

Top genes by P-value Permulated

Gene	Rho	N	P	p.adj	permPValue	qValueNoperm	qValuePerm
SCYL3	0.257146726	44	4.114e-02	1.000e+00	0.000e+00	1.000e+00	0.000e+00
LAS1L	-0.175139721	62	9.652e-02	1.000e+00	0.000e+00	1.000e+00	0.000e+00
LASP1	-0.194938124	62	6.434e-02	1.000e+00	0.000e+00	1.000e+00	0.000e+00
ICA1	-0.012467322	61	9.066e-01	1.000e+00	0.000e+00	1.000e+00	0.000e+00
CFLAR	0.381385036	11	1.573e-01	1.000e+00	0.000e+00	1.000e+00	0.000e+00
ABCB5	0.253085534	18	2.135e-01	1.000e+00	0.000e+00	1.000e+00	0.000e+00
SLC4A1	-0.117337615	24	4.995e-01	1.000e+00	0.000e+00	1.000e+00	0.000e+00
CALCR	0.000000000	21	1.000e+00	1.000e+00	0.000e+00	1.000e+00	0.000e+00
HCCS	0.081912198	46	5.059e-01	1.000e+00	0.000e+00	1.000e+00	0.000e+00
UPF1	-0.129426661	67	2.012e-01	1.000e+00	0.000e+00	1.000e+00	0.000e+00
SKAP2	0.180686308	29	2.496e-01	1.000e+00	0.000e+00	1.000e+00	0.000e+00
MCUB	-0.182500140	60	8.862e-02	1.000e+00	0.000e+00	1.000e+00	0.000e+00
KMT2E	-0.181760828	48	1.309e-01	1.000e+00	0.000e+00	1.000e+00	0.000e+00
CACNG3	-0.160934850	27	3.237e-01	1.000e+00	0.000e+00	1.000e+00	0.000e+00
PHTF2	-0.047027916	54	6.778e-01	1.000e+00	0.000e+00	1.000e+00	0.000e+00
VPS41	-0.009137725	62	9.309e-01	1.000e+00	0.000e+00	1.000e+00	0.000e+00
GAS7	-0.104574723	48	3.848e-01	1.000e+00	0.000e+00	1.000e+00	0.000e+00
TRAPPC6A	-0.009103799	57	9.341e-01	1.000e+00	0.000e+00	1.000e+00	0.000e+00
PLX6	-0.049660889	24	7.750e-01	1.000e+00	0.000e+00	1.000e+00	0.000e+00
TSR3	0.000000000	65	1.000e+00	1.000e+00	0.000e+00	1.000e+00	0.000e+00
PSMB1	0.032643546	66	7.490e-01	1.000e+00	0.000e+00	1.000e+00	0.000e+00
CRY1	0.019166936	65	8.522e-01	1.000e+00	0.000e+00	1.000e+00	0.000e+00
RHOBTB2	0.000000000	57	1.000e+00	1.000e+00	0.000e+00	1.000e+00	0.000e+00
UBE3C	-0.098459285	65	3.384e-01	1.000e+00	0.000e+00	1.000e+00	0.000e+00
POMT2	-0.171471375	64	9.812e-02	1.000e+00	0.000e+00	1.000e+00	0.000e+00

Top genes by P-value non-permulated

Gene	Rho	N	P	p.adj	permPValue	qValueNoperm	qValuePerm
RGSA	-0.47999759	58	1.080e-05	1.593e-01	1.813e-01	1.000e+00	1.000e+00
FSTL3	-0.41905036	65	4.609e-05	3.399e-01	1.919e-01	1.000e+00	1.000e+00
RANBP3L	-0.40737422	64	8.511e-05	4.185e-01	3.090e-01	1.000e+00	1.000e+00
DCTPP1	-0.42455342	56	1.323e-04	4.877e-01	0.000e+00	1.000e+00	0.000e+00
TSPAN6	0.02491137	64	8.101e-01	1.000e+00	8.240e-01	1.000e+00	1.000e+00
DPM1	-0.05579490	68	5.787e-01	1.000e+00	9.999e-01	1.000e+00	1.000e+00
SCYL3	0.25714673	44	4.114e-02	1.000e+00	0.000e+00	1.000e+00	0.000e+00
C1orf112	-0.05656972	56	6.105e-01	1.000e+00	1.000e+00	1.000e+00	1.000e+00
FGR	-0.16876196	58	1.218e-01	1.000e+00	7.236e-01	1.000e+00	1.000e+00
CFH	-0.10193702	60	3.416e-01	1.000e+00	9.999e-01	1.000e+00	1.000e+00
FUCA2	0.03296971	68	7.428e-01	1.000e+00	9.999e-01	1.000e+00	1.000e+00
GCLC	-0.04284988	68	6.745e-01	1.000e+00	4.619e-01	1.000e+00	1.000e+00
NFYA	-0.10271334	68	3.067e-01	1.000e+00	9.999e-01	1.000e+00	1.000e+00
NIPAL3	-0.04927305	55	6.603e-01	1.000e+00	1.419e-01	1.000e+00	8.820e-01
LAS1L	-0.17513972	62	9.652e-02	1.000e+00	0.000e+00	1.000e+00	0.000e+00
ENPP4	0.03170165	64	6.130e-01	1.000e+00	9.999e-01	1.000e+00	1.000e+00
SEMA3F	-0.03352508	37	8.079e-01	1.000e+00	1.000e+00	1.000e+00	1.000e+00
CFTR	0.06802170	64	5.117e-01	1.000e+00	1.000e+00	1.000e+00	1.000e+00
ANKIB1	0.07230918	66	4.785e-01	1.000e+00	1.000e+00	1.000e+00	1.000e+00
CYP51A1	0.03170165	68	7.524e-01	1.000e+00	6.851e-01	1.000e+00	1.000e+00
KRIT1	0.03749365	66	7.133e-01	1.000e+00	7.833e-01	1.000e+00	1.000e+00
RAD52	-0.07559289	25	6.565e-01	1.000e+00	6.736e-01	1.000e+00	1.000e+00
BAD	0.01052312	62	9.205e-01	1.000e+00	9.999e-01	1.000e+00	1.000e+00
LAP3	-0.03505884	68	7.238e-01	1.000e+00	4.577e-01	1.000e+00	1.000e+00
HS3ST1	0.05615848	44	6.556e-01	1.000e+00	6.390e-01	1.000e+00	1.000e+00

