

p.adj

5.382e-05 0.000e+00

permP

permPValue

0.000e+00

qValueNoperm

2.295e-02

qValuePerm

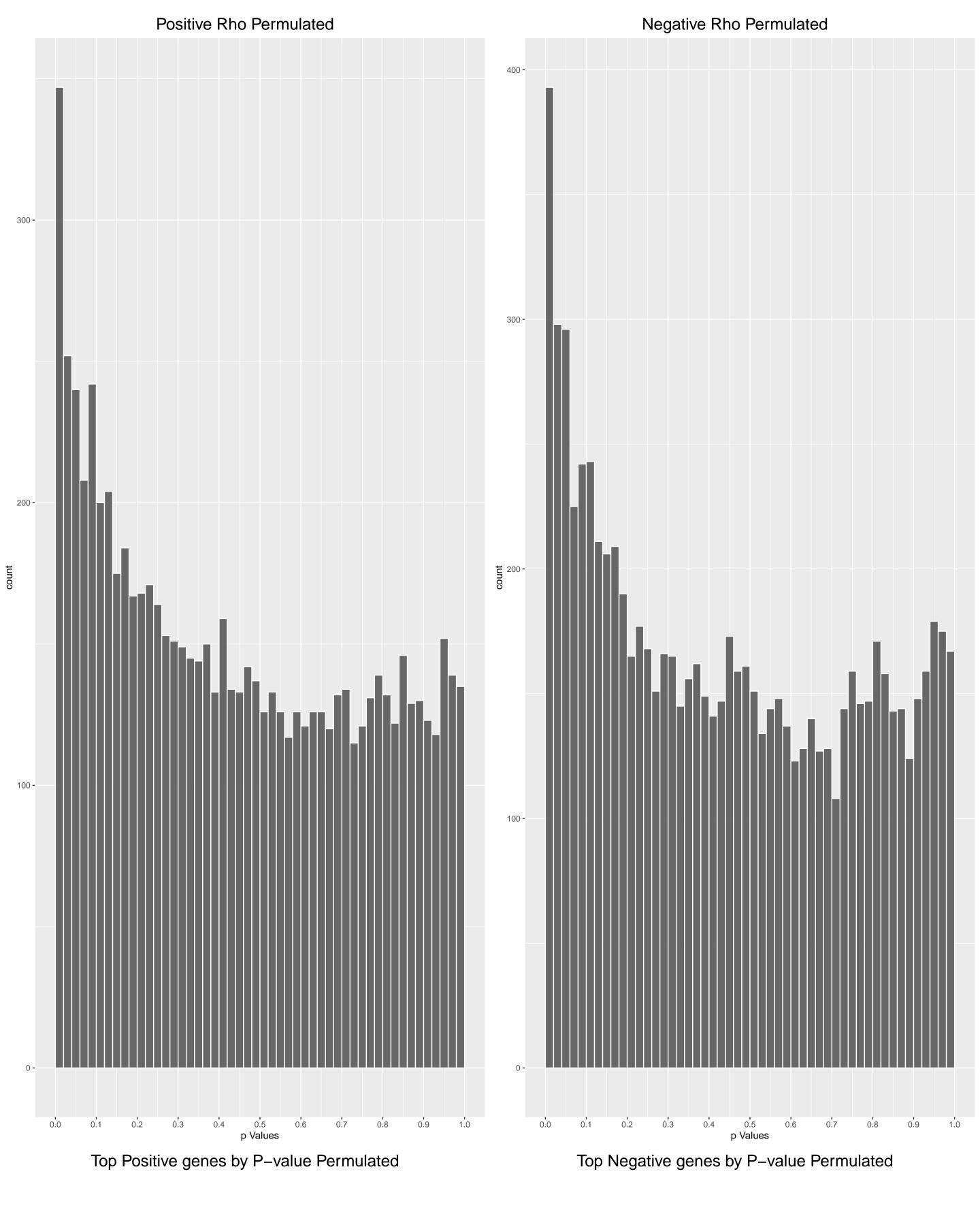
0.000e+00

Gene

PPFIA3

Rho

-5.484826 1.241630e-07



RAB8A	-3.921970	2.634834e-04	1.274e-02	3.444e-05	3.444e-05	6.049e-01	1.076e-0
ABCB1	-4.422030	2.933337e-05	2.898e-03	4.486e-05	4.486e-05	2.845e-01	1.112e-0
HAS2	-4.641299	1.038676e-05	1.389e-03	5.919e-05	5.919e-05	1.844e-01	1.112e-0
RGPD8	-4.769531	5.539656e-06	8.714e-04	9.069e-05	9.069e-05	1.371e-01	1.514e-0
SDS	-4.446206	2.622010e-05	2.639e-03	1.417e-04	1.417e-04	2.655e-01	1.539e-0
FNBP4	-5.508997	1.082651e-07	4.873e-05	1.484e-04	1.484e-04	2.193e-02	1.539e-0
UBR2	-4.881997	3.150512e-06	5.867e-04	1.654e-04	1.654e-04	1.089e-01	1.539e-0
PROM1	-6.306251	8.576256e-10	1.390e-06	1.666e-04	1.666e-04	1.910e-03	1.539e-0
ABHD11	-5.146905	7.944563e-07	2.384e-04	2.050e-04	2.050e-04	7.132e-02	1.539e-0

PPFIA3 -5.484826 1.241630e-07 5.382e-05 0.000e+00 0.000e+00 2.295e-02 0.000e+00

P p.adj permP permPValue qValueNoperm qValuePerm

C1QTNF8	4.770376	5.516465e-06	8.714e-04	5.892e-05	5.892e-05	1.371e-01	1.112e-01
OVOL1	4.076234	1.373129e-04	8.240e-03	1.179e-04	1.179e-04	4.923e-01	1.539e-01
TACR2	5.843973	1.529109e-08	1.032e-05	1.314e-04	1.314e-04	6.969e-03	1.539e-01
CFAP45	5.595518	6.598918e-08	3.449e-05	1.471e-04	1.471e-04	1.790e-02	1.539e-01
ARHGEF12	5.174211	6.866275e-07	2.139e-04	1.901e-04	1.901e-04	6.666e-02	1.539e-01
VPS11	4.185160	8.548963e-05	5.894e-03	2.437e-04	2.437e-04	4.051e-01	1.539e-01
SFTPA1	4.345771	4.163610e-05	3.627e-03	3.058e-04	3.058e-04	3.159e-01	1.588e-01
PDCL	4.634848	1.071601e-05	1.412e-03	3.080e-04	3.080e-04	1.859e-01	1.588e-01

