

Positive Rho Permulated

permP

permPValue

qValueNoperm

qValuePerm

Gene

PANK3

RPL8

YPEL5

0.000000

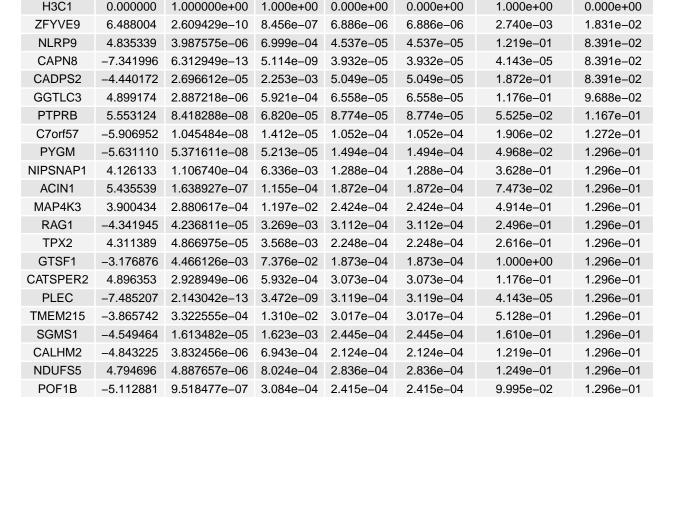
0.000000

0.000000

1.000000e+00

1.000000e+00

1.000000e+00



Negative Rho Permulated

p.adj

1.000e+00

1.000e+00

1.000e+00

permP

0.000e+00

0.000e+00

0.000e+00

permPValue

0.000e+00

0.000e+00

0.000e+00

qValueNoperm

1.000e+00

1.000e+00

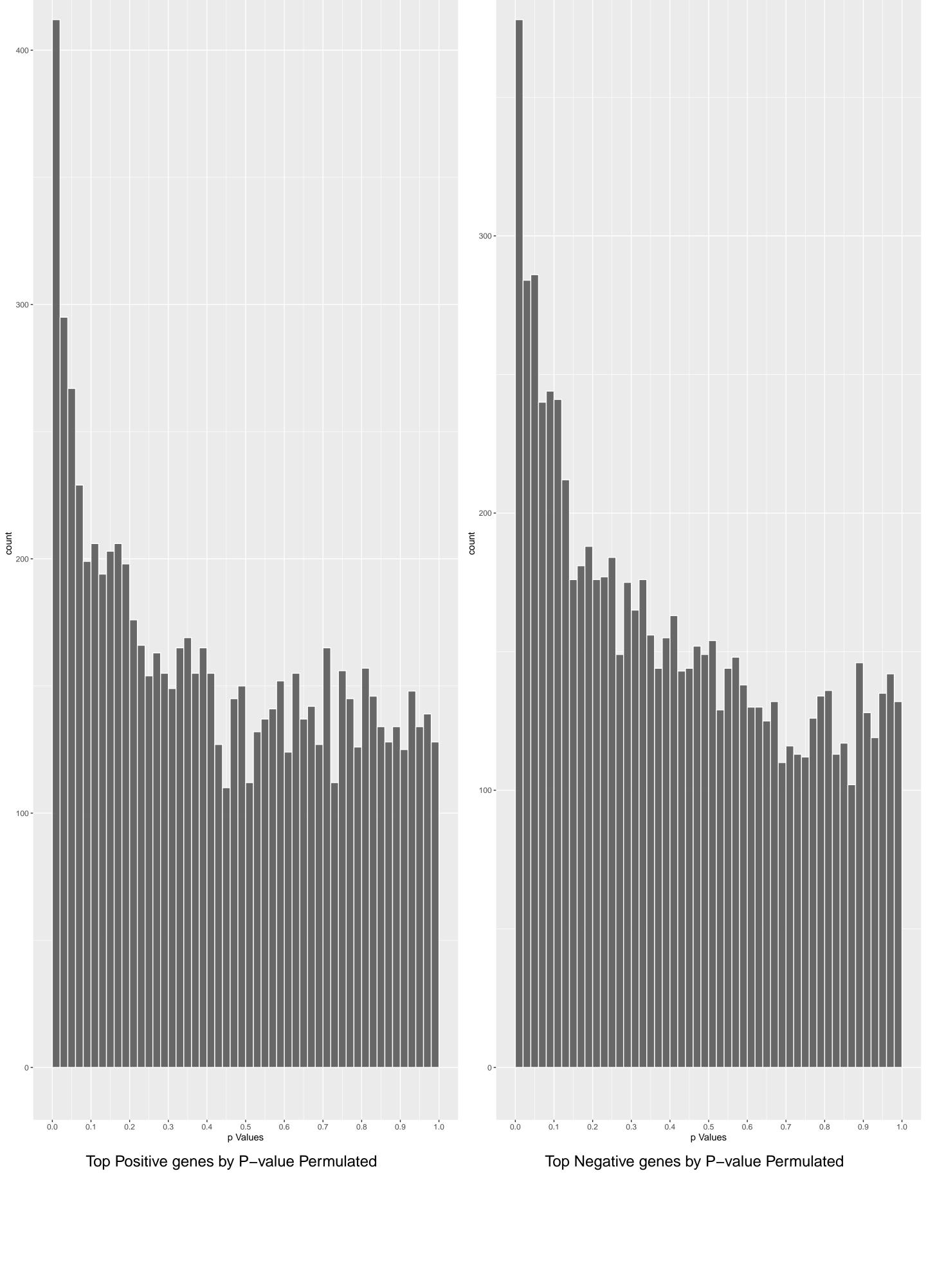
1.000e+00

qValuePerm

0.000e+00

0.000e+00

0.000e+00



Gene	Rho	Р	p.adj	permP	permPValue	qValueNoperm	qValuePerm	Gene	Rho	Р	p.adj	permP	permPValue	qValueNoperm	qValuePer
ZFYVE9	6.488004	2.609429e-10	8.456e-07	6.886e-06	6.886e-06	2.740e-03	1.831e-02	CAPN8	-7.341996	6.312949e-13	5.114e-09	3.932e-05	3.932e-05	4.143e-05	8.391e-0
NLRP9	4.835339	3.987575e-06	6.999e-04	4.537e-05	4.537e-05	1.219e-01	8.391e-02	CADPS2	-4.440172	2.696612e-05	2.253e-03	5.049e-05	5.049e-05	1.872e-01	8.391e-0
GGTLC3	4.899174	2.887218e-06	5.921e-04	6.558e-05	6.558e-05	1.176e-01	9.688e-02	C7orf57	-5.906952	1.045484e-08	1.412e-05	1.052e-04	1.052e-04	1.906e-02	1.272e-0
PTPRB	5.553124	8.418288e-08	6.820e-05	8.774e-05	8.774e-05	5.525e-02	1.167e-01	OFD1	-6.149700	2.328884e-09	4.193e-06	1.389e-04	1.389e-04	7.547e-03	1.296e-0
NIPSNAP1	4.126133	1.106740e-04	6.336e-03	1.288e-04	1.288e-04	3.628e-01	1.296e-01	PYGM	-5.631110	5.371611e-08	5.213e-05	1.494e-04	1.494e-04	4.968e-02	1.296e-0
ACIN1	5.435539	1.638927e-07	1.155e-04	1.872e-04	1.872e-04	7.473e-02	1.296e-01	GTSF1	-3.176876	4.466126e-03	7.376e-02	1.873e-04	1.873e-04	1.000e+00	1.296e-0
TPX2	4.311389	4.866975e-05	3.568e-03	2.248e-04	2.248e-04	2.616e-01	1.296e-01	EVPL	-6.330639	7.324434e-10	1.695e-06	1.922e-04	1.922e-04	3.924e-03	1.296e-0
MAP4K3	3.900434	2.880617e-04	1.197e-02	2.424e-04	2.424e-04	4.914e-01	1.296e-01	CLIC3	-4.761165	5.774365e-06	8.664e-04	2.036e-04	2.036e-04	1.249e-01	1.296e-0
EIF4E1B	4.714582	7.266219e-06	9.571e-04	2.617e-04	2.617e-04	1.249e-01	1.296e-01	CALHM2	-4.843225	3.832456e-06	6.943e-04	2.124e-04	2.124e-04	1.219e-01	1.296e-0
NDUFS5	4.794696	4.887657e-06	8.024e-04	2.836e-04	2.836e-04	1.249e-01	1.296e-01	CAB39L	-3.639186	8.205050e-04	2.417e-02	2.337e-04	2.337e-04	7.121e-01	1.296e-0

Geneset	stat	num.genes	pval	p.adj	gene.vals
Negative Regulation Of Gene Expression V	0.4443979	5		2.555e-02	USP7:105 HELLS:341 UHRF1:431 UHRF2:738 ZNF445:2794 NA
