

GeDiPNet Cluster 48 -- 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: 2026-10-10 03:30:08. · Rows: 15 · Generated: 2026-10-10 06:09:12

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
PI3K Cascade	Reactome	5	FGFR2, FGF3, FGF8, FGFR1, KLB	39	49	31.42	4.756e-7	2.735e-5
Negative regulation of FGFR1 signaling	Reactome	4	FGF3, FGF8, ANOS1, FGFR1	26	49	37.71	3.422e-6	1.492e-4
Constitutive Signaling by Aberrant PI3K in Cancer	Reactome	5	FGFR2, FGF3, FGF8, FGFR1, KLB	75	49	16.34	1.277e-5	4.346e-4
FGFR1c ligand binding and activation	Reactome	3	FGF8, ANOS1, FGFR1	12	49	61.28	1.368e-5	4.596e-4
Phospholipase C-mediated cascade: FGFR1	Reactome	3	FGF3, FGF8, FGFR1	16	49	45.96	3.443e-5	9.843e-4
PIP3 activates AKT signaling	Reactome	5	FGFR2, FGF3, FGF8, FGFR1, KLB	93	49	13.18	3.640e-5	1.029e-3
Activated point mutants of FGFR2	Reactome	3	FGFR2, FGF3, FGF8	17	49	43.25	4.169e-5	1.154e-3
Phospholipase C-mediated cascade; FGFR2	Reactome	3	FGFR2, FGF3, FGF8	18	49	40.85	4.989e-5	1.335e-3
Downstream signaling of activated FGFR1	Reactome	3	FGF3, FGF8, FGFR1	18	49	40.85	4.989e-5	1.335e-3
COPI-independent Golgi-to-ER retrograde traffic	Reactome	4	RAB18, RAB3GAP1, RAB3GAP2, TUBB3	51	49	19.22	5.307e-5	1.403e-3
PI5P, PP2A and IER3 Regulate PI3K/AKT Signaling	Reactome	5	FGFR2, FGF3, FGF8, FGFR1, KLB	103	49	11.90	5.947e-5	1.534e-3
PI-3K cascade:FGFR1	Reactome	3	FGF3, FGF8, FGFR1	21	49	35.01	8.061e-5	1.958e-3
SHC-mediated cascade:FGFR1	Reactome	3	FGF3, FGF8, FGFR1	21	49	35.01	8.061e-5	1.958e-3
FRS-mediated FGFR1 signaling	Reactome	3	FGF3, FGF8, FGFR1	23	49	31.97	1.067e-4	2.446e-3
PI-3K cascade:FGFR2	Reactome	3	FGFR2, FGF3, FGF8	23	49	31.97	1.067e-4	2.446e-3