

## GeDiPNet Cluster 39 -- 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 08:50:10

| GO Term                                                                                          | GO ID      | Overlap Genes | Overlap Gene Names     | Term Gene Count | Cluster Gene Count | Fold Enrichment | P-value  | FDR Q-value |
|--------------------------------------------------------------------------------------------------|------------|---------------|------------------------|-----------------|--------------------|-----------------|----------|-------------|
| facultative heterochromatin formation                                                            | GO:0140718 | 3             | EED, EZH2, SUZ12       | 7               | 15                 | 533.91          | 1.462e-8 | 2.347e-6    |
| liver development                                                                                | GO:0001889 | 3             | PIK3CA, ALDH1A2, HLX   | 87              | 15                 | 42.96           | 4.259e-5 | 1.626e-3    |
| positive regulation of protein serine/threonine kinase activity                                  | GO:0071902 | 2             | RHOA, EZH2             | 15              | 15                 | 166.11          | 6.277e-5 | 2.178e-3    |
| cardiac muscle tissue development                                                                | GO:0048738 | 2             | ZFPM2, ALDH1A2         | 24              | 15                 | 103.82          | 1.643e-4 | 4.473e-3    |
| chromatin organization                                                                           | GO:0006325 | 4             | EED, EZH2, NSD1, SUZ12 | 449             | 15                 | 11.10           | 3.637e-4 | 7.857e-3    |
| oligodendrocyte differentiation                                                                  | GO:0048709 | 2             | EED, SUZ12             | 45              | 15                 | 55.37           | 5.836e-4 | 1.086e-2    |
| endothelial cell migration                                                                       | GO:0043542 | 2             | PIK3CA, RHOA           | 48              | 15                 | 51.91           | 6.641e-4 | 1.181e-2    |
| determination of bilateral symmetry                                                              | GO:0009855 | 1             | ALDH1A2                | 1               | 15                 | 1245.80         | 8.027e-4 | 1.336e-2    |
| angiotensin-mediated vasoconstriction involved in regulation of systemic arterial blood pressure | GO:0001998 | 1             | RHOA                   | 1               | 15                 | 1245.80         | 8.027e-4 | 1.336e-2    |
| alpha-beta T cell lineage commitment                                                             | GO:0002363 | 1             | RHOA                   | 1               | 15                 | 1245.80         | 8.027e-4 | 1.336e-2    |
| mitotic cleavage furrow formation                                                                | GO:1903673 | 1             | RHOA                   | 1               | 15                 | 1245.80         | 8.027e-4 | 1.336e-2    |
| regulation of peptidyl-serine phosphorylation                                                    | GO:0033135 | 1             | NSD1                   | 1               | 15                 | 1245.80         | 8.027e-4 | 1.336e-2    |
| regulation of RNA polymerase II regulatory region sequence-specific DNA binding                  | GO:1903025 | 1             | NSD1                   | 1               | 15                 | 1245.80         | 8.027e-4 | 1.336e-2    |
| response to butyrate                                                                             | GO:1903544 | 1             | PIK3CA                 | 1               | 15                 | 1245.80         | 8.027e-4 | 1.336e-2    |
| regulation of ERBB signaling pathway                                                             | GO:1901184 | 1             | SH3TC2                 | 1               | 15                 | 1245.80         | 8.027e-4 | 1.336e-2    |