

Top genes by P-value Permulated

Gene	Rho	N	P	p.adj	permPValue	qValueNoPerm	qValuePerm
PTCD1	0.2793375	164	2.920e-04	9.991e-01	2.171e-03	9.999e-01	1.000e+00
LINC00514	0.2827197	123	1.533e-03	9.991e-01	2.628e-03	9.999e-01	1.000e+00
ATP5MF-PTCD1	0.2885243	159	2.258e-04	9.991e-01	2.857e-03	9.999e-01	1.000e+00
MCC	0.3098003	140	1.955e-04	9.991e-01	2.971e-03	9.999e-01	1.000e+00
MFAP5	-0.2836889	124	1.408e-03	9.991e-01	3.657e-03	9.999e-01	1.000e+00
CADPS	0.3775398	86	3.390e-04	9.991e-01	3.885e-03	9.999e-01	1.000e+00
KRTAP10-1	0.1987248	135	2.086e-02	9.991e-01	4.228e-03	9.999e-01	1.000e+00
TCAM	-0.2925997	144	3.725e-04	9.991e-01	5.028e-03	9.999e-01	1.000e+00
GCM1	-0.2582119	147	1.590e-03	9.991e-01	5.599e-03	9.999e-01	1.000e+00
CYP2W1	-0.2339568	140	5.399e-03	9.991e-01	6.171e-03	9.999e-01	1.000e+00
SPRR2B	0.3210103	79	3.921e-03	9.991e-01	7.428e-03	9.999e-01	1.000e+00
ABL2	0.2656947	143	1.340e-03	9.991e-01	7.656e-03	9.999e-01	1.000e+00
GAS2L3	-0.2216252	162	4.592e-03	9.991e-01	7.656e-03	9.999e-01	1.000e+00
CLIP1	0.2715619	165	4.182e-04	9.991e-01	8.685e-03	9.999e-01	1.000e+00
ZC3H13	-0.2394264	158	2.447e-03	9.991e-01	8.799e-03	9.999e-01	1.000e+00
SCFD2	0.2397081	158	2.417e-03	9.991e-01	8.913e-03	9.999e-01	1.000e+00
KCNH3	0.2397794	144	3.796e-03	9.991e-01	9.028e-03	9.999e-01	1.000e+00
DPM1	0.2662007	129	2.294e-03	9.991e-01	9.370e-03	9.999e-01	1.000e+00
KIF15	-0.1857470	159	1.679e-02	9.991e-01	1.006e-02	9.999e-01	1.000e+00
OTUD7B	0.2699077	133	1.679e-03	9.991e-01	1.017e-02	9.999e-01	1.000e+00
RINL	0.2063346	156	5.399e-03	9.991e-01	1.028e-02	9.999e-01	1.000e+00
KRTAP4-12	0.2708312	94	8.285e-03	9.991e-01	1.051e-02	9.999e-01	1.000e+00
SLC22A8	-0.1881628	148	2.201e-02	9.991e-01	1.063e-02	9.999e-01	1.000e+00
TEX10	-0.2230786	136	9.041e-03	9.991e-01	1.086e-02	9.999e-01	1.000e+00
CIT	0.2523954	154	1.589e-03	9.991e-01	1.097e-02	9.999e-01	1.000e+00

Top genes by P-value non-permulated

Gene	Rho	N	P	p.adj	permPValue	qValueNoPerm	qValuePerm
A1BG	-0.111644190	123	2.189e-01	9.991e-01	1.986e-01	9.999e-01	1.000e+00
A1CF	-0.024569127	128	7.831e-01	9.991e-01	7.988e-01	9.999e-01	1.000e+00
A2M	-0.160699562	169	3.687e-02	9.991e-01	6.502e-02	9.999e-01	1.000e+00
A2ML1	0.052890311	134	5.439e-01	9.991e-01	4.221e-01	9.999e-01	1.000e+00
A3GALT2	0.013537910	132	8.776e-01	9.991e-01	8.713e-01	9.999e-01	1.000e+00
A4GALT	-0.065096551	154	4.225e-01	9.991e-01	4.917e-01	9.999e-01	1.000e+00
A4GNT	0.054749291	151	5.043e-01	9.991e-01	4.707e-01	9.999e-01	1.000e+00
AAAS	-0.007388264	132	9.330e-01	9.991e-01	9.636e-01	9.999e-01	1.000e+00
AACS	0.019104271	156	8.129e-01	9.991e-01	7.752e-01	9.999e-01	1.000e+00
AADAC	-0.065142631	107	5.059e-01	9.991e-01	5.055e-01	9.999e-01	1.000e+00
AADACL2	0.019040428	120	8.355e-01	9.991e-01	7.951e-01	9.999e-01	1.000e+00
AADACL3	0.024884968	158	7.563e-01	9.991e-01	7.273e-01	9.999e-01	1.000e+00
AADACL4	-0.023590944	141	7.813e-01	9.991e-01	8.335e-01	9.999e-01	1.000e+00
AADAT	-0.058886959	152	4.711e-01	9.991e-01	5.047e-01	9.999e-01	1.000e+00
AAGAB	-0.010550651	136	9.030e-01	9.991e-01	9.834e-01	9.999e-01	1.000e+00
AAK1	0.140113651	145	9.278e-02	9.991e-01	2.111e-01	9.999e-01	1.000e+00
AAMDC	0.138093817	88	1.995e-01	9.991e-01	3.761e-01	9.999e-01	1.000e+00
AAMP	0.242451740	95	1.792e-02	9.991e-01	9.702e-02	9.999e-01	1.000e+00
ANAT	-0.106992984	138	2.117e-01	9.991e-01	3.568e-01	9.999e-01	1.000e+00
AAR2	0.188222061	133	3.004e-02	9.991e-01	4.217e-02	9.999e-01	1.000e+00
AARD	-0.111536350	105	2.573e-01	9.991e-01	5.427e-01	9.999e-01	1.000e+00
AARS1	-0.068495717	145	4.130e-01	9.991e-01	5.875e-01	9.999e-01	1.000e+00
AARS2	-0.031408831	165	6.888e-01	9.991e-01	6.514e-01	9.999e-01	1.000e+00
AARSD1	0.007615327	145	9.276e-01	9.991e-01	9.879e-01	9.999e-01	1.000e+00
AASDH	0.090375908	165	2.483e-01	9.991e-01	3.356e-01	9.999e-01	1.000e+00