ANKRD35 6.627095 1.027075e-10 2.377e-07 1.944e-05 1.944e-05

DNAH2 8.123462 1.359214e-15 2.202e-11 3.583e-05 3.583e-05

Rho P p.adj permP permPValue qValueNoperm qValuePerm

5.502e-04

3.568e-07

9.733e-02

1.076e-01

Geneset	stat	num.genes	pval	p.adj	gene.vals
Cilium Movement Involved In Cell Motilit	0.4327000	7	7.355e-05	9.907e-03	TEKT2:243 GAS8:333 TEKT1:397 TEKT4:832 TEKT5:1091 TEKT3:2070
RIG-I Signaling Pathway (GO:0039529)	0.4066996	4	4.845e-03	1.450e-01	TRIM25:86 RNF135:683 OAS3:2142 PHB2:3254 NA NA
snRNA Modification (GO:0040031)	-0.3982016	4	5.811e-03	1.630e-01	NHP2:664 MEPCE:1041 METTL4:2120 METTL16:2700 NA NA
Striated Muscle Hypertrophy (GO:0014897)	0.3974506	4	5.904e-03	1.631e-01	HTR2B:174 MYOC:1067 TCAP:2410 RYR2:3117 NA NA
snRNA Transcription By RNA Polymerase II	-0.3933399	4	6.438e-03	1.660e-01	SNAPC5:205 ICE2:540 ZC3H8:2547 SNAPC1:3569 NA NA
Glucocorticoid Biosynthetic Process (GO:	-0.3930256	3	1.838e-02	2.845e-01	CYP17A1:643 CYP11A1:1144 CYP21A2:3366 NA NA NA
Negative Regulation Of Leukocyte Prolife	-0.3909163	5	2.467e-03	1.099e-01	IL33:138 LYN:264 ENPP3:440 GREM1:1056 TNFAIP3:6899 NA
SA Node Cell Action Potential (GO:008601	0.3895723	5	2.554e-03	1.106e-01	SCN3B:70 SCN5A:315 CACNA1G:909 CACNA1D:1118 HCN4:6695 NA
Hepoxilin Biosynthetic Process (GO:00511	0.3894269	4	6.986e-03	1.729e-01	ALOX15B:393 ALOXE3:871 ALOX15:873 ALOX12B:5173 NA NA
Hepoxilin Metabolic Process (GO:0051121)	0.3894269	4	6.986e-03	1.729e-01	ALOX15B:393 ALOXE3:871 ALOX15:873 ALOX12B:5173 NA NA
Negative Regulation Of Gene Expression V	-0.3824887	5	3.056e-03	1.160e-01	USP7:410 HELLS:1164 UHRF2:1205 UHRF1:2635 ZNF445:4002 NA
Intracellular Sequestering Of Iron Ion (-0.3736859	3	2.498e-02	3.109e-01	SRI:1130 FTH1:1336 FTMT:3594 NA NA NA
Cellular Response To Leptin Stimulus (GO	-0.3723909	6	1.583e-03	7.973e-02	UGCG:655 STAT3:795 SIRT1:995 LEPR:1091 NR4A3:4201 LEP:4562
Regulation Of Endodeoxyribonuclease Acti	-0.3713529	7	6.679e-04	4.443e-02	HMGB1:921 SIRT1:995 GZMA:1536 PRKCD:1678 RPS3:2046 DDX11:2091
Cellular Response To UV-A (GO:0071492)	0.3706472	9	1.179e-04	1.444e-02	MME:362 TIMP1:420 MMP9:548 MMP3:596 OPN1SW:1300 OPN3:2066
Positive Regulation Of Mast Cell Activat	-0.3663043	4	1.117e-02	2.249e-01	TSLP:116 SPHK2:505 NECTIN2:3754 NR4A3:4201 NA NA
Chitin Catabolic Process (GO:0006032)	0.3658710	2	7.310e-02	4.439e-01	CTBS:1703 CHIT1:2715 NA NA NA NA
Chitin Metabolic Process (GO:0006030)	0.3658710	2	7.310e-02	4.439e-01	CTBS:1703 CHIT1:2715 NA NA NA NA
Serine Family Amino Acid Biosynthetic Pr	-0.3651139	10	6.391e-05	8.830e-03	SRR:68 SEPHS2:275 SERINC3:278 CTH:407 SERINC5:874 PSPH:1373
Positive Regulation Of Toll–Like Recepto	0.3548468	3	3.328e-02	3.448e-01	PTPN22:424 RSAD2:2707 SLC15A4:4075 NA NA NA
Regulation Of Toll–Like Receptor 7 Signa	0.3548468	3	3.328e-02	3.448e-01	PTPN22:424 RSAD2:2707 SLC15A4:4075 NA NA NA
Regulation Of Heterochromatin Formation	-0.3547256	7	1.154e-03	6.757e-02	SAMD1:1252 L3MBTL3:1732 CDK2:2002 TPR:2108 KDM1A:2776 MACROH2A1:
Cellular Response To Caffeine (GO:007131	0.3535853	5	6.177e-03	1.658e-01	RYR3:229 CASQ2:1175 RYR2:3117 RYR1:3384 SLC8A1:4212 NA
Response To Caffeine (GO:0031000)	0.3535853	5	6.177e-03	1.658e-01	RYR3:229 CASQ2:1175 RYR2:3117 RYR1:3384 SLC8A1:4212 NA
Regulation Of Monoatomic Anion Transport	-0.3533639	5	6.210e-03	1.658e-01	CA2:242 RAB11B:343 STC1:689 PDZK1:4901 ATP8B1:5660 NA
TRAIL-activated Apoptotic Signaling Path	-0.3528443	3	3.428e-02	3.456e-01	ZDHHC3:1612 SPI1:1683 FADD:3761 NA NA NA
Organic Hydroxy Compound Catabolic Proce	-0.3503321	6	2.960e-03		HSD17B6:11 FGF23:742 LCT:1677 CYP24A1:2502 LDHD:3551 PDXP:5920
Negative Regulation Of CD8–positive, Alp	0.3503057	6	2.962e-03	1.160e-01	SOCS1:361 ZBTB7B:831 DAPL1:2341 VSIR:3468 SLC4A2:3855 HFE:4005
Regulation Of Relaxation Of Muscle (GO:1	-0.3483387	3	3.664e-02	3.571e-01	SRI:1130 NEUROG1:2456 TIFAB:3684 NA NA NA
Peptide Transport (GO:0015833)	0.3465613	4	1.637e-02		CDH17:1053 DISP1:1441 TAP2:2377 TAP1:5277 NA NA
Membrane Lipid Catabolic Process (GO:004	-0.3426956	7	1.690e-03	8.355e-02	ENPP2:102 PPT1:741 SMPD2:2321 MGST2:2544 NAGA:2701 SGPL1:3481
Axonemal Central Apparatus Assembly (GO:	0.3419322	5		1.895e-01	DNAJB13:626 SPAG17:1473 SPEF1:2508 RSPH9:2838 HYDIN:5615 NA
Inositol Metabolic Process (GO:0006020)	-0.3413715	6		1.316e-01	MIOX:234 PPIP5K1:266 IMPA2:1082 ISYNA1:1658 SLC5A3:5213 PPIP5K2:680
Glucocorticoid Metabolic Process (GO:000	-0.3400190	5		1.914e-01	CYP17A1:643 CYP11A1:1144 HSD11B2:3099 CYP21A2:3366 YWHAH:4567 N
Transmembrane Receptor Protein Tyrosine	0.3333004	4	2.096e-02		PTPRD:1284 PTN:2579 PTPRF:3200 TRIO:3947 NA NA
Leptin–Mediated Signaling Pathway (GO:00	-0.3298298	7	2.511e-03		UGCG:655 STAT3:795 SIRT1:995 LEPR:1091 MKKS:3718 LEP:4562
Cilium–Dependent Cell Motility (GO:00602	0.3282355	17		9.437e-04	DNAH2:2 DNAH17:15 TEKT2:243 GAS8:333 TEKT1:397 TEKT4:832
Valine Metabolic Process (GO:0006573)	-0.3272274	5	1.127e-02		HIBCH:428 BCAT1:481 BCAT2:596 ILVBL:6110 HIBADH:6319 NA
Copper Ion Import (GO:0015677)	0.3264548	6			STEAP4:922 STEAP2:1762 SLC31A2:2338 ATP7B:2734 SLC31A1:3544 STEAP3:
Negative Regulation Of cAMP-dependent Pr		6			PRKAR1A:465 SIRT1:995 PRKAR2A:1524 PKIB:2753 PRKAR2B:3870 PRKAR1B

