





Top Positive genes by P-value non-permulated

Top Negative genes by P-value non-permulated

JOAD	0.52-115	1 .0002116-10	2.33-6-00	1.0736-02
ADGRG4	6.481391	5.452837e-10	2.934e-06	1.579e-02
MCF2L	6.099376	6.389014e-09	2.579e-05	6.238e-02
EME2	5.997321	1.203598e-08	3.886e-05	6.238e-02
ANKRD11	5.884617	2.393864e-08	4.467e-05	6.238e-02
TASOR2	5.887209	2.356631e-08	4.467e-05	6.238e-02
PIEZO1	5.828959	3.346444e-08	4.801e-05	6.238e-02
PPL	5.846099	3.019405e-08	4.801e-05	6.238e-02
PRUNE2	5.818236	3.568321e-08	4.801e-05	6.238e-02
ARHGEF6	5.669355	8.600189e-08	9.917e-05	1.091e-01

Gene Rho P p.adj qValueNoperm

JCAD 6.524775 4.086211e-10 2.934e-06 1.579e-02

CHL1	-5.878089	2.490178e-08	4.467e-05	6.238e-02
ANK2	-5.894989	2.248243e-08	4.467e-05	6.238e-02
LRRN3	-5.797233	4.045084e-08	5.023e-05	6.238e-02
DENND1B	-5.569866	1.529616e-07	1.441e-04	1.091e-01
AP1AR	-5.535020	1.867154e-07	1.486e-04	1.091e-01
KDM5B	-5.522645	2.003602e-07	1.486e-04	1.091e-01
SCN9A	-5.520761	2.025213e-07	1.486e-04	1.091e-01
WWP1	-5.465629	2.767611e-07	1.787e-04	1.154e-01
TMEM64	-5.436245	3.264910e-07	2.027e-04	1.259e-01

 Gene
 Rho
 P
 p.adj
 qValueNoperm

 HERC2
 -6.572040
 2.977833e-10
 2.934e-06
 1.579e-02

Geneset stat num.genes pval p.adj gene.vals Schizophrenia -0.04247106 1625 2.945e-08 2.889e-04 HERC2:1 CHL1:3 APOA1:12 UGT8:17 LTN1:19 S Neoplasm Metastasis -0.02857344 3142 1.395e-06 6.841e-03 CHL1:3 KDM5B:7 WWP1:9 APOA1:12 TJP1:14	
Neoplasm Metastasis -0.02857344 3142 1.395e-06 6.841e-03 CHL1:3 KDM5B:7 WWP1:9 APOA1:12 TJP1:14	LC26A7:32
	UGT8:17
Bilateral cataracts (disorder) -0.13051022 104 4.395e-06 1.437e-02 AKR1B1:43 TDRD7:99 HSF4:143 STOM:334 COL4A1:	340 CRYM:632
Alzheimer's Disease -0.03370734 1666 8.683e-06 1.879e-02 CHL1:3 APOA1:12 VCAM1:21 SLC26A7:32 BLMH:	37 F13B:40
Hepatitis C -0.05359554 596 9.577e-06 1.879e-02 APOA1:12 TJP1:14 AKR1B1:43 CLU:88 TNFSF10:97	GGTLC3:123
Glioblastoma -0.03352049 1597 1.401e-05 2.291e-02 APOA1:12 VCAM1:21 KIF14:29 AKR1B1:43 ZNF131:	46 MMP16:48
Neuroblastoma -0.03429693 1452 2.001e-05 2.804e-02 HERC2:1 ANK2:2 CHL1:3 LRRN3:4 KDM5B:7 V	CAM1:21
Central neuroblastoma -0.03391847 1413 3.076e-05 3.772e-02 HERC2:1 ANK2:2 CHL1:3 LRRN3:4 KDM5B:7 V	CAM1:21
Rheumatoid Arthritis -0.03319175 1456 3.591e-05 3.914e-02 APOA1:12 PHTF1:20 VCAM1:21 N4BP1:34 F13B:40	0 MMP16:48
Autism Spectrum Disorders -0.05413200 483 5.274e-05 4.466e-02 HERC2:1 LRRN3:4 ATP10A:31 MMP16:48 CSMD1:5	4 EHMT1:61
Autistic Disorder -0.04813064 615 5.463e-05 4.466e-02 CHL1:3 CNTN3:13 ZNF277:23 ATP10A:31 EHMT1:61	TUBGCP5:98
Neuralgia -0.12838207 83 5.380e-05 4.466e-02 SCN9A:8 CXCL13:50 SLC12A5:91 GRM2:209 TNF:24	8 SCN11A:308
Thyroid Neoplasm -0.05720790 417 6.869e-05 5.184e-02 TJP1:14 BAX:84 CLU:88 TNFSF10:97 SELP:130 F	PROM1:131
Diabetes Mellitus, Insulin-Dependent -0.04200998 744 1.166e-04 7.625e-02 APOA1:12 TJP1:14 VCAM1:21 CAMSAP2:35 AKR1B1	:43 EHMT1:61
Epilepsy, Cryptogenic -0.14317178 61 1.114e-04 7.625e-02 SLC12A5:91 VDAC2:142 UBE3A:156 SCN2A:265 ALB:3	73 GABRB3:618
Amyloidosis -0.04259303 707 1.367e-04 8.382e-02 APOA1:12 VCAM1:21 CYLD:81 CLU:88 HSPB1:96	OSMR:132
Epilepsy, Temporal Lobe -0.08515318 164 1.745e-04 8.708e-02 SLC12A5:91 TNFSF10:97 VDAC2:142 PAG1:169 GRM	2:209 CRH:212
Aura -0.14122645 59 1.775e-04 8.708e-02 SLC12A5:91 VDAC2:142 UBE3A:156 SCN2A:265 ALB:3	73 GABRB3:618
Awakening Epilepsy -0.14122645 59 1.775e-04 8.708e-02 SLC12A5:91 VDAC2:142 UBE3A:156 SCN2A:265 ALB:3	73 GABRB3:618
Degenerative polyarthritis -0.03897887 830 1.680e-04 8.708e-02 SCN9A:8 APOA1:12 VCAM1:21 CXCL13:50 CALCR	:65 DDR2:87
Seminoma -0.08253845 173 1.875e-04 8.760e-02 BAX:84 CLU:88 GGTLC3:123 PROM1:131 TNF:24	8 GH1:328
Allergic Reaction -0.16168183 44 2.083e-04 9.087e-02 SELP:130 TNF:248 MTHFR:280 ALB:373 IL5RA:49	91 IL18:605
Liver carcinoma -0.02275491 2819 2.157e-04 9.087e-02 KDM5B:7 WWP1:9 APOA1:12 TJP1:14 VCAM1:2	1 E2F5:26
Mammary Neoplasms -0.02593267 1999 2.223e-04 9.087e-02 HERC2:1 KDM5B:7 WWP1:9 CNTN3:13 TJP1:14 P	PP1R12B:16
Malignant lymphoma, lymphocytic, interme -0.06309278 289 2.392e-04 9.327e-02 BAX:84 TNFSF10:97 MRC1:144 CCNE1:154 PAG1:	169 TNF:248
insulinoma -0.08661366 151 2.472e-04 9.327e-02 EHMT1:61 HSPD1:136 MRC1:144 KCNH4:153 ATF6	:183 YY1:266
Lymphoma, T-Cell, Cutaneous -0.07268804 213 2.681e-04 9.507e-02 BAX:84 TNFSF10:97 TNF:248 TP53:435 IL2:570	CD80:595
Rheumatoid Nodule -0.24732135 18 2.810e-04 9.507e-02 VCAM1:21 TLR9:231 TNF:248 MTR:443 SELE:47	'6 IL2:570
Tumor Progression -0.02711649 1730 2.773e-04 9.507e-02 CHL1:3 KDM5B:7 APOA1:12 VCAM1:21 KIF14:29	AKR1B1:43
Neurodegenerative Disorders -0.04176275 652 3.189e-04 1.009e-01 APOA1:12 BLMH:37 CXCL13:50 TRPM7:75 GDAP1	1:77 BAX:84
Seizures -0.03293590 1088 3.169e-04 1.009e-01 SCN9A:8 UGT8:17 PIGG:22 SEC24D:38 NSD2:6	2 CLU:88
HIV Infections -0.04191193 639 3.463e-04 1.062e-01 APOA1:12 VCAM1:21 SAMHD1:27 CXCL13:50 CYL	D:81 BAX:84
Other cataract -0.19795018 27 3.719e-04 1.106e-01 AKR1B1:43 GSR:536 IL18:605 MAP2K1:699 CRYBA4:	:742 GJA3:867
Presenile dementia -0.05842118 314 3.969e-04 1.145e-01 APOA1:12 VCAM1:21 BLMH:37 TRPM7:75 BAX:8	34 CLU:88
Pain, Postoperative -0.22165933 21 4.385e-04 1.197e-01 SCN9A:8 TNF:248 SCN11A:308 CRHR1:431 TRPV1:75	52 ABCB1:1103
Myocardial Ischemia -0.05318471 375 4.391e-04 1.197e-01 ANK2:2 APOA1:12 VCAM1:21 AKR1B1:43 HSPB1:96	BHLHE40:112
Cholecystolithiasis 0.12492887 65 5.011e-04 1.263e-01 ABCB4:155 MYO10:260 ABCB11:342 ABCC3:362 APOBEC	C1:519 ABCG5:659
Epilepsy -0.03190427 1082 5.022e-04 1.263e-01 ANK2:2 SCN9A:8 UGT8:17 PIGG:22 CAMSAP2:35	5 NSD2:62
Glioma -0.02564981 1779 5.019e-04 1.263e-01 CHL1:3 TJP1:14 VCAM1:21 SAMHD1:27 KIF14:29	AKR1B1:43
	:212 TNF:248

