

GeDiPNet Cluster 464 -- Enriched Pathways

Pathway enrichment: KEGG + Reactome, upper-tail hypergeometric test, Benjamini-Hochberg FDR-corrected. Fold enrichment = (overlap / cluster gene count) / (pathway gene count / universe size). Top 15 pathways per cluster by q-value. See [scripts/build_cluster_enrichment.php](scripts/build_cluster_enrichment.php) on gedipnet.bicnirrh.res.in. Data as of: 2026-10-20 03:30:09. · Rows: 15 · Generated: 2026-10-20 00:02:44

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
RNA degradation	KEGG	2	DDX6, PABPC1	78	10	30.79	1.812e-3	1.771e-2
mRNA decay by 5' to 3' exoribonuclease	Reactome	1	DDX6	14	10	85.79	1.160e-2	6.220e-2
Thermogenesis	KEGG	2	PPARGC1A, SMARCA2	234	10	10.26	1.534e-2	7.359e-2
Deadenylation of mRNA	Reactome	1	PABPC1	24	10	50.04	1.981e-2	8.517e-2
Circadian Clock	Reactome	1	PPARGC1A	28	10	42.89	2.308e-2	9.301e-2
RUNX1 interacts with co-factors whose precise effect on RUNX1 targets is not known	Reactome	1	SMARCA2	38	10	31.61	3.121e-2	1.105e-1
Deactivation of the beta-catenin transactivating complex	Reactome	1	SOX4	42	10	28.60	3.444e-2	1.168e-1
Glycosphingolipid metabolism	Reactome	1	UGT8	46	10	26.11	3.766e-2	1.232e-1
Ether lipid metabolism	KEGG	1	UGT8	50	10	24.02	4.088e-2	1.289e-1
Transcriptional activation of mitochondrial biogenesis	Reactome	1	PPARGC1A	51	10	23.55	4.168e-2	1.304e-1
Sphingolipid metabolism	KEGG	1	UGT8	54	10	22.24	4.408e-2	1.347e-1
AUF1 (hnRNP D0) binds and destabilizes mRNA	Reactome	1	PABPC1	56	10	21.45	4.568e-2	1.373e-1
Translation initiation complex formation	Reactome	1	PABPC1	58	10	20.71	4.727e-2	1.402e-1
Regulation of RUNX2 expression and activity	Reactome	1	PPARGC1A	59	10	20.36	4.807e-2	1.416e-1
Transcriptional regulation of white adipocyte differentiation	Reactome	1	PPARGC1A	67	10	17.93	5.443e-2	1.519e-1