EnrichmentHsSymbolsFile2 Top pathways by non-permulation

Geneset	stat	num.genes	pval	p.adj	gene.vals
REACTOME_SENSORY_PERCEPTION	-0.11600886	308	-	1.894e-08	CALHM1:14 OPN1SW:24 OR10Z1:25 ANO2:34 OTOF:44 RBP4:47
REACTOME_FORMATION_OF_THE_CORNIFIED_ENVE	-0.21349958	78	7.266e-11		DSP:3 TGM1:5 KRT80:10 DSG3:17 PKP1:21 KRT31:26
REACTOME_KERATINIZATION	-0.19938218	85		4.658e-07	DSP:3 TGM1:5 KRT80:10 DSG3:17 PKP1:21 KRT31:26
FISCHER_DREAM_TARGETS	0.06205544	846		1.973e-06	CENPC:5 MIS18BP1:8 GABPB2:12 WDR76:13 KIF18A:16 FANCM:24
REACTOME_NEURONAL_SYSTEM	-0.08928214	374		4.495e-06	KCNS3:66 KCNV2:88 KCNK18:98 CACNA1E:99 PPFIA4:140 GNAT3:154
REACTOME_OLFACTORY_SIGNALING_PATHWAY	-0.15146635	116		1.502e-05	OR10Z1:25 ANO2:34 OR6B1:54 CNGA4:60 OR52M1:96 CNGA2:139
KEGG_CYTOKINE_CYTOKINE_RECEPTOR_INTERACT	0.11336825	208		1.502e-05	IFNAR1:66 EGF:89 IL4R:121 FAS:168 CSF2RA:207 CXCL6:248
KEGG_OLFACTORY_TRANSDUCTION	-0.14308095	130		1.502e-05	OR10Z1:25 OR6B1:54 CNGA4:60 OR52M1:96 OR10G3:160 OR2C3:209
MIKKELSEN_MEF_HCP_WITH_H3K27ME3	-0.06880750	546		3.249e-05	TRPM3:19 THBS4:31 MYO5C:42 CACNA1E:99 JAG2:106 DSG2:124
BENPORATH_ES_WITH_H3K27ME3	-0.04988425	964	2.054e-07		PLEC:2 PKP1:21 RBP4:47 CHAD:49 MYO5B:63 KCNS3:66
FLORIO_NEOCORTEX_BASAL_RADIAL_GLIA_DN	0.10682184	176		6.085e-04	MIS18BP1:8 KIF18A:16 BRCA2:26 CDCA2:81 CENPE:124 SGO1:134
MARSON_BOUND_BY_E2F4_UNSTIMULATED	0.05703242	629	1.219e-06		GABPB2:12 WDR76:13 FANCM:24 BRCA2:26 ZMYM1:44 TCF19:54
BIOCARTA_TH1TH2_PATHWAY	0.32237869	19		6.085e-04	IL4R:121 IL12RB1:279 CD28:299 CD86:437 IL18R1:619 IFNGR1:747
KEGG_STEROID_HORMONE_BIOSYNTHESIS	0.26410490	28	1.321e-06		CYP17A1:58 HSD17B2:84 HSD3B2:247 CYP7B1:406 HSD17B1:526 SULT1E1:655
WP_STRIATED_MUSCLE_CONTRACTION_PATHWAY	-0.25212387	30	1.763e-06		MYH8:41 NEB:50 TNNT2:61 TNNI2:79 MYBPC2:123 MYBPC1:231
MIKKELSEN_MCV6_HCP_WITH_H3K27ME3	-0.23212307	414		8.649e-04	RBP4:47 CHAD:49 SDK2:53 CLSTN2:67 AEBP1:85 FAM83G:129
REACTOME_STRIATED_MUSCLE_CONTRACTION	-0.24532422	31		8.708e-04	MYH8:41 NEB:50 TNNT2:61 TNNI2:79 MYBPC2:123 MYBPC1:231
HAMAI_APOPTOSIS_VIA_TRAIL_UP	0.05686894	585		1.069e-03	CENPC:5 BDP1:7 MIS18BP1:8 KIF18A:16 ZNF302:19 CPLANE1:31
WP_CALCIUM_REGULATION_IN_CARDIAC_CELLS	-0.12024207	126		1.1009e-03	RGS9:71 CACNA1E:99 SLC8A3:175 ANXA6:178 RYR3:249 CACNA1C:306
DODD_NASOPHARYNGEAL_CARCINOMA_DN	0.03987357	1175		1.738e-03	LRPPRC:15 KIF18A:16 FANCM:24 BRCA2:26 TFB2M:28 CLEC4E:45
