

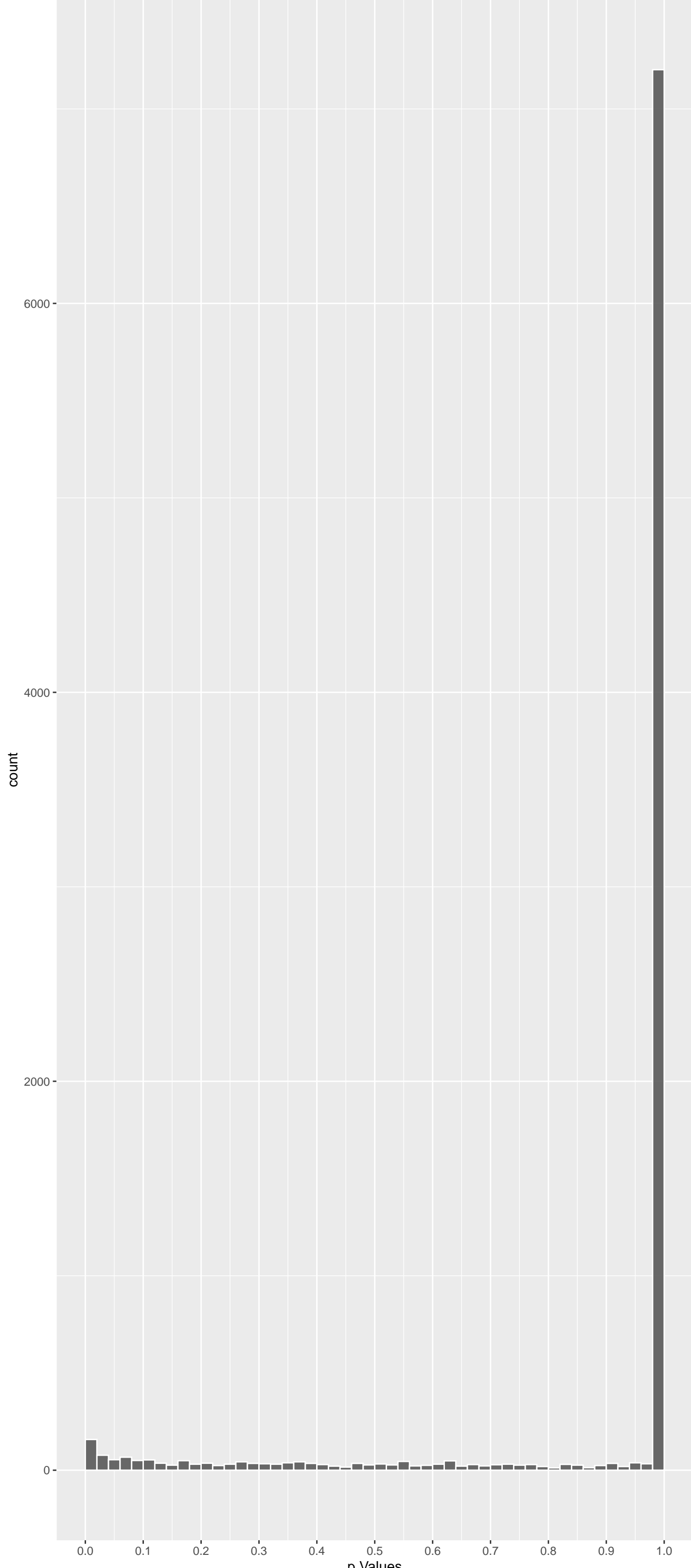
Top genes by P-value non-permuted

Gene	Rho	P	p.adj	qValueNoperm
HERC2	-6.572040	2.977833e-10	2.934e-06	1.579e-02
JCAD	6.524775	4.086211e-10	2.934e-06	1.579e-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
CHL1	-5.878089	2.490178e-08	4.467e-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
ANK2	-5.894989	2.248243e-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
LRRN3	-5.797233	4.045084e-08	5.023e-05	6.238e-02
ARHGEF6	5.669355	8.600189e-08	9.917e-05	1.091e-01
SLC2A7	5.617274	1.163963e-07	1.253e-04	1.091e-01
ZBTB8B	5.596760	1.310371e-07	1.322e-04	1.091e-01
CEP250	5.561323	1.606422e-07	1.441e-04	1.091e-01
DENND1B	-5.569866	1.529616e-07	1.441e-04	1.091e-01
ANKRD10	5.541207	1.802366e-07	1.486e-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
SVIL	5.492450	2.378381e-07	1.669e-04	1.154e-01
CTU2	5.477843	2.583246e-07	1.738e-04	1.154e-01
WWP1	-5.465629	2.767611e-07	1.787e-04	1.154e-01

Top genes by Q-value non-permuted

Gene	Rho	P	p.adj	qValueNoperm
HERC2	-6.572040	2.977833e-10	2.934e-06	1.579e-02
