

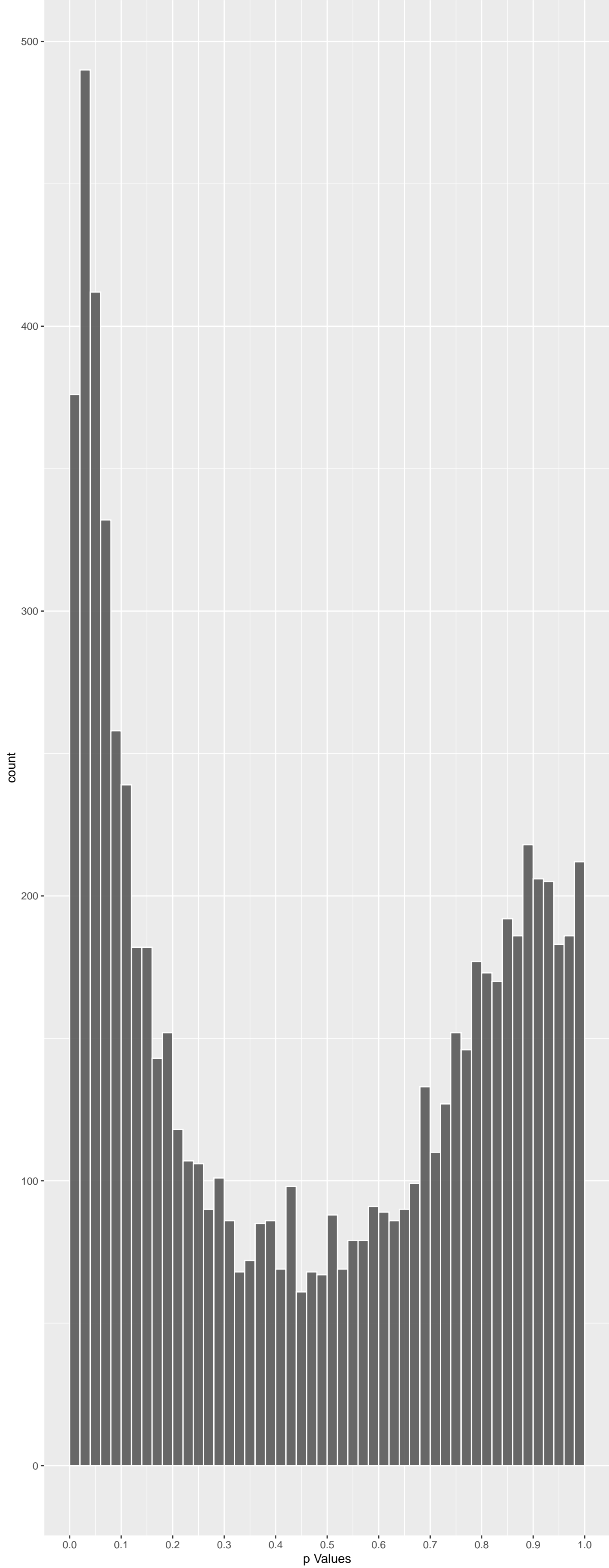
Top genes by P-value Permulated

Gene	Rho	N	P	p.adj	permPValue	qValueNoperm	qValuePerm
AC010255	0.2862415	46	1.999e-02	1.496e-01	2.233e-03	1.000e+00	4.918e-01
CEP19	0.2620941	57	1.725e-02	1.375e-01	2.257e-03	1.000e+00	4.918e-01
TMEM216	0.2968999	54	8.714e-03	9.321e-02	2.456e-03	9.946e-01	4.918e-01
MARCHF4	0.2118844	91	1.435e-02	1.238e-01	2.460e-03	1.000e+00	4.918e-01
COP22	0.2881240	57	8.849e-03	9.398e-02	2.887e-03	9.946e-01	4.918e-01
SLC14A2	-0.3020572	118	6.757e-05	4.309e-03	3.069e-03	2.748e-01	4.918e-01
DZIP1	0.3280493	110	2.970e-05	2.450e-01	3.186e-03	2.007e-01	4.918e-01
FXYD6	0.2185245	68	2.965e-02	1.860e-01	3.372e-03	1.000e+00	4.918e-01
FNDC11	0.3917569	98	2.582e-06	5.228e-04	3.602e-03	1.055e-01	4.918e-01
RAB3B	0.3379367	42	8.814e-03	9.382e-02	3.634e-03	9.946e-01	4.918e-01
SAV1	-0.4623103	42	3.395e-04	1.278e-02	3.692e-03	4.731e-01	4.918e-01
RASL11B	0.2680241	54	1.789e-02	1.400e-01	3.851e-03	1.000e+00	4.918e-01
ZHX2	0.2551538	97	2.318e-03	4.210e-02	3.878e-03	7.622e-01	4.918e-01
PHLDB1	0.2122769	111	6.637e-03	7.982e-02	3.909e-03	9.423e-01	4.918e-01
SLC8A3	0.3213759	94	1.595e-04	7.762e-03	3.952e-03	3.777e-01	4.918e-01
CADPS2	0.3171220	100	1.204e-04	6.312e-03	4.016e-03	3.307e-01	4.918e-01
CD84	0.2108018	112	6.769e-03	8.044e-02	4.021e-03	9.423e-01	4.918e-01
ADARB2	-0.2328861	94	6.217e-03	7.642e-02	4.040e-03	9.385e-01	4.918e-01
SORCS1	0.2396231	102	3.335e-03	5.239e-02	4.160e-03	8.229e-01	4.918e-01
CMTR1	-0.2243401	65	2.916e-02	1.838e-01	4.175e-03	1.000e+00	4.918e-01
APCDD1	-0.2857765	91	9.589e-04	2.473e-02	4.234e-03	6.377e-01	4.918e-01
PROKR1	0.2286249	88	9.342e-03	9.681e-02	4.278e-03	1.000e+00	4.918e-01
SPIRE1	-0.1793261	101	2.885e-02	1.828e-01	4.335e-03	1.000e+00	4.918e-01
TNFRSF11B	0.2931201	98	4.351e-04	1.465e-02	4.353e-03	4.935e-01	4.918e-01
DNAH11	0.2388423	137	6.764e-04	1.968e-02	4.364e-03	5.727e-01	4.918e-01