Transmembrane Receptor Protein Tyrosine	-0.4173782	4		9.078e-02	TRIO:437 PTN:1193 PTPRD:1777 PTPRF:2041 NA NA
Striated Muscle Hypertrophy (GO:0014897)	-0.4146901	4		9.377e-02	TCAP:388 MYOC:1391 RYR2:1609 HTR2B:2232 NA NA
snRNA Transcription By RNA Polymerase II	0.4122589	4		9.766e-02	SNAPC5:84 ICE2:1182 SNAPC1:1866 ZC3H8:2427 NA NA
Atrial Cardiac Muscle Cell To AV Node Ce	-0.4093389	6		2.417e-02	GJA1:638 SCN3B:822 KCNQ1:1341 SCN5A:1561 GJC1:1769 KCNE5:2838
Atrial Cardiac Muscle Cell Action Potent	-0.4082423	11		4.792e-04	KCNN2:93 CACNB2:377 GJA1:638 SCN3B:822 KCNJ3:1219 KCNQ1:1341
Positive Regulation Of Peptidyl–Serine P	0.3911883	4	6.734e-03		IFNG:257 LIF:403 IFNK:669 IFNE:5676 NA NA
Regulation Of Peptidyl–Serine Phosphoryl	0.3911883	4		1.295e-01	IFNG:257 LIF:403 IFNK:669 IFNE:5676 NA NA
SA Node Cell Action Potential (GO:008601	-0.3804143	5		8.299e-02	CACNA1G:66 CACNA1D:583 SCN3B:822 SCN5A:1561 HCN4:6779 NA
Positive Regulation Of Opsonization (GO:	-0.3784986	4	8.747e-03		COLEC11:302 COLEC10:997 PLA2G5:3134 MYO18A:3607 NA NA
Regulation Of Glycogen (Starch) Synthase	0.3685854	5		9.766e-02	INPP5K:699 PPP1R3F:924 IGF2:2372 GSK3B:2946 GSK3A:3527 NA
RIG-I Signaling Pathway (GO:0039529)	-0.3677064	4	1.086e-02		RNF135:510 TRIM25:1117 OAS3:2368 PHB2:4719 NA NA
Plasma Membrane Phospholipid Scrambling	-0.3653594	5	4.664e-03		PLSCR3:92 ANO7:360 P2RX7:411 PLSCR5:3087 PLSCR4:7127 NA
Organic Hydroxy Compound Catabolic Proce	0.3555406	6		7.225e-02	PDXP:843 FGF23:859 HSD17B6:1256 LCT:1516 CYP24A1:1836 LDHD:7517
Establishment Of Mitotic Sister Chromati	0.3551057	6		7.275e-02	STAG1:824 NIPBL:948 SMC3:1217 RAD21:2361 STAG2:2857 SMC1A:5679
Hepoxilin Biosynthetic Process (GO:00511	-0.3497193	4	1.542e-02		ALOXE3:488 ALOX15B:2296 ALOX12B:2757 ALOX15:4358 NA NA
Hepoxilin Metabolic Process (GO:0051121)	-0.3497193	4	1.542e-02		ALOXE3:488 ALOX15B:2296 ALOX12B:2757 ALOX15:4358 NA NA
Positive Regulation Of DNA Methylation–D	0.3490984	8		2.739e-02	TASOR:349 SETDB2:437 PPHLN1:828 ATF7IP2:1595 TRIM28:2274 MORC2:2819
Cellular Response To UV-A (GO:0071492)	-0.3489810	9		1.603e-02	MME:236 OPN1SW:531 PPID:596 MMP9:1060 OPN3:1133 MMP3:1808
Androgen Biosynthetic Process (GO:000670	0.3431339	7		5.397e-02	MED1:333 HSD3B2:943 HSD17B3:1051 HSD17B6:1256 SRD5A1:4241 SRD5A3:4513
