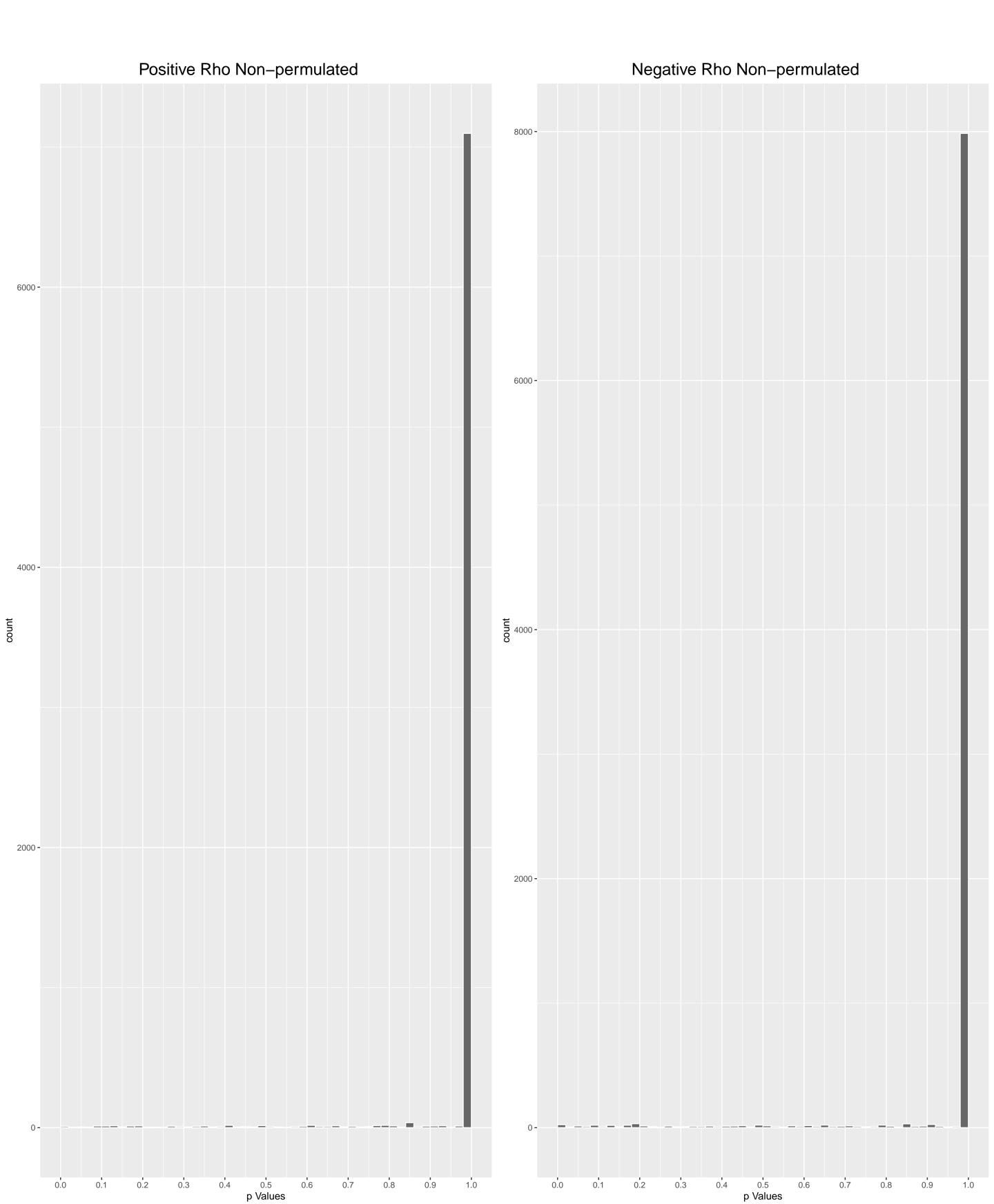


Gene

qValueNoperm

p.adj



Top Positive genes by P-value non-permulated

Top Negative genes by P-value non-permulated

PTCD3	5.077052	2.300014e-06	3.973e-03	1.000e+00
THADA	4.746728	1.240405e-05	9.806e-03	1.000e+00
TMEM116	4.758887	1.167982e-05	9.806e-03	1.000e+00
PIP	4.606413	2.458050e-05	1.450e-02	1.000e+00
HASPIN	4.614143	2.368329e-05	1.450e-02	1.000e+00
N4BP2L2	4.594788	2.599133e-05	1.450e-02	1.000e+00
BRWD1	4.583641	2.741691e-05	1.466e-02	1.000e+00
LRPPRC	4.548109	3.247799e-05	1.592e-02	1.000e+00
CATSPERE	4.448589	5.186185e-05	2.397e-02	1.000e+00

 Gene
 Rho
 P
 p.adj
 qValueNoperm

 CATSPERB
 6.101508
 6.304335e-09
 8.668e-05
 7.011e-01

Gene	Rho	Р	p.adj	qValueNoperm
CTNND1	-6.016147	1.071704e-08	8.668e-05	7.011e-01
PER2	-5.238162	9.731000e-07	3.863e-03	1.000e+00
ABCB4	-5.283561	7.601792e-07	3.863e-03	1.000e+00
OFD1	-5.166260	1.432950e-06	3.863e-03	1.000e+00
RIMS1	-5.166852	1.428419e-06	3.863e-03	1.000e+00
MAP3K15	-5.093083	2.113730e-06	3.973e-03	1.000e+00
LGR6	-5.107603	1.957630e-06	3.973e-03	1.000e+00
S100A6	-5.064535	2.456390e-06	3.973e-03	1.000e+00
BDNF	-5.017294	3.144256e-06	4.624e-03	1.000e+00
TRPV6	-4.963328	4.157719e-06	5.605e-03	1.000e+00

