

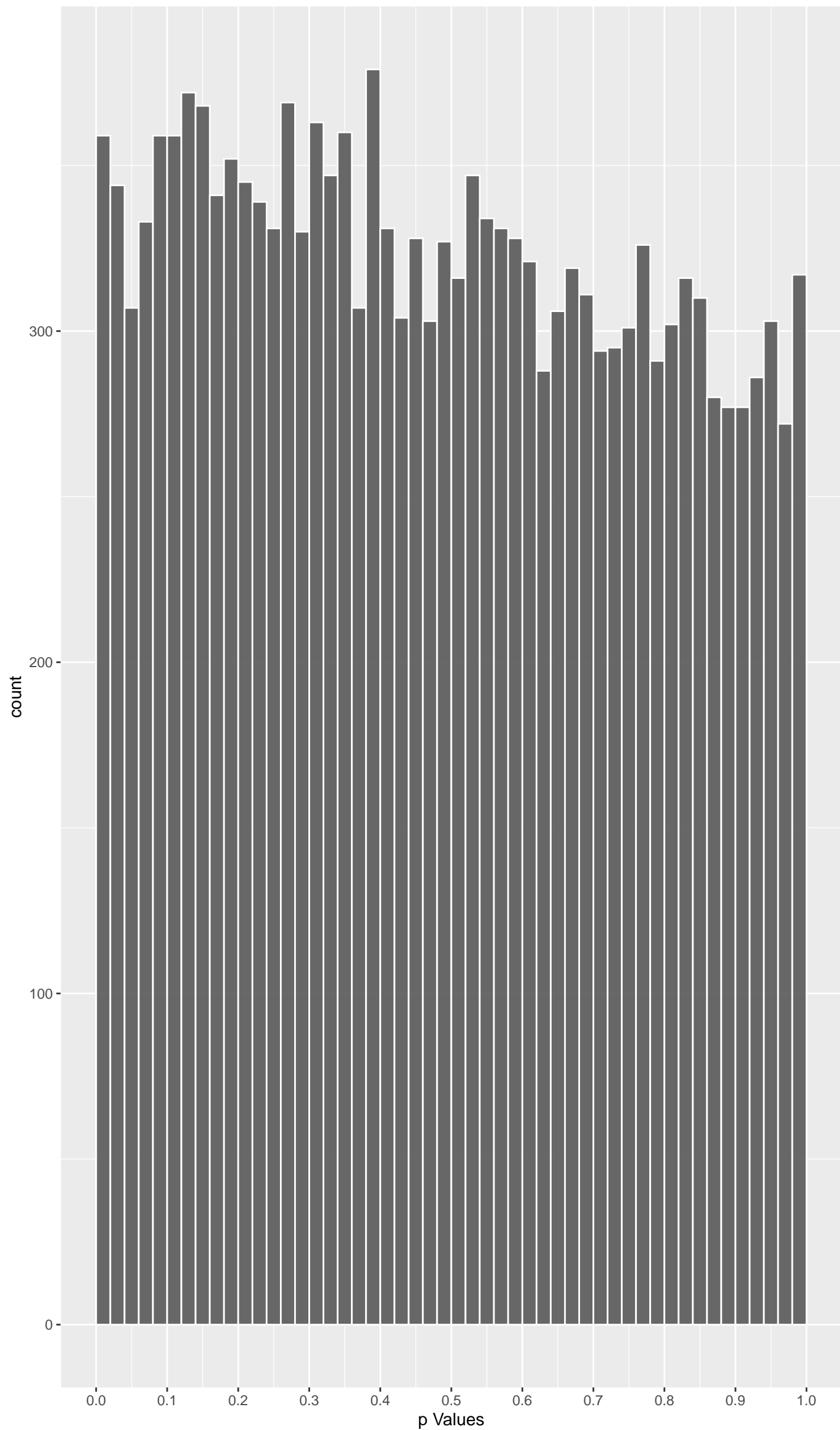
Top genes by P–value Permulated

Gene	Rho	N	P	p.adj	permP	permPValue	qValueNoperm	qValuePerm
PTCD3	0.09932340	313	1.866e-07	4.455e-05	1.515e-05	1.515e-05	9.596e-03	2.195e-01
PPFIA3	0.17794716	171	2.698e-07	5.909e-05	3.970e-04	3.970e-04	1.187e-02	6.964e-01
ABCB1	0.07230963	288	3.116e-05	1.476e-03	5.303e-04	5.303e-04	6.358e-02	6.964e-01
BAX	0.18734038	105	5.878e-05	2.279e-03	6.455e-04	6.455e-04	8.105e-02	6.964e-01
ARHGEF12	0.09204905	293	1.457e-06	1.785e-04	7.273e-04	7.273e-04	1.980e-02	6.964e-01
OFD1	0.16618570	274	1.407e-10	1.755e-07	7.394e-04	7.394e-04	2.007e-04	6.964e-01
CADPS2	0.08121832	251	3.899e-05	1.694e-03	9.606e-04	9.606e-04	6.749e-02	6.964e-01
CASR	0.09342518	251	8.477e-06	5.700e-04	1.027e-03	1.027e-03	3.515e-02	6.964e-01
DNAH2	0.21574345	312	2.693e-15	4.364e-11	1.027e-03	1.027e-03	6.486e-07	6.964e-01
TACR2	0.15034267	256	4.733e-09	2.841e-06	1.045e-03	1.045e-03	1.564e-03	6.964e-01
ZFYVE9	0.14857597	286	6.384e-10	5.747e-07	1.073e-03	1.073e-03	4.746e-04	6.964e-01
ANKRD35	0.15249551	289	2.905e-10	3.363e-07	1.118e-03	1.118e-03	3.570e-04	6.964e-01
CFAP45	0.11550068	273	1.507e-07	3.942e-05	1.285e-03	1.285e-03	9.381e-03	6.964e-01
ESYT3	0.11976678	299	1.778e-08	7.582e-06	1.297e-03	1.297e-03	2.874e-03	6.964e-01
GGTLC3	0.10623403	248	2.005e-06	2.166e-04	1.355e-03	1.355e-03	2.146e-02	6.964e-01
PTPRB	0.09626052	324	1.772e-07	4.350e-05	1.385e-03	1.385e-03	9.596e-03	6.964e-01
SDS	0.08252280	243	4.607e-05	1.924e-03	1.424e-03	1.424e-03	7.372e-02	6.964e-01
SLC10A6	0.09033010	277	3.857e-06	3.572e-04	1.427e-03	1.427e-03	3.028e-02	6.964e-01
MZF1	0.11725148	252	4.068e-07	7.434e-05	1.427e-03	1.427e-03	1.241e-02	6.964e-01
WIPF3	0.08197540	137	3.794e-03	3.631e-02	1.452e-03	1.452e-03	3.186e-01	6.964e-01
NUP88	0.18840808	267	1.310e-11	4.246e-08	1.473e-03	1.473e-03	1.262e-04	6.964e-01
ALYREF	0.14952497	96	8.231e-04	1.323e-02	1.473e-03	1.473e-03	1.949e-01	6.964e-01
SP3	0.08035184	147	2.835e-03	2.976e-02	1.509e-03	1.509e-03	2.864e-01	6.964e-01
ABCB4	0.10082176	291	4.477e-07	7.886e-05	1.570e-03	1.570e-03	1.274e-02	6.964e-01
ZNF606	0.07759741	249	6.625e-05	2.438e-03	1.591e-03	1.591e-03	8.190e-02	6.964e-01

Top genes by Q–Value Permulated

Gene	Rho	N	P	p.adj	permP	permPValue	qValueNoperm	qValuePerm
PTCD3	0.09932340	313	1.866e-07	4.455e-05	1.515e-05	1.515e-05	9.596e-03	2.195e-01
PYGM	0.14280726	224	1.215e-07	3.455e-05	2.330e-03	2.330e-03	9.010e-03	6.964e-01
SUPT4H1	0.42948718	25	5.777e-03	4.783e-02	1.931e-03	1.931e-03	3.623e-01	6.964e-01