Detection Of Muscle Stretch (GO:0035995)	-0.3431090	5	7.882e-03		TCAP:388 PTK2:2125 CDH2:2549 CTNNB1:3471 CSRP3:4397 NA
Glucocorticoid Biosynthetic Process (GO:	0.3427544	3	3.976e-02		CYP17A1:248 CYP21A2:3245 CYP11A1:4086 NA NA NA
Actin–Myosin Filament Sliding (GO:003327	-0.3420364	11		6.505e-01	MYH8:153 MYH2:312 MYH6:664 TPM1:919 MYH4:955 TNNT2:993
Positive Regulation Of Mast Cell Activat	0.3355274	4	2.012e-02		TSLP:18 SPHK2:1020 NECTIN2:3843 NR4A3:5702 NA NA
•					GLRA1:402 INSYN2A:1178 NLGN3:2399 NPAS4:2963 INSYN1:3211 INSYN2B:6191
Inhibitory Postsynaptic Potential (GO:00	-0.3344799	6	4.549e-03		
Glucocorticoid Metabolic Process (GO:000	0.3324978	5	1.003e-02		CYP17A1:248 HSD11B2:2886 YWHAH:2960 CYP21A2:3245 CYP11A1:4086 NA
Regulation Of DNA Methylation–Dependent	0.3323028	14	1.673e-05		TASOR:349 TET1:395 SETDB2:437 L3MBTL3:538 PPHLN1:828 SAMD1:981
Positive Regulation Of CD4–positive, CD2	0.3297362	3	4.792e-02		IFNG:257 HLA-DRA:1240 KLHL25:6716 NA NA NA
snRNA Modification (GO:0040031)	0.3294592	4	2.248e-02		METTL16:869 NHP2:2194 MEPCE:3101 METTL4:4751 NA NA
Muscle Filament Sliding (GO:0030049)	-0.3280494	10		1.786e-02	MYH8:153 MYH6:664 TPM1:919 MYH4:955 TNNT2:993 MYL6B:1497
Membrane Lipid Catabolic Process (GO:004		7		7.778e-02	SMPD2:857 MGST2:1147 PPT1:2595 SMPDL3B:2959 SGPL1:3217 ENPP2:3952
MHC Class II Protein Complex Assembly (G	0.3240637	7			HLA-DOA:66 GNAO1:967 HLA-DOB:977 HLA-DRA:1240 HLA-DPA1:4273 HLA-DMA:4357
Peptide Antigen Assembly With MHC Class	0.3240637	7			HLA-DOA:66 GNAO1:967 HLA-DOB:977 HLA-DRA:1240 HLA-DPA1:4273 HLA-DMA:4357
Regulation Of Thymocyte Apoptotic Proces	0.3231736	4	2.518e-02		TP53:1394 BMP4:1773 ZC3H8:2427 JAK3:5719 NA NA
Chitin Catabolic Process (GO:0006032)	-0.3224901	2	1.142e-01		CTBS:1223 CHIT1:4615 NA NA NA NA
Chitin Metabolic Process (GO:0006030)	-0.3224901	2	1.142e-01		CTBS:1223 CHIT1:4615 NA NA NA NA
Adenylate Cyclase–Inhibiting Serotonin R	-0.3203648	6	6.575e-03		HTR1B:18 HTR1D:44 HTR1F:1671 HTR5A:3432 HTR1E:4268 HTR1A:8224
Positive Regulation Of Chemokine (C–X–C	0.3201099	4	2.660e-02	2.681e-01	TNF:1142 HMGB1:2063 TLR4:2553 LCP1:5752 NA NA
Ventricular Cardiac Muscle Cell Membrane	-0.3198836	7	3.380e-03	8.591e-02	KCNJ3:1219 KCNQ1:1341 KCNJ5:1985 KCNE1:2854 KCNE2:3086 KCNH2:4475
Positive Regulation Of Heterochromatin F	0.3197136	11	2.411e-04	1.412e-02	TASOR:349 SETDB2:437 PPHLN1:828 ATF7IP2:1595 TRIM28:2274 MORC2:2819

