

# EnrichmentHsSymbolsFile2 Top pathways by non-permulation

Geneset	stat	num.genes	pval	p.adj	gene.vals
FISCHER_DREAM_TARGETS	0.07526136	882	5.347e-14	3.237e-10	CEP192:17 KIF18A:27 RBL1:42 SMCHD1:43 ZNF518A:46 EHBP1:80
JOHNSTONE_PARVB_TARGETS_3_DN	0.07841489	790	9.979e-14	3.237e-10	TFAM:13 QSER1:20 KIF18A:27 NDUFS5:33 RBL1:42 SMCHD1:43
DODD_NASOPHARYNGEAL_CARCCINOMA_UP	-0.05739325	1463	4.375e-13	9.462e-10	PER2:5 CAMSAP1:6 DNAH9:7 C7orf57:8 EVPL:11 TGM1:12
DODD_NASOPHARYNGEAL_CARCCINOMA_DN	0.06125876	1244	6.797e-13	1.102e-09	LRPPRC:10 TFAM:13 CEP192:17 QSER1:20 KIF18A:27 TMEM70:30
RODRIGUES_THYROID_CARCCINOMA_POORLY_DIFFE	0.08228366	598	8.095e-12	1.050e-08	LRPPRC:10 TFAM:13 KIF18A:27 ZNF644:37 RBL1:42 ADAM9:51
HAMAI_APOPTOSIS_VIA_TRAIL_UP	0.07863949	595	7.111e-11	7.689e-08	CEP192:17 QSER1:20 ZNF302:22 BPTF:26 KIF18A:27 RLF:29
WP_GPCRS_CLASS_A_RHODOPSINLIKE	-0.12548679	208	4.734e-10	4.388e-07	BDKRB1:58 SSTR4:76 FFAR2:85 GPR37L1:89 HTR1B:174 P2RY4:194
PUJANA_BRCA1_PCC_NETWORK	0.04749485	1501	1.332e-09	1.080e-06	DAXX:4 TMEM131L:9 TFAM:13 RBL1:42 NR2C1:57 TCL1A:71
REACTOME_FORMATION_OF_THE_CORNIFIED_ENVE	-0.19249212	78	4.244e-09	3.060e-06	EVPL:11 TGM1:12 DSP:13 KRT80:50 KRT20:51 KRT15:83
REACTOME_KERATINIZATION	-0.18314672	85	5.435e-09	3.526e-06	EVPL:11 TGM1:12 DSP:13 KRT80:50 KRT20:51 KRT15:83
KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP	0.04928145	1201	1.296e-08	7.645e-06	KIF18A:27 TMEM70:30 LARP4:89 TPX2:98 TEAD2:106 TMPO:129
MIKKELSEN_MEF_HCP_WITH_H3K27ME3	-0.06972889	555	2.279e-08	1.232e-05	SLC47A1:41 JAG2:47 CAMK2B:64 PCNX2:158 DSG2:177 THBS4:214
REACTOME_RESPIRATORY_ELECTRON_TRANSPORT_	0.15995050	101	2.849e-08	1.422e-05	LRPPRC:10 TMEM126B:18 NDUFS5:33 NDUFB4:74 NDUFA12:202 NDUFC2:270
REACTOME_RNA_POLYMERASE_II_TRANSCRIPTION	0.05120458	1026	3.935e-08	1.824e-05	DAXX:4 LRPPRC:10 MGA:14 ZNF302:22 RBL1:42 NR2C1:57
NIKOLSKY_BREAST_CANCER_20Q12_Q13_AMPLICO	-0.13865741	128	6.233e-08	2.594e-05	HELZ2:96 FAM217B:170 ARFGAP1:260 COL20A1:270 TOMM34:324 NPBWR2:407
REACTOME_SIGNALING_BY_GPCR	-0.06342328	631	6.397e-08	2.594e-05	TACR2:17 GPR132:32 ARHGEF11:42 BDKRB1:58 CAMK2B:64 SSTR4:76
DACOSTA_UV_RESPONSE_VIA_ERCC3_COMMON_DN	0.07418927	452	7.247e-08	2.766e-05	ZFYVE9:1 LRPPRC:10 BPTF:26 UBR2:36 SMCHD1:43 EIF4G3:52
MARSON_BOUND_BY_E2F4_UNSTIMULATED	0.06147432	661	8.368e-08	3.016e-05	ETAA1:39 RBL1:42 TPX2:98 HASPIN:105 FANCM:116 WDR76:130
REACTOME_RESPIRATORY_ELECTRON_TRANSPORT	0.17077547	81	1.094e-07	3.735e-05	LRPPRC:10 TMEM126B:18 NDUFS5:33 NDUFB4:74 NDUFA12:202 NDUFC2:270
REACTOME_NEURONAL_SYSTEM	-0.07854928	386	1.292e-07	4.190e-05	KCNV2:62 CAMK2B:64 KCNN3:183 KCNF1:195 PANX1:216 CACNA1E:235
