Geneset	stat	num.genes	pval	p.adj	gene.vals
Negative Regulation Of Leukocyte Prolife	-0.4471042	4	1.955e-03	2.522e-01	TNFAIP3:492 IL33:554 ENPP3:986 LYN:1062 NA NA
Nephron Tubule Development (GO:0072080)	0.4332989	3	9.340e-03	3.466e-01	HNF1B:415 MTSS1:1287 OXSR1:1435 NA NA NA
Cellular Response To Nitrogen Levels (GO	-0.4312031	4	2.819e-03	2.984e-01	GABARAPL1:550 BECN2:840 ATG7:952 BECN1:1697 NA NA
Cellular Response To Nitrogen Starvation	-0.4312031	4	2.819e-03	2.984e-01	GABARAPL1:550 BECN2:840 ATG7:952 BECN1:1697 NA NA
Positive Regulation Of Intrinsic Apoptot	-0.4135717	2	4.278e-02	4.893e-01	MYC:858 MSX1:1679 NA NA NA NA
Positive Regulation Of Osteoblast Prolif	-0.4095427	3	1.402e-02	3.789e-01	SOX8:277 CCNA2:1839 HPSE:1896 NA NA NA
Response To Peptidoglycan (GO:0032494)	-0.4047233	5	1.723e-03	2.506e-01	INAVA:402 IL6:430 IRAK3:721 IRF5:2460 RELA:2974 NA
Positive Regulation Of Toll-Like Recepto	0.4033954	3	1.552e-02	3.834e-01	SLC15A4:1238 PTPN22:1240 RSAD2:2062 NA NA NA
Regulation Of Toll-Like Receptor 7 Signa	0.4033954	3	1.552e-02	3.834e-01	SLC15A4:1238 PTPN22:1240 RSAD2:2062 NA NA NA
Cilium Movement Involved In Cell Motilit	0.3980911	7	2.650e-04	1.002e-01	TEKT2:365 TEKT5:791 GAS8:1163 TEKT3:1764 TEKT1:2092 TEKT4:2462
Axonemal Central Apparatus Assembly (GO:	0.3936735	5	2.299e-03	2.689e-01	SPAG17:247 SPEF1:1441 DNAJB13:1934 HYDIN:2157 RSPH9:2559 NA
Valine Metabolic Process (GO:0006573)	-0.3917083	5	2.418e-03	2.711e-01	BCAT2:101 ILVBL:561 HIBCH:2203 HIBADH:2419 BCAT1:2663 NA
Cell Junction Disassembly (GO:0150146)	-0.3865811	4	7.412e-03		C1QB:98 CX3CR1:274 C1QC:489 DKK1:5797 NA NA
Cellular Response To Potassium Ion (GO:0	0.3816254	4	8.208e-03	3.416e-01	DLG4:135 SLC12A2:756 DLG2:890 CRHBP:5565 NA NA
Response To Potassium Ion (GO:0035864)	0.3816254	4	8.208e-03	3.416e-01	DLG4:135 SLC12A2:756 DLG2:890 CRHBP:5565 NA NA
Protein Retention In ER Lumen (GO:000662	0.3732334	3	2.515e-02	4.371e-01	GPAA1:64 KDELR3:927 OS9:4892 NA NA NA
Toll-Like Receptor 9 Signaling Pathway (0.3713153	5	4.034e-03	3.191e-01	IRAK4:591 PIK3AP1:749 IRAK1:2048 UNC93B1:2736 TNIP2:3935 NA
Gastrulation With Mouth Forming Second (-0.3695565	3	2.663e-02	4.408e-01	LRP5:674 UGDH:2075 MEGF8:3006 NA NA NA
Positive Regulation Of Gastrulation (GO:	0.3684619	2	7.110e-02	5.639e-01	OXSR1:1435 SCX:2683 NA NA NA NA
TRAIL-activated Apoptotic Signaling Path	-0.3657934	3	2.821e-02	4.503e-01	FADD:1220 SPI1:1479 ZDHHC3:3229 NA NA NA
Protein Modification By Small Protein Co	-0.3594737	3		4.695e-01	ATG7:952 UBA6:1503 SENP6:3735 NA NA NA
Regulation Of Translation In Response To	-0.3590882	4	1.287e-02		EIF4G1:563 SESN2:1036 NCK1:2637 NCK2:4026 NA NA
Regulation Of Cilium Beat Frequency (GO:	0.3519910	5	6.414e-03		DNAH11:19 CFAP206:481 CFAP43:1915 CYB5D1:2519 CCDC40:6549 NA
snRNA Modification (GO:0040031)	-0.3516117	4	1.487e-02		MEPCE:290 METTL16:2367 METTL4:2585 NHP2:3460 NA NA
L-phenylalanine Catabolic Process (GO:00	-0.3507499	5		3.320e-01	TAT:33 HGD:198 QDPR:640 GSTZ1:2049 IL4I1:8036 NA
L-phenylalanine Metabolic Process (GO:00	-0.3507499	5	6.604e-03		TAT:33 HGD:198 QDPR:640 GSTZ1:2049 IL4I1:8036 NA
Erythrose 4–Phosphate/Phosphoenolpyruvat		5	6.604e-03		TAT:33 HGD:198 QDPR:640 GSTZ1:2049 IL4I1:8036 NA
Negative Regulation Of Actin Filament De	0.3475394	4	1.607e-02		SCIN:355 PLEKHH2:378 VIL1:3087 LIMA1:5643 NA NA
Negative Regulation Of CD8-positive, Alp	0.3473551	6		3.116e-01	SOCS1:275 DAPL1:351 VSIR:1791 HFE:2339 ZBTB7B:3804 SLC4A2:5687
Regulation Of Monoatomic Anion Transport	-0.3471947	4	1.618e-02		CA2:263 ATP8B1:1350 STC1:2071 PDZK1:5295 NA NA
ATP Synthesis Coupled Electron Transport	0.3460955	5			NDUFV1:76 NDUFB6:2653 NDUFS2:2764 NDUFA12:3041 NDUFV3:3480 N
Positive Regulation Of CD4–positive, CD2	-0.3454843	3		4.809e-01	KLHL25:255 HLA-DRA:1410 IFNG:5140 NA NA NA
Negative Regulation Of Mitochondrial Fus	-0.3408040	6		3.191e-01	OMA1:121 SLC18A1:272 HUWE1:288 PRKN:3226 TFRC:3836 MUL1:6284
Signal Complex Assembly (GO:0007172)	-0.3373901	5	8.982e-03		PXN:835 MAPK8IP2:1323 NCK1:2637 SRC:3111 NCK2:4026 NA
Cellular Response To Histamine (GO:00714	-0.3369591	5		3.466e-01	GABRB3:1344 DIAPH1:1407 GABRG2:1470 DHX8:3701 GABRB1:4049 NA
Positive Regulation Of Epithelial Cell D	-0.3366368		4.344e-02		PROM1:269 LIF:566 PAX8:6354 NA NA NA
Positive Regulation Of Translation In Re	-0.3326295	3	4.344e=02 2.122e=02		EIF4G1:563 IMPACT:2587 NCK1:2637 NCK2:4026 NA NA
Regulation Of Lysosomal Protein Cataboli	-0.3326295 -0.3311640	4		3.191e-01	LRP1:91 LAPTM4B:236 USP8:832 MARCHF2:2253 MGAT3:2960 LDLR:853
Mesodermal Cell Differentiation (GO:0048		6			
•	0.3306751	8		2.307e-01	ITGA3:358 ITGB4:951 ITGB1:1752 HMGA2:2252 ITGB3:2909 KDM6B:3230
Alpha–Amino Acid Biosynthetic Process (G	-0.3304389	10	2.9686-04	1.002e-01	BCAT2:101 SDS:167 SDSL:384 ILVBL:561 CPS1:909 MTHFD1:2006