## EnrichmentHsSymbolsFile2 Top pathways by permulation

Geneset	stat	num.genes	pval	p.adj	gene.vals
REACTOME_SPERM_MOTILITY_AND_TAXES	0.4327112	8			CATSPER2:12 CATSPERG:43 CATSPERB:79 CATSPERD:380 CATSPER4:812 KCNU1:1183
WP_AFLATOXIN_B1_METABOLISM	-0.4113276	2	4.392e-02	2.285e-01	EPHX1:1046 CYP1A2:1817 NA NA NA NA
MIKHAYLOVA OXIDATIVE STRESS RESPONSE VIA	0.3978723	6	7.373e-04	1.454e-02	PGAM1:38 HSPB1:317 CTSD:404 CALU:907 OAT:3537 AKR1B1:4722
REACTOME_ESTABLISHMENT_OF_SISTER_CHROMAT	0.3927351	11	6.468e-06	3.019e-04	ESCO1:128 PDS5B:653 WAPL:762 STAG1:824 SMC3:1217 PDS5A:1375
WP_NIPBL_ROLE_IN_DNA_DAMAGE_CORNELIA_DE_	0.3677627	7	7.524e-04	1.470e-02	RNF8:277 RNF168:327 H2AX:541 NIPBL:948 CBX3:3253 ATR:3509
REACTOME_MINERALOCORTICOID_BIOSYNTHESIS	0.3674805	4	1.091e-02	9.969e-02	CGA:456 HSD3B2:943 CYP21A2:3245 LHB:3927 NA NA
REACTOME_GLUCOCORTICOID_BIOSYNTHESIS	0.3662302	6	1.891e-03	3.014e-02	CYP17A1:248 HSD3B2:943 HSD11B1:1291 HSD11B2:2886 CYP21A2:3245 SERPINA6:4378
REACTOME_PREDNISONE_ADME	0.3621584	5	5.036e-03	5.940e-02	ALB:1283 HSD11B1:1291 ABCB1:1314 HSD11B2:2886 SERPINA6:4378 NA
WP_PILOCYTIC_ASTROCYTOMA	0.3612640	6	2.179e-03	3.313e-02	SOS1:445 RAF1:861 GRB2:1307 BRAF:2046 NF1:2736 PTPN11:6081
NIKOLSKY_BREAST_CANCER_17P11_AMPLICON	-0.3479529	10	1.388e-04	3.865e-03	ALDH3A2:267 ULK2:368 SLC47A1:477 EPN2:706 RNF112:2016 SLC47A2:2297
MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_1	0.3474594	3	3.712e-02	2.096e-01	GATA1:1199 WAS:1974 TFE3:4230 NA NA NA
CHOI_ATL_ACUTE_STAGE	0.3402176	4	1.844e-02	1.383e-01	MBD1:237 MET:833 LHX2:4603 ETV1:4666 NA NA
REACTOME_MET_ACTIVATES_PTPN11	0.3369180	5	9.074e-03	8.830e-02	GAB1:418 MET:833 GRB2:1307 HGF:4558 PTPN11:6081 NA
REACTOME_FORMYL_PEPTIDE_RECEPTORS_BIND_F	-0.3347935	4	2.039e-02	1.457e-01	APP:255 HEBP1:375 ANXA1:3526 FPR2:6566 NA NA
NIKOLSKY_BREAST_CANCER_21Q22_AMPLICON	-0.3307171	14	1.831e-05	7.379e-04	PCBP3:248 COL6A1:436 DIP2A:843 SPATC1L:1211 YBEY:2156 COL6A2:2530
OHASHI_AURKA_TARGETS	0.3250838	4	2.433e-02	1.645e-01	DLGAP5:1246 TP53:1394 CDC25B:3713 MBD3:4967 NA NA
REACTOME_ELECTRIC_TRANSMISSION_ACROSS_GA	-0.3242662	5	1.203e-02	1.066e-01	PANX1:220 GJA10:1151 GJC1:1769 PANX2:5303 GJD2:5805 NA
REACTOME_LEUKOTRIENE_RECEPTORS	-0.3234565	5	1.224e-02	1.075e-01	LTB4R2:508 LTB4R:1002 CYSLTR2:1390 GPR17:3658 CYSLTR1:7742 NA
BERGER_MBD2_TARGETS	-0.3225602	2	1.141e-01	3.839e-01	TFF2:552 CELA2A:5200 NA NA NA NA
REACTOME_COHESIN_LOADING_ONTO_CHROMATIN	0.3191736	10	4.738e-04	1.032e-02	PDS5B:653 WAPL:762 STAG1:824 NIPBL:948 SMC3:1217 PDS5A:1375
HEIDENBLAD_AMPLIFIED_IN_BONE_CANCER	0.3168598	7	3.692e-03	4.810e-02	MDM2:392 TSPAN31:763 FGF23:859 CCND2:2187 CDK4:3471 STK38L:3663
WALLACE_PROSTATE_CANCER_DN	-0.3147394	5	1.479e-02	1.208e-01	GJA1:638 GPM6B:2592 LAMA4:2750 CAV2:3045 RAP1B:5993 NA
CROSBY_E2F4_TARGETS	0.3139116	6	7.744e-03	8.000e-02	CENPE:1016 CDC6:1475 BUB1B:2075 NDC80:2206 PTTG1:2529 CHEK1:8772
REACTOME_BIOSYNTHESIS_OF_MARESIN_LIKE_SP	-0.3129467	2	1.253e-01	4.054e-01	CYP1A2:1817 CYP2E1:4240 NA NA NA NA
WP_STEROID_HORMONE_PRECURSOR_BIOSYNTHESI	0.3119430	7	4.259e-03	5.300e-02	CYP17A1:248 HSD3B2:943 AKR1D1:3241 CYP21A2:3245 CYP11A1:4086 SRD5A1:4241
REACTOME_NEGATIVE_FEEDBACK_REGULATION_OF	0.3064465	6	9.330e-03	9.008e-02	MAP2K2:485 RAF1:861 MAP2K1:882 BRAF:2046 MAPK1:5771 MAPK3:8759
REACTOME_TYPE_I_HEMIDESMOSOME_ASSEMBLY	-0.3063766	11	4.337e-04	9.637e-03	PLEC:16 ITGB4:192 LAMB3:361 LAMC2:492 KRT14:721 ITGA6:2177
TURASHVILI_BREAST_NORMAL_DUCTAL_VS_LOBUL	0.3056030	6	9.527e-03	9.143e-02	EHBP1:203 RHOBTB3:725 TSPAN5:835 DCN:3763 MBTPS2:5057 ARHGEF9:8301
WP_IRINOTECAN_PATHWAY	0.3039092	4	3.527e-02	2.034e-01	SLCO1B1:372 ABCC1:613 BCHE:2914 UGT1A1:8804 NA NA
REACTOME_ANDROGEN_BIOSYNTHESIS	0.3027715	9	1.658e-03	2.723e-02	CYP17A1:248 CGA:456 HSD3B2:943 HSD17B3:1051 LHB:3927 SRD5A1:4241
REACTOME_ESTROGEN_STIMULATED_SIGNALING_T	0.3024543	4	3.616e-02	2.071e-01	PDPK1:1180 NRAS:1780 KRAS:4052 MAPK1:5771 NA NA
REACTOME_ACTIVATION_OF_NOXA_AND_TRANSLOC	0.3013315	4	3.686e-02	2.090e-01	TP53:1394 E2F1:1942 TFDP1:2573 TFDP2:6958 NA NA
JI_CARCINOGENESIS_BY_KRAS_AND_STK11_UP	-0.2987281	10	1.071e-03	1.940e-02	TIAM1:143 BNC1:420 PKP1:972 KRT5:2486 LYPD3:3453 TP63:3845
REACTOME_BIOSYNTHESIS_OF_MARESINS	-0.2981846	4	3.887e-02	2.154e-01	ALOX5:278 CYP1A2:1817 CYP2E1:4240 EPHX2:6751 NA NA
SMID_BREAST_CANCER_ERBB2_DN	-0.2963027	4	4.012e-02	2.188e-01	NPY1R:566 FGFR2:1822 GABRP:3916 SOX10:6899 NA NA
REACTOME_SARS_COV_1_MODULATES_HOST_TRANS	0.2944289	31	1.403e-08	1.423e-06	RPS24:210 RPS8:535 RPS27L:539 RPS2:719 RPS15:945 RPS6:1023
CHEN_HOXA5_TARGETS_6HR_DN	0.2941549	5	2.272e-02	1.571e-01	ZBED8:1034 NPTXR:1397 TUBA1A:3257 FJX1:3829 PRPF31:7140 NA
REACTOME_ROLE_OF_SECOND_MESSENGERS_IN_NE	-0.2940138	10	1.284e-03	2.215e-02	TRPC4:303 DCC:614 TRPC5:886 TRPC6:1536 NTN1:1634 TRPC3:2302
KUMANAOTO DECRONICE TO NUITUNI OA DNI	0.0007550	-	7 000 - 00	7 705 00	000104 400 000 040 1/1504 004 1/1500 4004 000140 5070 001/10 0004