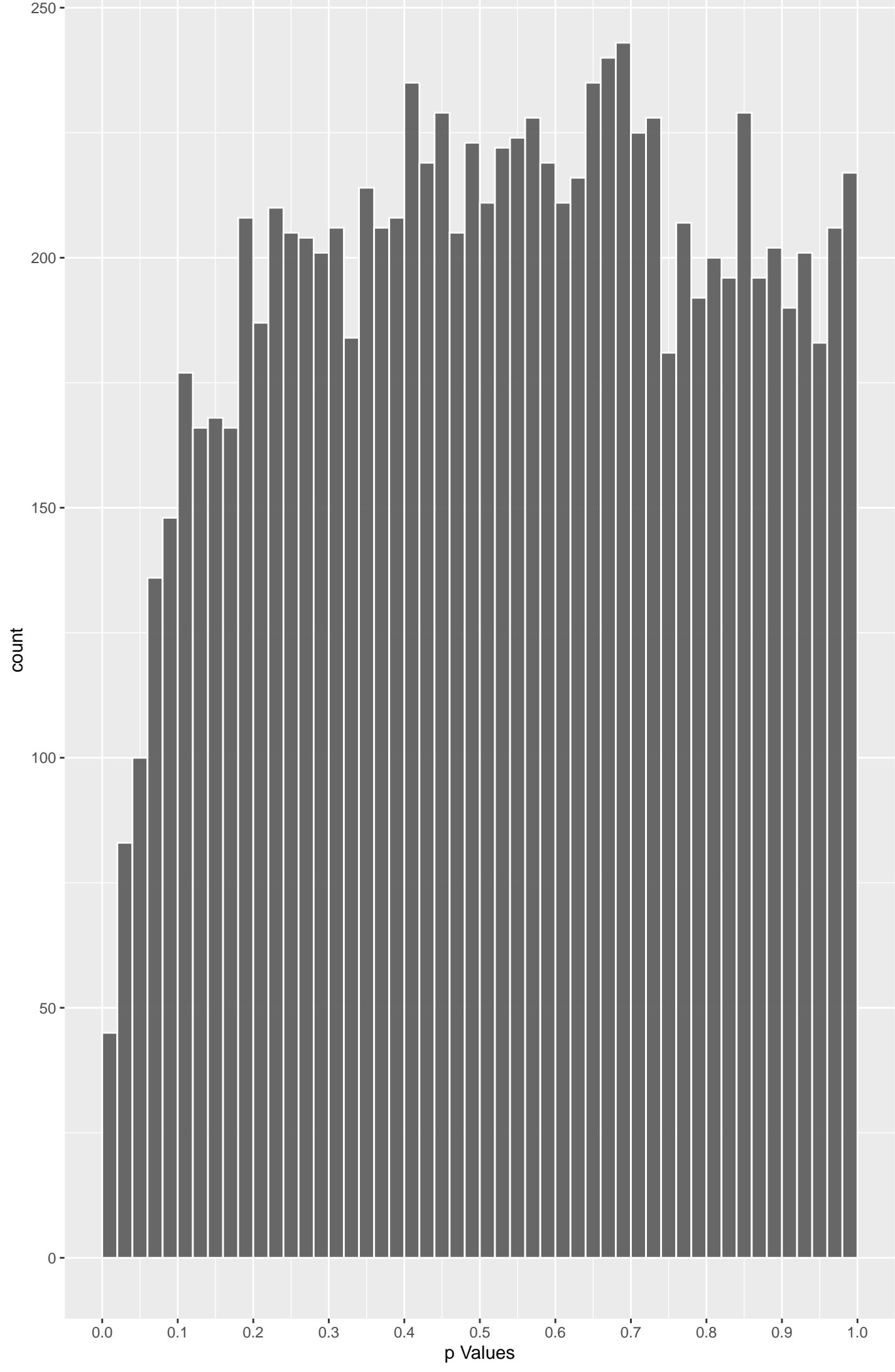
Top genes by Q-Value Permulated

Gene	Rho	N	P	p.adj	permPValue	qValueNoPerm	qValuePerm
A1BG	-0.111644190	123	2.189e-01	9.991e-01	1.986e-01	9.999e-01	1.000e+00
A1CF	-0.024569127	128	7.831e-01	9.991e-01	7.988e-01	9.999e-01	1.000e+00
A2M	-0.160699562	169	3.687e-02	9.991e-01	6.502e-02	9.999e-01	1.000e+00
A2ML1	0.052890311	134	5.439e-01	9.991e-01	4.221e-01	9.999e-01	1.000e+00
A3GALT2	0.013537910	132	8.776e-01	9.991e-01	8.713e-01	9.999e-01	1.000e+00
A4GALT	-0.065096551	154	4.225e-01	9.991e-01	4.917e-01	9.999e-01	1.000e+00
A4GNT	0.054749291	151	5.043e-01	9.991e-01	4.707e-01	9.999e-01	1.000e+00
AAAS	-0.007388264	132	9.330e-01	9.991e-01	9.636e-01	9.999e-01	1.000e+00
AACS	0.019104271	156	8.129e-01	9.991e-01	7.752e-01	9.999e-01	1.000e+00
AADAC	-0.065142631	107	5.059e-01	9.991e-01	5.055e-01	9.999e-01	1.000e+00
AADACL2	0.019040428	120	8.355e-01	9.991e-01	7.951e-01	9.999e-01	1.000e+00
AADACL3	0.024884968	158	7.563e-01	9.991e-01	7.273e-01	9.999e-01	1.000e+00
AADACL4	-0.023590944	141	7.813e-01	9.991e-01	8.335e-01	9.999e-01	1.000e+00
AADAT	-0.058886959	152	4.711e-01	9.991e-01	5.047e-01	9.999e-01	1.000e+00
AAGAB	-0.010550651	136	9.030e-01	9.991e-01	9.834e-01	9.999e-01	1.000e+00
AAK1	0.140113651	145	9.278e-02	9.991e-01	2.111e-01	9.999e-01	1.000e+00
AAMDC	0.138093817	88	1.995e-01	9.991e-01	3.761e-01	9.999e-01	1.000e+00
AAMP	0.242451740	95	1.792e-02	9.991e-01	9.702e-02	9.999e-01	1.000e+00
ANAT	-0.106992984	138	2.117e-01	9.991e-01	3.568e-01	9.999e-01	1.000e+00
AAR2	0.188222061	133	3.004e-02	9.991e-01	4.217e-02	9.999e-01	1.000e+00
AARD	-0.111536350	105	2.573e-01	9.991e-01	5.427e-01	9.999e-01	1.000e+00
AARS1	-0.068495717	145	4.130e-01	9.991e-01	5.875e-01	9.999e-01	1.000e+00
AARS2	-0.031408831	165	6.888e-01	9.991e-01	6.514e-01	9.999e-01	1.000e+00
AARSD1	0.007615327	145	9.276e-01	9.991e-01	9.879e-01	9.999e-01	1.000e+00
AASDH	0.090375908	165	2.483e-01	9.991e-01	3.356e-01	9.999e-01	1.000e+00