Top genes by Q-value Permulated

Gene	Rho	N	P	p.adj	permPValue	qValueNoperm	qValuePerm
M6PR	0.2756626	59	1.078e-02	1.047e-01	3.329e-02	1.000e+00	4.918e-01
CFTR	0.3181211	116	3.179e-05	2.561e-03	8.017e-03	2.062e-01	4.918e-01
YBX2	0.3897005	72	6.496e-05	4.251e-03	1.467e-02	2.733e-01	4.918e-01
ITGA3	0.2007961	112	9.895e-03	9.979e-02	1.937e-02	1.000e+00	4.918e-01
KRT33A	-0.2106794	74	2.854e-02	1.818e-01	2.146e-02	1.000e+00	4.918e-01
PGLYRP1	-0.2817490	74	3.405e-03	5.309e-02	1.622e-02	8.263e-01	4.918e-01
MGST1	-0.2914512	76	2.132e-03	3.984e-02	4.142e-02	7.426e-01	4.918e-01
UBR7	0.2715188	93	1.511e-03	3.272e-02	4.486e-03	7.076e-01	4.918e-01
RTN4R	-0.2022418	88	2.160e-02	1.567e-01	1.797e-02	1.000e+00	4.918e-01
CLDN11	0.1638936	41	2.106e-01	5.177e-01	2.880e-02	1.000e+00	4.918e-01
PKP2	0.1337284	103	9.973e-02	3.537e-01	4.710e-02	1.000e+00	4.918e-01
TRIB2	0.1997584	39	1.364e-01	4.186e-01	2.753e-02	1.000e+00	4.918e-01
LMCD1	0.1953246	78	3.699e-02	2.087e-01	5.943e-02	1.000e+00	4.918e-01
ANO8	-0.1701267	92	4.805e-02	2.399e-01	2.950e-02	1.000e+00	4.918e-01
KRT14	0.2076997	88	1.831e-02	1.422e-01	6.174e-02	1.000e+00	4.918e-01
KRT20	0.3226627	93	1.631e-04	7.885e-03	3.515e-02	3.797e-01	4.918e-01
NTN1	0.2406358	36	8.546e-02	3.258e-01	4.412e-02	1.000e+00	4.918e-01
TIGAR	-0.2470831	91	4.301e-03	6.180e-02	4.876e-02	8.822e-01	4.918e-01
FAM107B	-0.1255388	106	1.169e-01	3.851e-01	3.958e-02	1.000e+00	4.918e-01
CDK13	-0.0946497	95	2.636e-01	5.768e-01	4.993e-02	1.000e+00	4.918e-01
FAP	0.1289521	97	1.237e-01	3.961e-01	2.008e-02	1.000e+00	4.918e-01
DMRT3	0.2640984	72	6.795e-03	8.054e-02	5.706e-02	9.423e-01	4.918e-01
FLOD1	0.1822955	95	3.129e-02	1.911e-01	2.888e-02	1.000e+00	4.918e-01
MOGAT2	-0.2664729	98	1.384e-03	3.079e-02	1.693e-02	6.847e-01	4.918e-01
DIMT1	0.1037822	57	3.457e-01	6.490e-01	5.564e-02	1.000e+00	4.918e-01

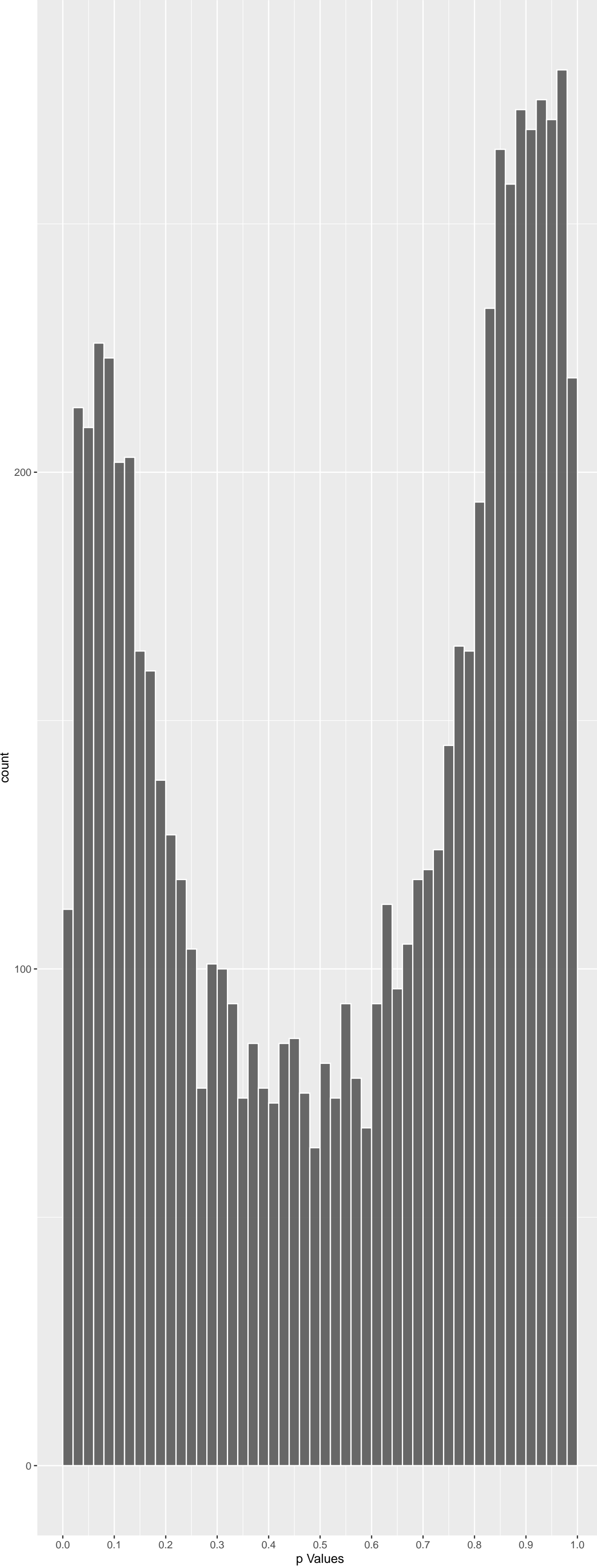
Positive Rho Permulated



Top Positive genes by P-value Permulated

Gene	Rho	N	P	p.adj	permPValue	qValueNoperm	qValuePerm
AC010255	0.2862415	46	1.999e-02	1.496e-01	2.233e-03	1.000e+00	4.918e-01
CEP19	0.2620941	57	1.725e-02	1.375e-01	2.257e-03	1.000e+00	4.918e-01
TMEM216	0.2968999	54	8.714e-03	9.321e-02	2.456e-03	9.946e-01	4.918e-01
MARCHF4	0.2118844	91	1.435e-02	1.238e-01	2.460e-03	1.000e+00	4.918e-01
COP22	0.2881240	57	8.849e-03	9.398e-02	2.887e-03	9.946e-01	4.918e-01
DZIP1	0.3280493	110	2.970e-05	2.450e-01	3.186e-03	2.007e-01	4.918e-01
FXYD6	0.2185245	68	2.965e-02	1.860e-01	3.372e-03	1.000e+00	4.918e-01
FNDC11	0.3917569	98	2.582e-06	5.228e-04	3.602e-03	1.055e-01	4.918e-01
RAB3B	0.3379367	42	8.814e-03	9.382e-02	3.634e-03	9.946e-01	4.918e-01
RASL11B	0.2680241	54	1.789e-02	1.400e-01	3.851e-03	1.000e+00	4.918e-01