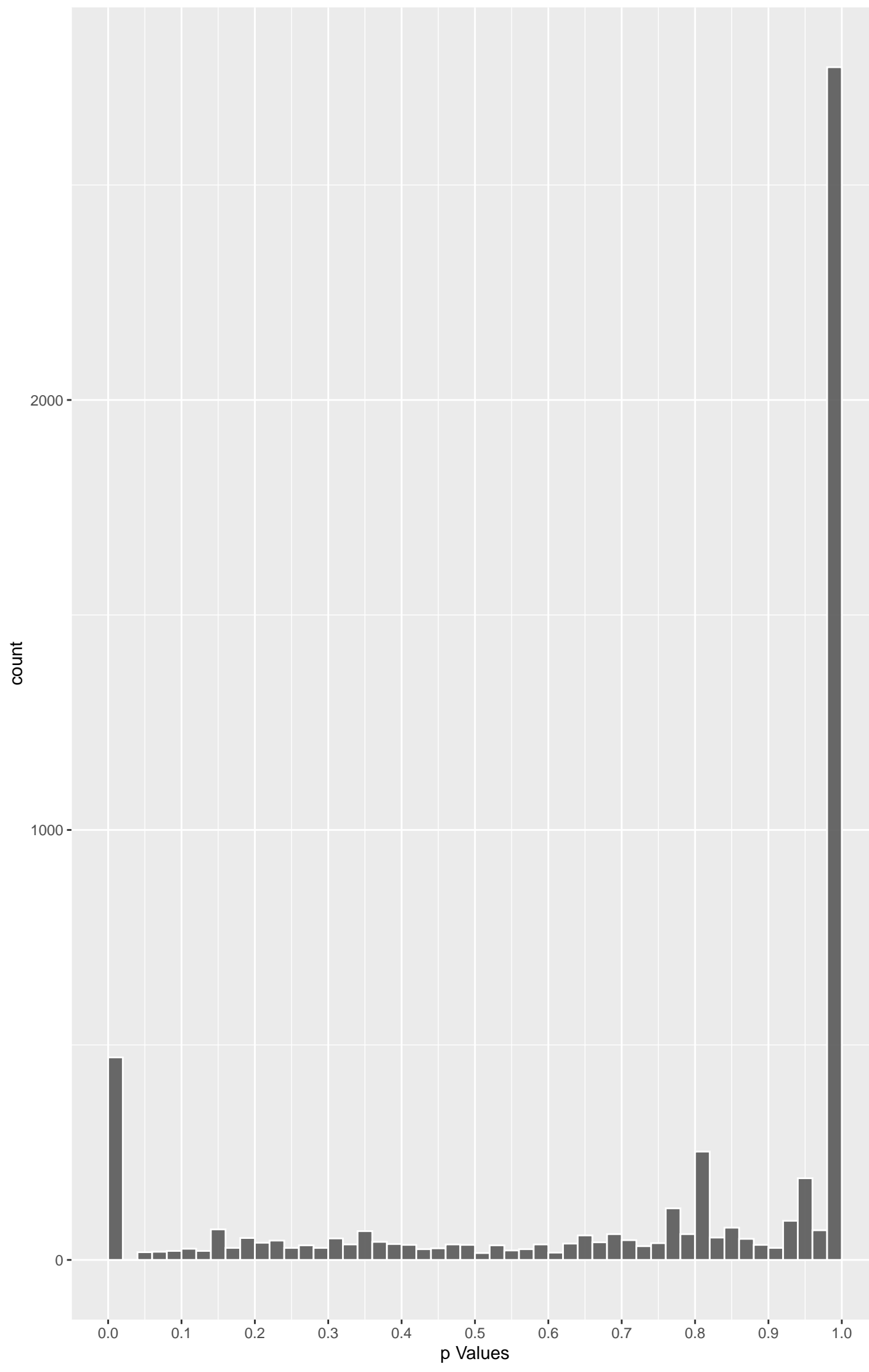
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Gene	Rho	N	P	p.adj	permPValue	qValueNoperm	qValuePerm
SCYL3	0.257146726	44	4.114e-02	1.000e+00	0.000e+00	1.000e+00	0.000e+00
LAS1L	-0.175139721	62	9.652e-02	1.000e+00	0.000e+00	1.000e+00	0.000e+00
LASP1	-0.194938124	62	6.434e-02	1.000e+00	0.000e+00	1.000e+00	0.000e+00
ICA1	-0.012467322	61	9.066e-01	1.000e+00	0.000e+00	1.000e+00	0.000e+00
CFLAR	0.381385036	11	1.573e-01	1.000e+00	0.000e+00	1.000e+00	0.000e+00
ABCB5	0.253085534	18	2.135e-01	1.000e+00	0.000e+00	1.000e+00	0.000e+00
SLC4A1	-0.117337615	24	4.995e-01	1.000e+00	0.000e+00	1.000e+00	0.000e+00
CALCR	0.000000000	21	1.000e+00	1.000e+00	0.000e+00	1.000e+00	0.000e+00
HCCS	0.081912198	46	5.059e-01	1.000e+00	0.000e+00	1.000e+00	0.000e+00
UPF1	-0.129426661	67	2.012e-01	1.000e+00	0.000e+00	1.000e+00	0.000e+00
SKAP2	0.180686308	29	2.496e-01	1.000e+00	0.000e+00	1.000e+00	0.000e+00
MCUB	-0.182500140	60	8.862e-02	1.000e+00	0.000e+00	1.000e+00	0.000e+00
KMT2E	-0.181760828	48	1.309e-01	1.000e+00	0.000e+00	1.000e+00	0.000e+00
CACNG3	-0.160934850	27	3.237e-01	1.000e+00	0.000e+00	1.000e+00	0.000e+00
PHTF2	-0.047027916	54	6.778e-01	1.000e+00	0.000e+00	1.000e+00	0.000e+00
VPS41	-0.009137725	62	9.309e-01	1.000e+00	0.000e+00	1.000e+00	0.000e+00
GAS7	-0.104574723	48	3.848e-01	1.000e+00	0.000e+00	1.000e+00	0.000e+00
TRAPPC6A	-0.009103799	57	9.341e-01	1.000e+00	0.000e+00	1.000e+00	0.000e+00
PLX6	-0.049660889	24	7.750e-01	1.000e+00	0.000e+00	1.000e+00	0.000e+00
TSR3	0.000000000	65	1.000e+00	1.000e+00	0.000e+00	1.000e+00	0.000e+00
PSMB1	0.032643546	66	7.490e-01	1.000e+00	0.000e+00	1.000e+00	0.000e+00
CRY1	0.019166936	65	8.522e-01	1.000e+00	0.000e+00	1.000e+00	0.000e+00
RHOBTB2	0.000000000	57	1.000e+00	1.000e+00	0.000e+00	1.000e+00	0.000e+00
UBE3C	-0.098459285	65	3.384e-01	1.000e+00	0.000e+00	1.000e+00	0.000e+00
POMT2	-0.171471375	64	9.812e-02	1.000e+00	0.000e+00	1.000e+00	0.000e+00

