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 MACROH2A1:2838
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	1.160e-01	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	2.641e-01	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	8.098e-03	1.895e-01	DNAJB13:626 SPAG17:1473 SPEF1:2508 RSPH9:2838 HYDIN:5615 NA
Inositol Metabolic Process (GO:0006020)	-0.3413715	6	3.782e-03	1.316e-01	MIOX:234 PPIP5K1:266 IMPA2:1082 ISYNA1:1658 SLC5A3:5213 PPIP5K2:6860
Glucocorticoid Metabolic Process (GO:000	-0.3400190	5	8.460e-03	1.914e-01	CYP17A1:643 CYP11A1:1144 HSD11B2:3099 CYP21A2:3366 YWHAH:4567 NA
Transmembrane Receptor Protein Tyrosine	0.3333004	4	2.096e-02	2.949e-01	PTPRD:1284 PTN:2579 PTPRF:3200 TRIO:3947 NA NA
Leptin–Mediated Signaling Pathway (GO:00	-0.3298298	7	2.511e-03	1.106e-01	UGCG:655 STAT3:795 SIRT1:995 LEPR:1091 MKKS:3718 LEP:4562
Cilium-Dependent Cell Motility (GO:00602	0.3282355	17	2.802e-06	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	2.250e-01	HIBCH:428 BCAT1:481 BCAT2:596 ILVBL:6110 HIBADH:6319 NA
Copper Ion Import (GO:0015677)	0.3264548	6		1.620e-01	STEAP4:922 STEAP2:1762 SLC31A2:2338 ATP7B:2734 SLC31A1:3544 STEAP3:5878
Negative Regulation Of cAMP-dependent Pr	-0.3252161	6	5.802e-03	1.630e-01	PRKAR1A:465 SIRT1:995 PRKAR2A:1524 PKIB:2753 PRKAR2B:3870 PRKAR1B:7211