Negative Rho Permulated



Top Negative genes by P-value Permulated

Gene	Rho	N	P	p.adj	permPValue	qValueNoperm	qValuePerm
SLC14A2	-0.3020572	118	6.757e-05	4.309e-03	3.069e-03	2.748e-01	4.918e-01
SAV1	-0.4623103	42	3.395e-04	1.278e-02	3.692e-03	4.731e-01	4.918e-01
ADARB2	-0.2328861	94	6.217e-03	7.642e-02	4.040e-03	9.385e-01	4.918e-01
CMTR1	-0.2243401	65	2.916e-02	1.838e-01	4.175e-03	1.000e+00	4.918e-01
APCDD1	-0.2857765	91	9.589e-04	2.473e-02	4.234e-03	6.377e-01	4.918e-01
SPIRE1	-0.1793261	101	2.885e-02	1.828e-01	4.335e-03	1.000e+00	4.918e-01
IGGAP2	-0.1877200	123	1.143e-02	1.089e-01	4.458e-03	1.000e+00	4.918e-01
PRODH	-0.2070884	110	8.388e-03	9.150e-02	4.640e-03	9.946e-01	4.918e-01
SLC26A3	-0.2552085	107	1.359e-03	3.050e-02	4.656e-03	6.825e-01	4.918e-01
COMT	-0.2792792	95	9.707e-04	2.495e-02	4.764e-03	6.397e-01	4.918e-01

GO_Biological_Process_2023 Top pathways by permutation

Negative Regulation Of Leukocyte Prolif	-0.4471042	4	1.955e-03	2.522e-01	TNFAIP3:492 IL33:554 ENP3:986 LY6E:1062 NA NA
Nephron Tubule Development (GO:0072080)	0.4332989	3	9.340e-03	3.466e-01	HNFB:1415 MTS51:1287 OXSR1:1435 NA NA NA
Cellular Response To Nitrogen Levels (GO	-0.4312031	4	2.819e-03	2.984e-01	GABARAP1:550 BECN2:840 ATG7:952 BECN1:1697 NA NA
Cellular Response To Nitrogen Starvation	-0.4312031	4	2.819e-03	2.984e-01	GABARAP1:550 BECN2:840 ATG7:952 BECN1:1697 NA NA
Positive Regulation Of Intrinsic Apoptot	-0.4135717	2	4.278e-02	4.893e-01	MYC:858 MSL1:1679 NA NA NA NA
Positive Regulation Of Osteoblast Prolif	-0.4095427	3	1.402e-02	3.789e-01	SOMX2:277 CCSD2:1839 HPSE1:1896 NA NA NA
Response To Peptidoglycan (GO:0032434)	-0.4047233	5	1.723e-03	2.506e-01	INAAV:402 IL6:430 IRAK3:721 IFI5:2460 RELTA:2974 NA
Positive Regulation Of Toll-Like Recepto	0.4033954	3	1.552e-02	3.834e-01	SLC15A4:1238 PTPN22:1240 RSAD2:2062 NA NA NA
Regulation Of Toll-Like Receptor 7 Signa	0.4033954	3	1.552e-02	3.834e-01	SLC15A4:1238 PTPN22:1240 RSAD2:2062 NA NA NA
Cilium Movement Involved In Cell Motilit	0.3980911	7	2.650e-04	1.002e-01	TEKT2:365 TEKT5:791 GAS8:1163 TEKT3:1764 TEKT1:2092 TEKT4:2462
Axonemal Central Apparatus Assembly (GO:	0.3936735	5	2.299e-03	2.689e-01	SPAG17:247 SPEF1:1441 DNAJB13:1934 HYDIN:2157 RSPH9:2559 NA
Valine Metabolic Process (GO:0006573)	-0.3917083	5	2.418e-03	2.711e-01	BCAT2:101 ILVBL5:61 HIBCH:2203 HIBADH:2149 BCAT1:2663 NA
Cell Junction Disassembly (GO:0150146)	-0.3865811	4	7.412e-03	3.416e-01	C1QB:98 CX3CR1:274 C1QC:489 DKK1:5797 NA NA
Cellular Response To Potassium Ion (GO:0	0.3816254	4	8.208e-03	3.416e-01	DLG4:135 SLC12A2:756 DLG2:890 CRHPB:5565 NA NA
Response To Potassium Ion (GO:0035864)	0.3816254	4	8.208e-03	3.416e-01	DLG4:135 SLC12A2:756 DLG2:890 CRHPB:5565 NA NA