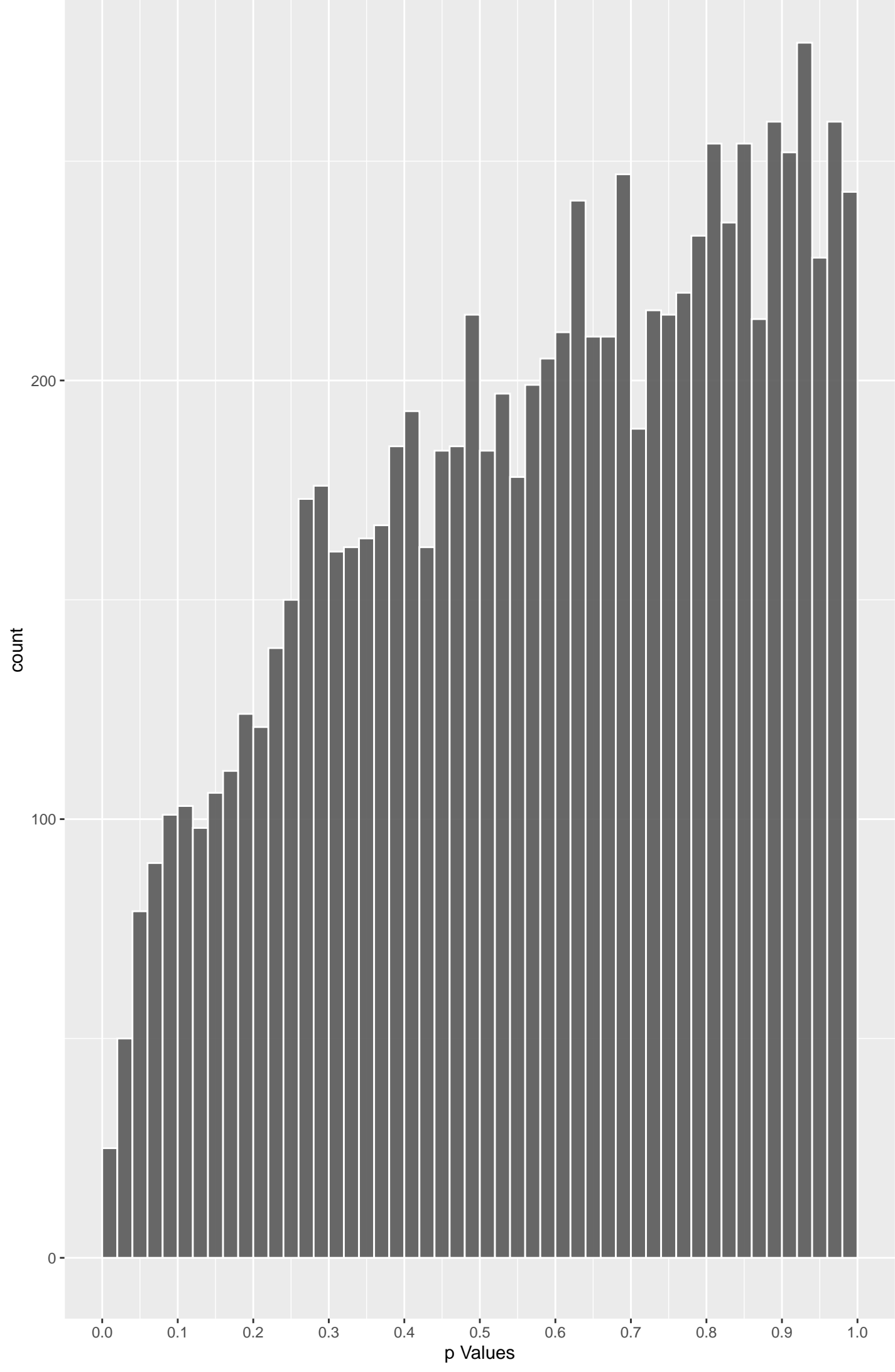
Top genes by Q-Value non-permulated

Gene	Rho	N	P	p.adj	permPValue	qValueNoPerm	qValuePerm
A1BG	-0.111644190	123	2.189e-01	9.991e-01	1.986e-01	9.999e-01	1.000e+00
A1CF	-0.024569127	128	7.831e-01	9.991e-01	7.988e-01	9.999e-01	1.000e+00
A2M	-0.160699562	169	3.687e-02	9.991e-01	6.502e-02	9.999e-01	1.000e+00
A2ML1	0.052890311	134	5.439e-01	9.991e-01	4.221e-01	9.999e-01	1.000e+00
A3GALT2	0.013537910	132	8.776e-01	9.991e-01	8.713e-01	9.999e-01	1.000e+00
A4GALT	-0.065096551	154	4.225e-01	9.991e-01	4.917e-01	9.999e-01	1.000e+00
A4GNT	0.054749291	151	5.043e-01	9.991e-01	4.707e-01	9.999e-01	1.000e+00
AAAS	-0.007388264	132	9.330e-01	9.991e-01	9.636e-01	9.999e-01	1.000e+00
AACS	0.019104271	156	8.129e-01	9.991e-01	7.752e-01	9.999e-01	1.000e+00
AADAC	-0.065142631	107	5.059e-01	9.991e-01	5.055e-01	9.999e-01	1.000e+00
AADACL2	0.019040428	120	8.355e-01	9.991e-01	7.951e-01	9.999e-01	1.000e+00
AADACL3	0.024884968	158	7.563e-01	9.991e-01	7.273e-01	9.999e-01	1.000e+00
AADACL4	-0.023590944	141	7.813e-01	9.991e-01	8.335e-01	9.999e-01	1.000e+00
AADAT	-0.058886959	152	4.711e-01	9.991e-01	5.047e-01	9.999e-01	1.000e+00
AAGAB	-0.010550651	136	9.030e-01	9.991e-01	9.834e-01	9.999e-01	1.000e+00
AAK1	0.140113651	145	9.278e-02	9.991e-01	2.111e-01	9.999e-01	1.000e+00
AAMDC	0.138093817	88	1.995e-01	9.991e-01	3.761e-01	9.999e-01	1.000e+00
AAMP	0.242451740	95	1.792e-02	9.991e-01	9.702e-02	9.999e-01	1.000e+00
ANAT	-0.106992984	138	2.117e-01	9.991e-01	3.568e-01	9.999e-01	1.000e+00
AAR2	0.188222061	133	3.004e-02	9.991e-01	4.217e-02	9.999e-01	1.000e+00
AARD	-0.111536350	105	2.573e-01	9.991e-01	5.427e-01	9.999e-01	1.000e+00
AARS1	-0.068495717	145	4.130e-01	9.991e-01	5.875e-01	9.999e-01	1.000e+00
AARS2	-0.031408831	165	6.888e-01	9.991e-01	6.514e-01	9.999e-01	1.000e+00
AARSD1	0.007615327	145	9.276e-01	9.991e-01	9.879e-01	9.999e-01	1.000e+00
AASDH	0.090375908	165	2.483e-01	9.991e-01	3.356e-01	9.999e-01	1.000e+00