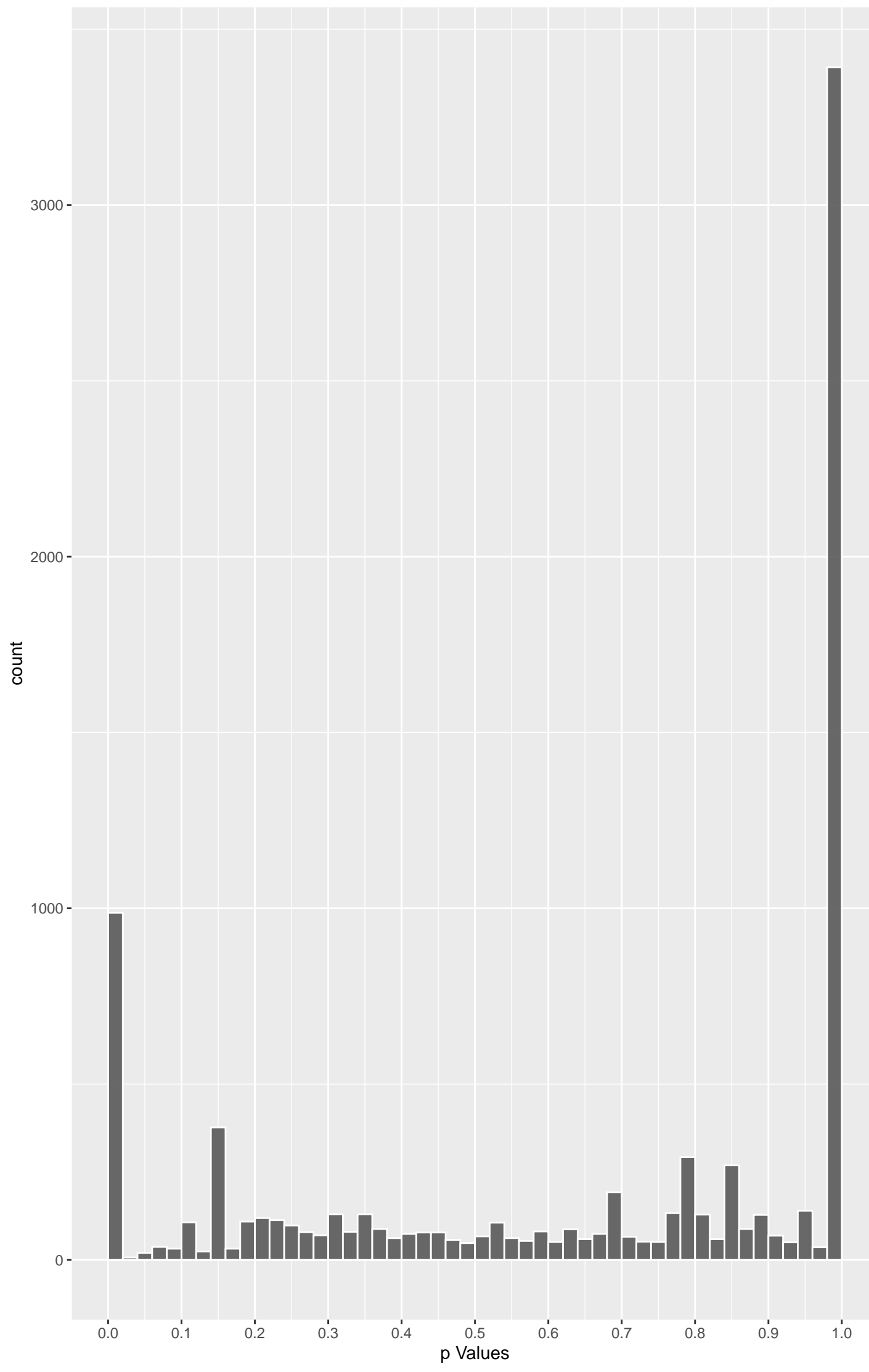
Top genes by Q-Value non-permulated

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TSPAN6	0.02491137	64	8.101e-01	1.000e+00	8.240e-01	1.000e+00	1.000e+00
DPM1	-0.05579490	68	5.787e-01	1.000e+00	9.999e-01	1.000e+00	1.000e+00
SCYL3	0.25714673	44	4.114e-02	1.000e+00	0.000e+00	1.000e+00	0.000e+00
C1orf112	-0.05656972	56	6.105e-01	1.000e+00	1.000e+00	1.000e+00	1.000e+00
FGR	-0.16876196	58	1.218e-01	1.000e+00	7.236e-01	1.000e+00	1.000e+00
CFH	-0.10193702	60	3.416e-01	1.000e+00	9.999e-01	1.000e+00	1.000e+00
FUCA2	0.03296971	68	7.428e-01	1.000e+00	9.999e-01	1.000e+00	1.000e+00
GCLC	-0.04284988	68	6.745e-01	1.000e+00	4.619e-01	1.000e+00	1.000e+00
NFYA	-0.10271334	68	3.067e-01	1.000e+00	9.999e-01	1.000e+00	1.000e+00
NIPAL3	-0.04927305	55	6.603e-01	1.000e+00	1.419e-01	1.000e+00	8.820e-01
LAS1L	-0.17513972	62	9.652e-02	1.000e+00	0.000e+00	1.000e+00	0.000e+00
ENPP4	-0.05243340	64	6.130e-01	1.000e+00	9.999e-01	1.000e+00	1.000e+00
SEMA3F	-0.03352508	37	8.079e-01	1.000e+00	1.000e+00	1.000e+00	1.000e+00
CFTR	0.06802170	64	5.117e-01	1.000e+00	1.000e+00	1.000e+00	1.000e+00
ANKIB1	0.07230918	66	4.785e-01	1.000e+00	1.000e+00	1.000e+00	1.000e+00
CYP51A1	0.03170165	68	7.524e-01	1.000e+00	6.851e-01	1.000e+00	1.000e+00
KRIT1	0.03749365	66	7.133e-01	1.000e+00	7.833e-01	1.000e+00	1.000e+00
RAD52	-0.07559289	25	6.565e-01	1.000e+00	6.736e-01	1.000e+00	1.000e+00
BAD	0.01052312	62	9.205e-01	1.000e+00	9.999e-01	1.000e+00	1.000e+00
LAP3	-0.03505884	68	7.238e-01	1.000e+00	4.577e-01	1.000e+00	1.000e+00
WNT16	-0.06332476	20	7.415e-01	1.000e+00	4.016e-01	1.000e+00	1.000e+00
MAD1L1	0.07366181	62	4.846e-01	1.000e+00	8.106e-01	1.000e+00	1.000e+00
LASP1	-0.19493812	62	6.434e-02	1.000e+00	0.000e+00	1.000e+00	0.000e+00