Protein Retention In ER Lumen (GO:000662	0.3732334	3	2.515e-02	4.371e-01	GPAA1:64 KDEL3:327 OS9:4892 NA NA NA
Toll-Like Receptor 9 Signaling Pathway (I	0.3713153	5	5.034e-03	3.191e-01	IRAK4:591 PIK3AP1:749 IRAK1:2048 USG9381:2736 TNIP2:3935 NA
Gastrulation With Mouth Forming Second (I	-0.3695565	3	2.663e-02	4.408e-01	LFP5:674 UGDH:2075 MEGF8:3006 NA NA NA
Positive Regulation Of Gastrulation (GO:	0.3684619	2	7.110e-02	5.639e-01	OXSR1:1435 SCX:2683 NA NA NA NA
TIRAL-activated Apoptotic Signaling Path	-0.3657934	3	2.821e-02	4.503e-01	RDD2:1220 SPI1:1479 ZDHHC3:3229 NA NA NA
Protein Modification By Small Protein Co	-0.3594737	3	3.105e-02	4.695e-01	ATG7:952 UBAB6:1503 SENP6:3735 NA NA NA
Regulation Of Translation In Response To	-0.3590882	4	1.287e-02	3.681e-01	EIF4G1:563 SESN2:1036 NCK1:2637 NCK2:4026 NA NA
Regulation Of Cilium Beat Frequency (GO:	0.3519910	5	6.414e-03	3.320e-01	DNAH11:19 CFAP206:481 CFAP43:1915 CYBD51:2519 CCDC40:6549 NA
snRNA Modification (GO:0040031)	-0.3516117	4	1.487e-02	3.834e-01	MERCE:290 METTL6:16267 METTL4:2585 NUTR2:3460 NA NA
L-phenylalanine Catabolic Process (GO:00	-0.3507499	5	6.604e-03	3.320e-01	TAT3:33 HGD:198 ODRP:640 GSTZ1:2049 IL4I1:8036 NA
L-phenylalanine Metabolic Process (GO:000	-0.3507499	5	6.604e-03	3.320e-01	TAT3:33 HGD:198 ODRP:640 GSTZ1:2049 IL4I1:8036 NA
Erythrose 4--Phosphate/Phosphoenolpyruvat	-0.3507499	5	6.604e-03	3.320e-01	TAT3:33 HGD:198 ODRP:640 GSTZ1:2049 IL4I1:8036 NA
Negative Regulation Of Actin Filament De	0.3475394	4	1.607e-02	3.834e-01	SCIN:355 PLEKHH2:378 VILI:3087 LAM1:5643 NA NA
Negative Regulation Of CD8--positive, Alp	0.3473551	6	3.214e-03	3.116e-01	SOC3:125 PDAE1:351 VSNR:1191 HFE:2339 ZBTB78:3804 SLC4A2:5687
Regulation Of Monoatomic Anion Transport	-0.3471947	4	1.618e-02	3.834e-01	CA2:265 ATP8B1:1350 STC1:2071 PDZK1:5295 NA NA
ATP Synthase Coupled Electron Transport	0.3405955	5	7.359e-03	3.416e-01	NDUFV1:76 NDUFB6:2653 NDUFS2:2764 NDUF1A:21301 NDUFV3:3480 NA
Positive Regulation Of CD4--positive, CD2	-0.3454843	3	3.821e-02	4.809e-01	KLHL25:255 HLA-DRA:1140 IFNG:5140 NA NA NA
Negative Regulation Of Mitochondrial Fun	-0.3408040	6	3.841e-03	3.191e-01	OMA1:121 SLC18A1:272 HUWE1:1288 PRKN:3226 TFR:3836 MUL1:6284
Signal Complex Assembly (GO:0007172)	-0.3373901	5	8.982e-03	3.466e-01	PXN:835 MAPK8IP2:1323 NCK1:2637 SCR3:3111 NCK2:4026 NA
Cellular Response To Histamine (GO:007174	-0.3366991	5	9.070e-03	3.466e-01	GABRB3:1344 DIAPH1:1407 GABRG2:1470 DHX8:3701 GABRB1:4049 NA
Positive Regulation Of Epithelial Cell D	-0.3363688	3	3.434e-02	4.899e-01	PROM1:269 IMPF:556 PAX8:6354 NA NA NA
Positive Regulation Of Translation In Re	-0.3326295	4	2.122e-02	4.167e-01	EIF4G1:563 MPACT:5587 NCK1:2637 NCK2:4026 NA NA
Regulation Of Lysosomal Protein Cataboli	-0.3311640	6	4.967e-03	3.191e-01	LRP1:91

