

# GSEA-c5-HsSymbols Top pathways by permulation

Geneset	stat	num.genes	pval	p.adj	gene.vals
GOCC_9PLUS0_MOTILE_CILIUM	0.4904229	4	6.808e-04	3.280e-02	CFAP45:6 DNAH5:48 DNAH11:237 ENKUR:340 NA NA
GOCC_CUL4B_RING_E3_UBIQUITIN_LIGASE_COMP	-0.4662063	4	1.240e-03	4.962e-02	DDB2:153 DTL:559 CUL4B:667 RBX1:805 NA NA
GOMF_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_P	-0.4540627	2	2.613e-02	2.723e-01	CYP2U1:328 CYP11A1:1144 NA NA NA NA
GOBP_L_Glutamine_IMPORT_across_plasma_me	-0.4181716	4	3.771e-03	1.013e-01	SLC38A1:430 SLC38A2:1182 SLC38A3:1666 SLC38A5:1962 NA NA
GOBP_SNRNA_TRANSCRIPTION_BY_RNA_POLYMERASE	-0.4143882	5	1.331e-03	5.179e-02	ELL:12 SNAPC5:205 ICE2:540 ZC3H8:2547 SNAPC1:3569 NA
GOBP_CHITIN_METABOLIC_PROCESS	0.4048441	3	1.515e-02	2.058e-01	CHI3L1:234 CTBS:1703 CHIT1:2715 NA NA NA
GOMF_CHITINASE_ACTIVITY	0.4048441	3	1.515e-02	2.058e-01	CHI3L1:234 CTBS:1703 CHIT1:2715 NA NA NA
GOMF_WD40_REPEAT_DOMAIN_BINDING	-0.4035606	3	1.548e-02	2.076e-01	CDC5L:1029 CCT6A:1055 USP47:2550 NA NA NA
GOMF_MINUS_END_DIRECTED_MICROTUBULE_MOTO	0.4034967	16	2.299e-08	1.064e-05	DNAH2:2 DNAH17:15 DNAH9:34 DNAH5:48 DNAH14:99 DNAH11:237
GOBP_BRANCHED_CHAIN_AMINO_ACID_BIOSYNTHESIS	-0.3993161	5	1.985e-03	6.816e-02	SDS:6 BCAT1:481 BCAT2:596 SDSL:919 ILVBL:6110 NA
GOMF_OPSIN_BINDING	0.3985195	4	5.770e-03	1.310e-01	SPTBN5:74 ARR3:253 IFT20:1262 SAG:5048 NA NA
GOBP GRANULOCYTE COLONY STIMULATING FACTOR	-0.3944861	4	6.283e-03	1.373e-01	TSLP:116 CD34:645 ISL1:1441 HAVCR2:4578 NA NA
GOBP ELASTIN CATABOLIC PROCESS	0.3942844	2	5.343e-02	3.828e-01	MMP12:979 CELA1:2476 NA NA NA NA
GOBP REGULATION OF CYTOPLASMIC MRNA PROCESSING	-0.3917875	7	3.309e-04	1.885e-02	PAN3:128 CNOT6:188 CNOT6L:427 PATL2:563 CNOT1:2158 CNOT2:3650
HP_UNILATERAL_PRIMARY_PULMONARY_DYSGENESIS	-0.3908572	5	2.470e-03	7.839e-02	TBX1:710 DGCR8:963 DGCR2:1105 DGCR6:1160 ESS2:4827 NA
GOBP_NEGATIVE_REGULATION_OF_GENE_EXPRESSION	-0.3893021	7	3.610e-04	2.000e-02	USP7:410 HELLS:1164 DNMT1:1167 UHRF2:1205 CTCF:1845 UHRF1:2635
GOBP_HEPOXILIN_METABOLIC_PROCESS	0.3883946	4	7.136e-03	1.456e-01	ALOX15B:393 ALOXE3:871 ALOX15:873 ALOX12B:5173 NA NA
GOCC_GPI_ANCHOR_TRANSAMIDASE_COMPLEX	0.3869506	4	7.353e-03	1.474e-01	GPAA1:12 PIGS:1777 PIGK:2167 PIGT:3430 NA NA
HP_HYOPLASTIC_Dermoepidermal hemidesmosomes	0.3869210	7	3.922e-04	2.114e-02	PLEC:18 ITGB4:50 ITGA6:267 LAMC2:272 LAMB3:2108 LAMA3:4764
GOBP_MEMBRANE_DEPOLARIZATION_DURING_AV_NA_CURRENT	0.3850408	5	2.864e-03	8.517e-02	SCN5A:315 CACNB2:657 CACNA1G:909 TRPM4:2790 CACNA1C:4724 NA
