

Top genes 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
COPZ2	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-03	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	0.2288249	88	9.342e-03	9.681e-02	4.276e-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 Q-Value Permulated

Gene	Rho	N	P	p.adj	permPValue	qValueNoperm	qValuePerm
DNAH2	0.5944088	123	1.161e-15	1.740e-11	1.045e-01	2.607e-07	5.300e-01
SLC47A1	0.5399089	95	1.799e-10	8.991e-07	9.845e-02	3.884e-03	5.213e-01
ANKRD35	0.4890758	113	2.767e-10	1.037e-06	4.573e-03	3.884e-03	4.918e-01
DNAH14	0.4942081	113	1.800e-10	8.991e-07	5.288e-02	3.884e-03	4.918e-01
KIAA0753	0.4530631	120	1.660e-09	3.517e-06	6.079e-02	6.588e-03	4.918e-01
CAPN8	0.5086260	95	1.878e-09	3.517e-06	7.558e-02	6.588e-03	5.031e-01
CRB1	-0.4457119	125	1.408e-09	3.517e-06	1.249e-01	6.588e-03	5.512e-01
PROM1	-0.4408997	127	1.564e-09	3.517e-06	3.656e-02	6.588e-03	4.918e-01
ICAM2	-0.4351785	123	4.540e-09	7.560e-06	3.965e-02	1.259e-02	4.918e-01
CABIN1	-0.4247582	126	6.902e-09	1.034e-05	2.231e-02	1.550e-02	4.918e-01
ITGB4	0.4110191	123	3.065e-08	2.871e-05	4.410e-02	2.209e-02	4.918e-01
MAN2A1	-0.4212335	118	2.747e-08	2.744e-05	8.145e-02	2.209e-02	5.056e-01
FNBP4	-0.4260675	116	2.519e-08	2.744e-05	1.178e-01	2.209e-02	5.447e-01
ABCC3	0.3980704	126	5.658e-08	3.686e-05	5.755e-02	2.209e-02	4.918e-01
PIEZO1	0.4129537	118	5.105e-08	3.477e-05	1.922e-01	2.209e-02	6.399e-01
MTBP	-0.4129659	121	3.433e-08	3.027e-05	1.666e-01	2.209e-02	6.051e-01
PLEC	0.4709115	92	4.446e-08	3.477e-05	1.285e-01	2.209e-02	5.529e-01
PCDH11X	0.4523406	99	4.847e-08	3.477e-05	5.561e-03	2.209e-02	4.918e-01
SLC7A4	-0.4231884	111	6.245e-08	3.801e-05	1.642e-02	2.209e-02	4.918e-01
DNAH17	0.4009639	127	4.002e-08	3.332e-05	4.714e-02	2.209e-02	4.918e-01
PPP1R12B	-0.4345012	114	1.779e-08	2.222e-05	8.311e-01	2.209e-02	1.000e+00
RPAIN	0.4365287	106	4.960e-08	3.477e-05	6.966e-02	2.209e-02	5.003e-01
TMEM131L	-0.3934174	128	6.340e-08	3.801e-05	1.320e-01	2.209e-02	5.570e-01
SPECC1L	-0.4739411	98	1.286e-08	1.752e-05	2.379e-02	2.209e-02	4.918e-01
SPATA6L	0.4288558	114	2.713e-08	2.744e-05	4.095e-02	2.209e-02	4.918e-01

