

## GeDiPNet Cluster 110 -- 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: 2026-10-07 03:23:06. · Rows: 15 · Generated: 2026-10-07 01:44:22

| GO Term                                             | GO ID      | Overlap Genes | Overlap Gene Names                                                                    | Term Gene Count | Cluster Gene Count | Fold Enrichment | P-value   | FDR Q-value |
|-----------------------------------------------------|------------|---------------|---------------------------------------------------------------------------------------|-----------------|--------------------|-----------------|-----------|-------------|
| smoothened signaling pathway                        | GO:0007224 | 27            | B9D1, CC2D2A, CD3E, CDON, CTNNA1, DISP1, DYRK2, FOXF1, GLI1, GLI2, GLI3, HHAT         | 94              | 76                 | 70.63           | 3.400e-44 | 5.406e-40   |
| determination of left/right symmetry                | GO:0007368 | 15            | FGF8, FOXH1, CC2D2A, DISP1, FOXF1, IFT172, IFT52, NME7, SMO, SUFU, DLL1, NODAL        | 83              | 76                 | 44.44           | 3.117e-21 | 6.023e-18   |
| heart looping                                       | GO:0001947 | 13            | FGF8, FOXH1, C2CD3, IFT172, IFT52, IHH, SMO, SUFU, TGFB2, DLL1, NODAL, SHH            | 64              | 76                 | 49.94           | 3.154e-19 | 4.541e-16   |
| dorsal/ventral pattern formation                    | GO:0009953 | 11            | FGF8, DISP1, GLI1, GLI3, HHIP, IFT172, IFT52, PTCH1, SMO, SHH, TGIF1                  | 47              | 76                 | 57.55           | 3.668e-17 | 3.841e-14   |
| negative regulation of smoothened signaling pathway | GO:0045879 | 10            | CD3E, GLI3, GLIS2, HHIP, IFT172, PTCH1, PTCH2, RB1, SUFU, TULP3                       | 35              | 76                 | 70.25           | 1.133e-16 | 1.054e-13   |
| lung development                                    | GO:0030324 | 11            | FGF8, PDGFRA, FOXF1, GLI1, GLI2, GLI3, TGFB2, FGFR1, LAMA5, NODAL, SHH                | 108             | 76                 | 25.04           | 5.977e-13 | 2.868e-10   |
| embryonic digit morphogenesis                       | GO:0042733 | 9             | B9D1, C2CD3, GLI3, IFT52, IHH, TMEM231, TULP3, SHH, LMBR1                             | 57              | 76                 | 38.82           | 1.436e-12 | 6.382e-10   |
| positive regulation of smoothened signaling pathway | GO:0045880 | 8             | CTNNA1, GLI1, IFT172, IHH, NDST1, SMO, STK36, SHH                                     | 39              | 76                 | 50.44           | 2.849e-12 | 1.186e-9    |
| cilium assembly                                     | GO:0060271 | 13            | B9D1, C2CD3, CC2D2A, IFT172, IFT52, IFT88, KIF3A, NME7, RAB23, STK36, TMEM17, TMEM231 | 237             | 76                 | 13.49           | 1.190e-11 | 4.322e-9    |
| regulation of smoothened signaling pathway          | GO:0008589 | 7             | C2CD3, GLI1, GLI3, IFT172, PTCH1, TULP3, GAS1                                         | 29              | 76                 | 59.35           | 2.015e-11 | 6.883e-9    |
| in utero embryonic development                      | GO:0001701 | 13            | PDGFRA, B9D1, C2CD3, FOXF1, GLI3, IHH, PTCH1, SMO, TGFB2, TMEM231, FGFR1, NODAL       | 252             | 76                 | 12.68           | 2.572e-11 | 8.495e-9    |
| cell population proliferation                       | GO:0008283 | 13            | FGF8, KIT, GLI3, HIPK1, HIPK2, IHH, NDST1, RB1, SMO, FGFR1, NODAL, SHH                | 263             | 76                 | 12.15           | 4.387e-11 | 1.373e-8    |
| spinal cord dorsal/ventral patterning               | GO:0021513 | 5             | GLI2, GLI3, SMO, SUFU, SHH                                                            | 8               | 76                 | 153.68          | 5.399e-11 | 1.654e-8    |
| brain development                                   | GO:0007420 | 12            | C2CD3, GLI3, IFT172, NME7, PTCH1, STK36, TGFB2, TULP3, FGFR1, NODAL, SIX3, ZIC2       | 244             | 76                 | 12.09           | 2.778e-10 | 7.150e-8    |
| camera-type eye development                         | GO:0043010 | 8             | B9D1, CC2D2A, GLI3, IHH, TMEM231, SHH, SIX3, TWSG1                                    | 74              | 76                 | 26.58           | 6.231e-10 | 1.478e-7    |