Geneset	stat	num.genes	pval	p.adj	gene.vals
Increased CSF lactate	0.158782803	53	6.443e-05	6.321e-01	LRPPRC:9 TMEM126B:49 COX20:117 TIMMDC1:134 SCO1:146 TRMT10C:379
46, XX Testicular Disorders of Sex Devel	-0.119156347	7	2.749e-01	9.862e-01	SOX9:346 SOX3:574 NR5A1:8402 RSPO1:8402 FOXL2:8402 NR0B1:8402
46, XY Disorders of Sex Development	-0.083947749	15	2.603e-01	9.862e-01	SOX9:346 WT1:520 CYB5A:866 TLX1:879 ZFPM2:1744 CYP11A1:1792
46, XY female	-0.019573910	16	7.864e-01	9.862e-01	SOX9:346 DMRT1:571 STAR:1399 UBL4A:2748 NR0B1:8402 HSD17B3:8402
46,XY partial gonadal dysgenesis	-0.118475652	10	1.945e-01	9.862e-01	SOX9:346 WT1:520 ZFPM2:1744 NR5A1:8402 NR0B1:8402 MAP3K1:8402
5,10-Methylenetetrahydrofolate reductase	0.034439797	18	6.130e-01	9.862e-01	AKAP9:96 XRCC4:1520 MTHFR:2057 CASP9:2072 GPX3:7775 SERPINE1:7775
Abortion, Habitual	-0.016907839	4	9.068e-01	9.862e-01	VEGFA:196 F2:8402 F5:8402 MTHFR:14120 NA NA
Abortion, Tubal	0.044630694	93	1.374e-01	9.862e-01	SPAG5:67 ECM2:147 ARNT:244 IL9:252 FN1:860 CD84:879
Achondrogenesis, type IB (disorder)	0.186325646	5	1.490e-01	9.862e-01	DCN:823 SLC26A2:1436 SLC26A3:7775 SLC26A5:7775 SLC26A4:7775 NA
Acidosis, Lactic	0.047703268	151	4.352e-02	9.862e-01	LRPPRC:9 TMEM126B:49 POLG:66 COX20:117 TIMMDC1:134 SCO1:146
ACROMESOMELIC DYSPLASIA, MAROTEAUX TYPE	0.021937631	4	8.792e-01	9.862e-01	IGF1:7775 NPPC:7775 NPR2:7775 GDF5:7775 NA NA
ACTH Syndrome, Ectopic	-0.132587835	5	3.045e-01	9.862e-01	GHSR:1879 AVPR1B:2437 CRH:8402 NR3C1:8402 PAK3:8402 NA
Acute Myeloid Leukemia, M1	0.012438814	105	6.601e-01	9.862e-01	CSF1R:114 ASXL2:200 NF1:255 KMT2A:307 KIT:614 MN1:694
Acute myeloid leukemia, minimal differen	0.058537749	19	3.771e-01	9.862e-01	KMT2A:307 FLT3:744 NCR1:869 DNMT3A:918 ZMYND11:1909 RUNX1:7775
Adenocarcinoma of lung, stage I	0.015389780	18	8.212e-01	9.862e-01	ADAM12:831 ACTN4:996 MET:7775 HOXA9:7775 MYC:7775 EIF4EBP1:7775
Adenocarcinoma of lung, stage IV	0.026144550	18	7.010e-01	9.862e-01	ERBB2:604 BRAF:858 MET:7775 TP53:7775 KRAS:7775 RET:7775
Adenocarcinoma, Basal Cell	-0.012082927	103	6.722e-01	9.862e-01	NR1I2:142 VEGFA:196 HRH4:199 CA2:220 DAPK1:363 CDKN1C:707
Adenocarcinoma, Clear Cell	0.003775512	95		9.862e-01	ATF1:239 HAGH:266 BRCA2:365 ERBB2:604 NEU3:683 TFAM:748
Adenocarcinoma, Endometrioid	0.014647367	54	7.098e-01	9.862e-01	ABCC1:410 NDC80:483 CCL22:581 ERBB2:604 BRAF:858 SHBG:882
Adenocarcinoma, intestinal type	0.013162989	12	8.746e-01	9.862e-01	BRAF:858 CDX2:1499 TP53:7775 KRAS:7775 EGFR:7775 CDKN2A:7775
Adenocarcinoma, metastatic	0.048615950	12		9.862e-01	ERBB2:604 HSPA5:1913 MYC:7775 KRAS:7775 EGF:7775 ESR2:7775
Adenocarcinoma, Oxyphilic	-0.010736755	105		9.862e-01	NR1I2:142 VEGFA:196 HRH4:199 CA2:220 DAPK1:363 CDKN1C:707
Adenocarcinoma, Scirrhous	0.082933467	6		9.862e-01	FGFR2:1475 MMP15:1586 MET:7775 MMP14:7775 FUT1:7775 TIMP3:14366
Adenocarcinoma, Tubular	-0.009513873	108		9.862e-01	NR1I2:142 VEGFA:196 HRH4:199 CA2:220 DAPK1:363 CDKN1C:707
Adenoma, Basal Cell	-0.035625897	27		9.862e-01	TXNRD1:1037 KCNJ5:1560 VHL:2140 ALOX5:2310 ATP1A1:2401 IGF1:8402
Adenoma, Microcystic	-0.023779433	34	6.315e-01	9.862e-01	TXNRD1:1037 KCNJ5:1560 VHL:2140 ALOX5:2310 ATP1A1:2401 IGF1:8402
Adenoma, Monomorphic	-0.035625897	27		9.862e-01	TXNRD1:1037 KCNJ5:1560 VHL:2140 ALOX5:2310 ATP1A1:2401 IGF1:8402
Adenoma, Trabecular	-0.033571262	28	5.388e-01		TXNRD1:1037 KCNJ5:1560 VHL:2140 ALOX5:2310 ATP1A1:2401 IGF1:8402
Adenoma, Villous	0.079858614	14	3.009e-01	9.862e-01	BRAF:858 MLH1:1591 TP53:7775 KRAS:7775 APC:7775 TP63:7775
Adrenal hyperplasia, bilateral	-0.119390282	3	4.738e-01	9.862e-01	KCNJ5:1560 PRKAR1A:8402 REN:8402 NA NA NA
Adrenoleukodystrophy, Neonatal	-0.089567844	15			PEX11B:1447 PEX3:1472 PEX10:1728 HSD17B4:1990 PEX19:8402 PEX1:8402
Affective Disorders, Psychotic	0.073970835	12		9.862e-01	FKBP5:226 DISC1:1616 BCL2L10:1661 MTHFR:2057 IL1RN:7775 HP:7775
Agammaglobulinemia, non-Bruton type	0.018260725	7		9.862e-01	LRRC8A:1863 CD79B:7775 CD79A:7775 PIK3R1:7775 BLNK:7775 TCF3:7775
Aganglionosis, Colonic	-0.047277902	19		9.862e-01	RASGEF1A:762 F2R:1498 FH:1804 EDN3:2622 TP53:8402 RET:8402
Aganglionosis, Rectosigmoid Colon	0.021625126	8		9.862e-01	NRG1:2045 RET:7775 CAVIN2:7775 UTP25:7775 ECE1:7775 EDNRB:7775
Albinism, Ocular	-0.014101349	27		9.862e-01	GPR143:108 PMPCA:647 XG:785 SLC45A2:1469 BLOC1S6:1986 TYRP1:8402
Albinism, Oculocutaneous	0.035190354	30		9.862e-01	BRCA2:365 KIT:614 BRAF:858 CSF3:7775 NRAS:7775 PIK3CA:7775
ALBINOIDISM, OCULOCUTANEOUS, AUTOSOMAL D	0.025659588	25		9.862e-01	HPS3:32 DBH:140 MLANA:886 SOX10:7775 TYRP1:7775 ZEB2:7775
Alcoholic Intoxication, Chronic	-0.019586364	376		9.862e-01	BDNF:9 ADH7:49 SLC6A6:68 IGSF22:101 DUSP8:186 NPY2R:266
	-0.009540626	27		9.862e-01	CD34:307 VDR:378 ZDHHC13:536 PARP1:905 ZFP36:2116 GGCT:2593