REACTOME_SIGNALING_BY_GPCR	-0.05333735	615		2.206e-03	SSTR4:6 TACR2:15 FFAR2:22 OPN1SW:24 OPN3:29 RGS9:71
REACTOME_SIGNALING_BT_GFCK REACTOME_SPERM_MOTILITY_AND_TAXES	0.45239488	8			CATSPERG:1 CATSPERB:3 CATSPERD:29 CATSPER2:115 KCNU1:426 HVCN1:1160
KEGG_CALCIUM_SIGNALING_PATHWAY	-0.09873779	169		2.760e-03	TACR2:15 CACNA1E:99 SLC25A31:148 SLC8A3:175 GRPR:180 CACNA1G:182
MEBARKI_HCC_PROGENITOR_FZD8CRD_UP	0.05763663	491	1.344e-05		MIS18BP1:8 SLAMF7:10 WDR76:13 KIF18A:16 GPRIN1:22 FANCM:24
REACTOME_DEVELOPMENTAL_BIOLOGY	-0.04425902	856		3.229e-03	DSP:3 TGM1:5 KRT80:10 DSG3:17 PKP1:21 KRT31:26
REACTOME_MUSCLE_CONTRACTION	-0.09398529	181		3.229e-03	MYH8:41 NEB:50 TNNT2:61 TNNI2:79 KCNK18:98 MYBPC2:123
WP_GPCRS_CLASS_A_RHODOPSINLIKE	-0.09390329	207		3.229e-03	SSTR4:6 FFAR2:22 OPN1SW:24 OPN3:29 OR6B1:54 MTNR1B:108
GOBERT_OLIGODENDROCYTE_DIFFERENTIATION_U	0.05501041	533		3.462e-03	MIS18BP1:8 WDR76:13 KIF18A:16 BRCA2:26 TCF19:54 CDCA2:81
WP_MITOCHONDRIAL_COMPLEX_I_ASSEMBLY_MODE	0.03301041	47	1.547e-05		TMEM126B:39 NDUFB4:150 NDUFB10:202 TMEM70:219 NDUFS5:360 ECSIT:452
BENPORATH_EED_TARGETS	-0.04166967	902		5.402e-03	PLEC:2 DSP:3 PKP1:21 C7orf57:37 RBP4:47 MYO5B:63
MIKKELSEN_NPC_HCP_WITH_H3K27ME3	-0.04100907	326		6.624e-03	KCNS3:66 CLSTN2:67 ABCG1:68 JAG2:106 TMEM132E:136 ZNF536:236
RODRIGUES THYROID CARCINOMA POORLY DIFFE				7.084e-03	WDR76:13 LRPPRC:15 KIF18A:16 ADAM9:126 MFN1:129 DLGAP5:194
KEGG_ALLOGRAFT_REJECTION	0.05082320 0.25457857	572 22		7.084e-03	HLA-DOA:73 CD80:160 FAS:168 CD28:299 CD86:437 IFNG:1261
REACTOME_CELL_CELL_COMMUNICATION REACTOME COMPLEMENT CASCADE	-0.10909875	119		7.600e-03	PLEC:2 ITGB4:16 SDK2:53 ACTN1:132 AFDN:234 KRT14:269 CR2:63 C5AR2:250 CPB2:314 ELANE:348 C1S:514 C3AR1:780
KEGG_TIGHT_JUNCTION	0.18517539 -0.10907680	41		7.600e-03 1.052e-02	MYH13:1 MYH7B:9 MYH8:41 MYH2:104 MAP3K20:115 ACTN1:132
REACTOME_CELL_CYCLE		114		1.052e-02 1.059e-02	CENPC:5 MIS18BP1:8 KIF18A:16 BRCA2:26 CEP192:90 CENPE:124
	0.04959316	566			
REACTOME_VOLTAGE_GATED_POTASSIUM_CHANNEL		42		1.103e-02	KCNS3:66 KCNV2:88 KCNA10:197 KCNF1:216 KCNQ5:238 KCNA6:475 SSTR4:6 TACR2:15 MTNR1B:108 GRM8:144 HTR1B:169 GRPR:180
KEGG_NEUROACTIVE_LIGAND_RECEPTOR_INTERAC	-0.07214180	259		1.110e-02	
REACTOME_COMPLEX_I_BIOGENESIS	0.16504515	48	7.0016-05	1.243e-02	TMEM126B:39 NDUFB4:150 NDUFB10:202 NDUFS5:360 ECSIT:452 NDUFB11:510