

GSEA-c5-HsSymbols Top pathways by permulation

Geneset	stat	num.genes	pval	p.adj	gene.vals
HP_SPHEROCYTOSIS	-0.4909120	8	1.522e-06	7.105e-04	SLC4A1:27 EPB42:42 RHAG:75 SPTB:85 ANK1:119 SPTA1:135
GOCC_9PLUS0_MOTILE_CILIUM	0.4706930	4	1.112e-03	7.732e-02	DNAH11:19 CFAP45:132 DNAH5:728 ENKUR: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_BIOSYNTH	-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	2.003e-02	3.045e-01	LRP1:91 HLA-DRA:1410 MBTPS2:3498 NA NA NA
GOCC_INNER_DYNEIN_ARM	0.3874496	4	7.278e-03	2.012e-01	DNAH1:1176 DNHD1:1468 DNAH2:1926 DNAH7:2355 NA NA
GOCC_PREFOLDIN_COMPLEX	0.3844835	3	2.108e-02	3.091e-01	VBP1:530 PFDN2:1028 PDRG1:3752 NA NA NA
GOCC_GPI_ANCHOR_TRANSAMIDASE_COMPLEX	0.3817825	4	8.179e-03	2.113e-01	GPAA1:64 PIGK:455 PIGT:3026 PIGS:3696 NA NA
GOBP_SRP_DEPENDENT_COTRANSLATIONAL_PROTE	0.3808102	2	6.213e-02	4.722e-01	SRPRB:1701 SRPRA:1964 NA NA NA NA
GOBP_ATTACHMENT_OF_GPI_ANCHOR_TO_PROTEIN	0.3807917	5	3.188e-03	1.331e-01	GPAA1:64 PIGK:455 PGAP1:1898 PIGT:3026 PIGS:3696 NA
GOBP_LEUKOTRIENE_SIGNALING_PATHWAY	0.3769341	5	3.511e-03	1.396e-01	LTB4R:329 CYSLTR2:855 LTB4R2:1490 CYSLTR1:2852 RGS1:3903 NA
HP_FALCIFORM_RETINAL_FOLD	-0.3758978	5	3.602e-03	1.422e-01	ZNF408:671 LRP5:674 NDP:2526 FZD4:2574 TSPAN12:2774 NA
HP_HYPOPLASTIC_DERMOEPIDERMAL_HEMIDESMOS	0.3732250	7	6.270e-04	5.456e-02	LAMC2:427 ITGB4:951 LAMA3:1863 LAMB3:1910 PLEC:2200 ITGA6:2330
GOMF_RIBOSOMAL_PROTEIN_S6_KINASE_ACTIVIT	0.3723733	4	9.897e-03	2.303e-01	RPS6KA1:154 RPS6KA6:157 RPS6KA2:2241 RPS6KA4:5263 NA NA
HP_PERIPHERAL_RETINAL_AVASCULARIZATION	-0.3711074	6	1.643e-03	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	1.588e-01	ADIPOQ:770 EPM2AIP1:1155 IGF2:1206 GSK3A:2713 PPP1R3G:3948 NA
GOBP_NEGATIVE_REGULATION_OF_PROTEIN_CATA	-0.3669162	5	4.490e-03	1.619e-01	LAPTM4B:236 USP8:832 VPS35:1269 MGAT3:2960 ATP13A2:4568 NA
HP_FAILURE_TO_THRIVE_SECONDARY_TO_RECURRE	0.3667770	6	1.862e-03	1.012e-01	CD3E:721 RAG1:781 CD3D:1763 IL7R:2213 CD247:3108 RAG2:3676
GOMF_PHOSPHATIDYLSERINE_FLIPPASE_ACTIVIT	-0.3654336	5	4.654e-03	1.636e-01	ATP11A:138 ATP11C:1005 ATP8B1:1350 ATP8A1:1558 ATP8A2:5920 NA
GOMF_MHC_CLASS_II_RECEPTOR_ACTIVITY	-0.3653929	4	1.137e-02	2.485e-01	HLA-DOB:673 HLA-DRA:1410 HLA-DOA:2845 HLA-DPA1:3070 NA NA
HP_RECURRENT	-0.3641814	5	4.797e-03	1.643e-01	ADORA2A:176 BCKDHA:1038 DBT:1399 BCKDHB:3382 PTH:4065 NA
HP_PARTIAL_ABSENCE_OF_SPECIFIC_ANTIBODY_	-0.3622382	5	5.027e-03	1.679e-01	TNFRSF13B:258 CD19:565 CR2:2474 ICOS:2676 SASH3:4241 NA
GOMF_MINUS_END_DIRECTED_MICROTUBULE_MOTO	0.3617653	16	5.451e-07	3.521e-04	DNAH11:19 DNAH3:232 DNAH10:368 DNAH9:435 DYNC2H1:487 DNAH5:728
GOCC_AXONEMAL_DYNEIN_COMPLEX	0.3615223	16	5.548e-07	3.521e-04	DNAI2:36 DNAH3:232 CCDC65:326 DNAH9:435 DNAH5:728 DNAH17:1027
GOBP_RNA_MEDIATED_HETEROCHROMATIN_FORMAT	-0.3613890	5	5.131e-03	1.692e-01	SIRT6:866 FAM172A:1620 HELLS:1683 ZNFX1:2720 CENPV:3392 NA
GOBP_PARATHYROID_GLAND_DEVELOPMENT	-0.3581282	6	2.381e-03	1.135e-01	GATA3:1405 TBX1:1600 GCM2:1880 TGFB1:1921 HOXA3:2606 CRKL:3210
GOBP_NEGATIVE_REGULATION_OF_SYNAPTIC_VES	-0.3522943	3	3.456e-02	3.812e-01	FMR1:1021 BRAF:2130 SYT4:3421 NA NA NA
GOBP_POSITIVE_REGULATION_OF_RNA_EXPORT_F	-0.3517053	2	8.492e-02	5.181e-01	DHX9:2018 NRDE2:2382 NA NA NA NA
GOMF_RNA_POLYMERASE_II_CTD_HEPTAPEPTIDE_	-0.3484598	6	3.116e-03	1.315e-01	CDK7:118 BRD4:181 CDK13:417 CDK12:1032 DYRK1A:4390 CCNK:7328