PTK7	0.04657853	280	1.507e-03	1.993e-02	3.867e-03	3.867e-03	2.419e-01	6.964e-01
RARS1	0.05524878	255	8.969e-04	1.402e-02	3.133e-03	3.133e-03	2.009e-01	6.964e-01
DHX58	0.03808004	296	3.636e-03	3.521e-02	2.748e-03	2.748e-03	3.126e-01	6.964e-01
CKMT2	0.09831331	186	1.123e-04	3.468e-03	3.009e-03	3.009e-03	9.802e-02	6.964e-01
NARS1	0.07761724	243	8.341e-05	2.834e-03	3.548e-03	3.548e-03	8.826e-02	6.964e-01
SDS	0.08252280	243	4.607e-05	1.924e-03	1.424e-03	1.424e-03	7.372e-02	6.964e-01
PDCL	0.11137572	194	2.149e-05	1.106e-03	3.691e-03	3.691e-03	5.210e-02	6.964e-01
ABCB4	0.10082176	291	4.477e-07	7.886e-05	1.570e-03	1.570e-03	1.274e-02	6.964e-01
ABCB1	0.07230963	288	3.116e-05	1.476e-03	5.303e-04	5.303e-04	6.358e-02	6.964e-01
CSAD	0.03766079	260	7.619e-03	5.738e-02	3.076e-03	3.076e-03	3.959e-01	6.964e-01
NCOR1	0.09276775	285	1.901e-06	2.146e-04	1.873e-03	1.873e-03	2.146e-02	6.964e-01
SLC10A6	0.09033010	277	3.857e-06	3.572e-04	1.427e-03	1.427e-03	3.028e-02	6.964e-01
C11orf53	0.08954310	265	7.358e-06	5.165e-04	2.227e-03	2.227e-03	3.323e-02	6.964e-01
PRSS53	0.08168560	295	6.097e-06	4.796e-04	3.655e-03	3.655e-03	3.323e-02	6.964e-01
ZFYVE9	0.14857597	286	6.384e-10	5.747e-07	1.073e-03	1.073e-03	4.746e-04	6.964e-01
PIP	0.12368616	250	2.053e-07	4.685e-05	3.018e-03	3.018e-03	9.808e-03	6.964e-01
ALB	0.07914234	303	6.456e-06	4.935e-04	3.215e-03	3.215e-03	3.323e-02	6.964e-01
HPS3	0.06782127	305	3.334e-05	1.544e-03	3.127e-03	3.127e-03	6.555e-02	6.964e-01
RAB8A	0.19976468	78	4.569e-04	9.005e-03	3.630e-03	3.630e-03	1.618e-01	6.964e-01
HAS2	0.23169520	105	5.855e-06	4.721e-04	1.612e-03	1.612e-03	3.323e-02	6.964e-01
SP3	0.08035184	147	2.835e-03	2.976e-02	1.509e-03	1.509e-03	2.864e-01	6.964e-01
SPTBN5	0.13306984	284	6.645e-09	3.846e-06	3.106e-03	3.106e-03	1.828e-03	6.964e-01

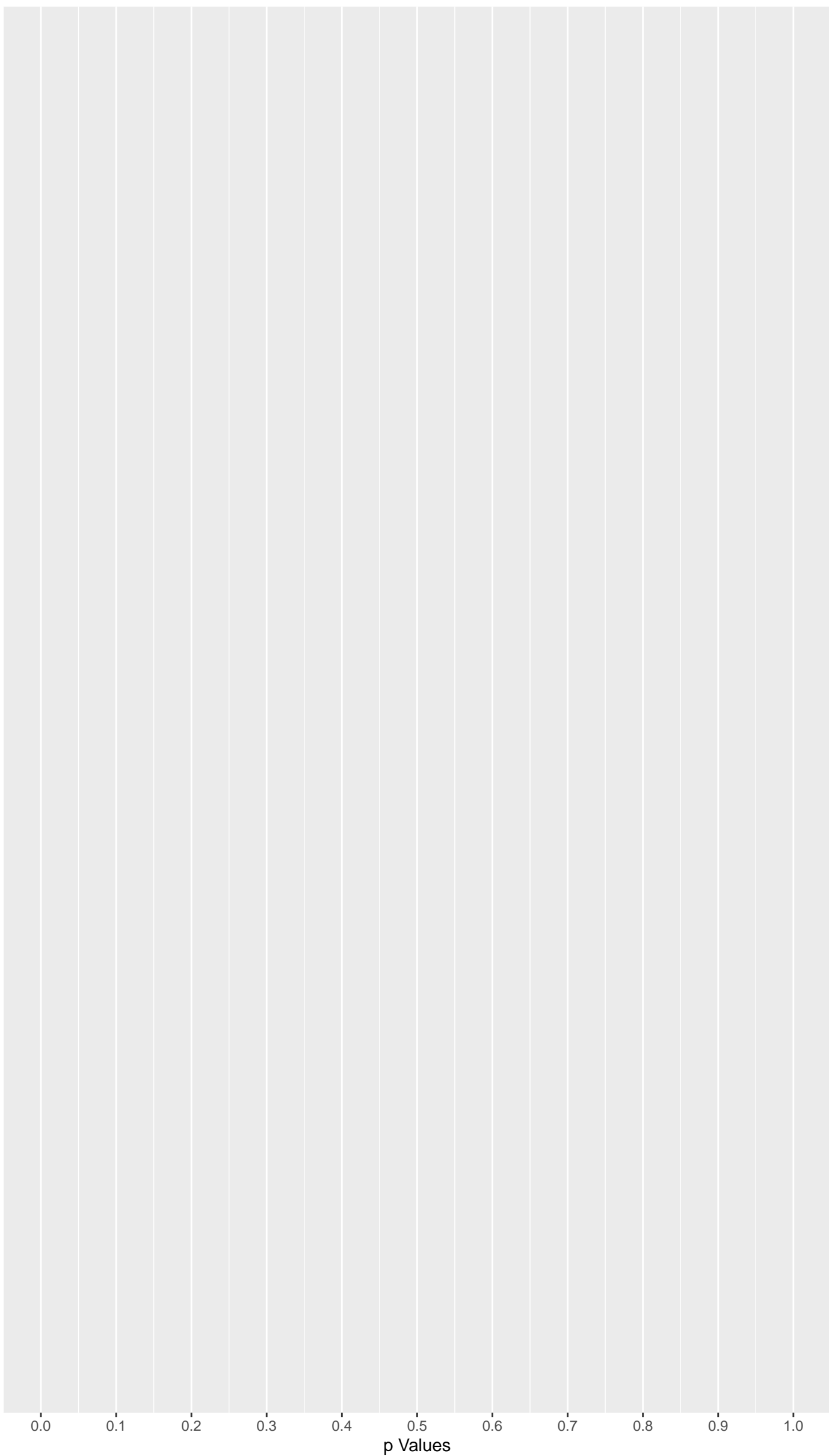
Positive Rho Permulated



Top Positive genes by P–value Permulated

Gene	Rho	N	P	p.adj	permP	permPValue	qValueNoperm	qValuePerm
PTCD3	0.09932340	313	1.866e-07	4.455e-05	1.515e-05	1.515e-05	9.596e-03	2.195e-01
PPFIA3	0.17794716	171	2.698e-07	5.909e-05	3.970e-04	3.970e-04	1.187e-02	6.964e-01
ABCB1	0.07230963	288	3.116e-05	1.476e-03	5.303e-04	5.303e-04	6.358e-02	6.964e-01
BAX	0.18734038	105	5.878e-05	2.279e-03	6.455e-04	6.455e-04	8.105e-02	6.964e-01
ARHGEF12	0.09204905	293	1.457e-06	1.785e-04	7.273e-04	7.273e-04	1.980e-02	6.964e-01
OFD1	0.16618570	274	1.407e-10	1.755e-07	7.394e-04	7.394e-04	2.007e-04	6.964e-01
CADPS2	0.08121832	251	3.899e-05	1.694e-03	9.606e-04	9.606e-04	6.749e-02	6.964e-01