RODRIGUES_THYROID_CARCCINOMA_ANAPLASTIC_U	0.06100706	637	1.742e-07	5.381e-05	QSER1:20 KIF18A:27 RLF:29 TPTE:31 ZNF644:37 MFN1:73
REACTOME_CLASS_A_1_RHODOPSIN_LIKE_RECEPT	-0.08789174	295	2.217e-07	6.539e-05	TACR2:17 GPR132:32 BDKRB1:58 SSTR4:76 FFAR2:85 GPR37L1:89
REACTOME_THE_CITRIC_ACID_TCA_CYCLE_AND_R	0.12282450	149	2.355e-07	6.545e-05	LRPPRC:10 TMEM126B:18 NDUFS5:33 NDUFB4:74 NDUFA12:202 NDUFC2:270
BENPORATH_CYCLING_GENES	0.06175136	606	2.421e-07	6.545e-05	ZNF414:72 CSH2:86 TPX2:98 TMPO:129 CCNB1:141 LRIF1:145
REACTOME_CELL_CYCLE	0.06057985	622	2.906e-07	7.251e-05	DAXX:4 CEP192:17 KIF18A:27 CENPT:41 RBL1:42 RNF168:66
REACTOME_COMPLEX_I_BIOGENESIS	0.21432722	48	2.808e-07	7.251e-05	TMEM126B:18 NDUFS5:33 NDUFB4:74 NDUFA12:202 NDUFC2:270 TIMMDC1:328
SHEDDEN_LUNG_CANCER_POOR_SURVIVAL_A6	0.07191598	427	3.821e-07	9.183e-05	LRPPRC:10 QSER1:20 KIF18A:27 RBL1:42 AFP:79 TPX2:98
WP_MITOCHONDRIAL_COMPLEX_I_ASSEMBLY_MODE	0.21264431	47	4.599e-07	1.066e-04	TMEM126B:18 TMEM70:30 NDUFS5:33 NDUFB4:74 DMAC1:112 NDUFA12:202
KEGG_NEUROACTIVE_LIGAND_RECEPTOR_INTERAC	-0.09087926	260	4.801e-07	1.074e-04	TACR2:17 BDKRB1:58 SSTR4:76 GRM3:113 TAAR6:129 HTR1B:174
ZHANG_BREAST_CANCER_PROGENITORS_UP	0.07155700	415	6.269e-07	1.356e-04	CEP192:17 RBL1:42 SMCHD1:43 SYDE2:53 ADAMTS20:78 TMPO:129
DACOSTA_UV_RESPONSE_VIA_ERCC3_DN	0.05036052	827	1.042e-06	2.181e-04	ZFYVE9:1 TMEM131L:9 LRPPRC:10 ATP2B4:21 BPTF:26 RLF:29
SHEN_SMARCA2_TARGETS_UP	0.07021190	408	1.242e-06	2.519e-04	TMEM126B:18 ZNF302:22 UBR2:36 MAP4K3:91 ANKHD1:99 AGGF1:123
WP_ELECTRON_TRANSPORT_CHAIN_OXPPOS_SYSTE	0.16113155	75	1.419e-06	2.743e-04	NDUFS5:33 NDUFB4:74 NDUFA12:202 NDUFC2:270 NDUFB5:358 NDUFB10:401
WONG_MITOCHONDRIA_GENE_MODULE	0.09950710	198	1.438e-06	2.743e-04	LRPPRC:10 TFAM:13 NDUFS5:33 NIPSNA1:69 NDUFB4:74 NDUFA12:202
DIAZ_CHRONIC_MYELOGENOUS_LEUKEMIA_UP	0.03932040	1338	1.875e-06	3.476e-04	ZNF302:22 NIPSNA1:69 CASP8:126 RBBP7:134 PPP4R1:156 CTH:160
KIM_WT1_TARGETS_DN	0.06605558	432	2.728e-06	4.916e-04	ZNF302:22 KIF18A:27 TPTE:31 LARP4:89 MAP4K3:91 CENPC:127
NIKOLSKY_BREAST_CANCER_7P22_AMPLICON	-0.21642022	38	3.917e-06	6.572e-04	IQCE:375 TMEM184A:376 BRAT1:512 MRM2:552 MAD1L1:601 FBXL18:658
REACTOME_RESOLUTION_OF_SISTER_CHROMATID_	0.12256632	119	3.950e-06	6.572e-04	KIF18A:27 CENPT:41 CENPC:127 CCNB1:141 SPDL1:149 CENPE:206
REACTOME_MUSCLE_CONTRACTION	-0.09712311	190	4.038e-06	6.572e-04	NEB:26 CACNA1G:54 CAMK2B:64 MYBPC2:71 RYR3:205 TNNI2:207
JAEGEER_METASTASIS_DN	-0.09115185	216	4.052e-06	6.572e-04	PER2:5 EVPL:11 DSP:13 ITGB4:37 NRCAM:48 CLIC3:57