GeDiPNet Cluster 651 -- 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: 2026-10-21 12:16:30. · Rows: 15 · Generated: 2026-10-21 08:36:33

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
LGI-ADAM interactions	Reactome	2	DLG4, STX1A	14	27	63.54	4.356e-4	5.660e-3
PCP/CE pathway	Reactome	2	DVL2, FZD3	18	27	49.42	7.283e-4	8.445e-3
PKA-mediated phosphorylation of key metabolic factors	Reactome	1	MLXIPL	1	27	444.81	2.248e-3	1.983e-2
Fatty acid degradation	KEGG	2	ACADL, ACADVL	43	27	20.69	4.152e-3	3.079e-2
Hippo signaling pathway	KEGG	3	DLG4, DVL2, FZD3	157	27	8.50	5.092e-3	3.539e-2
Toxicity of botulinum toxin type C (BoNT/C)	Reactome	1	STX1A	3	27	148.27	6.730e-3	4.251e-2
Beta oxidation of myristoyl-CoA to lauroyl-CoA	Reactome	1	ACADL	3	27	148.27	6.730e-3	4.251e-2
Beta oxidation of palmitoyl-CoA to myristoyl-CoA	Reactome	1	ACADVL	3	27	148.27	6.730e-3	4.251e-2
Fatty acid metabolism	KEGG	2	ACADL, ACADVL	57	27	15.61	7.199e-3	4.454e-2
Asymmetric localization of PCP proteins	Reactome	2	DVL2, FZD3	62	27	14.35	8.470e-3	4.935e-2
Basal cell carcinoma	KEGG	2	DVL2, FZD3	63	27	14.12	8.736e-3	5.027e-2
Beta oxidation of lauroyl-CoA to decanoyl-CoA-CoA	Reactome	1	ACADL	5	27	88.96	1.119e-2	5.881e-2
mitochondrial fatty acid beta-oxidation of unsaturated fatty acids	Reactome	1	ACADL	6	27	74.14	1.342e-2	6.575e-2
ChREBP activates metabolic gene expression	Reactome	1	MLXIPL	7	27	63.54	1.564e-2	7.226e-2
Activation of the mRNA upon binding of the cap-binding complex and eIFs, and subsequent binding to 43S	Reactome	1	EIF4H	7	27	63.54	1.564e-2	7.226e-2