CASR	0.09342518	251	8.477e-06	5.700e-04	1.027e-03	1.027e-03	3.515e-02	6.964e-01
DNAH2	0.21574345	312	2.693e-15	4.364e-11	1.027e-03	1.027e-03	6.486e-07	6.964e-01
TACR2	0.15034267	256	4.733e-09	2.841e-06	1.045e-03	1.045e-03	1.564e-03	6.964e-01

Negative Rho Permulated



Top Negative genes by P–value Permulated

Gene	Rho	N	P	p.adj	permP	permPValue	qValueNoperm	qValuePerm
NA	NA	NA	NA	NA	NA	NA	NA	NA
NA.1	NA	NA	NA	NA	NA	NA	NA	NA
NA.2	NA	NA	NA	NA	NA	NA	NA	NA
NA.3	NA	NA	NA	NA	NA	NA	NA	NA
NA.4	NA	NA	NA	NA	NA	NA	NA	NA
NA.5	NA	NA	NA	NA	NA	NA	NA	NA
NA.6	NA	NA	NA	NA	NA	NA	NA	NA
NA.7	NA	NA	NA	NA	NA	NA	NA	NA
NA.8	NA	NA	NA	NA	NA	NA	NA	NA
NA.9	NA	NA	NA	NA	NA	NA	NA	NA

Geneset		stat	num_genes	pval	padj	gene.vals
bladder		-0.160117878	24	6.677e-03	1.202e-01	UPK2:134 PLA2G2F:217 SLC14A1:306 MSX2:309 SEMA3E:1381 ACER2:2230
vagina		0.112320956	91	2.263e-04	1.222e-02	RNF222:82 EVPL:126 GJB3:257 ENDOU:339 SULT1E1:410 KRT13:492
hippocampus.proper		-0.066351284	11	4.463e-01	8.654e-01	NEUROG3:248 NTS:1086 NEUROD6:4732 GRP:5569 SLC17A7:6436 OLIG2:6778
caudate.nucleus		0.061706366	26	2.766e-01	8.654e-01	GRM3:80 GPR88:95 ANO3:334 RGS14:1114 TAC1:1338 AQP4:1961
left.ventricle		0.061445305	69	7.851e-02	6.056e-01	CKMT2:54 S100A1:123 MYH7B:181 MYL3:321 SMPX:520 ASB1:542
fallopian.tube		-0.059554967	52	1.383e-01	6.789e-01	CFAP157:73 HOXC4:332 HOXA6:415 ADAMTS3:645 EGR1:1591 CRISPLD2:1650
endocervix		0.056094196	72	1.009e-01	6.657e-01	BDKRB1:91 PLPP3:115 NXNL2:209 MSX1:350 TGM2:569 PWP2:947
leg.skin		0.055028346	217	5.693e-03	1.202e-01	ANKRD35:12 POF1B:66 RNF222:82 EVPL:126 GGT6:139 FAM83F:188
breast		0.051782294	15	4.877e-01	8.654e-01	LMXB1B:125 THRSP:2823.5 GSC:3105 NPY2R:3277 ABCB5:4003 TFAP2B:6113
suprapubic.skin		0.050664190	194	1.591e-02	1.718e-01	SLC10A6:18.5 RNF222:82 WNT4:90 EVPL:126 GGT6:139 FAM83F:188
coronary.artery		-0.049413688	15	5.078e-01	8.654e-01	HEYL:484 SOST:632 CCDC190:1096 MYO18B:2351 COL4A1:2733 MTHFD1L:3246
skeletal.muscle		0.046787336	239	1.377e-02	1.718e-01	PYGM:42 CKMT2:54 SLC2A4:160 TNNI2:186 MSS51:194.5 USP13:197
pancreas		0.044847150	94	1.346e-01	6.789e-01	CASR:8.5 PRODH2:111 CATSPERB:132.5 GCG:299 PNLP1RP1:337 ONECUT1:392
ectocervix		-0.043309474	25	5.450e-01	8.654e-01	ADRA1D:1000 TSKU:1808 ADRA2A:2027 KCNK6:2692 MATN2:3244 FGF10:3561
nucleus.accumbens		0.037904216	99	1.945e-01	8.654e-01	GPR88:95 KCNP1:158 PTPN5:184 ANO3:334 PENK:364 GPR6:608.5
esophagus.mucosa		0.037017906	220	6.115e-02	5.504e-01	RNF222:82 BDKRB1:91 CLIC3:92.5 DENND2C:113 EVPL:126 TGM1:131