EnrichmentHsSymbolsFile2 Top pathways by permutation

Geneset	stat	num.genes	pval	p.adj	gene.vals
REACTOME_ERYTHROCYTES_TAKE_UP_OXYGEN_AND WP_CELLULAR_PROTEOSTASIS	-0.4666062	6	9.310e-05	1.232e-02	SLC4A1:27 RHAG:75 CA4:132 CA2:263 CA1:1219 AQP1:1829 VBP1:500 PFDN2:1028 NA NA NA NA
WP_ARACHIDONATE_EPOXYGENASE_EPOXIDE_HYDR BIOCARTA_TERT_PATHWAY	-0.4090380	2	4.511e-02	3.770e-01	EPHX2:1139 COX5A:1574 NA NA NA NA
NIKOLSKY_BREAST_CANCER_12024_AMPLICON	-0.4064353	6	6.560e-04	4.071e-02	SP1:558 MZF1:311 MYC:858 SP3:1257 W71:1910 TP53:2991
REACTOME_LOSS_OF_FUNCTION_OF_SMD2_3_IN REACTOME_SIGNALING_BY_TGF_BETA_RECEPTOR	-0.4020973	4	5.347e-03	1.425e-01	NOCAL:116 GALTNT9:313 PLE:580 FSWAP:595 ULK1:660 CHFR:712 ZFVY9:588 TGFBR1:994 TGFBR1:1921 TGFBR2:2348 NA NA
STARK_HYPOCAPMUS_22011_DELETION_DN WP_METHIONINE_METABOLISM_LEADING_TO_SULF	-0.3836416	20	2.866e-09	3.098e-06	PRODHD8 COMT:10 ARVCF:33 TRMT2A:62 RTNR4:102 TANGO2:251 BHMT:153 AHCY:195 CSAD:94 CBS:621 MAT1A:666 GNMT:868
TESAR_ALK_TARGETS_EPISC_4D_UP	-0.3607690	2	7.719e-02	1.657e-01	MSX1:1679 PAX6:2478 NA NA NA NA
TESAR_ALK_AND_JAK_TARGETS_MOUSE_ES_D4_UP	-0.3607690	2	7.719e-02	1.657e-01	MSX1:1679 PAX6:2478 NA NA NA NA
MIKHAYLOVA_OXIDATIVE_STRESS_RESPONSE_VIA REACTOME_ABACAVIR_TRANSMEMBRANE_TRANSPOR	-0.3600579	6	2.255e-03	8.970e-02	HSPB1:309 AKR1B1:559 PGMAL:889 CTSD:2433 CALU:3487 AQT8:4869 ABCB1:201 SLC22A1:1671 SLC22A3:1984 SLC22A2:4595 NA NA
BIOCARTA_TERC_PATHWAY	-0.3451296	4	1.416e-02	2.294e-01	SP1:558 SP3:1257 NPYR:2391 RB1:4502 NA NA
RANKIN_ANGIOGENESIS_TARGETS_OF_VHL_HIF2A_D WP_EICOSANOID_METABOLISM_VIA_CYTOCHROME_C	-0.3398805	3	4.144e-02	3.647e-01	VEGFA:446 PPARA:175 EPHX2:1139 PPARG:5310 NA NA NA PPARGA:175
MANN_RESPONSE_TO_AMIFOSTINE_DN CASTELLANO_HRAS_TARGETS_UP	-0.3366223	5	8.534e-03	1.802e-01	TWTF1:908 BLMH:1352 PRKACB:1473 RRM2:2752 CNB1:5482 NA NNAT:1319 PRDX2:1424 GFER:4515 NA NA
REACTOME_SARS_COV_2_MODULATES_AUTOPHAGY WUNDER_INFLAMMATORY_RESPONSE_AND_CHOLEST	0.3370961	10	2.231e-04	2.372e-02	VPS11:237 VPS16:578 PIP5K1B:338 VPS4:1545 TUFM:2250 VPS41:2824 ALB:80 APODQ7:70 CDKN1C:1457 XCLN1:1640 JCHAIN:2639 MPEG1:5451
REACTOME_HIGHLY_SODIUM_PERMEABLE_POSTSYN REACTOME_DOPAMINE_CLEARANCE_FROM_THE_SYN	0.3306169	7	2.451e-03	9.405e-02	CHRNA2:42 CHRNA14:43 CHRNA51:341 CHRNA31:4299 CHRNG:4724 COMT:10 SLC6A3:680 LRTOAM:2240 MAOA:7220 NA NA
CHEN_HOXA5_TARGETS_6HR_DN SASAI_TARGETS_OF_CXCR6_AND_PTC1_DN	-0.3299747	3	4.845e-02	2.877e-01	ZBED8:1791 NPYR:2422 FXJ1:3450 NA NA NA
WP_HB_X TARGETS_3_DN BIOCARTA_VOESBITY_PATHWAY	-0.3252589	7	2.880e-03	1.032e-01	TFPI:1300 MDK:1326 PIP5K1A:1926 OTX1:2352 APOD:2436 ADAM28:3069 IL6:430 TGFBR1:994 GLG1:1289 GSTA4:1376 GASE:1596 MAP2K2:1606
REACTOME_CIPROFLOXACIN_ADME REACTOME_RUNX3_REGULATES_BCL2L11_BIM_TRA	-0.3123888	4	3.047e-02	3.219e-01	ALB:80 SLC01A2:681 SLC22A1:1671 SLC22A8:8754 NA NA BCL2L11:585 FOXO3:3625 RUNX3:42215 NA NA
KUROKAWA_LIVER_CANCER_EARLY_RECURRENCE_D REACTOME_LEUKOTRIEN_RECEPTORS	-0.3027063	4	3.601e-02	3.437e-01	VPS35:1269 IGFBP2:2739 LCAT:13269 RB1:4502 NA NA LTBR4:329 CYSLTR2:585 LTBR4:329 CYSLTR1:2852 GPR17:9372 NA
MIKKELSEN_PLURIPOTEST_STATE_DN REACTOME_ABACAVIR_ADME	-0.3023770	6	1.031e-02	1.967e-01	CASP8:191 CND2:1127 TGFBR2:2348 CDBK:2463 JAK2:3096 CAMK2D:8492 ABCB1:209 ADAM:851 NTSC5:1106 SLC22A1:1671 SLC22A3:1984 SLC22A2:4595
CHOI_ATL_ACTUATE_STAGE REACTOME_ACTIVATION_OF_THE_PHOTOTRANSDUC	-0.3006842	3	1.725e-02	5.432e-01	MET:678 T1V71 MB01:5074 NA NA NA
BRUNEAU_HEART_GREAT_VESSELS_AND_VALVULOG REACTOME_RUNX1_REGULATES_ESTROGEN_RECEPT	-0.2974618	5	2.105e-02	2.840e-01	PDE6A:289 CNGA1:443 SAG:1604 RHO:4270 PDE6B:8648 NA JAG1:993 MED13:1282 TBX1:1600 NOTCH1:1701 PTPN11:3352 NOTCH2:3556
REACTOME_PP2A_MEDIATED_DEPHOSPHORYLATION WP_COVID19_THROMBOSIS_AND_ANTICOAGULATION	-0.2941187	4	1.461e-02	3.147e-01	AXIN1:360 GPM1:1901 NUCN1:3974 ESR1:6753 NA NA PP2PB1R:1285 PPS2PD5:209 MLXIP:3436 PFKFB1:5540 NA NA
REACTOME_SLPB_DEPENDENT_PROCESSING_OF_RE AMUNDSON_DNA_DAMAGE_RESPONSE_TP53	-0.2939023	6	1.266e-02	2.639e-01	FGG:638 F13B:706 PLG:629 F4G:4689 F13A1:4776 F2:6811 LSM10:1761 LSM11:3399 NCBP1:3576 SLBP:3750 NA NA
	-0.2910052	4	3.828e-02	3.724e-01	
	-0.2890886	18	8.998e-04	5.453e-02	MDM2:345 LIF:566 LTM2:1684 NDBP1:2372 CSD2:2433 XPC:2925

