

GeDiPNet Cluster 264 -- 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: 2026-10-08 03:30:07. · Rows: 15 · Generated: 2026-10-08 06:18:43

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Gastrin-CREB signalling pathway via PKC and MAPK	Reactome	2	MAPK1, RPS6KA3	9	14	190.63	4.522e-5	1.195e-3
MAPK1 (ERK2) activation	Reactome	2	MAPK1, PTPN11	9	14	190.63	4.522e-5	1.195e-3
Chronic myeloid leukemia	KEGG	3	RUNX1, MAPK1, PTPN11	77	14	33.42	8.767e-5	2.036e-3
ERK/MAPK targets	Reactome	2	MAPK1, RPS6KA3	14	14	122.55	1.139e-4	2.516e-3
Growth hormone receptor signaling	Reactome	2	GHR, MAPK1	14	14	122.55	1.139e-4	2.516e-3
Regulation of RUNX1 Expression and Activity	Reactome	2	RUNX1, PTPN11	16	14	107.23	1.500e-4	3.135e-3
Spry regulation of FGF signaling	Reactome	2	MAPK1, PTPN11	16	14	107.23	1.500e-4	3.135e-3
Negative regulation of FGFR3 signaling	Reactome	2	MAPK1, PTPN11	22	14	77.99	2.876e-4	5.261e-3
Neurotrophin signaling pathway	KEGG	3	MAPK1, PTPN11, RPS6KA3	120	14	21.45	3.268e-4	5.823e-3
Negative regulation of FGFR4 signaling	Reactome	2	MAPK1, PTPN11	24	14	71.49	3.432e-4	6.062e-3
Negative regulation of FGFR1 signaling	Reactome	2	MAPK1, PTPN11	26	14	65.99	4.036e-4	6.895e-3
Negative regulation of FGFR2 signaling	Reactome	2	MAPK1, PTPN11	27	14	63.54	4.356e-4	7.319e-3
Oocyte meiosis	KEGG	3	MAPK1, RPS6KA3, YWHAG	138	14	18.65	4.925e-4	8.044e-3
Efferocytosis	KEGG	3	DNMT3A, MAPK1, PTPN11	157	14	16.39	7.176e-4	1.080e-2
RUNX1 interacts with co-factors whose precise effect on RUNX1 targets is not known	Reactome	2	ARID1A, RUNX1	38	14	45.15	8.661e-4	1.244e-2