





Top Positive genes by P-value non-permulated

Top Negative genes by P-value non-permulated

CCPG1	0.3169889	206	7.556e-16	1.417e-11	2.658e-07
MRGPRE	0.4673325	125	2.690e-14	2.266e-10	1.345e-06
PER2	0.2583903	223	3.624e-14	2.266e-10	1.345e-06
SHANK2	0.2669847	212	6.116e-14	2.868e-10	1.345e-06
AFDN	0.2488617	212	4.281e-13	1.439e-09	4.498e-06
SORL1	0.2435694	216	4.603e-13	1.439e-09	4.498e-06
USP43	0.2397915	216	6.961e-13	1.865e-09	4.998e-06
TET1	0.2295643	221	1.189e-12	2.712e-09	5.510e-06
TMEM126B	0.2580885	196	1.301e-12	2.712e-09	5.510e-06
TET2	0.2230513	225	1.566e-12	2.938e-09	5.510e-06

Gene Rho N P p.adj qValueNoperm

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

Gene Rho N P p.adj qValueNoperm

Geneset	stat	num.genes	pval	p.adj	gene.vals
Skin Development (GO:0043588)	0.17289050	66	1.210e-06	6.545e-03	DSP:51 OPN3:367 ITGB4:406 MED1:466 COL3A1:815 EVPL:861
NADH Dehydrogenase Complex Assembly (GO:	0.18430286	49	8.153e-06	1.469e-02	TMEM126B:9 NDUFA11:112 ECSIT:136 NDUFAF1:152 NDUFB8:335 NDUFB5:419
Mitochondrial Respiratory Chain Complex	0.18430286	49	8.153e-06	1.469e-02	TMEM126B:9 NDUFA11:112 ECSIT:136 NDUFAF1:152 NDUFB8:335 NDUFB5:419
Calcium Ion Transmembrane Import Into Cy	0.13956176	79	1.829e-05	2.073e-02	TRPV6:52 CACNA1I:278 CACNA1S:283 CACNA1E:310 SLC24A4:313 CACNA1G:528
Calcium Ion Transmembrane Transport (GO:	0.14010667	78	1.917e-05	2.073e-02	TRPM5:19 TRPV6:52 SLC24A3:237 CACNA1S:283 SLC24A4:313 ATP2C2:397
Keratinocyte Differentiation (GO:0030216	0.18654782	40	4.483e-05	4.040e-02	DSP:51 OPN3:367 MED1:466 EVPL:861 KRT16:1278 TGM1:1291
Natural Killer Cell Activation Involved	0.24586600	22	6.564e-05	4.436e-02	IFNA5:414 IFNA10:985 IFNA1:1066 IFNA2:1093 FCGR3A:1832 IFNA7:2164
Regulation Of Peptidyl–Serine Phosphoryl	0.27234135	18	6.338e-05	4.436e-02	IFNA5:414 IFNA10:985 IFNA1:1066 IFNA2:1093 IFNG:1395 IFNA7:2164
Positive Regulation Of Intracellular Tra	0.18140351	39	8.901e-05	5.347e-02	SORL1:6 SPAG5:369 MBD1:686 NEDD4:1044 PRR5L:1322 KIF20B:1349
Epidermis Development (GO:0008544)	0.11824992	84	1.819e-04	7.632e-02	DSP:51 HOXB13:169 FLOT2:610 EVPL:861 LCE2B:935 MANSC4:968
Intermediate Filament Organization (GO:0	0.13516074	65	1.659e-04	7.632e-02	PKP1:12 DSP:51 KRT17:196 KRT80:222 KRT20:247 DES:402
mRNA Methylation (GO:0080009)	0.27758403	15	1.976e-04	7.632e-02	TRMT61B:632 TRMT10C:646 METTL8:787 NSUN2:1916 CMTR1:1970 TRMT61A:2821
Mitochondrial Respiratory Chain Complex	0.11951587	82	1.855e-04	7.632e-02	TMEM126B:9 NDUFA11:112 ECSIT:136 NDUFAF1:152 NDUFB8:335 NDUFB5:419
Positive Regulation Of Peptidyl-Serine P	0.26217905	17	1.824e-04	7.632e-02	IFNA5:414 IFNA10:985 IFNA2:1093 IFNG:1395 IFNA7:2164 IFNA14:2417
Epidermal Cell Differentiation (GO:00099	0.14786169	52	2.273e-04	7.951e-02	DSP:51 OPN3:367 MED1:466 EVPL:861 OVOL3:1046 KRT16:1278
Homophilic Cell Adhesion Via Plasma Memb	0.13678365	60	2.500e-04	7.951e-02	SDK1:32 TRO:59 DSG2:195 ITGB1:346 NEXN:371 L1CAM:594
Positive Regulation Of Neuron Apoptotic	-0.22115776	23	2.416e-04	7.951e-02	ITGAM:427 FBXW7:508 BAX:877 TFAP2A:1104 TNF:1615 CDK5R1:2334