Anemia, hereditary spherocytic hemolysis	-0.4941793	5	1.297e-04	4.956e-02	SLCA41:27 EPB42:42 SPTB:85 ANK1:119 SPTA1:135 NA
Spherocytosis	-0.4941793	5	1.297e-04	4.956e-02	SLCA41:27 EPB42:42 SPTB:85 ANK1:119 SPTA1:135 NA
Angiokeratoma	-0.4740601	3	4.457e-03	2.579e-01	MANBA:142 VEGFA:446 GLA:507 NA NA NA
Abnormality of cranial vault shape	-0.4169462	2	4.112e-02	4.572e-01	SPECC1L:151 PEX19:2323 NA NA NA NA
Abnormality of cranium shape	-0.4169462	2	4.112e-02	4.572e-01	SPECC1L:151 PEX19:2323 NA NA NA NA
Abnormality of head shape	-0.4169462	2	4.112e-02	4.572e-01	SPECC1L:151 PEX19:2323 NA NA NA NA
Asymmetry of head	-0.4169462	2	4.112e-02	4.572e-01	SPECC1L:151 PEX19:2323 NA NA NA NA
Malformation of cranial vault shape	-0.4169462	2	4.112e-02	4.572e-01	SPECC1L:151 PEX19:2323 NA NA NA NA
Malformation of cranium shape	-0.4169462	2	4.112e-02	4.572e-01	SPECC1L:151 PEX19:2323 NA NA NA NA
Malformation of head shape	-0.4169462	2	4.112e-02	4.572e-01	SPECC1L:151 PEX19:2323 NA NA NA NA
Aase Smith syndrome 2	-0.4093731	3	1.392e-02	3.404e-01	TSR2:1233 RPS10:1273 GATA1:1475 NA NA NA
Monilethrix	0.4092319	2	4.501e-02	4.695e-01	KRT80:954 DSG4:1826 NA NA NA NA
Maple Syrup Urine Disease, Thiamine Resp	-0.4079594	5	1.582e-03	1.782e-01	BCAT2:101 PPM1K:861 BCKDHA:1038 DBT:1399 BCKDHB:3382 NA
Classic Maple Syrup Urine Disease	-0.4079594	5	1.582e-03	1.782e-01	BCAT2:101 PPM1K:861 BCKDHA:1038 DBT:1399 BCKDHB:3382 NA
Intermediate Maple Syrup Urine Disease	-0.4079594	5	1.582e-03	1.782e-01	BCAT2:101 PPM1K:861 BCKDHA:1038 DBT:1399 BCKDHB:3382 NA
Intermittent Maple Syrup Urine Disease	-0.4079594	5	1.582e-03	1.782e-01	BCAT2:101 PPM1K:861 BCKDHA:1038 DBT:1399 BCKDHB:3382 NA
Heritiz Disease	0.4026420	5	1.820e-03	1.959e-01	LAMC2:427 ITGB4:951 LAMA3:1863 LAMB3:1910 ITGA6:2330 NA
delta beta ⁰ α Thalassaemia	0.3967382	2	5.197e-02	4.927e-01	PSMB6:543 DLL1:2626 NA NA NA NA
Miller Fisher Syndrome	0.3950418	3	1.769e-02	3.684e-01	PSMB6:543 SMUG1:1645 DLL1:2626 NA NA NA NA
Junctional split	0.3951658	6	8.020e-04	1.289e-01	LAMC2:427 ITGB4:951 LAMA3:1863 LAMB3:1910 PLEC:2200 ITGA6:2330
Desmoplastic infantile astrocytoma	-0.3921741	6	8.878e-04	1.367e-01	HDAC8:158 DIAPH2:411 LIF:566 BRAF:2130 TP53:2991 PTPN11:3352
PAROXYSMAL EXTREME PAIN DISORDER	-0.3909982	5	2.464e-03	2.147e-01	SCN9A:735 SCN10A:786 SCN11A:1151 IDS:1200 MCF2L2:4195 NA
Progression of non-small cell lung cancer	0.3900721	2	5.604e-02	4.970e-01	CCRT7:1333 CD274:2251 NA NA NA NA
Sepsis of the newborn	-0.3899952	3	1.934e-02	3.809e-01	IL6:430 SERAC1:1490 ST14:2980 NA NA NA
Occipital myelomeningocele	-0.3893590	9	5.241e-05	3.022e-02	COMT:10 ARVCF:32 UFD1:383 HIRA:1025 TX1:1600 GP1B:2218
Z2q11 partial monosomy syndrome	-0.3889745	11	7.942e-06	7.786e-03	COMT:10 ARVCF:32 UFD1:383 P14K4:789 HIRA:1025 TX1:1600
Bacterial sepsis of newborn	-0.3852926	2	5.912e-02	5.005e-01	IL6:430 ST14:2980 NA NA NA NA
Visually threatening diabetic retinopathy	-0.3811640	4	8.285e-03	3.088e-01	VEGFA:446 TNF:1662 CXCL12:2465 LTA:2524 NA NA
EPIDERMOLYSIS BULLIOSA, JUNCTIONAL, LOCAL	0.3810702	5	3.167e-03	2.197e-01	LAMC2:427 ITGB4:951 LAMA3:1863 LAMB3:1910 COL17A1:3959 NA
Adult junctional epidermolysis bullosa (0.3810702	5	3.167e-03	2.197e-01	LAMC2:427 ITGB4:951 LAMA3:1863 LAMB3:1910 COL17A1:3959 NA
Epidermolysis Bullosa Progressiva	0.3810702	5	3.167e-03	2.197e-01	LAMC2:427 ITGB4:951 LAMA3:1863 LAMB3:1910 COL17A1:3959 NA
JEB-I	0.3810702	5	3.167e-03	2.197e-01	LAMC2:427 ITGB4:951 LAMA3:1863 LAMB3:1910 COL17A1:3959 NA
Palmar hyperhidrosis	0.3810702	5	3.167e-03	2.197e-01	LAMC2:427 ITGB4:951 LAMA3:1863 LAMB3:1910 COL17A1:3959 NA
Sclerium measurement	-0.3777256	4	8.886e-03	4.174e-01	BHMT:153 CBS6:621 DMGDH:2503 ARSB:3977 NA NA
Plantar hyperkeratosis	0.3717178	6	1.376e-03	1.752e-01	LAMC2:427 ITGB4:951 LAMA3:1863 LAMB3:1910 PLEC:2200 COL17A1:3959
Vulvar Neoplasia	-0.3770650	3	2.370e-02	4.097e-01	CA9:1415 CASP3:1995 PTGS2:2086 NA NA NA
Exudative vitreoretinopathy	-0.3767089	5	3.531e-03	3.255e-01	ZNF408:617 LRP5:674 NDP:2526 FZD4:2574 TSPAN12:2774 NA
Chronic idrocytitis	-0.3764464	2	2.619e-02	5.133e-01	IL6:430 RBM45:3228 NA NA NA NA
prenatal alcohol exposure	-0.3759644	4	9.209e-03	3.174e-01	VEGFA:446 IGF2:1260 HAND1:2027 NTRK2:3675 NA NA
Myelitis	0.3742033	4	9.542e-03	3.174e-01	LAMC2:427 CSF2:1157 P