putamen		0.03691357	15	6.201e-01	9.050e-01	GRM3:80 GPR88:95 ANO3:334 KCNH4:2081.5 RGS9:2717 LRRCL10B:3136
Brodmann.area.24		0.034009398	31	5.128e-01	8.654e-01	SLC39A12:309 SLC25A18:478 DDN:1413 SLC6A1:2491 SHANK1:2878 UPP2:3217
subcutaneous.adipose		-0.033559582	72	3.264e-01	8.654e-01	PLIN1:728 FZD4:792 PNPLA2:1203 G0S2:1241 ANGPTL4:1301 BMP6:1369
esophagogastric.junction		-0.032693923	8	7.489e-01	9.240e-01	COL4A5:2383 BARX1:5206 NKX6-1:5763 GADL1:7900 ADCY5:8233 HOKA4:9210
aorta		-0.029175763	154	2.148e-01	8.654e-01	LTBP1:125 MYO1D:185 TBXA2R:234 ART4:305 PMEP4:1368 IRAG1:428
eye.development		-0.029146938	67	4.107e-01	8.654e-01	CITED2:389 PROX1:621 FZD4:792 CDH11:879 KLF4:1015 MEIS2:1168
sigmoid.colon		-0.028927434	52	4.716e-01	8.654e-01	SLC5A7:11 TTC:453 VIP:469 HLX:1387 HAND1:1822 HMCN2:1911
greater.omentum		-0.027563112	33	5.842e-01	8.822e-01	UPK3B:519 PLIN1:728 ADAMTS4:1044 HBEGF:1150 SPRY1:2060 ATF3:2573
spleen		-0.027230574	298	1.109e-01	6.657e-01	NOX5:36 CD180:74 BLK:90 BANK1:96 TNFRSF4:204 TAS1R3:235
hypothalamus		0.027214551	66	4.459e-01	8.654e-01	SYTL5:312 DLX2:450 SCN9A:484 ENKUR:556 OXT:910 GABRG3:1163
substantia.nigra		-0.026723172	12	7.487e-01	9.240e-01	FOXB1:130 CHRM5:861 RPE65:3248 SPX:3861 SLC6A3:4464 RET:6738
cerebral.cortex		0.026592321	107	3.443e-01	8.654e-01	CALHM1:40 RIMKLA:83 PACSIN1:138 KCNF1:194.5 EIF4E1B:274 HTR3B:515
C1.spinal.cord		-0.025345457	182	2.423e-01	8.654e-01	GFAP:64 FOXB1:130 HHIP:224 SLC5A11:458 FAM222A:460 COLGALT2:599
esophagus.mucularis.mucosa		0.025039952	26	6.589e-01	9.145e-01	PRUNE2:130 KCNMB1:1064 SYNM:1698 NTN1:3444 FAM83B:3537 F2RL2:4238
ovary		0.023667029	103	4.088e-01	8.654e-01	WIPF3:20 BTNL2:53 KCNT2:403 C21orf62:422 CCDC170:436 TMEM21:747
adrenal.gland		0.020876066	108	4.558e-01	8.654e-01	ABCB1:3 SLC47A1:96 MGST1:262 CYSLTR2:305 KCNN2:612.5 MAP3K15:725
blood		-0.020364754	276	2.505e-01	8.654e-01	CTSW:6 ARHGDB123: AQP10:29 NFE2:32 RGS19:33 BLK:90
pituitary.gland		-0.019676417	213	3.272e-01	8.654e-01	NAALAD2:18 RXRG:38 OTOG:211 ZSWIM2:308 CRYBA2:455 VWA07:461
transverse.colon		0.019482835	149	4.150e-01	8.654e-01	B3GNT6:30 EPS8L3:65 ETHE1:155 GCG:299 TMEM54:419 LGLAL59C:487
amygdala		0.018819337	9	8.450e-01	9.240e-01	LHPFL3:1480 PCDH15:1496 PTPR21:3438 NEUROD2:6882 SLC17A7:9770 TNR:10465
transformed.skin.fibroblast		-0.014560148	259	4.256e-01	8.654e-01	KDELR3:76 PRKD1:197 SPOCD1:287 SEPTIN11:382 CITED2:389 MXRA5:532
tibial.nerve		-0.013085956	192	5.355e-01	8.763e-01	GFR3A3:55.5 SCARA5:172 SLC27A6:261 GLDN:336 IL1RAPL1:443 LGI2:510
