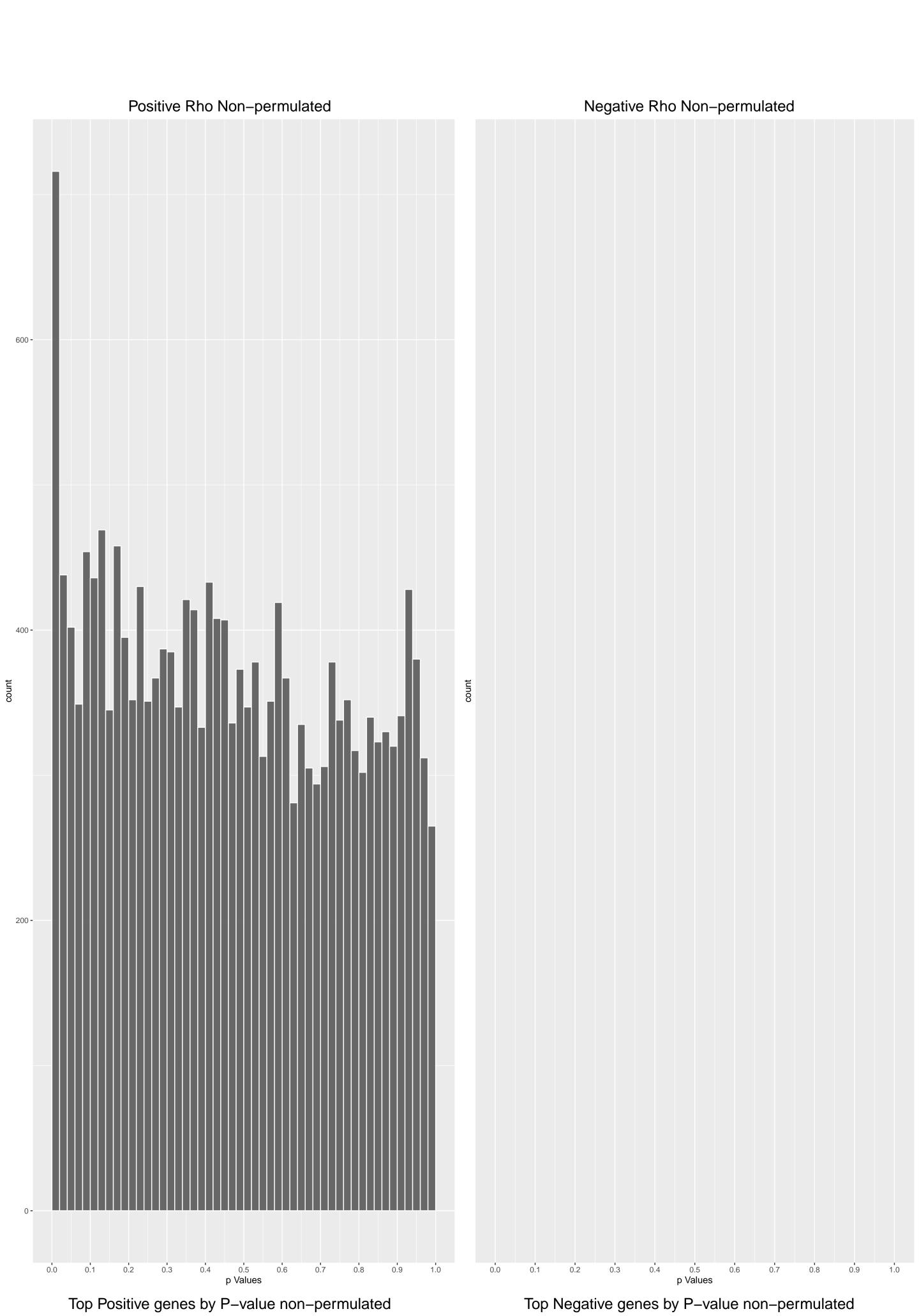
Gene	Rho	N	P	p.adj	qValueNoperm
CAPN8	0.2881746	204	1.230e-12	2.291e-08	3.725e-04
ANKRD35	0.2744398	203	5.540e-12	5.160e-08	4.196e-04
RXFP4	0.2552635	161	7.063e-09	4.386e-05	1.433e-01
DNAH2	0.1866714	213	1.312e-08	6.108e-05	1.433e-01
BNC1	0.2002449	196	1.696e-08	6.318e-05	1.433e-01
ADGRG4	0.2235319	172	2.534e-08	7.446e-05	1.433e-01
USP43	0.1854671	206	2.798e-08	7.446e-05	1.433e-01
PPP4R1	0.1968052	192	3.452e-08	8.038e-05	1.433e-01
AGGF1	0.1996389	188	3.913e-08	8.100e-05	1.433e-01
ITGB4	0.1791397	201	8.143e-08	1.264e-04	1.433e-01
NSD1	0.1748890	206	8.047e-08	1.264e-04	1.433e-01
TMEM131L	0.1692543	213	7.931e-08	1.264e-04	1.433e-01
ZNF292	0.1706157	209	9.607e-08	1.377e-04	1.433e-01
POLM	0.1706697	202	1.708e-07	1.989e-04	1.433e-01
PRUNE2	0.1554104	222	1.675e-07	1.989e-04	1.433e-01
ZZEF1	0.1631185	212	1.617e-07	1.989e-04	1.433e-01
KIAA0753	0.1649811	208	1.841e-07	2.017e-04	1.433e-01
ACAD10	0.1665332	204	2.177e-07	2.027e-04	1.433e-01
CCPG1	0.1751602	194	2.177e-07	2.027e-04	1.433e-01
MR1	0.1883105	179	2.503e-07	2.027e-04	1.433e-01
PLEC	0.1674169	202	2.348e-07	2.027e-04	1.433e-01
SSTR4	0.2520543	134	2.498e-07	2.027e-04	1.433e-01
STYXL2	0.1608269	210	2.391e-07	2.027e-04	1.433e-01
DAXX	0.1791397	184	3.579e-07	2.626e-04	1.482e-01
HERC2	0.1636672	201	3.666e-07	2.626e-04	1.482e-01





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ANKRD35	0.2744398	203	5.540e-12	5.160e-08	4.196e-04
RXFP4	0.2552635	161	7.063e-09	4.386e-05	1.433e-01
DNAH2	0.1866714	213	1.312e-08	6.108e-05	1.433e-01
BNC1	0.2002449	196	1.696e-08	6.318e-05	1.433e-01
ADGRG4	0.2235319	172	2.534e-08	7.446e-05	1.433e-01
USP43	0.1854671	206	2.798e-08	7.446e-05	1.433e-01
PPP4R1	0.1968052	192	3.452e-08	8.038e-05	1.433e-01
AGGF1	0.1996389	188	3.913e-08	8.100e-05	1.433e-01
ITGB4	0.1791397	201	8.143e-08	1.264e-04	1.433e-01