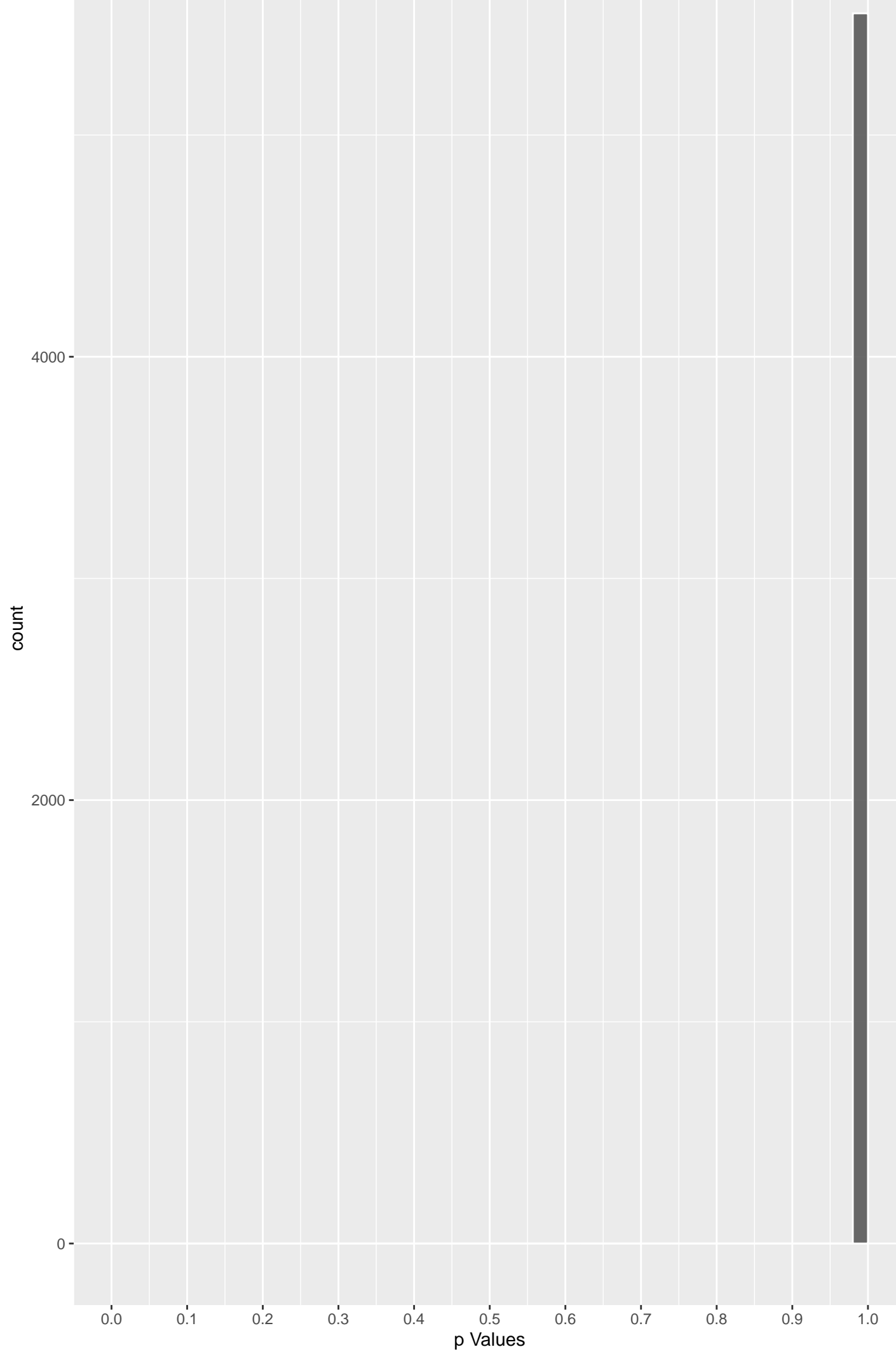
Positive Rho Permulated



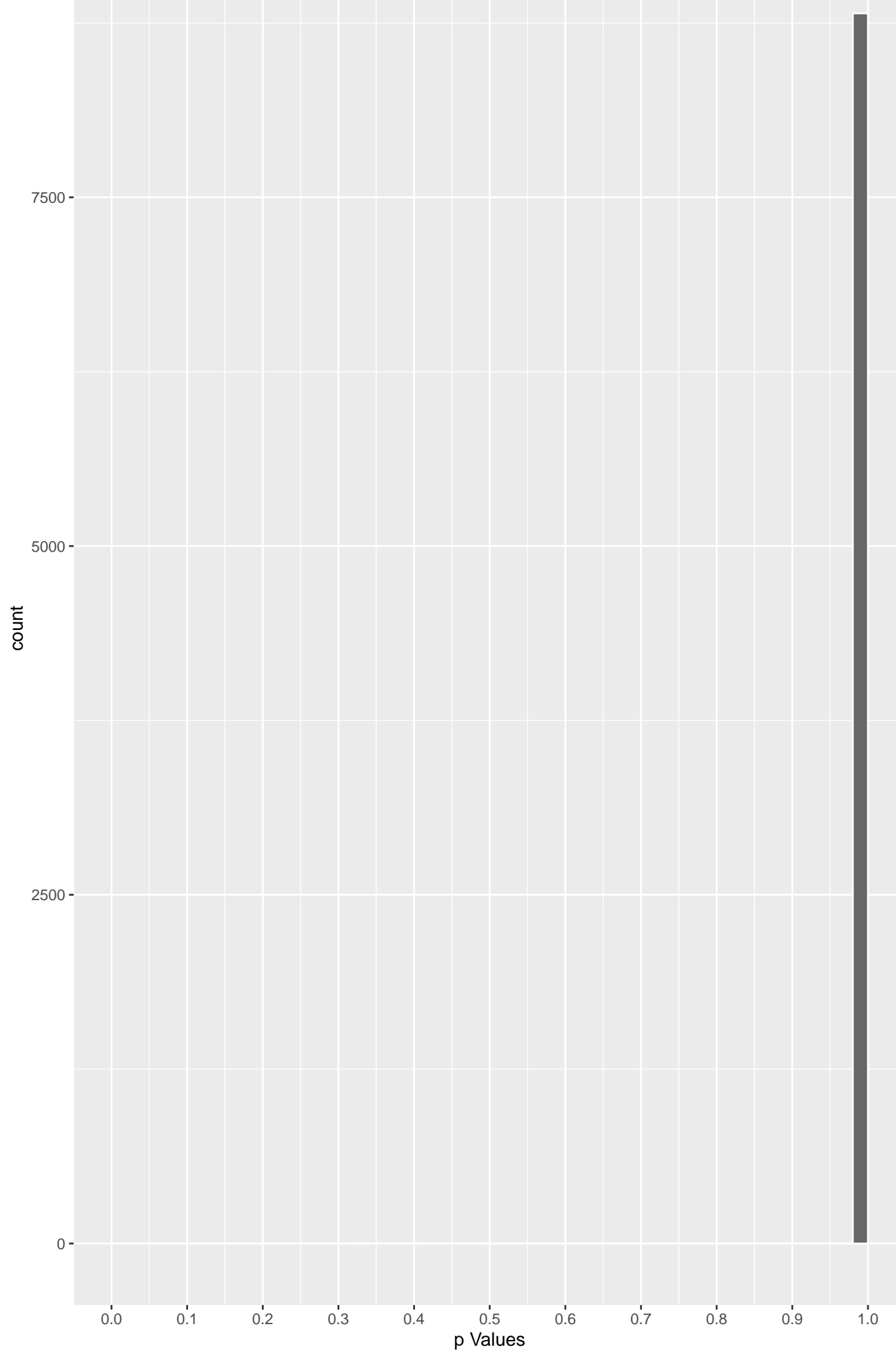
Negative Rho Permulated



Positive Rho Non-permulated



Negative Rho Non-permulated



Top Positive genes by P-value Permulated

SCYL3	0.25714673	44	4.114e-02	1.000e+00	0.000e+00	1.000e+00	0.000e+00
CFLAR	0.38138504	11	1.573e-01	1.000e+00	0.000e+00	1.000e+00	0.000e+00
ABCB5	0.25308553	18	2.135e-01	1.000e+00	0.000e+00	1.000e+00	0.000e+00
HCCS	0.03296971	68	6.505e-01	1.000e+00	0.000e+00	1.000e+00	0.000e+00
SKAP2	0.18068631	29	2.496e-01	1.000e+00	0.000e+00	1.000e+00	0.000e+00
PSMB1	0.03264355	66	7.490e-01	1.000e+00	0.000e+00	1.000e+00	0.000e+00
CRY1	0.01916694	65	8.522e-01	1.000e+00	0.000e+00	1.000e+00	0.000e+00
STAB1	0.06527183	62	4.184e-01	1.000e+00	0.000e+00	1.000e+00	0.000e+00
NPCL1	0.07230918	66	4.785e-01	1.000e+00	0.000e+00	1.000e+00	0.000e+00
NUDCD3	0.11919819	68	2.355e-01	1.000e+00	0.000e+00	1.000e+00	0.000e+00

DisGeNET Top pathways by permutation

Geneset	stat	num.genes	pval	p.adj	gene.vals
Adenoma, Villous	0.16726084	13	3.681e-02	0.194e-01	CDKN2A:419 GNAS:493 PMS2:1183 BRAF:1652 5 TP53:1771 MLH1:2116
Alzheimer Disease, Late Onset	0.04352323	193	3.854e-02	0.194e-01	HLA-DPB1:15 SGP1L:40 SIRT1:122.5 ALOX5:170 CNTNL:180 PFH1:200
AMYLOIDOSIS, HEREDITARY, TRANSTHYRETIN-R	-0.10288992	28	5.961e-02	0.194e-01	ETP1:509 MMP9:100 SERPINE1:206 PKD2:437 CCL4L2:443 SMARCA4:472
Angina, Unstable	-0.10667684	53	7.273e-03	0.194e-01	TNNI3:18 TLR4:94.5 EEF1A2:121.5 SERPINE1:206 GDF002:273 CCL2:334
Aortic Aneurysm, Thoracic	-0.06059513	78	6.466e-02	0.194e-01	TLR4:94.5 MMP9:100 SERPINE1:206 PKD2:437 CCL4L2:443 SMARCA4:472
Aphasia, Progressive	-0.28210455	5	2.892e-02	0.194e-01	PLAT:959.5 L1CAM:1944.5 FANCD2:2088 PSEN1:4106 BRCA2:6880.5 NA
Arsenic Poisoning, Inorganic	-0.07509972	51	6.378e-02	0.194e-01	KRT10:91 MRBP2L2:92 CCL20:127 TAF1D:387 CXCL2:534 CD44:512
Bartter syndrome, type 3	0.07052614	5	3.618e-02	0.194e-01	CLCNKB:100 KCNJ1:109 SLC12A2:544 SLC12A3:2049 APB3B1:3802 NA