EnrichmentHsSymbolsFile2 Top pathways by non-permulation

Geneset	stat	num.genes	pval	p.adj	gene.vals
BLALOCK_ALZHEIMERS_DISEASE_DN	-0.04876459	1165	2.882e-08	1.870e-04	HERC2:1 CHL1:3 LRRN3:4 LTN1:19 PHTF1:20 UAP1:52
KIM_ALL_DISORDERS_CALB1_CORR_UP	-0.06425308	528	4.958e-07	1.608e-03	CHL1:3 CAMSAP2:35 AKR1B1:43 ATP1B1:85 SLC12A5:91 BHLHE40:112
WP_PRADERWILLI_AND_ANGELMAN_SYNDROME	-0.17705131	56	4.619e-06	7.492e-03	HERC2:1 ATP10A:31 TUBGCP5:98 UBE3A:156 GABRA5:284 TP53:435
DIAZ_CHRONIC_MYELOGENOUS_LEUKEMIA_UP	-0.03827447	1337	3.523e-06	7.492e-03	KDM5B:7 ZNF277:23 BLMH:37 URI1:49 MIS18A:109 ZNF281:148
NIKOLSKY_BREAST_CANCER_16P13_AMPLICON	0.13092581	100	6.159e-06	7.992e-03	EME2:4 C1QTNF8:125 PTX4:187 PGAP6:366 WFIKKN1:386 CRAMP1:435
NIKOLSKY_BREAST_CANCER_15Q26_AMPLICON	-0.27783636	20	1.698e-05	1.746e-02	ARRDC4:102 PCSK6:140 LRRK1:377 ALDH1A3:433 MEF2A:722 IGF1R:1039
REACTOME_POST_TRANSLATIONAL_PROTEIN_MODI	-0.03579824	1297	1.884e-05	1.746e-02	HERC2:1 ANK2:2 APOA1:12 CNTN3:13 ADAMTS6:15 PIGG:22
KIM_ALL_DISORDERS_OLIGODENDROCYTE_NUMBER	-0.04702367	704	2.397e-05	1.944e-02	CHL1:3 AKR1B1:43 PRR3:74 HSPD1:136 APBA2:170 OAT:234
REACTOME_INFECTIOUS_DISEASE	-0.04268928	834	3.239e-05	2.335e-02	TJP1:14 SEC24D:38 NUP133:42 ATP1B1:85 MRC1:144 SEH1L:172
WP_ALLOGRAFT_REJECTION	-0.14150168	71	3.775e-05	2.449e-02	CXCL13:50 TNF:248 LRRK2:407 CD86:499 IL2:570 CD80:595
REACTOME_ADAPTIVE_IMMUNE_SYSTEM	-0.04582322	668	5.954e-05	3.370e-02	HERC2:1 WWP1:9 LTN1:19 VCAM1:21 BLMH:37 SEC24D:38
REACTOME_RNA_POLYMERASE_II_TRANSCRIPTION	-0.03714319	1026	6.752e-05	3.370e-02	KDM5B:7 WWP1:9 TJP1:14 MOV10:24 E2F5:26 EHMT1:61
BORCZUK_MALIGNANT_MESOTHELIOMA_UP	-0.06739754	297	6.738e-05	3.370e-02	KDM5B:7 BLMH:37 SEC24D:38 OSMR:132 MFN1:294 HPRT1:382
NIKOLSKY_BREAST_CANCER_16Q24_AMPLICON	0.16890983	46	7.415e-05	3.436e-02	ANKRD11:6 PIEZO1:8 CTU2:16 CBFA2T3:53 GSE1:55 SNAI3:123
NIKOLSKY_BREAST_CANCER_8P12_P11_AMPLICON	0.15687032	52	9.153e-05	3.554e-02	RAB11FIP1:72 ANK1:116 STAR:226 ERLIN2:363 EIF4EBP1:617 CHRNA6:652
REACTOME_SIGNALING_BY_RECEPTOR_TYROSINE_	-0.05112369	503	9.311e-05	3.554e-02	WWP1:9 ATP6V0D2:66 BAX:84 HSPB1:96 COL6A3:128 PCSK6:140
SCHLOSSER_SERUM_RESPONSE_DN	-0.04553516	644	8.848e-05	3.554e-02	E2F5:26 SEC24D:38 TDRD7:99 PDS5B:121 LARP7:151 UBE3A:156
WP_NEUROINFLAMMATION_AND_GLUTAMATERGIC_S	-0.09523276	138	1.142e-04	3.881e-02	SLC38A5:162 SLC38A3:175 GRM2:209 TNF:248 GLUL:268 CAMK2D:319
WP_NETWORK_MAP_OF_SARSCOV2_SIGNALING_PAT	-0.08349681	180	1.142e-04	3.881e-02	APOA1:12 CXCL13:50 TNFSF10:97 FGG:110 SELP:130 TNF:248
WP_CONTROL_OF_IMMUNE_TOLERANCE_BY_VASOAC	-0.30717213	13	1.256e-04	3.881e-02	CD86:499 IL2:570 CD80:595 TGFB1:939 IFNG:1184 VIP:1244
FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_OK_VS_	-0.04997385	508	1.239e-04	3.881e-02	ANK2:2 WWP1:9 UGT8:17 LTN1:19 VCAM1:21 N4BP1:34
NIKOLSKY_BREAST_CANCER_8Q12_Q22_AMPLICON	-0.09907603	122	1.593e-04	4.699e-02	TMEM64:10 SLC26A7:32 OSGIN2:45 MMP16:48 GDAP1:77 RBM12B:127
BLANCO_MELO_BETA_INTERFERON_TREATED_BRON	0.08184309	174	2.000e-04	5.643e-02	PLXNB3:23 HROB:49 KRT78:62 A2ML1:166 EVPL:178 EME1:190
BRIDEAU_IMPRINTED_GENES	-0.14941386	51	2.241e-04	5.815e-02	CNTN3:13 ATP10A:31 CALCR:65 UBE3A:156 FRAT1:214 DDC:475
WP_PHOTODYNAMIC_THERAPYINDUCED_AP1_SURVI	-0.15248910	49	2.227e-04	5.815e-02	BAX:84 TNFSF10:97 CCNE1:154 TNF:248 TP53:435 IL2:570
MARTORIATI_MDM4_TARGETS_NEUROEPITHELIUM_	-0.08601226	149	2.950e-04	7.140e-02	VCAM1:21 CXCL13:50 GDAP1:77 LRRN1:115 MRC1:144 PLCXD2:237
REACTOME_CYTOKINE_SIGNALING_IN_IMMUNE_SY	-0.04272811	622	2.971e-04	7.140e-02	VCAM1:21 SAMHD1:27 N4BP1:34 NUP133:42 OSMR:132 TSLP:137
WP_NUCLEAR_RECEPTORS_IN_LIPID_METABOLISM	0.20007061	27	3.206e-04	7.428e-02	ABCB4:155 ABCB11:342 ABCC3:362 CYP8B1:602 ABCG5:659 VDR:796
CHIANG_LIVER_CANCER_SUBCLASS_INTERFERON_	-0.23099670	20	3.486e-04	7.800e-02	KCNT2:70 ISG15:447 CALCRL:495 TDO2:640 HPGD:819 NNMT:1112
BIOCARTA_NUCLEARRS_PATHWAY	0.19742965	27	3.844e-04	8.045e-02	ABCB4:155 ABCB11:342 ABCC3:362 CYP8B1:602 ABCG5:659 VDR:796
KEGG_CYTOKINE_CYTOKINE_RECEPTOR_INTERACT	-0.07171201	208	3.724e-04	8.045e-02	CXCL13:50 TNFSF10:97 OSMR:132 TSLP:137 IFNAR1:210 TNF:248
KOKKINAKIS_METHIONINE_DEPRIVATION_48HR_U	-0.09186879	122	4.629e-04	9.385e-02	BAX:84 HSPB1:96 TNFSF10:97 CCNE1:154 IGFBP3:250 IGFBP2:278
ROYLANCE_BREAST_CANCER_16Q_COPY_NUMBER_D	-0.21431356	22	5.021e-04	9.871e-02	NETO2:64 SHCBP1:195 ORC6:200 ITFG1:201 VPS35:220 PHKB:296
GRATIAS_RETINOBLASTOMA_16Q24	0.23553946	18	5.409e-04	1.009e-01	ANKRD11:6 USP10:48 KIAA0513:64 SPG7:180 MBTPS1:356 MEAK7:464
WP_GABA_RECEPTOR_SIGNALING	-0.17946893	31	5.443e-04	1.009e-01	GABRA5:284 GAD1:395 GABRB3:618 GPHN:1133 GABRD:1217 AP2A2:1449
REACTOME_DNA_DAMAGE_TELOMERE_STRESS_INDU	-0.13614717	53	6.089e-04	1.087e-01	CCNE1:154 NBN:364 TP53:435 H1-3:559 LMNB1:685 CDKN1B:721
REACTOME_MITOTIC_G1_PHASE_AND_G1_S_TRANS	-0.08243757	145	6.198e-04	1.087e-01	E2F5:26 CCNE1:154 RBL2:159 LYN:188 ORC6:200 RBBP4:585
REACTOME_TRANSPORT_OF_INORGANIC_CATIONS_	-0.09737341	102	6.850e-04	1.111e-01	SLC26A7:32 SLC12A5:91 SLC38A5:162 SLC38A3:175 SLC6A15:453 SLC43A2:48
DEACTOME CARRIAG CONDUCTION	0.00004.404	101	0.540 04	4 4 4 4 4 6 4	000104 0 470404 05 1/001144 400 00/00 400 000104 005 0001444 000