3.725e-04

CAPN8 0.2881746 204 1.230e-12 2.291e-08

NA	NA	NA	NA	NA	NA
NA.1	NA	NA	NA	NA	NA
NA.2	NA	NA	NA	NA	NA
NA.3	NA	NA	NA	NA	NA
NA.4	NA	NA	NA	NA	NA
NA.5	NA	NA	NA	NA	NA
NA.6	NA	NA	NA	NA	NA
NA.7	NA	NA	NA	NA	NA
NA.8	NA	NA	NA	NA	NA
NA.9	NA	NA	NA	NA	NA

Geneset	stat	num.genes	pval	p.adj	gene.vals
HOUNKPE_HOUSEKEEPING_GENES	-0.09130440	1073	1.004e-23	6.519e-20	USB1:9 PTEN:21 PA2G4:48 PPP1R11:51 EDC3:59 SNX27:73
DIAZ_CHRONIC_MYELOGENOUS_LEUKEMIA_UP	-0.04740120	1336	7.896e-09	2.564e-05	MAN2A2:25 PTPN6:38 ASAP2:41 BCL2L1:57 TAF7:64 NQO2:65
KIM_ALL_DISORDERS_OLIGODENDROCYTE_NUMBER	-0.06201641	711	2.000e-08	3.662e-05	RPLP1:2 SLC25A4:20 MAN2A2:25 PPP1R11:51 PSMD7:114 TUBA1A:125
KIM_BIPOLAR_DISORDER_OLIGODENDROCYTE_DEN	-0.06484147	643	2.256e-08	3.662e-05	RPLP1:2 SLC25A4:20 MAN2A2:25 PPP1R11:51 RPL12:69 CDK16:77
REACTOME_METABOLISM_OF_RNA	-0.06372328	654	3.029e-08	3.935e-05	RPLP1:2 A1CF:33 EDC3:59 RPL12:69 PSMC3:89 TRMT9B:94
REACTOME_MRNA_SPLICING	-0.11753720	183	4.271e-08	4.623e-05	RNPS1:284 POLR2D:334 LENG1:355 HNRNPF:374 SF3A1:431 DDX46:467
REACTOME_PROCESSING_OF_CAPPED_INTRON_CON	-0.09528719	254	1.764e-07	1.636e-04	ZC3H11A:171 RNPS1:284 THOC6:310 POLR2D:334 LENG1:355 HNRNPF:374
SPIELMAN_LYMPHOBLAST_EUROPEAN_VS_ASIAN_D	-0.06208345	573	4.108e-07	3.335e-04	PTEN:21 ERGIC3:111 MRPL49:157 DCTN4:170 COX7A2L:173 RPA3:178
REACTOME_INFECTIOUS_DISEASE	-0.05000121	878	5.636e-07	4.067e-04	RPLP1:2 SLC25A4:20 PTPN6:38 BCL2L1:57 TAF7:64 RPL12:69
BLALOCK_ALZHEIMERS_DISEASE_DN	-0.04262467	1189	8.774e-07	5.698e-04	PTEN:21 SYT5:35 PPP1R11:51 CDK16:77 MAP2K4:127 DIO2:160
REACTOME_HIV_INFECTION	-0.09460231	216	1.695e-06	1.001e-03	SLC25A4:20 TAF7:64 PSMC3:89 PSMD3:113 PSMD7:114 GTF2E1:121
KIM_ALL_DISORDERS_CALB1_CORR_UP	-0.06078117	517	2.395e-06	1.296e-03	SLC25A4:20 MAN2A2:25 PSMD7:114 MAP2K4:127 PRKAR2B:164 COX7A2L:173
KARLSSON_TGFB1_TARGETS_UP	-0.12579219	115	3.199e-06	1.598e-03	SRM:108 GEMIN6:122 TCP1:223 EIF5:300 SHMT2:311 GADD45G:332
REACTOME_ADAPTIVE_IMMUNE_SYSTEM	-0.05059337	727	3.704e-06	1.718e-03	RNF25:10 PTEN:21 PTPN6:38 PSMC3:89 DET1:110 PSMD3:113
REACTOME_METABOLISM_OF_AMINO_ACIDS_AND_D	-0.07157779	348	4.657e-06	2.016e-03	RPLP1:2 SLC6A8:19 RPL12:69 PSMC3:89 SRM:108 PSMD3:113
FLORIO_NEOCORTEX_BASAL_RADIAL_GLIA_DN	0.09696056	186	5.200e-06	2.111e-03	KIF18A:64 SPAG5:87 APOD:139 DLGAP5:145 NCAPD2:219 TRIM59:321
REACTOME_DISEASES_OF_SIGNAL_TRANSDUCTION	-0.06509909	414	5.779e-06	2.207e-03	FZD8:7 PTEN:21 FGF18:29 DLL4:46 BCL2L1:57 PSMC3:89
CHAUHAN_RESPONSE_TO_METHOXYESTRADIOL_DN	-0.13359256	93	8.547e-06	2.828e-03	PTPN6:38 HERPUD1:49 RPL12:69 EIF3M:809 NME4:843 MARCKS:994