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ADGRG4	6.481391	5.452837e-10	2.934e-06	1.579e-02
CHL1	-5.878089	2.490178e-08	4.467e-05	6.238e-02
PIEZO1	5.828959	3.346444e-08	4.801e-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
PPL	5.846099	3.019405e-08	4.801e-05	6.238e-02
MCF2L	6.099376	6.389014e-09	2.579e-05	6.238e-02
PRUNE2	5.818236	3.568321e-08	4.801e-05	6.238e-02
LRRN3	-5.797233	4.045084e-08	5.023e-05	6.238e-02
EME2	5.997321	1.203598e-08	3.886e-05	6.238e-02
ANK2	-5.894989	2.248243e-08	4.467e-05	6.238e-02
ARHGEF6	5.669355	8.600189e-08	9.917e-05	1.091e-01
ANKRD10	5.541207	1.802366e-07	1.486e-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
CEP250	5.561323	1.606422e-07	1.441e-04	1.091e-01
SLC2A7	5.617274	1.163963e-07	1.253e-04	1.091e-01
SCN9A	-5.520761	2.025213e-07	1.486e-04	1.091e-01
ZBTB8B	5.596760	1.310371e-07	1.322e-04	1.091e-01
DENND1B	-5.569866	1.529616e-07	1.441e-04	1.091e-01
SVIL	5.492450	2.378381e-07	1.669e-04	1.154e-01
WWP1	-5.465629	2.767611e-07	1.787e-04	1.154e-01
CTU2	5.477843	2.583246e-07	1.738e-04	1.154e-01