DisGeNET Top pathways by permulation

7.308e-03 7.735e-02

CCNB1:160 SPAG5:343 KIFC1:961 KIF2C:1664 CCNA2:5872 CDKN3:6861

CFAP45:13 ENKUR:556 DNAH11:1124 DNAH5:1259 NA NA

1.327e-02 1.129e-01 HSD11B1:1291 HSD11B2:2886 AKR1D1:3241 CYP21A2:3245 SRD5A1:4241 SRD5A2:5297

KUMAMOTO\_RESPONSE\_TO\_NUTLIN\_3A\_DN

WP\_GLUCOCORTICOID\_BIOSYNTHESIS

GOCC\_9PLUS0\_MOTILE\_CILIUM

GOCC\_B\_CELL\_RECEPTOR\_COMPLEX

MP0010352 gastrointestinal tract polyps

MP0008260 abnormal autophagy

MP0004957 abnormal blastocyst morpholog

MP0008877 abnormal DNA methylation

0.1042249

0.1034792

0.1026718

0.1012537

16

84

16

0.2927550

0.2919065

Deficiency of monooxygenase	0.4345238	2	3.330e-02	3.243e-01	CYP17A1:248 CYP24A1:1836 NA NA NA NA
Acute postoperative pain	0.4299714	4	2.898e-03	1.245e-01	TAOK3:198 COMT:1229 ABCB1:1314 OPRM1:1717 NA NA
Monilethrix	-0.4286487	2	3.576e-02	3.341e-01	KRT80:161 DSG4:2109 NA NA NA NA
Junctional split	-0.4238195	6	3.241e-04	4.076e-02	PLEC:16 ITGB4:192 LAMB3:361 LAMC2:492 ITGA6:2177 LAMA3:4062
Rheumatoid Vasculitis	0.4141543	2	4.249e-02	3.533e-01	CD28:935 RBM45:1802 NA NA NA NA
Sequoiosis	0.4131107	2	4.301e-02	3.557e-01	GNAO1:967 RBM45:1802 NA NA NA NA
Central nervous system depression (disor	0.4105528	3	1.378e-02	2.303e-01	COMT:1229 ABCB1:1314 OPRM1:1717 NA NA NA
Human metapneumovirus infection	0.4103998	5	1.482e-03	9.693e-02	TSLP:18 PPIP5K1:40 TNF:1142 NCR1:2359 ISYNA1:3676 NA
Herlitz Disease	-0.4086677	5	1.552e-03	9.895e-02	ITGB4:192 LAMB3:361 LAMC2:492 ITGA6:2177 LAMA3:4062 NA
Localized vitiligo	0.4076994	2	4.582e-02	3.643e-01	TNF:1142 RBM45:1802 NA NA NA NA
Congenital pyloric atresia	-0.4069048	5	1.626e-03	1.006e-01	PLEC:16 ITGB4:192 LAMC2:492 ITGA6:2177 COL17A1:4556 NA
Bulla of lung	-0.3992733	2	5.049e-02	3.773e-01	EPHX1:1046 TIMP2:2139 NA NA NA NA
Plantar hyperkeratosis	-0.3991391	6	7.095e-04	6.446e-02	PLEC:16 ITGB4:192 LAMB3:361 LAMC2:492 LAMA3:4062 COL17A1:4556
Ineffective erythropoiesis	0.3958478	5	2.173e-03	1.099e-01	RPL26:98 COX4I2:995 KLF1:1184 GATA1:1199 SEC23B:5003 NA
Opticospinal Multiple Sclerosis	0.3894387	4	6.984e-03	1.730e-01	CD2AP:590 RBM45:1802 AQP4:1987 PLA2G7:2673 NA NA
T-lymphocyte immunodeficiency	-0.3890736	6	9.651e-04	7.910e-02	RAG1:15 CD3E:1383 LBR:1431 SFTPA1:1491 SMARCAL1:2365 SIPA1:3895
Abnormality of finger	0.3884336	4	7.132e-03	1.749e-01	SIL1:679 INPP5K:699 NRAS:1780 KRAS:4052 NA NA
Epidermolysis bullosa inversa dystrophic	-0.3836865	6	1.135e-03	8.419e-02	ITGB4:192 LAMB3:361 LAMC2:492 LAMC1:1461 LAMA3:4062 COL17A1:4556
Candidiasis of the esophagus	-0.3795516	3	2.279e-02	2.815e-01	ADAM17:771 NFKB1:946 IL1B:4040 NA NA NA
EPIDERMOLYSIS BULLOSA, JUNCTIONAL, LOCAL	-0.3790536	5	3.331e-03	1.318e-01	ITGB4:192 LAMB3:361 LAMC2:492 LAMA3:4062 COL17A1:4556 NA
Adult junctional epidermolysis bullosa (	-0.3790536	5	3.331e-03	1.318e-01	ITGB4:192 LAMB3:361 LAMC2:492 LAMA3:4062 COL17A1:4556 NA
Epidermolysis Bullosa Progressiva	-0.3790536	5	3.331e-03	1.318e-01	ITGB4:192 LAMB3:361 LAMC2:492 LAMA3:4062 COL17A1:4556 NA
JEB-I	-0.3790536	5	3.331e-03	1.318e-01	ITGB4:192 LAMB3:361 LAMC2:492 LAMA3:4062 COL17A1:4556 NA
Palmar hyperhidrosis	-0.3790536	5	3.331e-03	1.318e-01	ITGB4:192 LAMB3:361 LAMC2:492 LAMA3:4062 COL17A1:4556 NA
Benign neoplasm of thyroid gland	-0.3777993	3	2.342e-02	2.841e-01	APP:255 IQGAP1:1885 ALK:3706 NA NA NA
Microcystic stromal tumor	-0.3733318	5	3.838e-03	1.396e-01	MME:236 VIM:309 DICER1:1249 CTNNB1:3471 FOXL2:4831 NA
Papillary and follicular adenocarcinoma	0.3701925	5	4.146e-03	1.437e-01	EGF:390 TP53:1394 BRAF:2046 EDNRA:2564 KRAS:4052 NA
Papillary transitional cell carcinoma	0.3692013	4	1.055e-02	2.037e-01	EGF:390 ERBB2:944 TP53:1394 VEGFA:5779 NA NA
Empyema, Pleural	0.3680663	6	1.794e-03	1.012e-01	NFKBIA:451 NFKBIB:1410 NFKBIE:1433 SMC4:2352 SMC2:2417 TNFRSF6B:4687
Intestinal obstruction co-occurrent and	-0.3677232	3	2.738e-02	3.046e-01	CFTR:773 MUC1:1021 SLC26A9:4520 NA NA NA
Congenital muscular hypertrophy-cerebral	0.3669450	5	4.488e-03	1.477e-01	BRD4:571 NIPBL:948 SMC3:1217 RAD21:2361 SMC1A:5679 NA
Cornelia de Lange Syndrome 3	0.3669450	5	4.488e-03	1.477e-01	BRD4:571 NIPBL:948 SMC3:1217 RAD21:2361 SMC1A:5679 NA
Liver Abscess	-0.3646718	5	4.742e-03	1.501e-01	NCF1:687 NCF2:1364 DECR1:1756 CYBB:3242 CYBA:3741 NA
Myelodysplastic syndrome, no ICD-O subty	0.3633493	6	2.054e-03	1.066e-01	TET2:791 PAFAH1B1:1010 SF3B1:1649 YWHAE:1922 SETBP1:3122 FANCB:4755
Myopathy, Centronuclear, Autosomal Reces	-0.3604260	4	1.254e-02	2.177e-01	SPEG:898 AMPH:1398 BIN1:2934 DNM2:3668 NA NA
Phocomelia	0.3598469	5	5.325e-03	1.586e-01	GNAS:886 NIPBL:948 SMC3:1217 ESCO2:1631 WNT7A:6675 NA
Serous cystadenoma, borderline malignanc	0.3597696	5	5.334e-03	1.586e-01	ERBB2:944 DERL2:1888 BRAF:2046 MYC:2342 KRAS:4052 NA
Small anterior fontanelle	0.3561526	3	3.263e-02	3.238e-01	ORC1:107 MYCN:3411 ATR:3509 NA NA NA
Anterior Horn Cell Disease	-0.3558228	6	2.541e-03	1.170e-01	VIM:309 PNPLA6:476 SOD1:722 GLE1:806 PRDX3:2870 SMN1:8655
Acanthamoeba Keratitis	0.3542440	2	8.270e-02	4.464e-01	ARSA:2092 TLR4:2553 NA NA NA NA