Regulation Of Protein Localization To Nu	-0.14268264	51	4.263e-04	1.281e-01	PARP9:167 KAT7:263 DTX3L:369 YWHAZ:437 OTUD7B:839 TYK2:887
Internal Protein Amino Acid Acetylation	-0.35641964	8	4.811e-04	1.369e-01	KAT7:263 MAPT:350 NAA10:955 KAT5:1702 KAT2A:2218 KAT2B:2985
Calcium Ion Transport (GO:0006816)	0.09393830	110	6.753e-04	1.826e-01	TRPM5:19 TRPV6:52 SLC24A3:237 CACNA1S:283 SLC24A4:313 ATP2C2:397
Actin-Myosin Filament Sliding (GO:003327	0.30312187	10	9.027e-04	2.236e-01	MYH2:16 MYL6B:461 TNNT2:704 MYH3:783 MYH4:944 MYH8:3483
Calcium Ion Import Across Plasma Membran	0.16092912	34	1.168e-03	2.236e-01	TRPV6:52 CACNA1I:278 CACNA1S:283 CACNA1E:310 SLC24A4:313 CACNA1G:528
Gene Expression (GO:0010467)	-0.05890262	266	9.807e-04	2.236e-01	RBM39:16.5 RPS4Y2:16.5 GSPT2:98 CHTOP:128 MRPS21:169 EXOSC9:198
Lymphocyte Activation Involved In Immune	0.19584182	23	1.151e-03	2.236e-01	IFNA5:414 IFNA10:985 IFNA1:1066 IFNA2:1093 IFNA7:2164 IFNA14:2417
mRNA Modification (GO:0016556)	0.18349639	27	9.681e-04	2.236e-01	TRMT61B:632 TRMT10C:646 METTL8:787 PUS7L:1000 DKC1:1209 NSUN2:1916
Natural Killer Cell Activation (GO:00301	0.14090453	44	1.227e-03	2.236e-01	IFNA5:414 IFNA10:985 IFNA1:1066 IFNA2:1093 CD2:1483 NCR3:1616
Protein Insertion Into ER Membrane (GO:0	-0.17792637	28	1.122e-03	2.236e-01	MMGT1:252 TRAM1:1127 CCDC47:1414 RAB5IF:1611 GET3:1771 EMC4:2305.5
Regulation Of Vesicle Size (GO:0097494)	-0.24928030	14	1.241e-03	2.236e-01	BLOC1S1:1154 KXD1:1893 BORCS8:2110 BORCS7:2355 RAB5A:2966 AP2M1:3456
Semaphorin-Plexin Signaling Pathway Invo	0.27245284	12	1.083e-03	2.236e-01	PLXNC1:766 PLXNA4:842 PLXNB2:1102 PLXNB3:2191 SEMA3A:2999 PLXNA1:3281
Transcription Initiation At RNA Polymera	-0.10953006	73	1.224e-03	2.236e-01	MED20:142 TAF11L3:539 GTF2H2:722 GTF2B:735 TAF11L5:752 MED30:927
Mitotic Sister Chromatid Segregation (GO	0.08903716	109	1.339e-03	2.263e-01	DLGAP5:27 KIF18A:78 CEP192:96 KIF22:192 OFD1:224 KIF2C:231
Regulation Of Neuron Migration (GO:20012	0.17516094	28	1.339e-03	2.263e-01	KIF26A:120 TNN:456 COL3A1:815 ULK4:962 IGSF10:1014 PLXNB2:1102
ERBB Signaling Pathway (GO:0038127)	0.12674094	53	1.422e-03	2.330e-01	PTK2:705 AKT1:1040 PLCG1:1068 PLCE1:1177 EGFR:1249 PIK3C2A:1328
mRNA Processing (GO:0006397)	-0.06716858	187	1.575e-03	2.505e-01	RBM22:16.5 MTREX:135 SFPQ:265 WDR83:321 CPSF7:699 SART3:847
Positive Regulation Of Calcium Ion Trans	0.14187187	41	1.677e-03	2.591e-01	CASQ1:277 GPER1:336 CAPN3:834 CEMIP:909 P2RX7:1001 PLCG1:1068
Muscle Contraction (GO:0006936)	0.09468339	91	1.817e-03	2.730e-01	MYH2:16 MYH13:89 MYOF:243 CACNA1S:283 DES:402 MYH1:438
Establishment Or Maintenance Of Apical/B	0.18325259	24	1.889e-03		PATJ:228 SCRIB:258 PARD3B:633 DLG3:1710 LLGL1:1783 OOEP:1819
Negative Regulation Of Inflammatory Resp	-0.08650726	107		2.734e-01	TRIM65:45 FNDC4:133 TNFAIP6:278 APOA1:286 IL22:322 PRKCD:357
Presynaptic Active Zone Organization (GO	-0.39910733	5		2.734e-01	ERC2:277 ERC1:545 CAST:2550 PCLO:2855 RAB3A:3194 NA
Regulation Of Smooth Muscle Contraction	0.19941021	20		2.734e-01	CTTN:279 TACR2:615 PLCE1:1177 KCNB2:1411 SETD3:1793 CHRM2:1938