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

DisGeNET Top pathways by permulation

6.861e-04 1.855e-02

5.148e-02 2.691e-01

-0.2830402 12

-0.2811314

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

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

gene.vals

REACTOME_INTERLEUKIN_35_SIGNALLING

CHOI_ATL_ACUTE_STAGE

Diabetes-deafness syndrome maternally tr Color Blindness, Red Spondylitis Congenital pyloric atresia Junctional split Localized vitiligo Valvular disease Monilethrix Diabetes-deafness syndrome maternally tr -0.45e 0.43e 0.42e 0.42e 0.42e 0.42e 0.42e 0.41e 0.40e Monilethrix	3827 3018 4851 3061 9687	2 5 4 5 6 2 4	2.871e-03 1.008e-03	6.460e-02	GCG:320 RAPGEF5:1120 NA NA NA NA GNAT2:115 TEX28:423 OPN1LW:709 ATF6:1719 PDE6H:1964 NA TNF:99 IL6:845 IL4:1133 VCAN:2299 NA NA PLEC:18 ITGB4:50 ITGA6:267 LAMC2:272 COL17A1:5471 NA
Spondylitis -0.430 Congenital pyloric atresia 0.422 Junctional split 0.422 Localized vitiligo -0.420 Valvular disease 0.407 Monilethrix 0.404	3827 6018 4851 3061 9687 1440	4 5 6 2	2.871e-03 1.008e-03 3.385e-04	1.461e-01 8.912e-02	TNF:99 IL6:845 IL4:1133 VCAN:2299 NA NA PLEC:18 ITGB4:50 ITGA6:267 LAMC2:272 COL17A1:5471 NA
Congenital pyloric atresia 0.424 Junctional split 0.422 Localized vitiligo -0.420 Valvular disease 0.412 Herlitz Disease 0.407 Monilethrix 0.404	6018 4851 3061 9687 1440	5 6 2	1.008e-03 3.385e-04	8.912e-02	PLEC:18 ITGB4:50 ITGA6:267 LAMC2:272 COL17A1:5471 NA
Junctional split 0.422 Localized vitiligo -0.420 Valvular disease 0.412 Herlitz Disease 0.407 Monilethrix 0.404	4851 3061 9687 1440	6 2	3.385e-04		
Localized vitiligo -0.420 Valvular disease 0.412 Herlitz Disease 0.407 Monilethrix 0.404	3061 9687 1440	2		4.427e-02	DI FC:40 ITCD4.50 ITCAC:207 I AMC2:272 I AMD2:2400 I AMA2:4704
Valvular disease 0.412 Herlitz Disease 0.407 Monilethrix 0.404	9687 1440		3.951e-02		PLEC:18 ITGB4:50 ITGA6:267 LAMC2:272 LAMB3:2108 LAMA3:4764
Herlitz Disease 0.407 Monilethrix 0.404	1440	4		3.887e-01	TNF:99 RBM45:2418 NA NA NA NA
Monilethrix 0.404			4.229e-03	1.700e-01	TIMP1:420 MMP9:548 TIMP2:2106 MMP2:2505 NA NA
	2668	5	1.616e-03	1.117e-01	ITGB4:50 ITGA6:267 LAMC2:272 LAMB3:2108 LAMA3:4764 NA
NOONANI OVAIDDOME O		2	4.767e-02	4.079e-01	KRT80:303 DSG4:2753 NA NA NA NA
NOONAN SYNDROME 3 -0.402	0566	5	1.848e-03	1.148e-01	SHOC2:459 SOS1:554 PTPN11:714 RAF1:835 KRAS:5235 NA
Neonatal alloimmune thrombocytopenia (NA 0.400	8118	4	5.497e-03	1.909e-01	POU2F3:678 ITGB3:1325 PLA2G6:1975 PLA2G1B:2387 NA NA
Deficiency of monooxygenase -0.400	2087	2	4.995e-02	4.146e-01	CYP17A1:643 CYP24A1:2502 NA NA NA NA
X-Linked Infantile Nystagmus 0.399	4022	3	1.657e-02	2.960e-01	FRMD7:179 CASK:885 GPR143:3782 NA NA NA
Angiokeratoma –0.398	0826	5	2.050e-03	1.221e-01	MANBA:259 VEGFA:482 GLA:720 DCAF7:1640 PTEN:5008 NA