EnrichmentHsSymbolsFile2 Top pathways by non-permulation

Geneset	stat	num.genes	pval	p.adj	gene.vals
REACTOME_RESPIRATORY_ELECTRON_TRANSPORT_	0.14280990	101	7.208e-07	3.506e-03	LRPPRC:9 TMEM126B:49 ATP5PD:69 UQCRH:87 NDUFB7:97 COX20:117
REACTOME_RESPIRATORY_ELECTRON_TRANSPORT	0.15412451	81	1.646e-06	3.506e-03	LRPPRC:9 TMEM126B:49 UQCRH:87 NDUFB7:97 COX20:117 TIMMDC1:134
REACTOME_COMPLEX_I_BIOGENESIS	0.19771154	48	2.161e-06	3.506e-03	TMEM126B:49 NDUFB7:97 TIMMDC1:134 NDUFB10:196 NDUFB4:411 NDUFA9:541
WP_MITOCHONDRIAL_COMPLEX_I_ASSEMBLY_MODE	0.20402989	47	1.311e-06	3.506e-03	TMEM126B:49 DMAC1:64 NDUFB7:97 TIMMDC1:134 TMEM70:190 NDUFB10:196
REACTOME_TRANSPORT_OF_SMALL_MOLECULES	-0.05023780	669	1.059e-05	1.374e-02	ABCB4:2 TRPV6:10 ASIC3:19 ANO6:37 SLC43A1:51 ATP6V0D2:52
REACTOME_THE_CITRIC_ACID_TCA_CYCLE_AND_R	0.10323753	149	1.395e-05	1.509e-02	LRPPRC:9 TMEM126B:49 ATP5PD:69 UQCRH:87 NDUFB7:97 COX20:117
REACTOME_SLC_MEDIATED_TRANSMEMBRANE_TRAN	-0.08072167	237	1.935e-05	1.794e-02	SLC43A1:51 SLCO2A1:56 SLC6A20:59 SLC6A6:68 SLC27A4:72 SLC25A18:124
NIKOLSKY_BREAST_CANCER_7P22_AMPLICON	-0.19603025	38	2.904e-05	2.204e-02	FBXL18:31 TNRC18:107 BRAT1:116 SNX8:122 SUN1:176 TMEM184A:224
WP_ELECTRON_TRANSPORT_CHAIN_OXPHOS_SYSTE	0.13930894	75	3.057e-05	2.204e-02	ATP5PD:69 UQCRH:87 NDUFB7:97 SCO1:146 NDUFB10:196 ATP5PO:316
FISCHER_DREAM_TARGETS	0.04118708	882	3.837e-05	2.489e-02	HASPIN:5 AHCTF1:15 NEIL3:42 SPAG5:67 CEP295:76 LCORL:113
FLORIO_NEOCORTEX_BASAL_RADIAL_GLIA_DN	0.08684125	179	6.287e-05	3.399e-02	SPAG5:67 CKAP2L:127 MELK:175 BLM:213 NSUN7:224 C21orf62:241
WP_OXIDATIVE_PHOSPHORYLATION	0.17061710	46	6.264e-05	3.399e-02	ATP5PD:69 NDUFB7:97 NDUFB10:196 ATP5PO:316 ATP5PB:335 NDUFB4:411
REACTOME_NEURONAL_SYSTEM	-0.05872053	386	7.908e-05	3.745e-02	RIMS1:4 PPFIA4:62 KCNC2:91 EPB41L3:127 PRKAR1B:137 KCNH4:146
RODRIGUES_THYROID_CARCINOMA_POORLY_DIFFE	0.04744323	598	8.080e-05	3.745e-02	BRWD1:8 LRPPRC:9 HPS3:32 GTPBP10:74 ENO1:115 CIT:129
REACTOME_SPERM_MOTILITY_AND_TAXES	0.39177148	8	1.243e-04	5.377e-02	CATSPERB:1 CATSPERG:77 CATSPER3:704 CATSPER4:1113 CATSPER2:1296 HVCN1:1539
DODD_NASOPHARYNGEAL_CARCINOMA_DN	0.03253679	1244	1.360e-04	5.513e-02	PTCD3:2 LRPPRC:9 AHCTF1:15 NEIL3:42 SPAG5:67 GTPBP10:74
BENPORATH_ES_WITH_H3K27ME3	-0.03487528	983	2.446e-04	9.052e-02	RASGEF1C:12 RGS9:20 SLC27A2:55 SLCO2A1:56 SLC6A20:59 LYSMD2:73
KEGG_NEUROACTIVE_LIGAND_RECEPTOR_INTERAC	-0.06609280	260	2.511e-04	9.052e-02	HRH2:118 P2RY4:121 PTH2R:166 HRH4:199 HRH1:207 NPY2R:266