GO_Biological_Process_2023 Top pathways by non-permulation

6.518e-04 1.111e-01

6.842e-04 1.111e-01

121

-0.08981401

-0.04255026

SCN9A:8 ATP1B1:85 KCNJ14:193 RYR2:196 SCN2A:265 SCN11A:308

ANK2:2 CHL1:3 SCN9A:8 LHX9:59 COL6A3:128 APH1B:166

REACTOME_CARDIAC_CONDUCTION

REACTOME_NERVOUS_SYSTEM_DEVELOPMENT

Cacium Ion Import Across Plasma Membran 0.104-05902 3.10790-03 3.654-0-01 SCN9A-8 TRPM1:69 CLU-88 CACNAIS-T52 CACNAIS-259 SON2A-265 Immunoglobulin V(DJ Recombination (GO:00 0.44722575 5.534-0-4 3.654-0-01 PRROCC59 LE4-130 TCT-2132 NHELI-974 RRCC42291 NA 1.0790-03 3.654-0-01 Responsibility of the process of th						
Immunoglobalin V(D) Recombination (GO: 0. 44722875 5 5.3548-04 3.6548-01 PRIXOCSP LIGATION TOTALISM PRIES INCLUDES 19 1.04804289 41 1.2218-03 3.6548-01 CLDMs.218 SYM.1:227 SHANKS.698 NLCDMY.781 GPR88:963 INSR-1004 mRNA Stabilization (GO:0.004255) -0.15077888 47 3.5168-04 3.6548-01 CLDMs.218 SYM.1:227 SHANKS.698 NLCDMY.781 GPR88:963 INSR-1004 mRNA Stabilization (GO:0.004255) -0.15077888 47 3.5168-04 3.6548-01 CLDMs.218 SYM.1:227 SHANKS.698 NLCDMY.781 GPR88:963 INSR-1004 mRNA Stabilization (GO:0.0040500) -0.00670002 314 2.3398-04 3.6548-01 CLDMs.218 SYM.1:227 SHANKS.698 NLCDMY.781 (GR88.963 INSR-1004) -0.00670002 314 2.3398-04 3.6548-01 SCN9A.8 KEW157 TRPM7.75 CLDMS.218 MARDEV.227 INTR-248 Positive Regulation Of Gene Expression (Co.00400009) -0.00670002 314 2.3398-04 3.6548-01 TJP114 KIRDS.60 CD81.687 TINFSF4.935 RSADC.1599 Positive Regulation Of Typen Prosphor -0.00471555 132 1.168-03 3.6548-01 DENDITIS.5 CD82.498 LILOS CD81.687 TINFSF4.935 RSADC.1599 Positive Regulation Of Typen Prosphor -0.00471555 132 1.168-03 3.6548-01 TSLP.117 KIRDS INTR-248 GRANG.132 CD81.289 CD82.698 (L2570 TSLP.117 KIRDS INTR-248 GRANG.147 CD81.289 CD82.698 (L2570 TSLP.117 KIRDS INTR-248 GRANG.147 CD81.2898 CD82.698 CD82.698 (L2570 TSLP.117 KIRDS INTR-248 GRANG.147 CD81.2898 CD82.698 CD82.698 (L2570 TSLP.117 KIRDS INTR-248 GRANG.147 CD81.2898 CD82.698 C		stat	num.genes	pval	p.adj	
Learning (GO-0007612)	Calcium Ion Import Across Plasma Membran	-0.16450492	33	1.079e-03	3.654e-01	SCN9A:8 TRPM1:69 CLU:88 CACNA1B:157 CACNA1S:259 SCN2A:265
Laaming (GO:0007612)	Immunoglobulin V(D)J Recombination (GO:0	0.44722575	5	5.334e-04	3.654e-01	PRKDC:59 LIG4:130 TCF3:192 NHEJ1:674 XRCC4:3291 NA
MRNA Stabilization (GO:0048255)	Inorganic Cation Import Across Plasma Me	-0.10291417	96	5.022e-04	3.654e-01	SCN9A:8 TRPM1:69 ATP1B1:85 CLU:88 SLC12A5:91 CACNA1B:157
Mesial Ion Transport (GO:0030001) -0.08258457 156 3.840e-04 3.654e-01 SCN9A-8 KCNV1.57 TRPM7.75 CLU28 RAMP2-107 KCNA-113	Learning (GO:0007612)	-0.14604289	41	1.221e-03	3.654e-01	CLDN5:219 SYNJ1:227 SHANK3:698 NLGN4Y:781 GPR88:963 INSR:1004
Negative Regulation Of Gene Expression (mRNA Stabilization (GO:0048255)	-0.15077888	47	3.516e-04	3.654e-01	DHX9:388 DAZL:557 IREB2:560 ZAR1:578 NOCT:1026 TENT5D:1083
Positive Regulation Of Cell Population P	Metal Ion Transport (GO:0030001)	-0.08258457	156	3.840e-04	3.654e-01	SCN9A:8 KCNV1:57 TRPM7:75 CLU:88 RAMP2:107 KCNA4:113
Positive Regulation Of Type 2 Immune Res -0.29560555 11 6.871e-04 3.654e-01 TSLP:137 LYN:188 TNF:248 GH1:328 CSR-2398 Robustion of Transmembrane Transport (G -0.08171555 132 1.216e-03 3.654e-01 TSLP:137 LYN:188 TNF:248 GH1:328 CSR-2360 IL2:570 Potassium fon Transmembrane Transport (G -0.08171555 132 1.216e-03 3.654e-01 TSLP:137 LYN:188 TNF:248 GH1:328 CSR-2360 IL2:570 Robustion of Michordorial mRNA Stabili 0.2873628 18 4.939e-04 3.654e-01 FTSJ:330 NSUB:71 NOP2:179 EMG1:494 ZCCHG4:889 FDXACB1:1384 Regulation Of Michordorial mRNA Stabili 0.38314176 6 1.153e-03 3.654e-01 FTSJ:330 NSUB:71 NOP2:179 EMG1:494 ZCCHG4:889 FDXACB1:1384 Regulation Of Protein Phosphorylation (G -0.0618885 246 9.579e-04 3.654e-01 ROPNIB:92 ROPNIB:93 RPSPI:96 LYN:188 MYADM:222 TNF:248 Regulation Of Protein Phosphorylation (G -0.0618885 4 9.676e-04 3.654e-01 RRM:209 PLPPR4:211 TSHZ3:228 TNF:246 CDH2:363 ERRE2407 Somatic Recombination Of Immunoglobulin 0.33046262 8 1.039e-03 3.654e-01 RRM:209 PLPPR4:211 TSHZ3:228 TNF:246 CDH2:363 ERRE2407 Somatic Recombination Of Immunoglobulin 0.33046262 8 1.269e-03 3.654e-01 RRM:209 PLPPR4:211 TSHZ3:228 TNF:248 CDH2:363 ERRE2407 Somatic Recombination Of Immunoglobulin 0.11854464 77 4.735e-04 3.654e-01 SLC38A5:162 SLC38A3:175 SLC38A2:566 ABCC5:589 ABCC6:589 ABCC6:	Negative Regulation Of Gene Expression (-0.06070092	314	2.339e-04	3.654e-01	N4BP1:34 ZNF281:148 RBL2:159 CLDN5:219 MYADM:222 TNF:248
Positive Regulation Of Tyrosine Phosphor Polassium Ion Transmembrane Transport (G -0.08171555 132 1.216e-03 3.654e-01 KCNV1:75 KCNT2:70 ATPIB1:85 SLC12A5:91 KCNA4:113 KCNH4:153 (RNA Methylation (GO:0031167) 0.23723628 18 4.393e-04 3.654e-01 FSL33:30 NSUN5:121 ATPIB1:85 SLC12A5:91 KCNA4:113 KCNH4:153 (RNA Methylation (GO:0031167) 0.23723628 18 4.393e-04 3.654e-01 FSL33:30 NSUN5:121 ATPIB1:85 SLC12A5:91 KCNA4:113 KCNH4:153 (Regulation Of Mitochondrial mRNA Stabili 0.38314176 6 1.153e-03 3.654e-01 FSL33:30 NSUN5:121 ATPIB1:85 SLC12A5:91 FSL7A51705:148 FASTKD1:565 PDE12:769 TBRG4:1284 FASTKD2:8642.5 Regulation Of Protein Phosphorylation (G -0.06138855 246 9.579e-04 3.654e-01 ROPNIB:92 ROPNIB:92 ROPNIB:93 HSPB1:96 LVN:188 MYADAV2Z2 TNF:248 CDH2:363 LRRK2-407 Somatic Recombination Of Immunoglobulin 0.33046262 8 1.209e-03 3.654e-01 PRKDC:59 LG4:130 TCF3:192 MSH3:488 NHEJ1:674 XRCC4:3291 Transport Across Blood-Brain Barrier (GO -0.11584464 77 4.735e-04 3.654e-01 FSL3345-162 SLC3345-3175 SLC3342-256 ABCC5:589 ABCC6:565 CD36:692 Vascular Transport (GO:0010232) -0.1185398 75 8.213e-04 3.654e-01 SLA345-162 SLC3345-3175 SLC3342-256 ABCC5:589 ABCC5:589 ABCC5:589 ABCC5:589 ABCC5:589 ABCC5:589 ABCC5:589 ABCC5:589 ABCC3:561 ATPRA1:735 CO3465-01 SLC3345-162 SLC3345-175 SLC3342-256 ABCC5:589 ABCC5:589 ABCC5:589 ABCC5:589 ABCC5:589 ABCC5:589 ABCC3:561 ATPRA1:735 CD345-01 ABCC1-1674-03 A192e-01 CALCR:55 DR2:37 LYN:188 TNF:248 GH1:328 NSN:384 CNN:12:488 TND:2640 CD345-184 CNN:12:488 TND:2640 CNN:12:488 CNN:12:488 TND:2640 CNN:12:488	Positive Regulation Of Cell Population P	-0.04805869	434	6.546e-04	3.654e-01	TJP1:14 KIF14:29 AKR1B1:43 DDR2:87 OSMR:132 TSLP:137
Potassium Ion Transmembrane Transport (G	Positive Regulation Of Type 2 Immune Res	-0.29560955	11	6.871e-04	3.654e-01	DENND1B:5 CD86:499 IL18:605 CD81:667 TNFSF4:935 RSAD2:1599
Regulation Of Mitochondrial mRNA Stabili	Positive Regulation Of Tyrosine Phosphor	-0.13542404	49	1.048e-03	3.654e-01	TSLP:137 LYN:188 TNF:248 GH1:328 CSH2:360 IL2:570