EnrichmentHsSymbolsFile2 Top pathways by non-permulation

Geneset	stat	num.genes	pval	p.adj	gene.vals
HOUNKPE_HOUSEKEEPING_GENES	-0.06632010	1063	3.793e-13	2.463e-09	ARL8B:16.5 CAB39:16.5 CUL3:16.5 TMEM203:16.5 PDCD7:54 PSMD10:76
REACTOME_METABOLISM_OF_RNA	-0.07958533	645	6.273e-12	2.037e-08	RBM39:16.5 RBM22:16.5 SNRPC:16.5 RPS4Y2:16.5 PDCD7:54 PSMD10:76
REACTOME_KERATINIZATION	0.12923156	214	7.558e-11	1.636e-07	PKP1:12 DSP:51 KRTAP6-1:55 KRTAP10-1:163 KRTAP10-3:164 DSG2:195
REACTOME_FORMATION_OF_THE_CORNIFIED_ENVE	0.15619422	128	1.065e-09	1.730e-06	PKP1:12 DSP:51 DSG2:195 KRT17:196 KRT80:222 KRT20:247
BLALOCK_ALZHEIMERS_DISEASE_DN	-0.05241809	1180	1.672e-09	2.172e-06	CAB39:16.5 STAM:16.5 NQO1:16.5 TBPL1:16.5 MEMO1:16.5 SEC61A2:16.5
REACTOME_CELLULAR_RESPONSES_TO_STIMULI	-0.06327535	749	4.334e-09	4.020e-06	CUL3:16.5 NQO1:16.5 H2AC18:16.5 H2BC3:16.5 RPS4Y2:16.5 AKT3:34.5
DIAZ_CHRONIC_MYELOGENOUS_LEUKEMIA_UP	-0.04846457	1329	3.933e-09	4.020e-06	CAB39:16.5 STAM:16.5 RBM39:16.5 TBPL1:16.5 PSMD10:76 SAV1:103
NIKOLSKY_BREAST_CANCER_7P22_AMPLICON	0.27003870	37	1.316e-08	1.003e-05	INTS1:203 GPER1:336 ZFAND2A:357 SNX8:722 MAD1L1:854 AP5Z1:942
MARTENS_TRETINOIN_RESPONSE_DN	-0.06179440	733	1.390e-08	1.003e-05	TRIM65:45 OR7G2:55 HDGF:77 IRAK3:105 ATG4D:107 CHMP2A:119
REACTOME_INFECTIOUS_DISEASE	-0.05651316	876	1.610e-08	1.045e-05	CUL3:16.5 STAM:16.5 H2AC18:16.5 H2BC3:16.5 RPS4Y2:16.5 AKT3:34.5
REACTOME_POST_TRANSLATIONAL_PROTEIN_MODI	-0.04114297	1379	3.715e-07	2.027e-04	CUL3:16.5 STAM:16.5 H2AC18:16.5 TRAPPC2:16.5 WDR48:16.5 COPZ2:16.5
REACTOME_REGULATION_OF_EXPRESSION_OF_SLI	-0.12190487	146	3.746e-07	2.027e-04	RPS4Y2:16.5 PSMD10:76 GSPT2:98 RPLP0:232 PSMB6:282 PSMA4:492
PUJANA_BRCA1_PCC_NETWORK	-0.03907607	1514	4.714e-07	2.355e-04	RAP1B:16.5 TBPL1:16.5 SNRPC:16.5 FAM120A:41.5 MMP20:48 BRAF:67
HSIAO_HOUSEKEEPING_GENES	-0.07790012	349	5.994e-07	2.780e-04	H2AC18:16.5 PSD:64 CD164:65 STOM:176 AARS1:184 RPLP0:232
SPIELMAN_LYMPHOBLAST_EUROPEAN_VS_ASIAN_D	-0.05830100	573	1.977e-06	8.560e-04	CD164:65 YME1L1:106 CNOT2:181 ARPC5L:196 CCNC:216 STK17A:218
DANG_BOUND_BY_MYC	-0.04443417	1001	2.237e-06	9.080e-04	RBM39:16.5 H2AC18:16.5 CD164:65 PSMD10:76 HMOX1:122 CNPY2:163
BENPORATH_MYC_MAX_TARGETS	-0.05146216	727	2.511e-06	9.592e-04	RBM39:16.5 H2AC18:16.5 CD164:65 PSMD10:76 SAV1:103 MED20:142
REACTOME_UB_SPECIFIC_PROCESSING_PROTEASE	-0.09202678	214	3.566e-06	1.286e-03	H2AC18:16.5 WDR48:16.5 H2BC3:16.5 PSMD10:76 USP17L24:209 H2AC12:233
REACTOME_TRANSCRIPTIONAL_REGULATION_BY_R	-0.08916174	221	5.046e-06	1.725e-03	H2AC18:16.5 H2BC3:16.5 PSMD10:76 KMT2D:172 GPAM:178 PSMB6:282