EnrichmentHsSymbolsFile2 Top pathways by permulation

Geneset	stat	num.genes	pval	p.adj	gene.vals
MIKHAYLOVA_OXIDATIVE_STRESS_RESPONSE_VIA	-0.3972802	6	7.509e-04	1.988e-02	HSPB1:231 CALU:282 PGAM1:289 AKR1B1:2689 OAT:3241 CTSD:3245
REACTOME_TRAIL_SIGNALING	-0.3694706	5	4.218e-03	5.962e-02	CASP8:345 TNFSF10:370 CASP10:2968 CFLAR:3103 FADD:3761 NA
SASAI_TARGETS_OF_CXCR6_AND_PTCH1_DN	-0.3639744	7	8.529e-04	2.145e-02	OTX1:513 ADAM28:1687 PIP5K1A:2141 APOD:2179 DAZL:2229 MDK:2358
NIKOLSKY_BREAST_CANCER_21Q22_AMPLICON	0.3553845	14	4.142e-06	3.347e-04	COL6A1:125 SPATC1L:676 PCBP3:905 PCNT:949 DIP2A:1306 POFUT2:1574
REACTOME_MET_ACTIVATES_PTPN11	-0.3543166	5	6.069e-03	7.617e-02	PTPN11:714 GRB2:907 MET:1880 GAB1:3365 HGF:4918 NA
WP_DUAL_HIJACK_MODEL_OF_VIF_IN_HIV_INFEC	-0.3440852	7	1.617e-03	3.209e-02	RBX1:805 CUL5:1319 CBFB:2475 ELOC:2721 ELOB:2922 RUNX1:3128
WP_AFLATOXIN_B1_METABOLISM	0.3425762	2	9.332e-02	3.664e-01	EPHX1:1261 CYP1A2:3875 NA NA NA NA
BIOCARTA_TERT_PATHWAY	-0.3370366	8	9.623e-04	2.312e-02	MZF1:24 SP3:44 MYC:601 WT1:2000 TP53:2447 MAX:2480
SMID_BREAST_CANCER_RELAPSE_IN_PLEURA_UP	0.3360426	6	4.361e-03	6.053e-02	TENM3:111 CHN2:124 TPPP3:2531 GJA1:2632 SYNGR3:4611 CXCL14:6009
BERGER_MBD2_TARGETS	0.3316365	2	1.043e-01	3.863e-01	CELA2A:2326 TFF2:3162 NA NA NA NA
NIKOLSKY_BREAST_CANCER_17P11_AMPLICON	0.3310199	10	2.891e-04	1.008e-02	SLC47A1:40 ALDH3A2:715 ULK2:921 MAPK7:1307 EPN2:1956 RNF112:2616
REACTOME_LEUKOTRIENE_RECEPTORS	0.3305484	5	1.047e-02	1.071e-01	CYSLTR2:41 LTB4R:244 LTB4R2:1460 CYSLTR1:3033 GPR17:8999 NA
REACTOME_ERYTHROCYTES_TAKE_UP_OXYGEN_AND	-0.3283365	6	5.346e-03	6.999e-02	CA4:107 CA2:242 RHAG:3496 CA1:3512 AQP1:4278 SLC4A1:5011
REACTOME_MINERALOCORTICOID_BIOSYNTHESIS	-0.3279629	4	2.310e-02	1.751e-01	CGA:1616 HSD3B2:2812 LHB:3323 CYP21A2:3366 NA NA
REACTOME_PREDNISONE_ADME	-0.3267535	5	1.139e-02	1.127e-01	ABCB1:3 ALB:29 HSD11B1:54 HSD11B2:3099 SERPINA6:10826 NA
REACTOME_HIGHLY_SODIUM_PERMEABLE_POSTSYN	0.3265726	7	2.769e-03	4.574e-02	CHRNE:485 CHRND:819 CHRNA4:1131 CHRNB2:2625 CHRNB4:3070 CHRNA3:3732
GARGALOVIC_RESPONSE_TO_OXIDIZED_PHOSPHOL	-0.3231802	11	2.059e-04	7.859e-03	USP12:141 UGDH:542 ABHD3:991 SIRT1:995 RBBP6:1015 PIM1:1329
REACTOME_CHOLINE_CATABOLISM	-0.3219376	6	6.312e-03	7.875e-02	SLC44A1:368 DMGDH:1590 BHMT:1764 CHDH:3901 SARDH:4095 ALDH7A1:5563
REACTOME_TYPE_I_HEMIDESMOSOME_ASSEMBLY	0.3194070	11	2.442e-04	9.032e-03	PLEC:18 ITGB4:50 ITGA6:267 LAMC2:272 KRT14:507 LAMB3:2108
WP_LNCRNAMEDIATED_MECHANISMS_OF_THERAPEU	-0.3149905	6	7.536e-03	8.778e-02	ABCB1:3 TP53:2447 HIF1A:2449 BCL2L1:3568 CDKN1A:4590 WNT6:4885
HEIDENBLAD_AMPLIFIED_IN_BONE_CANCER	-0.3136956	7	4.049e-03	5.795e-02	MDM2:311 CCND2:480 FGF23:742 TSPAN31:2725 STK38L:3900 CDK4:4301
REACTOME_ESTABLISHMENT_OF_SISTER_CHROMAT	-0.3094044	11	3.802e-04	1.233e-02	STAG1:165 WAPL:653 STAG2:748 PDS5B:1430 SMC3:1839 ESCO1:1944
WP_NICOTINE_EFFECT_ON_CHROMAFFIN_CELLS	0.3092904	4	3.215e-02	2.126e-01	CACNA1G:909 CHRNB4:3070 CHRNA3:3732 CACNA1C:4724 NA NA
TURJANSKI_MAPK11_TARGETS	-0.3083739	5	1.693e-02	1.461e-01	MEF2C:1534 ELK1:1907 FOS:2213 MEF2A:4838 ATF2:5001 NA
WIEMANN_TELOMERE_SHORTENING_AND_CHRONIC_	-0.3064883	3	6.596e-02	3.096e-01	HMGCR:1194 NR1D2:2832 CCL5:5363 NA NA NA
REACTOME_MAPK1_ERK2_ACTIVATION	-0.3048755	9	1.538e-03	3.139e-02	MAP2K2:92 PTPN11:714 IL6:845 IL6ST:1603 JAK1:2874 TYK2:3793
REACTOME_CONJUGATION_OF_BENZOATE_WITH_GL	0.2996712	2	1.421e-01	4.413e-01	GLYATL3:1919 ACSM2B:4606 NA NA NA NA
WP_NIPBL_ROLE_IN_DNA_DAMAGE_CORNELIA_DE_	-0.2972222	7	6.461e-03	8.031e-02	CBX3:177 NIPBL:801 H2AX:1383 RNF8:2309 RNF168:3290 ATR:4070
NIKOLSKY_BREAST_CANCER_1Q21_AMPLICON	0.2947028	34	2.746e-09	5.484e-07	SCAMP3:321 THBS3:356 EFNA3:412 DCST1:538 RUSC1:587 PBXIP1:630
NIKOLSKY_BREAST_CANCER_19P13_AMPLICON	-0.2945734	5	2.253e-02	1.726e-01	NR2F6:1417 OCEL1:1659 MYO9B:1715 USHBP1:3229 USE1:8590 NA
WALLACE_PROSTATE_CANCER_DN	0.2916514	5	2.390e-02	1.783e-01	LAMA4:912 GJA1:2632 GPM6B:3142 RAP1B:4034 CAV2:6253 NA
BIOCARTA_RANMS_PATHWAY	-0.2915412	10	1.410e-03	2.970e-02	TPX2:217 NUMA1:922 KPNB1:1217 KPNA2:1908 KIF15:2464 RANBP1:2783
KORKOLA_CHORIOCARCINOMA	-0.2865071	4	4.718e-02	2.555e-01	CGA:1616 LHB:3323 TFPI:4300 LEP:4562 NA NA
REACTOME_GLUCOCORTICOID_BIOSYNTHESIS	-0.2855682	6	1.541e-02	1.377e-01	HSD11B1:54 CYP17A1:643 HSD3B2:2812 HSD11B2:3099 CYP21A2:3366 SERPINA6:10826
MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_1	-0.2851768	3	8.711e-02	3.543e-01	GATA1:579 TFE3:2600 WAS:7245 NA NA NA
REACTOME_ANDROGEN_BIOSYNTHESIS	-0.2850109	9	3.067e-03	4.876e-02	CYP17A1:643 HSD17B3:1092 CGA:1616 HSD3B2:2812 HSD17B12:3031 LHB:3323
WP_METHIONINE_METABOLISM_LEADING_TO_SULF	-0.2837163	11	1.120e-03	2.550e-02	GNMT:223 CTH:407 AHCY:903 CSAD:975 BHMT:1764 CDO1:4088
REACTOME_ELECTRIC_TRANSMISSION_ACROSS_GA	0.2836064	5	2.806e-02	1.965e-01	GJA10:38 PANX1:1629 PANX2:3760 GJC1:5773 GJD2:6420 NA
					W