Cardiomyopathy, Dilated	-0.02874560	350	6.652e-02	0.194e-01	TNNI3:18 ACTC1:59 NKX2-5:83 PRARG:1A:88 TLR4:94.5 MMP9:100
Cardiomyopathy, Familial Idiopathic	-0.03552843	315	3.118e-02	0.194e-01	TACSTD2:14 TNNI3:18 ACTC1:59 NKX2-5:83 TLR4:94.5 MMP9:100
CATARACT, ANTERIOR POLAR	-0.10095812	29	5.998e-02	0.194e-01	SFTPD:72 MMP9:100 SERPINE1:206 CD44:512 BDNF:784 CRYBB3:1249.5
CHARCOT-MARIE-TOOTH DISEASE, AXONAL, TYP	0.28832637	6	1.445e-02	0.194e-01	HSPB8:226.5 HSPB1:1448.5 HSPB3:2061 MACD1:1BP:2667 KIF1B:3844.5 HSPB2:8137
Charcot-Marie-Tooth Disease, Type Ib	-0.20306970	9	3.490e-02	0.194e-01	ACKR1:329 F1C4:388 LRSA1:1380.5 MPZ:4913.5 HOXD10:5051.5 SLC25A4:6.5324.5
Cholangitis, Sclerosing	0.05514544	105	5.134e-02	0.194e-01	IL1R1:139 ITGAL:153 DAP:213 HIPK1:304 ERAP2:405 CDKN2A:419
Choledochal Cyst, Type I	0.33212157	5	1.011e-02	0.194e-01	PKHD1:92 AQP1:1089 CFTR:2059.5 SLC4A2:2898 SCT:6012.5 NA
Choledochal Cyst, Type II	0.33212157	5	1.011e-02	0.194e-01	PKHD1:92 AQP1:1089 CFTR:2059.5 SLC4A2:2898 SCT:6012.5 NA
Choledochal Cyst, Type III	0.33212157	5	1.011e-02	0.194e-01	PKHD1:92 AQP1:1089 CFTR:2059.5 SLC4A2:2898 SCT:6012.5 NA
Choledochal Cyst, Type IV	0.33212157	5	1.011e-02	0.194e-01	PKHD1:92 AQP1:1089 CFTR:2059.5 SLC4A2:2898 SCT:6012.5 NA
Choledochal Cyst, Type V	0.33212157	5	1.011e-02	0.194e-01	PKHD1:92 AQP1:1089 CFTR:2059.5 SLC4A2:2898 SCT:6012.5 NA
Chromosome 12, 12p trisomy	-0.28111698	5	2.948e-02	0.194e-01	CD79B:1607 MSAA1:1823.5 BIRC3:2661.5 NOTCH1:4193 SF3B1:5812 NA
Colitis, Ischemic	-0.21470770	8	3.549e-02	0.194e-01	MMP9:100 SERPINE1:206 HSPA5:1807 ABCO2:2161.5 VEGFA:3178.5 MMP2:3253.5
Cone-rood sensory disorder, congenital n	-0.16685121	10	6.771e-02	0.194e-01	LRIT3:1153 GNAT1:1277.5 GNB3:2607 GPR179:3237.5 SAG:3289.5 GRM6:3836
Congenital secretory diarrhea, sodium ty	-0.21161543	8	3.821e-02	0.194e-01	HGF:873.1 F1C4:388 LRSA1:1380.5 MPZ:4913.5 HOXD10:5051.5 SLC25A4:6.5324.5
Deafness, Acquired	-0.17064870	16	1.813e-02	0.194e-01	POLD1:340 MTF:632.5 BDNF:784 ESPN:1527 GJB3:2174.5 JAG1:2242