Regulation Of Mitochondrial mRNA Stabili 0.38314176 6 1.153e-03 3.654e-01 FASTKD3:52 FASTKD5:148 FASTKD1:585 PDE12:769 TBRG4:1284 FASTKD2:8642.5 Regulation Of Protein Phosphorylation (G -0.0613885 246 9.579e-04 3.654e-01 ROPNIB:92 ROPNIB:93 HSPB1:96 LYN:188 MYADM:222 THS:248 Regulation Of Synaptic Transmission, Glu -0.12981383 54 9.579e-04 3.654e-01 ROPNIB:92 ROPNIB:93 HSPB1:96 LYN:188 MYADM:222 THS:248 REGULATION OF Synaptic Transmission, Glu -0.12981383 54 1.209e-03 3.654e-01 ROPNIB:92 ROPNIB:93 HSPB1:96 LYN:188 MYADM:222 TMS:248 CDH2:363 LARKE:407 ROPNIB:92 ROPNIB:93 HSPB1:96 LYN:188 MYADM:222 TMS:248 CDH2:363 LARKE:407 ROPNIB:92 ROPNIB:93 HSPB1:96 LYN:188 MYADM:222 TMS:248 CDH2:363 LARKE:407 ROPNIB:92 ROPNIB:93 HSPB1:96 LYN:188 HYADM:222 HSPB1:96 LYN:188 HYADM:232 HSPB1:96 LYN:188 HYADM:232 HSPB1:96 LYN:188 HYADM:246 ROPNIB:92 ROPNIB:93 ROPNIB:94 ROPNIB:95 HSPB1:96 LYN:188 HYADM:248 ROPNIB:96 HSPB1:96 LYN:188 HYADM:248 ROPNIB:96 HSPB1:96 LYN:188 HYADM:248 ROPNIB:96 LYN:188 HYADM:248 ROPNIB:96 HSPB1:96 LYN:188 HYADM:248 ROPNIB:96 HSPB1:97 LYN:188 HYADM:248 ROPNIB:97 LYN:188 HYADM:248 ROPNIB:98 HYADM:248 ROPNIB:97 LYN:188 HYADM:248 ROPNIB:97 LYN:188 HYADM:248 ROPNIB:97 LYN:188 HYADM:248 ROPNIB:97 LYN:188 HYADM:	Potassium Ion Transmembrane Transport (G	-0.08171555	132	1.216e-03	3.654e-01	KCNV1:57 KCNT2:70 ATP1B1:85 SLC12A5:91 KCNA4:113 KCNH4:153
Regulation Of Protein Phosphorylation (G	rRNA Methylation (GO:0031167)	0.23723628	18	4.939e-04	3.654e-01	FTSJ3:30 NSUN5:121 NOP2:179 EMG1:494 ZCCHC4:889 FDXACB1:1384
Regulation Of Synaptic Transmission, Glu	Regulation Of Mitochondrial mRNA Stabili	0.38314176	6	1.153e-03	3.654e-01	FASTKD3:52 FASTKD5:148 FASTKD1:585 PDE12:769 TBRG4:1284 FASTKD2:8642.5
Somatic Recombination Of Immunoglobulin 0.33046262 8 1.209e-03 3.654e-01 PRKDC:59 LIG4:130 TCF3:192 MSH3:488 NHEJ1:674 XRCC4:3291	Regulation Of Protein Phosphorylation (G	-0.06138885	246	9.579e-04	3.654e-01	ROPN1B:92 ROPN1:93 HSPB1:96 LYN:188 MYADM:222 TNF:248
Transport Across Blood-Brain Barrier (GO	Regulation Of Synaptic Transmission, Glu	-0.12981383	54	9.761e-04	3.654e-01	GRM2:209 PLPPR4:211 TSHZ3:228 TNF:248 CDH2:363 LRRK2:407
Vascular Transport (GO:0010232) -0.11185398 75 8.213e-04 3.654e-01 SLC38A3:175 SLC38A3:175 SLC38A2:556 ABCC5:589 ABCC9:651 ATP8A1:735	Somatic Recombination Of Immunoglobulin	0.33046262	8	1.209e-03	3.654e-01	PRKDC:59 LIG4:130 TCF3:192 MSH3:488 NHEJ1:674 XRCC4:3291
Positive Regulation Of Protein Phosphory	Transport Across Blood-Brain Barrier (GO	-0.11534464	77	4.735e-04	3.654e-01	SLC38A5:162 SLC38A3:175 SLC38A2:556 ABCC5:589 ABCC9:651 CD36:692
Protein Homotetramerization (GC:0051289) -0.13061809 50 1.408e-03 3.905e-01 SAMHD1:27 CLU:88 HPRT1:382 ALDH1A3:433 KCNJ12:468 TDO2:640 Cobalamin Transport (GC:00015889) 0.36970538 6 1.712e-03 4.192e-01 CBLIF:103 CUBN:304 TCN1:772 ABCD4:1307 ABCD1:1696 TCN2:8642.5 Positive Regulation Of Cellular Componen -0.09063755 101 1.674e-03 4.192e-01 ATP10A:31 AKR1B1:43 BAX:84 CLU:88 TNF:248 CLIP3:546 Regulation Of Gene Expression (GO:001046 -0.03032264 948 1.870e-03 4.380e-01 ANK2:2 AKR1B1:43 ZNF131:46 BTN3A3:60 NSD2:62 CALCR:65 Protein Tetramerization (GC:0051262) -0.10886820 67 2.080e-03 4.514e-01 SAMHD1:27 CLU:88 HPRT1:382 ALDH1A3:433 KCNJ12:468 TDO2:640 Regulation Of Neuron Death (GC:00051262) -0.10886820 67 2.080e-03 4.514e-01 SAMHD1:27 CLU:88 HPRT1:382 ALDH1A3:433 KCNJ12:468 TDO2:640 Regulation Of Neuron Death (GC:00051262) -0.10886820 67 2.080e-03 4.514e-01 SAMHD1:27 CLU:88 HPRT1:382 ALDH1A3:433 KCNJ12:468 TDO2:640 Regulation Of Neuron Death (GC:000124) -0.12058330 54 2.192e-03 4.514e-01 KIF14:29 CLU:88 VPS35:220 FAIM2:372 LRRK2:407 CSF1:490 Regulation Of Neitric Oxide Metabolic Pro -0.35995508 6 2.262e-03 4.514e-01 KIF14:29 CLU:88 VPS35:220 FAIM2:372 LRRK2:407 CSF1:490 Regulation Of Meiotic Recombination Inte 0.23338508 14 2.591e-03 4.813e-01 CTU:16 ARS2:160 THADA:215 ALKBH8:294 KTIT2:373 TRMT1:899 Right Regulation Of Amide Metabolic Pro -0.09253910 87 2.886e-03 4.993e-01 MOV10:24 CNOT6:1287 TNRC6C:1300 TNRC6A:1629 AJUBA:1655 AGO2:1690 Negative Regulation Of Amide Metabolic Pro -0.09253910 87 2.886e-03 4.993e-01 CLU:88 EIF2AK2:470 CPEB3:577 ZAR1:578 BIN1:763 EIF2AK3:1078 Positive Regulation Of Cellular Process -0.09350483 527 2.724e-03 4.993e-01 AKR1B1:43 EIF2AK2:470 CPEB3:577 ZAR1:578 TGFB1:939 EIF2AK3:1078 Regulation Of Cellular Process -0.0339927 696 3.099e-03 4.993e-01 TJP1:14 KIF14:29 AKR1B1:43 CUI:88 PDS5B:121 OSMR:132 CRD-mediated mRNA Stabilization (GC:00070 -0.04427604 367 3.790e-03 5.287e-01 CXCL13:50 CLU:88 BINP3:133 LYN:188 PDK4:236 CAMK2D:319 Inorganic Cation Transmembrane Transport -0.05099025 276 3.	Vascular Transport (GO:0010232)	-0.11185398	75	8.213e-04	3.654e-01	SLC38A5:162 SLC38A3:175 SLC38A2:556 ABCC5:589 ABCC9:651 ATP8A1:735
Cobalamin Transport (GO:0015889) 0.36970538 6 1.712e-03 4.192e-01 CBLIF:103 CUBN:304 TCN1:772 ABCD4:1307 ABCD1:1696 TCN2:8642.5 Positive Regulation Of Cellular Componen -0.09063755 101 1.674e-03 4.192e-01 ATP10A:31 AKR1B1:43 BAX:84 CLU:88 TNF:248 CLIP3:546 Regulation Of Gene Expression (GO:001046 -0.03032264 948 1.870e-03 4.380e-01 ANK2:2 AKR1B1:43 DAX:84 CLU:88 TNF:248 CLIP3:546 Protein Tetramerization (GO:0051262) -0.10886820 67 2.080e-03 4.514e-01 SAMHD1:27 CLU:88 PPS35:220 FAIM2:372 LRRK2:407 CSF1:490 Regulation Of Neuron Death (GO:1901214) -0.12058330 54 2.192e-03 4.514e-01 KIF14:29 CLU:88 VPS35:220 FAIM2:372 LRRK2:407 CSF1:490 Regulation Of Nitric Oxide Metabolic Pro -0.35995508 6 2.262e-03 4.514e-01 NOS1AP:155 CX3CR1:900 SELENOS:1267 RAC1:1559 JAK2:2082 TMEM106A:7502.5 tRNA Modification (GO:0006400) 0.10914401 66 2.188e-03 4.514e-01 CTU2:16 AARS2:160 THADA:215 ALKBH8:294 KT112:373 TRMT1:899 Pint1:1350 miRNA-mediated Gene Silencing (GO:003519 -0.16785965 26 3.058e-03 4.993e-01 MOV10:24 CNOT6:1287 TNRC6C:1300 TNRC6A:1629 AJUBA:1655 AGO2:1690 Negative Regulation Of Macromolecule Bio -0.09110650 90 2.852e-03 4.993e-01 AKR181:43 EIF2AK2:470 CPEB3:577 ZAR1:578 BIN1:763 EIF2AK3:1078 Positive Regulation Of Cellular Process -0.03850483 527 2.724e-03 4.993e-01 TJP1:14 KIF14:29 AKR181:43 OSMR:132 TSLP:137 P4HB:185 Regulation Of Cellular Process -0.03850483 527 2.724e-03 4.993e-01 TJP1:14 KIF14:29 AKR181:43 GF2BP3:1591 SYNCRIP:1697 IGF2BP2:1798 Cellular Response To Oxygen-Containing C -0.04427604 367 3.790e-03 5.287e-01 DHX9:388 HINRNPU:1441 PAIP1:1453 IGF2BP3:1591 SYNCRIP:1697 IGF2BP2:1798 Mitochondrial Transmembrane Transport -0.05099025 276 3.707e-03 5.287e-01 GATB:36 FASTKD1:57 TRPM1:69 TRPM7:75 ATP181:85 Mitochondrial Transmembrane Transport -0.05161133 273 3.480e-03 5.287e-01 GATB:36 GFMZ:181 PTCD3:198 TNFRT:75 ATP181:85 Mitochondrial Transmembrane Transpor -0.05161133 273 3.480e-03 5.287e-01 GATB:36 GFMZ:181 PTCD3:198 TRPM7:75 ATP181:85	Positive Regulation Of Protein Phosphory	-0.04956364	354	1.449e-03	3.905e-01	CALCR:65 DDR2:87 LYN:188 TNF:248 GH1:328 NBN:364