DisGeNET Top pathways by permulation

6.861e-04 1.855e-02

5.148e-02 2.691e-01

IL12RB2:338 STAT3:795 IL6ST:1603 CANX:2437 IL27RA:2647 JAK1:2874

MBD1:1719 MET:1880 ETV1:4778 LHX2:5785 NA NA

REACTOME_INTERLEUKIN_35_SIGNALLING

CHOI_ATL_ACUTE_STAGE

-0.2830402

-0.2811314

Geneset	stat	num.genes	pval	p.adj	gene.vals
Diabetes-deafness syndrome maternally tr	-0.4540079	2	2.615e-02	3.330e-01	GCG:320 RAPGEF5:1120 NA NA NA NA
Color Blindness, Red	0.4388124	5	6.782e-04	6.460e-02	GNAT2:115 TEX28:423 OPN1LW:709 ATF6:1719 PDE6H:1964 NA
Spondylitis	-0.4303827	4	2.871e-03	1.461e-01	TNF:99 IL6:845 IL4:1133 VCAN:2299 NA NA
Congenital pyloric atresia	0.4246018	5	1.008e-03	8.912e-02	PLEC:18 ITGB4:50 ITGA6:267 LAMC2:272 COL17A1:5471 NA
Junctional split	0.4224851	6	3.385e-04	4.427e-02	PLEC:18 ITGB4:50 ITGA6:267 LAMC2:272 LAMB3:2108 LAMA3:4764
Localized vitiligo	-0.4203061	2	3.951e-02	3.887e-01	TNF:99 RBM45:2418 NA NA NA NA
Valvular disease	0.4129687	4	4.229e-03	1.700e-01	TIMP1:420 MMP9:548 TIMP2:2106 MMP2:2505 NA NA
Herlitz Disease	0.4071440	5	1.616e-03	1.117e-01	ITGB4:50 ITGA6:267 LAMC2:272 LAMB3:2108 LAMA3:4764 NA
Monilethrix	0.4042668	2	4.767e-02	4.079e-01	KRT80:303 DSG4:2753 NA NA NA NA
NOONAN SYNDROME 3	-0.4020566	5	1.848e-03	1.148e-01	SHOC2:459 SOS1:554 PTPN11:714 RAF1:835 KRAS:5235 NA
Neonatal alloimmune thrombocytopenia (NA	0.4008118	4	5.497e-03	1.909e-01	POU2F3:678 ITGB3:1325 PLA2G6:1975 PLA2G1B:2387 NA NA
Deficiency of monooxygenase	-0.4002087	2	4.995e-02	4.146e-01	CYP17A1:643 CYP24A1:2502 NA NA NA NA
X-Linked Infantile Nystagmus	0.3994022	3	1.657e-02	2.960e-01	FRMD7:179 CASK:885 GPR143:3782 NA NA NA
Angiokeratoma	-0.3980826	5	2.050e-03	1.221e-01	MANBA:259 VEGFA:482 GLA:720 DCAF7:1640 PTEN:5008 NA
T-lymphocyte immunodeficiency	0.3974587	6	7.472e-04	7.035e-02	SFTPA1:9 RAG1:43 CD3E:1166 SMARCAL1:1223 LBR:1624 SIPA1:5855
Chronic iridocyclitis	-0.3966144	2	5.204e-02	4.152e-01	IL6:845 RBM45:2418 NA NA NA NA
Bulla of lung	0.3949525	2	5.303e-02	4.152e-01	EPHX1:1261 TIMP2:2106 NA NA NA NA
Unilateral primary pulmonary dysgenesis	-0.3897480	5	2.542e-03	1.379e-01	TBX1:710 DGCR8:963 DGCR2:1105 DGCR6:1160 ESS2:4827 NA
Profound sensorineural hearing impairmen	0.3844221	4	7.748e-03	2.172e-01	RDX:391 CIB2:907 TRIOBP:2685 MYO15A:3438 NA NA
C3 Glomerulonephritis	0.3812874	3	2.217e-02	3.178e-01	CFHR5:1077 C3:1835 CFB:2798 NA NA NA
Papillary transitional cell carcinoma	-0.3810012	4	8.312e-03	2.198e-01	EGF:263 VEGFA:482 TP53:2447 ERBB2:4396 NA NA
Chilblain lupus 1	-0.3801020	3	2.259e-02	3.199e-01	GZMA:1536 TREX1:1848 SAMHD1:2257 NA NA NA
Small anterior fontanelle	-0.3793805	3	2.285e-02	3.199e-01	ORC1:736 MYCN:959 ATR:4070 NA NA NA
Focal Dermal Hypoplasia	-0.3769939	7	5.521e-04	5.616e-02	ALB:29 CYP26C1:245 TWIST2:820 GC:938 HCCS:2312 WNT3A:3778
Sore Throat	-0.3717820	4	1.002e-02	2.426e-01	TNF:99 SFI1:1220 CNOT1:2158 SMN2:4694 NA NA
Ineffective erythropoiesis	-0.3687181	5	4.298e-03	1.721e-01	GATA1:579 RPL26:1309 KLF1:1767 COX4I2:2797 SEC23B:3947 NA
Melanoma-Associated Retinopathy	0.3686096	3	2.701e-02	3.359e-01	RCVRN:1409 TRPM1:2432 IMMT:2456 NA NA NA
Plantar hyperkeratosis	0.3685791	6	1.768e-03	1.143e-01	PLEC:18 ITGB4:50 LAMC2:272 LAMB3:2108 LAMA3:4764 COL17A1:5471
Phosphorus measurement	-0.3659644	4	1.125e-02	2.554e-01	IP6K3:236 ENPP3:440 RGS14:1270 CSTA:6643 NA NA
Microcystic stromal tumor	0.3650379	5	4.700e-03	1.812e-01	MME:362 DICER1:814 VIM:2228 CTNNB1:3539 FOXL2:3873 NA
Chorioretinitis	-0.3602289	5	5.276e-03	1.885e-01	TNF:99 IL6:845 IFNG:1322 IL2:4283 IL10:4620 NA
Exudative age-related macular degenerati	-0.3592301	3	3.116e-02	3.541e-01	VEGFA:482 KDR:1230 FLT1:5021 NA NA NA
Hypermagnesiuria	-0.3587335	6	2.341e-03	1.335e-01	CASR:34 CNNM2:154 EGF:263 CLDN16:360 GNA11:5146 CLDN19:7703
Human metapneumovirus infection	-0.3576929	5	5.605e-03	1.909e-01	TNF:99 TSLP:116 PPIP5K1:266 ISYNA1:1658 NCR1:9347 NA
Laryngismus	0.3575184	4	1.327e-02	2.702e-01	LAMC2:272 UBE3B:1999 LAMB3:2108 LAMA3:4764 NA NA
Female Pseudo-Turner Syndrome	-0.3556192	10	9.862e-05	2.546e-02	MAP2K2:92 MAP2K1:208 SHOC2:459 SOS1:554 PTPN11:714 RAF1:835
Rheumatoid Vasculitis	-0.3530958	2	8.370e-02	4.853e-01	CD28:2220 RBM45:2418 NA NA NA NA
Vitamin D-resistant rickets	-0.3519870	5	6.414e-03	2.015e-01	PTH:402 FGF23:742 RELB:2415 CYP24A1:2502 VDR:5749 NA
Myelitis	0.3518942	5	6.428e-03	2.015e-01	LAMC2:272 POU2F3:678 S100B:818 CSF2:2535 AQP4:7666 NA
Acute inflammatory demyelinating polyneu	-0.3516468	5	6.465e-03	2.020e-01	ALB:29 TNF:99 RBM45:2418 PMP22:2744 PTGDS:6593 NA