Dentin dysplasia, type 1	0.26097395	5	4.328e-02	0.194e-01	CDH11:679 SMOCC2:1207 SSUH4:2295 DSSP:6102.5 VPS4B:7014 NA
Dermatitis, Allergic Contact	-0.07167155	82	2.507e-02	0.194e-01	ASRGL1:50 QPCT:54 MMP9:100 CD3D:310 CCL2:334 CCL4:3234
Dermatomyositis, Childhood Type	-0.13072288	28	1.937e-02	0.194e-01	TLR4:94.5 NCAM1:320 WTI:1370 SAMHD1:831 RNA5E:24.5 RNASEH2A:1408
Diaphragm, Complete Agenesis Of	-0.31609910	5	1.437e-02	0.194e-01	FREM2:503 FRAS1:1150 ROBO4:3148.5 GLIS3:3772.5 FBN1:4947.5 NA
Electron Transport Chain Deficiencies, M	0.07052614	9	6.511e-02	0.194e-01	NUPB:1863 POLG:1817.5 HADHA:159.5 HADHB:11914 FOXRED1:2518 NOS2:3730 COG5:346.5
Endometrial stromal sarcoma, high grade	-0.20478542	7	6.062e-02	0.194e-01	CTNNB1:758 JAZF1:1881.5 CNOT1:2332 SMARCB1:2874.5 VWA4:5202 SUI2:12595.5
Encephalitis, Tropical	-0.28988113	6	1.423e-02	0.194e-01	TLR4:94.5 HPGD5:720 PTGDS:772 GAT3:2610 RAG2:5583 MYD88:8781.5
Epilepsy, Cryptogenic	0.07347615	56	5.742e-02	0.194e-01	TGFB1:457 FOLR1:481 ADRA2A:582 SLC12A2:644 ABCB1:717 ERN1:728
Familial Partial Lipodystrophy, Type 2	0.14784651	13	6.496e-02	0.194e-01	PLIN1:76 LPL:691 LMNA:752.5 CNDN3:1319 HNF4A:2565.5 PPP1R3A:3062
Fatty Liver, Alcoholic	0.09693739	46	2.303e-02	0.194e-01	ACACB:18 HLA-A:88.5 SIRT1:122.5 HLA-B:226 DGT52:396.5 OPA1:444.5
Fracture, spiral	-0.16996283	11	5.097e-02	0.194e-01	IRX5:501 BMP7:536 FAM20A:600 DKK1:1158 TNFSF18:3679 SPTBN1:4813.5
Gait, Scissors	-0.21071550	7	5.353e-02	0.194e-01	TBL1XR1:441 L1CAM:1944.5 KIF1A:2095 TTC19:3867.5 ARL6IP1:3929.5 AMPD2:4165
Hearing Loss, Extreme	-0.17064870	16	1.813e-02	0.194e-01	POLD1:340 MTF:632.5 BDNF:784 ESPN:1527 GJB3:2174.5 JAG1:2242
Hepatitis B, Chronic	0.04195577	160	6.788e-02	0.194e-01	HLA-DPB1:15 CD80:58 TGFAB5 HLA-A:88.5 HLA-B:226 JMD1:624 ILR1:139
Hyperbilirubinemia, Hereditary	0.23453666	8	2.161e-02	0.194e-01	CALB1:349 ABCA3:499.5 HMGBI:194.5 F7:2227 HMB5:2907.5 BCL2:3517
Hypoxia-Ischemia, Brain	0.19893441	7	6.836e-02	0.194e-01	HIF1A:1789 IRACK1:1609 TNF:1996 ILKAP4:2085 NTS2:37.5 C11B:8967