REACTOME_PROCESSING_OF_CAPPED_INTRON_CON	-0.08315536	250	6.116e-06	1.986e-03	RBM39:16.5 RBM22:16.5 SNRPC:16.5 PDCD7:54 CHTOP:128 MTREX:135
REACTOME_METABOLISM_OF_AMINO_ACIDS_AND_D	-0.07042464	347	6.804e-06	2.008e-03	NQO1:16.5 RPS4Y2:16.5 PSMD10:76 BCKDK:91 RPLP0:232 OAZ3:235
REACTOME_SARS_COV_1_INFECTION	-0.11858563	121	6.694e-06	2.008e-03	RPS4Y2:16.5 CHMP2A:119 PARP9:167 NMI:201 ST3GAL4:289 YWHAZ:437
REACTOME_RUNX1_REGULATES_TRANSCRIPTION_O	-0.12133253	114	7.708e-06	2.176e-03	H2AC18:16.5 H2BC3:16.5 PSMD10:76 PSMB6:282 H2BC10:447 PSMA4:492
REACTOME_RRNA_PROCESSING	-0.09366094	182	1.334e-05	3.609e-03	RPS4Y2:16.5 MTREX:135 EXOSC9:198 RPLP0:232 WDR3:498 UTP14A:538
FLORIO_NEOCORTEX_BASAL_RADIAL_GLIA_DN	0.09138853	186	1.749e-05	4.542e-03	MKI67:14 DLGAP5:27 PARPBP:76 KIF18A:78 SGO2:135 KIF22:192
DAZARD_RESPONSE_TO_UV_SCC_UP	-0.12310743	100	2.115e-05	5.282e-03	CCNC:216 TACSTD2:225 KYAT3:379 YWHAZ:437 PMAIP1:548 MAP2K1:558
REACTOME_CYCLIN_A_CDK2_ASSOCIATED_EVENTS	-0.13648570	80	2.452e-05	5.897e-03	AKT3:34.5 PSMD10:76 PSMB6:282 PSMA4:492 MNAT1:728 RBL2:790
BRUINS_UVC_RESPONSE_LATE	-0.03767346	1077	3.311e-05	7.194e-03	ARL8B:16.5 CAB39:16.5 MEMO1:16.5 TRAPPC2:16.5 COPZ2:16.5 TCF19:50
REACTOME_SRP_DEPENDENT_COTRANSLATIONAL_P	-0.12561462	92	3.144e-05	7.194e-03	SEC61A2:16.5 RPS4Y2:16.5 RPLP0:232 RPL36:769 SSR3:891 RPL3L:897
REACTOME_TRANSCRIPTIONAL_REGULATION_BY_R	-0.11112684	117	3.324e-05	7.194e-03	AKT3:34.5 PSMD10:76 PSMB6:282 RUNX2:429.5 PSMA4:492 FBXW7:508
REACTOME_INFLUENZA_INFECTION	-0.10309685	132	4.354e-05	9.122e-03	RPS4Y2:16.5 RPLP0:232 KPNA4:296 SLC25A6:299 NUP35:541 SEC13:623
REACTOME_TCF_DEPENDENT_SIGNALING_IN_RESP	-0.08093347	214	4.573e-05	9.279e-03	CUL3:16.5 H2AC18:16.5 H2BC3:16.5 PSMD10:76 KMT2D:172 CSNK1G2:257
REACTOME_HIV_INFECTION	-0.08053527	215	4.788e-05	9.422e-03	PSMD10:76 CHMP2A:119 TAF15:159 PSMB6:282 SLC25A6:299 LCK:360
REACTOME_HCMV_LATE_EVENTS	-0.11552157	103	5.133e-05	9.805e-03	H2AC18:16.5 H2BC3:16.5 CHMP2A:119 H2AC12:233 H2BC10:447 NUP35:541
THUM_SYSTOLIC_HEART_FAILURE_UP	-0.05969294	389	5.497e-05	1.020e-02	ARL8B:16.5 CP:102 IRF8:109 ZNF672:200 KPNA4:296 FAS:361
REACTOME_SPERM_MOTILITY_AND_TAXES	0.38418630	9	6.567e-05	1.057e-02	CATSPER2:99 CATSPERB:536 CATSPER3:587 CATSPERD:760 CATSPERG:1188 HVCN1:210
REACTOME_SIGNALING_BY_ROBO_RECEPTORS	-0.08404975	188	7.161e-05	1.057e-02	RPS4Y2:16.5 PSMD10:76 GSPT2:98 RPLP0:232 PSMB6:282 PSMA4:492
REACTOME_OTHER_SEMAPHORIN_INTERACTIONS	0.27149927	18	6.661e-05	1.057e-02	SEMA7A:97 ITGB1:346 PLXNC1:766 PLXNA4:842 PTPRC:1714 SEMA4D:2068