prostate		-0.012034885	38	7.977e-01	9.240e-01	NTF4:855 GLIS1:1119 TULP1:1917 SRD5A2:2029 P2RX2:2490 SP8:2704
testis		0.009100238	1381	2.972e-01	8.654e-01	DNAH2:8.5 CFAP45:13 SLAMF9:26 GSG1:37 C11orf53:41 OVOL1:46

Geneset	stat	num_genes	pval	padj	gene.vals
GOCC_9PLUS0_MOTILE_CILIUM	0.4546269	4	1.637e-03	5.422e-01	CFAP45:13 ENKUR:556 DNAH11:1124 DNAH5:1259 NA NA
GOCC_B_CELL_RECEPTOR_COMPLEX	-0.4107645	3	1.373e-02	7.190e-01	SYK:1076 CD79B:1561 CD79A:1707 NA NA NA
HP_APLASIA_CUTIS_CONGENITA_ON_TRUNK_OR_L	0.3852853	6	1.081e-03	4.775e-01	ITGB4:134 PLEC:147 KRT14:905 ITGA6:1212 ARHGAP31:1607 KRT5:7146
GOMF_ANDROGEN_BINDING	0.3768753	4	9.037e-03	7.035e-01	ALDH1A1:1092 TSPO:1523 SHBG:2329 SLC39A9:3012 NA NA
HP_BRONCHIAL_WALL_THICKENING	-0.3754813	6	1.446e-03	5.053e-01	ABCA3:608 HYDIN:1101 FNIP1:1866 SFTPC:2457 PAK2:2935 TTC26:3169
HP_TALL_CHIN	0.3750714	5	3.676e-03	9.594e-01	MYH8:382 NSD1:975 TLK2:2008 APC2:2163 OPHN1:4559 NA
GOCC_CUL4B_RING_E3_UBIQUITIN_LIGASE_COMP	0.3738549	4	9.606e-03	7.097e-01	CUL4B:583 DDB2:1421 DTL:2811 RBX1:3331 NA NA
GOMF_MELANOCORTIN_RECEPTOR_BINDING	-0.3723779	4	9.895e-03	7.097e-01	AGRP:1497 ASIP:1601 MRAP:2208 MRAP2:2994 NA NA
HP_PECTUS_EXCAVATUM_OF_INFERIOR_STERNUM	0.3709487	5	4.069e-03	5.954e-01	NF1:522 PTPN11:1349 MAP2K1:2117.5 BRAF:2370 SOS1:4070 NA
GOBP_CELL_CELL_JUNCTION_DISASSEMBLY	0.3690699	5	4.260e-03	5.954e-01	FER:751 SNAI2:1530 TGFβ3:2504 ABCC8:2629 TGFβR1:3169 NA
GOBP_NEGATIVE_REGULATION_OF_HEMATOPOIETI	0.3682289	4	1.075e-02	7.137e-01	ZFP36:1541 NFE2L2:1576 N4BP2L2:1928 TCF15:3478 NA NA
GOMF_MHC_CLASS_II_RECEPTOR_ACTIVITY	0.3644865	4	1.158e-02	7.137e-01	HLA-DOA:243 HLA-DOB:1690 HLA-DPA1:2852.5 HLA-DRA:3972 NA NA
GOCC_PAR_POLARITY_COMPLEX	-0.3597092	5	5.341e-03	6.152e-01	PRKCI:564 PARD6B:951 PARD6B:1738 PARD3:3725 PARD6A:4399 NA
GOCC_B_WICH_COMPLEX	0.3571460	6	2.447e-03	5.954e-01	DEK:247 ERCC6:1037 MYBBP1A:2177 DDX21:2241 SF3B1:2955 SMARCA5:5185
GOBP_RESPONSE_TO_PHEROMONE	-0.3543741	2	8.258e-02	8.580e-01	TMEM145:778 GPR180:3945 NA NA NA NA
HP_GENERALIZED_AMYLOID_DEPOSITION	0.3534351	3	3.398e-02	8.370e-01	APOA1:1827 GSN:2086 B2M:3195 NA NA NA
HP_RECURRENT_NEISSERIAL_INFECTIONS	-0.3495784	5	6.784e-03	6.687e-01	C8B:98 C6:433 C5:2207 CFB:4609 CFI:4850 NA
GOBP_POSITIVE_REGULATION_OF_EXTRACELLULA	-0.3463307	4	1.644e-02	7.377e-01	CPB2:1176.5 RGCC:2007 BMP2:2792 AGT:4003 NA NA
HP_ABNORMAL_MIDDLE_EAR_REFLEXES	0.3452500	5	7.501e-03	6.744e-01	OTOF:853 PRORP:859 AIFM1:1196 MPDU1:1595 DIAPH3:8032 NA