1.6376-03 5.4226-01

-0.4107645 3 1.373e-02 7.190e-01 SYK:1076 CD79B:1561 CD79A:1707 NA NA NA

GSEA-c5-HsSymbols Top pathways by permulation

	-0.4107645	3	1.0700 02	7.1906-01	51K:1076 CD79B:1561 CD79A:1707 NA NA NA
HP_APLASIA_CUTIS_CONGENITA_ON_TRUNK_OR_L	0.3852853	6	1.081e-03	4.775e-01	ITGB4:134 PLEC:147 KRT14:905 ITGA6:1212 ARHGAP31:1607 KRT5:7146
GOMF_ANDROGEN_BINDING	0.3768753	4	9.037e-03	7.035e-01	ALDH1A1:1092 TSPO:1523 SHBG:2329 SLC39A9:3012 NA NA
HP_BRONCHIAL_WALL_THICKENING	-0.3754813	6	1.446e-03	5.053e-01	ABCA3:608 HYDIN:1101 FNIP1:1866 SFTPC:2457 PAK2:2935 TTC26:3169
HP_TALL_CHIN	0.3750714	5	3.676e-03	5.954e-01	MYH8:382 NSD1:975 TLK2:2008 APC2:2163 OPHN1:4559 NA
GOCC_CUL4B_RING_E3_UBIQUITIN_LIGASE_COMP	0.3738549	4	9.606e-03	7.097e-01	CUL4B:583 DDB2:1421 DTL:2811 RBX1:3331 NA NA
GOMF_MELANOCORTIN_RECEPTOR_BINDING	-0.3723779	4	9.895e-03	7.097e-01	AGRP:1497 ASIP:1601 MRAP:2208 MRAP2:2994 NA NA
HP_PECTUS_EXCAVATUM_OF_INFERIOR_STERNUM	0.3709487	5	4.069e-03	5.954e-01	NF1:522 PTPN11:1349 MAP2K1:2117.5 BRAF:2370 SOS1:4070 NA
GOBP_CELL_CELL_JUNCTION_DISASSEMBLY	0.3690699	5	4.260e-03	5.954e-01	FER:751 SNAI2:1530 TGFB3:2504 ABCC8:2629 TGFBR1:3169 NA
GOBP_NEGATIVE_REGULATION_OF_HEMATOPOIETI	0.3682289	4	1.075e-02	7.137e-01	ZFP36:1541 NFE2L2:1576 N4BP2L2:1928 TCF15:3478 NA NA
GOMF_MHC_CLASS_II_RECEPTOR_ACTIVITY	0.3644865	4	1.158e-02	7.137e-01	HLA-DOA:243 HLA-DOB:1690 HLA-DPA1:2852.5 HLA-DRA:3972 NA NA
GOCC_PAR_POLARITY_COMPLEX	-0.3597092	5	5.341e-03	6.152e-01	PRKCI:564 PARD6G:951 PARD6B:1738 PARD3:3725 PARD6A:4399 NA
GOCC_B_WICH_COMPLEX	0.3571460	6	2.447e-03	5.954e-01	DEK:247 ERCC6:1037 MYBBP1A:2177 DDX21:2241 SF3B1:2955 SMARCA5:518
GOBP_RESPONSE_TO_PHEROMONE	-0.3543741	2	8.258e-02	8.580e-01	TMEM145:778 GPR180:3945 NA NA NA NA
HP_GENERALIZED_AMYLOID_DEPOSITION	0.3534351	3	3.398e-02	8.370e-01	APOA1:1827 GSN:2086 B2M:3195 NA NA NA
HP_RECURRENT_NEISSERIAL_INFECTIONS	-0.3495784	5	6.784e-03	6.687e-01	C8B:98 C6:433 C5:2207 CFB:4609 CFI:4850 NA
GOBP_POSITIVE_REGULATION_OF_EXTRACELLULA	-0.3463307	4	1.644e-02	7.377e-01	CPB2:1176.5 RGCC:2007 BMP2:2792 AGT:4003 NA NA
HP_ABNORMAL_MIDDLE_EAR_REFLEXES	0.3452500	5	7.501e-03	6.744e-01	OTOF:853 PRORP:859 AIFM1:1196 MPDU1:1595 DIAPH3:8032 NA
GOBP_PEPTIDYL_ARGININE_N_METHYLATION	0.3449578	5	7.551e-03	6.744e-01	PRMT5:1500 PRMT3:1662 PRMT8:2791 NDUFAF7:3213 PRMT6:3356 NA
