

GeDiPNet Cluster 54 -- 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: 2026-10-07 03:30:09. · Rows: 15 · Generated: 2026-10-07 12:59:32

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	4	ZFYVE16, ACVR2B, LEFTY2, NODAL	108	55	8.09	1.483e-3	1.832e-2
Motor proteins	KEGG	5	DNAH5, DNAH6, DNAH9, DNAH7, DNAH11	194	55	5.63	1.888e-3	2.186e-2
Transcriptional regulation of pluripotent stem cells	Reactome	2	ZIC3, FOXP1	17	55	25.69	2.680e-3	2.838e-2
Signaling pathways regulating pluripotency of stem cells	KEGG	4	ZIC3, ACVR2B, LEFTY2, NODAL	144	55	6.07	4.210e-3	3.905e-2
Signaling by BMP	Reactome	2	ZFYVE16, ACVR2B	28	55	15.60	7.212e-3	5.576e-2
Huntington disease	KEGG	5	DNAH5, DNAH6, DNAH9, DNAH7, DNAH11	308	55	3.54	1.312e-2	8.026e-2
RHO GTPases Activate ROCKs	Reactome	1	ROCK2	5	55	43.67	2.269e-2	1.105e-1
Amyotrophic lateral sclerosis	KEGG	5	DNAH5, DNAH6, DNAH9, DNAH7, DNAH11	368	55	2.97	2.615e-2	1.194e-1
Sema4D induced cell migration and growth-cone collapse	Reactome	1	ROCK2	11	55	19.85	4.926e-2	1.702e-1
Signaling by Activin	Reactome	1	ACVR2B	11	55	19.85	4.926e-2	1.702e-1
POU5F1 (OCT4), SOX2, NANOG activate genes related to proliferation	Reactome	1	ZIC3	13	55	16.80	5.795e-2	1.852e-1
Pathways of neurodegeneration - multiple diseases	KEGG	5	DNAH5, DNAH6, DNAH9, DNAH7, DNAH11	480	55	2.27	6.787e-2	2.010e-1
Chromatin modifying enzymes	Reactome	1	BRWD1	20	55	10.92	8.778e-2	2.308e-1
Sphingolipid signaling pathway	KEGG	2	ROCK2, CERS1	122	55	3.58	1.074e-1	2.582e-1
Platelet degranulation	Reactome	2	LEFTY2, TAGLN2	123	55	3.55	1.089e-1	2.599e-1