

EnrichmentHsSymbolsFile2 Top pathways by non-permutation

| Geneset | stat | num.genes | pval | p.adj | gene.vals |
|---|--------------|-----------|-----------|-----------|--|
| NIKOLSKY_BREAST_CANCER_15Q26_AMPLICON | -0.32785611 | 21 | 1.979e-07 | 1.285e-03 | PCSK6:244 TARSK:497 LYSMD4:547 ARDCD4:710 LRRK1:766 SNRPA1:828 |
| DODD_NASOPHARYNGEAL_CARCCINOMA_DN | -0.03993861 | 1274 | 1.974e-06 | 6.410e-03 | NUP133:7 APOC1:19 NUP205:22 GALNT2:30 NUP155:34 NSD2:82 |
| ZHANG_BREAST_CANCER_PROGNETITORS_LP | -0.06207104 | 414 | 1.538e-05 | 2.497e-02 | MET:5 PRPS2:26 TRPS1:28 NUP155:34 BCLAF3:48 PAXBP1:109 |
| REACTOME_RNA_POLYMERASE_II_TRANSCRIPTION | -0.03602415 | 1306 | 1.430e-05 | 2.497e-02 | MET:5 EHMT1:14 ZNF274:29 ZIM2:49 ZNF214:51 NUP1:52 |
| KEGG_CYTOKINE_CYTOKINE_RECEPTOR_INTERACT | -0.07605665 | 258 | 2.661e-05 | 3.456e-02 | MET:5 PRL:92 TGFBI:97 TSLP:117 TNF:254 FLT1:312 |
| BLALOCK_ALZHEIMERS_DISEASE_DN | -0.03604673 | 1189 | 3.215e-05 | 3.479e-02 | HERC2:1 MET:5 LTN1:15 SCN2A:16 ARHGEF4:32 ATP2B1:56 |
| NIKOLSKY_BREAST_CANCER_1Q21_AMPLICON | 0.20294201 | 34 | 4.219e-05 | 3.914e-02 | THBS3:14 ADAM15:60 DCST1:98 ZBTB78:226 PYGO2:259 RUCP1:318 |
| BRIDEAU_IMPRINTED_GENES | -0.15143650 | 58 | 6.650e-05 | 5.398e-02 | ATP10A:20 IGFB1:05 UBE3A:201 CNTN3:224 MAGEL2:234 CALCR:314 |
| REACTOME_PROLACTIN_RECEPTOR_SIGNALING | -0.28533212 | 15 | 1.300e-04 | 9.383e-02 | PRL:92 PRLR:805 JAK2:812 GH1:821 CSH1:835 GH1:982 |
| WP_PRADERWILLI_AND_ANGELMAN_SYNDROME | -0.13786708 | 63 | 1.544e-04 | 1.003e-01 | HERC2:1 GABRA5:2 ATP10A:20 MDM4:85 GABRG3:148 OCA2:170 |
| WP_PHOTODYNAMIC_THERAPYINDUCED_AP1_SURVI | -0.15598790 | 48 | 1.849e-04 | 1.092e-01 | FOS:169 TNF:254 BAX:283 BCL2L1:1139 CCNE1:466 MAPK8:494 |
| REACTOME_FORMATION_OF_SENESCENCE_ASSOCIA | -0.25942608 | 17 | 1.227e-04 | 1.151e-01 | H1-4:172 H1-1374 UBN1:478 H1-3:720 CABIN1:741 EP400:919 |
| WP_OVERVIEW_OF_PROINFLAMMATORY_AND_PROFI | -0.09259063 | 126 | 3.341e-04 | 1.669e-01 | AREG:95 TGFBI:97 TSLP:117 IL33:146 TNF:254 IL18:321 |
| REACTOME_PROCESSING_OF_CAPPED_INTRON_CON | -0.06463052 | 253 | 4.072e-04 | 1.889e-01 | NUP133:7 NUP205:22 NUP155:34 SYMPK:68 U2AF1L4:300 THOC5:364 |
| RODRIGUES_THYROID_CARCCINOMA_POORLY_DIFFE | -0.04199629 | 602 | 4.518e-04 | 1.956e-01 | NUP155:34 MPHOSPH10:43 E2F5:57 GPM52:174 ORC6:193 NETO2:221 |
| BIOCARTA_PEP1_PATHWAY | 0.34902846 | 8 | 6.058e-04 | 2.149e-01 | CELA1:27 CELA2B:468 SLPI:511 CELA3B:611 CELA2A:778 ELANE:1483 |