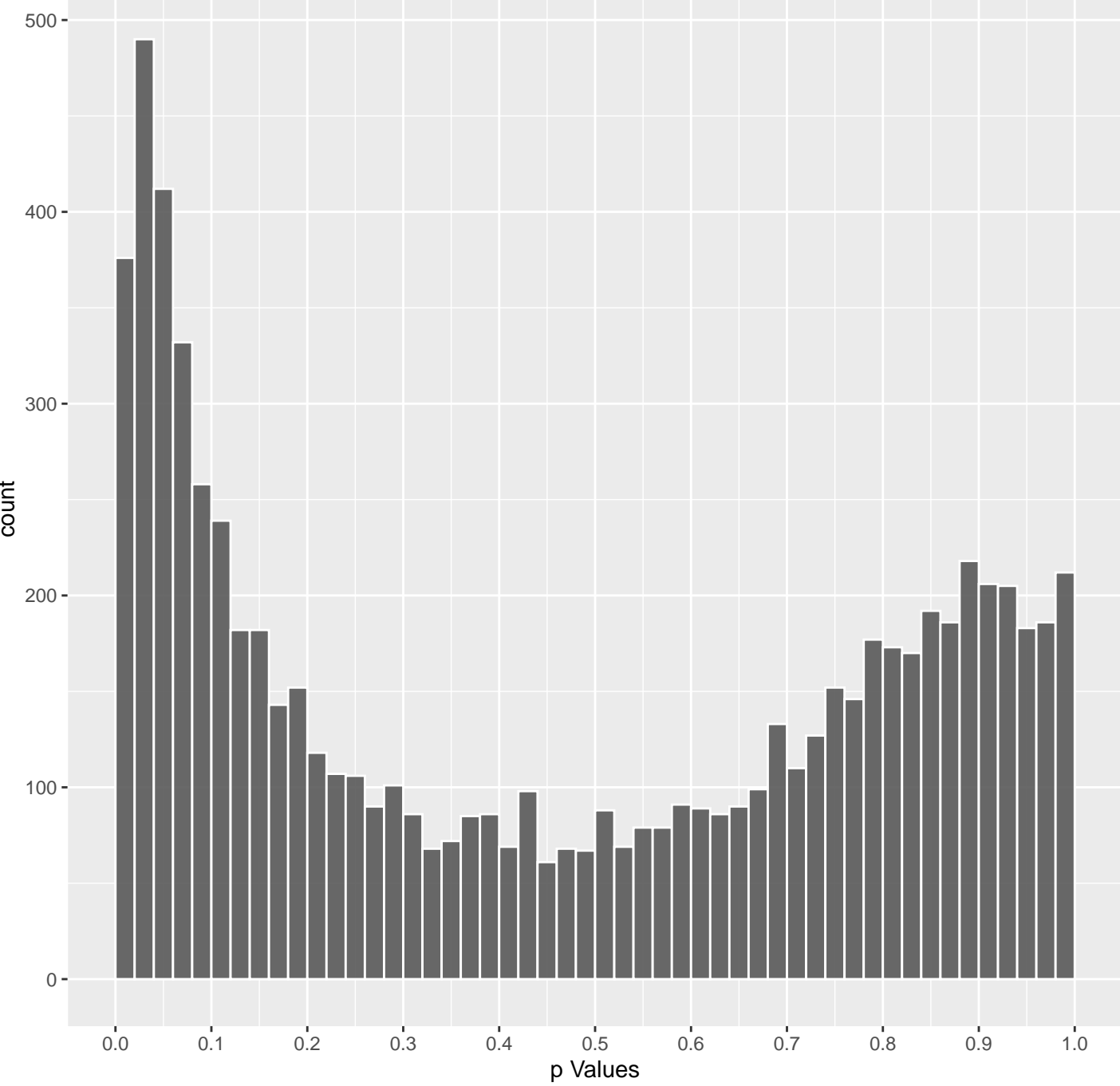
Top genes non-permulated

Gene	Rho	N	P	p.adj	permPValue	qValueNoperm	qValuePerm
DNAH2	0.5944088	123	1.161e-15	1.740e-11	1.045e-01	2.607e-07	5.300e-01
SLC47A1	0.5399089	95	1.799e-10	8.991e-07	9.845e-02	3.884e-03	5.213e-01
DNAH14	0.4942081	113	1.800e-10	8.991e-07	5.288e-02	3.884e-03	4.918e-01
ANKRD35	0.4890758	113	2.767e-10	1.037e-06	4.573e-03	3.884e-03	4.918e-01
KIAA0753	0.4530631	120	1.660e-09	3.517e-06	6.079e-02	6.588e-03	4.918e-01
CAPN8	0.5086260	95	1.878e-09	3.517e-06	7.558e-02	6.588e-03	5.031e-01
CRB1	-0.4457119	125	1.408e-09	3.517e-06	1.249e-01	6.588e-03	5.512e-01
PROM1	-0.4408997	127	1.564e-09	3.517e-06	3.656e-02	6.588e-03	4.918e-01
ICAM2	-0.4351785	123	4.540e-09	7.560e-06	3.965e-02	1.259e-02	4.918e-01
CABIN1	-0.4247582	126	6.902e-09	1.034e-05	2.231e-02	1.550e-02	4.918e-01
SPECC1L	-0.4739411	98	1.286e-08	1.752e-05	2.379e-02	2.209e-02	4.918e-01
PPP1R12B	-0.4345012	114	1.779e-08	2.222e-05	8.311e-01	2.209e-02	1.000e+00
MAN2A1	-0.4212335	118	2.747e-08	2.744e-05	8.145e-02	2.209e-02	5.056e-01
FNBP4	-0.4260675	116	2.519e-08	2.744e-05	1.178e-01	2.209e-02	5.447e-01
SPATA6L	0.4288558	114	2.713e-08	2.744e-05	4.095e-02	2.209e-02	4.918e-01
ITGB4	0.4110191	123	3.065e-08	2.871e-05	4.410e-02	2.209e-02	4.918e-01
MTBP	-0.4129659	121	3.433e-08	3.027e-05	1.666e-01	2.209e-02	6.051e-01
DNAH17	0.4009639	127	4.002e-08	3.332e-05	4.714e-02	2.209e-02	4.918e-01
PIEZO1	0.4129537	118	5.105e-08	3.477e-05	1.922e-01	2.209e-02	6.399e-01
PLEC	0.4709115	92	4.446e-08	3.477e-05	1.285e-01	2.209e-02	5.529e-01
PCDH11X	0.4523406	99	4.847e-08	3.477e-05	5.561e-03	2.209e-02	4.918e-01
RPAIN	0.4365287	106	4.960e-08	3.477e-05	6.966e-02	2.209e-02	5.003e-01
ABCC3	0.3980704	126	5.658e-08	3.686e-05	5.755e-02	2.209e-02	4.918e-01
SLC7A4	-0.4231884	111	6.245e-08	3.801e-05	1.642e-02	2.209e-02	4.918e-01
TMEM131L	-0.3934174	128	6.340e-08	3.801e-05	1.320e-01	2.209e-02	5.570e-01