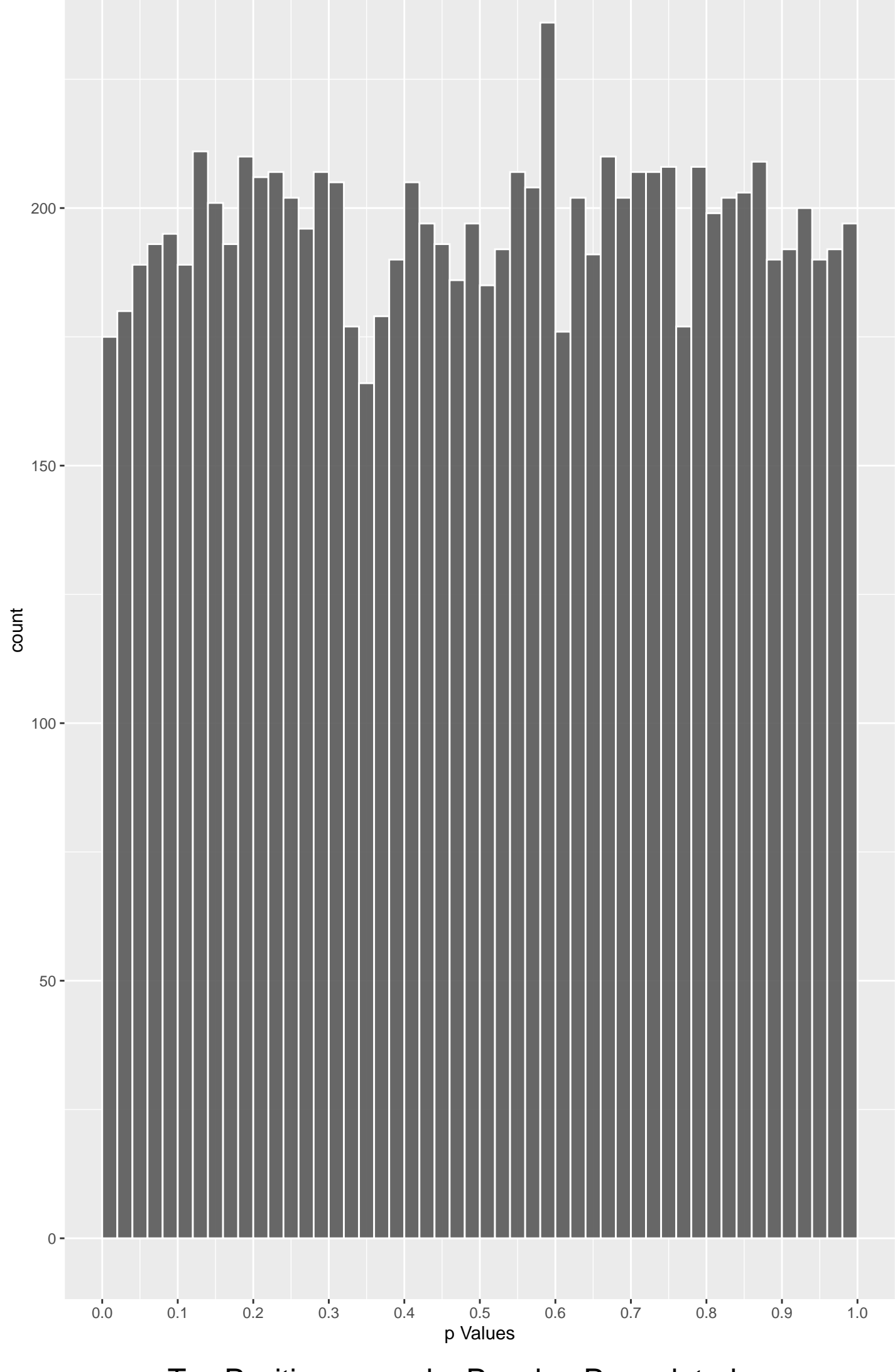
Positive Rho Permulated



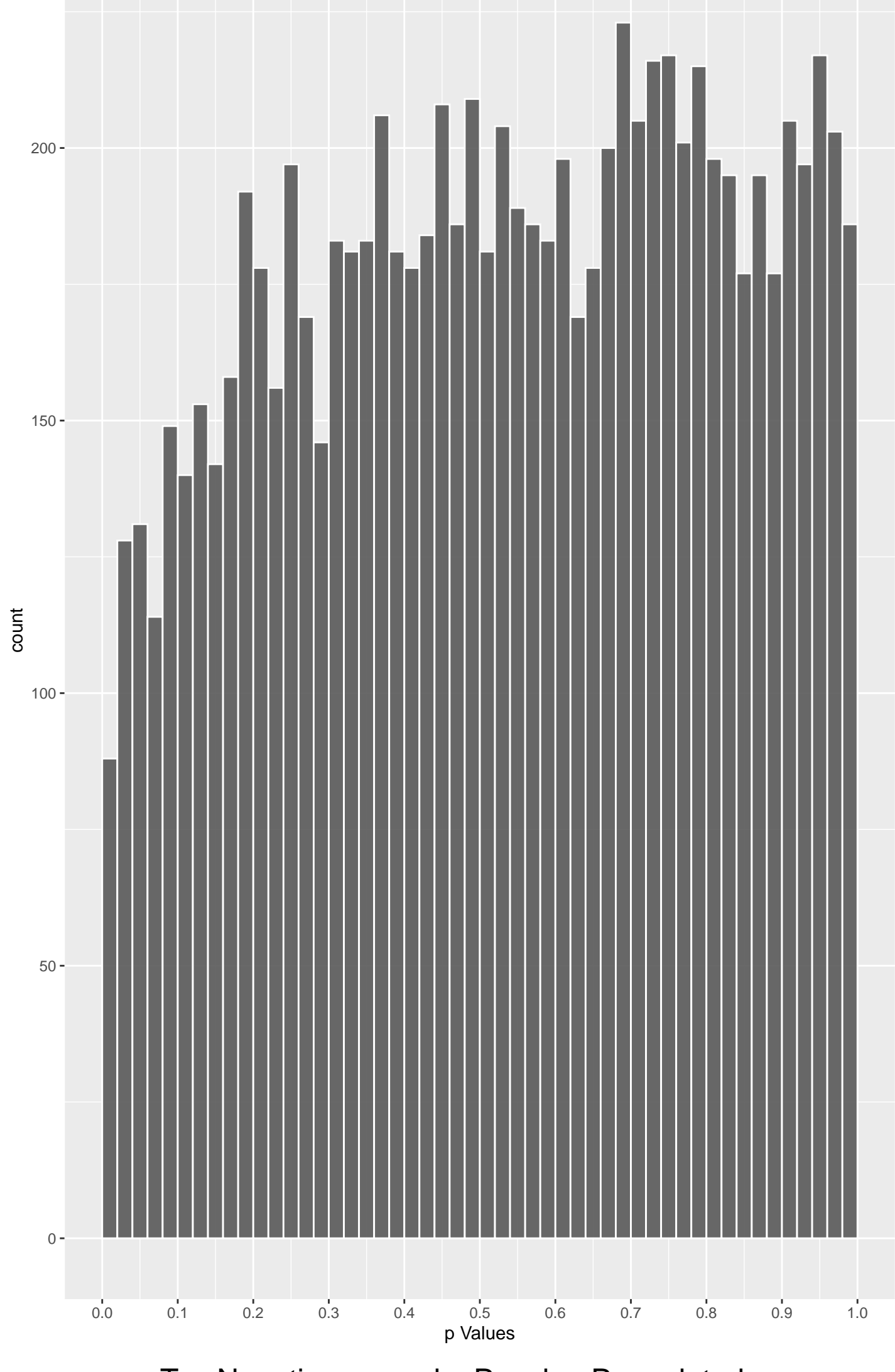
Negative Rho Permulated



Positive Rho Non-permulated



Negative Rho Non-permulated



Top Positive genes by P-value Permulated

						q-value	permPValue	qValueNoPerm
PTCD1	0.2793375	164	2.920e-04	9.991e-01	2.171e-03	9.999e-01	1.000e+00	
LINC00514	0.2827197	123	1.533e-03	9.991e-01	2.628e-03	9.999e-01	1.000e+00	
ATP5MF-PTCD1	0.2885243	159	2.258e-04	9.991e-01	2.857e-03	9.999e-01	1.000e+00	
MCC	0.3098003	140	1.955e-04	9.991e-01	2.971e-03	9.999e-01	1.000e+00	
CADPS	0.3775398	86	3.390e-04	9.991e-01	3.885e-03	9.999e-01	1.000e+00	
KRTAP10-1	0.1987248	135	2.086e-02	9.991e-01	4.228e-03	9.999e-01	1.000e+00	
SPR2Z	-0.2925997	79	3.971e-03	9.991e-01	7.432e-03	9.999e-01	1.000e+00	
ABL2	0.2656947	143	1.340e-03	9.991e-01	7.656e-03	9.999e-01	1.000e+00	
CLIP1	0.2715619	165	4.182e-04	9.991e-01	8.685e-03	9.999e-01	1.000e+00	
SCFD2	0.2397081	158	2.417e-03	9.991e-01	8.913e-03	9.999e-01	1.000e+00	