T–lymphocyte immunodeficiency 0.397	4587	6	7.472e-04	7.035e-02	SFTPA1:9 RAG1:43 CD3E:1166 SMARCAL1:1223 LBR:1624 SIPA1:5855
Chronic iridocyclitis -0.39	6144	2	5.204e-02	4.152e-01	IL6:845 RBM45:2418 NA NA NA NA
Bulla of lung 0.394	9525	2	5.303e-02	4.152e-01	EPHX1:1261 TIMP2:2106 NA NA NA NA
Unilateral primary pulmonary dysgenesis -0.389	7480	5	2.542e-03	1.379e-01	TBX1:710 DGCR8:963 DGCR2:1105 DGCR6:1160 ESS2:4827 NA
Profound sensorineural hearing impairmen 0.384	4221	4	7.748e-03	2.172e-01	RDX:391 CIB2:907 TRIOBP:2685 MYO15A:3438 NA NA
C3 Glomerulonephritis 0.381	2874	3	2.217e-02	3.178e-01	CFHR5:1077 C3:1835 CFB:2798 NA NA NA
Papillary transitional cell carcinoma -0.38	0012	4	8.312e-03	2.198e-01	EGF:263 VEGFA:482 TP53:2447 ERBB2:4396 NA NA
Chilblain lupus 1 -0.38	1020	3	2.259e-02	3.199e-01	GZMA:1536 TREX1:1848 SAMHD1:2257 NA NA NA
Small anterior fontanelle -0.379	3805	3	2.285e-02	3.199e-01	ORC1:736 MYCN:959 ATR:4070 NA NA NA
Focal Dermal Hypoplasia -0.37	9939	7	5.521e-04	5.616e-02	ALB:29 CYP26C1:245 TWIST2:820 GC:938 HCCS:2312 WNT3A:3778
Sore Throat -0.37	7820	4	1.002e-02	2.426e-01	TNF:99 SFI1:1220 CNOT1:2158 SMN2:4694 NA NA
Ineffective erythropoiesis -0.366	7181	5	4.298e-03	1.721e-01	GATA1:579 RPL26:1309 KLF1:1767 COX4I2:2797 SEC23B:3947 NA
Melanoma-Associated Retinopathy 0.368	6096	3	2.701e-02	3.359e-01	RCVRN:1409 TRPM1:2432 IMMT:2456 NA NA NA
Plantar hyperkeratosis 0.368	5791	6	1.768e-03	1.143e-01	PLEC:18 ITGB4:50 LAMC2:272 LAMB3:2108 LAMA3:4764 COL17A1:5471
Phosphorus measurement -0.368	9644	4	1.125e-02	2.554e-01	IP6K3:236 ENPP3:440 RGS14:1270 CSTA:6643 NA NA
Microcystic stromal tumor 0.365	0379	5	4.700e-03	1.812e-01	MME:362 DICER1:814 VIM:2228 CTNNB1:3539 FOXL2:3873 NA
Chorioretinitis -0.366	2289	5	5.276e-03	1.885e-01	TNF:99 IL6:845 IFNG:1322 IL2:4283 IL10:4620 NA
Exudative age-related macular degenerati -0.35	2301	3	3.116e-02	3.541e-01	VEGFA:482 KDR:1230 FLT1:5021 NA NA NA
Hypermagnesiuria -0.35	7335	6	2.341e-03	1.335e-01	CASR:34 CNNM2:154 EGF:263 CLDN16:360 GNA11:5146 CLDN19:7703
Human metapneumovirus infection -0.35	6929	5	5.605e-03	1.909e-01	TNF:99 TSLP:116 PPIP5K1:266 ISYNA1:1658 NCR1:9347 NA
Laryngismus 0.357	5184	4	1.327e-02	2.702e-01	LAMC2:272 UBE3B:1999 LAMB3:2108 LAMA3:4764 NA NA
Female Pseudo-Turner Syndrome -0.35	6192	10	9.862e-05	2.546e-02	MAP2K2:92 MAP2K1:208 SHOC2:459 SOS1:554 PTPN11:714 RAF1:835
Rheumatoid Vasculitis -0.353	0958	2	8.370e-02	4.853e-01	CD28:2220 RBM45:2418 NA NA NA NA
Vitamin D–resistant rickets –0.35	9870	5	6.414e-03	2.015e-01	PTH:402 FGF23:742 RELB:2415 CYP24A1:2502 VDR:5749 NA
Myelitis 0.351	3942	5	6.428e-03	2.015e-01	LAMC2:272 POU2F3:678 S100B:818 CSF2:2535 AQP4:7666 NA
Acute inflammatory demyelinating polyneu -0.35	6468	5	6.465e-03		ALB:29 TNF:99 RBM45:2418 PMP22:2744 PTGDS:6593 NA