Positive Regulation Of Cellular Componen Regulation Of Gene Expression (GO:001046 Regulation Of Gene Expression (GO:001046 Protein Tetramerization (GO:0051262) -0.10886820 67 2.080e-03 4.514e-01 SAMHD1:27 CLU:88 HPRT1:382 ALDH1A3:433 KCNJ12:468 TDO2:640 Regulation Of Neuron Death (GO:1901214) -0.12058330 54 2.192e-03 4.514e-01 Regulation Of Nitric Oxide Metabolic Pro -0.35995508 6 2.262e-03 4.514e-01 NOS1AP:155 CX3CR1:900 SELENOS:1267 RAC1:1559 JAK2:2082 TMEM106A:7502.5 tRNA Modification (GO:0006400) 0.10914401 66 2.188e-03 4.514e-01 CTU2:16 AARS2:160 THADA:215 ALKBHB:294 KTI12:373 TRMT1:899 Resolution Of Meiotic Recombination Inte 0.23338508 14 2.501e-03 4.813e-01 EME2:4 SLX4:177 EME1:190 MEIOB:681 MUS81:809 HFM1:1350 miRNA-mediated Gene Silencing (GO:003519 -0.16785965 26 3.058e-03 4.993e-01 Negative Regulation Of Amide Metabolic P Positive Regulation Of Cellular Process -0.03850483 527 2.724e-03 4.993e-01 TJP1:14 KIF14:29 AKR1B1:43 DAX:84 CLU:88 TNF:248 CLIP3:546 ANK2:2 AKR1B1:43 ZNF131:46 BTN3A3:60 NSD2:62 CALCR:65 ANHD1:248 HPRT1:382 ALDH1A3:433 KCNJ12:468 TDO2:640 ANK2:2 AKR1B1:43 ZNF131:46 BTN3A3:60 NSD2:62 CALCR:65 AMHD1:27 CLU:88 HPRT1:382 ALDH1A3:433 KCNJ12:468 TDO2:640 KIF14:29 CLU:88 VPS35:220 FAIM2:372 LRRK2:407 CSF1:490 AKS14:29 CLU:88 LPRT1:359 AKR2:2 AKR1B1:43 ZNF131:46 BTN3A3:60 NSD2:62 CALCR:65 AKR1B1:43 ZNF131:46 BTN3A3:60 NSD2:62 CALCR:65 AKH1B1:43 ZNF131:46 BTN3A3:40 NSD2:62 CALCR:65 AKH1B1:43 ZNF131:46 BTN3A3:40 NSD2:62 CALCR:65 AKH1B1:43 ZNF131:46 BTN3A3:40 NSD2:62 CALCR:65 AKH1B1:43 ZNF131:46 DTN3A3:60 NSD2:62 CALCR:65 AKH1B1:43 ZNF131:46 DTN3A3:40 NSD2:62 CALCR:65 AKH1B1:43 ZNF131:46 DTN3A3:40 NSD2:62 CALCR:65 AKH1B1:	Protein Homotetramerization (GO:0051289)	-0.13061809	50	1.408e-03	3.905e-01	SAMHD1:27 CLU:88 HPRT1:382 ALDH1A3:433 KCNJ12:468 TDO2:640
Regulation Of Gene Expression (GO:001046	Cobalamin Transport (GO:0015889)	0.36970538	6	1.712e-03	4.192e-01	CBLIF:103 CUBN:304 TCN1:772 ABCD4:1307 ABCD1:1696 TCN2:8642.5
Protein Tetramerization (GO:0051262)	Positive Regulation Of Cellular Componen	-0.09063755	101	1.674e-03	4.192e-01	ATP10A:31 AKR1B1:43 BAX:84 CLU:88 TNF:248 CLIP3:546
Regulation Of Neuron Death (GO:1901214) -0.12058330 54 2.192e-03 4.514e-01 KIF14:29 CLU:88 VPS35:220 FAIM2:372 LRRK2:407 CSF1:490 Regulation Of Nitric Oxide Metabolic Pro -0.35995508 6 2.262e-03 4.514e-01 NOS1AP:155 CX3CR1:900 SELENOS:1267 RAC1:1559 JAK2:2082 TMEM106A:7502.5 tRNA Modification (GO:0006400) 0.10914401 66 2.188e-03 4.514e-01 CTU2:16 AARS2:160 THADA:215 ALKBH8:294 KTI12:373 TRMT1:899 Resolution Of Meiotic Recombination Inte 0.23338508 14 2.501e-03 4.813e-01 EME2:4 SLX4:177 EME1:190 MEIOB:681 MUS81:809 HFM1:1350 miRNA-mediated Gene Silencing (GO:003619 -0.16785965 26 3.058e-03 4.993e-01 MOV10:24 CNOT6:1287 TNRC6C:1300 TNRC6A:1629 AJUBA:1655 AGO2:1690 Negative Regulation Of Amide Metabolic P -0.09253910 87 2.886e-03 4.993e-01 CLU:88 EIF2AK2:470 CPEB3:577 ZAR1:578 BIN1:763 EIF2AK3:1078 Positive Regulation Of Cellular Process -0.09110650 90 2.852e-03 4.993e-01 AKR1B1:43 EIF2AK2:470 CPEB3:577 ZAR1:578 TGFB1:939 EIF2AK3:1078 Regulation Of Cell Population Proliferat -0.03339827 696 3.093e-01 TJP1:14 KIF14:29 AKR1B1:43 OSMR:132 TSLP:137 P4HB:185 CRD-m	Regulation Of Gene Expression (GO:001046	-0.03032264	948	1.870e-03	4.380e-01	ANK2:2 AKR1B1:43 ZNF131:46 BTN3A3:60 NSD2:62 CALCR:65
Regulation Of Nitric Oxide Metabolic Pro	Protein Tetramerization (GO:0051262)	-0.10886820	67	2.080e-03	4.514e-01	SAMHD1:27 CLU:88 HPRT1:382 ALDH1A3:433 KCNJ12:468 TDO2:640
tRNA Modification (GO:0006400) 0.10914401 66 2.188e-03 4.514e-01 CTU2:16 AARS2:160 THADA:215 ALKBH8:294 KTI12:373 TRMT1:899 Resolution Of Meiotic Recombination Inte 0.23338508 14 2.501e-03 4.813e-01 EME2:4 SLX4:177 EME1:190 MEIOB:681 MUS81:809 HFM1:1350 miRNA-mediated Gene Silencing (GO:003519 -0.16785965 26 3.058e-03 4.993e-01 MOV10:24 CNOT6:1287 TNRC6C:1300 TNRC6A:1629 AJUBA:1655 AGO2:1690 Negative Regulation Of Amide Metabolic P -0.09253910 87 2.886e-03 4.993e-01 CLU:88 EIF2AK2:470 CPEB3:577 ZAR1:578 BIN1:763 EIF2AK3:1078 Negative Regulation Of Macromolecule Bio -0.09110650 90 2.852e-03 4.993e-01 AKR1B1:43 EIF2AK2:470 CPEB3:577 ZAR1:578 TGFB1:939 EIF2AK3:1078 Positive Regulation Of Cellular Process -0.03850483 527 2.724e-03 4.993e-01 TJP1:14 KIF14:29 AKR1B1:43 OSMR:132 TSLP:137 P4HB:185 Regulation Of Cell Population Proliferat -0.03339827 696 3.009e-03 4.993e-01 TJP1:14 KIF14:29 AKR1B1:43 CLU:88 PDS5B:121 OSMR:132 CRD-mediated mRNA Stabilization (GO:0070 -0.26064547 10 4.317e-03 5.287e-01 DHX9:388 HNRNPU:1441 PAIP1:1453 IGF2BP3:1591 SYNCRIP:1697 IGF2BP2:1798	Regulation Of Neuron Death (GO:1901214)	-0.12058330	54	2.192e-03	4.514e-01	KIF14:29 CLU:88 VPS35:220 FAIM2:372 LRRK2:407 CSF1:490
Resolution Of Meiotic Recombination Inte 0.23338508 14 2.501e-03 4.813e-01 EME2:4 SLX4:177 EME1:190 MEIOB:681 MUS81:809 HFM1:1350 miRNA-mediated Gene Silencing (GO:003519 -0.16785965 26 3.058e-03 4.993e-01 MOV10:24 CNOT6:1287 TNRC6C:1300 TNRC6A:1629 AJUBA:1655 AGO2:1690 Negative Regulation Of Amide Metabolic P -0.09253910 87 2.886e-03 4.993e-01 CLU:88 EIF2AK2:470 CPEB3:577 ZAR1:578 BIN1:763 EIF2AK3:1078 Negative Regulation Of Macromolecule Bio -0.09110650 90 2.852e-03 4.993e-01 AKR1B1:43 EIF2AK2:470 CPEB3:577 ZAR1:578 TGFB1:939 EIF2AK3:1078 Positive Regulation Of Cellular Process -0.03850483 527 2.724e-03 4.993e-01 TJP1:14 KIF14:29 AKR1B1:43 OSMR:132 TSLP:137 P4HB:185 Regulation Of Cell Population Proliferat -0.03339827 696 3.009e-03 4.993e-01 TJP1:14 KIF14:29 AKR1B1:43 CLU:88 PDS5B:121 OSMR:132 CRD-mediated mRNA Stabilization (GO:0070 -0.26064547 10 4.317e-03 5.287e-01 DHX9:388 HNRNPU:1441 PAIP1:1453 IGF2BP3:1591 SYNCRIP:1697 IGF2BP2:1798 Cellular Response To Oxygen-Containing C -0.04427604 367 3.790e-03 5.287e-01 CXCL13:50 CLU:88 BRINP3:133 LYN:188 PDK4:236 CAMK2D:319 Inorganic Cation Transmembrane Transport -0.05099025 276 3.707e-03 5.287e-01 GATB:36 FASTKD3:52 FASTKD5:148 GFM2:181 PTCD3:198 FASTKD1:585 Mitochondrial Gene Expression (GO:014005 0.08338551 100 4.015e-03 5.287e-01 GATB:36 GFM2:181 PTCD3:198 MTRF1:880 DAP3:970 TSFM:1067 Monoatomic Cation Transmembrane Transpor -0.05161133 273 3.480e-03 5.287e-01 SCN9A:8 CNGB3:30 KCNV1:57 TRPM1:69 TRPM7:75 ATP1B1:85	Regulation Of Nitric Oxide Metabolic Pro	-0.35995508	6	2.262e-03	4.514e-01	NOS1AP:155 CX3CR1:900 SELENOS:1267 RAC1:1559 JAK2:2082 TMEM106A:7502.5
miRNA-mediated Gene Silencing (GO:003519 -0.16785965 26 3.058e-03 4.993e-01 MOV10:24 CNOT6:1287 TNRC6C:1300 TNRC6A:1629 AJUBA:1655 AGO2:1690 Negative Regulation Of Amide Metabolic P -0.09253910 87 2.886e-03 4.993e-01 CLU:88 EIF2AK2:470 CPEB3:577 ZAR1:578 BIN1:763 EIF2AK3:1078 Negative Regulation Of Macromolecule Bio -0.09110650 90 2.852e-03 4.993e-01 AKR1B1:43 EIF2AK2:470 CPEB3:577 ZAR1:578 TGFB1:939 EIF2AK3:1078 Positive Regulation Of Cellular Process -0.03850483 527 2.724e-03 4.993e-01 TJP1:14 KIF14:29 AKR1B1:43 OSMR:132 TSLP:137 P4HB:185 Regulation Of Cell Population Proliferat -0.03339827 696 3.009e-03 4.993e-01 TJP1:14 KIF14:29 AKR1B1:43 OSMR:132 TSLP:137 P4HB:185 CRD-mediated mRNA Stabilization (GO:0070 -0.26064547 10 4.317e-03 5.287e-01 DHX9:388 HNRNPU:1441 PAIP1:1453 IGF2BP3:1591 SYNCRIP:1697 IGF2BP2:1798 Cellular Response To Oxygen-Containing C -0.04427604 367 3.790e-03 5.287e-01 CXCL13:50 CLU:88 BRINP3:133 LYN:188 PDK4:236 CAMK2D:319 Inorganic Cation Transmembrane Transport -0.05099025 276 3.707e-03 5.287e-01 GATB:36 FASTKD3:52 FASTKD5:148 GFM2:181 PTCD3:198 FASTKD	tRNA Modification (GO:0006400)	0.10914401	66	2.188e-03	4.514e-01	CTU2:16 AARS2:160 THADA:215 ALKBH8:294 KTI12:373 TRMT1:899