| HOLLERN_EMT_BREAST_TUMOR_DN | 0.09143831 | 118 | 6.255e-04 | 2.149e-01 | CLIC3:156 SDR42E1:230 EVPL:297 ENDOU:328 POF1B:391 PTPRF:425 |
| REACTOME_FORMATION_OF_THE_CORNIFIED_ENVE | 0.08905522 | 126 | 5.599e-04 | 2.149e-01 | KRT39:139 KRT84:170 SPRR2A:204 EVPL:297 KRT20:322 KRT72:454 |
| RODRIGUES_THYROID_CARCCINOMA_ANAPLASTIC_U | -0.03896305 | 673 | 5.952e-04 | 2.149e-01 | COL7A1:25 MPHOSPH10:43 CNOT1:55 ATP2B1:56 CDH2:87 AREG:95 |
| NIKOLSKY_BREAST_CANCER_8Q12_Q22_AMPLICON | -0.08674479 | 127 | 7.404e-04 | 2.193e-01 | RBM12B:35 ZBTB10:118 SNX16:134 RALYL:200 PIRAP2:213 MMP16:242 |
| REACTOME_CELL_SURFACE_INTERACTIONS_AND_TH | -0.08374567 | 137 | 7.190e-04 | 2.193e-01 | TGFB1:97 GRB14:223 PIK3CA:308 GYPC:378 SIRPA:485 JAML:489 |
| KEGG_P53_SIGNALING_PATHWAY | -0.11919283 | 67 | 7.431e-04 | 2.193e-01 | MDM4:85 IGFBP3:111 SHIS45:132 BAX:283 CHEK1:369 CCNE1:466 |
| MILI_PEGUODODIA_HAPTOXIS_UP | -0.04392626 | 496 | 1.043e-04 | 2.635e-01 | LTN1:15 CAMSAP2:47 BCLAF3:48 WPM1:52 SHEN1:139 RNF1:31:149 |
| DANG_BOUND_BY_MYC | -0.03081833 | 1010 | 9.878e-04 | 2.635e-01 | MET:5 ZNF134:6 PRPS2:26 ZNF274:29 NUP155:34 SYMPK:68 |
| KIM_ALL_OBSTRUCTS_CALB1_CORR_UP | -0.04291957 | 517 | 9.485e-04 | 2.635e-01 | GABRA5:2 CAMSAP2:47 ATP2B1:56 CHL1:62 SARSL:121 DCTN1:147 |
| PID_E2F_PATHWAY | -0.11405483 | 69 | 1.055e-03 | 2.635e-01 | E2F5:57 RBL2:80 CASP7:131 CDC25A:150 MYBL2:391 CCNE1:466 |
| REACTOME_TP53_REGULATES_TRANSCRIPTION_OF | -0.13697975 | 47 | 1.160e-03 | 2.660e-01 | CNOT1:55 RBL2:80 BAX:283 CCNE1:466 CDK1:852 CNOT11:946 |
| JOHNSTONE_PARVB_TARGETS_3_DN | -0.03414968 | 793 | 1.133e-03 | 2.660e-01 | PRPS2:26 SETD2:27 ZNF274:29 UAP1:71 MDM4:85 ZNF22:119 |
| BLUM_RESPONSE_TO_SALIRASIB_DN | -0.05231811 | 326 | 1.188e-03 | 2.660e-01 | GALTNT2:30 CDC25A:150 FOS:169 GPM52:174 ORC6:193 PCK1:361 |
| SHEN_SMARCA2_TARGETS_UP | -0.04638322 | 410 | 1.300e-03 | 2.814e-01 | PALNT2:11 NUP133:7 PSMF1:206 CAPN7:287 NPTN:376 WDR1:503 |
| KEGG_GRAFT_VERSUS_HOST_DISEASE | -0.14999908 | 37 | 1.593e-03 | 3.336e-01 | TNF:254 HLA-DQB3:384 HLA-DQA1:502 ATG5:265 CDK1:852 |
| REACTOME_CYTOKINE_SIGNALING_IN_IMMUNE_SY | -0.03504975 | 698 | 1.670e-03 | 3.388e-01 | TGFB1:97 TSLP:117 CRK1:37 TNF:254 CALCR:314 HLA-DQA1:502 |
| REACTOME_SPERM_MOTILITY_AND_TAXES | -0.130130682 | 9 | 1.746e-03 | 3.459e-01 | BFSPP2:93 CRYBB1:214 CRYAA2:956 STS:1054 GJA8:1828 MIP:2175 |
| ROYLANCE_BREAST_CANCER_16Q_COPY_NUMBER_D | -0.08462091 | 23 | 1.908e-03 | 3.556e-01 | TGFB1:97 CRK1:37 PHB2:199 PDE6B:247 TNF:254 TLR8:267 |
