

GSEA-c5-HsSymbols Top pathways by permulation

Geneset	stat	num.genes	pval	p.adj	gene.vals
GOCC_9PLUS0_MOTILE_CILIUM	0.4546269	4	1.637e-03	5.422e-01	CFAP45:13 ENKUR:556 DNAH11:1124 DNAH5:1259 NA NA
GOCC_B_CELL_RECEPTOR_COMPLEX	-0.4107645	3	1.373e-02	7.190e-01	SYK: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 TGFB1:3169 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 SMARCA5:5185
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 TGFB2:3006 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