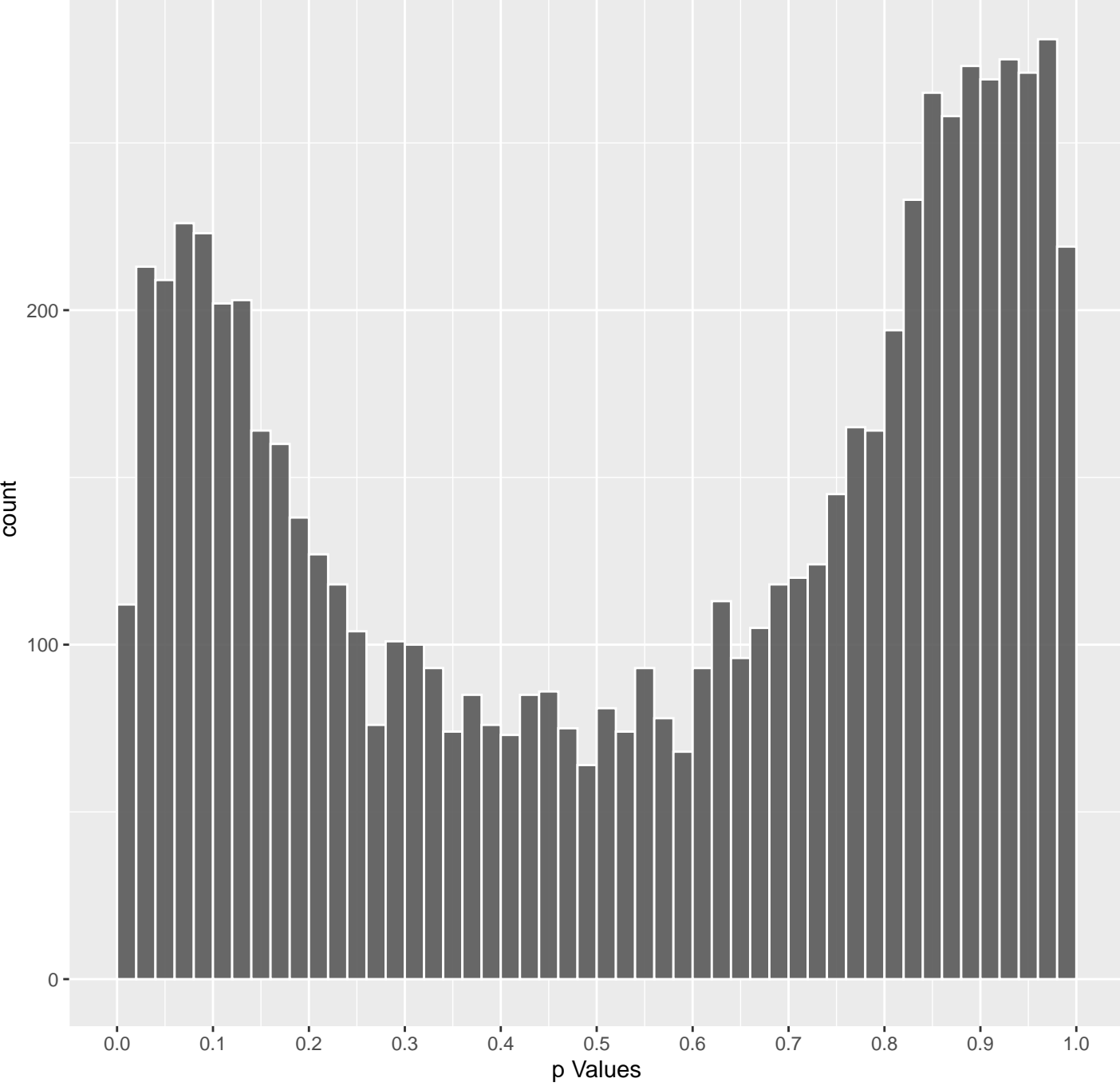
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SLC47A1	0.5399089	95	1.799e-10	8.991e-07	9.845e-02	3.884e-03	5.213e-01
ANKRD35	0.4890758	113	2.767e-10	1.037e-06	4.573e-03	3.884e-03	4.918e-01
DNAH14	0.4942081	113	1.800e-10	8.991e-07	5.288e-02	3.884e-03	4.918e-01
KIAA0753	0.4530631	120	1.660e-09	3.517e-06	6.079e-02	6.588e-03	4.918e-01
CAPN8	0.5086260	95	1.878e-09	3.517e-06	7.558e-02	6.588e-03	5.031e-01
CRB1	-0.4457119	125	1.408e-09	3.517e-06	1.249e-01	6.588e-03	5.512e-01
PROM1	-0.4408997	127	1.564e-09	3.517e-06	3.656e-02	6.588e-03	4.918e-01
ICAM2	-0.4351785	123	4.540e-09	7.560e-06	3.965e-02	1.259e-02	4.918e-01
CABIN1	-0.4247582	126	6.902e-09	1.034e-05	2.231e-02	1.550e-02	4.918e-01
ITGB4	0.4110191	123	3.065e-08	2.871e-05	4.410e-02	2.209e-02	4.918e-01
MAN2A1	-0.4212335	118	2.747e-08	2.744e-05	8.145e-02	2.209e-02	5.056e-01
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MTBP	-0.4129659	121	3.433e-08	3.027e-05	1.666e-01	2.209e-02	6.051e-01
PLEC	0.4709115	92	4.446e-08	3.477e-05	1.285e-01	2.209e-02	5.529e-01
PCDH11X	0.4523406	99	4.847e-08	3.477e-05	5.561e-03	2.209e-02	4.918e-01
SLC7A4	-0.4231884	111	6.245e-08	3.801e-05	1.642e-02	2.209e-02	4.918e-01
DNAH17	0.4009639	127	4.002e-08	3.332e-05	4.714e-02	2.209e-02	4.918e-01
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SPATA6L	0.4288558	114	2.713e-08	2.744e-05	4.095e-02	2.209e-02	4.918e-01