| MIKKELSEN_ES_LCP_WITH_H3K4ME3 | 0.03648595 | 684 | 2.096e-03 | 3.565e-01 | CYLD:42 TDRD7:46 ARSF:79 AREG:95 TGFBI:97 HERC5:108 |
| REACTOME_TLR1_SIGNALING | -0.31340549 | 8 | 2.141e-03 | 3.565e-01 | GPBAR1:31 PEX1:173 HAMP:271 SLC10A2:273 LIPA:287 MPI:288 |
| REACTOME_UPTAKE_OF_DIETARY_COBALAMINS_IN | -0.03532171 | 655 | 2.122e-03 | 3.565e-01 | CYLD:42 TDRD7:46 ARSF:79 AREG:95 TGFBI:97 HERC5:108 |
| SCHLOSSER_SERUM_RESPONSE_DN | 0.23697885 | 14 | 2.139e-03 | 3.565e-01 | TGFBI:97 TSLP:117 CRK1:37 TNF:254 CALCR:314 HLA-DQA1:502 |
| NIKOLSKY_BREAST_CANCER_1Q21_AMPLICON | 0.07738365 | 131 | 2.238e-03 | 3.624e-01 | BFSPP2:93 CRYBB1:214 CRYAA2:956 STS:1054 GJA8:1828 MIP:2175 |

DisGeNET Top pathways by non-permutation

| Geneset | stat | num.genes | pval | p.adj | gene.vals |
|--|--------------|-----------|-----------|-----------|--|
| Adenocarcinoma in Situ | -0.22462139 | 29 | 2.842e-05 | 2.791e-01 | CDH2:87 ASAP1:488 DPYD:507 SEC14L2:664 PAPOLA:918 STS:1054 |
| Carcinosarcoma | -0.17316279 | 43 | 8.589e-05 | 4.217e-01 | MET:5 TGFBI:97 IGFB1:05 PHB2:199 PIK3CA:308 SOX9:515 |
| Allergic Reaction | -0.12627535 | 61 | 6.522e-04 | 6.250e-01 | KNG1:45 TGFBI:97 TNF:254 IL18:321 HLA-DQA1:502 CX3CL1:625 |
| Anal squamous cell carcinoma | -0.28741944 | 12 | 5.659e-04 | 6.250e-01 | PIK3CA:308 MDM2:757 DCC:1247 NLFIE:1264 TP53:139 CDKN2A:1536 |
| Cataract | -0.04542582 | 484 | 6.695e-04 | 6.250e-01 | CNGB3:8 COL7A1:25 TDRD7:46 ATP2B1:56 SUMF1:76 RBP3:83 |
| Cervical Squamous Intraepithelial Neopla | -0.14195945 | 47 | 7.638e-04 | 6.250e-01 | MET:5 TGFBI:97 TNF:254 LAMB2:286 HMGB1:551 MTHFR:662 |
| Hepatitis C | -0.03838935 | 677 | 7.359e-04 | 6.250e-01 | MET:5 APOA1:13 APOC1:19 TGFBI:97 CLU:101 IGFB1:05 |
| insulinoma | -0.08206995 | 164 | 2.953e-04 | 6.250e-01 | MET:5 EHMT1:14 PRL:92 TGFBI:97 IGFB1:05 SDS:173 |
| Liver carcinoma | -0.02026726 | 3047 | 6.026e-04 | 6.250e-01 | MET:5 APOA1:13 SETD2:27 GALNT2:30 CYLD:42 KNG1:45 |
| Prader-Willi Syndrome | -0.10739578 | 88 | 5.035e-04 | 6.250e-01 | HERC2:1 GABRA5:2 ATP10A:20 ZNF274:29 GABRG3:148 OCA2:170 |
| Stable angina | -0.12132354 | 70 | 4.525e-04 | 6.250e-01 | APOA1:13 TGFBI:97 IGFB1:05 IL33:146 TNF:254 CX3CL1:625 |
| Tumor Immunity | -0.09083163 | 122 | 5.398e-04 | 6.250e-01 | AREG:95 IL33:146 FOS:169 HAVCR1:198 TNF:254 TLR8:267 |
| Leukemia, Myelocytic, Acute | -0.02567732 | 1494 | 1.152e-03 | 6.286e-01 | MET:5 SETD2:27 TRPS1:28 CHL1:62 ZNF331:74 MDM4:85 |