BILANGES_RAPAMYCIN_SENSITIVE_VIA_TSC1_AN	-0.15676213	67	9.146e-06	2.828e-03	NAA10:79 TCP1:223 PRDX3:283 PAICS:1026 TUBB4A:1047 ACOT1:1383
LOPEZ_MBD_TARGETS	-0.04395523	895	9.061e-06	2.828e-03	NKIRAS2:1 COQ4:18 PA2G4:48 IRX4:63 NQO2:65 CDK16:77
DACOSTA_UV_RESPONSE_VIA_ERCC3_UP	-0.07490212	299	8.650e-06	2.828e-03	SLC6A8:19 SLC25A4:20 LIN37:24 CDK16:77 PSMC3IP:81 PSMC3:89
BRUINS_UVC_RESPONSE_VIA_TP53_GROUP_B	-0.05515801	525	1.614e-05	4.765e-03	TSPAN17:67 PGLYRP1:71 EDEM1:124 HYLS1:133 MSX2:146 WIPI2:250
CASORELLI_ACUTE_PROMYELOCYTIC_LEUKEMIA_D	-0.04989694	643	1.689e-05	4.768e-03	SLC25A4:20 EDC3:59 PSMC3IP:81 PSMC3:89 TUBB2B:119 TJP2:137
DANG_BOUND_BY_MYC	-0.03979154	1010	2.102e-05	5.689e-03	MAN2A2:25 PTPN6:38 PA2G4:48 HERPUD1:49 CDK16:77 MKNK1:78
MOOTHA_PGC	-0.06161821	403	2.277e-05	5.915e-03	SLC25A4:20 RPA3:178 PDHB:183 GUK1:187 CDKN2D:261 TIMM10B:276
REACTOME_ANTIGEN_PROCESSING_UBIQUITINATI	-0.07173766	293	2.462e-05	5.921e-03	RNF25:10 PSMC3:89 DET1:110 PSMD3:113 PSMD7:114 KLHL9:200
WP_MRNA_PROCESSING	-0.11723329	109	2.371e-05	5.921e-03	CELF2:37 RNPS1:284 SF3A1:431 CLASRP:501 SRSF2:616 SRSF7:722
REACTOME_MRNA_SPLICING_MINOR_PATHWAY	-0.19246742	39	3.196e-05	7.353e-03	POLR2D:334 SRSF2:616 SRSF7:722 SNRNP40:867 DDX23:992 RNPC3:1023
HSIAO_HOUSEKEEPING_GENES	-0.06427675	355	3.284e-05	7.353e-03	RPLP1:2 SLC6A8:19 PTPN6:38 RPL12:69 PSMD7:114 CLIC1:251
REACTOME_SIGNALING_BY_WNT	-0.06950681	300	3.553e-05	7.483e-03	FZD8:7 PSMC3:89 AXIN1:97 PSMD3:113 PSMD7:114 AP2A1:188
BENPORATH_MYC_MAX_TARGETS	-0.04489804	736	3.617e-05	7.483e-03	RPLP1:2 PTPN6:38 PA2G4:48 CDK16:77 MKNK1:78 MAP2K7:107
ENK_UV_RESPONSE_KERATINOCYTE_UP	-0.05372796	506	3.687e-05	7.483e-03	SLC6A8:19 INSL4:50 PPP1R11:51 TAF7:64 RPL12:69 CDK16:77
GRAESSMANN_APOPTOSIS_BY_DOXORUBICIN_UP	-0.03702530	1096	3.915e-05	7.704e-03	SLC6A8:19 FGF18:29 AQP1:42 PA2G4:48 PSMC3IP:81 SCIN:95
MARTENS_TRETINOIN_RESPONSE_DN	-0.04469529	731	4.156e-05	7.938e-03	PA2G4:48 TAF7:64 CDK16:77 SRM:108 PSMD7:114 PDHB:183
REACTOME_SIGNALING_BY_NOTCH	-0.08081683	214	4.692e-05	8.705e-03	DLL4:46 PSMC3:89 PSMD3:113 PSMD7:114 ST3GAL4:145 TNRC6B:219
WAKABAYASHI_ADIPOGENESIS_PPARG_RXRA_BOUN	-0.04185924	822	4.917e-05	8.869e-03	RASSF6:36 PTPN6:38 PEX11G:56 EDC3:59 CLN3:211 MKNK2:220
REACTOME_CELLULAR_RESPONSES_TO_STIMULI	-0.04318626	752	5.964e-05	1.047e-02	RPLP1:2 HERPUD1:49 RPL12:69 PSMC3:89 MAP2K7:107 PSMD3:113
GRADE_COLON_AND_RECTAL_CANCER_UP	-0.07000982	274	6.801e-05	1.162e-02	PA2G4:48 NQO2:65 NAA10:79 ZDHHC9:117 GEMIN6:122 MDC1:132