GOBP_PPTIDYL_ARGININE_N_METHYLATION	0.3449578	5	7.551e-03	6.744e-01	PRMT5:1500 PRMT3:1662 PRMT8:2791 NDUFAF7:3213 PRMT6:3356 NA
HP_ELEVATED_CIRCULATING_LONG_CHAIN_FATTY	-0.3424484	5	8.000e-03	6.830e-01	ABCD1:699 PEX19:700 PEX1:1212 PEX5:4881 CPT2:5280 NA
GOBP_TRICUSPID_VALVE_MORPHOGENESIS	-0.3416423	4	1.795e-02	7.377e-01	HEY2:429 BMPR2:2367 TGFβR2:3006 BMPR1A:4473 NA NA
GOMF_INTERLEUKIN_2_RECEPTOR_BINDING	-0.3396734	5	8.524e-03	7.022e-01	GATA3:576 IL2:1880 TIMM50:3264 IL21:3460 ECM1:3839 NA
GOBP GRANULOCYTE_COLONY_STIMULATING_FACT	0.3395927	4	1.865e-02	7.377e-01	CD34:683 TSLP:709 ISL1:4083 HAVCR2:4879.5 NA NA
GOBP_POSITIVE_REGULATION_OF_RESPONSE_TO_	-0.3388384	6	4.047e-03	5.954e-01	RIPK1:578 ENDOG:1284 HDAC6:1821 ABL1:2142.5 FOXPI1:4244 PAWR:5617
GOCC_CCAAT_BINDING_FACTOR_COMPLEX	-0.3377705	6	4.165e-03	5.954e-01	NFYB:245 NFYC:1588 ATF2:1910 ING2:2021 NFYA:3378 CEBPZ:6673
GOBP_SKELETAL_MUSCLE_SATELLITE_CELL_ACTI	-0.3377407	8	9.390e-04	4.665e-01	EPHB1:69 GJD4:1079 MEGF10:2381 CAPN3:2507 WNT7A:2913 SOX15:3455
HP_APLASIA_CUTIS_CONGENITA_OVER_THE_SCAL	0.3374607	6	4.199e-03	5.954e-01	ITGB4:134 PLEC:147 MCTP2:1043 BMS1:3150 DLL4:4367 UBA2:6909
GOMF_PEROXISOME_TARGETING_SEQUENCE_BINDI	-0.3373764	5	9.891e-03	7.035e-01	PEX19:700 PEX5L:904 BABAM2:3022 PEX7:3691 PEX5:4881 NA
HP_CONGENITAL_ADRENAL_HYPERPLASIA	0.3360661	4	1.991e-02	7.450e-01	POR:1825 CYP17A1:2556 STAR:2615 HSD3B2:3596 NA NA
GOBP_ESTABLISHMENT_OF_LEFT_RIGHT_ASYMMET	0.3345227	4	2.049e-02	7.552e-01	CFAP45:13 CFAP52:173 ENKUR:556 CCDC39:9977 NA NA
GOCC_MCRD_MEDIATED_MRNA_STABILITY_COMPLE	0.3334727	5	9.807e-03	7.097e-01	PAIP1:285 SYNCNRP1:1467 CSDE1:1538 HNRNPD:3429 PABPC1:6740 NA
GOBP_PHENYLPROPANOID_METABOLIC_PROCESS	0.3331674	2	1.027e-01	8.609e-01	PON3:1308 CYP1A1:4086 NA NA NA NA
GOBP_REGULATION_OF_FAS_SIGNALING_PATHWAY	-0.3329904	3	4.575e-02	8.580e-01	ZDHHC7:789 TMBIM1:1080 SMAD5:6249 NA NA NA
GOBP_HYPOTHALAMUS_CELL_MIGRATION	-0.3326495	5	9.990e-03	7.097e-01	FOXB1:130 SEMA3E:1381 NDNF:1925 NRP2:2141 NRP1:8022 NA
GOBP_POSITIVE_REGULATION_OF_HYDROGEN_PER	-0.3326225	4	2.122e-02	7.566e-01	ENDOG:1284 HDAC6:1821 ABL1:2142.5 PAWR:5617 NA NA
GOBP_SPHINGOLIPID_TRANSLOCATION	0.3312035	4	2.178e-02	7.584e-01	ABCB1:3 ABCB4:24 ABCC1:3415 ABCA2:7474 NA NA
GOBP_BRANCHED_CHAIN_AMINO_ACID_BIOSYNTH	0.3308770	5	1.039e-02	7.137e-01	SDS:17 BCAT2:1648 BCAT1:2244.5 SDSL:3421 ILVLB:6330 NA
GOCC_DNA_REPLICATION_FACTOR_A_COMPLEX	-0.3271269	3	4.970e-02	8.580e-01	RPA2:380 RPA1:2077 RPA3:5950 NA NA NA
GOBP_CHONDROBLAST_DIFFERENTIATION	-0.3271128	5	1.130e-02	7.137e-01	RARA:126 GDF5:1242 CCN1:1726 FGF2:5431 FGF4:5494 NA