MGI_Mammalian_Phenotype_Level_4 Top pathways by permulation

MP0003646 muscle fatigue MP0010386 abnormal urinary bladder MP0003121 genomic imprinting MP0003787 abnormal imprinting MP0003122 maternal imprinting MP0002837 dystrophic cardiac calcinosis MP0004043 abnormal pH regulation MP0002653 abnormal ependyma morphology MP0003183 abnormal peptide metabolism MP0002139 abnormal hepatobiliary system MP0003656 abnormal erythrocyte physiolo MP0003678 abnormal parathyroid gland MP0002822 catalepsy MP0002822 catalepsy MP0004858 abnormal nervous system MP0004858 abnormal hair follicle MP000383 abnormal olfactory placode MP0003123 paternal imprinting MP0006292 abnormal olfactory placode MP0003123 paternal imprinting MP0006054 spinal hemorrhage MP0010352 gastrointestinal tract polyps MP0005275 abnormal skin tensile MP0003221 abnormal respiratory mucosa MP0003221 abnormal cardiomyocyte apopto -0.11	291535 268251 240429 188482 268343 939993 770517 728209 726155 724022 635099 633836 629702 695956 682470 666211 607007 427596 419630	5 9 14 23 10 14 9 14 11 10 8 10 22 21 6 9 14 22 12	1.852e-02 3.733e-03 2.860e-04 2.361e-02 1.204e-02 6.602e-02 2.529e-02 4.759e-02 5.921e-02 1.094e-01 7.358e-02 8.073e-03 9.829e-03 1.759e-01 1.004e-01 4.264e-02	4.196e-01 2.056e-01 8.462e-02 1.513e-02 2.391e-01 1.784e-01 3.928e-01 2.508e-01 3.407e-01 3.838e-01 4.736e-01 4.196e-01 1.609e-01 5.792e-01 4.634e-01	GNAQ:418 RPS20:776 RPS19:3860 GNA11:5146 EGFR:11843 NA SLC2A4:46 NOS1:305 MB:379 PPARGC1A:408 COX10:1798 MTOR:2657 TAC1:327 AGA:1244 KCNMA1:1443 CHRM3:1657 CHRNB2:2625 MYLK:3022 SMCHD1:341 HDAC8:396 GNAS:414 MEST:738 NDN:932 HELLS:1164 SMCHD1:341 GNAS:414 CDKN1C:1514 ARID4A:1554 ARID4B:2426 SNRPN:4362 GNAS:414 MEST:738 NDN:932 SGCE:1317 ARID4A:1554 DLK1:2371 SLC2A4:46 MMP9:548 SCG5:2455 MYH6:3426 DES:4176 DNM1L:5732 RHCG:896 SLC26A7:968 SLC4A10:1411 SLC12A1:2380 WNK4:3453 SLC4A4:4337 E2F5:537 NR1H2:1288 DLL3:1560 SOX2:3555 VAX1:4162 BBS1:5234 NCF1:613 ACE2:1023 TRIP11:2428 GNPTG:2605 VAV2:3161 ATE1:4063 ALDH1A1:77 INSIG1:844 FABP1:2313 NR1H3:3903 SLC22A1:6008 ABCG8:7650 SOCS1:361 SYT7:916 ITGB3:1325 SH3BP2:2068 RYR2:3117 CEBPB:3321 MAN2A1:84 NFE2L2:167 MAFG:755 PRKAA1:1005 KLF1:1767 AQP9:1817 CASR:34 PTH:402 VEGFA:482 TBX1:710 FOXG1:813 HOXA3:1857 DRD2:565 DBH:1373 CHRM4:4757 RXRG:7340 CNR1:8542 FAAH:10244 RGS5:2787 PRKDC:2794 RB1:3301 PDCD4:4015 CDKN1B:5486 KLF4:5800
MP0010386 abnormal urinary bladder MP0003121 genomic imprinting —0.21 MP0003787 abnormal imprinting —0.19 MP0003122 maternal imprinting —0.19 MP0002837 dystrophic cardiac calcinosis MP0004043 abnormal pH regulation —0.17 MP0002653 abnormal ependyma morphology MP0003183 abnormal peptide metabolism MP0002139 abnormal hepatobiliary system MP0004510 myositis MP0003656 abnormal erythrocyte physiolo MP0003678 abnormal parathyroid gland MP0002822 catalepsy MP000209 preneoplasia MP0004858 abnormal nervous system MP0004858 abnormal hair follicle MP000383 abnormal hair follicle MP0003123 paternal imprinting MP0006292 abnormal olfactory placode MP0003123 paternal imprinting MP0006054 spinal hemorrhage MP0010352 gastrointestinal tract polyps MP0005275 abnormal skin tensile MP0008260 abnormal autophagy MP0003221 abnormal cardiomyocyte apopto —0.11	240429 188482 068343 939993 770517 728209 726155 724022 635099 633836 629702 695956 682470 666211 607007 427596 419630	14 23 10 14 9 14 11 10 8 10 22 21 6 9 14 22	3.733e-03 2.860e-04 2.361e-02 1.204e-02 6.602e-02 2.529e-02 4.759e-02 5.921e-02 1.094e-01 7.358e-02 8.073e-03 9.829e-03 1.759e-01 1.004e-01 4.264e-02	8.462e-02 1.513e-02 2.391e-01 1.784e-01 3.928e-01 2.508e-01 3.407e-01 3.838e-01 4.736e-01 4.196e-01 1.453e-01 1.609e-01 5.792e-01	TAC1:327 AGA:1244 KCNMA1:1443 CHRM3:1657 CHRNB2:2625 MYLK:3022 SMCHD1:341 HDAC8:396 GNAS:414 MEST:738 NDN:932 HELLS:1164 SMCHD1:341 GNAS:414 CDKN1C:1514 ARID4A:1554 ARID4B:2426 SNRPN:4362 GNAS:414 MEST:738 NDN:932 SGCE:1317 ARID4A:1554 DLK1:2371 SLC2A4:46 MMP9:548 SCG5:2455 MYH6:3426 DES:4176 DNM1L:5732 RHCG:896 SLC26A7:968 SLC4A10:1411 SLC12A1:2380 WNK4:3453 SLC4A4:4337 E2F5:537 NR1H2:1288 DLL3:1560 SOX2:3555 VAX1:4162 BBS1:5234 NCF1:613 ACE2:1023 TRIP11:2428 GNPTG:2605 VAV2:3161 ATE1:4063 ALDH1A1:77 INSIG1:844 FABP1:2313 NR1H3:3903 SLC22A1:6008 ABCG8:7650 SOCS1:361 SYT7:916 ITGB3:1325 SH3BP2:2068 RYR2:3117 CEBPB:3321 MAN2A1:84 NFE2L2:167 MAFG:755 PRKAA1:1005 KLF1:1767 AQP9:1817 CASR:34 PTH:402 VEGFA:482 TBX1:710 FOXG1:813 HOXA3:1857 DRD2:565 DBH:1373 CHRM4:4757 RXRG:7340 CNR1:8542 FAAH:10244
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MP0003183 abnormal peptide metabolism MP0002139 abnormal hepatobiliary system —0.16 MP0003656 abnormal erythrocyte physiolo MP0000678 abnormal parathyroid gland MP0002822 catalepsy MP0002009 preneoplasia MP0004858 abnormal nervous system MP000383 abnormal hair follicle MP0006292 abnormal olfactory placode MP0003123 paternal imprinting MP0006054 spinal hemorrhage MP0010352 gastrointestinal tract polyps MP0005275 abnormal respiratory mucosa MP0008260 abnormal autophagy MP0003221 abnormal cardiomyocyte apopto —0.11	724022 635099 635009 633836 629702 695956 682470 666211 607007 427596 419630	10 8 10 22 21 6 9 14 22	5.921e-02 1.094e-01 7.358e-02 8.073e-03 9.829e-03 1.759e-01 1.004e-01 4.264e-02	3.838e-01 4.736e-01 4.196e-01 1.453e-01 1.609e-01 5.792e-01	NCF1:613 ACE2:1023 TRIP11:2428 GNPTG:2605 VAV2:3161 ATE1:4063 ALDH1A1:77 INSIG1:844 FABP1:2313 NR1H3:3903 SLC22A1:6008 ABCG8:7650 SOCS1:361 SYT7:916 ITGB3:1325 SH3BP2:2068 RYR2:3117 CEBPB:3321 MAN2A1:84 NFE2L2:167 MAFG:755 PRKAA1:1005 KLF1:1767 AQP9:1817 CASR:34 PTH:402 VEGFA:482 TBX1:710 FOXG1:813 HOXA3:1857 DRD2:565 DBH:1373 CHRM4:4757 RXRG:7340 CNR1:8542 FAAH:10244