DisGeNET Top pathways by non-permulation

H2AC18:16.5 H2BC3:16.5 GPAM:178 STAG2:347 H2BC10:447 SP1:593

RPS4Y2:16.5 GSPT2:98 RPLP0:232 RPL36:769 RPL3L:897 RPS3:948.5

REACTOME_ESTROGEN_DEPENDENT_GENE_EXPRESS -0.10093025 131 6.696e-05 1.057e-02

Geneset	stat	num.genes	pval	p.adj	gene.vals
Cerebral Ischemia	-0.07316557	240	9.904e-05	4.867e-01	ASIC1:16.5 KCNK3:56 REN:132 KCNJ13:171 BDNF:193 CREB1:221
Esophagitis	-0.14786041	58	9.914e-05	4.867e-01	NQO1:16.5 PDLIM3:188 PLCL1:242 YWHAZ:437 IL10:581 GPHN:900.5
Bell Palsy	0.11296138	87	2.742e-04	4.921e-01	SMCHD1:293 COL6A1:294 DES:402 DNA2:425 SLC18A3:454 MGME1:485
Erythrokeratoderma	0.16605376	41	2.353e-04	4.921e-01	DSP:51 DSG2:195 KRT17:196 DES:402 SLURP1:458 GJB4:521
Leukokeratosis	0.21915410	23	2.750e-04	4.921e-01	KRT17:196 CTTN:279 CTC1:756 DKC1:1209 KRT16:1278 ACD:1302
Thyroid Agenesis	-0.20101517	27	3.007e-04	4.921e-01	FOXE1:70 THRA:346 PRKAR1A:637 TSHB:870 LHX4:1055 DUOX2:1201
Stiff-Person Syndrome	-0.27551525	14	3.581e-04	5.023e-01	GAD1:63 GP6:514.5 GPHN:900.5 NUDT10:2115 SLC6A5:2189 HLA-DQB1:2574
Anaphylaxis (non medication)	-0.16535181	38	4.218e-04	5.176e-01	CD63:306 F9:423 IL10:581 HACD1:668 STAT6:823 TM7SF2:1153
Abnormality of the skull	0.11904777	68	6.928e-04	5.233e-01	CENPJ:337 ESCO2:567 CEP152:831 CENPE:846 IFT122:880 RBBP8:1122
Facial Paresis	0.10632062	88	5.729e-04	5.233e-01	SMCHD1:293 COL6A1:294 DES:402 DNA2:425 SLC18A3:454 MGME1:485
Hyperdiploid B Acute Lymphoblastic Leuke	-0.18773742	28	5.865e-04	5.233e-01	CEBPE:154 KRAS:970 CD19:991 ASPG:1413 PIP4K2A:1568 TNF:1615
Long Qt Syndrome 2	0.29593776	11	6.773e-04	5.233e-01	GOLGA2:250 KCNH2:663 ALG10:923 KCNQ1:2351 SCN5A:3466 KCNE1:3620
Sarcoma	-0.04123981	605	5.862e-04	5.233e-01	NQO1:16.5 BRAF:67 HDGF:77 LIN28A:78 IRF8:109 MITF:111
Facial muscle weakness of muscles innerv	0.10447054	84	9.434e-04	6.617e-01	SMCHD1:293 COL6A1:294 DES:402 DNA2:425 SLC18A3:454 MGME1:485
46, XX Testicular Disorders of Sex Devel	-0.24074597	9	1.238e-02	6.715e-01	SOX10:694 FOXL2:1561 NR5A1:2066 SOX9:3151 AR:3201 RSPO1:4096
Bulbocavernosus Reflex, Decreased	0.32153499	5	1.277e-02	6.715e-01	PMP22:1991 CHRNB2:2399 TTPA:2852 ABAT:4487 ATXN7:5003 NA
Child Development Disorders, Specific	0.15439931	23	1.038e-02	6.715e-01	CHRNA4:732 DRD2:964 KCNT1:1030 KCNQ2:1366 SLC6A8:1549 SHANK3:1682
Conjunctivitis, recurrent	-0.11712136	39	1.140e-02	6.715e-01	BLNK:551 ERCC6:765 CD19:991 TP63:1069 XPC:1332 SAT1:1846