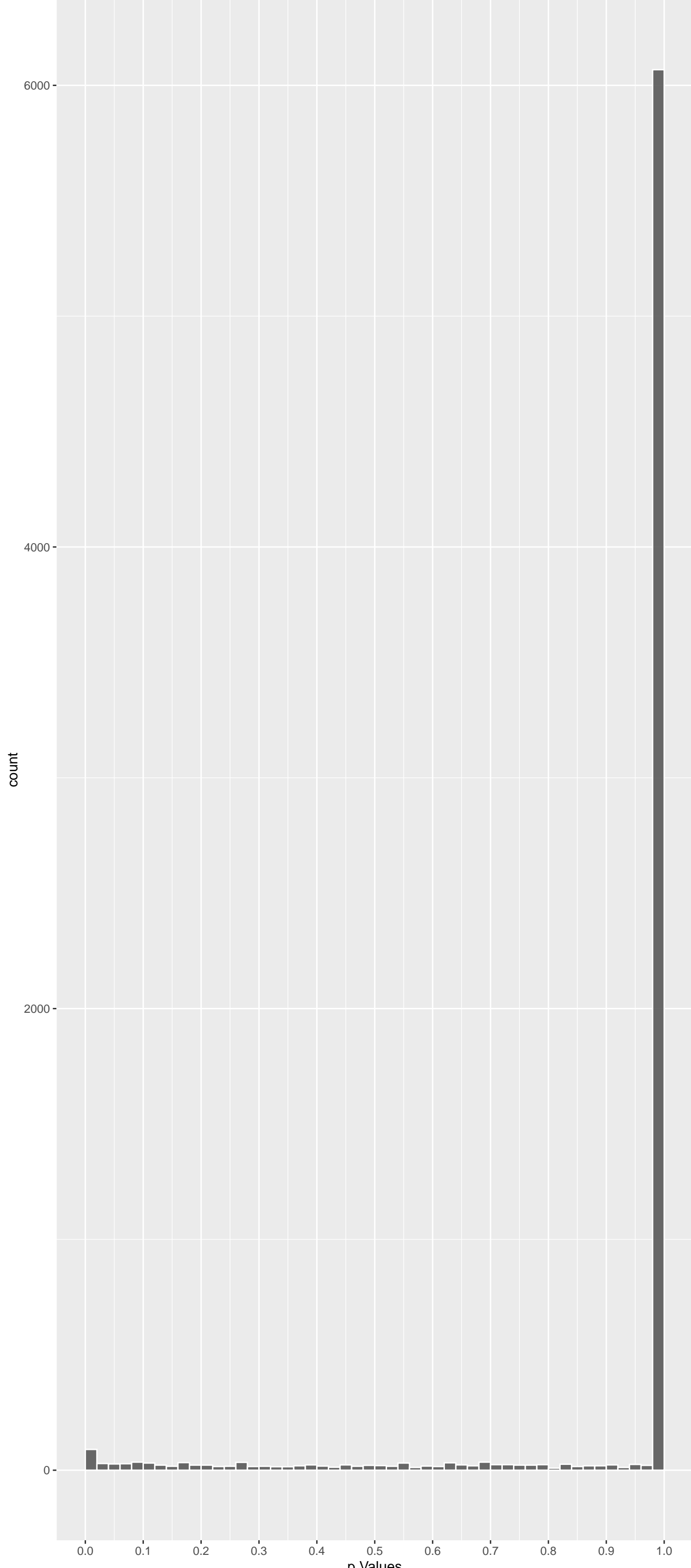
Positive Rho Non-permuted



Top Positive genes by P-value non-permuted

Gene	Rho	P	p.adj	qValueNoperm
JCAD	6.524775	4.086211e-10	2.934e-06	1.579e-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

Negative Rho Non-permuted



Top Negative genes by P-value non-permuted

Gene	Rho	P	p.adj	qValueNoperm
HERC2	-6.572040	2.977833e-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	1.159e-01
TMEM64	-5.436245	3.264910e-07	2.027e-04	1.259e-01