HP_ELEVATED_CIRCULATING_LONG_CHAIN_FATTY	-0.3424484	5	8.000e-03	6.830e-01	ABCD1:699 PEX19:700 PEX1:1212 PEX5:4881 CPT2:5280 NA
GOBP_TRICUSPID_VALVE_MORPHOGENESIS	-0.3416423	4	1.795e-02	7.377e-01	HEY2:429 BMPR2:2367 TGFBR2:3006 BMPR1A:4473 NA NA
GOMF_INTERLEUKIN_2_RECEPTOR_BINDING	-0.3396734	5	8.524e-03	7.022e-01	GATA3:576 IL2:1880 TIMM50:3264 IL21:3460 ECM1:3839 NA
GOBP_GRANULOCYTE_COLONY_STIMULATING_FACT	0.3395927	4	1.865e-02	7.377e-01	CD34:683 TSLP:709 ISL1:4083 HAVCR2:4879.5 NA NA
GOBP_POSITIVE_REGULATION_OF_RESPONSE_TO_	-0.3388384	6	4.047e-03	5.954e-01	RIPK1:578 ENDOG:1284 HDAC6:1821 ABL1:2142.5 FOXP1:4244 PAWR:5617
GOCC_CCAAT_BINDING_FACTOR_COMPLEX	-0.3377705	6	4.165e-03	5.954e-01	NFYB:245 NFYC:1588 ATF2:1910 ING2:2021 NFYA:3378 CEBPZ:6673
GOBP_SKELETAL_MUSCLE_SATELLITE_CELL_ACTI	-0.3377407	8	9.390e-04	4.665e-01	EPHB1:69 GJD4:1079 MEGF10:2381 CAPN3:2507 WNT7A:2913 SOX15:3455
HP_APLASIA_CUTIS_CONGENITA_OVER_THE_SCAL	0.3374607	6	4.199e-03	5.954e-01	ITGB4:134 PLEC:147 MCTP2:1043 BMS1:3150 DLL4:4367 UBA2:6909
GOMF_PEROXISOME_TARGETING_SEQUENCE_BINDI	-0.3373764	5	8.981e-03	7.035e-01	PEX19:700 PEX5L:904 BABAM2:3022 PEX7:3691 PEX5:4881 NA
HP_CONGENITAL_ADRENAL_HYPERPLASIA	0.3360661	4	1.991e-02	7.450e-01	POR:1825 CYP17A1:2556 STAR:2615 HSD3B2:3596 NA NA
GOBP_ESTABLISHMENT_OF_LEFT_RIGHT_ASYMMET	0.3345227	4	2.049e-02	7.552e-01	CFAP45:13 CFAP52:173 ENKUR:556 CCDC39:9977 NA NA
GOCC_MCRD_MEDIATED_MRNA_STABILITY_COMPLE	0.3334727	5	9.807e-03	7.097e-01	PAIP1:285 SYNCRIP:1467 CSDE1:1538 HNRNPD:3429 PABPC1:6740 NA
GOBP_PHENYLPROPANOID_METABOLIC_PROCESS	0.3331674	2	1.027e-01	8.609e-01	PON3:1308 CYP1A1:4086 NA NA NA NA
GOBP_REGULATION_OF_FAS_SIGNALING_PATHWAY	-0.3329904	3	4.575e-02	8.580e-01	ZDHHC7:789 TMBIM1:1080 SMAD5:6249 NA NA NA
GOBP_HYPOTHALAMUS_CELL_MIGRATION	-0.3326495	5	9.990e-03	7.097e-01	FOXB1:130 SEMA3E:1381 NDNF:1925 NRP2:2141 NRP1:8022 NA
GOBP_POSITIVE_REGULATION_OF_HYDROGEN_PER	-0.3326225	4	2.122e-02	7.566e-01	ENDOG:1284 HDAC6:1821 ABL1:2142.5 PAWR:5617 NA NA
GOBP_SPHINGOLIPID_TRANSLOCATION	0.3312035	4	2.178e-02	7.584e-01	ABCB1:3 ABCB4:24 ABCC1:3415 ABCA2:7474 NA NA
GOBP_BRANCHED_CHAIN_AMINO_ACID_BIOSYNTHE	0.3308770	5	1.039e-02	7.137e-01	SDS:17 BCAT2:1648 BCAT1:2244.5 SDSL:3421 ILVBL:6330 NA
GOCC_DNA_REPLICATION_FACTOR_A_COMPLEX	-0.3271269	3	4.970e-02	8.580e-01	RPA2:380 RPA1:2077 RPA3:5950 NA NA NA
GOBP_CHONDROBLAST_DIFFERENTIATION	-0.3271128	5	1.130e-02	7.137e-01	RARA:126 GDF5:1242 CCN1:1726 FGF2:5431 FGF4:5494 NA