MP0002139 abnormal hepatobiliary system MP0004510 myositis 0.16 MP0003656 abnormal erythrocyte physiolo MP0000678 abnormal parathyroid gland MP0002822 catalepsy 0.15 MP0002009 preneoplasia 0.15 MP0004858 abnormal nervous system MP0000383 abnormal hair follicle MP0006292 abnormal olfactory placode MP0003123 paternal imprinting MP0006054 spinal hemorrhage MP0010352 gastrointestinal tract polyps MP0005275 abnormal skin tensile 0.13 MP0002277 abnormal respiratory mucosa MP0008260 abnormal autophagy MP0003221 abnormal cardiomyocyte apopto -0.11	635099 635009 633836 629702 695956 682470 666211 607007 427596 419630	8 10 22 21 6 9 14 22	1.094e-01 7.358e-02 8.073e-03 9.829e-03 1.759e-01 1.004e-01 4.264e-02	4.736e-01 4.196e-01 1.453e-01 1.609e-01 5.792e-01	ALDH1A1:77 INSIG1:844 FABP1:2313 NR1H3:3903 SLC22A1:6008 ABCG8:7650 SOCS1:361 SYT7:916 ITGB3:1325 SH3BP2:2068 RYR2:3117 CEBPB:3321 MAN2A1:84 NFE2L2:167 MAFG:755 PRKAA1:1005 KLF1:1767 AQP9:1817 CASR:34 PTH:402 VEGFA:482 TBX1:710 FOXG1:813 HOXA3:1857 DRD2:565 DBH:1373 CHRM4:4757 RXRG:7340 CNR1:8542 FAAH:10244
MP0004510 myositis 0.16 MP0003656 abnormal erythrocyte physiolo -0.16 MP0000678 abnormal parathyroid gland -0.16 MP0002822 catalepsy 0.15 MP0002009 preneoplasia 0.15 MP0004858 abnormal nervous system 0.15 MP0000383 abnormal hair follicle 0.15 MP0006292 abnormal olfactory placode -0.14 MP0003123 paternal imprinting -0.14 MP0006054 spinal hemorrhage -0.13 MP0010352 gastrointestinal tract polyps -0.13 MP0005275 abnormal skin tensile 0.13 MP0002277 abnormal respiratory mucosa -0.12 MP0008260 abnormal autophagy -0.11 MP0003221 abnormal cardiomyocyte apopto -0.11	635009 633836 629702 695956 682470 666211 607007 427596 419630	10 22 21 6 9 14 22	7.358e-02 8.073e-03 9.829e-03 1.759e-01 1.004e-01 4.264e-02	4.196e-01 1.453e-01 1.609e-01 5.792e-01	SOCS1:361 SYT7:916 ITGB3:1325 SH3BP2:2068 RYR2:3117 CEBPB:3321 MAN2A1:84 NFE2L2:167 MAFG:755 PRKAA1:1005 KLF1:1767 AQP9:1817 CASR:34 PTH:402 VEGFA:482 TBX1:710 FOXG1:813 HOXA3:1857 DRD2:565 DBH:1373 CHRM4:4757 RXRG:7340 CNR1:8542 FAAH:10244
MP0003656 abnormal erythrocyte physiolo -0.16 MP0000678 abnormal parathyroid gland -0.16 MP0002822 catalepsy 0.15 MP0002009 preneoplasia 0.15 MP0004858 abnormal nervous system 0.15 MP0000383 abnormal hair follicle 0.15 MP0006292 abnormal olfactory placode -0.14 MP0003123 paternal imprinting -0.14 MP0006054 spinal hemorrhage -0.13 MP0010352 gastrointestinal tract polyps -0.13 MP0005275 abnormal skin tensile 0.13 MP0002277 abnormal respiratory mucosa -0.12 MP0008260 abnormal autophagy -0.11 MP0003221 abnormal cardiomyocyte apopto -0.11	633836 629702 695956 682470 666211 607007 427596 419630	22 21 6 9 14 22	8.073e-03 9.829e-03 1.759e-01 1.004e-01 4.264e-02	1.453e-01 1.609e-01 5.792e-01	MAN2A1:84 NFE2L2:167 MAFG:755 PRKAA1:1005 KLF1:1767 AQP9:1817 CASR:34 PTH:402 VEGFA:482 TBX1:710 FOXG1:813 HOXA3:1857 DRD2:565 DBH:1373 CHRM4:4757 RXRG:7340 CNR1:8542 FAAH:10244
MP0000678 abnormal parathyroid gland MP0002822 catalepsy 0.15 MP0002009 preneoplasia 0.15 MP0004858 abnormal nervous system 0.15 MP0000383 abnormal hair follicle 0.15 MP0006292 abnormal olfactory placode MP0003123 paternal imprinting -0.14 MP0006054 spinal hemorrhage -0.13 MP0010352 gastrointestinal tract polyps -0.13 MP0005275 abnormal skin tensile 0.13 MP0002277 abnormal respiratory mucosa MP0008260 abnormal autophagy -0.11 MP0003221 abnormal cardiomyocyte apopto -0.11	629702 695956 682470 666211 607007 427596 419630	21 6 9 14 22	9.829e-03 1.759e-01 1.004e-01 4.264e-02	1.609e-01 5.792e-01	CASR:34 PTH:402 VEGFA:482 TBX1:710 FOXG1:813 HOXA3:1857 DRD2:565 DBH:1373 CHRM4:4757 RXRG:7340 CNR1:8542 FAAH:10244
MP0002822 catalepsy 0.15 MP0002009 preneoplasia 0.15 MP0004858 abnormal nervous system 0.15 MP0000383 abnormal hair follicle 0.15 MP0006292 abnormal olfactory placode -0.14 MP0003123 paternal imprinting -0.14 MP0006054 spinal hemorrhage -0.13 MP0010352 gastrointestinal tract polyps -0.13 MP0005275 abnormal skin tensile 0.13 MP0002277 abnormal respiratory mucosa -0.12 MP0008260 abnormal autophagy -0.11 MP0003221 abnormal cardiomyocyte apopto -0.11	595956 582470 566211 507007 427596 419630	6 9 14 22	1.759e-01 1.004e-01 4.264e-02	5.792e-01	DRD2:565 DBH:1373 CHRM4:4757 RXRG:7340 CNR1:8542 FAAH:10244