GO\_Biological\_Process\_2023 Top pathways by permutation

Geneset	stat	num.genes	pval	p.adj	gene.vals
Sensory Perception Of Smell (GO:0007608)	0.14618253	208	4.198e-13	2.270e-09	OR21P:43 OR5M3:78 OR13G1:89 OR5D3P:102 OR4E2:106 OR10Z1:121.5
Detection Of Chemical Stimulus Involved	0.14697539	129	8.613e-09	2.328e-05	OR21P:43 OR13G1:89 OR4E2:106 OR10Z1:121.5 OR6K3:244.5 OR2T33:304
Detection Of Chemical Stimulus Involved	0.14515771	127	1.691e-08	3.047e-05	OR21P:43 OR5M3:78 OR13G1:89 OR4E2:106 OR10Z1:121.5 OR6K3:244.5 OR2T33:304
Fatty Acid Metabolic Process (GO:0006631)	-0.140016631	120	1.220e-07	1.649e-04	ACOT8:16 THEM4:38 GNPAT:151 LCP1:155 LPHAL6B:211 SC2P:390.5
Monocarboxylic Acid Metabolic Process (G	-0.14347655	96	1.216e-06	1.315e-03	THEM4:38 LDHAL6A:64 GNPAT:151 LCP1:155 LPHAL6B:211 SC2P:390.5
Peptide Biosynthetic Process (GO:0043043)	0.11155620	93	1.995e-06	1.798e-03	RPS17:34 RPS16:135 AGO2:159.5 RPL9:283 RPS19:302.5 RPL34:367
Cytoplasmic Translation (GO:0002181)	0.14136982	151	3.219e-06	2.486e-03	RPS17:34 RPS16:135 RPL28:283 RPS19:302.5 RPL34:367 RPL23A:411
Brain Development (GO:0007420)	0.10630067	157	4.473e-06	3.023e-03	NDRG4:128 ZIC1:133.5 EML1:181 GRN2D:291 ROB2D:293.5 PLN8:383
Macromolecular Biosynthetic Process (GO:0	0.09437649	179	1.222e-05	6.005e-03	RPS17:34 RPS16:135 AGO2:159.5 RPL9:283 RPS19:302.5 GTPBP1:318.5
Sensory Perception Of Chemical Stimulus	0.12823008	98	1.176e-05	6.005e-03	OR5M3:78 OR5D3P:102 CALH2:140 OR8K1:194 OR5I1:242.5 OR5M9:376.5
Triglyceride Metabolic Process (GO:000666	-0.19309326	43	1.189e-05	6.005e-03	APOC3:29 LCP1:155 LMD2:206.5 LPIN1:256 GK5:558.5 PNPLA4:582
Steroid Biosynthetic Process (GO:0006694)	-0.17787624	49	1.665e-05	7.503e-03	ACOT8:16 CYP8B1:163.5 OSBP:226 CYP39A1:311.5 SCP2:390.5 PRLR:536
Nitrogen Compound Transport (GO:00071705)	-0.09351927	161	4.371e-05	1.818e-02	ABCC2:84.5 CD320:92 SLC13A1:196 SLC22A4:222 SLC2A4:260.5 SLC6A13:372
Gene Expression (GO:0010467)	0.06943954	286	5.663e-05	5.048e-02	RPS17:34 H3C1:103 HNRNP3:123.5 RPS16:135 AGO2:159.5 ALYREF:162.5
Vitamin Transport (GO:0051180)	-0.18878962	38	5.676e-05	2.046e-02	SLC5A6:34 CD320:92 SLC25A32:128 SLC2A8:190 TNCN:388 SLC46A1:598.5
Cellular Lipid Catabolic Process (GO:0004	-0.23646837	23	8.667e-05	2.757e-02	ACOT8:16 LPN2:206.5 LPIN1:256 ACOX1:319 PLBD1:343 PLD1:1397.5
Translation (GO:0006412)	0.07591019	228	8.207e-05	2.757e-02	RPS17:34 RPS16:135 AGO2:159.5 RPL9:283 RPS19:302.5 GTPBP1:318.5
Cell Mitogenesis Involved In Neuron Di	0.12899038	76	1.024e-04	2.915e-02	NEFH1:123.5 MAP1B:168.5 DVL1:523 POU4F1:532.5 MAP1B:703 APLF2:283.5
Diet Biosynthetic Process (GO:0034312)	-0.28126773	16	9.919e-05	2.915e-02	SPHK2:21 SPTSSB:40.5 ACER1:321 SPTLC1:496.5 DHFR:542.5 SPHK1:900
Neuron Projection Morphogenesis (GO:0048	0.09432961	140	1.196e-04	3.233e-02	SRGAP3:82 NEFH:123.5 MAP1B:168.5 EPHA4:251.5 SGK1:261.5 SHANK3:429
Fatty Acid Catabolic Process (GO:0009062)	-0.14211675	60	1.409e-04	3.493e-02	ACOT8:16 ECHDC1:159.5 LPN2:206.5 NUDT8:219 LPIN1:256 ACOX1:319
Serine Family Amino Acid Metabolic Proces	-0.30475009	13	1.421e-04	3.493e-02	GCLC:320 ACOT1:831 SRR:1310 CTH:1712 GLYT4:1995.5 BAAT:2016.5
Lipid Biosynthetic Process (GO:0008610)	-0.13224147	68	1.643e-04	3.554e-02	LCP1:155 SPC2:390.5 MVD:53.5 PRLR:536 ACACB:624 CYP17A1:625
Sphingolipid Biosynthetic Process (GO:0046	-0.31482171	12	1.593e-04	3.554e-02	SPHK2:21 SPTSSB:40.5 ACER1:321 SPTLC1:496.5 SPHK1:900 ASAH2:908
Sphingosine Biosynthetic Process (GO:0045	-0.31482171	12	1.593e-04	3.554e-02	SPHK2:21 SPTSSB:40.5 ACER1:321 SPTLC1:496.5 SPHK1:900 ASAH2:908
NADH Dehydrogenase Complex Assembly (GO:	-0.15405705	49	1.922e-04	3.849e-02	ECISIT:70.5 NDUFB10:271.5 NDUFAF1:469 NUBPL:474.5 NDUFA3:606 NDUFC2:614.5
Mitochondrial Respiratory Chain Complex	-0.15405705	49	1.922e-04	3.849e-02	ECISIT:70.5 NDUFB10:271.5 NDUFAF1:469 NUBPL:474.5 NDUFA3:606 NDUFC2:614.5
Positive Regulation Of Cell Migration (GO:	-0.06587634	267	2.214e-04	4.127e-02	PDGFRB:27 EPHA2:60 MYADM:65.5 CTSN:90.5 SEMA7A:148 GRB7:295.5
Positive Regulation Of Leukocyte Activat	-0.23880495	20	2.173e-04	4.127e-02	NECTIN2:526 TSLP:612 CD226:63.5 HAVCR1:1039 WNT5A:1473.5 TLR6:2032
Embryonic Limb Morphogenesis (GO:0030326	0.18233352	34	2.347e-04	4.230e-02	INTU2:17 WDPCP:625 CREBBP:877 TPAP2A:396 TBX2:1135.5 ZNF358:1164.5
Mitochondrial Respiratory Chain Complex	-0.11687195	82	2.568e-04	4.340e-02	ECISIT:70.5 NDUFB10:271.5 NDUFAF1:469 NUBPL:474.5 CHCHD7:600 NDUFA3:606
protein-RNA Complex Assembly (GO:0022618	0.08949784	141	2.494e-04	4.340e-02	AGO1:32 TCFR1:234 MAP2K2:50 MYH69:769 TUBA1A:71.5 IFNA1:1474
Wnt Signaling Pathway (GO:0016055)	0.12170534	74	2.979e-04	4.350e-02	FZD8:59 TCFR1:234 CDC8C:223 WNT2B:347 FZD3:487 DVL1:523
acyl-CoA Metabolic Process (GO:0006637)	-0.19406240	28	3.800e-04	4.350e-02	ACOT8:16 MCEE:445 ACACB:624 OGDH:631 SUGLC7:94 SUGLC2:1257
Amide Biosynthetic Process (GO:0043604)	-0.14905911	50	2.669e-04	4.350e-02	SPTSSB:40.5 CER3:101 CER56:187 OSBP:226 CYP4F2:490 SPTLC1:496.5
Amide Transport (GO:0042886)	-0.18457077	31	3.768e-04	4.350e-02	SLC5A6:34 SLC25A32:128 OSBP:226 GIPC1:313 DISP1:438 TAP1:576.5
Cholesterol Transport (GO:0030301)	-0.14404802	51	3.751e-04	4.350e-02	APOC3:29 OSBP:226 STARO5:349 SOAT1:403 CD36:728.5 NPC1:787.5
Dicarboxylic Acid Metabolic Process (GO:00	-0.14840342	49	3.279e-04	4.350e-02	ACOT8:16 SLC25A32:128 GCLC:320 LZHGHD:442.5 DHFR:542.5 SLC46A1:598.5
Import into Cell (GO:0009857)	-0.17046163	37	3.345e-04	4.350e-02	SLC5A6:34 SLC22A4:222 SLC16A2:242 SLC16A1:372 SLC46A1:598.5 SLC6A6:738
mRNA Processing (GO:0006397)	0.07239027	25	3.650e-04	4.350e-02	HNRNP3:123.5 ALYREF:162.5 SART1:195 RBMX:238.5 SNRNP1:242.5 DHX15:283