EnrichmentHsSymbolsFile2 Top pathways by permulation

Geneset	stat	num.genes	pval	p.adj	gene.vals
REACTOME_ERYTHROCYTES_TAKE_UP_OXYGEN_AND	-0.4606602	6	9.310e-05	1.232e-02	SLC4A1:27 RHAG:75 CA4:132 CA2:263 CA1:1219 AQP1:1829
WP_CELLULAR_PROTEOSTASIS	0.4482417	2	2.811e-02	3.183e-01	VBP1:530 PFDN2:1028 NA NA NA NA
WP_ARACHIDONATE_EPOXYGENASE_EPOXIDE_HYDR	-0.4090380	2	4.511e-02	3.770e-01	EPHX2:1139 COX5A:1574 NA NA NA NA
BIOCARTA_TERT_PATHWAY	-0.4064353	6	5.650e-04	4.071e-02	SP1:558 MZF1:811 MYC:858 SP3:1257 WT1:1910 TP53:2991
NIKOLSKY_BREAST_CANCER_12Q24_AMPLICON	0.4059417	15	5.230e-08	2.609e-05	NOC4L:116 GALNT9:313 POLE:580 SFSWAP:595 ULK1:660 CHFR:712
REACTOME_LOSS_OF_FUNCTION_OF_SMAD2_3_IN_	-0.4020973	4	5.347e-03	1.425e-01	ZFYVE9:588 TGFB1:994 TGFBR1:1921 TGFBR2:2348 NA NA
REACTOME_SIGNALING_BY_TGF_BETA_RECEPTOR_	-0.4020973	4	5.347e-03	1.425e-01	ZFYVE9:588 TGFB1:994 TGFBR1:1921 TGFBR2:2348 NA NA
STARK_HYPPOCAMPUS_22Q11_DELETION_DN	-0.3836416	20	2.866e-09	3.098e-06	PRODH:8 COMT:10 ARVCF:32 TRMT2A:62 RTN4R:102 TANGO2:251
WP_METHIONINE_METABOLISM_LEADING_TO_SULF	-0.3668945	11	2.514e-05	4.406e-03	BHMT:153 AHCY:195 CSAD:494 CBS:621 MAT1A:666 GNMT:868
TESAR_ALK_TARGETS_EPISC_4D_UP	-0.3607690	2	7.719e-02	4.657e-01	MSX1:1679 PAX6:2478 NA NA NA NA
TESAR_ALK_AND_JAK_TARGETS_MOUSE_ES_D4_UP	-0.3607690	2	7.719e-02	4.657e-01	MSX1:1679 PAX6:2478 NA NA NA NA
MIKHAYLOVA_OXIDATIVE_STRESS_RESPONSE_VIA	-0.3600579	6	2.255e-03	8.970e-02	HSPB1:301 AKR1B1:559 PGAM1:889 CTSD:2433 CALU:3489 OAT:4869
REACTOME_ABACAVIR_TRANSMEMBRANE_TRANSPOR	-0.3582866	4	1.307e-02	2.202e-01	ABCB1:209 SLC22A1:1671 SLC22A3:1984 SLC22A2:4595 NA NA
BIOCARTA_TERC_PATHWAY	-0.3541296	4	1.416e-02	2.294e-01	SP1:558 SP3:1257 NFYC:2399 RB1:4502 NA NA
RANKIN_ANGIOGENIC_TARGETS_OF_VHL_HIF2A_D	-0.3413519	6	3.782e-03	1.179e-01	VEGFA:446 ANGPTL3:882 PLXND1:1391 CDH5:2731 EGFL7:3442 ITGAV:5318
WP_EICOSANOID_METABOLISM_VIA_CYTOCHROME_	-0.3398905	3	4.144e-02	3.647e-01	PPARA:715 EPHX2:1139 PPARG:5310 NA NA NA
MANN_RESPONSE_TO_AMIFOSTINE_DN	-0.3396223	5	8.534e-03	1.802e-01	TWF1:908 BLMH:1352 PRKACB:1473 RRM2:2752 CCNB1:5482 NA
CASTELLANO_HRAS_TARGETS_UP	-0.3379291	3	4.263e-02	3.682e-01	NNAT:1319 PRDX2:1424 GFER:4513 NA NA NA
REACTOME_SARS_COV_2_MODULATES_AUTOPHAGY	0.3370961	10	2.231e-04	2.372e-02	VPS11:237 VPS16:578 VPS33B:1304 VPS45:1538 TUFM:2250 VPS41:2824
WUNDER_INFLAMMATORY_RESPONSE_AND_CHOLEST	-0.3309688	7	2.425e-03	9.361e-02	ALB:80 ADIPOQ:770 CDKN1C:1457 CXCL9:1604 JCHAIN:2639 MPEG1:5451
REACTOME_HIGHLY_SODIUM_PERMEABLE_POSTSYN	0.3306169	7	2.451e-03	9.405e-02	CHRNE:42 CHRNA4:143 CHRND:514 CHRNB4:3111 CHRNA3:4299 CHRNG:4724
REACTOME_DOPAMINE_CLEARANCE_FROM_THE_SYN	-0.3299747	4	2.227e-02	2.877e-01	COMT:10 SLC6A3:680 LRTOMT:2240 MAOA:7220 NA NA
CHEN_HOXA5_TARGETS_6HR_DN	-0.3289429	3	4.845e-02	3.841e-01	ZBED8:1791 NPTXR:2422 FJX1:3450 NA NA NA
SASAI_TARGETS_OF_CXCR6_AND_PTCH1_DN	-0.3252589	7	2.880e-03	1.032e-01	TFPI:1300 MDK:1326 PIP5K1A:1926 OTX1:2352 APOD:2436 ADAM28:3069
WU_HBX_TARGETS_3_DN	-0.3199754	10	4.586e-04	3.765e-02	IL6:430 TGFB1:994 GLG1:1289 GSTA4:1376 GAS6:1596 MAP2K2:1606
BIOCARTA_VOBESITY_PATHWAY	-0.3127738	8	2.187e-03	8.809e-02	LPL:67 RXRA:229 ADIPOQ:770 TNF:1662 RETN:1845 HSD11B1:3473
REACTOME_CIPROFLOXACIN_ADME	-0.3123888	4	3.047e-02	3.219e-01	ALB:80 SLCO1A2:681 SLC22A1:1671 SLC22A8:8754 NA NA
REACTOME_RUNX3_REGULATES_BCL2L11_BIM_TRA	-0.3116319	3	6.155e-02	4.237e-01	BCL2L11:585 FOXO3:3625 RUNX3:4215 NA NA NA
KUROKAWA_LIVER_CANCER_EARLY_RECURRENCE_D	-0.3027063	4	3.601e-02	3.437e-01	VPS35:1269 IGF2R:2739 LCLAT1:3269 RB1:4502 NA NA
REACTOME_LEUKOTRIENE_RECEPTORS	0.3023814	5	1.919e-02	2.688e-01	LTB4R:329 CYSLTR2:855 LTB4R2:1490 CYSLTR1:2852 GPR17:9372 NA
MIKKELSEN_PLURIPOTENT_STATE_DN	-0.3023770	6	1.031e-02	1.967e-01	CASP8:191 CCND2:1127 TGFBR2:2348 CDK6:2438 JAK2:3096 CAMK2D:8492
REACTOME_ABACAVIR_ADME	-0.3009328	7	5.827e-03	1.482e-01	ABCB1:209 ADAL:853 NT5C2:1106 SLC22A1:1671 SLC22A3:1984 SLC22A2:4595
CHOI_ATL_ACUTE_STAGE	-0.3006842	3	7.125e-02	4.532e-01	MET:668 ETV1:3177 MBD1:5074 NA NA NA
REACTOME_ACTIVATION_OF_THE_PHOTOTRANSDUC	0.2979060	5	2.105e-02	2.840e-01	PDE6A:289 CNGA1:443 SAG:1604 RHO:4270 PDE6B:8648 NA
BRUNEAU_HEART_GREAT_VESSELS_AND_VALVULOG	-0.2974618	7	6.420e-03	1.549e-01	JAG1:993 MED13L:1282 TBX1:1600 NOTCH1:1701 PTPN11:3352 NOTCH2:3556
REACTOME_RUNX1_REGULATES_ESTROGEN_RECEPT	-0.2941700	4	4.158e-02	3.647e-01	AXIN1:360 GPAM:1197 RUNX1:3974 ESR1:6753 NA NA
REACTOME_PP2A_MEDIATED_DEPHOSPHORYLATION	0.2941187	4	4.161e-02	3.647e-01	PPP2R1B:1285 PPP2R5D:2209 MLXIPL:3436 PFKFB1:5540 NA NA
WP_COVID19_THROMBOSIS_AND_ANTICOAGULATIO	-0.2939023	6	1.266e-02	2.193e-01	FGG:638 F13B:706 PLG:829 FGB:4689 F13A1:4776 F2:6811
REACTOME_SLBP_DEPENDENT_PROCESSING_OF_RE	-0.2910052	4	4.382e-02	3.724e-01	LSM10:1761 LSM11:3384 NCBP1:3576 SLBP:3750 NA NA
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DisGeNET Top pathways by permulation