MGI_Mammalian_Phenotype_Level_4 Top pathways by permulation

MP0009379 abnormal foot pigmentation	-0.2291535	5	7.606e-02	4.196e-01	GNAQ:418 RPS20:776 RPS19:3860 GNA11:5146 EGFR:11843 NA
MP0003646 muscle fatigue	0.2268251	9	1.852e-02	2.056e-01	SLC2A4:46 NOS1:305 MB:379 PPARGC1A:408 COX10:1798 MTOR:2657
MP0010386 abnormal urinary bladder	0.2240429	14	3.733e-03	8.462e-02	TAC1:327 AGA:1244 KCNMA1:1443 CHRM3:1657 CHRNB2:2625 MYLK:3022
MP0003121 genomic imprinting	-0.2188482	23	2.860e-04	1.513e-02	SMCHD1:341 HDAC8:396 GNAS:414 MEST:738 NDN:932 HELLS:1164
MP0003787 abnormal imprinting	-0.2068343	10	2.361e-02	2.391e-01	SMCHD1:341 GNAS:414 CDKN1C:1514 ARID4A:1554 ARID4B:2426 SNRPN:4362
MP0003122 maternal imprinting	-0.1939993	14	1.204e-02	1.784e-01	GNAS:414 MEST:738 NDN:932 SGCE:1317 ARID4A:1554 DLK1:2371
MP0002837 dystrophic cardiac calcinosis	0.1770517	9	6.602e-02	3.928e-01	SLC2A4:46 MMP9:548 SCG5:2455 MYH6:3426 DES:4176 DNM1L:5732
MP0004043 abnormal pH regulation	-0.1728209	14	2.529e-02	2.508e-01	RHCG:896 SLC26A7:968 SLC4A10:1411 SLC12A1:2380 WNK4:3453 SLC4A4:4337
MP0002653 abnormal ependyma morphology	-0.1726155	11	4.759e-02	3.407e-01	E2F5:537 NR1H2:1288 DLL3:1560 SOX2:3555 VAX1:4162 BBS1:5234
MP0003183 abnormal peptide metabolism	0.1724022	10	5.921e-02	3.838e-01	NCF1:613 ACE2:1023 TRIP11:2428 GNPTG:2605 VAV2:3161 ATE1:4063
MP0002139 abnormal hepatobiliary system	-0.1635099	8	1.094e-01	4.736e-01	ALDH1A1:77 INSIG1:844 FABP1:2313 NR1H3:3903 SLC22A1:6008 ABCG8:7650
MP0004510 myositis	0.1635009	10	7.358e-02	4.196e-01	SOCS1:361 SYT7:916 ITGB3:1325 SH3BP2:2068 RYR2:3117 CEBPB:3321
MP0003656 abnormal erythrocyte physiolo	-0.1633836	22	8.073e-03	1.453e-01	MAN2A1:84 NFE2L2:167 MAFG:755 PRKAA1:1005 KLF1:1767 AQP9:1817
MP0000678 abnormal parathyroid gland	-0.1629702	21	9.829e-03	1.609e-01	CASR:34 PTH:402 VEGFA:482 TBX1:710 FOXG1:813 HOXA3:1857
MP0002822 catalepsy	0.1595956	6	1.759e-01	5.792e-01	DRD2:565 DBH:1373 CHRM4:4757 RXRG:7340 CNR1:8542 FAAH:10244
MP0002009 preneoplasia	0.1582470	9	1.004e-01	4.634e-01	RGS5:2787 PRKDC:2794 RB1:3301 PDCD4:4015 CDKN1B:5486 KLF4:5800
MP0004858 abnormal nervous system	0.1566211	14	4.264e-02	3.307e-01	AVIL:35 NOS1:305 NGFR:2294 PTPRF:3200 GAL:3308 TNFRSF1B:4083
MP0000383 abnormal hair follicle	0.1507007	22	1.455e-02	1.823e-01	FGFR2:24 KRT14:507 PKP3:646 DICER1:814 TRPV3:1060 KSR1:1545
MP0006292 abnormal olfactory placode	-0.1427596	12	8.707e-02	4.555e-01	FOXG1:813 HESX1:1024 OTX2:2110 CHRD:2823 PAX6:3138 HHEX:3426
MP0003123 paternal imprinting	-0.1419630	8	1.646e-01	5.792e-01	GNAS:414 HELLS:1164 CDKN1C:1514 UBE3A:3225 AXIN1:5511 GRB10:8764
MP0006054 spinal hemorrhage	-0.1349325	9	1.612e-01	5.792e-01	PSEN1:1209 C1GALT1:2950 COL1A1:3291 TFPI:4300 SPHK1:5595 C1GALT1C1:6490
MP0010352 gastrointestinal tract polyps	-0.1321466	15	7.668e-02	4.196e-01	STAT3:795 PTGS2:829 SMAD4:1318 SAV1:1508 PPARD:1671 ITGB1:3722