NIKOLSKY_BREAST_CANCER_16P13_AMPLICON	0.10405672	100	3.268e-04	1.116e-01	MMP25:58 HS3ST6:181 NDUFB10:196 PRSS27:240 HAGH:266 NPW:391
MEBARKI_HCC_PROGENITOR_FZD8CRD_UP	0.04518910	501	5.654e-04	1.834e-01	HASPIN:5 PLEKHG4:31 SH3GL3:119 CDC7:124 CKAP2L:127 CIT:129
MIKKELSEN_MEF_HCP_WITH_H3K27ME3	-0.04248905	555	6.595e-04	1.945e-01	RASGEF1C:12 SLC27A2:55 SLC6A20:59 HRH2:118 SPRN:132 PSD:197
REACTOME_TRANSPORT_OF_INORGANIC_CATIONS_	-0.09795797	102	6.356e-04	1.945e-01	SLC43A1:51 SLC6A20:59 SLC6A6:68 SLC25A18:124 SLC6A14:129 SLC4A1:381
NIKOLSKY_BREAST_CANCER_5P15_AMPLICON	-0.20822667	22	7.227e-04	1.993e-01	LPCAT1:117 LRRC14B:482 TPPP:1208 IRX4:1226 SLC9A3:1293 SLC12A7:1671
SCHAEFFER_PROSTATE_DEVELOPMENT_48HR_DN	-0.05086104	376	7.371e-04	1.993e-01	PER2:3 ENPP3:71 LYSMD2:73 GPRASP1:98 MMP16:144 AHR:169
DACOSTA_UV_RESPONSE_VIA_ERCC3_COMMON_DN	0.04629055	452	7.796e-04	2.023e-01	LRPPRC:9 FAT1:17 GOLGA4:26 USP13:27 ZFYVE9:52 FILIP1L:65
MOOTHA_VOXPHOS	0.11282403	72	9.374e-04	2.339e-01	ATP5PD:69 UQCRH:87 NDUFB7:97 ATP5PO:316 ATP5PB:335 NDUFB4:411
REACTOME_CELL_CYCLE	0.03865575	622	1.064e-03	2.556e-01	AHCTF1:15 MLH3:61 CENPT:70 AKAP9:96 CDC7:124 PSMB11:128
MARSON_BOUND_BY_E2F4_UNSTIMULATED	0.03723610	661	1.170e-03	2.711e-01	HASPIN:5 AHCTF1:15 ANKFY1:25 NEIL3:42 SPAG5:67 ATP5PD:69
GRESHOCK_CANCER_COPY_NUMBER_UP	0.05308983	312	1.299e-03	2.907e-01	BIRC3:18 BLM:213 ATF1:239 ARNT:244 NF1:255 DDX6:267
KEGG_HUNTINGTONS_DISEASE	0.07582335	149	1.418e-03	3.067e-01	DNAH2:38 ATP5PD:69 UQCRH:87 NDUFB7:97 NDUFB10:196 ATP5PO:316
VILLANUEVA_LIVER_CANCER_KRT19_UP	0.07308321	158	1.544e-03	3.106e-01	CDC7:124 CKAP2L:127 CEP135:142 MELK:175 BLM:213 ARID3A:290
RODRIGUES_THYROID_CARCINOMA_ANAPLASTIC_U	0.03703657	637	1.514e-03	3.106e-01	BRWD1:8 BIRC3:18 SYTL2:30 HPS3:32 GTPBP10:74 LCORL:113
HAMAI_APOPTOSIS_VIA_TRAIL_UP	0.03811858	595	1.580e-03	3.106e-01	N4BP2L2:7 ARMT1:14 AHCTF1:15 GOLGA4:26 CSPP1:44 NARS1:90
WP_PROXIMAL_TUBULE_TRANSPORT	-0.12831693	49	1.893e-03	3.611e-01	ATP6V0D2:52 SLC6A20:59 CA2:220 SLC22A6:247 ATP6V1B1:382 SLC1A1:495
REACTOME_SLC_TRANSPORTER_DISORDERS	-0.09428769	90	2.004e-03	3.714e-01	SLCO2A1:56 SLC6A20:59 SLC27A4:72 SLC6A14:129 NUP160:177 NUP210:273
REACTOME_TRANSPORT_OF_BILE_SALTS_AND_ORG	-0.09731370	82	2.330e-03	4.199e-01	SLC6A20:59 SLC6A6:68 SLC6A14:129 SLC30A10:133 SLC22A6:247 RHCG:260
REACTOME_PI3K_AKT_SIGNALING_IN_CANCER	0.08632113	102	2.611e-03	4.458e-01	CHUK:104 GAB1:183 KL:263 RPS6KB2:332 FGFR1:373 MLST8:375
REACTOME_TRIGLYCERIDE_METABOLISM	-0.14519593	36	2.576e-03	4.458e-01	MOGAT3:259 LPIN2:373 MOGAT2:719 FABP5:934 ABHD5:1195 DGAT2:1270