8.998e-04 5.453e-02

MDM2:345 LIF:566 BTG2:1699 DDB2:1792 CTSD:2433 XPC:2925

AMUNDSON_DNA_DAMAGE_RESPONSE_TP53

Geneset
HP_SPHEROCYTOSIS

GOCC_9PLUS0_MOTILE_CILIUM

MP0001661 extended life span

MP0002090 abnormal vision

MP0005171 absent coat pigmentation

MP0002877 abnormal melanocyte morpholog -0.1031842

0.1034317

0.1033343

-0.1030260

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Geneset	Stat	num.genes	Pvai	p.auj	yene.vais
Anemia, hereditary spherocytic hemolytic	-0.4941793	5	1.297e-04	4.956e-02	SLC4A1:27 EPB42:42 SPTB:85 ANK1:119 SPTA1:135 NA
Spherocytosis	-0.4941793	5	1.297e-04	4.956e-02	SLC4A1:27 EPB42:42 SPTB:85 ANK1:119 SPTA1:135 NA
Angiokeratoma	-0.4740601	3	4.457e-03	2.579e-01	MANBA:142 VEGFA:446 GLA:507 NA NA NA
Abnormality of cranial vault shape	-0.4169462	2	4.112e-02	4.572e-01	SPECC1L:151 PEX19:2323 NA NA NA NA
Abnormality of cranium shape	-0.4169462	2	4.112e-02	4.572e-01	SPECC1L:151 PEX19:2323 NA NA NA NA
Abnormality of head shape	-0.4169462	2	4.112e-02	4.572e-01	SPECC1L:151 PEX19:2323 NA NA NA NA
Asymmetry of head	-0.4169462	2	4.112e-02	4.572e-01	SPECC1L:151 PEX19:2323 NA NA NA NA
Malformation of cranial vault shape	-0.4169462	2	4.112e-02	4.572e-01	SPECC1L:151 PEX19:2323 NA NA NA NA
Malformation of cranium shape	-0.4169462	2	4.112e-02	4.572e-01	SPECC1L:151 PEX19:2323 NA NA NA NA
Malformation of head shape	-0.4169462	2	4.112e-02	4.572e-01	SPECC1L:151 PEX19:2323 NA NA NA NA
Aase Smith syndrome 2	-0.4099371	3	1.392e-02	3.404e-01	TSR2:1233 RPS10:1273 GATA1:1475 NA NA NA
Monilethrix	0.4092319	2	4.501e-02	4.695e-01	KRT80:954 DSG4:1826 NA NA NA NA
Maple Syrup Urine Disease, Thiamine Resp	-0.4079594	5	1.582e-03	1.782e-01	BCAT2:101 PPM1K:861 BCKDHA:1038 DBT:1399 BCKDHB:3382 NA
Classic Maple Syrup Urine Disease	-0.4079594	5	1.582e-03	1.782e-01	BCAT2:101 PPM1K:861 BCKDHA:1038 DBT:1399 BCKDHB:3382 NA
Intermediate Maple Syrup Urine Disease	-0.4079594	5	1.582e-03	1.782e-01	BCAT2:101 PPM1K:861 BCKDHA:1038 DBT:1399 BCKDHB:3382 NA
Intermittent Maple Syrup Urine Disease	-0.4079594	5	1.582e-03	1.782e-01	BCAT2:101 PPM1K:861 BCKDHA:1038 DBT:1399 BCKDHB:3382 NA
Herlitz Disease	0.4026420	5	1.820e-03	1.959e-01	LAMC2:427 ITGB4:951 LAMA3:1863 LAMB3:1910 ITGA6:2330 NA
delta beta^0^ Thalassemia	0.3967382	2	5.197e-02	4.927e-01	PSMB6:543 DLL1:2626 NA NA NA NA
Miller Fisher Syndrome	0.3954018	3	1.769e-02	3.684e-01	PSMB6:543 SMUG1:1645 DLL1:2626 NA NA NA
Junctional split	0.3951658	6	8.020e-04	1.289e-01	LAMC2:427 ITGB4:951 LAMA3:1863 LAMB3:1910 PLEC:2200 ITGA6:2330
Desmoplastic infantile astrocytoma	-0.3921741	6	8.787e-04	1.367e-01	HDAC6:158 DIAPH2:411 LIF:566 BRAF:2130 TP53:2991 PTPN11:3352
PAROXYSMAL EXTREME PAIN DISORDER	-0.3909838	5	2.464e-03	2.147e-01	SCN9A:735 SCN10A:766 SCN11A:1111 IDS:1200 MCF2L2:4195 NA
Progression of non-small cell lung cance	0.3900721	2	5.604e-02	4.970e-01	CCR7:1133 CD274:2251 NA NA NA NA
Sepsis of the newborn	-0.3898952	3	1.934e-02	3.809e-01	IL6:430 SERAC1:1490 ST14:2980 NA NA NA
Occipital myelomeningocele	-0.3893550	9	5.241e-05	3.022e-02	COMT:10 ARVCF:32 UFD1:383 HIRA:1025 TBX1:1600 GP1BB:2218
22q11 partial monosomy syndrome	-0.3889745	11	7.942e-06	7.786e-03	COMT:10 ARVCF:32 UFD1:383 PI4KA:789 HIRA:1025 TBX1:1600
Bacterial sepsis of newborn	-0.3852926	2	5.912e-02	5.005e-01	IL6:430 ST14:2980 NA NA NA NA
Visually threatening diabetic retinopath	-0.3811640	4	8.285e-03	3.088e-01	VEGFA:446 TNF:1662 CXCL12:2465 LTA:2524 NA NA
EPIDERMOLYSIS BULLOSA, JUNCTIONAL, LOCAL	0.3810702	5	3.167e-03	2.197e-01	LAMC2:427 ITGB4:951 LAMA3:1863 LAMB3:1910 COL17A1:3959 NA
Adult junctional epidermolysis bullosa (0.3810702	5	3.167e-03	2.197e-01	LAMC2:427 ITGB4:951 LAMA3:1863 LAMB3:1910 COL17A1:3959 NA
Epidermolysis Bullosa Progressiva	0.3810702	5	3.167e-03	2.197e-01	LAMC2:427 ITGB4:951 LAMA3:1863 LAMB3:1910 COL17A1:3959 NA
JEB-I	0.3810702	5	3.167e-03	2.197e-01	LAMC2:427 ITGB4:951 LAMA3:1863 LAMB3:1910 COL17A1:3959 NA
Palmar hyperhidrosis	0.3810702	5	3.167e-03	2.197e-01	LAMC2:427 ITGB4:951 LAMA3:1863 LAMB3:1910 COL17A1:3959 NA
Selenium measurement	-0.3777256	4	8.886e-03	3.174e-01	BHMT:153 CBS:621 DMGDH:2503 ARSB:3977 NA NA
Plantar hyperkeratosis	0.3771878	6	1.376e-03	1.752e-01	LAMC2:427 ITGB4:951 LAMA3:1863 LAMB3:1910 PLEC:2200 COL17A1:3959
Vulvar Neoplasms	-0.3770650	3	2.370e-02	4.097e-01	CA9:1415 CASP3:1995 PTGS2:2086 NA NA NA
Exudative vitreoretinopathy	-0.3767089	5	3.531e-03	2.355e-01	ZNF408:671 LRP5:674 NDP:2526 FZD4:2574 TSPAN12:2774 NA
Chronic iridocyclitis	-0.3764464	2	6.519e-02	5.133e-01	IL6:430 RBM45:3228 NA NA NA NA
prenatal alcohol exposure	-0.3759644	4	9.209e-03	3.174e-01	VEGFA:446 IGF2:1206 HAND1:2027 NTRK2:3675 NA NA
Myelitis	0.3742033	4	9.542e-03	3.174e-01	LAMC2:427 CSF2:1157 POU2F3:1450 AQP4:4657 NA NA

1.522e-06 7.105e-04 SLC4A1:27 EPB42:42 RHAG:75 SPTB:85 ANK1:119 SPTA1:135

0.4706930 4 1.112e-03 7.732e-02 DNAH11:19 CFAP45:132 DNAH5:728 ENKUR:916 NA NA

GSEA-c5-HsSymbols Top pathways by permulation

GOCC_9PL030_MOTILE_CILIDIVI	0.4706930	4	1.1126-03	1.1326-02	DNAH 11.19 GFAF45.132 DNAH5.726 ENKUK.916 NA NA
GOMF_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_P	-0.4502446	2	2.742e-02	3.489e-01	CYP11A1:14 CYP2U1:1454 NA NA NA NA
GOBP_BRANCHED_CHAIN_AMINO_ACID_BIOSYNTHE	-0.4478230	5	5.242e-04	5.041e-02	BCAT2:101 SDS:167 SDSL:384 ILVBL:561 BCAT1:2663 NA
GOBP_REGULATION_OF_PROTEIN_TYROSINE_PHOS	-0.4360294	3	8.902e-03	2.205e-01	SLC39A10:471 PTPRC:946 MGAT5:1418 NA NA NA
GOBP_ESTABLISHMENT_OF_LEFT_RIGHT_ASYMMET	0.4315091	4	2.799e-03	1.237e-01	CFAP45:132 CFAP52:536 ENKUR:916 CCDC39:2623 NA NA
GOBP_L_CYSTEINE_METABOLIC_PROCESS	-0.4274072	4	3.070e-03	1.313e-01	CSAD:494 CBS:621 AGXT:1531 CDO1:1648 NA NA
GOBP_POSITIVE_REGULATION_OF_CONNECTIVE_T	0.4179378	2	4.063e-02	4.023e-01	ROCK2:1193 ROCK1:1322 NA NA NA NA
GOBP_NEURON_NEURON_SYNAPTIC_TRANSMISSION	0.4071315	4	4.800e-03	1.643e-01	DRD2:170 KIF1B:1181 TMOD2:1280 DLGAP2:3057 NA NA
GOBP_REGULATION_OF_TOLL_LIKE_RECEPTOR_7_	0.4013936	3	1.604e-02	2.782e-01	SLC15A4:1238 PTPN22:1240 RSAD2:2062 NA NA NA
GOBP_LEUKOTRIENE_CATABOLIC_PROCESS	0.3946611	2	5.321e-02	4.493e-01	DPEP2:1230 DPEP1:2003 NA NA NA NA
GOMF_C3HC4_TYPE_RING_FINGER_DOMAIN_BINDI	0.3941574	2	5.351e-02	4.500e-01	KCNH2:878 PINK1:2374 NA NA NA NA
HP_ABNORMAL_ISOHEMAGGLUTININ_LEVEL	-0.3926089	5	2.362e-03	1.135e-01	SLC35C1:350 CD19:565 ARHGEF1:857 CR2:2474 PRKCD:3712 NA
HP_MULTIPLE_GLOMERULAR_CYSTS	0.3923749	3	1.858e-02	2.981e-01	HNF1B:415 NPHP3:1504 MYOCD:3029 NA NA NA
HP_DECREASED_SERUM_COMPLEMENT_FACTOR_I	-0.3917854	4	6.650e-03	1.925e-01	C1QB:98 C1QA:335 C1QC:489 CFI:5494 NA NA
HP_ABNORMAL_PERIFOLLICULAR_MORPHOLOGY	-0.3876736	3		3.045e-01	LRP1:91 HLA-DRA:1410 MBTPS2:3498 NA NA NA
GOCC INNER DYNEIN ARM	0.3874496	4	7.278e-03		DNAH1:1176 DNHD1:1468 DNAH2:1926 DNAH7:2355 NA NA
GOCC_PREFOLDIN_COMPLEX	0.3844835	3		3.091e-01	VBP1:530 PFDN2:1028 PDRG1:3752 NA NA NA
GOCC_GPI_ANCHOR_TRANSAMIDASE_COMPLEX	0.3817825	4		2.113e-01	GPAA1:64 PIGK:455 PIGT:3026 PIGS:3696 NA NA
GOBP_SRP_DEPENDENT_COTRANSLATIONAL_PROTE	0.3808102	2		4.722e-01	SRPRB:1701 SRPRA:1964 NA NA NA NA
GOBP_ATTACHMENT_OF_GPI_ANCHOR_TO_PROTEIN	0.3807917	5		1.331e-01	GPAA1:64 PIGK:455 PGAP1:1898 PIGT:3026 PIGS:3696 NA
GOBP_LEUKOTRIENE_SIGNALING_PATHWAY	0.3769341	5		1.396e-01	LTB4R:329 CYSLTR2:855 LTB4R2:1490 CYSLTR1:2852 RGS1:3903 NA
HP_FALCIFORM_RETINAL_FOLD	-0.3758978	5		1.422e-01	ZNF408:671 LRP5:674 NDP:2526 FZD4:2574 TSPAN12:2774 NA
HP_HYPOPLASTIC_DERMOEPIDERMAL_HEMIDESMOS	0.3732250	7		5.456e-02	LAMC2:427 ITGB4:951 LAMA3:1863 LAMB3:1910 PLEC:2200 ITGA6:2330
GOMF_RIBOSOMAL_PROTEIN_S6_KINASE_ACTIVIT	0.373233	4		2.303e-01	RPS6KA1:154 RPS6KA6:157 RPS6KA2:2241 RPS6KA4:5263 NA NA
HP_PERIPHERAL_RETINAL_AVASCULARIZATION	-0.3711074	6		9.585e-02	ZNF408:671 LRP5:674 DLK1:2272 NDP:2526 FZD4:2574 TSPAN12:2774
GOBP_POSITIVE_REGULATION_OF_GLYCOGEN_STA	-0.3678086	5	4.394e-03		ADIPOQ:770 EPM2AIP1:1155 IGF2:1206 GSK3A:2713 PPP1R3G:3948 NA
GOBP_NEGATIVE_REGULATION_OF_PROTEIN_CATA	-0.3669162	5		1.619e-01	LAPTM4B:236 USP8:832 VPS35:1269 MGAT3:2960 ATP13A2:4568 NA
HP_FAILURE_TO_THRIVE_SECONDARY_TO_RECURR	0.3667770	6		1.019e-01	CD3E:721 RAG1:781 CD3D:1763 IL7R:2213 CD247:3108 RAG2:3676
GOMF_PHOSPHATIDYLSERINE_FLIPPASE_ACTIVIT	-0.3654336	5		1.636e-01	ATP11A:138 ATP11C:1005 ATP8B1:1350 ATP8A1:1558 ATP8A2:5920 NA
GOMF_MHC_CLASS_II_RECEPTOR_ACTIVITY	-0.3653929	4		2.485e-01	HLA-DOB:673 HLA-DRA:1410 HLA-DOA:2845 HLA-DPA1:3070 NA NA
HP RECURRENT	-0.3641814	5		1.643e-01	ADORA2A:176 BCKDHA:1038 DBT:1399 BCKDHB:3382 PTH:4065 NA
HP_PARTIAL_ABSENCE_OF_SPECIFIC_ANTIBODY_	-0.3622382	5		1.679e-01	TNFRSF13B:258 CD19:565 CR2:2474 ICOS:2676 SASH3:4241 NA
GOMF MINUS END DIRECTED MICROTUBULE MOTO					
GOCC_AXONEMAL_DYNEIN_COMPLEX	0.3617653	16			DNAH11:19 DNAH3:232 DNAH10:368 DNAH9:435 DYNC2H1:487 DNAH5:72 DNAI2:36 DNAH3:232 CCDC65:326 DNAH9:435 DNAH5:728 DNAH17:1027
	0.3615223	16			
GOBP_RNA_MEDIATED_HETEROCHROMATIN_FORMAT	-0.3613890	5		1.692e-01	SIRT6:866 FAM172A:1620 HELLS:1683 ZNFX1:2720 CENPV:3392 NA
GOBP_PARATHYROID_GLAND_DEVELOPMENT	-0.3581282	6		1.135e-01	GATA3:1405 TBX1:1600 GCM2:1880 TGFBR1:1921 HOXA3:2606 CRKL:321
GOBP_NEGATIVE_REGULATION_OF_SYNAPTIC_VES	-0.3522943	3		3.812e-01	FMR1:1021 BRAF:2130 SYT4:3421 NA NA NA
GOBP_POSITIVE_REGULATION_OF_RNA_EXPORT_F GOMF_RNA_POLYMERASE_II_CTD_HEPTAPEPTIDE_	-0.3517053	2		5.181e-01	DHX9:2018 NRDE2:2382 NA NA NA NA
	-0.3484598	6	3.116e-03	1.315e-01	CDK7:118 BRD4:181 CDK13:417 CDK12:1032 DYRK1A:4390 CCNK:7328

