

GeDiPNet Cluster 473 -- 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 on gedipnet.bicnirrh.res.in. Data as of: 2026-10-20 03:30:09. · Rows: 15 · Generated: 2026-10-20 00:03:51

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
TGF-beta signaling pathway	KEGG	2	ZFYVE16, NODAL	108	8	27.80	2.166e-3	2.019e-2
RHO GTPases Activate ROCKs	Reactome	1	ROCK2	5	8	300.25	3.327e-3	2.738e-2
Signaling pathways regulating pluripotency of stem cells	KEGG	2	ZIC3, NODAL	144	8	20.85	3.813e-3	3.022e-2
Sema4D induced cell migration and growth-cone collapse	Reactome	1	ROCK2	11	8	136.48	7.306e-3	4.669e-2
POU5F1 (OCT4), SOX2, NANOG activate genes related to proliferation	Reactome	1	ZIC3	13	8	115.48	8.629e-3	5.192e-2
Transcriptional regulation of pluripotent stem cells	Reactome	1	ZIC3	17	8	88.31	1.127e-2	6.122e-2
Signaling by BMP	Reactome	1	ZFYVE16	28	8	53.62	1.850e-2	8.204e-2
EPHB-mediated forward signaling	Reactome	1	ROCK2	39	8	38.49	2.569e-2	9.901e-2
RNA Polymerase II Transcription Elongation	Reactome	1	SUPT16H	59	8	25.44	3.864e-2	1.251e-1
Formation of RNA Pol II elongation complex	Reactome	1	SUPT16H	61	8	24.61	3.993e-2	1.273e-1
VEGFA-VEGFR2 Pathway	Reactome	1	ROCK2	62	8	24.21	4.057e-2	1.283e-1
TP53 Regulates Transcription of DNA Repair Genes	Reactome	1	SUPT16H	65	8	23.10	4.250e-2	1.320e-1
G alpha (12/13) signalling events	Reactome	1	ROCK2	80	8	18.77	5.208e-2	1.481e-1
RNA Polymerase II Pre-transcription Events	Reactome	1	SUPT16H	84	8	17.87	5.462e-2	1.521e-1
Regulation of TP53 Activity through Phosphorylation	Reactome	1	SUPT16H	92	8	16.32	5.968e-2	1.600e-1