DisGeNET Top pathways by non-permulation

7.312e-05 1.216e-02

FSTL1:54 PSMC3:89 PDCD6IP:190 MCM2:195 KIF23:381 CXCL12:405

7.493e-05 1.216e-02 SEL1L3:209 ANP32A:319 ST6GALNAC4:385 GAPDH:805 KDELR1:1533 HSPA8:1612

2.767e-03 5.117e-01 SCN2A:211 CHRNA4:736 LGI4:1646 KCNQ3:1910 SLC2A1:2871 CSTB:4068 2.485e-03 5.117e-01 TREH:159 AFP:226 ALG1:1476 NPHS1:1607 NPHS2:2089 APLP1:10561

> NA NA

CHRM3:78 MUC2:266 AIRE:395 STK11:412 LAMC2:630 PRKDC:1064

-0.08350840

-0.22017858

PAL_PRMT5_TARGETS_UP

TIEN_INTESTINE_PROBIOTICS_2HR_UP

Familial benign neonatal epilepsy

Finnish congenital nephrotic syndrome

NA.35

MP0005381 digestive/alimentary phenotyp

0.08246217

0.23970903

Geneset	Stat	num.genes	pvai	p.auj	gene.vais
Nephrosis, congenital	0.28936355	14	1.778e-04	3.678e-01	TREH:159 AFP:226 CD2AP:960 CRB2:1311 SIRPA:1364 NPHS1:1607
Acanthosis	0.18562834	33	2.247e-04	3.678e-01	CARD14:107 ALOX12B:478 TGM1:625 KRT13:772 ALOXE3:1086 ENPP1:1596
Epileptic encephalopathy	-0.05064618	447	2.622e-04	3.678e-01	ALG2:4 ALG9:16 COQ4:18 SLC6A8:19 PTEN:21 SRPX2:90
Erythrokeratoderma	0.16551733	41	2.465e-04	3.678e-01	CARD14:107 DSP:407 ALOX12B:478 KRT17:706 ALOXE3:1086 DES:1567
Non-Small Cell Lung Carcinoma	-0.02628227	1886	2.325e-04	3.678e-01	SLC6A8:19 PTEN:21 PTPN6:38 AQP1:42 DLL4:46 LIN28A:47
Palmoplantar Keratosis	0.11505943	95	1.081e-04	3.678e-01	PLEC:20 CARD14:107 DSP:407 ALOX12B:478 PKP1:508 TGM1:625
Primary microcephaly	0.10242299	110	2.101e-04	3.678e-01	KNL1:195 FANCG:244 CDK5RAP2:290 ERCC6:309 TRMT10A:382 FANCM:391
Pruritus	0.09112783	131	3.229e-04	3.964e-01	SSTR4:22 SCN9A:90 COL7A1:91 CARD14:107 GPBAR1:135 TRPV1:209
Absent earlobe	0.29611221	12	3.827e-04	4.176e-01	COL3A1:917 CENPJ:941 RBBP8:1429 ESCO2:1637 ATRIP:1745 CEP152:1805
Epilepsy	-0.03171990	1108	4.460e-04	4.379e-01	ALG2:4 ALG9:16 SLC6A8:19 PTEN:21 AQP1:42 NAA10:79
Angina, Unstable	-0.12626774	62	5.894e-04	5.117e-01	BDNF:470 TNFRSF11A:510 ITGA2B:517 GP1BA:529 F2:562 FSD1L:587
DEAFNESS, AUTOSOMAL RECESSIVE (disorder)	0.15485892	35	1.526e-03	5.117e-01	OTOF:487 PTPRQ:526 RIPOR2:681 CDH23:878 BDP1:1379 TFF1:1827
Hyalinosis, Segmental Glomerular	0.16869416	26	2.912e-03	5.117e-01	HAVCR1:110 MYH10:369 CD2AP:960 TGFB1:1272 CRB2:1311 NPHS1:1607
Hyperkeratosis, Epidermolytic	0.22927282	16	1.498e-03	5.117e-01	COL7A1:91 KRT80:276 DSP:407 ALOX12B:478 TGM1:625 ALOXE3:1086
Mammary Carcinoma, Animal	-0.07417974	128	3.804e-03	5.117e-01	AQP1:42 TUBB2B:119 PSME1:324 KITLG:384 SLC25A10:397 CASK:488
Mammary Neoplasms, Experimental	-0.07377260	148	1.984e-03	5.117e-01	AQP1:42 MAP2K7:107 TUBB2B:119 PSME1:324 KITLG:384 SLC25A10:397
Other specified forms of pleural effusio	0.22778053	15	2.256e-03	5.117e-01	PTAFR:165 BDKRB1:529 PLA2G6:1083 TNF:2479 ELANE:3043 BDKRB2:3147
Abnormality of the hypothalamus-pituitar	0.25050544	14	1.174e-03	5.117e-01	PRTN3:423 RNF216:435 PTPN22:514 HESX1:548 LHX4:582 PROP1:1051
Adult Rickets	0.18842560	20	3.535e-03	5.117e-01	LRP2:112 DMP1:786 TGFB1:1272 ENPP1:1596 TNFSF11:2704 FGF23:2718
alpha 1-Antitrypsin Deficiency	0.15163550	35	1.912e-03	5.117e-01	ATF6:187 PRTN3:423 CRP:549 BPI:809 A2M:1031 TGFB1:1272
Anaplastic carcinoma	-0.06230899	190	3.126e-03	5.117e-01	PTEN:21 AQP1:42 BCL2L1:57 TUBB2B:119 LY96:130 PSME1:324
Animal Mammary Neoplasms	-0.07417974	128	3.804e-03	5.117e-01	AQP1:42 TUBB2B:119 PSME1:324 KITLG:384 SLC25A10:397 CASK:488
Arthralgia	0.08198940	120	1.949e-03	5.117e-01	CALCA:324 CYP17A1:332 PRTN3:423 PTPN22:514 CRP:549 PTH1R:579
Arthropathy	0.08202515	117	2.209e-03	5.117e-01	LRPPRC:48 CPB1:259 CHI3L1:448 CRP:549 GHR:693 NOD2:821
Autosomal Recessive Primary Microcephaly	0.17833440	25	2.029e-03	5.117e-01	KNL1:195 CDK5RAP2:290 SASS6:913 STIL:926 CENPJ:941 CEP135:1592
Carcinoma	-0.06818457	191	1.187e-03	5.117e-01	PTEN:21 AQP1:42 BCL2L1:57 TUBB2B:119 LY96:130 PSME1:324
Cellulitis of periorbital region	0.21026633	17	2.688e-03	5.117e-01	PIEZO1:320 PRTN3:423 PTPN22:514 BAZ1B:1184 GTF2I:1540 SUMF1:1559
Cerebral Infarction	-0.05644323	255	1.975e-03	5.117e-01	MAP2K7:107 TLX2:212 JUND:392 EPHX2:393 CXCL12:405 BDNF:470
Cholestasis in newborn	0.09453796	87	2.326e-03	5.117e-01	GPBAR1:135 ABCB11:339 PKHD1:799 MPI:971 PEX1:1141 ABCB4:1168
Chondroma	-0.28503820	10	1.801e-03	5.117e-01	BCL2L1:57 IDH1:813 RUNX2:1331 CD6:2076 IDH2:2673 SOX4:5187
Clubbed Fingers	0.21130552	21	8.030e-04	5.117e-01	DSP:407 STK11:412 PTH1R:579 SLCO2A1:1039 RTEL1:1388 SFTPA1:2733
Communication delay	0.37536949	5	3.649e-03	5.117e-01	NSD1:11 SRCAP:1002 GNE:1989 RAI1:3791 FLCN:4925 NA
Congenital ichthyosis	0.13364234	47	1.533e-03	5.117e-01	ALOX12B:478 TGM1:625 CYP4F22:758 ALOXE3:1086 DMD:1273 TGM5:1320
Craniofacial Abnormalities	-0.06678024	177	2.226e-03	5.117e-01	PTEN:21 MSX2:146 MED13L:169 B3GAT3:180 RAX:233 FOXC2:383
Deficit in expressive language	0.30215825	9	1.695e-03	5.117e-01	NSD1:11 BPTF:475 SRCAP:1002 GNE:1989 UBE3A:3097 RAI1:3791
Disease of capillaries	-0.15886255	28	3.626e-03	5.117e-01	WDTC1:181 PLG:672 AGT:703 SMPD1:766 SLC9C1:1375 PEMT:1849
Exaggerated acoustic startle response	-0.27161856	10	2.937e-03	5.117e-01	ARHGEF9:835 GPHN:842 ASNS:1233 HEXA:1997 KLC2:2696 SLC6A9:3520
Exaggerated startle response	-0.25292150	11	3.677e-03	5.117e-01	ARHGEF9:835 GPHN:842 ASNS:1233 HEXA:1997 KLC2:2696 SLC6A9:3520
Familial having gasestel aniles	0.00070000	40	0.707- 00	E 447- 04	CCNIQA 244 CUIDNIA 2700 I CIA 4040 I/ONIQQ 4040 CU CQA 42074 CCTD 4000