MP0002009 preneoplasia 0.15 MP0004858 abnormal nervous system 0.15 MP0000383 abnormal hair follicle 0.15 MP0006292 abnormal olfactory placode -0.14 MP0003123 paternal imprinting -0.14 MP0006054 spinal hemorrhage -0.13 MP0010352 gastrointestinal tract polyps -0.13 MP0005275 abnormal skin tensile 0.13 MP0002277 abnormal respiratory mucosa MP0008260 abnormal autophagy -0.11 MP0003221 abnormal cardiomyocyte apopto -0.11	582470 566211 507007 427596 419630	9 14 22	1.004e-01 4.264e-02		
MP0004858 abnormal nervous system MP0000383 abnormal hair follicle MP0006292 abnormal olfactory placode MP0003123 paternal imprinting MP0006054 spinal hemorrhage MP0010352 gastrointestinal tract polyps MP0005275 abnormal skin tensile MP0002277 abnormal respiratory mucosa MP0008260 abnormal autophagy MP0003221 abnormal cardiomyocyte apopto 0.15 0.15 0.16 0.17 0.18 0.19 0.19 0.19 0.11	566211 507007 427596 419630	14 22	4.264e-02	4.634e-01	DCCC-2707 DDVDC-2704 DDC-2201 DDCD4-4045 CDVN4D-5406 VLF4-5000
MP000383 abnormal hair follicle MP0006292 abnormal olfactory placode MP0003123 paternal imprinting MP0006054 spinal hemorrhage MP0010352 gastrointestinal tract polyps MP0005275 abnormal skin tensile MP0002277 abnormal respiratory mucosa MP0008260 abnormal autophagy MP0003221 abnormal cardiomyocyte apopto -0.11	507007 427596 419630	22			NG33.2101 FRNDC.2134 RD1.3301 FDCD4.4013 CDRNTD.3400 KLF4:5800
MP0006292 abnormal olfactory placode MP0003123 paternal imprinting MP0006054 spinal hemorrhage MP0010352 gastrointestinal tract polyps MP0005275 abnormal skin tensile MP0002277 abnormal respiratory mucosa MP0008260 abnormal autophagy MP0003221 abnormal cardiomyocyte apopto -0.11	427596 419630		1 455 - 00	3.307e-01	AVIL:35 NOS1:305 NGFR:2294 PTPRF:3200 GAL:3308 TNFRSF1B:4083
MP0003123 paternal imprinting -0.14 MP0006054 spinal hemorrhage -0.13 MP0010352 gastrointestinal tract polyps -0.13 MP0005275 abnormal skin tensile 0.13 MP0002277 abnormal respiratory mucosa MP0008260 abnormal autophagy -0.11 MP0003221 abnormal cardiomyocyte apopto -0.11	419630	12	1.4556-02	1.823e-01	FGFR2:24 KRT14:507 PKP3:646 DICER1:814 TRPV3:1060 KSR1:1545
MP0006054 spinal hemorrhage -0.13 MP0010352 gastrointestinal tract polyps -0.13 MP0005275 abnormal skin tensile 0.13 MP0002277 abnormal respiratory mucosa -0.12 MP0008260 abnormal autophagy -0.11 MP0003221 abnormal cardiomyocyte apopto -0.11			8.707e-02	4.555e-01	FOXG1:813 HESX1:1024 OTX2:2110 CHRD:2823 PAX6:3138 HHEX:3426
MP0010352 gastrointestinal tract polyps -0.13 MP0005275 abnormal skin tensile 0.13 MP0002277 abnormal respiratory mucosa MP0008260 abnormal autophagy -0.11 MP0003221 abnormal cardiomyocyte apopto -0.11		8	1.646e-01	5.792e-01	GNAS:414 HELLS:1164 CDKN1C:1514 UBE3A:3225 AXIN1:5511 GRB10:8764
MP0005275 abnormal skin tensile 0.13 MP0002277 abnormal respiratory mucosa -0.12 MP0008260 abnormal autophagy -0.11 MP0003221 abnormal cardiomyocyte apopto -0.11	349325	9	1.612e-01	5.792e-01	PSEN1:1209 C1GALT1:2950 COL1A1:3291 TFPI:4300 SPHK1:5595 C1GALT1C1:6490
MP0002277 abnormal respiratory mucosa -0.12 MP0008260 abnormal autophagy -0.11 MP0003221 abnormal cardiomyocyte apopto -0.11	321466	15	7.668e-02	4.196e-01	STAT3:795 PTGS2:829 SMAD4:1318 SAV1:1508 PPARD:1671 ITGB1:3722
MP0008260 abnormal autophagy -0.11 MP0003221 abnormal cardiomyocyte apopto -0.11	320760	17	5.966e-02	3.838e-01	LAMC2:272 TNXB:751 DSE:1018 FMOD:1849 OGN:2112 COL5A2:2166
MP0003221 abnormal cardiomyocyte apopto -0.11	279104	20	4.796e-02	3.407e-01	RORA:644 DLX5:700 HESX1:1024 RELB:2415 HOXA5:2535 CXCR2:3315
, , , ,	189527	16	9.984e-02	4.634e-01	LRRK2:957 BECN1:1240 ATG4C:1378 PTHLH:2552 PMP22:2744 VCP:2926
	164469	37	1.448e-02	1.823e-01	MDM2:311 CASP8:345 PTPN11:714 RAF1:835 MAPK8:971 TFAM:1298
MP0005367 renal/urinary system phenotyp -0.11	152034	19	8.251e-02	4.364e-01	BMP4:790 FOXC1:1222 HOXA13:2176 SGPL1:3481 CDKN1A:4590 PAX1:4928
MP0000516 abnormal urinary system -0.11	152034	19	8.251e-02	4.364e-01	BMP4:790 FOXC1:1222 HOXA13:2176 SGPL1:3481 CDKN1A:4590 PAX1:4928
MP0005083 abnormal biliary tract 0.11	47850	8	2.611e-01	6.246e-01	MUC1:1494 CCKAR:2204 VTI1B:2217 XYLT2:2526 GPBAR1:4055 LDLR:10003
MP0009840 abnormal foam cell -0.11	144364	11	1.891e-01	5.792e-01	NR1H2:1288 MAPKAPK2:1390 APOA1:1743 SUPV3L1:3484 LDLR:6199 PLA2G15:6564
MP0000749 muscle degeneration 0.11	143910	36	1.782e-02	2.056e-01	DMD:11 PLEC:18 HSPB2:149 MYOZ1:342 BAG3:599 KY:767
MP0002254 reproductive system inflammat -0.11	135814	5	3.792e-01	6.903e-01	RELB:2415 PGR:3115 MFGE8:4001 EPHA1:9281 AIRE:12644 NA
MP0002909 abnormal adrenal gland -0.11	121078	21	7.573e-02	4.196e-01	PRKAR1A:465 CADPS:676 PTPN11:714 KCNK3:945 LRRK2:957 CYP11A1:1144
-	82746	17	1.226e-01	5.075e-01	MMP9:548 RAG2:1688 HIP1:2149 EP400:2719 TSC22D1:3351 LIG1:4395
MP0003303 peritoneal inflammation -0.10	055470	11	2.258e-01	6.038e-01	LYN:264 PTGS2:829 PECAM1:981 APC:4251 IL10:4620 ST6GAL1:6724
)46348	21		4.634e-01	DMD:11 PLEC:18 COL6A1:125 COL15A1:1121 COX10:1798 SLC25A4:1889
	043021	29		3.611e-01	FGFR2:24 KRT14:507 PKP3:646 DICER1:814 TRPV3:1060 KSR1:1545
	034136	25		4.196e-01	SLC35D1:706 HOXB4:1064 NKX3-2:1629 CBFB:2475 PTHLH:2552 COL1A1:3291
. 0,	028538	22		4.634e-01	CASP8:345 ATXN2:574 ARL3:3047 NR1H4:3183 NF2:4148 PKHD1:4544
	011023	16		5.792e-01	PTAFR:121 NOS1:305 MMP9:548 HRH3:2914 CTNNB1:3539 IL1B:3806