| Bilateral cataracts (disorder) | -0.09453982 | 104 | 8.768e-04 | 6.286e-01 | TDRD7:46 BFSPP2:93 TGFBI:97 MGST1:207 AKR1B1:212 EPHA2:356 |
| Cervical Intraepithelial Neoplasia | -0.06942076 | 187 | 1.089e-03 | 6.286e-01 | MET:5 TGFBI:97 SYCP3:196 TNF:254 BAX:283 LAMB2:286 |
| Cholestasis in newborn | 0.10161197 | 87 | 1.064e-03 | 6.286e-01 | GPBAR1:31 PEX1:173 HAMP:271 SLC10A2:273 LIPA:287 MPI:288 |
| Influenza | -0.04241087 | 508 | 1.150e-03 | 6.286e-01 | CYLD:42 TDRD7:46 ARSF:79 AREG:95 TGFBI:97 HERC5:108 |
| Myasthenia Gravis | -0.07077270 | 156 | 9.131e-04 | 6.286e-01 | TGFBI:97 TSLP:117 CRK1:37 TNF:254 CALCR:314 HLA-DQA1:502 |
| CATARACT, AUTOSOMAL DOMINANT | -0.29751104 | 9 | 1.997e-03 | 6.674e-01 | BFSPP2:93 CRYBB1:214 CRYAA2:956 STS:1054 GJA8:1828 MIP:2175 |
| Tuberculosis, Pulmonary | -0.07405264 | 150 | 1.779e-03 | 6.674e-01 | TGFB1:97 CRK1:37 PHB2:199 PDE6B:247 TNF:254 TLR8:267 |
| Acute inflammatory demyelinating polyneu | -0.32422268 | 7 | 2.971e-03 | 6.674e-01 | TNF:254 PTGDS:302 TNFRSF1A:858 ALB:1419 PMP22:1499 HLA-DRB1:9284.5 |
| Adenovirus Infections | -0.09567072 | 85 | 2.318e-03 | 6.674e-01 | TRPS1:28 MDM4:85 CDC25A:150 TNF:254 BAX:283 CHEK1:369 |
| Anasarca | -0.16972994 | 26 | 2.743e-03 | 6.674e-01 | APOA1:13 KNG1:45 TNF:254 VIP:917 PTGS2:964 CASP8:1005 |
| Anti-Basement Membrane Glomerulonephriti | -0.15029550 | 36 | 1.810e-03 | 6.674e-01 | CLU:101 TNF:254 MAPK8:494 CX3CL1:625 ITGA4:1477 PTK2B:1508 |
| Carcinoma of bladder | -0.02953013 | 1013 | 1.710e-03 | 6.674e-01 | MET:5 SETD2:27 KNG1:45 MDM4:85 CDH2:87 TGFBI:97 |
| Central neuroblastoma | -0.02391509 | 1507 | 2.374e-03 | 6.674e-01 | HERC2:1 SETD2:27 CYLD:42 KNG1:45 CNOT1:55 CHL1:62 |
| Cervix carcinoma | -0.02932364 | 943 | 2.668e-03 | 6.674e-01 | MET:5 SETD2:27 CYLD:42 CHL1:62 NSD2:82 TGFBI:97 |
| Choriocarcinoma | -0.05287199 | 279 | 2.456e-03 | 6.674e-01 | MDM4:85 TGFBI:97 IGFB1:05 PHB2:199 CRH:215 INSR:231 |
| Epithelial ovarian cancer | -0.02650156 | 1150 | 2.852e-03 | 6.674e-01 | MET:5 SETD2:27 KNG1:45 RBL2:80 MDM4:85 PRL:92 |
| Extramedullary Plasmacytoma | -0.24780234 | 12 | 2.956e-03 | 6.674e-01 | PECAM1:679 ANGP1:1132 ENG:1334 TP53:1339 CDKN2A:1536 PRM3:1703 |
| Generalized hypopigmentation | -0.23851841 | 14 | 2.002e-03 | 6.674e-01 | HERC2:1 MAGEL2:234 NDN:1164 OCLR1:1727 MKRN3:2059 LEMO3:2181 |
| Glioblastoma | -0.02250462 | 1686 | 2.672e-03 | 6.674e-01 | MET:5 APOA1:13 SETD2:27 CD109:31 CNOT1:55 RBL2:80 |