HP_SPHEROCTYSIS	-0.4909120	8	1.522e-06	7.105e-04	SLC4A1:27 EPB42:42 RHAG:75 SPTB:85 ANK1:119 SPTA1:135
GOCC_PLRUCYTO_MOTILE_CILIUM	0.4706930	4	1.112e-03	7.732e-02	DNAH1:115 CFAP45:132 DNAH5:728 ENKUR:916 NA NA
GOMB_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_P	-0.4502446	2	2.742e-02	3.489e-01	CYP11A1:14 CYP2U1:1454 NA NA NA
GOMB_BRANCHED_CHAIN_AMINO_ACID_BIOSYNTH	-0.4478230	5	5.242e-04	5.041e-02	BCAT2:101 SDS:167 SCD3A:184 ILVBL:561 BCAT1:2663 NA
GOMB_REGULATION_OF_PROTEIN_TYROSINE_PHOS	-0.4360294	3	8.902e-03	2.205e-01	SLC39A10:471 PTPRC:946 MGAT5:1418 NA NA NA
GOMB_ESTABLISHMENT_OF_LEFT_RIGHT_ASYMMET	0.4315091	4	2.799e-03	1.237e-01	CFAP45:132 CFAP45:536 ENKUR:916 CD3C39:2623 NA NA
GOMB_L_CYSSTEINE_METABOLIC_PROCESS	-0.4274072	4	4.070e-03	1.313e-01	CSAD:494 CBS:621 AGXT:1531 C001:164 NA NA
GOMB_POSITIVE_REGULATION_OF_CONNECTIVE_T	0.4179378	2	4.063e-02	4.023e-01	ROCK2:1193 ROCK1:1322 NA NA NA NA
GOMB_NEURON_NEURON_SYNAPTIC_TRANSMISSION	0.4071315	4	4.800e-03	1.643e-01	DRD2:170 KIF1B:1181 TMOD2:1280 DLGAP2:3057 NA NA
GOMB_REGULATION_OF_TOLL_LIKE_RECEPTOR_7	0.4013936	3	1.604e-02	2.782e-01	SLC15A4:1238 PTPN22:1240 SRD2:2062 NA NA NA
GOMB_LEUKOTRIENE_CATABOLIC_PROCESS	0.3946111	2	5.321e-02	4.493e-01	DPEP2:1230 DPEP1:2003 NA NA NA NA
GOMB_C3HC4_TYPE_RING_FINGER_DOMAIN_BINDI	0.3941574	2	5.351e-02	4.500e-01	CNN2:878 PINK1:2374 NA NA NA NA
HP_ABNORMAL_ISOHEMAGGLUTININ_LEVEL	-0.3926089	5	2.362e-03	1.135e-01	SLC35C1:350 CD19:565 ARHGEF1:857 CR2:2474 PRKCD:3712 NA
HP_MULTIPLE_GLOMERULAR_CYSTS	0.3923749	3	1.858e-02	2.981e-01	HNF1B:415 HNP3H:1504 MYOCD:3029 NA NA NA
HP_DECREASED_SERUM_COMPLEMENT_FACTOR_I	-0.3917854	4	6.505e-03	1.925e-01	C1QB:98 C1QA:335 C1QC:489 C1F:5494 NA NA
HP_ABNORMAL_PERIFOLLICULAR_MORPHOLOGY	-0.3877636	3	2.003e-02	3.045e-01	LRP1:91 HLA-DRA:1410 MBPT52:3484 NA NA NA
GOCC_INNER_DYNEIN_ARM	0.3874496	4	2.278e-03	2.012e-01	DNAH1:1176 DNHD1:1468 DNAH2:1926 DNHD7:2355 NA NA
GOCC_PREFOLDIN_COMPLEX	0.3848355	3	2.108e-02	3.091e-01	VPB1:530 PFDN2:1028 PDRG1:3752 NA NA NA
GOCC_GPI_ANCHOR_TRANSMIDASE_COMPLEX	0.3817825	4	8.179e-03	2.113e-01	GPA1:614 PI6K:455 PI6T:3026 PI6S:3696 NA NA
GOMB_SRP_DEPENDENT_COTRANSLATIONAL_PROTE	0.3808102	2	6.213e-02	4.722e-01	SRPRB:1701 SRPRA:1964 NA NA NA NA
GOMB_ATTACHMENT_OF_GPI_ANCHOR_TO_PROTEIN	0.3807917	5	3.188e-03	1.336e-01	GPA1:614 PI6T:455 GPA1:1898 PI6T:3026 PI6S:3696 NA
GOMB_LEUKOTRIENE_SIGNALING_PATHWAY	0.3769341	5	5.511e-03	1.396e-01	LTB4R:329 CYSLTR2:855 LTB4R:1420 CYSLTR1:2852 RGS1:3903 NA
HP_FALCIFORM_RETINAL_FOLD	-0.3758978	7	6.202e-03	1.422e-01	ZNF408:671 LRP5:674 NDP:256 FZD4:2574 TSPAN12:2774 NA
HP_HYPOPLASTIC_DERMOPIDERMAL_HEMIDESMOS	0.3725575	5	6.670e-04	5.456e-02	LAMC2:427 ITGB4:951 LAMA3:1863 LAMB3:1910 PLEC:2200 ITGA6:2330
GOMB_RIBOSOMAL_PROTEIN_S6_KINASE_ACTIVIZ	0.3723733	4	9.897e-03	2.303e-01	RPS6KA1:154 RPS6KA6:157 RPS6KA2:2241 RPS6KA4:5263 NA NA
HP_PERIPHERAL_RETINAL_AVSULARIZATION	0.3711074	6	1.643e-03	9.585e-02	ZNF406:671 LRP5:674 DLK1:2272 NDP:256 FZD4:2574 TSPAN12:2774
GOMB_POSITIVE_REGULATION_OF_GLYCOGEN_STA	0.3678086	5	4.394e-03	1.588e-01	ADIPOQ:770 EPM2AAT1:1155 IGFB:1206 GSK3A:2713 PPP1R3G:3948 NA
GOMB_NEGATIVE_REGULATION_OF_PROTEIN_CATA	-0.3669162	5	4.490e-03	1.619e-01	LAPTM4:256 USP8:832 VP53S:1269 MGAT3:2960 ATP13A2:4568 NA
HP_FAILURE_TO_THRIVE_SECONDARY_TO_RECURR	0.3667770	6	1.862e-03	1.012e-01	CD3E:721 RAG1:781 RAG2:1763 IL7R:2213 CD247:1108 RAG2:3676
GOMB_PHOSPHATIDYLSELINE_FLIPPASE_ACTIVITY	0.3654336	5	4.654e-03	1.636e-01	ATP11A:137 ATP11C:1005 ATP8B1:1350 ATP8A1:1558 ATP8A2:5920 NA
GOMB_MHC_CLASS_II_RECEPTOR_ACTIVITY	-0.3653929	4	1.137e-02	2.485e-01	HLA-DQB:673 HLA-DRA:1410 HLA-DQA:2845 HLA-DPA1:3070 NA NA
HP_RECURRENT	-0.3641814	5	4.797e-03	1.643e-01	ADORA2A:176 BCKDHA:1038 DBT:1399 BCKDHB:3382 PTH:4065 NA
HP_PARTIAL_ABSENCE_OF_SPECIFIC_ANTIBODY_	-0.3623283	5	5.027e-03	1.679e-01	TNFRSF13B:258 CD19:565 CR2:2474 ICOS:2676 SASH3:4241 NA
GOMB_MINUS_END_DIRECTED_MICROTUBULE_MOTO	0.3617653	16	5.451e-07	3.521e-04	DNAH1:119 DNAH3:232 DNAH10:368 DNAH3:445 DYNC2H1:487 DNAH5:728
GOCC_AXONEMAL_DYNEIN_COMPLEX	0.3615223	16	5.548e-07	3.521e-04	DNA2:36 DNAH3:232 CDDG5:362 DNAH9:435 DNAH2P:728 DNAH17:1027
GOMB_RNA_MEDIATED_HETEROCHROMATIN_FORMAT	0.3613890	5	5.131e-03	1.692e-01	SIRT6:866 FAM12A:720 HELLS:1863 ZNF1:2720 CENPF:3392 NA
GOMB_PARATHYROID_GLAND_DEVELOPMENT	-0.3582283	6	2.381e-03	1.135e-01	GATA3:1405 TSH:1600 GCM2:1880 TGFBRI:1921 HOXA3:2606 CRKL:3210
GOMB_NEGATIVE_REGULATION_OF_SYNAPTIC_VES	-0.3521294	3	3.456e-02	3.812e-01	FMRI:1102 BRAF:2