tissue_specific Top pathways by permulation

Geneset	stat	num.genes	pval	p.adj	gene.vals
left.ventricle	0.11690439	69	8.157e-04	5.506e-03	CKMT2:104 MYH7B:122 ASB10:178 NRAP:224 SCN5A:315 MB:379
hippocampus.proper	-0.11617152	11	1.823e-01	4.476e-01	CNIH2:1504 NEUROD2:2653 SLC17A7:3785 HRK:5991 FEZF2:6843 NTS:7322
substantia.nigra	-0.11190142	12	1.797e-01	4.476e-01	DBX2:404 RET:3741 RPE65:4387 C10orf105:4943 CHRM5:6466 TH:6491
skeletal.muscle	0.11124024	238	5.077e-09	2.742e-07	SLC2A4:46 MYH8:52 SLC8A3:93 CKMT2:104 ASB10:178 NRAP:224
vagina	0.10351567	91	6.772e-04	5.224e-03	RNF222:47 EVPL:103 KRT13:173 SLURP1:330 WFDC5:376 ALOX15B:393
ectocervix	-0.10245437	25	7.651e-02	2.582e-01	HOXD13:1305 MMRN1:1577 FGF7:2010 PTHLH:2552 LRFN5:2612 PAPPA2:2932
leg.skin	0.10136121	217	3.526e-07	4.946e-06	ANKRD35:1 GGT6:36 RNF222:47 FAM83F:66 POF1B:73 EVPL:103
esophagus.mucosa	0.10054595	220	3.664e-07	4.946e-06	RNF222:47 PTK6:60 SDCBP2:62 BDKRB1:80 EVPL:103 KRT4:117
thyroid	-0.09331728	151	8.501e-05	9.181e-04	CLCNKA:15 GGTLC1:52 CLUL1:114 MUC15:171 IDO2:172 MIOX:234
eye.development	-0.08201577	67	2.064e-02	1.013e-01	MSX1:633 BMP4:790 ONECUT1:1060 FOXC1:1222 PITX3:1389 PAX2:1458
suprapubic.skin	0.08109457	194	1.138e-04	1.025e-03	GGT6:36 RNF222:47 FAM83F:66 EVPL:103 KCNK7:241 LTB4R:244
pancreas	-0.07781810	94	9.427e-03	5.091e-02	PRODH2:26 CASR:34 GNMT:223 EGF:263 GCG:320 KCNK16:332
atrium.auricle	0.06909714	91	2.329e-02	1.048e-01	CKMT2:104 ASB10:178 NRAP:224 SCN5A:315 MB:379 LMOD3:421
sigmoid.colon	0.06209682	52	1.222e-01	3.667e-01	TACR2:5 PLA2G2C:116 PLEKHO1:245 NTSR1:732 DPT:1369 CHRM2:1408
EBV.lymphocyte	-0.06025027	674	2.518e-07	4.946e-06	TMEM131L:23 MTBP:33 BAX:45 TNF:99 HMGA1:119 CD80:122
esophagogastric.junction	-0.05923449	8	5.619e-01	7.535e-01	F2RL2:2341 ADCY5:3740 GADL1:4181 COL4A5:5726 NKX6-1:7345 BARX1:11706
cerebral.cortex	0.05730140	107	4.158e-02	1.727e-01	CALHM1:39 C1QL2:166 KCNH3:168 CIT:252 HTR3B:283 KCNF1:457
esophagus.muscularis.mucosa	0.05614488	26	3.223e-01	5.843e-01	PRUNE2:233 NTN1:619 SYNM:766 FAM83D:770 TPM1:1038 KCNMB1:1576
Brodmann.area.24	-0.05508713	31	2.891e-01	5.575e-01	DDN:598 SLC6A1:750 NTRK2:860 UPP2:1484 NCS1:1571 GAD1:2125
adrenal.gland	-0.05411780	108	5.320e-02	2.050e-01	ABCB1:3 MGST1:63 ADGRV1:399 SCARB1:555 CYP17A1:643 GSTA4:688
bladder	-0.05392157	24	3.610e-01	6.092e-01	UPK1A:2526 CLEC3A:3586 ID1:4508 TMC7:4612 ACER2:5228 ARL14:5244
liver	-0.04896514	328	2.696e-03	1.618e-02	SDS:6 HSD17B6:11 PRODH2:26 ALB:29 HSD11B1:54 ARG1:108
minor.salivary.gland	0.04347621	69	2.132e-01	4.978e-01	PIP:335 KRT19:554 MMP3:596 ITPRID1:977 KRTCAP3:1043 MMP7:1049
prostate	0.04347343	38	3.545e-01	6.092e-01	ANO7:194 LMAN1L:578 ACP3:1246 H2BC6:1685 CREB3L4:1716 STEAP2:1762
peyers.patch	0.04303399	167	5.695e-02	2.050e-01	EPS8L3:21 SLC28A1:164 ANPEP:189 TMEM236:219 ANKS4B:238 NLRP6:294
putamen	-0.04215741	15	5.721e-01	7.535e-01	ANO3:333 KCNH4:1768 FAM237A:3108 HPCA:6051 RASD2:6727 GBX2:7431
greater.omentum	-0.04015982	33	4.253e-01	6.751e-01	BTNL9:473 MEST:738 IL6:845 LPL:1154 TCF15:1540 GFPT2:3107
cortex.kidney	-0.03885442	114	1.540e-01	4.158e-01	PRODH2:26 CASR:34 CLCNKB:132 MIOX:234 ATP6V0D2:350 CLDN16:360
amygdala	0.03648703	9	7.047e-01	7.923e-01	PCDH15:1124 PTPRZ1:1439 BCAN:3373 SLC38A8:4605 TNR:4657 NEUROD6:6562
ovary	0.03373525	103	2.391e-01	4.978e-01	C21orf62:326 WIPF3:364 CCDC170:392 TCF23:553 ANGPTL5:870 LRRC17:1027
coronary.artery	-0.03370723	15	6.515e-01	7.676e-01	CCL19:1407 GJA5:2924 SPINK13:3430 CCN3:3802 PCOLCE2:4494 COL4A1:6311
endocervix	-0.03368276	72	3.246e-01	5.843e-01	PRSS12:381 METTL27:516 MSX1:633 GABRE:674 HOXD13:1305 LUM:1878
fallopian.tube	-0.03278040	52	4.146e-01	6.751e-01	LONRF2:977 HOXA3:1857 CDHR4:2072 RARRES1:2096 GMNC:2175 FOS:2213

transformed.skin.fibroblast -0.02710718
C1.spinal.cord -0.02621664

breast

caudate.nucleus

stomach

lung

0.02436904

-0.01896341

0.01680044

-0.01573022

15

26

86

139

259 1.379e-01 3.921e-01 HAS2:4 IGF2BP1:78 RHOBTB3:106 ADAM9:130 OSTC:174 FKBP14:219

THRSP:624 ABCB5:1054 TNN:2412 KRT5:3220 TFAP2B:5303 NPY2R:5368

ANO3:333 ETNPPL:1251 RGS14:1270 PSD2:2482 FAM237A:3108 NR2E1:4036 EPS8L3:21 GKN1:49 CAPN8:105 CYP2S1:210 TM4SF5:323 MYH13:556

GGTLC1:52 IL18R1:387 PTPRB:447 MSR1:686 TMEM100:754 PTGS2:829

182 2.265e-01 4.978e-01 SCD:80 ENPP2:102 SLC44A1:368 DBX2:404 PMP2:483 TMEM144:632

0.02575488 154 2.735e-01 5.470e-01 C1QTNF8:3 ACTN1:190 PCDH11X:255 MYH10:261 AEBP1:297 TNFRSF11B:318

7.440e-01 7.923e-01

7.381e-01 7.923e-01

5.917e-01 7.607e-01

5.247e-01 7.506e-01