DisGeNET Top pathways by non-permutation

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 SLC26A7:32
Neoplasm Metastasis	-0.02857344	3142	1.395e-06	6.841e-03	CHL1:3 KDM5B:7 WWP1:9 APOA1:12 TJP1:14 UGT8:17
Bilateral cataracts (disorder)	-0.13051022	104	4.395e-06	1.437e-02	AKR1B1:43 TDRD7:99 HSFA:143 STOM:334 COL4A1:340 CRYM:632
Alzheimer's Disease	-0.03370734	1666	6.683e-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 GTGLC3:123
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 VCAM1:21
Central neuroblastoma	-0.03391847	1413	3.076e-05	3.772e-02	HERC2:1 ANK2:2 CHL1:3 LRRN3:4 KDM5B:7 VCAM1:21
Rheumatoid Arthritis	-0.03319175	1456	3.591e-05	3.914e-02	APOA1:12 PHTF1:20 VCAM1:21 N4BP1:34 F13B:40 MMP16:48
Autism Spectrum Disorders	-0.05413200	483	5.274e-05	4.466e-02	HERC2:1 LRRN3:4 ATP10A:31 MMP16:48 CSMD1:54 EHMT1:61
Autistic Disorder	-0.04813064	615	5.463e-05	4.466e-02	CHL1:3 CNTN3:13 ZNF277:23 ATP10A:31 EHMT1:61 TUBGP5:98
Neuralgia	-0.12382077	83	5.380e-05	4.466e-02	SCN9A:8 CXCL13:50 SLC12A5:91 GRM2:209 TNF:248 SCN11A:308
Thyroid Neoplasm	-0.03720990	417	6.869e-05	5.184e-02	TJP1:14 BAX:84 CLU:88 TNFSF10:97 SELP:130 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 VDACC2:142 UBE3A:156 SCN2A:265 ALB:373 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 VDACC2:142 PAG1:169 GRM2:209 CRH2:12
Aura	-0.14122645	59	1.775e-04	8.708e-02	SLC12A5:91 VDACC2:142 UBE3A:156 SCN2A:265 ALB:373 GABRB3:618
Awakening Epilepsy	-0.14122645	59	1.775e-04	8.708e-02	SLC12A5:91 VDACC2:142 UBE3A:156 SCN2A:265 ALB:373 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 GTGLC3:123 PROM1:131 TNF:248 GH1:328
Allergic Reaction	-0.16168183	44	2.083e-04	9.087e-02	SELP:130 TNF:248 MTHFR:280 ALB:373 IL5RA:491 IL18:605
Liver carcinoma	-0.02275491	2819	2.157e-04	9.087e-02	KDM5B:7 WWP1:9 APOA1:12 TJP1:14 VCAM1:21 E2F5:26
Mammary Neoplasms	-0.02593267	1999	2.223e-04	9.087e-02	HERC2:1 KDM5B:7 WWP1:9 CNTN3:13 TJP1:14 PPP1R12B:16
Malignant lymphoma, lymphocytic, interme insulinoma	-0.0309278	289	2.392e-04	9.327e-02	BAX:84 TNFSF10:97 MRC1:144 CCNE1:154 PAG1:169 TNF:248
Lymphoma, T-Cell, Cutaneous	-0.07268804	213	2.681e-04	9.507e-02	EHMT1:61 HSPD1:136 MRC1:144 KCN4:153 ATF6:183 YY1:266
Rheumatoid Nodule	-0.24732135	18	2.810e-04	9.507e-02	BAX:84 TNFSF10:97 TNF:248 TP53:435 IL2:570 CD80:595
Tumor Progression	-0.02711499	1730	2.773e-04	9.507e-02	VCAM1:21 TLR5:231 TNF:248 MTR:443 SELE:476 IL2:570
Neurodegenerative Disorders	-0.04176275	652	3.189e-04	1.009e-01	CHL1:3 KDM5B:7 APOA1:12 VCAM1:21 KIF14:29 AKR1B1:43
Seizures	-0.03293590	1088	3.169e-04	1.009e-01	APOA1:12 BLMH:37 CXCL13:50 TRPM7:75 GDAP1:77 BAX:84
HIV Infections	-0.04191193	639	3.463e-04	1.062e-01	SCN9A:8 UGT8:17 PIGG:22 SEC24D:38 NSD2:62 CLU:88
Other cataract	-0.19795018	27	3.719e-04	1.106e-01	APOA1:12 VCAM1:21 SAMHD1:27 CXCL13:50 CYLD:81 BAX:84
Presenile dementia	-0.05842118	314	3.969e-04	1.145e-01	AKR1B1:43 GSR:536 IL18:605 MAP2K1:699 CRYBA4:742 GJA3:867
Pain, Postoperative	-0.22165933	21	4.385e-04	1.197e-01	APOA1:12 VCAM1:21 BLMH:37 TRPM7:75 BAX:84 CLU:88
Myocardial Ischemia	-0.05318471	375	4.391e-04	1.197e-01	SCN9A:8 TNF:248 SCN11A:308 CRRH1:431 TRPV1:752 ABCB1:1103
Cholecytolithiasis	0.12492887	65	5.011e-04	1.263e-01	ANK2:2 APOA1:12 VCAM1:21 AKR1B1:43 AKR1B1:96 BHLHE40:112
Epilepsy	-0.03190427	1082	5.022e-04	1.263e-01	ABCB4:155 MYO10:260 ABCB1:1342 ABCG3:362 APOBEC1:519 ABCG5:659
Gloma	-0.02564981	1779	5.019e-04	1.263e-01	ANK2:2 SCN9A:8 UGT8:17 PIGG:22 CAMSAP2:35 NSD2:62
Visual seizure	-0.07285112	191	5.368e-04	1.317e-01	CHL1:3 TJP1:14 VCAM1:21 SAMHD1:27 KIF14:29 AKR1B1:43
					CLU:88 SLC12A5:91 VDACC2:142 SLC38A3:175 CRH2:121 TNF:248