EnrichmentHsSymbolsFile2 Top pathways by permutation

Geneset	stat	num.genes	pval	p.adj	gene.vals
HOUNKPE_HOUSEKEEPING_GENES	0.07527272	1070	2.626e-16	1.480e-12	RANBP2:39 GPN2:74 PSM6:87 MRPS2:99 ARNT:103 TNKS2:105
LIU_OVARIAN_CANCER_TUMORS_AND_XENOGRAFTS	-0.06073443	1280	6.786e-13	2.184e-09	RS6A1 JAM3:6 NCF2:7 SERPIN1:95 SMMD2:20 CARD6:30
DIAZ_CHRONIC_MYELOGENOUS_LEUKEMIA	0.05336500	1320	1.543e-10	3.336e-07	RANBP2:39 SH3GLB2:47 TCEAL9:50 CNOT8:60 VAV3:90 RAP2C:119
NABA_MATRISOME	-0.06294634	714	1.346e-08	1.834e-05	FSTL3:2 SERPIN1:18 CNTF:25 SFRP5:32 EPO:45 ADAM22:47
GRAESSMANN_APOPTOSIS_BY_DOXORUBICIN_DN	0.04298425	1637	1.414e-08	1.834e-05	DHRS11:3 RAD18:12 ACACB:18 GDPD1:27 HLA-B:226 HGF:873
STARK_PREFRONTAL_CORTEX_B22Q11_DELETION_D	0.06783263	478	4.389e-07	4.744e-04	TOMM40L:29 TCEAL9:50 NDUFB1:64 PSM6:87 SEC61B:122.5 PPR25C:228.5
NABA_MATRISOME_ASSOCIATED	-0.06463960	494	1.005e-06	9.314e-04	FSTL3:2 SERPIN1:18 CNTF:25 SFRP5:32 EPO:45 ADAM22:47
MILI_PSEUDOPODIA_HAPTOTAXIS_UP	0.06340803	468	1.800e-06	1.319e-03	AGTPBP1:30 HRC4:38 CNE2:45 SERP1:66 CDCD141:69 USP46:75
YAO_TEMPORAL_RESPONSE_TO_PROGESTERONE_CL	0.10817380	164	1.831e-06	1.319e-03	PSAT1:55 PRPSAP2:211 DAP:213 ATP5MK:221 PPP2R5C:228.5 UOCR11:269
ACEVEDO_NORMAL_TISSUE_ADJACENT_TO_LIVER_	0.07913195	306	2.098e-06	1.360e-03	TGDS5:1 ARNT:103 DIAPH1:106 FGGY:145 DIAPH1:150 LTB1:166
LIM_MAMMARY_STEM_CELL_UP	-0.06581963	429	3.296e-06	1.781e-03	JAM3:8 AGPAT4:27 EPOR1:38 RAB34:52 CDCD8B:53 C19orf12:107
MOOTHA_HUMAN_MITOCH_8_2012	0.06945850	387	3.024e-06	1.781e-03	MRPS29:9 AK4:146 GPD2:263 UOCR11:269 FAR2:300 NME4:316
WAKABAYASHI_ADIPOGENESIS_PPARG_RXRA_BOUN	0.04819802	764	7.098e-06	3.298e-03	HCB17:5 ABHD1:10 ZMYND10:33 RANBP2:39 ZNF569-ZNF177:63 YAP1:68
REACTOME_PROTEIN_LOCALIZATION	0.10782351	146	7.120e-06	3.298e-03	SEC61B:122.5 PEK1B:127 UBE2D:143 CHCHD2:630.5 BAAT:706 TIMM10:714
REACTOME_METABOLISM_OF_AMINO_ACIDS_AND_D	0.07636698	292	7.666e-06	3.314e-03	PSAT1:55 PSM6:87 PHGDH:150 AUH:179 SERINC2:329 RPL3:334
GOTZMANN_EPITHELIAL_TO_MESENCHYMAL_TRANS	0.09503867	178	1.271e-05	4.849e-03	PLXNA2:81 HLA-A:88.5 IL1R1:139 KRT19:294 TPDS2:412 CKN2A:419
KIM_BIPOLAR_DISORDER_OLIGODENDROCYTE_DEN	0.05229586	607	1.254e-05	4.849e-03	RAB40B:26 ARLA4:44 FAPB7:59 LZTS3:62 PSM6:87 SEC61B:122.5
LINDGREN_BLADDER_CANCER_CLUSTER_2B	-0.06844527	336	1.748e-05	6.299e-03	JAM3:6 NRN1:12 STMN3:31 RCAN2:151 OLFML1:197 GLS:214
SCHUETZ_BREAST_CANCER_DUCTAL_INVASIVE_UP	-0.06833527	311	3.641e-05	1.181e-02	RGSA1:1 JAM3:6 ITGBL1:141 RCAN2:151 OLFML1:197 GLS:214
FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_REJECT	0.05445136	498	5.537e-05	1.181e-02	SLC22A2:2 USP29:9 RAB40B:26 ITGA6:86 SULT1C2:114.5 MPE11B:127
REACTOME_CELL_CYCLE_CHECKPOINTS	0.07548541	245	5.537e-05	1.529e-02	H2BC17:5 RANBP2:39 CNE2:45 PSM6:87 UBE2D:143 MPM10:156
BLAOTOME_ALZHEIMERS_DISEASE_DN	0.03581912	116	5.215e-05	1.537e-02	RANBP2:39 SH3GLB2:47 PSAT1:55 FAPB7:59 KCNJ3:748 VPEL5:184
PUJANA_CHEK2_PCC_NETWORK	0.04532130	687	5.672e-05	1.672e-02	CDE1:18 CNE2:45 TGDS5:1 FURP1:133 UBE2D:143 UBE2A:173
ACEVEDO_LIVER_CANCER_DN	0.05486984	465	6.554e-05	1.771e-02	ACACB:18 TGDS5:1 MRPS29:9 ARNT:103 DIAPH1:106 PHGDH:150
REACTOME_MITOTIC_METAPHASE_AND_ANAPHASE	0.07891926	210	8.279e-05	1.988e-02	RANBP2:39 PSM6:87 UBE2D:143 UBE2I:161 TUBA1:204 PPP2R5C:228.5
REACTOME_TRANSLATION	0.07613878	227	8.072e-05	1.988e-02	MRPS29:9 SEC61B:122.5 EEF1B2:182 FAR2:300 MRPS23:310 RPL3:334
GARY_CDS_TARGETS_UP	0.05690817	413	7.871e-05	1.988e-02	SESTD1:24 SH3GLB2:47 PSAT1:55 PHGDH:150 MDN:154 MIF4GD:169
HSIAO_HOUSEKEEPING_GENES	0.06465606	314	8.665e-05	2.007e-02	PSMB6:87 HLA-A:88.5 SEC61B:122.5 EEF1B2:182 HLA-B:226 RPL3:334
REACTOME_NEDDYLATION	0.07532316	227	9.618e-05	2.151e-02	PSMB6:87 UBE2D:143 FBXO11:302 CDCD22:327 COP5A:369 FBXO17:391
BOCHKIS_FOXA2_TARGETS	0.06115839	345	1.013e-04	2.189e-02	GDPD1:27 CHAC2:34 HRC4:38 ARHGAP12:46 MRPS29:9 EEF1B2:182
GRAESSMANN_RESPONSE_TO_MC_AND_DOXORUBICI	0.07668891	299	1.103e-04	2.235e-02	GDPD1:27 CHAC2:34 HRC4:38 RUFY3:49 ZNF280C:54 STEAP4:57
REACTOME_EUKARYOTIC_TRANSLATION_INITIATI	0.13694951	67	1.071e-04	2.235e-02	RPL3:334 EIF3Q:356 RPS7:521 EIF4A2:655 RPS16:743 EIF3F:759
MOOTHA_PGC	0.05763925	376	1.331e-04	2.615e-02	USP29:9 MRPS29:9 JMD1:624 CHRNE:222 HSPB8:226.5 DPYSL3:239
MARTENS_TREPMAT_RESPONSE_UP	-0.04651666	563	1.678e-04	3.201e-02	TACSTD2:14 TNNI3:18 ENO2:228 RRAD:43 PRRT1:75 NKX2-5:83
JAAITINEN_HEMATOPOIETIC_STEM_CELL_DN	-0.08196079	179	1.789e-04	3.201e-02	NCF2:7 OPTC5:140 CD86:116 CD247:196 LIT:268
SENGUPTA_NASOPHARYNGEAL_CARCINOMA_DN	-0.06697374	266	1.779e-04	3.201e-02	TMC4:29 FKBP1:840 RRAD:43 DNAAJ8:482 MUC11:204 PACRG:155.5
OUELLET_OVARIAN_CANCER_INVASIVE_VS_LMP_U	0.10368013	109	1.827e-04	3.201e-02	COX7B:424 GNAS:493 CDKN3:536 SNRPD:748 MEST:787 FH:950.5
WONG_MITOCHONDRIA_GENE_MODULE	0.07697315	197	2.018e-04	3.356e-02	NDUFB10:64 AUH:179 SLC16A5:224 GDPD2:263 UOCR11:269 NME4:316
MOOTHA_MITOCHONDRIA	0.05452962	399	1.989e-04	3.356e-02	MRPS29:9 AK4:146 GPD2:263 UOCR11:269 FAR2:300 NME4:316
WP_ESTROGEN_SIGNALING_PATHWAY	0.22828876	22	2.103e-04	3.410e-02	IKBKKG:452 MAPK9:472.5 GNAS:494 ELK1:707 PIK3CA:1234 NGMT1:574