MGI_Mammalian_Phenotype_Level_4 Top pathways by permulation

MP000069d spinal hemorrhage						
MP0003121 genomic imprinting	Geneset	stat	num.genes	pval	p.adj	gene.vals
MP0003122 maternal imprinting	MP0006054 spinal hemorrhage	-0.2188257	8	3.219e-02	3.058e-01	SPHK1:725 TFPI:1300 C1GALT1:1852 FLI1:2179 PSEN1:3166 FBLN1:4638
MP0003724 increased susceptibility to	MP0003121 genomic imprinting	-0.2068265	20	1.387e-03	6.818e-02	AXIN1:360 SGCE:1001 ARID4A:1205 CDKN1C:1457 HELLS:1683 NDN:1893
MP0003646 abnormal pituitary gland 0.1657007 18 1.507e-02 2.170e-01 GNRH:1:106 DRD2:170 RASGRF1:370 ARNT2:413 NF1:1248 PROP1:1599 MP0003306 abnormal irrinary bladder 0.1592785 14 3.927e-02 3.4560e-01 PECAMI:312 LYH:1062 PTGS2:2066 SCOS3:22487 STG6AL1:3151 IL:104:251 MP0010386 abnormal irrinary bladder 0.1592785 14 3.927e-02 3.456e-01 MR3:1023 PSNI-2035 PSNI-	MP0003122 maternal imprinting	-0.1997596	11	2.189e-02	2.692e-01	AXIN1:360 SGCE:1001 ARID4A:1205 IGF2:1206 NDN:1893 DLK1:2272
MP0003303 peritoneal inflammation	MP0003724 increased susceptibility to	-0.1667610	15	2.550e-02	2.692e-01	PECAM1:312 IFNGR1:341 FPR2:610 SOD3:2172 SOCS3:2847 TNFSF10:3272
MP000254 reproductive system inflammat	MP0005646 abnormal pituitary gland	0.1657007	18	1.507e-02	2.170e-01	GNRH1:106 DRD2:170 RASGRF1:370 ARNT2:413 NF1:1248 PROP1:1599
MP0002254 reproductive system inflammat	MP0003303 peritoneal inflammation	-0.1607388	10	7.860e-02	4.560e-01	PECAM1:312 LYN:1062 PTGS2:2086 SOCS3:2847 ST6GAL1:3151 IL10:4251
MP0005275 abnormal skin tensile 0.1559055 17 2.623e-02 2.692e-01 OGN:224 LAMC2:427 COL5A2:1543 DSE:1639 DSG4:1826 FBN1:2053 MP0004043 abnormal pH regulation -0.1486003 14 5.446e-02 4.116e-01 RHGG:202 SLC12A1:221 SLC26A7:1687 WWK4:1842 SLC4A10:2102 SLC4A7:2631 MP0008438 abnormal cutaneous collagen 0.1482985 14 5.505e-02 4.116e-01 MYOSA:725 CBL:999 MC1R:2073 DOCK7:3084 BLOC1S3:3615 KIT.4099 MP0003172 abnormal jvsosome physiology -0.1429867 21 2.356e-02 2.682e-01 NAGPA:12 MANBA:142 AP381:982 IDS:1500 HPS4:1403 CTSD:2433 MP0000575 myopathy -0.1425967 18 3.652e-02 2.336e-01 TCAF:145 DMI:228 ITGA7:555 PLEC:2200 COL6A1:220 LDB3:3414 MP0006292 abnormal olfactory placode -0.1328421 10 1.461e-01 5.640e-01 HHEX:599 HEX1:2469 PAX6:2478 POU2F1:3863 DKK1:5797 GBX2:6535 MP0003123 paternal imprinting -0.139116 7 2.306e-01 4.708e-01 AXIII:360 CDK/11:25 NF1:1248 UCP2:1627 AVP:194 PROKR2:2996 F6721-4787 MP0003203 gastrointestinal ulcer -0.1295960 14 9.350e-02 4.706e-01 AXIII:360 CDK/11:25 NF1:1248 UCP2:1627 AVP:194 PROKR2:2996 F6721-4787 MP0001234 abnormal c	MP0010386 abnormal urinary bladder	0.1592785	14	3.927e-02	3.406e-01	CHRM3:1023 FBN1:2053 PSAP:2058 CHRNB4:3111 UPK2:3431 KCNMA1:4062
MP0004043 abnormal pH regulation -0.1486003 14 5.446e-02 4.116e-01 RHCG:202 SLC12A1:221 SLC26A7:1687 WNK4:1842 SLC4A10:2102 SLC4A7:2631 MP0005174 abnormal tail pigmentation 0.1482395 14 5.505e-02 4.116e-01 MY05A:725 CBL:1999 MC1R:2073 DOCK7:3084 BLOC1S3:3615 KIT:4099 MP000372 abnormal givacome physiology -0.1429487 21 2.356e-02 2.692e-01 NAGPA:12 MANBA:142 AP381:3962 IDS:1200 HPS4:1403 CTSD:2433 MP0000751 myopathy 0.1425507 18 3.652e-02 3.336e-01 TCAP:145 DMD:228 ITGA7:555 PLEC:2200 COL6A1:2205 LDB3:3414 MP0000529 abnormal olfactory placode -0.1328421 10 1.461e-01 5.640e-01 ATG-4:145 DMD:228 ITGA7:555 PLEC:2200 COL6A1:2205 LDB3:3414 MP0005260 abnormal autophagy -0.1311174 15 7.904e-02 4.560e-01 ATG-4:45 DMD:228 ITGA7:555 PLEC:2200 COL6A1:2205 LDB3:3414 MP0005645 abnormal pyothalamus physiol 0.1309957 14 9.01e-02 4.766e-01 ATG-4:287 ATG-9:52 PMP22:1059 BNIP3L:1187 BECN1:1697 ATG-9:3320 MP0003123 paternal imprinting -0.1309116 7 2.366e-01 7.087e-01 ATG-4:287 ATG-9:52 PMP22:1059 BNIP3L:1187 BECN1:1697 ATG-9:3320 MP000300 gastroinetstinal ulcer -0.1295960 14 9.350e-02 4.706e-01 ATG-4:1376 PKHD1:2431 CYLD:3313 IL2:3749 IL10:4251 MP0001324 abnormal vibrissa follicle 0.1268649 4 3.797e-01 8.016e-01 PKP3:866 CHUK:3642 SPINK5:6419 ST14:12007 NA NA MP0003466 muscle fatigue 0.1263482 9 1.896e-01 ASG-9-01 ASG-9-02 BASE-2	MP0002254 reproductive system inflammat	-0.1580762	5	2.211e-01	7.048e-01	MFGE8:1508 RELB:2427 EPHA1:4254 PGR:4342 AIRE:12758 NA
MP0005174 abnormal tall pigmentation 0.1482395 14 5.505e-02 4.116e-01 MYOSA:725 CBL:999 MC1R:2073 DOCK7:3084 BLOC1S3:3615 KIT:4099 MP0003472 abnormal cutaneous collagen 0.1429851 15 5.546e-02 4.116e-01 OGN:224 PLOD1:610 COL5A2:1543 DSE:1639 FBM1:2063 TNXB:2066 MP0003172 abnormal lysosome physiology 0.1425507 18 3.652e-02 3.336e-01 TCAP:145 DMD:228 ITGAT:555 PLEC:2200 COL6A1:2205 LDB3:3414 MP0006292 abnormal olfactory placode -0.1328421 10 1.461e-01 5.640e-01 HHEX:599 HESX1:2469 PAX6:2478 POU2F1:3963 DKK1:5797 GBX2:6535 MP0008260 abnormal autophagy -0.1311174 15 7.904e-02 4.560e-01 ATG4C:874 ATG7:952 PMP22:1059 BNIP3L:1187 BECN1:1697 ATG9A:3124 MP0003646 abnormal hypothalamus physiol 0.1309957 14 9.001e-02 4.706e-01 NOS1:1025 NF1:1248 UCP2:1627 AVP:1941 PROKR2:2996 FGF21:4787 MP003320 gastrointestinal ulcer -0.1295960 14 9.350e-02 4.706e-01 TGFB1:994 VDR:1467 PKHD1:2431 CYLD:3313 IL2:3749 IL10:4251 MP0001324 abnormal chest morphology -0.1263750 22 4.050e-02 3.406e-01 PTCH1:718 HOXB4:973 NXX3-2:1164 PDGFA:1165 SLG35D1:1358 UNCX:1439 MP0003646 muscle fatigue 0.1263482 9 1.896e-01 A30e-01 PTCH1:718 HOXB4:973 NXX3-2:1164 PDGFA:1165 SLG35D1:1358 UNCX:1439 MP000379 abnormal vocalization 0.124357 7 2.657e-01 A30e-01 DRD2:170 TERFI:1095 MC1R2:073 KIR1:4099 CDKN2A:9791 TERF2:IP1044 MP0003890 abnormal embryonic-extraembry -0.1205357 8 2.330e-01 7.087e-01 ARIDA4:205 CDKN1C:1457 ATRX:2634 ARIDA8:4400 RB1:4502 SMCHD1:5014 MP0003890 abnormal embryonic-extraembry -0.1170:296 16 1.055e-01 A891e-01 GCLC:215 HSD17B12:487 HIRA:1025 PALB:21287 FOXH:1:1619 FOXA2:2417 MP0003666 abnormal autopic presentation 0.1149886 48 6.027e-03 4.301e-01 SCAPA:225 CBL:999 SLC24A5:1481 MC1R:2073 PCLH:3201 BLOC1S:3615 MP0000185 abnormal autopic presentation 0.1149886 48 6.027e-03 5.122e-01 MYOSA:725 CBL:999 SLC24A5:1481 MC1R:2073 PCLH:3201 BLOC1S:3615 MP00004270 analgesia 0.1087706	MP0005275 abnormal skin tensile	0.1559055	17	2.623e-02	2.692e-01	OGN:224 LAMC2:427 COL5A2:1543 DSE:1639 DSG4:1826 FBN1:2053