EnrichmentHsSymbolsFile2 Top pathways by permutation

Geneset	stat	num.genes	pval	p.adj	gene.vals
REACTOME_OILFACTORY_SIGNALING_PATHWAY	0.14513987	390	5.512e-29	3.590e-25	OR52B2:18.5 OR52W1:29 OR2AT:462 OR5M3:78 OR13G1:89 OR1102:104
REACTOME_OILFACTORY_TRANSDUCTION	0.12598558	380	2.536e-26	8.234e-23	OR52B2:18.5 OR52W1:29 CAMK2B:42 OR5A1:62 OR5M3:78 OR13G1:89
REACTOME_SENSORY_PERCEPTION	0.12097937	605	3.978e-24	8.610e-21	OR52B2:18.5 OR52W1:29 OR2AT:462 MYH69 OR5M3:78 OR13G1:89
REACTOME_DEVELOPMENTAL_BIOLOGY	0.08326744	1143	3.903e-21	6.337e-18	KRTAP10-1.6 SPRR2B:7 ABL2:8 RPS17:34 MAP2K2:50 MYH69:69
HOUNKPE_HOUSEKEEPING_GENES	0.06709069	1100	8.182e-14	1.063e-10	CBX1:19.5 DXD27:35 PDCD6:36.5 TBR3:39 PURB:41 MAP2K2:50
REACTOME_SIGNALING_BY_WNT	0.11693456	322	5.894e-13	6.379e-10	AGO1:32 FZD8:59 H3C1:103 H3C13:127 H2BC4:141 AGO2:159.5
HSIAO_LIVER_SPECIFIC_GENES	-0.14281771	240	4.388e-12	4.071e-09	APOC3:29 ABCD2:84.5 HNR1H4:130.5 ALDH1A1:139.5 LPN2:206.5 AZGP1:369
CARRILLOREIXACH_HEPATOBLASTOMA_VS_NORMAL	-0.06341643	1046	5.424e-12	4.403e-09	TME4M4:515 APOC3:29 ANO5:35 SLC6A16:53 ETNPLP:59 EPHA2:60
REACTOME_INFECTIONS_DISEASE	0.05116447	933	2.342e-10	1.690e-07	CBX1:19.5 RPS17:34 MAP2K2:50 MYH69:769 TUBA1A:71.5 IFNA1:1474
REACTOME_ACTIVATION_OF_ANTERIOR_HOX_GENE	0.16697291	116	5.322e-10	3.456e-07	H3C1:103 H3C13:127 H2BC4:141 H2AC14:261.5 H2AC19:308.5 ASH2L:394
REACTOME_NERVOUS_SYSTEM_DEVELOPMENT	0.07574312	570	7.112e-10	4.199e-07	ABL2:8 RPS17:34 MAP2K2:50 MYH69:769 TUBA1A:71.5 SRGAP3:82
REACTOME_METABOLISM_OF_LIPIDS	-0.06894441	726	9.558e-10	5.172e-07	MYH69:69 ACTR19:190 ARPC4:276 ARPC5:417.5 WNT4:748 FGR:49.5
REACTOME_CELLULAR_RESPONSES_TO_STIMULI	0.06411892	788	1.044e-09	6.214e-07	AGO1:32 RPS17:34 CAMK2B:42 TUBA1A:71.5 CALR:90 TNC2:95.5
REACTOME_RHO_GTPASES_ACTIVATE_PKNS	0.18409103	99	1.961e-09	9.096e-07	MYH69:69 WYHAQ:94 H3C1:103 H3C13:127 H2BC4:141 H2AC14:261.5
REACTOME_REGULATION_OF_EXPRESSION_OF_SL	0.13242352	169	2.937e-09	1.271e-06	RPS17:34 RPS16:135 PSMA4:225 PSMA7:258 RPL9:283 ROB2C:293.5
HOSHIDA_LIVER_CANCER_SUBCLASS_S3	-0.10411267	260	7.793e-09	3.163e-06	GGH:50 ALDH1A1:139.5 LPN2:206.5 SLC16A2:242 LPIN1:256 ADK:274
CAIRO_LIVER_DEVELOPMENT_DN	-0.11329995	217	9.121e-09	3.484e-06	CTSH:90.5 CAMP:104 LCP1:155 A2M:178 LPN2:206.5 SLC16A2:242
REACTOME_SIGNALING_BY_ROBO_RECEPTORS	-0.11316255	214	1.198e-08	4.322e-06	ABL2:8 RPS17:34 SRGAP3:82 RPS16:135 PSMA4:225 PSMA7:258
REACTOME_KERATINIZATION	0.11265690	214	1.391e-08	4.753e-06	KRTAP10-1.6 SPRR2B:7 KRTAP10-4.77 KRT81:91.5 KRTAP10-8:117.5 KRTAP5-8:130.5
REACTOME_BETA_CATENIN_INDEPENDENT_WNT_SI	0.13609902	145	1.568e-08	5.092e-06	AGO1:32 FZD8:59 AGO2:159.5 PDE6G:165.5 TNRC6B:176.5