GO_Biological_Process_2023 Top pathways by permutation

Colgi Vesicle Transport (GO:0048193)	0.05767787	183	7.323e-03	5.570e-01	STEEP1:66 TMEM115:135 MYO1B:140 RANGRF:408 KIF14C:258 RAB6A:513.5
acyl-CoA Metabolic Process (GO:0006637)	0.18305710	27	9.981e-04	5.570e-01	ACACB:18 ACSL6:413.5 ACOT7:591 GLYAT:604 BAAT:706 OGDH:756
Amyloid Precursor Protein Metabolic Proc	-0.20576862	15	5.802e-03	5.570e-01	ACHE:215 TMCC2:230 ADAM10:1408 APH1A:1575 ADAM17:2377.5 NSG1:2859
Axonal Transport (GO:0008930)	0.12757332	37	7.279e-03	5.570e-01	APEX1:389 OPA1:444.5 HIF1A:789 BLOC1S2:1250.5 ARLB8:1350.5 MGARP:1371
Axonal Transport Of Mitochondrion (GO:0008930)	0.24968048	12	2.749e-03	5.570e-01	APEX1:389 OPA1:444.5 HIF1A:789 MGARP:1371 TRAK2:1386 HDAC6:1463
Axonogenesis (GO:0007409)	-0.07879159	167	4.625e-04	5.570e-01	RAB3A:73 EPHA5:101 FEZ1:150 KIF5C:188 NELL2:303 SLIT2:608.5
Cardiac Cell Development (GO:0055006)	-0.22483346	13	5.009e-03	5.570e-01	NKX2-5:83 CXADR:225 TTN91:11 TCAP:1336.5 SLC8A1:1474 MYH11:2177.5
Cardiac Muscle Hypertrophy (GO:0003300)	-0.33679270	7	2.031e-03	5.570e-01	CSRP3:718 TTN91:11 TCAP:1336.5 ORC1:1732 RYR2:2794 HDAC4:3260
Cell Communication By Electrical Coupling	-0.21485103	13	7.321e-03	5.570e-01	FKBP1:840 GJC1:399 ATP1A3:990.5 ATP1A2:1348 SLC8A1:1474 RYR2:2794
Cellular Response To Osmotic Stress (GO:0006965)	-0.15576890	26	5.992e-03	5.570e-01	HSP45:45 DD3X3:390.5 PKD2:437 MTOR:781 SERPINB6:917 ZFP361:1833.5
Cellular Response To Toxicologically Inconsistent	0.18293546	19	5.782e-03	5.570e-01	EPOB8:228.5 ERN1:728 STUB1:1085 UBE2E:1186 DNAJB12:1460.5 HDAC6:1463
Cholesterol Biosynthetic Process (GO:0006067)	0.18752836	23	1.857e-03	5.570e-01	SC5D:885 LBR:1007 MVD:1073.5 MSMO1:1416 HMGCR:1589 LSS:1807.5
Cholesterol Metabolic Process (GO:0008020)	0.10060770	53	6.066e-03	5.570e-01	TSKU:468 LBR:1007 MVD:1073.5 SCARF1:1101 ACA2:214.5 MSMO1:1416
Cytoplasmic Translation (GO:0002181)	0.15168617	43	5.836e-04	5.570e-01	RPL3:334 PRS7:521 EIF4A2:655 RPS16:743 EIF3F:797 RPL18:802
Dendritic Spine Morphogenesis (GO:006099)	-0.23334444	13	3.584e-03	5.570e-01	ZNF365:392 NOL13:1004 COCOT10:1293.5 EPHB3:1937 CTNND2:234 PMK1:901.5
Endosome Organization (GO:0007032)	-0.11833448	49	4.198e-03	5.570e-01	PLEKHGA:130 TMEM9:243 WASHC4:438 TMOC1:528 ARFGEF2:841.5 DAK1:340.5
Establishment Of Protein Localization To	0.12325306	40	6.903e-03	5.570e-01	TOMM40L:29 TOMM3A:336 TMEM10:174 RALA:973.5 FBXO7:1366 MGARP:1371
Fatty Acid Metabolic Process (GO:0006631)	0.07668591	104	7.001e-03	5.570e-01	ACACB:18 GPT1:140 ALOX5:170 THM:322 ACSL6:413.5 CYP4F2:570
Filopodium Assembly (GO:0046847)	-0.21623718	15	3.742e-03	5.570e-01	EZR:385.5 FGDS:1135 SPATA13:1236 SFEF1:1656.5 SPYF2:1702 DMN3:6903
Granulocyte Chemotaxis (GO:0071621)	-0.12336935	37	6.938e-03	5.570e-01	CCL20:127 CXADR:225 TTN91:11 CCL3:334 CCL2L3:534 KIF26:574 SYK:1194
Hematopoietic Progenitor Cell Differentiation	-0.16304149	25	4.790e-03	5.570e-01	FSTL3:2 HXBFA:473 BATF:581 BMP4:822 INHBA:852.5 TNFRSF13B:920
Lymphocyte Differentiation (GO:0030098)	-0.14033537	66	3.537e-03	5.570e-01	RELB:24 ZOBTB7A:403 BLNK:455.5 HDAC6:1869 HANP1:992 NHEJ1:1031.5
Mitochondrial Cytochrome C Oxidase Assembly	0.13300103	16	7.533e-03	5.570e-01	COX1B:151 SORF1:580 COX5:977.5 SMDY1:259 COX17:2084 COX16:2668
Mitochondrial Transport (GO:0006839)	0.10807661	51	7.836e-03	5.570e-01	SLC25A31:30 TOMM3A:336 TMEM10:174 BCL2L1:84X SLC25A4:91.5 FBXO7:1366
Negative Regulation Of BMP Signaling Pathway	-0.14077404	35	3.970e-03	5.570e-01	FSTL3:2 SART2:255 GEMR1:345 CHRD:143 DLX1:524.5 GPR155:555
Negative Regulation Of Bone Remodeling (GO:0001501)	-0.28970071	10	1.514e-03	5.570e-01	CARTPT:297 GEMR1:345 UBASH3B:361 TNFAIP3:1160 INP5D:1675 SFRP1:1990
Negative Regulation Of Fibrinolysis (GO:0001111)	-0.31111111	8	2.311e-03	5.570e-01	THBD:169 SERPIN1:206 TPA:95.5 RPSFNP2:1997.5 NRG1:3798 PLA2G3B:55
Negative Regulation Of Intracellular Trafficking	-0.24017155	7	1.789e-03	5.570e-01	ARHGAP8:140 MLRN:518 CRYAA:947 PLN:143.5 CRYAB:2565.5 INSL1:363.5
Negative Regulation Of Leukocyte Chemotaxis	-0.3867765	9	2.952e-03	5.570e-01	GEMR1:345 SLIT2:608.5 NELL1:736.5 C-2855.5 UST:2861.5 DUSP1:3119
Negative Regulation Of Monocyte Chemotaxis	-0.34609197	5	4.810e-03	5.570e-01	GEMR1:345 SLIT2:608.5 NELL1:736.5 DUSP1:3119 SLAMF8:533.5 NA
Negative Regulation Of Myeloid Leukocyte Chemotaxis	-0.17359781	22	4.840e-03	5.570e-01	FSTL3:2 TLR4:94.5 CARTPT:297 INHBA:852.5 TLR3:1615.5 PTPN22:2765
Negative Regulation Of Nuclear Transcription	0.26186828	11	2.634e-03	5.570e-01	PAIP1:299 TENT4A:649 SYNCRIP:1504 HNRNPUL1:512 PABPC1:2241.5 YBX1:2454
Negative Regulation Of Protein Metabolic Processes	0.07134718	124	6.194e-03	5.570e-01	GSTP3:3 THAF52:140 CPB3:171 MAD2L2:247 CDM4:266 SNAI2:730
Neuron Projection Extension (GO:0019138)	-0.14386691	38	2.144e-03	5.570e-01	NRN1:12 NELL2:303 CTNNB1:758 IMPACT:1048 SEMA3A:1221 SLC9A6:1632