| HIV Infections | -0.03300997 | 717 | 2.856e-03 | 6.674e-01 | ZNF134:6 APOA1:13 CYLD:42 CNOT1:55 CDH2:87 TGFBI:97 |
| Human metapneumovirus infection | -0.32969415 | 7 | 2.521e-03 | 6.674e-01 | TSLP:117 TNF:254 NCR1:424 PIPPK1:903 ISYNA1:1940 SGT:9284.5 |
| Hyperinulsinim | -0.04804065 | 359 | 1.854e-03 | 6.674e-01 | HERC2:1 EHMT1:14 APOC1:19 MCR4:61 RBP3:83 PRL:92 |
| Infection | -0.043232542 | 463 | 1.494e-03 | 6.674e-01 | APOA1:13 APOC1:19 CYLD:42 TGFBI:97 IGFB1:05 IL33:146 |
| Male sterility due to Y-chromosome delet | -0.37276775 | 6 | 1.566e-03 | 6.674e-01 | DAZ1:567 DAZ4:714 DAZ3:851 DAZ2:997 USP9Y:1817 DDXX3Y:9284.5 |
| Neuroblastoma | -0.02309536 | 1547 | 2.990e-03 | 6.674e-01 | HERC2:1 MET:5 SETD2:27 CYLD:42 KNG1:45 CNOT1:55 |
| Oncocytic Neoplasm | -0.12687192 | 47 | 2.631e-03 | 6.674e-01 | PRL:92 ZFP42:123 MST1:329 CLDN8:651 PTGS2:964 CD8:1033 |
| Partial chromosome Y deletion | -0.37276775 | 6 | 1.566e-03 | 6.674e-01 | DAZ1:567 DAZ4:714 DAZ3:851 DAZ2:997 USP9Y:1817 DDXX3Y:9284.5 |

customGeneSet Top pathways by non-permutation

| Geneset | stat | num.genes | pval | p.adj | gene.vals |
|--------------------------------|-------------|-----------|-----------|-----------|---|
| HumanLocalAdaptionDietAll | 0.05735493 | 13 | 5.210e-01 | 7.814e-01 | SLC39A8:2409 LCT:9221.5 AS3MT:9221.5 GPX3:9221.5 CELF1:9221.5 SEPSECS:9221.5 |
| NAFLDGOVIA5 | -0.06787879 | 15 | 4.228e-01 | 7.814e-01 | INSR:231 TOR1B:959 GID4:1220 FTO:1677 GPAM:1954 PNPLA3:9284.5 |
| expressionDirectionalSelection | 0.01147959 | 42 | 8.714e-01 | 8.714e-01 | DEFB8:2262 HLA-DRB1:9221.5 FADS1:9221.5 POU5F1:9221.5 HLA-DRB5:9221.5 KAT8:9221.5 |
| NA | NA | NA | NA | NA | NA NA NA NA NA NA |
| NA.1 | NA | NA | NA | NA | NA NA NA NA NA NA |
| NA.2 | NA | NA | NA | NA | NA NA NA NA NA NA |
| NA.3 | NA | NA | NA | NA | NA NA NA NA NA NA |
| NA.4 | NA | NA | NA | NA | NA NA NA NA NA NA |
| NA.5 | NA | NA | NA | NA | NA NA NA NA NA NA |
| NA.6 | NA | NA | NA | NA | NA NA NA NA NA NA |
| NA.7 | NA | NA | NA | NA | NA NA NA NA NA NA |
| NA.8 | NA | NA | NA | NA | NA NA NA NA NA NA |
| NA.9 | NA | NA | NA | NA | NA NA NA NA NA NA |
| NA.10 | NA | NA | NA | NA | NA NA NA NA NA NA |
| NA.11 | NA | NA | NA | NA | NA NA NA NA NA NA |
| NA.12 | NA | NA | NA | NA | NA NA NA NA NA NA |
| NA.13 | NA | NA | NA | NA | NA NA NA NA NA NA |
| NA.14 | NA | NA | NA | NA | NA NA NA NA NA NA |
