

GeDiPNet Cluster 111 -- 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 17:49:01

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Signaling by BMP	Reactome	4	BMPR1B, SMAD4, BMP2, NOG	28	52	32.99	5.924e-6	2.175e-4
G alpha (s) signalling events	Reactome	6	GNAS, PTHLH, PDE3A, PTH1R, INSL3, RXFP2	140	52	9.90	2.952e-5	8.225e-4
TGF-beta signaling pathway	KEGG	5	BMPR1B, GDF5, SMAD4, BMP2, NOG	108	52	10.69	9.949e-5	2.244e-3
ADORA2B mediated anti-inflammatory cytokines production	Reactome	5	GNAS, PTHLH, PTH1R, INSL3, RXFP2	128	52	9.02	2.212e-4	4.241e-3
Relaxin receptors	Reactome	2	INSL3, RXFP2	8	52	57.74	5.063e-4	8.041e-3
Hippo signaling pathway	KEGG	5	CTNNB1, BMPR1B, GDF5, SMAD4, BMP2	157	52	7.36	5.672e-4	8.785e-3
Molecules associated with elastic fibres	Reactome	3	GDF5, BMP2, FBLN1	38	52	18.23	5.803e-4	8.953e-3
Apoptotic cleavage of cell adhesion proteins	Reactome	2	CTNNB1, CASP3	11	52	41.99	9.864e-4	1.344e-2
TGF-beta receptor signaling activates SMADs	Reactome	2	SMAD4, CBL	12	52	38.49	1.180e-3	1.534e-2
Pathways in cancer	KEGG	8	CTNNB1, GNAS, SMAD4, BMP2, AR, BCL2L1, CASP3, CBL	533	52	3.47	1.916e-3	2.205e-2
Hormone signaling	KEGG	5	BMPR1B, GNAS, SMAD4, PTHLH, PTH1R	219	52	5.27	2.494e-3	2.686e-2
Class B/2 (Secretin family receptors)	Reactome	2	PTHLH, PTH1R	18	52	25.66	2.691e-3	2.847e-2
Activation of SMO	Reactome	2	IHH, IQCE	18	52	25.66	2.691e-3	2.847e-2
Gastric acid secretion	KEGG	3	SLC9A4, GNAS, CHRM3	76	52	9.12	4.308e-3	3.977e-2
Defective SLC26A2 causes chondrodysplasias	Reactome	1	SLC26A2	1	52	230.96	4.330e-3	3.983e-2