Creatinine measurement, serum (procedure	0.09668360	63	7.993e-03	6.715e-01	WDR72:93 ALMS1:194 PTPN12:280 CACNA1S:283 CDK12:382 SPATA5L1:520
Epilepsy, Rolandic	0.13180789	30	1.248e-02	6.715e-01	KCNQ3:240 SNIP1:1205 RBFOX3:1299 KCNQ2:1366 ADAMTS4:1402 SHANK3:168
Keratoderma, Palmoplantar, Diffuse	0.23389964	12	5.024e-03	6.715e-01	SLURP1:458 RHBDF2:1174 KRT16:1278 TSC1:2208 KRT9:3404 SNAP29:3838
Mental Retardation, Psychosocial	0.06871815	130	6.901e-03	6.715e-01	SHANK2:4 NSD1:62 CALCA:109 AP4E1:230 NDST1:365 CACNA1G:528
Neoplasm Recurrence, Local	-0.12910220	36	7.366e-03	6.715e-01	LIMD2:72 YWHAZ:437 CXCL9:1338 TPD52:1509 SOX2:1797.5 DNMT3A:2024
Nephritis, Interstitial	-0.16242781	31	1.753e-03	6.715e-01	APOA1:286 BAX:877 CCL7:988 CYP2C9:990 TM7SF2:1153 CCL1:1704
ALMOPLANTAR KERATODERMA, NONEPIDERMOLYT	0.31773886	7	3.599e-03	6.715e-01	KRT80:222 RHBDF2:1174 KRT16:1278 TSC1:2208 AQP5:4073 KRT1:5086
Periodontitis, Juvenile	0.08736900	85	5.405e-03	6.715e-01	MUC2:342 NOD2:571 CAMP:920 HTRA1:995 IL12RB2:1019 AKT1:1040
PERIODONTITIS, LOCALIZED AGGRESSIVE	0.39580980	4	6.111e-03	6.715e-01	MYOM2:1389 CLU:1989 DGKA:2155 IL1B:2255 NA NA
Psychomotor retardation, mild	0.17607902	19	7.887e-03	6.715e-01	RNF168:117 CENPJ:337 CEP152:831 CENPE:846 RBBP8:1122 ATR:1306
Reflex, Abnormal	0.32153499	5	1.277e-02	6.715e-01	PMP22:1991 CHRNB2:2399 TTPA:2852 ABAT:4487 ATXN7:5003 NA
Reflex, Acoustic, Abnormal	0.32153499	5	1.277e-02	6.715e-01	PMP22:1991 CHRNB2:2399 TTPA:2852 ABAT:4487 ATXN7:5003 NA
Reflex, Anal, Absent	0.32153499	5		6.715e-01	PMP22:1991 CHRNB2:2399 TTPA:2852 ABAT:4487 ATXN7:5003 NA
Reflex, Anal, Decreased	0.32153499	5		6.715e-01	PMP22:1991 CHRNB2:2399 TTPA:2852 ABAT:4487 ATXN7:5003 NA
Reflex, Ankle, Abnormal	0.32153499	5		6.715e-01	PMP22:1991 CHRNB2:2399 TTPA:2852 ABAT:4487 ATXN7:5003 NA
Reflex, Ankle, Decreased	0.32153499	5	1.277e-02		PMP22:1991 CHRNB2:2399 TTPA:2852 ABAT:4487 ATXN7:5003 NA
Reflex, Biceps, Abnormal	0.32153499	5	1.277e-02		PMP22:1991 CHRNB2:2399 TTPA:2852 ABAT:4487 ATXN7:5003 NA
Reflex, Biceps, Absent	0.32153499	5		6.715e-01	PMP22:1991 CHRNB2:2399 TTPA:2852 ABAT:4487 ATXN7:5003 NA
Reflex, Biceps, Decreased	0.32153499	5		6.715e-01	PMP22:1991 CHRNB2:2399 TTPA:2852 ABAT:4487 ATXN7:5003 NA
Reflex, Corneal, Absent	0.32153499	5	1.277e-02		PMP22:1991 CHRNB2:2399 TTPA:2852 ABAT:4487 ATXN7:5003 NA
Reflex, Gag, Absent	0.32153499	5	1.277e 02 1.277e-02		PMP22:1991 CHRNB2:2399 TTPA:2852 ABAT:4487 ATXN7:5003 NA
Reflex, Gag, Decreased	0.32153499	5		6.715e-01	

