF3R:271
cortex.kidney	0.055919523	107	4.704e-02	2.842e-01	SLC22A2:2 PKHD1:92 FOXI1:97 CLCNKB:100 KCNJ1:109 SULT1C2:114.5
left.ventricle	-0.070853620	66	4.737e-02	2.842e-01	TNNI3:18 ACTC1:59 MYH7B:74 NKX2-5:83 CKMT2:183 SGCG:201
tibial.artery	0.059070487	108	3.508e-02	2.842e-01	SUSD5:151 AMIGO2:233 C1QTNF1:390 MSRB3:523 AVPR1A:634 HEY2:774
uterus	-0.077829116	59	3.933e-02	2.842e-01	RPRM:42 HOXA10:200 WT1:370 RSPO3:480 CHRDL2:483 HOXD9:532
pituitary.gland	0.040387560	174	6.894e-02	3.723e-01	GNG4:13 DLK1:142 RXRG:202 CFAP47:217 CHRNE:222 SLC6A5:340
	-0.045788676	116	9.067e-02	4.451e-01	TMEM54:5 CDC42EP5:35 MARVELD3:60 SULT1B1:130 HSD11B2:152 PTGDR2:163
spleen	-0.030595157	240	1.076e-01	4.469e-01	NKX2-5:83 GDPD5:90 MMP9:100 CSF3R:271 CD3D:310 GIMAP5:336
stomach	0.053598395	77	1.055e-01	4.469e-01	FBP2:14 CXCL17:88.5 SULT1C2:114.5 PIK3C2G:126 TM4SF5:275 RFLNA:301
breast	0.119101805	13	1.373e-01	4.668e-01	PLIN1:76 GLYAT:604 ABCB5:610 NPY2R:919 KRT5:1601 THRSP:1835
peyers.patch	0.038369670	127	1.383e-01	4.668e-01	DHRS11:3 SLC17A4:114.5 MYO7B:118 TM4SF20:149 CLDN15:199 TUBAL3:204
thyroid	0.038661355	130	1.309e-01	4.668e-01	ARHGAP8:104 SULT1C2:114.5 SLC16A11:177 MIOX:265 MARVELD2:385 GAL3ST3:386
testis	0.014036870	1038	1.536e-01	4.879e-01	USP2:9 ABHD1:10 HMGN5:17 ZMYND12:33 ARL4A:44 TTC39A:173
cerebellar.hemisphere	-0.018668957	448	1.877e-01	5.630e-01	NDP:11 NRN1:12 ENO2:28 MREG:37 TMEM145:44 ADAM22:47
coronary.artery	-0.105238291	12	2.071e-01	5.711e-01	HEYL:1837.5 MYO18B:1920 COL4A1:3037 CCDC3:3195 MTHFD1L:3825 CCN3:4606
prostate	0.064917627	31	2.117e-01	5.711e-01	SLC45A3:253 SRD5A2:1287 FOXA1:1295 KRT5:1601 EPHA3:1634 GLB1L2:2072
sigmoid.colon	-0.051617725	47	2.221e-01	5.711e-01	GJC1:399 FOXF1:559.5 PNCK:1136 SEMA3A:1221 ACTG2:1705.5 NKX2-3:2231
-	-0.027936046	142	2.545e-01	6.246e-01	PPP1R14A:164 FMOD:262.5 CYP4X1:295 STK38L:311 SLC22A3:423.5 OSR1:428
atrium.auricle	-0.034296898	79	2.942e-01	6.396e-01	TNNI3:18 ACTC1:59 NKX2-5:83 CKMT2:183 SGCG:201 PEBP4:352
substantia.nigra	-0.105079209	9	2.752e-01	6.396e-01	RET:882 KLHL1:936 CHRM5:2125 SLC6A3:3617 TH:4904 SLC6A11:6644.5
	-0.023530891	169	2.961e-01		CNTF:25 SFRP5:32 VWA1:153 CADM4:253 ARHGAP39:312 IL34:317
skeletal.muscle	0.017843627	225	3.629e-01	7.537e-01	FBP2:14 POPDC3:116 PDLIM3:212 MYOZ1:285 RBM24:485 MRLN:518
bladder	0.046786512	19		7.564e-01	ABCC4:198 PLA2G4A:557 TMC7:1397 SIGLEC15:2885 CYP4B1:3451 UPK1B:3481
Brodmann.area.9	0.018453262	159	4.264e-01	7.564e-01	PPP2R2B:162 VSNL1:288 CALHM1:339 GDA:402 KCNV1:418 NRCAM:588
caudate.nucleus	0.041429106	22	5.017e-01	7.564e-01	ACBD7:720 GPR88:2725 ANO3:2767 GPR37L1:2865 CHAT:3493.5 VAX1:4574
ectocervix	0.047306074	19	4.758e-01	7.564e-01	TSKU:468 ADRA2A:582 PTHLH:1978 CPXM1:2742.5 COL5A1:3979 GDF7:4439
esophagogastric.junction	0.086887169	7		7.564e-01	COL4A5:1233 GADL1:1466 BARX1:3907.5 F2RL2:5959 HOXA4:9436 NKX6-1:11013.5
	-0.042167325	25	4.661e-01	7.564e-01	SYNPO2:1893 RGS2:2025.5 MYH11:2177.5 S1PR3:2693.5 KCNMB1:2712 SMTN:2813
hippocampus.proper	0.070793644	8	4.882e-01		GRP:1591.5 CTXND1:2046 FEZF2:3802 NTS:3879.5 CABP7:7996 CNIH2:9897.5
	-0.021004601	110	4.496e-01		SFTPD:72 CCL20:127 CSF3R:271 RGCC:296 AGER:463 ADGRF5:537
minor.salivary.gland	0.031003834	57	4.197e-01		ELF5:251 KRT19:294 SERINC2:329 MMP7:377 GALNT3:1381 RUNX1:1451
subcutaneous.adipose	0.023436205	64		7.564e-01	ACACB:18 STEAP4:57 PLIN1:76 ANGPTL4:260 AKR1C2:496 GLYAT:604
·	-0.024665949	60		7.564e-01	FZD6:404 DLX1:524.5 BMP7:536 MITF:632.5 NBL1:736.5 BMP4:822
EBV.lymphocyte	0.007162507	602		7.830e-01	H2BC17:5 RAD18:12 HLA-DPB1:15 CHAC2:34 CD80:58 MCM10:156
, , , , , , , , , , , , , , , , , , , ,	-0.012907036	170		7.830e-01	KRT10:91 CHMP4C:431.5 MLANA:485 HS3ST6:533 ALOX12B:712.5 TREX2:722
leg.skin	3.0.200	., •		7.927e-01	LHFPL3:594 SLC17A7:3737 TNR:5580 BCAN:7228 PTPRZ1:9065 PCDH15:9358