MGI\_Mammalian\_Phenotype\_Level\_4 Top pathways by permulation

Geneset	stat	num.genes	pval	p.adj	gene.vals
MP0003787 abnormal imprinting	0.2671881	10	-	4.839e-02	SMCHD1:119 ATRX:823 GNAS:886 ARID4B:1089 ARID4A:1422 SNRPN:4608
MP0002837 dystrophic cardiac calcinosis	-0.2435404	9		1.090e-01	DES:88 SLC2A4:104 MYH6:664 MYBPC3:1024 MMP9:1060 SCG5:3692
MP0004510 myositis	-0.2109870	10		1.514e-01	SH3BP2:157 SYT7:394 CEBPB:1326 RYR2:1609 SGCB:1760 SOCS1:2131
MP0003646 muscle fatigue	-0.2018970	9		2.123e-01	SLC2A4:104 PPARGC1A:904 NOS1:1203 MTOR:1952 MB:2833 COX10:3324
MP0009379 abnormal foot pigmentation	0.1955535	5	1.300e-01	4.552e-01	GNAQ:819 RPS19:2791 GNA11:3735 RPS20:4587 EGFR:13579 NA
MP0006054 spinal hemorrhage	0.1874573	9	5.162e-02	2.730e-01	
MP0005083 abnormal biliary tract	-0.1871277	8	6.696e-02	3.125e-01	MUC1:1021 VTI1B:2255 CCKAR:3259 XYLT2:3990 ANK1:4910 GPBAR1:5248
MP0003121 genomic imprinting	0.1783485	23		4.539e-02	SMCHD1:119 DNMT1:200 HELLS:341 ATRX:823 GNAS:886 ARID4B:1089
MP0002653 abnormal ependyma morphology	0.1757310	11	4.372e-02	2.392e-01	SOX2:789 MSI1:1363 NR1H2:1803 DLL3:2185 E2F5:3298 BBS1:4694
MP0000678 abnormal parathyroid gland	0.1752148	21		6.899e-02	TBX1:517 HOXA3:585 GCM2:621 PTHLH:896 CHRD:1133 FOXG1:1711
MP0004233 abnormal muscle weight	-0.1736810	16	1.627e-02	1.291e-01	PPARGC1A:904 NOS1:1203 GRB10:1863 MTOR:1952 CHRNE:2394 ARNTL:2668
MP0003183 abnormal peptide metabolism	-0.1637430	10	7.315e-02	3.285e-01	NCF1:687 VAV2:937 VAV3:2303 ACE2:2935 NCSTN:3890 TRIP11:4584
MP0002277 abnormal respiratory mucosa	0.1611474	20		1.142e-01	HESX1:225 SOX2:789 CXCR2:881 RELB:989 C3AR1:1331 HOXA5:1413
MP0002254 reproductive system inflammat	0.1537302	5	2.340e-01	5.772e-01	RELB:989 PGR:3795 MFGE8:5659 AIRE:6695 EPHA1:12018 NA
MP0005275 abnormal skin tensile	-0.1519069	17	3.031e-02	2.004e-01	LAMC2:492 OGN:1089 COL5A2:1938 DSG4:2109 DSE:2754 COL14A1:3060
MP0010386 abnormal urinary bladder	-0.1457590	14	5.921e-02	2.914e-01	TAC1:151 CHRNB2:718 HTR3A:1222 MYLK:2380 ANXA4:3282 KCNMA1:3553
MP0003136 yellow coat color	0.1425514	7	1.917e-01	5.319e-01	ADAMTS20:494 SOX2:789 OCA2:3435 EDA:6304 EDNRB:6342 MITF:10332
MP0009278 abnormal bone marrow	-0.1397977	17	4.622e-02	2.500e-01	LIG1:323 MMP9:1060 TSC22D1:1646 RAG2:1934 HIP1:2087 SOCS3:2644
MP0002396 abnormal hematopoietic system	0.1357974	21	3.145e-02	2.041e-01	CASP8:117 MEOX2:1122 LDB1:1163 MAN2A1:1214 MYC:2342 CDK6:2354
MP0000569 abnormal digit pigmentation	-0.1355291	6	2.505e-01	5.796e-01	LYST:3249 MYO5A:3671 EN1:3772 DOCK7:3806 HPS5:6218 AP3B1:13469
MP0000383 abnormal hair follicle	-0.1321389	22	3.216e-02	2.041e-01	PKP3:582 KRT14:721 ADAM17:771 DICER1:1249 FGFR2:1822 TRPV3:1872
MP0008007 abnormal cellular replicative	0.1311550	29	1.469e-02	1.227e-01	SIRT6:115 CUL7:926 MAPKAPK5:1376 CDKN2A:1956 FLT3:2799 RAD9B:2882
MP0003950 abnormal plasma membrane	-0.1298324	10	1.554e-01	4.760e-01	CAV1:542 NPC1:1230 CDK5RAP2:1759 DMD:2293 GLRX:2480 TJP2:4457
MP0006292 abnormal olfactory placode	0.1286637	12	1.230e-01	4.432e-01	HESX1:225 OTX2:951 HHEX:1048 CHRD:1133 FOXG1:1711 TCOF1:2625
MP0000749 muscle degeneration	-0.1275834	36	8.226e-03	9.323e-02	PLEC:16 DES:88 HSPB2:266 MYOF:339 DYSF:414 BAG3:422
MP0002877 abnormal melanocyte morpholog	0.1272998	10	1.636e-01	4.837e-01	CDKN2A:1956 KIT:3050 KRAS:4052 PTPN11:6081 RAB27A:6218 MREG:6665
MP0004859 abnormal synaptic plasticity	-0.1262672	31	1.518e-02	1.246e-01	ADD2:73 CAMK2B:132 TNC:250 ADCY1:450 FOXP2:648 GRIN2B:1050
MP0002876 abnormal thyroid physiology	0.1257304	18	6.510e-02	3.068e-01	MED1:333 CGA:456 GHR:980 HPN:1344 GFRA4:3169 GNA11:3735
MP0003122 maternal imprinting	0.1220382	14	1.142e-01	4.346e-01	GNAS:886 ARID4A:1422 NDN:2096 IGF2:2372 MEST:2982 SNRPN:4608
MP0009780 abnormal chondrocyte physiolo	-0.1209272	9	2.093e-01	5.504e-01	CAV1:542 WNT9A:2360 THRA:3025 TRIP11:4584 ESR1:5740 THRB:6513
MP0005167 abnormal blood-brain barrier	-0.1168554	16	1.060e-01	4.134e-01	PTAFR:33 MMP9:1060 NOS1:1203 HRH3:1485 CLCN2:3412 CTNNB1:3471
MP0002735 abnormal chemical nociception	-0.1146968	28	3.602e-02	2.123e-01	ADCY8:341 PROKR1:407 ADCY1:450 BAMBI:577 PTGIR:983 GRIK1:1090
MP0000681 abnormal thyroid gland	0.1133487	43	1.034e-02	1.090e-01	CGA:456 TBX1:517 HOXA3:585 MANBA:797 HHEX:1048 CHRD:1133
MP0003221 abnormal cardiomyocyte apopto	0.1107107	37	2.010e-02	1.514e-01	CASP8:117 AIFM1:216 TFAM:220 MAPKAPK2:242 MDM2:392 RAF1:861
MP0000013 abnormal adipose tissue	0.1103759	15	1.392e-01	4.700e-01	COL1A1:1906 PRKAR1A:2030 SMTN:2743 FSTL3:2853 PYY:4078 PPARG:4605
MP0003693 abnormal embryo hatching	0.1050691	24	7.525e-02	3.326e-01	RBBP8:364 HSPA5:786 ATF1:1069 PARG:1268 KIF11:1497 AURKA:2108

1.626e-01 4.837e-01

1.523e-01 4.760e-01

1.221e-03 2.325e-02

1.613e-01 4.828e-01

STAT3:594 SAV1:682 SMAD4:2423 PTGS2:2550 ITGB1:2961 APC:3314

PMP22:498 LRRK2:878 PTHLH:896 VCP:923 ATG9A:968 ATG5:3778

CHD8:212 CUL3:218 BRD4:571 TPT1:777 HSPA5:786 ATRX:823

SMCHD1:119 DNMT3B:205 UHRF1:431 GNAS:886 ARID4B:1089 ARID4A:1422