MGI_Mammalian_Phenotype_Level_4 Top pathways by non-permulation

Geneset	stat	num.genes	pval	p.adj	gene.vals
MP0000467 abnormal esophagus morphology	0.13042352	42	3.538e-03	3.439e-01	IGHMBP2:322 ITGB1:346 ITGB4:406 BRCA1:669 EGFR:1249 RIPK4:1276
MP0000955 abnormal spinal cord	-0.05740173	211	4.615e-03	3.439e-01	CP:102 LRP8:164 ABCD1:237 RIMS1:245 AFG3L2:398 GRIA1:459
MP0004811 abnormal neuron physiology	-0.05741780	284	1.095e-03	3.439e-01	AKT3:34.5 GAD1:63 BRAF:67 LRP8:164 XRCC2:186 BDNF:193
MP0001502 abnormal circadian rhythm	0.11128155	49	7.225e-03	3.439e-01	PER2:3 TNC:557 PER1:578 RASD1:616 RAI1:712 MAGEL2:807
MP0000631 abnormal neuroendocrine gland	-0.08332869	92	6.043e-03	3.439e-01	HMX3:16.5 BRAF:67 THRA:346 SCG5:381 OTP:522 B4GALT1:720
MP0004142 abnormal muscle tone	-0.11952662	43	6.844e-03	3.439e-01	MOG:575 NFATC2:576 ERCC6:765 SLC7A7:819 PEX7:1483 DST:1711
MP0000749 muscle degeneration	0.14384471	36	2.884e-03	3.439e-01	PLEC:21 MYOF:243 CACNA1S:283 IGHMBP2:322 DES:402 PFKM:723
MP0002082 postnatal lethality	-0.02879610	926	5.592e-03	3.439e-01	HMX3:16.5 IRS1:43 NDRG3:59 BRAF:67 FOXE1:70 LIN28A:78
MP0010770 preweaning lethality	-0.02879610	926	5.592e-03	3.439e-01	HMX3:16.5 IRS1:43 NDRG3:59 BRAF:67 FOXE1:70 LIN28A:78
MP0002019 abnormal tumor incidence	-0.04037287	441	4.836e-03	3.439e-01	NQO1:16.5 AKT3:34.5 BRAF:67 SAV1:103 IRF8:109 SUV39H1:227
MP0002269 muscular atrophy	0.07248473	86	2.087e-02	5.525e-01	PLEC:21 CTH:242 CASQ1:277 ADARB1:290 IGHMBP2:322 ITGB1:346
MP0008961 abnormal basal metabolism	0.15294578	18	2.483e-02	5.525e-01	PER2:3 PER1:578 FTO:1418 HTR6:1647 NCOR1:2489 PTPN1:3672
MP0004036 abnormal muscle relaxation	0.10650263	40	2.009e-02	5.525e-01	CASQ1:277 ITGB1:346 DES:402 APOE:856 CLCN1:1117 NPR2:1482
MP0005381 digestive/alimentary phenotyp	0.06288275	111	2.310e-02	5.525e-01	IGHMBP2:322 MUC2:342 HSF1:560 SH3BP2:584 SLC27A4:770 TNS3:843
MP0002169 no abnormal phenotype	-0.02097726	1179	2.679e-02	5.525e-01	HMX3:16.5 AKT3:34.5 GAD1:63 BRAF:67 XRCC1:97 SNX2:99
MP0008775 abnormal heart ventricle	0.10236976	37	3.158e-02	5.525e-01	HIF3A:375 FSTL3:380 TNNT2:704 EGFR:1249 TTN:1492 SLC2A4:1493
MP0004087 abnormal muscle fiber	0.04144344	243	2.865e-02	5.525e-01	PLEC:21 XIRP2:70 CTH:242 MYOF:243 CASQ1:277 CACNA1S:283
MP0009672 abnormal birth weight	0.07494056	62	4.210e-02	5.525e-01	XIRP2:70 KIF1A:300 DHCR7:792 PLAGL1:906 LAMA1:939 AKT1:1040
MP0001286 abnormal eye development	-0.04662254	160	4.410e-02	5.525e-01	MITF:111 IKZF2:121 ABI2:246 EXT1:368 RHO:424 ZIC5:534
MP0000462 abnormal digestive system	0.11859357	30	2.484e-02	5.525e-01	HSF1:560 SLC27A4:770 TNS3:843 CLDN15:1211 APC:1871 LAMC2:2185
MP0000681 abnormal thyroid gland	-0.09694235	44	2.652e-02	5.525e-01	FOXE1:70 THRA:346 FAS:361 RUNX2:429.5 HOXA5:625 PAX9:1124
MP0000689 abnormal spleen morphology	-0.03090261	552	1.700e-02	5.525e-01	BRAF:67 CCR2:75 CP:102 IRF8:109 MITF:111 HMOX1:122
MP0004145 abnormal muscle electrophysio	0.16906051	15	2.352e-02	5.525e-01	CASQ1:277 KCNH2:663 CLCN1:1117 MUSK:1681 ENTPD1:1802 CACNG1:22
MP0005075 abnormal melanosome morpholog	0.12918043	21	4.070e-02	5.525e-01	ADAMTS20:25 KRT17:196 GPR143:361 RXRA:2231 HPS1:2309 LYST:2541
MP0003956 abnormal body size	-0.01767078	1482	4.361e-02	5.525e-01	NQO1:16.5 RAP1B:16.5 IRS1:43 BRAF:67 CCR2:75 BCKDK:91
MP0008260 abnormal autophagy	0.14839379	16	4.007e-02	5.525e-01	NOD2:571 LRRK2:824 CLCN7:1233 ATG4B:1974 PMP22:1991 PTHLH:4138
MP0002081 perinatal lethality	-0.02195086	844	4.193e-02	5.525e-01	RAP1B:16.5 GAD1:63 NPHS2:93 HMOX1:122 TRIP11:174 XRCC2:186
MP0002083 premature death	-0.02428955	821	2.605e-02	5.525e-01	STAM:16.5 IRS1:43 GAD1:63 BRAF:67 CCR2:75 BCKDK:91
MP0003252 abnormal bile duct	0.13791757	25	1.716e-02	5.525e-01	ABCB11:726 ATXN2:1094 PCTP:1244 SCP2:2223 PKHD1:2344 CASP8:295
MP0001145 abnormal male reproductive	-0.02929892	457	3.767e-02	5.525e-01	TBPL1:16.5 HMOX1:122 DMRT1:202 PICK1:239 THRA:346 SCG5:381
MP0001873 stomach inflammation	0.13042768	21	3.879e-02	5.525e-01	SH3BP2:584 IFNG:1395 IL4:2114 CTLA4:2161 TOP3B:3142 AIRE:3431
MP0000163 abnormal cartilage morphology	-0.03795365	250	4.222e-02	5.525e-01	IRS1:43 MITF:111 TRIP11:174 CLEC2D:259 COL11A2:305 THRA:346
MP0002873 normal phenotype	-0.02082545	1184	2.767e-02	5.525e-01	HMX3:16.5 AKT3:34.5 GAD1:63 BRAF:67 XRCC1:97 SNX2:99
MP0010769 abnormal survival	-0.02180342	1016	2.955e-02		HMX3:16.5 IRS1:43 NDRG3:59 BRAF:67 FOXE1:70 LIN28A:78
MP0010768 mortality/aging	-0.02111062	1039	3.356e-02	5.525e-01	HMX3:16.5 IRS1:43 NDRG3:59 BRAF:67 FOXE1:70 LIN28A:78
MP0005375 adipose tissue phenotype	-0.07624046	66	3.296e-02		BCKDK:91 TNKS2:303 PRKCI:337 SCG5:381 BGLAP:571 PRKAR1A:637
MP0000778 abnormal nervous system	-0.06142323	121	2.063e-02		AKT3:34.5 ABI2:246 EXT1:368 GAP43:382.5 EOMES:849 PURA:908
MP0002152 abnormal brain morphology	-0.02076955	968	4.195e-02	5.525e-01	HMX3:16.5 AKT3:34.5 GAD1:63 BRAF:67 BCKDK:91 SNX2:99
MP0002210 abnormal sex determination	-0.03035145	350		6.302e-01	TBPL1:16.5 HMOX1:122 DMRT1:202 SUV39H1:227 PICK1:239 THRA:346
MP0010155 abnormal intestine physiology	-0.04798876	136		6.302e-01	CCR2:75 SAV1:103 CEBPE:154 IL22:322 MAP3K7:338 THRA:346