customGeneSet Top pathways by non-permulation

Geneset	stat	num.genes	pval	p.adj	gene.vals
NAFLDGWAS	0.12060606	15	1.544e-01	4.632e-01	INSR:2306 PNPLA3:3707 ADH1B:4161 MTARC1:4655 GPAM:7099 FTO:7303
HumanLocalAdaptionDietAll	-0.06275304	13	4.825e-01	5.252e-01	SEPSECS:814 CREBRF:1304 CELF1:2701 AS3MT:4174 GPX3:5444 SLC22A4:5680
expressionDirectionalSelection	-0.04506803	42	5.252e-01	5.252e-01	AXIN1:97 FADS1:669 COMMD6:784 ITGAM:1062 LGALS2:1284 MAPT:1771
NA	NA	NA	NA	NA	NA NA NA NA NA
NA.1	NA	NA	NA	NA	NA NA NA NA NA
NA.2	NA	NA	NA	NA	NA NA NA NA NA
NA.3	NA	NA	NA	NA	NA NA NA NA NA
NA.4	NA	NA	NA	NA	NA NA NA NA NA
NA.5	NA	NA	NA	NA	NA NA NA NA NA
NA.6	NA	NA	NA	NA	NA NA NA NA NA
NA.7	NA	NA	NA	NA	NA NA NA NA NA
NA.8	NA	NA	NA	NA	NA NA NA NA NA
NA.9	NA	NA	NA	NA	NA NA NA NA NA
NA.10	NA	NA	NA	NA	NA NA NA NA NA
NA.11	NA	NA	NA	NA	NA NA NA NA NA
NA.12	NA	NA	NA	NA	NA NA NA NA NA
NA.13	NA	NA	NA	NA	NA NA NA NA NA
NA.14	NA	NA	NA	NA	NA NA NA NA NA
NA.15	NA	NA	NA	NA	NA NA NA NA NA
NA.16	NA	NA	NA	NA	NA NA NA NA NA
NA.17	NA	NA	NA	NA	NA NA NA NA NA
NA.18	NA	NA	NA	NA	NA NA NA NA NA
NA.19	NA	NA	NA	NA	NA NA NA NA NA
NA.20	NA	NA	NA	NA	NA NA NA NA NA
NA.21	NA	NA	NA	NA	NA NA NA NA NA
NA.22	NA	NA	NA	NA	NA NA NA NA NA
NA.23	NA	NA	NA	NA	NA NA NA NA NA
NA.24	NA	NA	NA	NA	NA NA NA NA NA
NA.25	NA	NA	NA	NA	NA NA NA NA NA
NA.26	NA	NA	NA	NA	NA NA NA NA NA
NA.27	NA	NA	NA	NA	NA NA NA NA NA
NA.28	NA	NA	NA	NA	NA NA NA NA NA
NA.29	NA	NA	NA	NA	NA NA NA NA NA
NA.30	NA	NA	NA	NA	NA NA NA NA NA
NA.31	NA	NA	NA	NA	NA NA NA NA NA
NA.32	NA	NA	NA	NA	NA NA NA NA NA
NA.33	NA	NA	NA	NA	NA NA NA NA NA
NA.34	NA	NA	NA	NA	NA NA NA NA NA

GO_Biological_Process_2023 Top pathways by non-permulation

Geneset	stat	num.genes	pval	p.adj	gene.vals
RNA Splicing, Via Transesterification Re	-0.12919957	157	2.460e-08	1.330e-04	GEMIN6:122 RNPS1:284 HNRNPF:374 SF3A1:431 DDX46:467 WDR83:574
mRNA Processing (GO:0006397)	-0.11249508	191	8.868e-08	2.397e-04	GEMIN6:122 RNPS1:284 KIN:288 HNRNPF:374 SF3A1:431 DDX46:467
mRNA Splicing, Via Spliceosome (GO:00003	-0.10856229	187	3.257e-07	5.870e-04	GEMIN6:122 RNPS1:284 HNRNPF:374 SF3A1:431 DDX46:467 WDR83:574
Intermediate Filament Organization (GO:0	0.17377106	65	1.288e-06	1.740e-03	KRT80:276 KRT20:316 DSP:407 BFSP2:489 PKP1:508 KRT28:558
RNA Splicing (GO:0008380)	-0.12620821	89	3.936e-05	4.257e-02	USB1:9 RNPS1:284 WDR83:574 SRSF2:616 SRSF7:722 U2AF1:758.5
Calcium Ion Import Across Plasma Membran	0.19903961	34	5.936e-05	5.349e-02	SCN9A:90 CLU:148 TRPV1:209 SCN2A:211 SLC8A3:295 CACNA1B:384
Positive Regulation Of Telomere Maintena	-0.20109921	31	1.070e-04	8.263e-02	MAP2K7:107 TCP1:223 AURKB:821 HMBOX1:900 TNKS2:1128 ATM:1281
Cellular Response To Starvation (GO:0009	-0.09929833	120	1.756e-04	1.055e-01	PICK1:15 NUPR2:165 WIPI2:250 MAP1LC3B:420 PRKD1:424 TTC5:447
Ubiquitin-Dependent Protein Catabolic Pr	-0.05887771	349	1.684e-04	1.055e-01	RNF25:10 HERPUD1:49 PPP1R11:51 PSMC3:89 AXIN1:97 PSMD3:113
RNA Processing (GO:0006396)	-0.08294775	170	1.965e-04	1.063e-01	USB1:9 CELF2:37 LIN28A:47 RNPS1:284 KIN:288 HNRNPF:374
Protein Localization To Centrosome (GO:0	0.25798753	17	2.310e-04	1.136e-01	KIAA0753:17 SPAG5:87 CEP250:116 MBD1:204 CEP192:207 C2CD3:368
Establishment Of Mitotic Spindle Localiz	0.17989527	33	3.495e-04	1.575e-01	CDK5RAP2:290 NUMA1:551 NDC80:657 PKHD1:799 ITGB1:895 HTT:974
Centromere Complex Assembly (GO:0034508)	0.27255774	14	4.142e-04	1.600e-01	CENPT:129 DLGAP5:145 CENPC:480 HJURP:698 NASP:1263 CENPF:1316
Monoatomic Cation Transport (GO:0006812)	0.15826985	42	3.887e-04	1.600e-01	TRPM6:56 LRP2:112 CALHM1:132 PKD1L3:251 CNGB3:262 CLDN16:289