MP0008438 abnormal cutaneous collagen 0.1429851 15 5.546e-02 4.116e-01 OGN:224 PLOD1:610 COL5A2:1543 DSE:1639 FBN1:2053 TNXB:2066 MP0003172 abnormal lysosome physiology -0.1429487 21 2.356e-02 2.692e-01 NAGRA:12 MANBA:142 AP3B1:962 IDS:1200 HPSA:1403 CTSD:2433 MP0006292 abnormal olfactory placode -0.1328421 10 1.461e-01 5.640e-01 HEX:599 HESX:1:2469 PAX6:2478 POUPE1:3963 DKK1:5797 GBX2:6535 MP0005292 abnormal olfactory placode -0.1328421 10 1.461e-01 5.640e-01 HEX:599 HESX:1:2469 PAX6:2478 POUPE1:3963 DKK1:5797 GBX2:6535 MP0005463 abnormal hypothalamus physiol 0.1309957 14 9.001e-02 4.708e-01 NOS1:1025 NF1:1248 UCP2:1627 AVP:1941 PROKR2:2996 FGF21:4787 MP0003123 paternal imprinting -0.1309116 7 2.306e-01 7.087e-01 AXIN1:360 CDXN1c:1457 HELLS:1683 GRB10:2997 UB23:33 IL2:3749 IL10:4251 MP0003302 gastrointestinal ulcer -0.126560 14 9.359e-02 4.708e-01 AXIN1:360 CDXN1c:1457 HELLS:1683 GRB10:2997 UB23:33 IL2:3749 IL10:4251 MP0001234 abnormal vibrissa follicle 0.1268649 4 3.797e-01 8.016e-01 PKP3:866 CHUK:3462 SPINK5:6419 STI4:12007 NA NA MP0000	MP0004043 abnormal pH regulation	-0.1486003	14	5.446e-02	4.116e-01	RHCG:202 SLC12A1:221 SLC26A7:1687 WNK4:1842 SLC4A10:2102 SLC4A7:2631
MP0003172 abnormal lysosome physiology MP0000751 myopathy MP0006292 abnormal olfactory placode MP0006292 abnormal olfactory placode MP0006292 abnormal autophagy MP0006292 abnormal autophagy MP0006292 abnormal autophagy MP0006260 abnormal autophagy MP0006260 abnormal autophagy MP0006260 abnormal autophagy MP0005645 abnormal hypothalamus physiol MP0005645 abnormal hypothalamus physiol MP0003139 paternal imprinting MP0003139 paternal imprinting MP0003230 gastrointestinal ulcer MP0003230 gastrointestinal ulc	MP0005174 abnormal tail pigmentation	0.1482395	14	5.505e-02	4.116e-01	MYO5A:725 CBL:999 MC1R:2073 DOCK7:3084 BLOC1S3:3615 KIT:4099
MP0000751 myopathy 0.1425507 18 3.652e-02 3.336e-01 TCAP:145 DMD:228 ITGA7:555 PLEC:2200 COL6A1:2205 LDB3:3414 MP0006292 abnormal olfactory placode -0.1328421 10 1.461e-01 5.640e-01 HHEX:599 HESX1:2469 PAX6:2478 POU2F1:3963 DKK1:5797 GBX2:6535 MP0005645 abnormal autophagy -0.1311174 15 7.904e-02 4.560e-01 AG4C:874 ATG7:952 PMP22:1059 BNIP3L:1187 BECN1:1697 ATG9A:3124 MP0005645 abnormal hypothalamus physiol 0.1309957 14 9.01e-02 4.706e-01 NOS1:1025 NF1:1248 UCP2:1627 AVP:1941 PROKR2:2996 FGF21:4787 MP0003123 paternal imprinting -0.139916 7 2.306e-01 7.087e-01 AXIN1:360 CDKN1C:1457 HELLS:1683 GRB10:2987 UBE3A:3320 GPC3:13904 MP00103300 gastrointestinal ulcer -0.1295960 14 9.350e-02 4.706e-01 TGFB1:994 VDR:1467 PKHD1:2431 CYLD:3313 IL2:3749 IL10:4251 MP0010234 abnormal vibrissa follicle 0.1268649 4 3.797e-01 8.016e-01 PKP3:866 CHUK:3642 SPINK5:6419 ST14:12007 NA NA MP0001529 abnormal wocalization 0.1263482 9 1.896e-01 6.433e-01 NOS1:1025 MB:2632 SLC2A4:2829 MTOR:3196 SOD2:3555 PPARGC14:5051 MP00001529 abnormal wocalization 0.	MP0008438 abnormal cutaneous collagen	0.1429851	15	5.546e-02	4.116e-01	OGN:224 PLOD1:610 COL5A2:1543 DSE:1639 FBN1:2053 TNXB:2066
MP0006292 abnormal olfactory placode -0.1328421 10 1.461e-01 5.640e-01 HHEX:599 HESX1:2469 PAX6:2478 POUZF1:3963 DKK1:5797 GBX2:6535 MP0008260 abnormal autophagy -0.1311174 15 7.904e-02 4.560e-01 ATG4C:874 ATG7:952 PMP22:1059 BNIP3L:1187 BECN1:1697 ATG9A:3124 MP0005645 abnormal hypothalamus physiol 0.1309957 14 9.001e-02 4.706e-01 NOS1:1025 NF1:1248 UCP2:1627 AVP:1941 PROKR2:2996 FGF21:4787 MP0003123 paternal imprinting -0.1309116 7 2.308e-01 7.087e-01 AXIN1:360 CDKN10:1457 HELLS:1683 GRB10:2987 UBE3A:3320 GPC3:13994 MP0003300 gastrointestinal ulcer -0.1295960 14 9.350e-02 4.706e-01 TGFB1:994 VDR:1467 PKHD1:2431 CYLD:3313 IL2:3749 IL10:4251 MP0010234 abnormal vibrissa follicle 0.1268649 4 3.797e-01 8.016e-01 PKP3:866 CHUK:3642 SPINK5:6419 ST14:1207 NA NA MP0003646 muscle fatigue 0.1263482 9 1.896e-01 4.301e-01 EZF4:92 DRD2:170 FOXP2:743 CHRM2:1927 TOR1A:2129 NDUFS4:2154 MP0001589 abnormal exponication 0.1215453 7 2.657e-01 7.294e-01 DRD2:170 TERF1:1095 MC1R:2073 KIT:4099 CDKN2A:9791 TERF2IP:10244 MP0003890 abnormal empryonic-extraembry <td>MP0003172 abnormal lysosome physiology</td> <td>-0.1429487</td> <td>21</td> <td>2.356e-02</td> <td>2.692e-01</td> <td>NAGPA:12 MANBA:142 AP3B1:962 IDS:1200 HPS4:1403 CTSD:2433</td>	MP0003172 abnormal lysosome physiology	-0.1429487	21	2.356e-02	2.692e-01	NAGPA:12 MANBA:142 AP3B1:962 IDS:1200 HPS4:1403 CTSD:2433
MP0008260 abnormal autophagy -0.1311174 15 7.904e-02 4.560e-01 ATG4C:874 ATG7:952 PMP22:1059 BNIP3L:1187 BECN1:1697 ATG9A:3124 MP0005645 abnormal hypothalamus physiol 0.1309957 14 9.001e-02 4.706e-01 NOS1:1025 NF1:1248 UCP2:1627 AVP:1941 PROKR2:2996 FGF21:4787 MP0003300 gastrointestinal ulcer -0.139960 14 9.350e-02 4.706e-01 TGFB1:994 VDR:1467 PKHD1:2431 CYLD:3313 IL2:3749 IL10:4251 MP0010234 abnormal vibrissa follicle 0.1268649 4 3.797e-01 8.016e-01 PKP3:666 CHUK:3642 SPINK5:6419 ST14:12007 NA NA MP0004134 abnormal chest morphology -0.1263750 22 4.050e-02 3.406e-01 PTCH1:718 HOXB4:973 NKX3-2:1164 PDGFA:1165 SLC35D1:1358 UNCX:1439 MP0001529 abnormal vocalization 0.1263482 9 1.896e-01 6.433e-01 NOS1:1025 MB:2632 SLC2A4:2829 MTOR:3196 SOD2:3555 PPARGC1A:5051 MP0001529 abnormal vocalization 0.1215453 7 2.657e-01 7.294e-01 DRD2:170 TERF1:1095 MCT:273 CHRM2:1927 TOR1A:2129 NDUFS4:2154 MP0003787 abnormal imprinting 0.1205357 8 2.380e-01 7.087e-01 A.8114:205 CDKN1C:1457 ATRX:2634 ARID48:4400 RB1:4502 SMCHD1:5014 MP0003890 abnormal embryonic-extra	MP0000751 myopathy	0.1425507	18	3.652e-02	3.336e-01	TCAP:145 DMD:228 ITGA7:555 PLEC:2200 COL6A1:2205 LDB3:3414