Negative Regulation Of Amide Metabolic P -0.09253910 87 2.886e-03 4.993e-01 CLU:88 EIF2AK2:470 CPEB3:577 ZAR1:578 BIN1:763 EIF2AK3:1078 Negative Regulation Of Macromolecule Bio -0.09110650 90 2.852e-03 4.993e-01 AKR1B1:43 EIF2AK2:470 CPEB3:577 ZAR1:578 TGFB1:939 EIF2AK3:1078 Positive Regulation Of Cellular Process -0.03850483 527 2.724e-03 4.993e-01 TJP1:14 KIF14:29 AKR1B1:43 OSMR:132 TSLP:137 P4HB:185 Regulation Of Cell Population Proliferat -0.03339827 696 3.009e-03 4.993e-01 TJP1:14 KIF14:29 AKR1B1:43 CLU:88 PDS5B:121 OSMR:132 CRD-mediated mRNA Stabilization (GO:0070 -0.26064547 10 4.317e-03 5.287e-01 DHX9:388 HNRNPU:1441 PAIP1:1453 IGF2BP3:1591 SYNCRIP:1697 IGF2BP2:1798 Cellular Response To Oxygen-Containing C -0.04427604 367 3.790e-03 5.287e-01 CXCL13:50 CLU:88 BRINP3:133 LYN:188 PDK4:236 CAMK2D:319 Inorganic Cation Transmembrane Transport -0.05099025 276 3.707e-03 5.287e-01 SCN9A:8 KCNV1:57 TRPM1:69 TRPM7:75 ATP1B1:85 CLU:88 Mitochondrial Gene Expression (GO:014005 0.08338551 100 4.015e-03 5.287e-01 GATB:36 GFM2:181 PTCD3:198 MTRF1:880 DAP3:970 TSFM:1067	Resolution Of Meiotic Recombination Inte	0.23338508	14	2.501e-03	4.813e-01	EME2:4 SLX4:177 EME1:190 MEIOB:681 MUS81:809 HFM1:1350
Negative Regulation Of Macromolecule Bio -0.09110650 90 2.852e-03 4.993e-01 AKR1B1:43 EIF2AK2:470 CPEB3:577 ZAR1:578 TGFB1:939 EIF2AK3:1078 Positive Regulation Of Cellular Process -0.03850483 527 2.724e-03 4.993e-01 TJP1:14 KIF14:29 AKR1B1:43 OSMR:132 TSLP:137 P4HB:185 Regulation Of Cell Population Proliferat -0.03339827 696 3.009e-03 4.993e-01 TJP1:14 KIF14:29 AKR1B1:43 CLU:88 PDS5B:121 OSMR:132 CRD-mediated mRNA Stabilization (GO:0070 -0.26064547 10 4.317e-03 5.287e-01 DHX9:388 HNRNPU:1441 PAIP1:1453 IGF2BP3:1591 SYNCRIP:1697 IGF2BP2:1798 Cellular Response To Oxygen-Containing C -0.04427604 367 3.790e-03 5.287e-01 CXCL13:50 CLU:88 BRINP3:133 LYN:188 PDK4:236 CAMK2D:319 Inorganic Cation Transmembrane Transport -0.05099025 276 3.707e-03 5.287e-01 SCN9A:8 KCNV1:57 TRPM1:69 TRPM7:75 ATP1B1:85 CLU:88 Mitochondrial Gene Expression (GO:014005 0.08338551 100 4.015e-03 5.287e-01 GATB:36 FASTKD3:52 FASTKD5:148 GFM2:181 PTCD3:198 FASTKD1:585 Mitochondrial Translation (GO:0032543) 0.08545160 96 3.863e-03 5.287e-01 GATB:36 GFM2:181 PTCD3:198 MTRF1:880 DAP3:970 TSFM:1067	miRNA-mediated Gene Silencing (GO:003519	-0.16785965	26	3.058e-03	4.993e-01	MOV10:24 CNOT6:1287 TNRC6C:1300 TNRC6A:1629 AJUBA:1655 AGO2:1690
Positive Regulation Of Cellular Process	Negative Regulation Of Amide Metabolic P	-0.09253910	87	2.886e-03	4.993e-01	CLU:88 EIF2AK2:470 CPEB3:577 ZAR1:578 BIN1:763 EIF2AK3:1078
Regulation Of Cell Population Proliferat -0.03339827 696 3.009e-03 4.993e-01 TJP1:14 KIF14:29 AKR1B1:43 CLU:88 PDS5B:121 OSMR:132 CRD-mediated mRNA Stabilization (GO:0070 -0.26064547 10 4.317e-03 5.287e-01 DHX9:388 HNRNPU:1441 PAIP1:1453 IGF2BP3:1591 SYNCRIP:1697 IGF2BP2:1798 Cellular Response To Oxygen-Containing C -0.04427604 367 3.790e-03 5.287e-01 CXCL13:50 CLU:88 BRINP3:133 LYN:188 PDK4:236 CAMK2D:319 Inorganic Cation Transmembrane Transport -0.05099025 276 3.707e-03 5.287e-01 SCN9A:8 KCNV1:57 TRPM1:69 TRPM7:75 ATP1B1:85 CLU:88 Mitochondrial Gene Expression (GO:014005 0.08338551 100 4.015e-03 5.287e-01 GATB:36 FASTKD3:52 FASTKD5:148 GFM2:181 PTCD3:198 MTRF1:880 DAP3:970 TSFM:1067 Monoatomic Cation Transmembrane Transpor -0.05161133 273 3.480e-03 5.287e-01 SCN9A:8 CNGB3:30 KCNV1:57 TRPM1:69 TRPM7:75 ATP1B1:85	Negative Regulation Of Macromolecule Bio	-0.09110650	90	2.852e-03	4.993e-01	AKR1B1:43 EIF2AK2:470 CPEB3:577 ZAR1:578 TGFB1:939 EIF2AK3:1078
CRD-mediated mRNA Stabilization (GO:0070	Positive Regulation Of Cellular Process	-0.03850483	527	2.724e-03	4.993e-01	TJP1:14 KIF14:29 AKR1B1:43 OSMR:132 TSLP:137 P4HB:185
Cellular Response To Oxygen-Containing C -0.04427604 367 3.790e-03 5.287e-01 CXCL13:50 CLU:88 BRINP3:133 LYN:188 PDK4:236 CAMK2D:319 Inorganic Cation Transmembrane Transport -0.05099025 276 3.707e-03 5.287e-01 SCN9A:8 KCNV1:57 TRPM1:69 TRPM7:75 ATP1B1:85 CLU:88 Mitochondrial Gene Expression (GO:014005 0.08338551 100 4.015e-03 5.287e-01 GATB:36 FASTKD3:52 FASTKD5:148 GFM2:181 PTCD3:198 FASTKD1:585 Mitochondrial Translation (GO:0032543) 0.08545160 96 3.863e-03 5.287e-01 GATB:36 GFM2:181 PTCD3:198 MTRF1:880 DAP3:970 TSFM:1067 Monoatomic Cation Transmembrane Transpor -0.05161133 273 3.480e-03 5.287e-01 SCN9A:8 CNGB3:30 KCNV1:57 TRPM1:69 TRPM7:75 ATP1B1:85	Regulation Of Cell Population Proliferat	-0.03339827	696	3.009e-03	4.993e-01	TJP1:14 KIF14:29 AKR1B1:43 CLU:88 PDS5B:121 OSMR:132
Inorganic Cation Transmembrane Transport -0.05099025 276 3.707e-03 5.287e-01 SCN9A:8 KCNV1:57 TRPM1:69 TRPM7:75 ATP1B1:85 CLU:88 Mitochondrial Gene Expression (GO:014005 0.08338551 100 4.015e-03 5.287e-01 GATB:36 FASTKD3:52 FASTKD5:148 GFM2:181 PTCD3:198 FASTKD1:585 Mitochondrial Translation (GO:0032543) 0.08545160 96 3.863e-03 5.287e-01 GATB:36 GFM2:181 PTCD3:198 MTRF1:880 DAP3:970 TSFM:1067 Monoatomic Cation Transmembrane Transpor -0.05161133 273 3.480e-03 5.287e-01 SCN9A:8 CNGB3:30 KCNV1:57 TRPM1:69 TRPM7:75 ATP1B1:85	CRD-mediated mRNA Stabilization (GO:0070	-0.26064547	10	4.317e-03	5.287e-01	DHX9:388 HNRNPU:1441 PAIP1:1453 IGF2BP3:1591 SYNCRIP:1697 IGF2BP2:1798
Mitochondrial Gene Expression (GO:014005 0.08338551 100 4.015e-03 5.287e-01 GATB:36 FASTKD3:52 FASTKD5:148 GFM2:181 PTCD3:198 FASTKD1:585 Mitochondrial Translation (GO:0032543) 0.08545160 96 3.863e-03 5.287e-01 GATB:36 GFM2:181 PTCD3:198 MTRF1:880 DAP3:970 TSFM:1067 Monoatomic Cation Transmembrane Transpor -0.05161133 273 3.480e-03 5.287e-01 SCN9A:8 CNGB3:30 KCNV1:57 TRPM1:69 TRPM7:75 ATP1B1:85	Cellular Response To Oxygen-Containing C	-0.04427604	367	3.790e-03	5.287e-01	CXCL13:50 CLU:88 BRINP3:133 LYN:188 PDK4:236 CAMK2D:319
Mitochondrial Translation (GO:0032543) 0.08545160 96 3.863e-03 5.287e-01 GATB:36 GFM2:181 PTCD3:198 MTRF1:880 DAP3:970 TSFM:1067 Monoatomic Cation Transmembrane Transpor -0.05161133 273 3.480e-03 5.287e-01 SCN9A:8 CNGB3:30 KCNV1:57 TRPM1:69 TRPM7:75 ATP1B1:85	Inorganic Cation Transmembrane Transport	-0.05099025	276	3.707e-03	5.287e-01	SCN9A:8 KCNV1:57 TRPM1:69 TRPM7:75 ATP1B1:85 CLU:88
Mitochondrial Translation (GO:0032543) 0.08545160 96 3.863e-03 5.287e-01 GATB:36 GFM2:181 PTCD3:198 MTRF1:880 DAP3:970 TSFM:1067 Monoatomic Cation Transmembrane Transpor -0.05161133 273 3.480e-03 5.287e-01 SCN9A:8 CNGB3:30 KCNV1:57 TRPM1:69 TRPM7:75 ATP1B1:85	Mitochondrial Gene Expression (GO:014005	0.08338551	100	4.015e-03	5.287e-01	GATB:36 FASTKD3:52 FASTKD5:148 GFM2:181 PTCD3:198 FASTKD1:585
Monoatomic Cation Transmembrane Transpor -0.05161133 273 3.480e-03 5.287e-01 SCN9A:8 CNGB3:30 KCNV1:57 TRPM1:69 TRPM7:75 ATP1B1:85	Mitochondrial Translation (GO:0032543)	0.08545160	96	3.863e-03	5.287e-01	GATB:36 GFM2:181 PTCD3:198 MTRF1:880 DAP3:970 TSFM:1067
Positive Regulation Of Macromolecule Met	Monoatomic Cation Transmembrane Transpor	-0.05161133	273	3.480e-03	5.287e-01	SCN9A:8 CNGB3:30 KCNV1:57 TRPM1:69 TRPM7:75 ATP1B1:85
	Positive Regulation Of Macromolecule Met	-0.04638632	325	4.248e-03	5.287e-01	ANK2:2 AKR1B1:43 CALCR:65 CLU:88 RAMP2:107 NOS1AP:155