REACTOME_METABOLISM_OF_STEROIDS	-0.13195689	152	2.006e-08	6.203e-06	ACOT8:16 STARDE3:1 TM7SF2:116 NR1H4:130.5 CYP8B1:163.5 AKR1B1:213
REACTOME_TRANSCRIPTIONAL_REGULATION_BY_R	0.10483904	233	3.539e-08	1.045e-05	AGO1:32 H3C1:103 H3C13:127 H2BC4:141 AGO2:159.5 CBX2:173
REACTOME_TRANSCRIPTIONAL_INFECTION	0.12822319	158	4.448e-08	1.234e-05	MYH69:69 ACTR19:190 ARPC4:276 ARPC5:417.5 WNT4:748 FGR:49.5
CHIANG_LIVER_CANCER_SUBCLASS_PROLIFERATI	-0.11969025	173	5.734e-08	1.552e-05	ETNPLP:59 CYP8B1:163.5 MYH69:769 SLC16A2:242 AZGP1:369 SCP2:390.5
CAIRO_HEPATOBLASTOMA_DN	-0.09717051	262	6.362e-08	1.653e-05	ETNPLP:59 EPHA2:60 MGLL:98 LEPR:182.5 LPN2:206.5 VIPR1:246
REACTOME_RHO_GTPASE_EFFECTORS	0.08729911	312	1.192e-07	2.848e-05	CLIP1:9 GUT1:6 MYH69:69 TUBA1A:71.5 WYHAQ:94 H3C1:103
REACTOME_OXIDATIVE_STRESS_INDUCED_SENESC	0.14145624	117	1.272e-07	2.848e-05	AGO1:32 H3C1:103 H3C13:127 H2BC4:141 CBX2:173 TNRC6B:176.5
REACTOME_GLYCOXYLATE_METABOLISM_AND_GLYCI	-0.27889902	30	1.242e-07	2.848e-05	DBT:201 DLD:242 GLDC:563.5 UAS:566 OGDH:631 PDHA2:637.5
REACTOME_ESR_MEDIATED_SIGNALING	0.10506695	214	1.209e-07	2.848e-05	AGO1:32 H3C1:103 H3C13:127 H2BC4:141 AGO2:159.5 TNRC6B:176.5
REACTOME_RUNX1_REGULATES_GENES_INVOLVED	0.15672222	92	2.061e-07	4.460e-05	AGO1:32 H3C1:103 H3C13:127 H2BC4:141 TNRC6B:176.5 SETD1B:246.5
REACTOME_ESTROGEN_DEPENDENT_GENE_EXPRESS	0.12340408	145	2.951e-07	5.861e-05	AGO1:32 H3C1:103 H3C13:127 H2BC4:141 AGO2:159.5 TNRC6B:176.5
WP_CYTOPLASMIC_RIBOSOMAL_PROTEINS	0.16018754	86	2.845e-07	5.861e-05	RPS17:34 RPS16:135 RPL9:283 RPS19:302.5 RPL34:367 RPL23A:411
HSIAO_HOUSEKEEPING_GENES	0.07661425	361	2.978e-07	5.861e-05	RPS17:34 MYH69:69 HINT1:86 WYHAQ:94 RPS16:135 SLC25A6:143
KEGG_VALINE_LEUCINE_AND_ISOLEUCINE_DEGRA	-0.22282627	44	3.137e-07	5.982e-05	DBT:201 DLD:242 ACAD3:266 HICB1:324 MCEE:445 SCAT2:474.5
REACTOME_SRP_DEPENDENT_COTRANSLATION_P	0.13893881	111	4.306e-07	7.990e-05	MYH69:69 CYP8B1:163.5 LPN2:213.5 RPL9:283 RPS19:302.5 RPL34:367
REACTOME_RUNX1_REGULATES_TRANSCRIPTION_O	0.13040311	125	4.837e-07	8.725e-05	H3C1:103 H3C13:127 H2BC4:141 PSMA4:225 PSMA7:258 H2AC14:261.5
MARTENS_TRETNIN_RESPONSE_DN	0.05394735	751	5.370e-07	9.425e-05	CLIP1:9 ARL6P4:43 PURB:41 ABT1:67 HINT1:86 CALR:90
REACTOME_SLC_MEDIATED_TRANSMEMBRANE_TRAN	-0.09268152	245	6.016e-07	1.002e-04	SLC22A8:8 SLC5A12:12 SLC5A6:34 SLC2A8:190 SLC13A1:196 SLC22A6:204
KIM_BIPOLAR_DISORDER_OLIGODENDROCYTE_DEN	0.05928659	655	5.926e-07	1.002e-04	RPS17:34 CAMK2B:42 VDAC3:58 HINT1:86 WYHAQ:94 NDRG4:128
REACTOME_TCF_DEPENDENT_SIGNALING_VN_RESP	0.09692966	226	6.908e-07	1.094e-04	FZD8:59 H3C1:103 H3C13:127 H2BC4:141 CDC08C:223 TCF71:223