MP0005645 abnormal hypothalamus physiol 0.1309957 14 9.001e-02 4.706e-01 NOS1:1025 NF1:1248 UCP2:1627 AVP:1941 PROKR2:2996 FGF21:4787 MP0003123 paternal imprinting -0.1309116 7 2.306e-01 7.087e-01 AXIN1:360 CDKN1C:1457 HELLS:1683 GRB10:2987 UBE3A:3320 GPC3:13904 MP0003300 gastrointestinal ulcer -0.1295960 14 9.350e-02 4.706e-01 TGFB1:994 VDR:1467 PKHD1:2431 CYLD:3313 IL2:3749 IL10:4251 MP0010234 abnormal vibrissa follicle 0.1268649 4 3.797e-01 8.016e-01 PKP3:866 CHUK:3642 SPINK5:6419 ST14:12007 NA NA MP0001484 abnormal chest morphology -0.1263750 22 4.050e-02 3.406e-01 PTCH1:718 HOXB4:973 NKX3-2:1164 PDGFA:1165 SLC35D1:1358 UNCX:1439 MP0001529 abnormal vocalization 0.1263482 9 1.896e-01 6.433e-01 NOS1:1025 MB:2632 SLC2A4:2829 MTOR:3196 SOD2:3555 PPARGC1A:5051 MP0001188 hyperpigmentation 0.1215453 7 2.657e-01 7.294e-01 DRD2:170 TERF1:1095 MC1R:2073 KIT:4099 CDKN2A:9791 TERF2IP:10244 MP0003890 abnormal embryonic-extraembry -0.1170296 16 1.055e-01 4.891e-01 GCLC:215 HSD17B12:487 HIRA:1025 PALB2:1287 FOXH1:1619 FOXA2:2417 MP0003656 abnormal em	MP0006292 abnormal olfactory placode	-0.1328421	10	1.461e-01	5.640e-01	HHEX:599 HESX1:2469 PAX6:2478 POU2F1:3963 DKK1:5797 GBX2:6535
MP0003123 paternal imprinting -0.1309116 7 2.306e-01 7.087e-01 AXIN1:360 CDKN1C:1457 HELLS:1683 GRB10:2987 UBE3A:3320 GPC3:13904 MP0003300 gastrointestinal ulcer -0.1295960 14 9.350e-02 4.706e-01 TGFB1:994 VDR:1467 PKHD1:2431 CYLD:3313 IL2:3749 IL10:4251 MP0010234 abnormal vibrissa follicle 0.1268649 4 3.797e-01 8.016e-01 PKP3:866 CHUK:3642 SPINK5:6419 ST14:12007 NA NA MP0004134 abnormal vibrissa follicle 0.1263750 22 4.050e-02 3.406e-01 PTCH1:718 HOXB4:973 NKX3-2:1164 PDGFA:1165 SLC35D1:1358 UNCX:1439 MP0001529 abnormal vocalization 0.1263482 9 1.896e-01 6.433e-01 NOS1:1025 MB:2632 SLC2A4:2829 MTOR:3196 SOD2:3555 PPARGC1A:5051 MP0001529 abnormal vocalization 0.1248371 18 6.707e-02 4.301e-01 E2F4:92 DRD2:170 FOXP2:743 CHRM2:1927 TOR1A:2129 NDUFS4:2154 MP0003787 abnormal imprinting 0.1205357 8 2.380e-01 7.087e-01 ARID4A:1205 CDKN1C:1457 ATRX:2634 ARID4B:4400 RB1:4502 SMCHD1:5014 MP0003890 abnormal embryonic-extraembry -0.1170296 16 1.055e-01 4.891e-01 GCLC:215 HSD17B12:487 HIRA:1025 PALB2:1287 FOXH1:1619 FOXA2:2417 MP0003656 abnormal embryo	MP0008260 abnormal autophagy	-0.1311174	15	7.904e-02	4.560e-01	ATG4C:874 ATG7:952 PMP22:1059 BNIP3L:1187 BECN1:1697 ATG9A:3124
MP0003300 gastrointestinal ulcer -0.1295960 14 9.350e-02 4.706e-01 TGFB1:994 VDR:1467 PKHD1:2431 CYLD:3313 IL2:3749 IL10:4251 MP0010234 abnormal vibrissa follicle 0.1268649 4 3.797e-01 8.016e-01 PKP3:866 CHUK:3642 SPINK5:6419 ST14:12007 NA NA MP0004134 abnormal chest morphology -0.1263750 22 4.050e-02 3.406e-01 PTCH1:718 HOXB4:973 NKX3-2:1164 PDGFA:1165 SLC35D1:1358 UNCX:1439 MP00036646 muscle fatigue 0.1263482 9 1.896e-01 6.433e-01 NOS1:1025 MB:2632 SLC2A4:2829 MTOR:3196 SOD2:3555 PPARGC1A:5051 MP0001188 hyperpigmentation 0.1248371 18 6.707e-02 4.301e-01 E2F4:92 DRD2:170 FOXP2:743 CHRM2:1927 TOR1A:2129 NDUFS4:2154 MP0001188 hyperpigmentation 0.1215453 7 2.657e-01 7.294e-01 DRD2:170 TERF1:1095 MC1R:2073 KIT:4099 CDKN2a:9791 TERF2IP:10244 MP0003890 abnormal imprinting -0.1205357 8 2.380e-01 7.087e-01 ARIDA4:1205 CDKN1C:1457 ATRX:2634 ARID4B:4400 RB1:4502 SMCHD1:5014 MP0003890 abnormal embryonic-extraembry -0.1170296 6 6.430e-02 4.891e-01 GCLC:215 HSD17B12:487 HIRA:1025 PALB2:1287 FOXH1:1619 FOXA2:2417 MP0000750 abnormal muscle regeneration<	MP0005645 abnormal hypothalamus physiol	0.1309957	14	9.001e-02	4.706e-01	NOS1:1025 NF1:1248 UCP2:1627 AVP:1941 PROKR2:2996 FGF21:4787
MP0010234 abnormal vibrissa follicle 0.1268649 4 3.797e-01 8.016e-01 PKP3:866 CHUK:3642 SPINK5:6419 ST14:12007 NA NA MP0004134 abnormal chest morphology -0.1263750 22 4.050e-02 3.406e-01 PTCH1:718 HOXB4:973 NKX3-2:1164 PDGFA:1165 SLC35D1:1358 UNCX:1439 MP0003646 muscle fatigue 0.1263482 9 1.896e-01 6.433e-01 NOS1:1025 MB:2632 SLC2A4:2829 MTOR:3196 SOD2:3555 PPARGC1A:5051 MP0001529 abnormal vocalization 0.1248371 18 6.707e-02 4.301e-01 E2F4:92 DRD2:170 FOXP2:743 CHRM2:1927 TOR1A:2129 NDUFS4:2154 MP0001188 hyperpigmentation 0.1215453 7 2.657e-01 7.294e-01 DRD2:170 TERF1:1095 MC1R:2073 KIT:4099 CDKN2A:9791 TERF2IP:10244 MP00038787 abnormal imprinting -0.1205357 8 2.380e-01 7.087e-01 ARID4A:1205 CDKN1C:1457 ATRX:2634 ARID4B:4400 RBI:4502 SMCHD1:5014 MP0003896 abnormal embryonic-extraembry -0.1170296 16 1.055e-01 4.891e-01 GCLC:215 HSD17B12:487 HIRA:1025 PALB2:1287 FOXH1:1619 FOXA2:2417 MP0000750 abnormal muscle regeneration 0.1159244 31 2.584e-02 2.692e-01 MYF5:82 DMD:228 CAV2:251 MYOZ1:1279 RP5:2232 IFRD1:3245 MP000015 abnormal ear pigmentation 0.1150872 15 1.232e-01 5.212e-0	MP0003123 paternal imprinting	-0.1309116	7	2.306e-01	7.087e-01	AXIN1:360 CDKN1C:1457 HELLS:1683 GRB10:2987 UBE3A:3320 GPC3:13904
MP0004134 abnormal chest morphology -0.1263750 22 4.050e-02 3.406e-01 PTCH1:718 HOXB4:973 NKX3-2:1164 PDGFA:1165 SLC35D1:1358 UNCX:1439 MP0003646 muscle fatigue 0.1263482 9 1.896e-01 6.433e-01 NOS1:1025 MB:2632 SLC2A4:2829 MTOR:3196 SOD2:3555 PPARGC1A:5051 MP0001529 abnormal vocalization 0.1248371 18 6.707e-02 4.301e-01 E2F4:92 DRD2:170 FOXP2:743 CHRM2:1927 TOR1A:2129 NDUFS4:2154 MP0001188 hyperpigmentation 0.1215453 7 2.657e-01 7.294e-01 DRD2:170 TERF1:1095 MC1R:2073 KIT:4099 CDKN2A:9791 TERF2IP:10244 MP0003787 abnormal imprinting -0.1205357 8 2.380e-01 7.087e-01 ARID4A:1205 CDKN1C:1457 ATRX:2634 ARID4B:4400 RB1:4502 SMCHD1:5014 MP0003890 abnormal embryonic-extraembry -0.1170296 16 1.055e-01 4.891e-01 GCLC:215 HSD17B12:487 HIRA:1025 PALB2:1287 FOXH1:1619 FOXA2:2417 MP0003656 abnormal erythrocyte physiolo -0.1168030 21 6.430e-02 4.301e-01 SLC4A1:27 ANK1:119 PFKM:194 MAN2A1:784 FECH:934 BNIP3L:1187 MP0000750 abnormal muscle regeneration 0.1159244 31 2.584e-02 2.692e-01 MYF5:82 DMD:228 CAV2:251 MYOZ1:1279 RNF5:2232 IFRD1:3245 MP0001835 abnor	MP0003300 gastrointestinal ulcer	-0.1295960	14	9.350e-02	4.706e-01	TGFB1:994 VDR:1467 PKHD1:2431 CYLD:3313 IL2:3749 IL10:4251