Geneset	stat	num_genes	pval	padj	gene_vals
REACTOME_CHYLOMICRON_CLEARANCE	-0.4270646	5	9.417e-04	7.207e-01	APOB:107 APOE:246 LDLR:1315 LIPC:1642 LDLRAP1:2603 NA
REACTOME_EICOSANOIDS	-0.3748340	4	9.417e-03	9.378e-01	TBXAS1:1054 CYP8B1:1278 CYP4B1:2853 PTGIS:2929 NA NA
REACTOME_BETA_OXIDATION_OF_DECANOYL_COA_	-0.3640254	6	2.014e-03	7.730e-01	HADH:66 ACADM:388 MECR:2183 ECHS1:2401 HADHA:2626 HADHB:5554
REACTOME_BETA_OXIDATION_OF_OCTANOYL_COA_	-0.3637663	5	4.845e-03	7.730e-01	HADH:66 ACADM:388 ECHS1:2401 HADHA:2626 HADHB:5554 NA
REACTOME_ALPHA_DEFENSINS	-0.3598466	3	3.087e-02	9.398e-01	ART1:1786 CD4:2248 PRSS3:2772 NA NA NA
IBRAHIM_NRF3_UP	-0.3402808	5	8.406e-03	9.378e-01	RPN2:1382 CMAS:1464 PSMD4:1875 HMOX1:3572 GCLM:4655 NA
BAFNA_MUC4_TARGETS_UP	-0.3296240	3	4.799e-02	9.398e-01	NEK6:275 AVPR2:2798 SNAI1:5209 NA NA NA
WP_PILOCYTIC_ASTROCYTOMA	0.3220873	6	6.288e-03	8.868e-01	NF1:522 PTPN11:1349 BRAF:2370 GRB2:4051 SOS1:4070 RAF1:4951
MCCOLLUM_GELDANAMYCIN_RESISTANCE_UP	-0.3179774	9	9.550e-04	7.207e-01	FOXN3:339 SMPD1:717 CDH11:879 PMCH:1639 SLC16A7:1851 SULF2:2927
REACTOME_BETA_OXIDATION_OF_LAURYL_COA_T	-0.3153029	5	1.461e-02	9.398e-01	HADH:66 ECHS1:2401 HADHA:2626 ACADL:4315 HADHB:5554 NA
WP_EFFECT_OF_INTESTINAL_MICROBIOME_ON_AN	0.3106366	7	4.423e-03	7.730e-01	NR12:886 VDR:1275 PPARA:2537 NPC1L1:3800 PPARD:4081 CD36:4307
REACTOME_ATORVASTATIN_ADME	0.2876818	5	2.588e-02	9.398e-01	ABCB1:3 PON3:1308 SLC01B1:2894 PON1:6359 SLC02B1:6659 NA
BIOCARTA_NPPI_PATHWAY	-0.2865456	10	1.702e-03	7.730e-01	SPP1:566 ALPL:661 COL4A2:1158 COL4A4:2014 ENPP1:2036 COL4A5:2383
SCHAEFFER_PROSTATE_DEVELOPMENT_AND_CANCE	0.2848615	5	2.738e-02	9.398e-01	ZNF22:1342 SOX9:1459 CDC27:2525 PDIA4:2882 IGFB1:9251 NA
REACTOME_PREDNISONE_ADME	0.2820033	5	2.896e-02	9.398e-01	ABCB1:3 ALB:64 HSD11B1:605 SERPINI6A:7506 HSD11B2:9492 NA
MIZUKAMI_HYPOXIA_DN	-0.2779689	5	3.134e-02	9.398e-01	PDGFB:529 LRP1:745 CXCL8:3229 FGF2:5431 CXCR1:8060 NA
WP_ALTERNATIVE_PATHWAY_OF_FETAL_ANDROGEN	0.2770188	9	4.003e-03	7.730e-01	HSD17B16:150 POR:1825 HSD17B3:2212 CYB5A:2320 CYP17A1:2556 STAR:2615
MIKKELSEN_IPS_LCP_WITH_H3K4ME3_AND_H3K27	-0.2757051	5	3.274e-02	9.398e-01	CDH7:184 SLC16A8:1899 PPPIR26:3927 FUT7:5752 SLC17A7:6436 NA
REACTOME_CA2_ACTIVATED_K_CHANNELS	0.2732905	9	4.522e-03	7.730e-01	KCNN3:174 KCNN2:612.5 KCNMB1:1064 KCNN1:1408 KCNN4:2896 KCNMB4:5762
DONATO_CELL_CYCLE_TRETINOIN	-0.2726870	6	2.071e-02	9.398e-01	SKAP2:1849 ABI1:2513 BTG2:3242 TOB1:3862 ATR:5148 MNT:5488
