

## GeDiPNet Cluster 486 -- 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: 2026-10-20 00:01:08

| GO Term                                                                             | GO ID      | Overlap Genes | Overlap Gene Names                                      | Term Gene Count | Cluster Gene Count | Fold Enrichment | P-value  | FDR Q-value |
|-------------------------------------------------------------------------------------|------------|---------------|---------------------------------------------------------|-----------------|--------------------|-----------------|----------|-------------|
| regulation of DNA-templated transcription                                           | GO:0006355 | 8             | BRPF1, ASH1L, NFIB, SETD5, MYT1L, ZFHX4, ZMYND8, ZBTB11 | 1454            | 21                 | 4.90            | 1.069e-4 | 3.249e-3    |
| chromatin organization                                                              | GO:0006325 | 5             | BRPF1, ASH1L, SETD5, ZMYND11, ZMYND8                    | 449             | 21                 | 9.91            | 1.159e-4 | 3.442e-3    |
| neuron fate specification                                                           | GO:0048665 | 2             | NFIB, MYT1L                                             | 24              | 21                 | 74.15           | 3.271e-4 | 7.127e-3    |
| regeneration                                                                        | GO:0031099 | 1             | NFIB                                                    | 1               | 21                 | 889.86          | 1.124e-3 | 1.550e-2    |
| lung ciliated cell differentiation                                                  | GO:0061141 | 1             | NFIB                                                    | 1               | 21                 | 889.86          | 1.124e-3 | 1.550e-2    |
| negative regulation of epithelial cell proliferation involved in lung morphogenesis | GO:2000795 | 1             | NFIB                                                    | 1               | 21                 | 889.86          | 1.124e-3 | 1.550e-2    |
| tarsal gland development                                                            | GO:1903699 | 1             | ASH1L                                                   | 1               | 21                 | 889.86          | 1.124e-3 | 1.550e-2    |
| uterine gland development                                                           | GO:1903709 | 1             | ASH1L                                                   | 1               | 21                 | 889.86          | 1.124e-3 | 1.550e-2    |
| cell differentiation involved in salivary gland development                         | GO:0060689 | 1             | NFIB                                                    | 2               | 21                 | 444.93          | 2.246e-3 | 2.244e-2    |
| negative regulation of mesenchymal cell proliferation involved in lung development  | GO:2000791 | 1             | NFIB                                                    | 2               | 21                 | 444.93          | 2.246e-3 | 2.244e-2    |
| selenocysteine biosynthetic process                                                 | GO:0016260 | 1             | SEPHS1                                                  | 2               | 21                 | 444.93          | 2.246e-3 | 2.244e-2    |
| glial cell fate specification                                                       | GO:0021780 | 1             | NFIB                                                    | 3               | 21                 | 296.62          | 3.368e-3 | 2.763e-2    |
| principal sensory nucleus of trigeminal nerve development                           | GO:0021740 | 1             | NFIB                                                    | 3               | 21                 | 296.62          | 3.368e-3 | 2.763e-2    |
| positive regulation of MDA-5 signaling pathway                                      | GO:1900245 | 1             | ANKRD17                                                 | 4               | 21                 | 222.46          | 4.488e-3 | 3.173e-2    |
| negative regulation of transcription by RNA polymerase III                          | GO:0016480 | 1             | SETD5                                                   | 4               | 21                 | 222.46          | 4.488e-3 | 3.173e-2    |