tissue_specific Top pathways by non-permulation

Geneset	stat	num.genes	pval	p.adj	gene.vals
leg.skin	0.06510063	288	1.709e-04	9.228e-03	PKP1:12 INAVA:34 BNC1:40 DSP:51 TRIM29:56 PSAPL1:121
cerebral.cortex	0.08534221	110	2.074e-03	3.733e-02	ADGRB1:63 NCAN:82 KIF1A:300 DPYSL4:470 POU6F2:791 HECW1:1007
EBV.lymphocyte	0.03511128	753	1.477e-03	3.733e-02	SORL1:6 MKI67:14 DLGAP5:27 ZNF267:67 ATAD2:72 PARPBP:76
suprapubic.skin	0.05164577	259	4.613e-03	6.228e-02	PKP1:12 BNC1:40 PSAPL1:121 AADACL2:171 NKPD1:186 KRT17:196
eye.development	-0.07446193	69	3.289e-02	3.552e-01	MITF:111 SP1:593 RAX:709 CHRDL1:1267 FGF1:1477 FOXC1:1481
blood	-0.02828284	347	7.416e-02	6.674e-01	LIMD2:72 CEBPE:154 SLC25A37:203 C5AR2:211 S1PR4:269 TNFAIP6:278
endocervix	0.05579029	79	8.740e-02	6.742e-01	MRGPRE:2 ANGPT4:45 ELFN1:65 COL24A1:91 KIF26A:120 ZNF516:177
cerebellar.hemisphere	-0.02024614	542	1.147e-01	7.743e-01	NDRG3:59 CDH7:85 CTXN2:155 SEZ6L:177 BDNF:193 UNCX:195
adrenal.gland	-0.03586957	116	1.840e-01	7.808e-01	KCNK3:56 FNDC4:133 TMEM52:258 C4B:409 FDXR:514.5 HTR2B:621
amygdala	-0.06403002	9	5.060e-01	7.808e-01	LHFPL3:34.5 BCAN:2016 NEUROD2:4143 SLC38A8:5756 SLC17A7:6347 NEUROD6:7696
atrium.auricle	-0.03135908	95	2.926e-01	7.808e-01	SYNPO2L:44 SBK3:348 LMOD3:353 ADPRHL1:732 RPL3L:897 KLHL31:968
bladder	-0.05801266	30	2.719e-01	7.808e-01	TMC7:862 UPK1A:1455 SIGLEC15:2287 PLA2G4A:2816 AKR1B10:2837 CYP4B1:3255
breast	0.06554570	20	3.105e-01	7.808e-01	TNN:456 ANKRD30A:629 THRSP:1155 ABCB5:2321 KRT5:3324 NPY2R:3763
Brodmann.area.24	-0.06988017	33	1.652e-01	7.808e-01	GAD1:63 HRK:272 CRH:1565 NCS1:2762.5 NPTXR:2932 FAM107A:3028
C1.spinal.cord	-0.02138066	194	3.081e-01	7.808e-01	PIEZO2:73 ANKS1B:95 MDGA2:230 PLCL1:242 MOG:575 HSPA2:595
caudate.nucleus	-0.07159151	28	1.902e-01	7.808e-01	ACBD7:366 SLC1A2:982 RGS14:2033 PPP1R1B:2459 SYNDIG1L:2742 SLC35D3:3046
cerebellum	-0.01138126	409	4.372e-01	7.808e-01	ASIC1:16.5 RGS11:108 BRSK2:115 PRAG1:165 UNCX:195 SEMA6C:240
ectocervix	-0.03986128	27	4.738e-01	7.808e-01	ADAMTSL5:652 PRLR:1772 ADRA2A:1956 FGF10:3141 CPXM1:5277 HOXD13:5626
esophagogastric.junction	-0.07928404	9	4.103e-01	7.808e-01	HOXA4:1306 COL4A5:3299 ADCY5:3789 GADL1:6176 CHRM3:6994 NKX6-1:9167
esophagus.mucosa	0.01287609	263	4.768e-01	7.808e-01	PKP1:12 BNC1:40 ADH7:60 LAD1:66 FAM83H:234 RNF222:345
fallopian.tube	-0.02758934	60	4.608e-01	7.808e-01	TCF23:553 HOXA5:625 RARRES1:757 CCDC71L:810 CFAP73:1257 PAGE4:1938
hippocampus.proper	-0.07244970	13	3.659e-01	7.808e-01	HRK:272 NEUROG3:4029 NEUROD2:4143 NTS:4886 FEZF2:5608 SLC17A7:6347
hypothalamus	-0.02203188	78	5.024e-01	7.808e-01	CTXN2:155 CALCR:260 OTP:522 ADCYAP1:697 CENPVL1:967 CALY:1165
liver	-0.01390833	399	3.480e-01	7.808e-01	UGT2B7:82 CP:102 FGB:285 APOA1:286 ALDH8A1:288 INSIG1:295
lung	0.02591768	161	2.594e-01	7.808e-01	SFTPB:423 SCGB3A1:618 FCN3:641 TFEC:706 BPIFA1:784 HGF:817
minor.salivary.gland	-0.03027475	91	3.198e-01	7.808e-01	AMTN:46 TMPRSS11E:168 BPIFB2:569 ENTPD3:589 OPRPN:635 SLC6A14:691
pancreas	-0.01976626	118	4.603e-01	7.808e-01	TMEM52:258 SHISAL2B:279 SLC4A4:613 SCTR:687 PDIA2:714 GPHA2:1131
sigmoid.colon	0.06062623	51	1.349e-01	7.808e-01	DES:402 HDAC4:537 TACR2:615 MRGPRD:666 NTSR1:958 TES:1317
skeletal.muscle	0.02416037	258	1.859e-01	7.808e-01	MYH2:16 PPP1R3A:46 XIRP2:70 MYBPC2:268 CASQ1:277 CACNA1S:283
spleen	-0.01127787	367	4.646e-01	7.808e-01	VPREB3:53 LIMD2:72 CCR2:75 IRAK3:105 HMOX1:122 CD180:329
stomach	0.03256159	99	2.647e-01	7.808e-01	MYH13:89 PIK3C2G:107 PSAPL1:121 EPS8L3:251 CAPN8:316 TMED6:416
thyroid	0.01498167	176	4.959e-01	7.808e-01	WDR72:93 PLA2R1:227 GOLGA8N:291 ZNF486:341 TLE6:344 HIRA:435
ansformed.skin.fibroblast	-0.01541238	276	3.833e-01	7.808e-01	NQO1:16.5 IRS1:43 PCDHGA10:79 RCN3:100 RUNX2:429.5 AJUBA:444
uterus	-0.04110669	63	2.603e-01	7.808e-01	LINGO2:302 LIPI:385 WT1:433 TCF23:553 GATA2:1084 SHISAL1:1820

5.725e-01 7.984e-01

5.833e-01 7.984e-01

5.911e-01 7.984e-01

6.082e-01 7.984e-01

119 2.254e-01 7.808e-01 PKP1:12 BNC1:40 RNF222:345 SLURP1:458 LCE3D:558 NOD2:571

38 5.304e-01 7.957e-01 BNC1:40 AADACL4:713 ITLN1:785 THRSP:1155 ADAMTS4:1402 FAM89A:1680

CCDC190:104 TIMP1:3495.5 PCOLCE2:4552 SUSD5:5134 CCN3:5331 SOST:5420

CUBN:28 CALCA:109 RNF186:260 CLRN3:648 KLHDC7A:658 TM4SF5:702

RGS2:646.5 SMTN:2093 TPM1:2227 PGM5:2996 NTN1:4471 KCNMB1:5729

SYNPO2L:44 LMOD3:353 HSPB7:693 ADPRHL1:732 RPL3L:897 HJV:1041

0.03231663

greater.omentum

esophagus.muscularis.mucosa -0.02935970

coronary.artery cortex.kidney

left.ventricle

0.02944769

-0.04211088

0.01389819

-0.01802245

28