MGI_Mammalian_Phenotype_Level_4 Top pathways by non-permulation

Geneset	stat	num.genes	pval	p.adj	gene.vals
MP0005083 abnormal biliary tract	0.31009705	8	2.399e-03	3.807e-01	ANK1:116 GPBAR1:453 CCKAR:1033 MUC1:1634 LDLR:2875 VTI1B:2888
MP0003252 abnormal bile duct	0.20671016	22	8.039e-04	3.807e-01	ABCB4:155 PKHD1:328 ABCB11:342 CYP8B1:602 PKD1:615 ABCG5:659
MP0001666 abnormal nutrient absorption	0.13916765	42	1.860e-03	3.807e-01	ABCB4:155 RSC1A1:246 MBTPS1:356 CLOCK:378 PLA2G1B:532 CYP8B1:602
MP0002095 abnormal skin pigmentation	0.10980100	46	1.022e-02	3.964e-01	ANK1:116 RAG1:120 HPS5:182 KRT4:437 POLH:478 DST:515
MP0003868 abnormal feces composition	0.16258004	25	4.967e-03	3.964e-01	ABCB4:155 CYP8B1:602 LIPE:622 ITPR2:810 SLC10A2:860 VWF:1010
MP0005085 abnormal gallbladder physiolo	0.15656619	25	6.826e-03	3.964e-01	ABCB4:155 ABCB11:342 GPBAR1:453 CYP8B1:602 ABCG5:659 SLC10A2:860
MP0005551 abnormal eye electrophysiolog	-0.06280008	138	1.166e-02	3.964e-01	CNGB3:30 USH2A:44 TRPM1:69 PROM1:131 MERTK:186 PDE6B:223
MP0008875 abnormal xenobiotic pharmacok	0.19546729	16	6.847e-03	3.964e-01	ABCC3:362 POR:788 SLC47A1:1213 CYP1A1:1356 MTF1:1410 ADH7:1492
MP0003121 genomic imprinting	-0.15512373	23	1.013e-02	3.964e-01	UBE3A:156 SMCHD1:297 HELLS:974 IGF1R:1039 ARID4B:1404 DIO3:1794
MP0010329 abnormal lipoprotein level	-0.08304309	81	1.019e-02	3.964e-01	APOA1:12 NDST3:41 SEC14L2:147 PEMT:187 PLTP:244 FOXO1:420
MP0002063 abnormal learning/memory/cond	-0.04007070	356	1.139e-02	3.964e-01	CHL1:3 EHMT1:61 ACSM4:80 UBE3A:156 CACNA1B:157 APBA2:170
MP0002932 abnormal joint morphology	0.07137536	108	1.098e-02	3.964e-01	ZEB1:28 FOXC2:45 PHC1:147 SYVN1:157 ENPP1:419 PHC2:646
MP0010094 abnormal chromosome stability	0.09522721	61	1.042e-02	3.964e-01	RAG1:120 LIG4:130 DCLRE1C:240 MCM7:266 NHEJ1:674 MUS81:809
MP0009745 abnormal behavioral response	-0.05701022	204	5.669e-03	3.964e-01	EHMT1:61 SLC12A5:91 BHLHE40:112 CACNA1B:157 RYR2:196 ADAMTS4:199
MP0000462 abnormal digestive system	0.13035865	29	1.531e-02	4.005e-01	LAMC2:217 DMD:1172 APC:1531 CFTR:1541 CYP26A1:1690 DACT1:1712
MP0002572 abnormal emotion/affect behav	-0.04136029	290	1.765e-02	4.005e-01	CHL1:3 NDST3:41 EHMT1:61 CACNA1B:157 APBA2:170 GRM2:209
MP0001849 ear inflammation	0.15175048	22	1.388e-02	4.005e-01	RAG1:120 LAMC2:217 NAGLU:231 MECOM:404 VDR:796 SALL4:1508
MP0001968 abnormal touch/ nociception	-0.12018933	33	1.712e-02	4.005e-01	SLC12A5:91 SCN11A:308 TACR1:354 TRPV1:752 TRPM8:788 SCN10A:984
MP0004019 abnormal vitamin homeostasis	0.10914462	41	1.589e-02	4.005e-01	RHO:210 CUBN:304 LASP1:598 VDR:796 RBP4:814 CYP27A1:1115
MP0002064 seizures	-0.04403141	254	1.767e-02	4.005e-01	SCN9A:8 SLC12A5:91 BHLHE40:112 KCNA4:113 UBE3A:156 RYR2:196
MP0003937 abnormal limbs/digits/tail de	0.07095616	101	1.442e-02	4.005e-01	PHC1:147 TBX5:268 MECOM:404 FMN1:571 GDF5:680 POR:788
MP0008058 abnormal DNA repair	0.10847256	39	1.939e-02	4.196e-01	POLK:74 LIG4:130 NHEJ1:674 TEX15:797 ALKBH2:905 APC:1531
MP0002429 abnormal blood cell	0.02199933	1191	2.036e-02	4.214e-01	ANKRD11:6 ARHGEF6:10 ZEB1:28 JAK3:38 CBFA2T3:53 PREX1:56
MP0005584 abnormal enzyme/coenzyme acti	-0.05714691	137	2.219e-02	4.401e-01	CYLD:81 IFNAR1:210 IGFBP3:250 CACNA1S:259 DBT:325 GAD1:395
MP0002398 abnormal bone marrow	0.02503534	794	2.410e-02	4.589e-01	ARHGEF6:10 ZEB1:28 JAK3:38 CBFA2T3:53 PRKDC:59 FCER1A:98
MP0002067 abnormal sensory capabilities	-0.04049107	261	2.710e-02	4.962e-01	LTN1:19 ACSM4:80 SLC12A5:91 SELP:130 ISLR2:150 UBE3A:156
MP0003646 muscle fatigue	0.21030635	9	2.900e-02	5.112e-01	SLC2A4:636 PPARGC1A:1706 MTOR:1847 COX10:2229 NOS1:3403 SOD2:8642
MP0001881 abnormal mammary gland	-0.07708471	64	3.373e-02	5.485e-01	CCNE1:154 RXFP1:353 CSF1:490 AGAP2:604 EGFR:905 VGF:936
MP0000358 abnormal cell content/	0.05518069	126	3.399e-02	5.485e-01	PRKDC:59 SYNE2:309 DYNC2H1:400 AATF:411 COL10A1:856 ULK1:885
MP0002272 abnormal nervous system	-0.04450858	195	3.457e-02	5.485e-01	SLC12A5:91 UBE3A:156 CACNA1B:157 RYR2:196 SCN11A:308 TACR1:354
MP0003959 abnormal lean body	-0.07734422	58	4.243e-02	6.516e-01	DDR2:87 FTO:525 RPTOR:534 VIPR2:704 VGF:936 MC4R:1066
MP0002697 abnormal eye size	-0.05495838	111	4.717e-02	7.017e-01	HSF4:143 MMP14:337 COL4A1:340 GJE1:390 LMX1B:452 NDST1:773
MP0002733 abnormal thermal nociception	-0.05930652	92	5.077e-02	7.324e-01	CACNA1B:157 PIRT:533 TRPV1:752 TRPM8:788 SCN10A:984 KCNIP3:1053
MP0004782 abnormal surfactant physiolog	0.12850787	19	5.277e-02	7.388e-01	LPCAT1:163 ABCA12:262 SFTPA1:1056 NOS2:2093 CYP1A2:2234 HIF1A:236
MP0005365 abnormal bile salt	0.10811366	26	5.680e-02	7.510e-01	ABCB11:342 ABCC3:362 GPBAR1:453 CYP8B1:602 POR:788 SLC10A2:860
MP0009765 abnormal xenobiotic induced	0.05793701	92	5.635e-02	7.510e-01	MMP7:212 MBTPS1:356 DNASE1:372 HIP1:482 VDR:796 MUS81:809
MP0001970 abnormal pain threshold	-0.04484179	149		7.711e-01	CACNA1B:157 TSHZ3:228 SCN11A:308 TACR1:354 PIRT:533 ADCY1:579
MP0004885 abnormal endolymph	0.11870907	21		7.711e-01	EFNB2:783 KCNJ10:1268 GJB6:1427 ESPN:1511 KIT:1814 ESRRB:2031
MP0008569 lethality at weaning	-0.06076045	79		7.731e-01	MMP14:337 GABRB3:618 CDKN1B:721 ITPR1:766 TGFB1:939 PTPRC:1038
	-0.01765289	1079	7.261e-02		HERC2:1 ANK2:2 LTN1:19 E2F5:26 KCNV1:57 EHMT1:61