Inorganic Cation Transmembrane Transport	0.06067629	280	4.985e-04	1.797e-01	SLC6A6:47 TRPM6:56 SCN9A:90 CLU:148 KCNN3:167 KCNA10:186
Mitochondrial RNA Metabolic Process (GO:	0.22271096	20	5.655e-04	1.911e-01	POLRMT:224 TFAM:271 TEFM:352 TFB2M:430 FASTKD1:443 TWNK:452
Mitochondrial RNA Processing (GO:0000963	0.32799965	9	6.557e-04	1.970e-01	TRMT10C:415 FASTKD1:443 FASTKD5:709 FASTKD2:771 SUPV3L1:2491 FASTKD3:2767
Mitochondrion Disassembly (GO:0061726)	-0.16960460	34	6.227e-04	1.970e-01	WIPI2:250 FIS1:398 MAP1LC3B:420 ATG2B:558 ATG3:613 CISD2:1031
Kinetochore Assembly (GO:0051382)	0.32329135	9	7.836e-04	2.118e-01	CENPT:129 DLGAP5:145 CENPC:480 CENPF:1316 NPC1:1727 MIS12:3033
Protein Localization To Microtubule Orga	0.25111302	15	7.596e-04	2.118e-01	KIAA0753:17 SPAG5:87 CEP250:116 MBD1:204 CEP192:207 C2CD3:368
Attachment Of Mitotic Spindle Microtubul	0.27749092	12	8.737e-04	2.147e-01	CENPC:480 NDC80:657 KIF2C:863 CDT1:2906 MIS12:3033 CENPE:3178
Folic Acid Metabolic Process (GO:0046655	-0.27234533	12	1.088e-03	2.147e-01	SHMT2:311 SLC19A1:567 DHFR2:583 MTHFD2:1329 SLC46A1:2001 SHMT1:3448
Kinetochore Organization (GO:0051383)	0.29776997	10	1.112e-03	2.147e-01	CENPT:129 DLGAP5:145 CENPC:480 CENPF:1316 NPC1:1727 MIS12:3033
Macroautophagy (GO:0016236)	-0.09603176	99	9.735e-04	2.147e-01	TBC1D5:80 VPS37B:155 CLN3:211 WIPI2:250 CHMP2A:280 MAP1LC3B:420
Monoatomic Cation Transmembrane Transpor	0.05761394	277	1.007e-03	2.147e-01	SLC6A6:47 TRPM6:56 SCN9A:90 CLU:148 KCNN3:167 KCNA10:186
Positive Regulation Of Telomere Capping	-0.24429859	15	1.054e-03	2.147e-01	MAP2K7:107 TNKS2:1128 NEK7:1291 MAPK1:1702 MAPK15:2112 MAP3K4:2309
Regulation Of Mitochondrial mRNA Stabili	0.39053763	6	9.230e-04	2.147e-01	FASTKD1:443 FASTKD5:709 FASTKD2:771 PDE12:2114 FASTKD3:2767 TBRG4:5555
Resolution Of Meiotic Recombination Inte	0.25690616	14	8.744e-04	2.147e-01	HFM1:234 SHOC1:313 FANCM:391 RMI1:828 EME1:1019 EME2:1417
Autophagosome Maturation (GO:0097352)	-0.14253202	42	1.399e-03	2.161e-01	CLN3:211 WIPI2:250 CHMP2A:280 MAP1LC3B:420 UBQLN1:605 CHMP1A:1134
Autophagy Of Mitochondrion (GO:0000422)	-0.13936954	44	1.387e-03	2.161e-01	WIPI2:250 FIS1:398 MAP1LC3B:420 ATG2B:558 ATG3:613 CISD2:1031
Positive Regulation Of DNA Biosynthetic	-0.11752693	63	1.264e-03	2.161e-01	MAP2K7:107 TCP1:223 SMOC2:777 AURKB:821 HMBOX1:900 KLF4:1018
Positive Regulation Of DNA-templated Tra	-0.02794451	1204	1.324e-03	2.161e-01	TAF7:64 HAS3:75 DYRK1B:87 PSMC3:89 AXIN1:97 MAP2K7:107
Positive Regulation Of Telomerase Activi	-0.16352386	32	1.371e-03	2.161e-01	MAP2K7:107 TCP1:223 AURKB:821 HMBOX1:900 KLF4:1018 HSP90AB1:1056
Positive Regulation Of Telomere Maintena	-0.16159984	33	1.319e-03	2.161e-01	MAP2K7:107 TCP1:223 AURKB:821 HMBOX1:900 TNKS2:1128 ATM:1281
Purine–Containing Compound Metabolic Pro	-0.35173540	7	1.270e-03	2.161e-01	GUK1:187 FHIT:1969 MACROD2:2089 TTR:2280 MACROD1:2990 PRPS1:3130
Sister Chromatid Segregation (GO:0000819	0.15766624	34	1.469e-03	2.207e-01	KIF18A:64 SPAG5:87 SMC4:565 NDC80:657 NUSAP1:983 SGO1:1603
Endonucleolytic Cleavage Of Tricistronic	0.26179719	12	1.689e-03	2.440e-01	NOL9:390 SDE2:1201 UTP20:1304 TSR1:1976 NOP14:1996 KRI1:4013
Vesicle Budding From Membrane (GO:000690	-0.16827027	29	1.715e-03	2.440e-01	TRAPPC13:304 TRAPPC3:504 GOLPH3L:1055 TMED10:1136 TRAPPC5:2164 CHMP4A:2215
Regulation Of Telomere Capping (GO:19043	-0.19705948	21	1.773e-03	2.459e-01	MAP2K7:107 USP7:543 AURKB:821 TNKS2:1128 NEK7:1291 MAPK1:1702
Homophilic Cell Adhesion Via Plasma Memb	0.11623849	60	1.857e-03	2.510e-01	HMCN1:247 CADM3:404 ROBO1:633 TENM3:822 ITGB1:895 PECAM1:1085