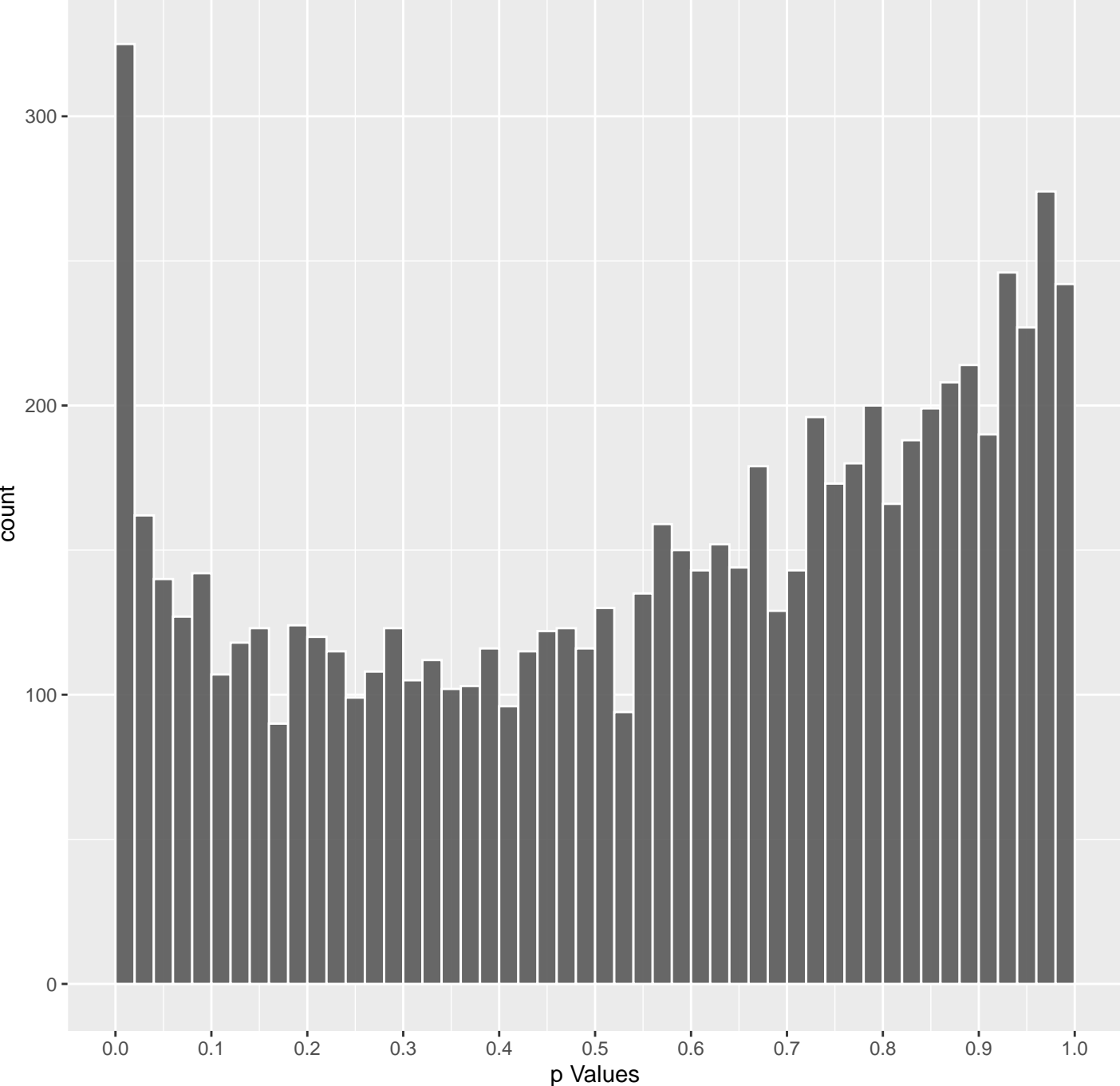
Positive Rho Permulated



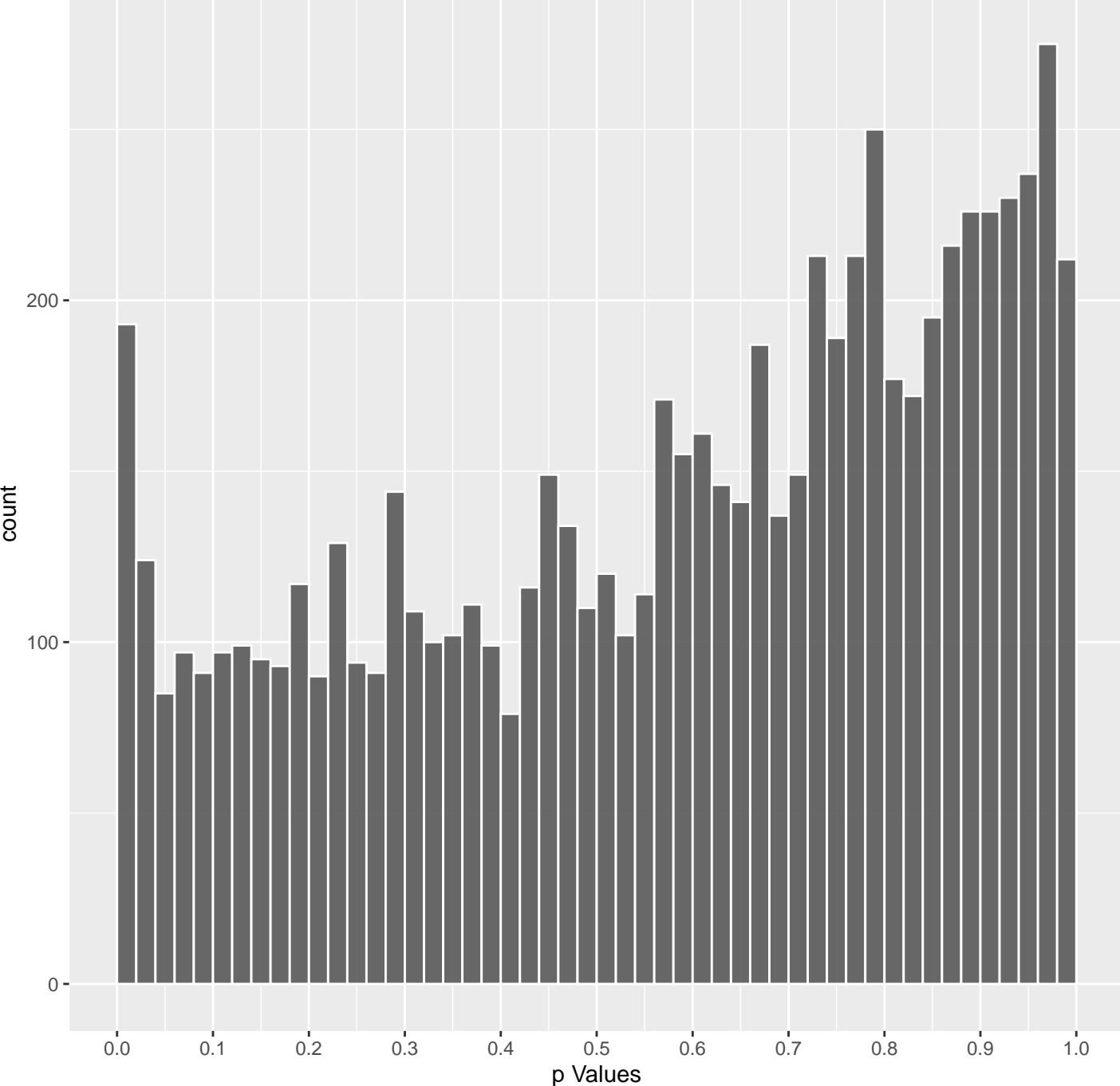
Positive Rho Permulated



Positive Rho Non-permulated



Positive Rho Non-permulated



Top Positive genes Permulated

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AC010255	0.2862415	46	1.999e-02	1.496e-01	2.233e-03	1.000e+00	4.918e-01
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FXYD6	0.2185245	68	2.965e-02	1.860e-01	3.372e-03	1.000e+00	4.918e-01
FNDCl1	0.3917569	98	2.582e-06	5.228e-04	3.602e-03	1.055e-01	4.918e-01
RAB3B	0.3393967	42	8.814e-03	9.382e-02	3.634e-03	9.946e-01	4.918e-01
RAS1 11R	0.7680241	54	1.789e-02	1.400e-01	3.851e-03	1.000e+00	4.918e-01