MP0003646 muscle fatigue 0.1263482 9 1.896e-01 6.433e-01 NOS1:1025 MB:2632 SLC2A4:2829 MTOR:3196 SOD2:3555 PPARGC1A:5051 MP0001529 abnormal vocalization 0.1248371 18 6.707e-02 4.301e-01 E2F4:92 DRD2:170 FOXP2:743 CHRM2:1927 TOR1A:2129 NDUFS4:2154 MP0001188 hyperpigmentation 0.1215453 7 2.657e-01 7.294e-01 DRD2:170 TERF1:1095 MC1R:2073 KIT:4099 CDKN2A:9791 TERF2IP:10244 MP0003787 abnormal imprinting -0.1205357 8 2.380e-01 7.087e-01 ARID4A:1205 CDKN1C:1457 ATRX:2634 ARID4B:4400 RB1:4502 SMCHD1:5014 MP0003890 abnormal embryonic-extraembry -0.1170296 16 1.055e-01 4.891e-01 GCLC:215 HSD17B12:487 HIRA:1025 PALB2:1287 FOXH1:1619 FOXA2:2417 MP0003656 abnormal erythrocyte physiolo -0.1168030 21 6.430e-02 4.301e-01 SLC4A1:27 ANK1:119 PFKM:194 MAN2A1:784 FECH:934 BNIP3L:1187 MP0000750 abnormal muscle regeneration 0.1159244 31 2.584e-02 2.692e-01 MYF5:82 DMD:228 CAV2:251 MYOZ1:1279 RNF5:2232 IFRD1:3245 MP0001835 abnormal ear pigmentation 0.1150872 15 1.232e-01 5.212e-01 MYO5A:725 CBL:999 SLC24A5:1481 MC1R:2073 POLH:3201 BLOC1S3:3615 MP00002396 abnorma	MP0010234 abnormal vibrissa follicle	0.1268649	4	3.797e-01	8.016e-01	PKP3:866 CHUK:3642 SPINK5:6419 ST14:12007 NA NA
MP0001529 abnormal vocalization 0.1248371 18 6.707e-02 4.301e-01 E2F4:92 DRD2:170 FOXP2:743 CHRM2:1927 TOR1A:2129 NDUFS4:2154 MP0001188 hyperpigmentation 0.1215453 7 2.657e-01 7.294e-01 DRD2:170 TERF1:1095 MC1R:2073 KIT:4099 CDKN2A:9791 TERF2IP:10244 MP0003787 abnormal imprinting -0.1205357 8 2.380e-01 7.087e-01 ARID4A:1205 CDKN1C:1457 ATRX:2634 ARID4B:4400 RB1:4502 SMCHD1:5014 MP0003890 abnormal embryonic-extraembry -0.1170296 16 1.055e-01 4.891e-01 GCLC:215 HSD17B12:487 HIRA:1025 PALB2:1287 FOXH1:1619 FOXA2:2417 MP0003656 abnormal erythrocyte physiolo -0.1168030 21 6.430e-02 4.301e-01 SLC4A1:27 ANK1:119 PFKM:194 MAN2A1:784 FECH:934 BNIP3L:1187 MP0000750 abnormal muscle regeneration 0.1159244 31 2.584e-02 2.692e-01 MYF5:82 DMD:228 CAV2:251 MYOZ1:1279 RNF5:2232 IFRD1:3245 MP0001835 abnormal ear pigmentation 0.1150872 15 1.232e-01 5.212e-01 MYO5A:725 CBL:999 SLC24A5:1481 MC1R:2073 POLH:3201 BLOC1S3:3615 MP0002396 abnormal hematopoietic system 0.1107924 19 9.501e-02 4.706e-01 CASP8:191 MAN2A1:784 MYC:858 ARHGAP1:1413 CDK6:2438 SNAI2:2571 MP0	MP0004134 abnormal chest morphology	-0.1263750	22	4.050e-02	3.406e-01	PTCH1:718 HOXB4:973 NKX3-2:1164 PDGFA:1165 SLC35D1:1358 UNCX:1439
MP0001188 hyperpigmentation 0.1215453 7 2.657e-01 7.294e-01 DRD2:170 TERF1:1095 MC1R:2073 KIT:4099 CDKN2A:9791 TERF2IP:10244 MP0003787 abnormal imprinting -0.1205357 8 2.380e-01 7.087e-01 ARID4A:1205 CDKN1C:1457 ATRX:2634 ARID4B:4400 RB1:4502 SMCHD1:5014 MP0003890 abnormal embryonic-extraembry -0.1170296 16 1.055e-01 4.891e-01 GCLC:215 HSD17B12:487 HIRA:1025 PALB2:1287 FOXH1:1619 FOXA2:2417 MP0003656 abnormal erythrocyte physiolo -0.1168030 21 6.430e-02 4.301e-01 SLC4A1:27 ANK1:119 PFKM:194 MAN2A1:784 FECH:934 BNIP3L:1187 MP0000750 abnormal muscle regeneration 0.1159244 31 2.584e-02 2.692e-01 MYF5:82 DMD:228 CAV2:251 MYOZ1:1279 RNF5:2232 IFRD1:3245 MP000153 abnormal ear pigmentation 0.1150872 15 1.232e-01 5.212e-01 MYO5A:725 CBL:999 SLC24A5:1481 MC1R:2073 POLH:3201 BLOC1S3:3615 MP0001835 abnormal antigen presentation 0.1149986 48 6.027e-03 1.301e-01 TNFRSF11B:18 PSMB8:401 PDCD1LG2:758 RAG1:781 CSF2:1157 MAP3K14:1677 MP0002396 abnormal hematopoietic system -0.1107924 19 9.501e-02 4.706e-01 CASP8:191 MAN2A1:784 MYC:858 ARHGAP1:1413 CDK6:2438 SNAI2:2571	MP0003646 muscle fatigue	0.1263482	9	1.896e-01	6.433e-01	NOS1:1025 MB:2632 SLC2A4:2829 MTOR:3196 SOD2:3555 PPARGC1A:5051
MP0003787 abnormal imprinting -0.1205357 8 2.380e-01 7.087e-01 ARID4A:1205 CDKN1C:1457 ATRX:2634 ARID4B:4400 RB1:4502 SMCHD1:5014 MP0003890 abnormal embryonic-extraembry -0.1170296 16 1.055e-01 4.891e-01 GCLC:215 HSD17B12:487 HIRA:1025 PALB2:1287 FOXH1:1619 FOXA2:2417 MP0003656 abnormal erythrocyte physiolo -0.1168030 21 6.430e-02 4.301e-01 SLC4A1:27 ANK1:119 PFKM:194 MAN2A1:784 FECH:934 BNIP3L:1187 MP0000750 abnormal muscle regeneration 0.1159244 31 2.584e-02 2.692e-01 MYF5:82 DMD:228 CAV2:251 MYOZ1:1279 RNF5:2232 IFRD1:3245 MP00001835 abnormal ear pigmentation 0.1150872 15 1.232e-01 5.212e-01 MYO5A:725 CBL:999 SLC24A5:1481 MC1R:2073 POLH:3201 BLOC1S3:3615 MP0001835 abnormal antigen presentation 0.1149986 48 6.027e-03 1.301e-01 TNFRSF11B:18 PSMB8:401 PDCD1LG2:758 RAG1:781 CSF2:1157 MAP3K14:1677 MP0002396 abnormal hematopoietic system -0.1107924 19 9.501e-02 4.706e-01 CASP8:191 MAN2A1:784 MYC:858 ARHGAP1:1413 CDK6:2438 SNAI2:2571 MP0005084 abnormal gallbladder morpholo 0.1102309 14 1.537e-01 5.748e-01 VTI1B:196 HNF1B:415 HLX:513 SOX17:1299 KLB:1515 NPC1L1:2855	MP0001529 abnormal vocalization	0.1248371	18	6.707e-02	4.301e-01	E2F4:92 DRD2:170 FOXP2:743 CHRM2:1927 TOR1A:2129 NDUFS4:2154
MP0003890 abnormal embryonic-extraembry -0.1170296 16 1.055e-01 4.891e-01 GCLC:215 HSD17B12:487 HIRA:1025 PALB2:1287 FOXH1:1619 FOXA2:2417 MP0003656 abnormal erythrocyte physiolo -0.1168030 21 6.430e-02 4.301e-01 SLC4A1:27 ANK1:119 PFKM:194 MAN2A1:784 FECH:934 BNIP3L:1187 MP0000750 abnormal muscle regeneration 0.1159244 31 2.584e-02 2.692e-01 MYF5:82 DMD:228 CAV2:251 MYOZ1:1279 RNF5:2232 IFRD1:3245 MP000015 abnormal ear pigmentation 0.1150872 15 1.232e-01 5.212e-01 MYO5A:725 CBL:999 SLC24A5:1481 MC1R:2073 POLH:3201 BLOC1S3:3615 MP0001835 abnormal antigen presentation 0.1149986 48 6.027e-03 1.301e-01 TNFRSF11B:18 PSMB8:401 PDCD1LG2:758 RAG1:781 CSF2:1157 MAP3K14:1677 MP0002396 abnormal hematopoietic system -0.1107924 19 9.501e-02 4.706e-01 CASP8:191 MAN2A1:784 MYC:858 ARHGAP1:1413 CDK6:2438 SNAI2:2571 MP0005084 abnormal gallbladder morpholo 0.1102309 14 1.537e-01 5.748e-01 VTI1B:196 HNF1B:415 HLX:513 SOX17:1299 KLB:1515 NPC1L1:2855 MP0004270 analgesia 0.1087706 17 1.210e-01 5.192e-01 MUSK:810 DLG2:890 KIF1B:1181 PLCB3:1902 NRG1:2188 RYR1:2891	MP0001188 hyperpigmentation	0.1215453	7	2.657e-01	7.294e-01	DRD2:170 TERF1:1095 MC1R:2073 KIT:4099 CDKN2A:9791 TERF2IP:10244