MP0006054 spinal hemorrhage	-0.2188257	8	3,219e-02	3.058e-01	SPHK1:725 FPLT:1300 C1GALT1:1852 F1L1:2179 PSEN1:3166 FBLM1:4638
MP0003121 genetic imprinting	-0.2686825	20	1,387e-03	8.618e-02	AXIN1:360 SGCE:1001 ARIDA1:1205 CCK1NC1:1457 LHBLS:1683 NDN:1893
MP0003122 maternal imprinting	-0.1997596	11	1,839e-02	2.692e-01	AXIN1:360 SGCE:1001 ARIDA1:1205 IGFB:1206 NDN:1893 DLD1:2272
MP0003274 increased susceptibility to	-0.1667610	15	2,550e-02	2.692e-01	PECAM1:312 IFNGR1:341 FPR2:810 SOD3:2172 SODCS:2847 TNFSF10:3272
MP0005646 abnormal pituitary gland	0.1657007	18	1,570e-02	2.170e-01	GNRH1:106 DRD2:170 RASGRF1:370 ARNT2:413 NF1:1248 PRP1:1599
MP0003303 peritoneal inflammation	-0.1607388	10	8,006e-02	4.560e-01	PECAM1:312 LYN:1062 PTGS2:2086 SODCS:2847 STEGAL:1351 IL10:4251
MP00010386 abnormal urinary bladder	0.1592785	14	3,927e-02	3.406e-01	CHRM3:1023 FBN1:2053 P5AP:2058 CHRN3:3141 UPK2:3431 KCNMA1:4062
MP0002254 reproductive system inflammat	-0.1806762	5	2,211e-01	7.048e-01	MGFB8:1508 RELB:2427 EPHA1:14254 PGR:4342 AIRC:12758 NA
MP0005275 abnormal skin tensile	0.1559055	17	2,623e-02	2.692e-01	OGN2:244 CLM1:2427 COL5A2:1543 DES:1639 DSG4:1826 FBN1:2053
MP0004043 abnormal pH regulation	-0.1486030	14	6,466e-02	4.116e-01	RHCG:202 LMC121:221 SLC26A7:1687 WNK4:1842 SLC4A11:102 SLC4AT:2631
MP0005174 abnormal tail pigmentation	0.1482395	14	5,505e-02	4.116e-01	MYO5A:725 CBL:999 M1CR:2073 DOCKY:3084 BLOC1:53:3615 KIT:4099
MP0008498 abnormal cutaneous collagen	0.1429851	15	5,546e-02	4.116e-01	OGN2:244 PLOD1:816 COL5A2:1543 DES:1639 FBN1:2053 TNXB:2066
MP0003172 abnormal lysosome physiology	-0.1429487	21	2,356e-02	2.692e-01	NAGPA:12 MABNA:142 AP3B1:962 IDS:1200 HPSA:1403 CTD3:2433
MP0000751 myopathy	0.1425907	18	3,652e-02	3.636e-01	TCAP:145 DMD:228 ITGA7:555 PLEC:2200 COL6A1:2205 LDBS:3414
MP0006292 abnormal olfactory placode	-0.1328421	10	1,461e-01	5.640e-01	HHEX:599 HESX1:2469 PAX6:2478 POU3F1:3963 DKO1:5797 BGD2:6535
MP0006280 abnormal autophagy	-0.1317414	15	7,904e-02	4.560e-01	ATG9A:874 ATG9:952 PMPE2:2259 BNP1L:1687 BECN1:1689 ATG9A:3124
MP0000165 abnormal hypothalamic pituitary	0.1309957	14	9,001e-02	4.709e-01	0.1309102 NF:1248 UBE3A:1248 UBE3A:1248 UBE3A:1248
MP0003123 peritoneal inflammation	-0.1309116	10	2,666e-01	7.087e-01	AXIN1:360 CCK1NC1:1457 LHBLS:1683 ORB1:2890 G45A:3320 GPC3:13904
MP0003300 gastrointestinal ulcer	-0.1295691	7	3,350e-02	4.706e-01	TGFB1:994 VDR:1467 PKHD1:2341 CYLD:3313 IL27A3:101 IL10:4251
MP00010234 abnormal vibrissa follicle	0.1266649	4	3,797e-01	8.016e-01	PKP3:866 CHUK:3642 SPINK5:6419 ST14:12007 NA:14
MP0004134 abnormal chest morphology	0.1263075	22	4,003e-02	3.406e-01	PTCH1:718 HMOX3:974 NKX3:2116 PDGF:1656 HSCD501:1358 UNCLN:1439
MP0003646 muscle fatigue	0.1263482	9	8,896e-01	6.433e-01	NTS1:1025 MB:2632 SLC24A:2829 MTOR:3196 SOD2:3255 PNFGA:CA:5051
MP0001529 abnormal vocalization	0.1248371	18	1,707e-02	4.301e-01	E2F4:92 DRD2:170 FOXO2P:743 CHRM2:1292 TOR1A:2129 PDARCA:2154
MP00011188 hyperpigmentation	0.1215453	7	2,657e-01	7.794e-01	DRD2:170 TERF1:1095 M1CR:2073 KIT:4099 CCKNA:9291 TERF2P1:10244
MP0003787 abnormal imprinting	-0.1205357	8	8,300e-02	7.028e-01	ARIDA1:1205 CCK1NC1:1457 ATRX:2634 ARID4B:440 RB1:4501 SMCHD1:5014
MP0003890 abnormal embryonic-extraembry	-0.1170296	16	1,055e-01	4.891e-01	GLC2C:155 HSD17B12:487 HIRA:1025 PALB2:1287 FCHL1:1619 FOXA2:2417
MP0003656 abnormal erythrocyte physiolo	-0.1168030	21	6,430e-02	4.301e-01	SLC4A1:27 ANK1:119 PFKM:194 MAN2A:1784 FECH:934 BNP3L:1847
MP0000750 abnormal muscle regeneration	0.1159244	31	2,584e-02	2.692e-01	MYF5:82 DMD:228 CAV2:251 MYOZ1:1279 NF5:2232 IFR1:3245
MP0001515 abnormal ear pigmentation	0.1150872	15	1,232e-01	5.121e-01	MYO5A:725 CBL:999 SLC2A5:1481 M1CR:2073 POLH:3201 BLOC1S3:3615
MP0001835 abnormal antigen presentation	0.1149986	48	6,027e-03	1.301e-01	TNFRSF11B:118 PSMB2:401 PDCD1:LG2:758 RAG1:781 CSF2:1157 MAP3K4:14677
MP0002396 abnormal hematopoietic system	-0.1107924	19	9,016e-02	4.706e-01	CASP8:191 PMAN1:784 MYC:858 ARHGAP:1414 CDK6:2438 SNIA2:2571
MP0005084 abnormal gallbladder morpholo	0.1102309	14	5,378e-01	5.748e-01	VT1B:196 HNF1B:415 HXL5:53 CUSP:127:1299 LK1B:1515 NPYRL1:2855
MP0004270 analgesia	0.1087706	17	1,210e-01	5.192e-01	CASP8:191 PMSB2:401 KIF1B:181 PCLX3:1902 NRG1:2188 RYR1:2891
MP0003806 abnormal nucleotide metabolis	0.1080727	9	6,219e-01	7.289e-01	TPMT:2493 TALDO1:2842 VPS