GSEA-c5-HsSymbols Top pathways by permulation

Geneset	stat	num.genes	pval	p.adj	gene.vals
HP_SPHEROCYTOSIS	-0.4909120	8	1.522e-06	7.105e-04	SLC4A1:27 EPB42:42 RHAG:75 SPTB:85 ANK1:119 SPTA1:135
GOCC_9PLUS0_MOTILE_CILIUM	0.4706930	4	1.112e-03	7.732e-02	DNAH11:19 CFAP45:132 DNAH5:728 ENKUR:916 NA NA
GOMF_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_P	-0.4502446	2	2.742e-02	3.489e-01	CYP11A1:14 CYP2U1:1454 NA NA NA NA
GOBP_BRANCHED_CHAIN_AMINO_ACID_BIOSYNTH	-0.4478230	5	5.242e-04	5.041e-02	BCAT2:101 SDS:167 SDSL:384 ILVBL:561 BCAT1:2663 NA
GOBP_REGULATION_OF_PROTEIN_TYROSINE_PHOS	-0.4360294	3	8.902e-03	2.205e-01	SLC39A10:471 PTPRC:946 MGAT5:1418 NA NA NA
GOBP_ESTABLISHMENT_OF_LEFT_RIGHT_ASYMMET	0.4315091	4	2.799e-03	1.237e-01	CFAP45:132 CFAP52:536 ENKUR:916 CCDC39:2623 NA NA
GOBP_L_CYSTEINE_METABOLIC_PROCESS	-0.4274072	4	3.070e-03	1.313e-01	CSAD:494 CBS:621 AGXT:1531 CDO1:1648 NA NA
GOBP_POSITIVE_REGULATION_OF_CONNECTIVE_T	0.4179378	2	4.063e-02	4.023e-01	ROCK2:1193 ROCK1:1322 NA NA NA NA
GOBP_NEURON_NEURON_SYNAPTIC_TRANSMISSION	0.4071315	4	4.800e-03	1.643e-01	DRD2:170 KIF1B:1181 TMOD2:1280 DLGAP2:3057 NA NA
GOBP_REGULATION_OF_TOLL_LIKE_RECEPTOR_7_	0.4013936	3	1.604e-02	2.782e-01	SLC15A4:1238 PTPN22:1240 RSAD2:2062 NA NA NA
GOBP_LEUKOTRIENE_CATABOLIC_PROCESS	0.3946611	2	5.321e-02	4.493e-01	DPEP2:1230 DPEP1:2003 NA NA NA NA
GOMF_C3HC4_TYPE_RING_FINGER_DOMAIN_BINDI	0.3941574	2	5.351e-02	4.500e-01	KCNH2:878 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	HNFB1B:415 NPHP3:1504 MYOCD:3029 NA NA NA
HP_DECREASED_SERUM_COMPLEMENT_FACTOR_I	-0.3917854	4	6.650e-03	1.925e-01	C1QB:98 C1QA:335 C1QC:489 CFI:5494 NA NA
HP_ABNORMAL_PERIFOLLICULAR_MORPHOLOGY	-0.3876736	3	2.003e-02	3.045e-01	LRP1:91 HLA-DRA:1410 MBTPS2:3498 NA NA NA
GOCC_INNER_DYNEIN_ARM	0.3874496	4	7.278e-03	2.012e-01	DNAH1:1176 DNHD1:1468 DNAH2:1926 DNAH7:2355 NA NA
GOCC_PREFOLDIN_COMPLEX	0.3844835	3	2.108e-02	3.091e-01	VBP1:530 PFDN2:1028 PDRG1:3752 NA NA NA
GOCC_GPL_ANCHOR_TRANSMIDASE_COMPLEX	0.3817825	4	8.179e-03	2.113e-01	GPAA1:64 PIGK:455 PIGT:3026 PIGS:3696 NA NA
GOBP_SRP_DEPENDENT_COTRANSLATIONAL_PROTE	0.3808102	2	6.213e-02	4.722e-01	SRPRB:1701 SRPRA:1964 NA NA NA NA
GOBP_ATTACHMENT_OF_GPL_ANCHOR_TO_PROTEIN	0.3807917	5	3.188e-03	1.331e-01	GPAA1:64 PIGK:455 PGAP1:1898 PIGT:3026 PIGS:3696 NA