DisGeNET Top pathways by permutation

Geneset	stat	num.genes	pval	p.adj	gene.vals
Steatohepatitis	-0.09003086	512	4.237e-12	4.161e-08	SLC22A8:8 APOC3:29 TM6SF2:68.5 DNASE2:77 TM7SF2:116 NR1H4:130.5
Fatty Liver	-0.08827839	401	1.571e-09	7.713e-06	SLC22A8:8 APOC3:29 TM6SF2:68.5 DNASE2:77 ABCD2:84.5 TM7SF2:116
Obesity	-0.04194108	1799	8.366e-09	2.739e-05	MFAP5:1 KRT11:61 ADAM28:22 APOC3:29 KLF8:136 THEM4:60
Endometriosis	-0.06046979	694	7.350e-08	1.805e-04	IL37:66 NAA18:109 HK1:101 ITGAV:130.5 ARHGAP28:136 SLC06A1:180.5
Cardiovascular Diseases	-0.05636487	724	3.077e-07	6.023e-04	APOC3:29 GGH:50 C1QTNF9:56.5 TM6SF2:68.5 TASZS03:83 CD320:92
Metabolic Syndrome X	-0.06060634	512	3.680e-07	6.023e-04	ADAM28:22 APOC3:29 TM6SF2:68.5 TM7SF2:116 NR1H4:130.5 LEPR:182.5
Hypertensive Diseases	-0.04367011	1212	4.998e-07	7.012e-04	MFAP5:1 GCM1:3 SLC22A8:8 PDGFRB:27 APOC3:29 SDHC:42
Non-alcoholic Fatty Liver Disease	-0.08190552	311	7.473e-07	9.174e-04	APOC3:29 TM6SF2:68.5 ABCD2:84.5 LAMA1:97 NR1H4:130.5 LCP1:155
Drug-Induced Liver Disease	-0.0880332	246	2.138e-06	2.100e-03	SLC22A8:8 GGH:50 ABCD2:84.5 NR1H4:130.5 ECHDC1:159.5 CYP8B1:163.5
Vomiting	-0.10445394	175	1.964e-06	2.100e-03	DBT:201 DLD:242 SLC17A5:277.5 CPOX:330.5 TPOC2:388 PPOX:466.5
Lethargy	-0.13410090	104	2.359e-06	2.106e-03	DBT:201 DLD:242 SLC25A20:355 TNCN:388 DHFR:542.5 NMDAP:1459
Atherosclerosis	-0.04379366	1033	2.653e-06	2.171e-03	PDE1A:26 APOC3:29 EPHA2:60 IL37:66 TM6SF2:68.5 CAMP:104
Hyperlipidemia	-0.09241972	210	4.124e-06	3.116e-03	APOC3:29 NR1H4:130.5 CDCP1:134 LEPR:182.5 AKR1B1:213 OLR1:223.5
Coronary Artery Disease	-0.04513434	898	5.749e-06	4.028e-03	MFAP5:1 APOC3:29 BCAS3:62.5 TM6SF2:68.5 MYO9B:84.5 ELL:95.5
Metabolic Diseases	-0.06684489	392	6.152e-06	4.028e-03	APOC3:29 OCA2:55 IL37:66 TM7SF2:116 NR1H4:130.5 LEPR:182.5
Nonalcoholic Steatohepatitis	-0.05936535	192	7.473e-06	4.587e-03	TM6SF2:68.5 LAMA1:97 NR1H4:130.5 CYP8B1:163.5 LEPR:182.5 OLR1:223.5
Hypercholesterolemia, Familial	-0.10511306	145	9.859e-06	5.379e-03	APOC3:29 OCA2:55 OLR1:223.5 ITGB3:338.5 MTTF:407.5 ABCA1:514
Hypertriglyceridemia	-0.10807565	141	9.715e-06	5.379e-03	APOC3:29 TM6SF2:68.5 NR1H4:130.5 LPN1:256 MTTF:407.5 ABCA1:514</