GOBP_INTESTINAL_HEXOSE_ABSORPTION	0.3843447	4	7.759e-03	1.514e-01	PLS1:368 VIL1:1250 SLC2A5:2278 EZR:3663 NA NA
HP_DOUBLE_AORTIC_ARCH	-0.3808433	6	1.234e-03	4.962e-02	TBX1:710 DGCR8:963 DGCR2:1105 DGCR6:1160 FLT4:2718 ESS2:4827
GOBP_POSITIVE_REGULATION_OF_CYTOPLASMIC_PROTEIN_FOLDING	-0.3795042	6	1.284e-03	5.067e-02	PAN3:128 CNOT6:188 CNOT6L:427 CNOT1:2158 CNOT2:3650 PAN2:5077
GOMF_SUMO_POLYMER_BINDING	-0.3759211	3	2.412e-02	2.652e-01	RNF111:507 SIMC1:2338 RNF4:3124 NA NA NA
GOMF_UBIQUITIN LIKE PROTEIN SPECIFIC ENDOPEPTIDASE	-0.3754532	5	3.641e-03	9.981e-02	SEN5:953 SENP7:1291 SENP6:2327 SENP2:2417 SENP1:2991 NA
GOCC_INNER_DYNEIN_ARM	0.3740539	4	9.567e-03	1.673e-01	DNAH2:2 DNHD1:663 DNAH7:1787 DNAH1:5782 NA NA
GOBP_SEQUESTERING_OF_IRON_ION	-0.3737967	3	2.493e-02	2.671e-01	SRI:1130 FTH1:1336 FTMT:3594 NA NA NA
GOBP_LEUKOTRIENE_SIGNALING_PATHWAY	0.3729832	5	3.870e-03	1.029e-01	CYSLTR2:41 LTB4R:244 LTB4R2:1460 CYSLTR1:3033 RGS1:5608 NA
GOCC_ALPHA_BETA_T_CELL_RECEPTOR_COMPLEX	0.3704203	5	4.122e-03	1.080e-01	PTPN6:1017 CD3E:1166 CD3D:2624 CD3G:2806 CD247:2972 NA
GOMF_MHC_CLASS_II_RECEPTOR_ACTIVITY	-0.3703857	4	1.030e-02	1.721e-01	HLA-DOB:261 HLA-DPA1:649 HLA-DOA:2038 HLA-DRA:5388 NA NA
HP_SINGLE_LINEAGE_MYELODYSPLASIA	-0.3635639	4	1.179e-02	1.829e-01	SF3B1:658 TET2:1207 ERBB3:3307 HSCB:3575 NA NA
HP_INCREASED_RED_CELL_SICKLING_TENDENCY	-0.3622876	2	7.595e-02	4.414e-01	KLF1:1767 BCL11A:2642 NA NA NA NA
GOBP_APOPTOTIC_PROCESS_INVOLVED_IN_BLOOD_CELL_DEVELOPMENT	-0.3620942	5	5.044e-03	1.230e-01	BAX:45 BAK1:1107 SPI1:1683 LEF1:1910 LRP5:6330 NA
GOCC_GAMMA_DELTA_T_CELL_RECEPTOR_COMPLEX	0.3582620	3	3.161e-02	3.001e-01	CD3E:1166 CD3G:2806 CD247:2972 NA NA NA
GOMF_PYRUVATE_DEHYDROGENASE_ACETYL_TRANSFERRASE	-0.3578182	5	5.587e-03	1.282e-01	PDK1:1221 PDK4:1712 PDK3:2104 BCKDK:3139 PDK2:3216 NA
GOBP_TYPE_III_INTERFERON_PRODUCTION	0.3565454	2	8.072e-02	4.520e-01	IFIH1:1029 TLR3:3667 NA NA NA NA
HP_APLASIA CUTIS CONGENITA ON TRUNK OR LIMBS	0.3557437	6	2.545e-03	7.998e-02	PLEC:18 ITGB4:50 ITGA6:267 KRT14:507 KRT5:3220 ARHGAP31:10044
GOBP_REGULATION_OF_BILE_ACID_SECRETION	-0.3556135	4	1.376e-02	1.952e-01	TNF:99 SLC10A1:395 PRKAA1:1005 ABCB11:7808 NA NA
GOBP_REGULATION_OF_TOLL LIKE RECEPTOR 7 SIGNALING	0.3529731	3	3.421e-02	3.138e-01	PTPN22:424 RSAD2:2707 SLC15A4:4075 NA NA NA
HP_APLASIA_HYOPLASIA_OF_THE_FALLOPIAN_TUBES	-0.3490904	4	1.560e-02	2.082e-01	WNT4:1692 DCAF17:2596 DHH:2672 WNT3:2714 NA NA