EnrichmentHsSymbolsFile2 Top pathways by non-permutation

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 TGF277:23 BLMH:37 URR1:49 MIS18A:109 ZNF281:148
NIKOLSKY_BREAST_CANCER_16P13_AMPLICON	0.13092581	100	6.159e-06	7.992e-03	EME2:4 C1QTNF8:125 PTK4:187 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 MEFA2:722 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	6.954e-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 EHTM1:61
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 CBF2A2T3:53 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 EIF4EBP1:67 CHRNA6:652
REACTOME_SIGNALING_BY_RECEPTOR_TYROSINE_SCHLOSSER_SERUM_RESPONSE_DN	-0.05112369	503	9.311e-05	3.554e-02	WWP1:9 ATP6V0D2:66 BAX:84 HSPB1:96 COL6A3:128 PCSK6:140
WP_NEUROINFLAMMATION_AND_GLUTAMATERGIC_S	-0.09523276	138	1.142e-04	3.881e-02	E2F5:26 SEC24D:38 TDRD7:99 PDS5B:121 LARP7:151 UBE3A:156
WP_NETWORK_MAP_OF_SARSCOV2_SIGNALING_PATH	-0.08349681	180	1.142e-04	3.881e-02	SLC38A5:162 SLC38A3:175 GRM2:209 TNF:248 GLUL:268 CAMK2D:319
WP_CONTROL_OF_IMMUNE_TOLERANCE_BY_VASOAC	-0.30717213	13	1.256e-04	3.881e-02	APOA1:12 CXCL13:50 TNFSF10:97 FGG:110 SELP:130 TNF:248
FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_OK_VS_	-0.04997385	508	1.239e-04	3.881e-02	CD86:499 IL2:570 CD80:595 TGFBI:939 IFNG:1184 VIP:1244
NIKOLSKY_BREAST_CANCER_8Q12_Q22_AMPLICON	-0.09907603	122	1.593e-04	4.699e-02	ANK2:2 WWP1:9 UGT8:17 LTN1:19 VCAM1:21 N4BP1:34
BLANCO_MELO_BETA_INTERFERON_TREATED_BRON	0.08184309	174	2.000e-04	5.643e-02	TMEM64:10 SLC26A7:32 OSGN2:45 MZM1:46 GDAP1:77 RBM12B:127
BRIDEAU_IMPRINTED_GENES	-0.14941386	51	2.241e-04	5.815e-02	PLXNB3:23 HROB:49 KRT78:248 NUP133:42 EVPL:178 EME1:190
WP_PHOTODYNAMIC_THERAPYINDUCED_AP1_SURVI	-0.15248910	49	2.227e-04	5.815e-02	CNTN3:13 ATP6A3:31 CALCR:65 UBE3A:156 FRAT1:214 DDC:475
MARTORIATI_MD04_TARGETS_NEUROEPITHELIUM_I	-0.08601226	149	2.950e-04	7.140e-02	BAX:84 TNFSF10:97 CCNE1:154 TNF:248 TP53:435 IL2:570
