

GeDiPNet Cluster 440 -- Enriched GO Terms (Biological Process)

GO term enrichment: Biological Process terms (gene2go, human/tax_id=9606 only), upper-tail hypergeometric test, fold enrichment = (overlap / cluster gene count) / (term gene count / universe size), Benjamini-Hochberg FDR-corrected. Top 15 terms per cluster by q-value. See scripts/build_cluster_go_enrichment.php on gedipnet.bicnirrh.res.in. Data as of: 2026-10-20 03:23:14. · Rows: 15 · Generated: 2026-10-19 23:18:28

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
cardiac muscle cell proliferation	GO:0060038	4	ABL1, FOXC2, SKI, TGFB2	28	7	381.37	1.407e-10	4.151e-8
neural tube closure	GO:0001843	4	ABL1, RARG, SKI, TGFB2	85	7	125.63	1.381e-8	2.338e-6
negative regulation of cartilage development	GO:0061037	2	RARG, TGFB2	10	7	533.91	5.405e-6	3.364e-4
regulation of extracellular matrix organization	GO:1903053	2	ABL1, TGFB2	12	7	444.93	7.924e-6	4.549e-4
positive regulation of cell adhesion mediated by integrin	GO:0033630	2	FOXC2, TGFB2	16	7	333.70	1.440e-5	7.220e-4
bone morphogenesis	GO:0060349	2	RARG, SKI	32	7	166.85	5.934e-5	2.098e-3
face morphogenesis	GO:0060325	2	SKI, TGFB2	33	7	161.79	6.316e-5	2.200e-3
positive regulation of cell migration involved in sprouting angiogenesis	GO:0090050	2	ABL1, FOXC2	37	7	144.30	7.961e-5	2.612e-3
blood vessel remodeling	GO:0001974	2	FOXC2, TGFB2	42	7	127.12	1.028e-4	3.160e-3
positive regulation of apoptotic process	GO:0043065	3	ABL1, RARG, TGFB2	326	7	24.57	1.748e-4	4.614e-3
embryonic limb morphogenesis	GO:0030326	2	SKI, TGFB2	59	7	90.49	2.037e-4	5.158e-3
heart morphogenesis	GO:0003007	2	FOXC2, TGFB2	61	7	87.53	2.178e-4	5.389e-3
collagen fibril organization	GO:0030199	2	FOXC2, TGFB2	65	7	82.14	2.474e-4	5.906e-3
positive regulation of neuron apoptotic process	GO:0043525	2	ABL1, TGFB2	65	7	82.14	2.474e-4	5.906e-3
positive regulation of endothelial cell migration	GO:0010595	2	ABL1, FOXC2	66	7	80.90	2.551e-4	6.036e-3