tissue_specific Top pathways by non-permulation

Geneset	stat	num.genes	pval	p.adj	gene.vals
esophagus.mucosa	0.077911663	219	8.430e-05	4.552e-03	PPL:7 ADGRF1:29 KRT78:62 ZNF185:67 RAB11FIP1:72 ESPL1:100
Brodmann.area.9	-0.078853796	181	2.860e-04	6.716e-03	CSMD1:54 KCNV1:57 PLPPR4:211 TMEM132D:226 B3GALT2:254 RXFP1:353
peyers.patch	0.080443977	167	3.731e-04	6.716e-03	SLC28A1:122 CREB3L3:127 TMEM236:227 DQX1:272 MALRD1:316 TINAG:324
transverse.colon	0.078163920	148	1.117e-03	1.507e-02	WNK4:102 LRRC31:109 TMEM236:227 DQX1:272 TINAG:324 URAD:412
cerebellar.hemisphere	-0.041530127	507	1.799e-03	1.943e-02	PHTF1:20 TMEM266:33 NDST3:41 GDAP1:77 SLC12A5:91 MAP7D2:95
leg.skin	0.060762714	216	2.319e-03	2.087e-02	GGT6:25 KRT78:62 POF1B:138 A2ML1:166 KRTDAP:171 EVPL:178
suprapubic.skin	0.051458241	193	1.459e-02	1.125e-01	GGT6:25 KRT78:62 FCER1A:98 A2ML1:166 KRTDAP:171 EVPL:178
caudate.nucleus	-0.134202987	26	1.798e-02	1.214e-01	GPR88:963 RGS14:1202 AQP4:1239 MLC1:1563 VAX1:1625 RLBP1:1647
C1.spinal.cord	-0.048277395	181	2.635e-02	1.378e-01	UGT8:17 SLC5A11:124 PCSK6:140 ANLN:164 PDE6B:223 GPR62:454
minor.salivary.gland	0.078542702	69	2.452e-02	1.378e-01	PIP:46 CRACR2A:78 ODAM:144 MMP7:212 AMTN:344 EHF:577
pituitary.gland	-0.044211618	212	2.807e-02	1.378e-01	TMEM130:184 PLPPR4:211 SPRED3:281 GH1:328 INSM1:344 CSH2:360
stomach	0.067575214	86	3.096e-02	1.393e-01	PGC:31 CAPN8:44 CBLIF:103 B4GALNT3:239 MECOM:404 CYP2S1:727
vagina	0.063657935	90	3.765e-02	1.564e-01	KRT78:62 A2ML1:166 KRTDAP:171 EVPL:178 RNF222:193 MAB21L4:348
transformed.skin.fibroblast	-0.034748605	258	5.770e-02	2.226e-01	CNTN3:13 ADAMTS6:15 SEC24D:38 FJX1:63 DDR2:87 ARSJ:105
cerebellum	-0.025111428	373	1.020e-01	3.672e-01	ANK2:2 PHTF1:20 TMEM266:33 CLEC4G:108 NOS1AP:155 CACNA1B:157
blood	0.027940517	274	1.162e-01	3.809e-01	BPI:26 JAK3:38 PREX1:56 DHX34:90 NLRP12:119 SNAI3:123
hypothalamus	-0.053956850	66	1.307e-01	3.809e-01	SCN9A:8 CALCR:65 BRINP3:133 TMEM255A:357 PIRT:533 FNDC9:679
putamen	-0.113964408	15	1.267e-01	3.809e-01	KCNH4:153 PDE10A:526 GPR88:963 LRRC10B:1774 ANO3:7502.5 FAM237A:7502.5
skeletal.muscle	0.028464968	239	1.340e-01	3.809e-01	SVIL:15 NRAP:281 TACC2:314 SMTNL2:354 RAPSN:440 XIRP1:479
greater.omentum	-0.069165225	32	1.763e-01	4.760e-01	GFPT2:129 ADAMTS4:199 MTARC1:1400 SPRY1:1481 LEP:2241 MEST:2395
hippocampus.proper	-0.106344310	11	2.222e-01	5.713e-01	NTS:1479 NEUROD6:1592 NEUROD2:7502.5 SLC17A7:7502.5 HRK:7502.5 OLIG2:7502.5
aorta	0.024481732	154	2.979e-01	6.995e-01	C1QTNF8:125 SUSD5:188 FILIP1L:345 KCNK17:463 MYO18B:491 MYH10:563
left.ventricle	0.036648870	68	2.975e-01	6.995e-01	NRAP:281 RBM20:329 XIRP1:479 MYO18B:491 TNNI3K:580 SMCO1:607
atrium.auricle	0.028760915	90	3.477e-01	7.231e-01	TBX5:268 NRAP:281 RBM20:329 XIRP1:479 MYO18B:491 TNNI3K:580
cerebral.cortex	-0.026546217	107	3.452e-01	7.231e-01	CSMD1:54 PACSIN1:141 FAIM2:372 HTR1A:422 RS1:463 CABP1:518
ovary	0.027013215	102	3.481e-01	7.231e-01	BAMBI:24 ADAMTS16:196 STAR:226 TSHZ2:311 PLIN5:447 CDK15:605
fallopian.tube	0.036118282	52	3.687e-01	7.374e-01	ADGRG4:2 CROCC2:82 CRISPLD2:830 ADAMTS3:1254 CCDC17:1592 CFAP73:1594
cortex.kidney	0.022664272	113	4.077e-01	7.387e-01	SLC28A1:122 KLHDC7A:242 KIF12:273 CUBN:304 TINAG:324 PKHD1:328
subcutaneous.adipose	0.028151527	72	4.104e-01	7.387e-01	ACACB:134 ITIH5:322 GPBAR1:453 SIGLEC1:581 LIPE:622 VWF:1010
testis	0.007141930	1373	4.102e-01	7.387e-01	PKD1L3:22 BPI:26 INCA1:32 TTLL6:37 CCDC154:41 HROB:49
coronary.artery	-0.043315960	15	5.616e-01	7.605e-01	CCDC190:125 COL4A1:340 SPINK13:1200 PCOLCE2:1266 CCL19:2296 CCN3:7502.5
EBV.lymphocyte	-0.008728381	671	4.561e-01	7.605e-01	KIF14:29 NETO2:64 ZGRF1:79 BAX:84 LYN:188 TICRR:192
ectocervix	0.032416420	25	5.752e-01	7.605e-01	COL27A1:33 RIPOR3:1014 F10:1945 PTHLH:2082 ADAMTSL5:2457 MATN2:2857
		_			

5.374e-01 7.605e-01

6.071e-01 7.605e-01

5.148e-01 7.605e-01

6.058e-01 7.605e-01

0.018485937

-0.024149460

0.026172037

0.008817094

38

52

298

pancreas

prostate

sigmoid.colon

spleen

PLA2G1B:532 RBPJL:663 CUZD1:768 AQP12A:1080 RNF186:1187 GUCA1C:1314

NR2E3:291 NKX3-1:430 ALDH1A3:433 TRPM8:788 NPY:1152 FOXA1:1327

MYLK:368 CCDC9B:510 HMCN2:878 BMP3:994 PLEKHO1:1111 TACR2:1670

ARHGAP4:66 AKNA:75 CROCC2:82 RAG1:120 STAB2:229 LIPA:315