GO_Biological_Process_2023 Top pathways by non-permulation

PTCD3:2 OXA1L:62 MRPS17:162 MRPL37:297 MRPS31:320 MTIF2:460

0.09058098 92 2.693e-03 4.479e-01

REACTOME_MITOCHONDRIAL_TRANSLATION

Geneset	stat	num.genes	pval	p.adj	gene.vals
NADH Dehydrogenase Complex Assembly (GO:	0.21641653	48	2.173e-07	3.902e-04	TMEM126B:49 OXA1L:62 DMAC1:64 NDUFB7:97 TIMM21:153 NDUFB10:196
Mitochondrial Respiratory Chain Complex	0.21641653	48	2.173e-07	3.902e-04	TMEM126B:49 OXA1L:62 DMAC1:64 NDUFB7:97 TIMM21:153 NDUFB10:196
Mitochondrial Respiratory Chain Complex	0.17669687	77	8.578e-08	3.902e-04	TMEM126B:49 OXA1L:62 DMAC1:64 NDUFB7:97 COX20:117 SCO1:146
Inorganic Cation Transmembrane Transport	-0.08580694	277	9.960e-07	1.342e-03	TRPV6:10 ASIC3:19 ANO6:37 SLC6A20:59 SLC6A6:68 KCNC2:91
Monoatomic Cation Transmembrane Transpor	-0.08226283	273	3.207e-06	3.455e-03	TRPV6:10 ASIC3:19 ANO6:37 SLC6A20:59 SLC6A6:68 KCNC2:91
Intermediate Filament Organization (GO:0	-0.18666349	50	5.041e-06	4.527e-03	KRT32:24 KRT31:65 KRT82:85 KRT27:198 KRT26:210 KRT40:261
Oxidative Phosphorylation (GO:0006119)	0.15607240	55	6.316e-05	4.254e-02	ATP5PD:69 UQCRH:87 NDUFB7:97 NDUFB10:196 ATP5PO:316 ATP5PB:335
Proton Motive Force–Driven Mitochondrial	0.16901750	47	6.167e-05	4.254e-02	ATP5PD:69 NDUFB7:97 NDUFB10:196 ATP5PO:316 ATP5PB:335 NDUFB4:411
Proton Motive Force-Driven ATP Synthesis	0.14977963	51	2.175e-04	1.302e-01	ATP5PD:69 NDUFB7:97 NDUFB10:196 ATP5PO:316 ATP5PB:335 NDUFB4:411
Very Long-Chain Fatty Acid Catabolic Pro	-0.42998285	6	2.648e-04	1.427e-01	SLC27A2:55 SLC27A4:72 ACOX1:971 ABCD4:1866 ABCD3:1912 ABCD2:2030
Mitochondrial Electron Transport, NADH T	0.18649945	31	3.275e-04	1.604e-01	NDUFB7:97 NDUFB10:196 NDUFB4:411 NDUFA9:541 NDUFC2:586 NDUFB6:722
Mitochondrial RNA Metabolic Process (GO:	0.23356879	19	4.251e-04	1.908e-01	FASTKD5:80 POLRMT:169 FASTKD1:186 TWNK:199 PNPT1:343 MTERF1:417
Aerobic Electron Transport Chain (GO:001	0.13255593	54	7.600e-04	2.711e-01	UQCRH:87 NDUFB7:97 NDUFB10:196 NDUFB4:411 UQCRFS1:476 NDUFA9:541
Aerobic Respiration (GO:0009060)	0.13329596	54	7.098e-04	2.711e-01	OXA1L:62 UQCRH:87 NDUFB7:97 NDUFB10:196 NDUFB4:411 NDUFA9:541
Interstrand Cross-Link Repair (GO:003629	0.16490447	35	7.389e-04	2.711e-01	NEIL3:42 RNF168:148 DCLRE1C:305 XPA:352 FANCI:356 FANCE:492
Mitochondrial ATP Synthesis Coupled Elec	0.13072895	55	8.051e-04	2.711e-01	UQCRH:87 NDUFB7:97 NDUFB10:196 NDUFB4:411 UQCRFS1:476 NDUFA9:541
Mitochondrial Gene Expression (GO:014005	0.09509888	100	1.034e-03	3.277e-01	PTCD3:2 FASTKD5:80 MRPS17:162 POLRMT:169 FASTKD1:186 TWNK:199
Cellular Respiration (GO:0045333)	0.11116116	71	1.215e-03	3.636e-01	OXA1L:62 UQCRH:87 NDUFB7:97 NDUFB10:196 NDUFB4:411 UQCRFS1:476
Potassium Ion Transmembrane Transport (G	-0.08094021	132	1.353e-03	3.838e-01	KCNC2:91 KCNH4:146 KCNT2:184 KCNE5:203 KCNQ5:231 NALCN:552