MP0005275 abnormal skin tensile	0.1320760	17	5.966e-02	3.838e-01	LAMC2:272 TNXB:751 DSE:1018 FMOD:1849 OGN:2112 COL5A2:2166
MP0002277 abnormal respiratory mucosa	-0.1279104	20	4.796e-02	3.407e-01	RORA:644 DLX5:700 HESX1:1024 RELB:2415 HOXA5:2535 CXCR2:3315
MP0008260 abnormal autophagy	-0.1189527	16	9.984e-02	4.634e-01	LRRK2:957 BECN1:1240 ATG4C:1378 PTHLH:2552 PMP22:2744 VCP:2926
MP0003221 abnormal cardiomyocyte apopto	-0.1164469	37	1.448e-02	1.823e-01	MDM2:311 CASP8:345 PTPN11:714 RAF1:835 MAPK8:971 TFAM:1298
MP0005367 renal/urinary system phenotyp	-0.1152034	19	8.251e-02	4.364e-01	BMP4:790 FOXC1:1222 HOXA13:2176 SGPL1:3481 CDKN1A:4590 PAX1:4928
MP0000516 abnormal urinary system	-0.1152034	19	8.251e-02	4.364e-01	BMP4:790 FOXC1:1222 HOXA13:2176 SGPL1:3481 CDKN1A:4590 PAX1:4928
MP0005083 abnormal biliary tract	0.1147850	8	2.611e-01	6.246e-01	MUC1:1494 CCKAR:2204 VTI1B:2217 XYLT2:2526 GPBAR1:4055 LDLR:10003
MP0009840 abnormal foam cell	-0.1144364	11	1.891e-01	5.792e-01	NR1H2:1288 MAPKAPK2:1390 APOA1:1743 SUPV3L1:3484 LDLR:6199 PLA2G15:6564
MP0000749 muscle degeneration	0.1143910	36	1.782e-02	2.056e-01	DMD:11 PLEC:18 HSPB2:149 MYOZ1:342 BAG3:599 KY:767
MP0002254 reproductive system inflammat	-0.1135814	5	3.792e-01	6.903e-01	RELB:2415 PGR:3115 MFGE8:4001 EPHA1:9281 AIRE:12644 NA
MP0002909 abnormal adrenal gland	-0.1121078	21	7.573e-02	4.196e-01	PRKAR1A:465 CADPS:676 PTPN11:714 KCNK3:945 LRRK2:957 CYP11A1:1144
MP0009278 abnormal bone marrow	0.1082746	17	1.226e-01	5.075e-01	MMP9:548 RAG2:1688 HIP1:2149 EP400:2719 TSC22D1:3351 LIG1:4395
MP0003303 peritoneal inflammation	-0.1055470	11	2.258e-01	6.038e-01	LYN:264 PTGS2:829 PECAM1:981 APC:4251 IL10:4620 ST6GAL1:6724
MP0000751 myopathy	0.1046348	21	9.739e-02	4.634e-01	DMD:11 PLEC:18 COL6A1:125 COL15A1:1121 COX10:1798 SLC25A4:1889
MP0010678 abnormal skin adnexa	0.1043021	29		3.611e-01	FGFR2:24 KRT14:507 PKP3:646 DICER1:814 TRPV3:1060 KSR1:1545
MP0004134 abnormal chest morphology	-0.1034136	25		4.196e-01	SLC35D1:706 HOXB4:1064 NKX3-2:1629 CBFB:2475 PTHLH:2552 COL1A1:3291
MP0003252 abnormal bile duct	-0.1028538	22	9.539e-02	4.634e-01	CASP8:345 ATXN2:574 ARL3:3047 NR1H4:3183 NF2:4148 PKHD1:4544
	0.1011023	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
sophagus.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	259	1.379e-01	3.921e-01	HAS2:4 IGF2BP1:78 RHOBTB3:106 ADAM9:130 OSTC:174 FKBP14:219
C1.spinal.cord	-0.02621664	182	2.265e-01	4.978e-01	SCD:80 ENPP2:102 SLC44A1:368 DBX2:404 PMP2:483 TMEM144:632
			0.705 0:		OLOTHEO C. ACTNIA 400 DODINAY OFF ANYWOOD AFED A COT THE COLOTH

7.440e-01 7.923e-01

7.381e-01 7.923e-01

5.917e-01 7.607e-01

5.247e-01 7.506e-01

0.02436904

-0.01896341

0.01680044

-0.01573022

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breast

caudate.nucleus

stomach

lung

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

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