MP0003656 abnormal erythrocyte physiolo -0.1168030 21 6.430e-02 4.301e-01 SLC4A1:27 ANK1:119 PFKM:194 MAN2A1:784 FECH:934 BNIP3L:1187 MP0000750 abnormal muscle regeneration 0.1159244 31 2.584e-02 2.692e-01 MYF5:82 DMD:228 CAV2:251 MYOZ1:1279 RNF5:2232 IFRD1:3245 MP0000015 abnormal ear pigmentation 0.1150872 15 1.232e-01 5.212e-01 MYO5A:725 CBL:999 SLC24A5:1481 MC1R:2073 POLH:3201 BLOC1S3:3615 MP0001835 abnormal antigen presentation 0.1149986 48 6.027e-03 1.301e-01 TNFRSF11B:18 PSMB8:401 PDCD1LG2:758 RAG1:781 CSF2:1157 MAP3K14:1677 MP0002396 abnormal hematopoietic system -0.1107924 19 9.501e-02 4.706e-01 CASP8:191 MAN2A1:784 MYC:858 ARHGAP1:1413 CDK6:2438 SNAI2:2571 MP0005084 abnormal gallbladder morpholo 0.1102309 14 1.537e-01 5.748e-01 VTI1B:196 HNF1B:415 HLX:513 SOX17:1299 KLB:1515 NPC1L1:2855 MP0004270 analgesia 0.1087706 17 1.210e-01 5.192e-01 MUSK:810 DLG2:890 KIF1B:1181 PLCB3:1902 NRG1:2188 RYR1:2891	MP0003787 abnormal imprinting	-0.1205357	8	2.380e-01	7.087e-01	ARID4A:1205 CDKN1C:1457 ATRX:2634 ARID4B:4400 RB1:4502 SMCHD1:5014
MP0000750 abnormal muscle regeneration 0.1159244 31 2.584e-02 2.692e-01 MYF5:82 DMD:228 CAV2:251 MYOZ1:1279 RNF5:2232 IFRD1:3245 MP0000015 abnormal ear pigmentation 0.1150872 15 1.232e-01 5.212e-01 MYO5A:725 CBL:999 SLC24A5:1481 MC1R:2073 POLH:3201 BLOC1S3:3615 MP0001835 abnormal antigen presentation 0.1149986 48 6.027e-03 1.301e-01 TNFRSF11B:18 PSMB8:401 PDCD1LG2:758 RAG1:781 CSF2:1157 MAP3K14:1677 MP0002396 abnormal hematopoietic system -0.1107924 19 9.501e-02 4.706e-01 CASP8:191 MAN2A1:784 MYC:858 ARHGAP1:1413 CDK6:2438 SNAI2:2571 MP0005084 abnormal gallbladder morpholo 0.1102309 14 1.537e-01 5.748e-01 VTI1B:196 HNF1B:415 HLX:513 SOX17:1299 KLB:1515 NPC1L1:2855 MP0004270 analgesia 0.1087706 17 1.210e-01 5.192e-01 MUSK:810 DLG2:890 KIF1B:1181 PLCB3:1902 NRG1:2188 RYR1:2891	MP0003890 abnormal embryonic-extraembry	-0.1170296	16	1.055e-01	4.891e-01	GCLC:215 HSD17B12:487 HIRA:1025 PALB2:1287 FOXH1:1619 FOXA2:2417
MP0000015 abnormal ear pigmentation 0.1150872 15 1.232e-01 5.212e-01 MY05A:725 CBL:999 SLC24A5:1481 MC1R:2073 POLH:3201 BLOC1S3:3615 MP0001835 abnormal antigen presentation 0.1149986 48 6.027e-03 1.301e-01 TNFRSF11B:18 PSMB8:401 PDCD1LG2:758 RAG1:781 CSF2:1157 MAP3K14:1677 MP0002396 abnormal hematopoietic system -0.1107924 19 9.501e-02 4.706e-01 CASP8:191 MAN2A1:784 MYC:858 ARHGAP1:1413 CDK6:2438 SNAI2:2571 MP0005084 abnormal gallbladder morpholo 0.1102309 14 1.537e-01 5.748e-01 VTI1B:196 HNF1B:415 HLX:513 SOX17:1299 KLB:1515 NPC1L1:2855 MP0004270 analgesia 0.1087706 17 1.210e-01 5.192e-01 MUSK:810 DLG2:890 KIF1B:1181 PLCB3:1902 NRG1:2188 RYR1:2891	MP0003656 abnormal erythrocyte physiolo	-0.1168030	21	6.430e-02	4.301e-01	SLC4A1:27 ANK1:119 PFKM:194 MAN2A1:784 FECH:934 BNIP3L:1187
MP0001835 abnormal antigen presentation 0.1149986 48 6.027e-03 1.301e-01 TNFRSF11B:18 PSMB8:401 PDCD1LG2:758 RAG1:781 CSF2:1157 MAP3K14:1677 MP0002396 abnormal hematopoietic system -0.1107924 19 9.501e-02 4.706e-01 CASP8:191 MAN2A1:784 MYC:858 ARHGAP1:1413 CDK6:2438 SNAI2:2571 MP0005084 abnormal gallbladder morpholo 0.1102309 14 1.537e-01 5.748e-01 VTI1B:196 HNF1B:415 HLX:513 SOX17:1299 KLB:1515 NPC1L1:2855 MP0004270 analgesia 0.1087706 17 1.210e-01 5.192e-01 MUSK:810 DLG2:890 KIF1B:1181 PLCB3:1902 NRG1:2188 RYR1:2891	MP0000750 abnormal muscle regeneration	0.1159244	31	2.584e-02	2.692e-01	MYF5:82 DMD:228 CAV2:251 MYOZ1:1279 RNF5:2232 IFRD1:3245
MP0002396 abnormal hematopoietic system -0.1107924 19 9.501e-02 4.706e-01 CASP8:191 MAN2A1:784 MYC:858 ARHGAP1:1413 CDK6:2438 SNAI2:2571 MP0005084 abnormal gallbladder morpholo 0.1102309 14 1.537e-01 5.748e-01 VTI1B:196 HNF1B:415 HLX:513 SOX17:1299 KLB:1515 NPC1L1:2855 MP0004270 analgesia 0.1087706 17 1.210e-01 5.192e-01 MUSK:810 DLG2:890 KIF1B:1181 PLCB3:1902 NRG1:2188 RYR1:2891	MP0000015 abnormal ear pigmentation	0.1150872	15	1.232e-01	5.212e-01	MYO5A:725 CBL:999 SLC24A5:1481 MC1R:2073 POLH:3201 BLOC1S3:3615
MP0005084 abnormal gallbladder morpholo 0.1102309 14 1.537e-01 5.748e-01 VTI1B:196 HNF1B:415 HLX:513 SOX17:1299 KLB:1515 NPC1L1:2855 MP0004270 analgesia 0.1087706 17 1.210e-01 5.192e-01 MUSK:810 DLG2:890 KIF1B:1181 PLCB3:1902 NRG1:2188 RYR1:2891	MP0001835 abnormal antigen presentation	0.1149986	48	6.027e-03	1.301e-01	TNFRSF11B:18 PSMB8:401 PDCD1LG2:758 RAG1:781 CSF2:1157 MAP3K14:1677
MP0004270 analgesia 0.1087706 17 1.210e-01 5.192e-01 MUSK:810 DLG2:890 KIF1B:1181 PLCB3:1902 NRG1:2188 RYR1:2891	MP0002396 abnormal hematopoietic system	-0.1107924	19	9.501e-02	4.706e-01	CASP8:191 MAN2A1:784 MYC:858 ARHGAP1:1413 CDK6:2438 SNAI2:2571
· ·	MP0005084 abnormal gallbladder morpholo	0.1102309	14	1.537e-01	5.748e-01	VTI1B:196 HNF1B:415 HLX:513 SOX17:1299 KLB:1515 NPC1L1:2855
MP0003806 abnormal nucleotide metabolis 0.1080727 9 2.619e-01 7.289e-01 TPMT:2493 TALDO1:2842 VPS54:2843 UPP1:3651 NQO1:6671 OTC:7365	MP0004270 analgesia	0.1087706	17	1.210e-01	5.192e-01	MUSK:810 DLG2:890 KIF1B:1181 PLCB3:1902 NRG1:2188 RYR1:2891
	MP0003806 abnormal nucleotide metabolis	0.1080727	9	2.619e-01	7.289e-01	TPMT:2493 TALDO1:2842 VPS54:2843 UPP1:3651 NQO1:6671 OTC:7365
MP0000383 abnormal hair follicle 0.1053727 21 9.511e-02 4.706e-01 FGFR2:39 PKP3:866 TRPV3:1211 KSR1:1234 KRT14:1318 DICER1:1759	MP0000383 abnormal hair follicle	0.1053727	21	9.511e-02	4.706e-01	FGFR2:39 PKP3:866 TRPV3:1211 KSR1:1234 KRT14:1318 DICER1:1759
MP0001879 abnormal lymphatic vessel -0.1038005 27 6.244e-02 4.301e-01 LYVE1:180 HEG1:261 VEGFA:446 PLCG2:1090 PDPN:1217 SOX18:1227	MP0001879 abnormal lymphatic vessel	-0.1038005	27	6.244e-02	4.301e-01	LYVE1:180 HEG1:261 VEGFA:446 PLCG2:1090 PDPN:1217 SOX18:1227

1.403e-01 5.508e-01 3.118e-01 7.484e-01

2.841e-01 7.312e-01

2.459e-02 2.692e-01

DMD:228 INHA:295 GHR:526 DSG4:1826 MTOR:3196 SHC1:3560

FBN1:2053 ATP7A:3422 EDNRB:4377 PAX3:4394 MITF:5178 RECQL4:6611

MREG:1355 RAB27A:1786 PTPN11:3352 ECE1:4428 RB1:4502 CDKN2A:5196

SLC6A6:53 ADORA2A:176 LRAT:524 TYR:626 POU4F2:843 AP3B1:962