Potassium Ion Transport (GO:0006813)	-0.08340288	120	1.634e-03	4.403e-01	KCNC2:91 KCNH4:146 KCNQ5:231 NALCN:552 KCNV1:560 KCNA4:573
Learning (GO:0007612)	-0.14142664	41	1.738e-03	4.458e-01	SHANK1:368 LGMN:372 TH:375 GPR88:400 MAPK8IP2:402 SHANK3:485
Chloride Transport (GO:0006821)	-0.10372887	73	2.205e-03	5.401e-01	ANO6:37 ANO3:300 GABRB3:333 SLC4A1:381 ANO8:450 SLC1A1:495
Cilium-Dependent Cell Motility (GO:00602	0.20721269	17	3.102e-03	6.287e-01	DNAH2:38 DNAH17:473 DNAH3:1462 TEKT1:1479 RSPH9:1544 RFX3:1943
Fatty Acid Transport (GO:0015908)	-0.14033726	37	3.151e-03	6.287e-01	SLCO2A1:56 SLC27A4:72 SLC22A6:247 SLC22A8:539 CD36:596 FABP5:934
Monoatomic Ion Transport (GO:0006811)	-0.08426366	104	3.033e-03	6.287e-01	ANO6:37 SLC25A18:124 PIEZO2:340 SLC4A1:381 SLC1A1:495 SLC17A1:566
Positive Regulation Of Long-Term Synapti	-0.24880896	12	2.843e-03	6.287e-01	LGMN:372 SHANK3:485 INS:501 SLC18A3:598 ZDHHC2:652 SHISA7:1657
Positive Regulation Of Metabolic Process	-0.08640351	101	2.737e-03	6.287e-01	PER2:3 PTH2R:166 EHMT1:168 VEGFA:196 GRB10:297 CNOT3:478
Acylglycerol Biosynthetic Process (GO:00	-0.17942042	21	4.431e-03	7.618e-01	MOGAT3:259 PLA2G4A:306 LPIN2:373 PNPLA3:379 MOGAT2:719 DGAT2:1270
Amino-Acid Betaine Transport (GO:0015838	-0.31146114	7	4.322e-03	7.618e-01	SLC6A20:59 SLC7A6:624 SLC22A4:1131 SLC25A29:1241 SLC22A5:1573 SLC22A16:8402
Axoneme Assembly (GO:0035082)	0.15132556	30	4.135e-03	7.618e-01	CCDC40:249 SPAG1:272 SPAG17:665 CFAP91:909 RSPH9:1544 RP1:1568
Long-Chain Fatty Acid Transport (GO:0015	-0.17105481	23	4.524e-03	7.618e-01	SLC27A2:55 SLC27A4:72 CD36:596 FABP5:934 SLC27A1:1123 ABCD4:1866
Positive Regulation Of Cold-Induced Ther	-0.08574343	93	4.321e-03	7.618e-01	PER2:3 PTH2R:166 EHMT1:168 VEGFA:196 GRB10:297 CNOT3:478
Cell Surface Pattern Recognition Recepto	-0.40244916	4	5.308e-03	7.748e-01	COLEC10:1193 FFAR2:1247 COLEC11:1813 EHHADH:2145 NA NA
Epithelial Cell Differentiation (GO:0030	-0.07589654	113	5.400e-03	7.748e-01	KRT32:24 KRT31:65 VEGFA:196 KRT27:198 KRT26:210 RHCG:260
Mitochondrial RNA Processing (GO:0000963	0.26931602	9	5.147e-03	7.748e-01	FASTKD5:80 FASTKD1:186 PNPT1:343 TRMT10C:379 FASTKD3:1587 SUPV3L1:7775
Protein Localization To Centrosome (GO:0	0.19465724	17	5.465e-03	7.748e-01	SPAG5:67 GOLGB1:453 CEP250:708 MBD1:851 CEP131:1087 C2CD3:1488
Skeletal System Morphogenesis (GO:004870	0.13101726	38	5.215e-03	7.748e-01	FGFR1:373 HOXD3:588 SPEF2:645 LAMA5:889 DSCAML1:984 LRP5:1041
Triglyceride Biosynthetic Process (GO:00	-0.19664924	17	5.005e-03	7.748e-01	MOGAT3:259 LPIN2:373 PNPLA3:379 MOGAT2:719 DGAT2:1270 GPAM:1398
Memory (GO:0007613)	-0.10794347	53	6.599e-03	9.117e-01	BDNF:9 KLK8:349 SHANK1:368 LGMN:372 TH:375 SHANK3:485
Regulation Of Nuclear Division (GO:00517	0.18874879	17	7.061e-03	9.492e-01	FBXO43:143 KIF20B:615 CDC25C:792 PDXP:1200 PRMT5:1224 FBXO5:2024