3.018e-03 4.562e-01

MGI_Mammalian_Phenotype_Level_4 Top pathways by non-permulation

MP0005085 abnormal gallbladder physiolo	0.15509737	30	3.340e-03	4.562e-01	CHRM3:78 GPBAR1:135 APOC1:297 ABCB11:339 CHRM2:1050 ABCB4:11
MP0003045 fibrosis	0.17187107	23	4.383e-03	4.562e-01	ENTPD1:403 PKHD1:799 DMD:1273 ARID4A:3044 IL13:3102 NF1:3493
MP0000579 abnormal nail morphology	0.18646064	21	3.136e-03	4.562e-01	ITGB4:12 COL7A1:91 KRT17:706 FGFR2:2332 KRT6B:2371 ATP2A2:2816
MP0001177 atelectasis	0.10841990	57	4.792e-03	4.562e-01	LRP2:112 SFTPB:258 TRPS1:683 CYLD:969 PROP1:1051 TSHZ3:1451
MP0002269 muscular atrophy	0.07750097	86	1.351e-02	5.187e-01	PLEC:20 SLC6A6:47 LTN1:140 CASQ1:420 CTH:462 PARL:654
MP0008775 abnormal heart ventricle	0.12606576	37	8.114e-03	5.187e-01	TRPV1:209 HIF3A:873 SLC2A4:909 TTN:1551 WRN:2686 MUS81:2728
MP0006036 abnormal mitochondrial physio	-0.07937273	86	1.141e-02	5.187e-01	SLC25A4:20 PDSS2:106 JUND:392 APAF1:449 TARDBP:785 SURF1:806
MP0003252 abnormal bile duct	0.13972533	25	1.576e-02	5.187e-01	ABCB11:339 PKHD1:799 ATXN2:1001 ABCB4:1168 CHUK:1473 CYP8B1:19
MP0010771 integument phenotype	0.05392290	187	1.205e-02	5.187e-01	ITGB4:12 PLEC:20 PTPRZ1:62 COL7A1:91 TRPV1:209 ERCC6:309
MP0003121 genomic imprinting	0.13854379	28	1.131e-02	5.187e-01	SMCHD1:249 MAGEL2:338 PLAGL1:545 PEG3:1106 GPC3:1760 PEG10:18
MP0001663 abnormal digestive system	0.07631957	87	1.443e-02	5.187e-01	CHRM3:78 MUC2:266 AIRE:395 STK11:412 PRKDC:1064 CLDN15:1068
MP0001666 abnormal nutrient absorption	0.10810416	46	1.144e-02	5.187e-01	TREH:159 MUC2:266 NPC1L1:346 TRPV6:734 ITGB1:895 SLC2A4:909
MP0003699 abnormal female reproductive	0.03495197	426	1.634e-02	5.187e-01	HERC2:26 PER2:31 SLC6A6:47 ZP1:103 DLGAP5:145 KCNN3:167
MP0002060 abnormal skin morphology	0.08067726	77	1.489e-02	5.187e-01	ITGB4:12 PLEC:20 COL7A1:91 LRIG1:364 NFKBIZ:422 LAMC2:630
MP0003635 abnormal synaptic transmissio	-0.03457377	426	1.754e-02	5.219e-01	PICK1:15 SYT5:35 RORA:193 SYN1:208 SPRED1:216 SLC32A1:340
MP0001845 abnormal inflammatory respons	0.03070882	508	2.230e-02	5.650e-01	MAN2A1:146 PTAFR:165 MET:191 TRPV1:209 CRLF2:217 ITGB7:231
MP0003122 maternal imprinting	0.16454312	16	2.282e-02	5.650e-01	MAGEL2:338 PLAGL1:545 PEG3:1106 IGF2:1598 GPC3:1760 PEG10:189
MP0001216 abnormal epidermal layer	0.04562996	215	2.307e-02	5.650e-01	ITGB4:12 PLEC:20 EVPL:35 COL7A1:91 LRIG1:364 POU2F3:381
1P0003705 abnormal hypodermis morpholog	0.18709813	12	2.493e-02	5.650e-01	DSE:1139 PPARD:1359 HR:3328 CBS:3455 BRCA1:4143 EFEMP2:5400
MP0005395 other phenotype	0.06822357	92	2.459e-02		ENTPD1:403 KL:666 NLRP5:710 PKHD1:799 MACF1:1214 DMD:1273
MP0004811 abnormal neuron physiology	-0.03869635	284	2.778e-02	5.750e-01	PTEN:21 BCL2L1:57 ST8SIA2:86 TUBA1A:125 OLIG3:205 SYN1:208
MP0005551 abnormal eye electrophysiolog	0.05382297	144	2.724e-02	5.750e-01	GJA10:150 PROM1:180 CNGB3:262 EGFLAM:341 CDHR1:524 LAMA1:67
MP0000490 abnormal crypts of	-0.07573589	70	2.919e-02	5.788e-01	MCM2:195 IGF2BP1:407 HTR2A:469 EPHB2:514 SLC19A1:567 NEUROG3:
MP0000462 abnormal digestive system	0.11101465	30	3.569e-02	6.589e-01	LAMC2:630 CLDN15:1068 TNS3:1267 DMD:1273 GLI1:1725 FGFR2:2332
MP0002080 prenatal lethality	-0.01888575	1338	3.706e-02	6.589e-01	PTEN:21 CPT1B:27 A1CF:33 SYT5:35 AQP1:42 DLL4:46
MP0005023 abnormal wound healing	0.07033186	74	3.737e-02	6.589e-01	BNC1:5 PLEC:20 MET:191 VIL1:520 EPPK1:793 SLPI:1182
MP0000049 abnormal middle ear	-0.07166540	68	4.191e-02	7.124e-01	PRRX1:305 FGFR3:326 FOXC2:383 PITX1:445 PBX1:770 TCOF1:873
MP0005501 abnormal skin physiology	0.06857056	73	4.380e-02	7.190e-01	ITGB4:12 PLEC:20 ERCC6:309 ALOX12B:478 TGM1:625 KL:666
MP0008438 abnormal cutaneous collagen	0.13066378	15	8.003e-02	7.479e-01	COL3A1:917 DSE:1139 DCN:1633 TNXB:1638 LOX:3576 THBS2:5419
MP0005369 muscle phenotype	0.03457633	213	8.651e-02	7.479e-01	PLEC:20 LTN1:140 ENTPD1:403 CASQ1:420 KCNH2:437 FBN2:450
MP0002066 abnormal motor capabilities/c	-0.01744392	1087	7.398e-02	7.479e-01	PTEN:21 AQP1:42 BCL2L1:57 B4GALT2:70 ST8SIA2:86 AXIN1:97
MP0002419 abnormal innate immunity	0.02550843	361	1.045e-01	7.479e-01	PLEC:20 SSTR4:22 MYO9B:36 PIK3R5:80 BIRC3:279 ENTPD1:403
MP0005384 cellular phenotype	0.02553924	431	7.775e-02	7.479e-01	PLEC:20 ATF6:187 SMCHD1:249 NFATC3:252 MUC2:266 TFAM:271
MP0008995 early reproductive senescence	0.12453771	16	8.489e-02	7.479e-01	PER2:31 CYP17A1:332 MAGEL2:338 NXF2:637 TAF4B:1937 AMHR2:262
MP0005388 respiratory system phenotype	0.04353118	130	8.933e-02	7.479e-01	SSTR4:22 CHRM3:78 LRP2:112 SFTPB:258 TRPS1:683 CYLD:969
MP0000428 abnormal craniofacial morphol	-0.06121685	79	6.131e-02	7.479e-01	AXIN1:97 IDUA:100 CDON:203 FGFR3:326 APAF1:449 RDH10:572
MP0002168 other aberrant phenotype	0.06276097	55	1.087e-01	7.479e-01	ENTPD1:403 KL:666 PKHD1:799 MACF1:1214 DMD:1273 ENPP1:1596
MP0000647 abnormal sebaceous gland	0.07071373	49	8.782e-02	7.479e-01	PER2:31 ITGB1:895 UACA:1977 FGFR2:2332 KRT71:2373 SUPV3L1:249
MP0005367 renal/urinary system phenotyp	-0.11787954	19	7.561e-02	7.479e-01	PTEN:21 UPK3A:824 UPK2:1687 CDKN1A:2195 RARA:3308 DACT1:3890