GOBP_LEUKOTRIENE_SIGNALING_PATHWAY	0.3769341	5	3.511e-03	1.396e-01	LTB4R:329 CYSLTR2:855 LTB4R2:1490 CYSLTR1:2852 RGS1:3903 NA
HP_FALCIFORM_RETINAL_FOLD	-0.3758978	5	3.602e-03	1.422e-01	ZNF408:671 LRP5:674 NDP:2526 FZD4:2574 TSPAN12:2774 NA
HP_HYPOPLASTIC_DERMOEPIDERMAL_HEMIDESMOS	0.3732250	7	6.270e-04	5.456e-02	LAMC2:427 ITGB4:951 LAMA3:1863 LAMB3:1910 PLEC:2200 ITGA6:2330
GOMF_RIBOSOMAL_PROTEIN_S6_KINASE_ACTIVIT	0.3723733	4	9.897e-03	2.303e-01	RPS6KA1:154 RPS6KA6:157 RPS6KA2:2241 RPS6KA4:5263 NA NA
HP_PERIPHERAL_RETINAL_AVASCULARIZATION	-0.3711074	6	1.643e-03	9.585e-02	ZNF408:671 LRP5:674 DLK1:2272 NDP:2526 FZD4:2574 TSPAN12:2774
GOBP_POSITIVE_REGULATION_OF_GLYCOGEN_STA	-0.3678086	5	4.394e-03	1.588e-01	ADIPOQ:770 EPM2AIP1:1155 IGF2:1206 GSK3A:2713 PPP1R3G:3948 NA
GOBP_NEGATIVE_REGULATION_OF_PROTEIN_CATA	-0.3669162	5	4.490e-03	1.619e-01	LAPTM4B:236 USP8:832 VPS35:1269 MGAT3:2960 ATP13A2:4568 NA
HP_FAILURE_TO_THRIVE_SECONDARY_TO_RECURRE	0.3667770	6	1.862e-03	1.012e-01	CD3E:721 RAG1:781 CD3D:1763 IL7R:2213 CD247:3108 RAG2:3676
GOMF_PHOSPHATIDYLSERINE_FLIPPASE_ACTIVIT	-0.3654336	5	4.654e-03	1.636e-01	ATP11A:138 ATP11C:1005 ATP8B1:1350 ATP8A1:1558 ATP8A2:5920 NA
GOMF_MHC_CLASS_II_RECEPTOR_ACTIVITY	-0.3653929	4	1.137e-02	2.485e-01	HLA-DOB:673 HLA-DRA:1410 HLA-DOA:2845 HLA-DPA1:3070 NA NA
HP_RECURRENENT	-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_	-0.3622382	5	5.027e-03	1.679e-01	TNFRSF13B:258 CD19:565 CR2:2474 ICOS:2676 SASH3:4241 NA
GOMF_MINUS_END_DIRECTED_MICROTUBULE_MOTO	0.3617653	16	5.451e-07	3.521e-04	DNAH11:19 DNAH3:232 CDNAH10:368 DNAH9:435 DYNC2H1:487 DNAH5:728
GOCC_AXONEMAL_DYNEIN_COMPLEX	0.3615223	16	5.548e-07	3.521e-04	DNAI2:36 DNAH3:232 CDC65:326 DNAH9:435 DNAH5:728 DNAH17:1027
GOBP_RNA_MEDIATED_HETEROCHROMATIN_FORMAT	-0.3613890	5	5.131e-03	1.692e-01	SIRT6:866 FAM172A:1620 HELLS:1683 ZNFX1:2720 CENPV:3392 NA
GOBP_PARATHYROID_GLAND_DEVELOPMENT	-0.3581282	6	2.381e-03	1.135e-01	GATA3:1405 TBX1:1600 GCM2:1880 TGFBR1:1921 HOXA3:2606 CRKL:3210
GOBP_NEGATIVE_REGULATION_OF_SYNAPTIC_VES	-0.3522943	3	3.456e-02	3.812e-01	FMR1:1021 BRAF:2130 SYT4:3421 NA NA NA
GOBP_POSITIVE_REGULATION_OF_RNA_EXPORT_F	-0.3517053	2	8.492e-02	5.181e-01	DHX9:2018 NRDE2:2382 NA NA NA NA
GOMF_RNA_POLYMERASE_II_CTD_HEPTAPEPTIDE_	-0.3484598	6	3.116e-03	1.315e-01	CDK7:118 BRD4:181 CDK13:417 CDK12:1032 DYRK1A:4390 CCNK:7328