REACTOME_CYTOKINE_SIGNALING_IN_IMMUNE_SY	-0.04272811	622	2.971e-04	7.140e-02	VCAM1:21 CXCL13:50 GDAP1:77 LRRN1:115 MRC1:144 PLCXD2:237
WP_NUCLEAR_RECEPTORS_IN_LIPID_METABOLISM	0.20007061	27	3.206e-04	7.428e-02	VCAM1:21 SAMHD1:27 N4BP1:34 NUP133:42 TSLP:137
CHIANG_LIVER_CANCER_SUBCLASS_INTERFERON_	-0.23099670	20	3.486e-04	7.800e-02	ABCB4:155 ABCB1:1342 ABCG3:362 CYP8B1:602 ABCG5:659 VDR:796
BIOCARTA_NUCLEAR_RNS_PATHWAY	0.19742965	27	3.844e-04	8.045e-02	KCNT2:70 ISG15:447 CALCR:495 TDO2:640 HPGD:819 NNMT:1112
KEGG_CYTOKINE_CYTOKINE_RECEPTOR_INTERACT	-0.07171201	208	3.724e-04	8.045e-02	ABCB4:155 ABCB1:1342 ABCG3:362 CYP8B1:602 ABCG5:659 VDR:796
KOKKINAKIS_METHIONINE_DEPRIVATION_48HR_U	-0.09186879	122	4.629e-04	9.385e-02	CXCL13:50 TNFSF10:97 OSMR:132 TSLP:137 IFNAR1:210 TNF:248
ROYLANCE_BREAST_CANCER_16Q_COPY_NUMBER_D	-0.21431356	22	5.021e-04	9.871e-02	BAX:84 HSPB1:96 TNFSF10:97 CCNE1:154 IGFBP3:250 IGFBP2:278
GRATIAS_RETINOBLASTOMA_16Q24	-0.23553946	18	5.409e-04	1.009e-01	NETO2:64 SHCBP1:195 ORC6:200 ITFG1:201 VPS35:220 PHK8:296
WP_GABA_RECEPTOR_SIGNALING	-0.17946893	31	5.443e-04	1.009e-01	ANKRD11:6 USP10:48 KIAA0513:64 SPB7:180 MBTPS1:356 MEAK7:464
REACTOME_DNA_DAMAGE_TELOMERE_STRESS_INDUC	-0.13614717	53	6.089e-04	1.087e-01	GABRA5:284 GAD1:395 GABRB3:618 GPHN:1133 GABRD:1217 AP2A2:1449
REACTOME_MITOTIC_G1_PHASE_AND_G1_S_TRANS	-0.08243757	145	6.198e-04	1.087e-01	CCNE1:154 NBN:364 TP53:435 H1-3:559 LMNB1:685 CDKN1B:721
REACTOME_TRANSPORT_OF_INORGANIC_CATIONS_	-0.09737341	102	6.850e-04	1.111e-01	E2F5:26 CCNE1:154 RBL2:159 LYN:188 ORC6:200 RBBP4:585
REACTOME_CARDIAC_CONDUCTION	-0.08981401	121	6.518e-04	1.111e-01	SLC26A7:32 SLC12A5:91 SLC38A5:162 SLC38A3:175 SLC6A15:453 SLC43A4:281
REACTOME_NERVOUS_SYSTEM_DEVELOPMENT	-0.04255026	550	6.842e-04	1.111e-01	SCN9A:8 ATP1B1:85 KCN1J:143 RYR2:196 SCN2A:265 SCN11A:308
					ANK2:2 CHL1:3 SCN9A:8 LHX9:59 COL6A3:128 APH1B:166