| NA.15 | NA | NA | NA | NA | NA NA NA NA NA NA |
| NA.16 | NA | NA | NA | NA | NA NA NA NA NA NA |
| NA.17 | NA | NA | NA | NA | NA NA NA NA NA NA |
| NA.18 | NA | NA | NA | NA | NA NA NA NA NA NA |
| NA.19 | NA | NA | NA | NA | NA NA NA NA NA NA |
| NA.20 | NA | NA | NA | NA | NA NA NA NA NA NA |
| NA.21 | NA | NA | NA | NA | NA NA NA NA NA NA |
| NA.22 | NA | NA | NA | NA | NA NA NA NA NA NA |
| NA.23 | NA | NA | NA | NA | NA NA NA NA NA NA |
| NA.24 | NA | NA | NA | NA | NA NA NA NA NA NA |
| NA.25 | NA | NA | NA | NA | NA NA NA NA NA NA |
| NA.26 | NA | NA | NA | NA | NA NA NA NA NA NA |
| NA.27 | NA | NA | NA | NA | NA NA NA NA NA NA |
| NA.28 | NA | NA | NA | NA | NA NA NA NA NA NA |
| NA.29 | NA | NA | NA | NA | NA NA NA NA NA NA |
| NA.30 | NA | NA | NA | NA | NA NA NA NA NA NA |
| NA.31 | NA | NA | NA | NA | NA NA NA NA NA NA |
| NA.32 | NA | NA | NA | NA | NA NA NA NA NA NA |
| NA.33 | NA | NA | NA | NA | NA NA NA NA NA NA |
| NA.34 | NA | NA | NA | NA | NA NA NA NA NA NA |
| NA.35 | NA | NA | NA | NA | NA NA NA NA NA NA |
| NA.36 | NA | NA | NA | NA | NA NA NA NA NA NA |

GO_Biological_Process_2023 Top pathways by non-permutation

| | | | | | |
|---|---------------|----|-----------|-----------|---|
| B Cell Receptor Signaling Pathway (GO:0033030) | 0.0370377705 | 32 | 4.653e-01 | 9.999e-01 | BTX447 PLCG2:960 NFAM1:1463 BCAR1:1497 LCK:1704 BCL2:2418 |
| BMP Signaling Pathway (GO:0030309) | 0.0172347396 | 61 | 6.418e-01 | 9.999e-01 | GDF3:105 AAMH2:378 INHBA:618 RGMB:790 SLC39A5:888 HIVPF1:1190 |
| C-terminal Protein Amino Acid Modification | -0.0060169575 | 11 | 9.449e-01 | 9.999e-01 | ATG5:992 AGBL5:9284.5 GPLD1:9284.5 ICMT:9284.5 AGTPBP1:9284.5 ATG16L1:9284.5 |
| C-terminal Protein Deglutamylation (GO:0006505) | 0.0943438670 | 4 | 5.134e-01 | 9.999e-01 | FOLH1:2728 AGBL5:9221.5 AGTPBP1:9221.5 AGBL4:9221.5 NA NA |
| C-terminal Protein Lipidation (GO:0006650) | -0.1113140656 | 4 | 4.407e-01 | 9.999e-01 | ATG5:992 GPLD1:9284.5 ATG16L1:9284.5 ATG7:9284.5 NA NA |
| C4-dicarboxylate Transport (GO:0015740) | 0.1173923221 | 12 | 1.591e-01 | 9.999e-01 | LRRCEB:158 SLC25A1:587 SLC25A18:844 SLC1A6:1113 SLC13A2:9221.5 SLC13A5:9221.5 |
| CD4-positive, Alpha-Beta T Cell Activation | -0.2278829542 | 4 | 1.144e-01 | 9.999e-01 | HLMG21:551 TNFSF4:1083 STOML2:9284.5 NKGF:9284.5 NA NA |
| CD40 Signaling Pathway (GO:0023030) | -0.1207738910 | 7 | 2.685e-01 | 9.999e-01 | PHB2:199 CD86:1566 RNF31:2310 ITGB1:9284.5 TNIP2:9284.5 ITGA5:9284.5 |