tissue_specific Top pathways by permulation

Geneset	stat	num.genes	pval	p.adj	gene.vals
bladder	-0.13534444	23	2.480e-02	1.418e-01	UGT1A6:625 SLC14A1:796 UPK1A:1996 ACER2:2283 ID1:3095 DHRS2:3160
ectocervix	-0.12891639	24	2.898e-02	1.423e-01	LRFN5:814 RIPOR3:862 MMRN1:1023 KRT34:1216 TRHDE:1226 PAPPA2:1583
substantia.nigra	-0.10772634	11	2.162e-01	4.704e-01	SLC6A3:680 DBX2:3240 TH:3510 C10orf105:4764 SLC6A11:5281 KCNE5:6143
left.ventricle	0.10636034	64	3.352e-03	2.586e-02	SCN5A:49 ASB15:53 TCAP:145 LMOD3:204 NRAP:231 MYLK3:325
greater.omentum	-0.10408703	31	4.519e-02	1.958e-01	TCF15:19 BTNL9:36 LPL:67 IL6:430 ADIPOQ:770 GFPT2:813
thyroid	-0.09365461	148	9.478e-05	1.279e-03	CLCNKA:51 GPAT3:143 IDO2:165 GGT2:248 VEGFA:446 INPP5J:501
putamen	-0.08925691	14	2.478e-01	4.821e-01	SYNDIG1L:915 ANO3:1003 KCNH4:3261 FAM237A:4721 SLC18A3:4795 GPR88:5681
testis	0.07674690	1352	2.050e-18	1.107e-16	CEP19:2 FNDC11:8 FBXO24:23 OPLAH:32 TPPP2:33 DNAI2:36
eye.development	-0.07339557	56	5.813e-02	2.089e-01	SOX8:277 SP1:558 TYR:626 WNT5A:689 MSX1:1679 NOTCH1:1701
esophagus.muscularis.mucosa	0.07127844	26	2.089e-01	4.704e-01	KCNMB1:703 NTN1:952 CHR3:1023 PRUNE2:1053 SYNM:1155 FAM83D:1376
atrium.auricle	0.06922450	87	2.627e-02	1.418e-01	CHRNE:42 SCN5A:49 ASB15:53 TCAP:145 LMOD3:204 NRAP:231
prostate	0.06812433	37	1.523e-01	3.916e-01	STEAP2:54 ACP3:55 NTF4:159 CHR2A:167 TULP1:270 LMAN1L:359
skeletal.muscle	0.06522793	230	7.561e-04	6.805e-03	SLC8A3:13 NEXN:45 ASB15:53 TCAP:145 LMOD3:204 NRAP:231
liver	-0.06448218	324	8.711e-05	1.279e-03	TM4SF4:16 ANGPTL8:22 TAT:33 SLC38A3:38 ITH2:49 RIDA:65
caudate.nucleus	-0.06417602	26	2.579e-01	4.821e-01	PSD2:35 MLC1:299 SYNDIG1L:915 ANO3:1003 RGS14:2064 SLC01C1:2151
ovary	0.05890821	96	4.713e-02	1.958e-01	RASL11B:10 SGCZ:84 C21orf62:171 SUS4:172 CCDC170:173 ADRB3:200
vagina	0.05828431	90	5.709e-02	2.089e-01	SCEL:211 RNF222:344 KRT13:524 TMPRSS11A:621 MAB21L4:685 LEXM:750
amygdala	0.05736470	7	5.993e-01	7.710e-01	PTPRZ1:836 SLC38A8:997 BCAN:4859 PCDH15:5275 NEUROD6:6827 TNR:12225
EBV.lymphocyte	-0.05642624	646	2.278e-06	6.151e-05	MIS18BP1:29 RHEBL1:60 CENPE:74 BUB1:76 HAUS8:81 WDH1:88
cerebellar.hemisphere	-0.05186306	451	2.268e-04	2.450e-03	SPRN:13 ARVCF:32 ANK1:119 C4A:132 PISD:157 PCDHGC4:160
sigmoid.colon	0.05158618	47	2.222e-01	4.704e-01	PLA2G2C:436 HLX:513 FOXP2:743 BMP3:962 PDE9A:1066 PLEKHO1:1283
breast	0.05113863	14	5.079e-01	7.413e-01	THRSP:386 ABCB5:1190 ALX4:1388 TNN:1402 HCAR1:2065 KRT5:3827
esophagus.mucosa	0.04663158	218	1.895e-02	1.279e-01	PTK6:122 RHOD:187 SCEL:211 EVOL1:221 THSD4:255 RNF222:344
Brodmann.area.9	-0.04338454	158	6.190e-02	2.089e-01	SERPINI1:468 INSM2:486 RXFP1:710 SYT16:717 FREM3:856 LRRMT4:876
minor.salivary.gland	-0.04224839	69	2.265e-01	4.704e-01	BP1FB1:31 PROM1:269 ENPP3:986 TRPV4:1271 OVOL2:1484 GABRP:1666
cortex.kidney	-0.04033182	108	1.498e-01	3.916e-01	CLCNKB:50 BHMT:153 SLC12A1:221 CASR:265 SLC22A6:660 SLC5A10:822
C1.spinal.cord	-0.03378932	170	1.318e-01	3.747e-01	ADARB2:3 PAQR4:128 SEC14L5:278 ZNF488:511 LRAT:524 SCC:557
transformed.skin.fibroblast	-0.03322162	247	7.581e-02	2.408e-01	ADAM9:47 DNAJB4:52 LRP1:91 PTGER2:137 NRP1:173 LOX:222
leg.skin	0.03294470	213	1.012e-01	3.035e-01	ANKRD35:26 PSORS1C2:44 POF1B:140 SCEL:211 EPHB3:261 RNF222:344
nucleus.accumbens	0.02859555	91	3.480e-01	6.018e-01	PCDH11X:38 CACNG4:85 KIRREL3:209 DACH2:383 POU3F4:459 OPRK1:635
subcutaneous.adipose	-0.02759553	70	4.262e-01	6.770e-01	ADGRL4:462 ACACB:611 ADIPOQ:770 GPAM:1197 AGTR1:1225 PRKAR2B:1375
pancreas	-0.02740500	93	3.633e-01	6.018e-01	PNLIPRP1:120 CASR:265 CPA2:300 TMED6:497 GNMT:868 MATN4:1028
suprapubic.skin	0.02600009	186	2.257e-01	4.704e-01	PSORS1C2:44 SCEL:211 LTB4R:329 RNF222:344 RNF39:396 ANXA8L1:529
Brodmann.area.24	-0.02589219	27	6.419e-01	7.710e-01	SHANK1:70 IDS:1200 SLC25A18:1524 SLC17A7:2039 NPTXR:2422 NTRK2:3675
coronary.artery	-0.02556957	15	7.319e-01	8.591e-01	CCL19:329 CN3:2232 GJA5:2975 PCOLCE2:3197 MTHFD1L:4075 COL4A1:4914
peyers.patch	0.02381057	164	2.967e-01	5.341e-01	TRPM5:342 HTR4:528 NLRP6:568 BCO1:713 KRT20:755 MUSK:810
stomach	-0.02194986	85	4.861e-01	7.291e-01	EPN3:82 MFSD4A:380 TMED6:497 PIK3C2G:1294 ATP4B:1371 GPRC5C:1372
aorta	0.02146840	150	3.677e-01	6.018e-01	TNFRSF11B:18 PDGFD:25 PCDH11X:38 PPP1R14A:83 S100A4:113 NOXA:156
blood	-0.02034884	267	2.589e-01	4.821e-01	SLC4A1:27 SLA:41 EPB42:42 SLC6A6:53 RHAG:75 PGLYRP1:83
esophagogastric.junction	0.01893773	8	8.529e-01	9.399e-01	CHRM3:1023 ADCY5:3607 BARX1:4017 HOXA4:7114 F2RL2:7639 GADL1:9154