REACTOME_LEUKOTRIENE_RECEPTORS	0.2680283	5	3.792e-02	9.398e-01	CYSLTR2:305 LTBR4:1121 LTBR4:2324 GPR7:17159 CYSLTR1:8200 NA
REACTOME_TERMINAL_PATHWAY_OF_COMPLEMENT	-0.2638915	6	2.518e-02	9.398e-01	C8B:98 C6:433 C5:2207 C8G:2879 C8A:8519 L C10:8826
REACTOME_REGULATION_OF_NP4S4_GENE_TRANSC	-0.2629308	4	6.855e-02	9.398e-01	NR3C1:1336 SRF:1407 CYP3A3:3221 NP4A:9404 NA NA NA
WILSON_PROTEASES_AT_TUMOR_BONE_INTERFAC	-0.2594649	5	4.410e-02	9.398e-01	SERPIN1:90 CTSH:3812 CTSH:4590 CTSE:4790 ADAM57:6163 NA
BYSTRYKH_TP53_TARGETS_OEISIS_STEM_CELL_FGF3	-0.2568035	6	2.936e-02	9.398e-01	EFNB1:30 SH3RF1:34 EFNB3:1512 PKNOX1:4813 POU5F1:7550 MAP2K6:9715
GALI_TPM53_TARGETS_APOPTOTIC_UP	0.2560171	7	1.898e-02	9.398e-01	BAX:4 GADD45A:1024 CASP8:11109 BIRC3:1804 BIRC2:6062 CD40:6618
IGARASHI_ATF4_TARGETS_UP	-0.2531141	4	7.954e-02	9.398e-01	ITFG2:676 PDP1:4113 SFYN4:4437 ASB4:6782 NA NA
BIOCARTA_RAN_PATHWAY	-0.2476446	4	8.626e-02	9.430e-01	RCO1:17 RANGAP1:1865 RAN:5397 RANBP1:9078 NA NA
IKEDA_MIR1_TARGETS_DN	-0.2472354	7	2.349e-02	9.398e-01	CLCN3:1378 SMM36:1628 EIF4E:1999 ST39:2773 MTS51:3162 HSPD1:6532
ERENJENO_TRANSFORMED_BY_RHOA_REVERSIBLY	-0.2448934	6	3.775e-02	9.398e-01	PIK3R1:270 DNMI:997 QSSTM1:4525 TNFRSF1B:4594 DAP:5978 MGST3:8442
BIOCARTA_NEUTROPHIL_PATHWAY	-0.2443868	8	1.667e-02	9.398e-01	ITGB2:129 ICAM1:807 ITGAL:1308 ITGAM:1860 CD44:3352 SELT:5686
SAMOLS_TARGETS_OF_KHSV_MIRNAS_UP	-0.2442821	6	8.323e-02	9.398e-01	CDH11:879 GALNT3:1721 SLC31A1:3765 COCH:4031 GAB:4887 AKC:9584
LIU_CD22_TARGETS_DN	0.2436449	5	5.917e-02	9.398e-01	KRT14:905 KRT15:920 KRT19:2546 SOX2:2674 HES1:13763 NA
REACTOME_COBALAMIN_CBL_METABOLISM	-0.2434498	7	2.570e-02	9.398e-01	MTR:656 MTRR:1163 MMADHC:1825 MMMA:2716 MMAB:4723 MMACHC:5597
REACTOME_SYNTHESIS_OF_5_EICOSATETRAENOIC	0.2427929	9	1.166e-02	9.378e-01	PON2:463 PON3:1308 GPX1:1447 GPX2:1556 ALOX5:2324 ALOX5AP:2391
MIKHAYLOVA_OXIDATIVE_STRESS_RESPONSE_VIA	0.2427749	6	3.944e-02	9.398e-01	PGAM1:165 CALU:1887 HSPB1:3062 CTSD:3746 AKR1B1:6329 AOT:9740
BIOCARTA_SLRP_PATHWAY	-0.2420635	6	4.002e-02	9.398e-01	EPYC:925 BGN:748 KERA:1213 LUM:6609 FMOD:6666 DCM:9860
REACTOME_BETA_OXIDATION_OF_HEXANOYL_COA_	-0.2415328	5	6.141e-02	9.398e-01	HADH:66 ECHS1:2401 HADHA:2626 HADHB:5554 ACADS:10292 NA
WP_SFCA_AND_SKELETAL_MUSCLE_SUBSTRATE_ME	0.2409621	6	4.094e-02	9.398e-01	SLC24A:160 GGC:299 FFAR2:2149 PPARD:4081 FFAR3:6844 PYY:11669
REACTOME_ARYL_HYDROCARBON_RECEPTOR_SIGNA	0.2406143	6	4.123e-02	9.398e-01	AHR:86 PTGES3:1634 ARNT:3459 AIP:3798 ARNT2:4740 HSP90AB1:11524