GO\_Biological\_Process\_2023 Top pathways by non-permutation

Geneset	stat	num.genes	pval	p.adj	gene.vals
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
Immunoglobulin V(D)J Recombination (GO:0	0.44722575	5	5.334e-04	3.654e-01	PRKDC:59 LIG4:130 TCF3:192 NHEJ1:674 XRC4:3291 NA
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
Learning (GO:0007612)	-0.14602489	41	1.221e-03	3.654e-01	CLDN5:219 SYNJ1:227 SHANK3:698 NLGN4:781 GPR88:963 INSR:1004
mRNA Stabilization (GO:0048255)	-0.15077888	47	3.156e-04	3.654e-01	DHX9:388 DAZL:557 IREB2:560 ZAR1:578 NOCT:1026 TENTED:1083
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
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 Cell Population P	-0.04805969	434	6.546e-04	3.654e-01	TJP1:14 KIF14:29 AKR1B1:43 DDR2:87 OSMR:132 TSLP:137
Positive Regulation Of Type 2 Immune Res	-0.29560955	11	6.871e-04	3.654e-01	DENDN01B:5 CD86:499 IL18:605 CD81:607 TNFSF4:935 RASD2:1599
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
Potassium Ion Transmembrane Transport (G	-0.08171555	132	1.216e-03	3.654e-01	KCNV1:57 KCNT2:70 ATP1B1:85 SLC12A5:91 KCNA4:113 KCNHA4:153
rRNA Methylation (GO:0031167)	0.23723628	18	4.939e-04	3.654e-01	FTJ3:30 NSUN5:121 NOP2:179 EMT1:494 ZCCHC4:889 FDXACB1:1384
Regulation Of Mitochondrial mRNA Stabili	0.38314176	6	1.153e-03	3.654e-01	FASTKD3:52 FASTKD5:148 FASTKD1:585 PDE1E:769 TBRC4:1284 FASTKD2:8642.5
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
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
Somatic Recombination Of Immunoglobulin	0.33042662	8	1.209e-03	3.654e-01	PRKDC:59 LIG4:130 TCF3:192 MSH3:488 NHEJ1:674 XRC4:3291
Transport Across Blood-Brain Barrier (GO	-0.11553444	77	4.735e-04	3.654e-01	SLC38A5:162 SLC38A3:175 SLC38A2:556 ABCG5:589 ABCG9:651 CD36:692
Vascular Transport (GO:0010232)	-0.11185398	75	8.213e-04	3.654e-01	SLC38A5:162 SLC38A3:175 SLC38A2:556 ABCG5:589 ABCG9:651 ATP8A1:735
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
Protein Homotetramerization (GO:0051289)	-0.13061809	50	1.408e-03	3.905e-01	SAMHD1:27 CLU:88 HPRT1:382 ALDH1A3:433 KCN1J:1468 TDO2:640
Cobalamin Transport (GO:0015889)	0.36970538	6	1.712e-03	4.192e-01	CBILF:103 CUBN:304 TON1:772 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 (GO:0051262)	-0.10896820	67	2.080e-03	4.514e-01	SAMHD1:27 CLU:88 HPRT1:382 ALDH1A3:433 KCN1J:1468 TDO2:640
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				NOS1AP:5 CX3CR1:90 SELENOI:1267 RAC1:1559 JAK2:2082 TMEM106A:7502.5
rRNA Modification (GO:0006040)	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	0.23385058	14	2.501e-03	4.813e-01	EME2:34 SNX4:127 EME1:190 MEOB:681 MUSJ1:809 HFM1:1350
miRNA-mediated Gene Silencing (GO:003519	-0.16785965	26	3.058e-03	4.993e-01	MOV10:24 CLN01:287 TNRC6:1300 TNMCA:1629 AJUBA:1655 AGO2:1690
Negative Regulation Of Amide Metabolic P	-0.09253910	87	2.886e-03	4.993e-01	CLU:88 EIF2AK2:470 CPB53:577 ZAR1:578 BFN1:763 EIF2AK3:1078
Negative Regulation Of Macromolecule Bio	-0.09110650	90	2.852e-03	4.993e-01	AKR1B1:43 EIF2AK2:470 CPB53:577 ZAR1:578 TGFBI:399 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	606	3.009e-03	4.993e-01	TJP1:14 KIF14:29 AKR1B1:43 CLU:88 PD55E: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 SYNCR1:1697 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 TRPM7:69 TRPM7:75 ATP1B1:85 CLU:88
Mitochondrial Gene Expression (GO:014005	0.03838551	100	4.015e-03	5.287e-01	GATB:36 FASTKD3:52 FASTKD5:148 GMTF:181 PTDG3:198 FASTKD1:585
Mitochondrial Translation (GO:0032543)	0.0854160	96	3.863e-03	5.287e-01	GATB:36 GMF2:181 PTDG3:198 GMTF:180 DAP3:970 TSMF:1067
Monatomic 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	235	4.248e-03	5.287e-01	ANK2:2 AKR1B1:43 CALCR:65 CLU:88 RAMP2:107 NOS1AP:155