| CENP-A Containing Chromatin Assembly (GO:0042820) | 0.091826542 | 6 | 4.360e-01 | 9.999e-01 | HJURP:95 NASP:1138 CENPW:9221.5 SCNP1:9221.5 OIP5:9221.5 MIS18A:16349 |
| COP1 Coating Of Golgi Vesicle (GO:004820) | -0.1523288460 | 5 | 2.381e-01 | 9.999e-01 | ARFGAP3:1984 TMDER:2426 TMDI0:9284.5 GBF1:9284.5 TMDI2:9284.5 NA |

MGI_Mammalian_Phenotype_Level_4 Top pathways by non-permutation

| Geneset | stat | num.genes | pval | p.adj | gene.vals |
|--|--------------|-----------|-----------|-----------|--|
| MP0008875 abnormal xenobiotic pharmacokinetics | 0.176566733 | 20 | 6.330e-03 | 9.112e-01 | ADH7:223 ABCC3:298 AHR:321 POR:705 ABCC2:841 SLC47A1:991 |
| MP0002086 abnormal extraembryonic tissue morphogenesis | -0.035487163 | 487 | 9.569e-03 | 9.112e-01 | MET5: SETD2:27 CDH28:97 TGFBI:91 IFG2:105 FGG:135 |
| MP0002080 prenatal lethality | -0.024703356 | 1338 | 6.387e-03 | 9.112e-01 | HERC2:1 MET5: NUP133:7 EHM11:14 LTN1:15 SETD2:27 |
| MP0003252 abnormal milk duct morphogenesis | 0.149938539 | 25 | 5.972e-03 | 9.112e-01 | MAP3K14:281 AHR:321 PKHD1:231 CYP8B1:371 ABCG5:428 ABCB4:563 |
| MP0001666 abnormal nutrient absorption | 0.126167022 | 46 | 3.162e-03 | 9.112e-01 | TREH:166 SLC22A4:180 SLC10A2:372 CYP8B1:371 ABCG5:428 ABCB4:563 |
| MP0008438 abnormal cutaneous collagen synthesis | -0.064579573 | 15 | 3.869e-01 | 9.188e-01 | FBN1:658 DGN:782 TNXB:2221 PLOD3:9284.5 THBS2:9284.5 COL3A1:9284.5 |
| MP0002909 abnormal adrenal gland development | -0.059920625 | 23 | 3.205e-01 | 9.188e-01 | LRRK2:64 KDNK3:1348 DRD5:1952 CHGB:9284.5 FOXA1:9284.5 CHGA:9284.5 |
| MP0001730 embryonic growth arrest | -0.019075390 | 182 | 3.807e-01 | 9.188e-01 | NUP133:7 RBL2:80 DCTN1:147 PIK3CA:308 FLT1:312 CHD8:530 |
| MP0001731 abnormal postnatal growth | -0.007862130 | 592 | 5.311e-01 | 9.188e-01 | MET5: LTN1:15 COL7A1:25 SUMF1:76 AREG:95 IFG2:105 |
| MP0002210 abnormal sex determination | -0.034019461 | 349 | 3.308e-02 | 9.188e-01 | SPAG16:103 OCA2:170 TAF4F:195 SYCP3:196 UBE3A:201 SLC14A1:228 |
| MP0000598 abnormal liver morphology | -0.016970750 | 482 | 2.175e-01 | 9.188e-01 | MET5: APOA1:13 TGFB1:97 F11:106 OCA2:170 ASAH1:211 |
| MP0005334 abnormal fat pad development | -0.035393033 | 152 | 1.361e-01 | 9.188e-01 | IGFBP3:111 IGF2:107 INSR:231 IL18:321 GPR12:423 HDG:471 |
| MP0005330 cardiomyopathy | -0.049576922 | 70 | 1.534e-01 | 9.188e-01 | MYO22:209 HEXIM1:384 IGF1R:878 MCOLN1:1079 CAV1:1483 ERBB4:1484 |