Geneset	stat	num.genes	pval	p.adj	gene.vals
testis	0.037490161	1655	2.454e-06	1.325e-04	DNAH2:4 BNC1:5 PSAPL1:24 SPEM2:27 FAM83F:44 OXCT2:60
C1.spinal.cord	-0.054033645	194	1.001e-02	1.465e-01	PRRG1:3 TUBB2B:119 TUBA1A:125 TP53INP2:152 COLGALT2:213 OLIG2:610
EBV.lymphocyte	0.027287270	752	1.356e-02	1.465e-01	TMEM131L:10 NCAPD3:50 KIF18A:64 ZNF267:98 ZFAT:115 DLGAP5:145
fallopian.tube	0.102008632	60	6.394e-03	1.465e-01	ADGRG4:6 LONRF2:136 SCGB2A1:649 CROCC2:661 BCHE:664 MRGPRD:692
leg.skin	0.043424101	286	1.248e-02	1.465e-01	ANKRD35:2 BNC1:5 PSAPL1:24 EVPL:35 FAM83F:44 ACER1:57
hippocampus.proper	-0.185966466	13	2.030e-02	1.716e-01	NEUROD2:523 OLIG2:610 NEUROG3:648 SLC17A7:2079 GRP:3205 NEUROD6:4004
pancreas	0.061460761	117	2.225e-02	1.716e-01	SLC17A4:58 CATSPERB:84 TMED6:236 RNF186:257 CPB1:259 ARSL:314
bladder	-0.115579039	29	3.139e-02	1.726e-01	MSX2:146 PLA2G2F:291 VGLL1:586 UPK3A:824 PLA2G4A:1073 ARL14:1169
Brodmann.area.9	-0.046176409	184	3.196e-02	1.726e-01	LRRTM4:40 CREG2:163 PPP2R2B:262 HTR2A:469 CPLX1:482 RGS7BP:485
eye.development	-0.077161313	69	2.706e-02	1.726e-01	RAX:233 FOXC2:383 MEIS2:576 ALDH3A1:598 NR2F2:667 MSX1:916
cerebellar.hemisphere	-0.024888989	537	5.356e-02	2.300e-01	TRMT9B:94 MTMR7:120 CDON:203 SEL1L3:209 SNAP91:267 SHF:277
ectocervix	-0.112542677	26	4.719e-02	2.300e-01	TSKU:253 HOXD13:1736 ADRA2A:2090 EDNRA:2458 CPXM1:2585 CCL23:3360
nucleus.accumbens	-0.054331741	105	5.538e-02	2.300e-01	GPR88:136 SLC32A1:340 EFNB3:342 PRMT8:810 PDYN:1150 GPC5:1307
liver	-0.027941039	397	6.004e-02	2.316e-01	A1CF:33 C2:104 APOC4-APOC2:142 GCHFR:242 SLC22A10:247 AMBP:298
substantia.nigra	-0.143889708	11	9.855e-02	3.548e-01	RET:462 TH:1009 KLHL1:1550 FOXB1:3139 SPX:4300 SLC6A11:4616
breast	-0.094858771	20	1.422e-01	4.767e-01	ALX4:597 LMX1B:1208 CIDEC:1525 LEP:2073 ADIPOQ:2461 GSC:2854
caudate.nucleus	-0.076995642	28	1.589e-01	4.767e-01	GPR88:136 LRRC10B:241 SLC35D3:643 SLCO1C1:1044 HS3ST5:1760 RGS14:2224
suprapubic.skin	0.025978660	257	1.558e-01	4.767e-01	BNC1:5 PSAPL1:24 EVPL:35 FAM83F:44 ACER1:57 COL7A1:91
skeletal.muscle	-0.024844496	258	1.738e-01	4.913e-01	TNNT3:174 MKNK2:220 KCNA7:299 TNNC2:428 KBTBD12:473 MYLK3:548
vagina	0.035732657	118	1.820e-01	4.913e-01	BNC1:5 EVPL:35 RNF222:227 FOXN1:287 PKP1:508 A2ML1:532
esophagus.mucosa	0.020851650	261	2.510e-01	6.455e-01	BNC1:5 EVPL:35 FAM83H:157 PTK6:175 RNF222:227 FOXN1:287
spleen	-0.016545155	366	2.840e-01	6.971e-01	GRAPL:28 GIMAP2:30 LY96:130 FOLR3:199 C1QC:336 LILRA1:533
blood	-0.016004886	345	3.137e-01	7.254e-01	EFHD2:11 C5AR2:31 PGLYRP1:71 KIR2DL1:116 FOLR3:199 CDKN2D:261
pituitary.gland	-0.018991102	233	3.224e-01	7.254e-01	SYT5:35 CNGA3:98 GNRHR:158 CD8B2:237 TBX19:295 TNFRSF11A:510
tibial.artery	-0.026123374	114	3.374e-01	7.288e-01	AOC3:232 FOXC2:383 PPP1R3C:660 KBTBD13:763 FAM207A:829 CRTAC1:959
cerebellum	-0.013588966	407	3.547e-01	7.368e-01	SAMD14:53 TRMT9B:94 TMEM132A:153 CCDC78:244 SHF:277 AIFM3:325
prostate	-0.034986137	51	3.883e-01	7.488e-01	SRD5A2:573 CHRNA2:618 KLK3:638 NKX3-1:644 SPDEF:1711 HOXD13:1736
stomach	0.025479997	99	3.828e-01	7.488e-01	CAPN8:1 PSAPL1:24 EPS8L3:92 TMPRSS2:153 TMED6:236 CBLIF:310
lung	0.017156124	161	4.554e-01	8.479e-01	LTK:32 PTPRB:128 SFTPB:258 LRRK2:307 SLC22A31:334 TM4SF19:504
adrenal.gland	-0.018364360	116	4.964e-01	8.935e-01	AGRP:719 IDH1:813 GNS:839 TSPAN12:930 MCOLN3:1068 TMEM150C:1325
cerebral.cortex	-0.016180599	109	5.611e-01	9.067e-01	NGEF:6 RIMS4:191 SYN1:208 PACSIN1:472 NEUROD2:523 RNF208:569
endocervix	0.020895709	76	5.300e-01	9.067e-01	COL24A1:121 ELFN1:406 ANGPT4:509 BDKRB1:529 METTL27:616 TGM2:766
esophagus.muscularis.mucosa	-0.029633468	28	5.877e-01	9.067e-01	COL4A6:234 CNTNAP3B:647 NKX6-1:1287 SYNPO2:1668 RGS2:2388 JPH2:3075
minor.salivary.gland	0.018718127	91	5.385e-01	9.067e-01	PROM1:180 ENPP3:759 CRACR2A:936 SLPI:1182 OPRPN:1299 KRT5:1425
subcutaneous.adipose	-0.018064310	82	5.729e-01	9.067e-01	PRKAR2B:164 EBF1:970 CD300LG:1057 ANGPTL4:1174 ACVR1C:1504 CIDEC:1525
amygdala	-0.022234594	9	8.174e-01	9.156e-01	NEUROD2:523 SLC17A7:2079 NEUROD6:4004 SLC38A8:4312 TNR:7268 BCAN:1112

AQP1:42 ADRA1B:339 PRDM6:366 FGL2:454 IGFBPL1:456 CRISPLD1:588

TNNI3K:283 ALPK2:554 LMOD2:694 PPP1R3A:845 CCDC141:1067 FSD2:1225

7.305e-01 9.156e-01 TMEM271:39 NEUROD2:523 SLC17A7:2079 NPTXR:2557 SLC6A1:3038 GRIN3A:3125 7.434e-01 9.156e-01 PLA2G2A:1523 CCDC190:2287 SUSD5:3867 CCDC3:5046 CCL19:6338 COL4A1:6803

-0.006503955

0.012080188

-0.017347441

0.024419133

156

95

33

7.805e-01 9.156e-01

6.851e-01 9.156e-01

aorta

atrium.auricle

Brodmann.area.24

coronary.artery