MGI_Mammalian_Phenotype_Level_4 Top pathways by non-permulation

Geneset	stat	num.genes	pval	p.adj	gene.vals
MP0001756 abnormal urination	-0.10305831	81	1.430e-03	3.552e-01	TRPV6:10 SCNN1G:149 VDR:378 SLC4A1:381 EPHB6:432 SLC26A7:569
MP0002080 prenatal lethality	0.02891910	1339	1.493e-03	3.552e-01	AHCTF1:15 UBE4B:22 NCOR1:29 NPHP3:45 POLG:66 FBXW8:102
MP0004043 abnormal pH regulation	-0.20384462	14	8.329e-03	5.704e-01	RHCG:260 SLC26A7:569 SCNN1B:611 WNK4:1072 SLC9A3:1293 SLC4A10:13
MP0005380 embryogenesis phenotype	0.03962071	407	7.773e-03	5.704e-01	POLG:66 PTK7:83 FBXW8:102 HINFP:121 DVL2:194 BLM:213
MP0005636 abnormal mineral homeostasis	-0.07003176	134	5.558e-03	5.704e-01	TRPV6:10 HPX:33 ANK1:36 CLDN16:77 SCNN1G:149 RHCG:260
MP0001672 abnormal embryogenesis/ devel	0.03962071	407	7.773e-03	5.704e-01	POLG:66 PTK7:83 FBXW8:102 HINFP:121 DVL2:194 BLM:213
MP0004264 abnormal extraembryonic tissu	0.17490294	19	8.388e-03	5.704e-01	CUBN:515 XBP1:630 NCOA6:946 HEPH:1045 MED1:1221 RB1:1447
MP0003656 abnormal erythrocyte physiolo	-0.15830531	22	1.027e-02	6.110e-01	ANK1:36 SLC4A1:381 PFKM:523 ADD2:662 MAN2A1:828 KCNN4:1418
MP0002069 abnormal eating/drinking beha	-0.03712391	401	1.325e-02	7.006e-01	PER2:3 BDNF:9 JAK1:46 SLC27A4:72 NPC1:76 EHMT1:168
MP0001765 abnormal ion homeostasis	-0.06742425	103	1.891e-02	7.058e-01	TRPV6:10 CLDN16:77 SCNN1G:149 RHCG:260 CASR:265 VDR:378
MP0002572 abnormal emotion/affect behav	-0.03797308	291	2.910e-02	7.058e-01	BDNF:9 NAV2:78 KCNC2:91 EHMT1:168 HRH1:207 NPY2R:266
MP0000266 abnormal heart morphology	0.02523345	699	3.114e-02	7.058e-01	UBE4B:22 NPHP3:45 POLG:66 PTK7:83 DLC1:108 DMD:109
MP0002136 abnormal kidney physiology	-0.03927950	279	2.691e-02	7.058e-01	TRPV6:10 HPX:33 CLDN16:77 SCNN1G:149 TOP3B:158 SLC22A6:247
MP0001501 abnormal sleep pattern	-0.10811548	35	2.723e-02	7.058e-01	PER2:3 KCNC2:91 NPAS2:264 NPY2R:266 DLGAP3:409 IL6:735
MP0002078 abnormal glucose homeostasis	-0.03097283	449	2.954e-02	7.058e-01	BDNF:9 SLC6A6:68 CD38:179 ERCC6:183 HRH1:207 NPY2R:266
MP0002925 abnormal cardiovascular devel	0.03084883	509	2.181e-02	7.058e-01	DLC1:108 RBL2:130 DVL2:194 CCNF:208 ARNT:244 NF1:255
MP0002084 abnormal developmental patter	0.03419204	360	2.997e-02	7.058e-01	NPHP3:45 PTK7:83 CHUK:104 RBL2:130 DVL2:194 CCNF:208
MP0002086 abnormal extraembryonic tissu	0.03263508	476	1.855e-02	7.058e-01	FBXW8:102 CHUK:104 DLC1:108 GAB1:183 CCNF:208 ACVR1B:228
MP0003693 abnormal embryo hatching	0.12998442	24	2.775e-02	7.058e-01	HINFP:121 ATF1:239 CDX2:1499 CDCA8:1663 RBBP8:1732 HSPA5:1913
MP0000534 abnormal ureter morphology	-0.09404359	52	1.941e-02	7.058e-01	SOX9:346 AGTR2:407 BMP5:418 AQP2:725 PYGO2:959 UPK3A:986
MP0009745 abnormal behavioral response	-0.04910352	204	1.718e-02	7.058e-01	PER2:3 BDNF:9 KCNC2:91 GPRASP1:98 NR1I2:142 EHMT1:168
MP0003635 abnormal synaptic transmissio	-0.03107936	425	3.319e-02	7.182e-01	RIMS1:4 BDNF:9 DGCR8:87 PRKAR1B:137 ENTPD1:164 SYN3:174
MP0002066 abnormal motor capabilities/c	-0.02056705	1079	3.644e-02	7.227e-01	PER2:3 BDNF:9 ANK1:36 SLC27A4:72 NPC1:76 GPRASP1:98
MP0002064 seizures	-0.03887372	254	3.620e-02	7.227e-01	BDNF:9 KCNC2:91 HRH2:118 SCN9A:205 DGKD:216 NPY2R:266
MP0009642 abnormal blood homeostasis	-0.01933542	1249	3.811e-02	7.255e-01	ABCB4:2 BDNF:9 TRPV6:10 HPX:33 SLC27A4:72 CLDN16:77
MP0003136 yellow coat color	0.21348718	7	5.056e-02	9.257e-01	ADAMTS20:174 SOX2:1027 EDA:1040 OCA2:7775 EDNRB:7775 MITF:7775
MP0000609 abnormal liver physiology	-0.01781176	374	2.498e-01	9.287e-01	ABCB4:2 NPC1:76 NR1I2:142 AHR:169 ERCC6:183 HRH1:207
MP0001731 abnormal postnatal growth	0.01798365	587	1.543e-01	9.287e-01	FBXW8:102 CHUK:104 DMD:109 CSF1R:114 ITGA9:120 DBH:140
MP0000604 amyloidosis	-0.05840752	33	2.466e-01	9.287e-01	ZDHHC13:536 LRPAP1:1390 CLU:1788 PSEN1:1933 SORL1:1960 KLC1:199
MP0000598 abnormal liver morphology	-0.01370268	472	3.247e-01	9.287e-01	ABCB4:2 ANK1:36 NPC1:76 LIG1:126 AHR:169 GRB10:297
MP0005334 abnormal fat pad	-0.01964842	150	4.112e-01	9.287e-01	NPC1:76 ERCC6:183 NPY2R:266 AGTR2:407 NPY1R:564 LPL:576
MP0005330 cardiomyopathy	-0.03127979	68	3.747e-01	9.287e-01	SLC6A6:68 PLRG1:362 MYBPC3:428 LY6E:570 DES:595 ERBB4:676
MP0008961 abnormal basal metabolism	-0.04715219	19	4.773e-01	9.287e-01	PER2:3 HTR6:1032 BRD2:1136 VGF:1342 HIF1AN:2241 DECR1:2611
MP0002837 dystrophic cardiac calcinosis	-0.12673708	9	1.882e-01	9.287e-01	MYBPC3:428 DES:595 MYH6:2051 GSTZ1:8402 SCG5:8402 SLC2A4:8402
MP0005369 muscle phenotype	0.01454667	206	4.782e-01	9.287e-01	DMD:109 NF1:255 KL:263 TGFBR3:300 FGFR1:373 TRDN:398
MP0009250 abnormal appendicular skeleto	0.03137175	74	3.532e-01	9.287e-01	CBX2:106 ARSB:251 PHC1:597 PBX1:1096 HOXA4:1100 TNFSF11:1125
MP0002998 abnormal bone remodeling	0.03378900	109	2.265e-01		CSF1R:114 KL:263 CTSK:340 FGFR1:373 CRTAP:415 TOB2:423
MP0005248 abnormal Harderian gland	-0.05287071	16		9.287e-01	PRLR:1081 OTX1:1775 RARB:1869 RARA:8402 CDKN1A:8402 CTNNB1:840
MP0004133 heterotaxia	0.08002029	31	1.239e-01		MGAT1:664 NODAL:714 LAMA5:889 RPGRIP1L:1025 RFX3:1943 BICC1:777
MP0002396 abnormal hematopoietic system	0.05731544	21		9.287e-01	BRCA2:365 FLT3:744 SNAI2:1363 LDB1:1704 CSF3R:2098 RAD50:7775

