

GeDiPNet Cluster 67 -- 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: 2026-10-08 03:23:04. · Rows: 15 · Generated: 2026-10-08 05:41:46

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
positive regulation of phosphatidylinositol 3-kinase/protein kinase B signal transduction	GO:0051897	34	CAT, CSF1R, FGFR3, FN1, INS, INSR, IRS1, PDGFC, RAC1, SIRT1, TCF7L2, TGFB1	217	623	4.70	4.985e-14	2.830e-11
response to hypoxia	GO:0001666	29	ADIPOQ, ASCL2, CAT, CPT1A, CYP1A1, ITGA2, KCNJ11, PML, SOD3, TFRC, TGFB1, UCP3	176	623	4.94	1.006e-12	4.544e-10
response to xenobiotic stimulus	GO:0009410	33	TFAP2B, ABCC8, ACSL1, ADIPOQ, BCL2, CALR, CAT, CCND1, CPT1A, CYBB, CYP1A1, ITGA2	248	623	3.99	1.223e-11	4.357e-9
positive regulation of MAPK cascade	GO:0043410	31	ADRB1, FGFR3, IL6, INS, INSR, KSR2, MAP3K5, SOD1, TGFB1, AR, FGF2, LEP	224	623	4.15	1.856e-11	6.383e-9
regulation of blood pressure	GO:0008217	19	POMC, ATP2B1, KCNQ1, PPARG, PTGS2, SOD1, LEP, SOD2, ACE, AGT, NOS3, GUCY1A1	83	623	6.87	2.293e-11	7.644e-9
positive regulation of cell population proliferation	GO:0008284	49	PTN, TFAP2B, ALDH1A2, BCL2, CALR, CCND1, CCND2, CSF1R, FGFR3, FN1, HMGA2, IGF2BP1	532	623	2.76	1.312e-10	3.652e-8
positive regulation of gene expression	GO:0010628	46	SEC16B, ALDH1A2, APOB, BCL3, CALR, CEBPB, ETS1, FN1, HFE, HMGA2, HNF1B, IL6	504	623	2.74	6.649e-10	1.505e-7
regulation of insulin secretion	GO:0050796	13	GIPR, TFAP2B, CPT1A, GCK, HNF4A, IL6, KCNJ11, MTNR1B, RFX6, LEP, IFNG, GIP	46	623	8.48	2.053e-9	4.134e-7
response to glucose	GO:0009749	15	GIPR, ADIPOQ, GCK, GCKR, HNF1B, HNF4A, LPL, SLC30A8, TCF7L2, TGFB1, TXNIP, CASP3	68	623	6.62	5.103e-9	9.251e-7
positive regulation of ERK1 and ERK2 cascade	GO:0070374	25	APOE, CSF1R, FGFR3, NOTCH2, PDE8B, PDGFC, PTPN22, TGFB1, TLR4, CCN2, FGF2, GAS6	201	623	3.73	1.550e-8	2.471e-6
negative regulation of neuron apoptotic process	GO:0043524	22	BDNF, TFAP2B, BCL2, CCND1, CEBPB, FAIM2, MTNR1B, SIRT1, SOD1, TFAP2D, WFS1, SOD2	160	623	4.12	1.809e-8	2.820e-6
positive regulation of endothelial cell migration	GO:0010595	14	BCAR1, CALR, ETS1, PROX1, RAC1, FGF2, AGT, KDR, VEGFA, NRP2, SASH1, ANGPT1	66	623	6.36	2.831e-8	4.164e-6
negative regulation of apoptotic process	GO:0043066	43	TFAP2B, BCL2, BCL3, CAT, CCND2, CSF1R, FAIM2, HMGA2, HNF1B, IL6, NOTCH2, PTGS2	524	623	2.46	5.562e-8	7.398e-6
positive regulation of transcription by RNA polymerase II	GO:0045944	76	MAP2K5, POMC, TFAP2B, ASCL2, AUTS2, BAZ1B, BCL3, BRD3, BSX, CDK12, CEBPB, CHD6	1208	623	1.89	6.166e-8	8.090e-6
positive regulation of blood vessel endothelial cell migration	GO:0043536	12	ETS1, PLCG1, SIRT1, TGFB1, FGF2, KDR, NFE2L2, NOS3, VEGFA, PLG, ANGPT1, THBS1	51	623	7.06	8.192e-8	1.031e-5