tissue_specific Top pathways by non-permulation

0	-1.1				
Geneset	stat	num.genes	pval	p.adj	gene.vals
EBV.lymphocyte	0.05023104	671		4.826e-04	HASPIN:5 BIRC3:18 NEIL3:42 SFMBT2:59 ENO1:115 CARMIL2:123
testis	0.03792263	1378		4.826e-04	CATSPERE:10 UTS2B:20 CCDC110:24 PLEKHG4:31 DNAH2:38 MAP3K19:55
nucleus.accumbens	-0.09092260	98		3.334e-02	PSD:197 ANKRD34B:201 LRRC7:294 ANO3:300 SORCS3:330 GPR6:369
putamen	-0.22587652	15		3.334e-02	RGS9:20 KCNH4:146 ANO3:300 GPR88:400 GRM3:585 SLC18A3:598
Brodmann.area.9	-0.06073467	182		5.490e-02	KCNC2:91 ZNF365:182 KCNQ5:231 SYT16:301 FAM81A:317 OLFM1:323
cerebellar.hemisphere	-0.03159286	510	1.725e-02		RIMS1:4 BDNF:9 MTBP:11 RASGEF1C:12 MTCL1:16 PDZD4:30
cerebellum	-0.03372171	376	2.749e-02		MTBP:11 MTCL1:16 ASIC3:19 TRANK1:25 CRB1:39 B4GALNT4:40
esophagus.mucosa	-0.04223408	220	3.267e-02		KRT32:24 ADH7:49 DSG3:81 EPS8L1:106 TMEM184A:224 GJB3:250
uterus	0.07776400	61	3.619e-02		PTK7:83 KLHL13:377 FRMD7:400 TCF23:416 HOXD3:588 HOXD8:797
caudate.nucleus	-0.11182516	26	4.867e-02		GPR37L1:21 ANO3:300 GPR88:400 GRM3:585 RGS14:929 LRRC10B:1272
fallopian.tube	0.07866318	52	5.027e-02		TUBA4B:137 TCF23:416 MSLNL:560 BCHE:608 CCDC198:649 RARRES1:724
endocervix	-0.06416435	72	6.060e-02	2.727e-01	PLPP3:230 VIPR2:318 PRSS12:347 SPON2:475 SMPDL3A:479 XKR5:514
substantia.nigra	-0.15336071	12	6.597e-02		KCNE5:203 TH:375 SLC6A11:1034 SLC6A3:2436 KLHL1:2580 CHRM5:8402
C1.spinal.cord	-0.03904381	181	7.245e-02		GJC2:95 PIEZO2:340 SEC14L5:357 PCDHA1:497 BCAS1:502 CNTN2:521
adrenal.gland	-0.04561845	108	1.032e-01	3.652e-01	MAP3K15:7 AOX1:225 CYB561A3:287 KLHL4:430 ABCB1:568 TPD52L1:764
minor.salivary.gland	-0.05504867	69	1.150e-01	3.652e-01	ENPP3:71 PROM1:119 SLC6A14:129 SOX9:346 ATP6V1B1:382 BPIFB1:451
stomach	-0.04970889	86	1.125e-01	3.652e-01	BAIAP2L1:162 CXCL17:512 SLC26A9:612 CBLIF:658 CLDN18:723 ANXA10:912
thyroid	-0.03528659	151	1.373e-01	4.119e-01	FHDC1:22 HIRA:66 MGAT4C:195 VEGFA:196 MARVELD2:282 TPO:303
breast	-0.10224688	15	1.706e-01	4.849e-01	NPY2R:266 CIDEC:974 TFAP2B:2160 GSC:2433 FABP4:2695 HCAR1:2773
cortex.kidney	-0.03474169	114	2.025e-01	5.419e-01	ATP6V0D2:52 CLDN16:77 PTH2R:166 SLC22A6:247 CASR:265 ATP6V1B1:382
skeletal.muscle	-0.02276018	239	2.308e-01	5.419e-01	SPTB:75 BEST3:125 NEB:194 OBSCN:255 YBX3:321 MLIP:332
spleen	0.02075379	298	2.244e-01	5.419e-01	MMP25:58 SCARF1:88 CSF1R:114 CXCR5:170 RENBP:242 NTN4:257
transformed.skin.fibroblast	0.02212396	258	2.269e-01	5.419e-01	FAT1:17 P4HA3:47 NEDD4:260 GPR1:303 PODNL1:345 CXCL6:461
prostate	0.05009195	38	2.861e-01	6.179e-01	CPAMD8:13 SCUBE2:111 TTC6:1011 LMAN1L:1053 CREB3L4:1632 SRD5A2:2148
vagina	-0.03266443	91	2.835e-01	6.179e-01	DSG3:81 SCNN1G:149 GJB3:250 RHCG:260 KRT16:309 NCCRP1:356
bladder	-0.06024735	24	3.074e-01	6.377e-01	PLA2G4A:306 UGT1A6:393 UPK3A:986 PSCA:1883 TMC7:2233 UPK1B:2533
coronary.artery	0.07438094	15	3.189e-01	6.377e-01	TIMP1:635 SUSD5:1405 GJA5:1925 PCOLCE2:1935 CCN3:7775 SPINK13:7775
aorta	0.02186048	154	3.526e-01	6.801e-01	FILIP1L:65 ITGA9:120 ECM2:147 FOXS1:289 NIBAN1:291 ITGA10:540
amygdala	-0.05999096	9	5.333e-01	7.502e-01	PCDH15:1345 LHFPL3:2378 BCAN:8402 NEUROD2:8402 NEUROD6:8402 PTPRZ1:8402
atrium.auricle	0.02137935	90	4.851e-01	7.502e-01	SMPX:149 IGSF5:763 S100A1:802 NRAP:863 LMAN1L:1053 C1orf105:1082
Brodmann.area.24	-0.03169962	31	5.418e-01	7.502e-01	SLC25A18:124 SHANK1:368 CSPG5:633 DDN:955 NTRK2:1336 SLC6A1:2363
cerebral.cortex	-0.02124908	107	4.499e-01	7.502e-01	LZTS1:69 PRKAR1B:137 ADGRB2:222 DLGAP3:409 CSMD1:489 RNF208:634
esophagus.muscularis.mucosa	0.03493455	26	5.380e-01	7.502e-01	PRUNE2:43 KCNMB1:116 CHRM3:939 SMTN:1493 NKX6-1:7775 CCDC69:7775
hypothalamus	-0.02980155	66	4.039e-01	7.502e-01	SCN9A:205 NPY2R:266 TACR3:472 LRRC55:591 GABRQ:702 MC4R:964
leg.skin	-0.01311556	217		7.502e-01	DSG3:81 INAVA:155 TREX2:218 GJB3:250 GPRIN2:262 KRT16:309
	0.01092700	0.4		7 5020 01	CATCHERD, 4 CCDC2,440 DDFD4,545 CCDC400,640 CFL A2A,744 CFL A2A,745

CAISPERBIT G0PC2:118 DPEP1:545 CCDC198:649 CELA3A:711 CELA2A:715

CASP5:53 ETHE1:223 MTMR11:236 TRIM15:360 TSPAN8:381 KRT18:674

SLCO2A1:56 LPCAT1:117 BPIFA1:141 AGTR2:407 BMP5:418 DRAM1:483

DES:595 NT5DC3:604 F2RL2:687 PNCK:961 SEMA3A:1153 TES:1225 SYTL2:30 WTIP:254 LPP:513 CPED1:587 PDE3A:650 RNF180:667

5.0836-01 7.5026-01

4.712e-01 7.502e-01

4.242e-01 7.502e-01

5.123e-01 7.502e-01

5.624e-01 7.593e-01

pancreas

sigmoid.colon

tibial.artery

transverse.colon

lung

0.01982709

-0.02894931

0.02216766

0.01566236

-0.01432320

110

149

139