

## GeDiPNet Cluster 270 -- 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 00:31:21

| GO Term                                                              | GO ID      | Overlap Genes | Overlap Gene Names                                 | Term Gene Count | Cluster Gene Count | Fold Enrichment | P-value  | FDR Q-value |
|----------------------------------------------------------------------|------------|---------------|----------------------------------------------------|-----------------|--------------------|-----------------|----------|-------------|
| epidermis development                                                | GO:0008544 | 6             | KRT14, CDKN1A, EGFR, SPRR1A, ALDH3A2, KRT5         | 114             | 32                 | 30.74           | 3.594e-8 | 5.119e-6    |
| positive regulation of epithelial cell proliferation                 | GO:0050679 | 5             | ERBB2, EGFR, HRAS, TGFA, TGFB1                     | 73              | 32                 | 40.00           | 1.468e-7 | 1.671e-5    |
| ERBB2-EGFR signaling pathway                                         | GO:0038134 | 3             | ERBB2, EGFR, TGFA                                  | 8               | 32                 | 218.99          | 2.539e-7 | 2.652e-5    |
| regulation of cell population proliferation                          | GO:0042127 | 6             | ERBB2, PTGS2, SMAD4, EGFR, HRAS, TGFB1             | 201             | 32                 | 17.43           | 1.032e-6 | 8.510e-5    |
| negative regulation of apoptotic process                             | GO:0043066 | 8             | BAG1, ERBB2, PTGS2, SOD2, EGFR, TERT, CRYAB, HSPB1 | 524             | 32                 | 8.92            | 2.105e-6 | 1.500e-4    |
| positive regulation of fibroblast proliferation                      | GO:0048146 | 4             | CDKN1A, EGFR, HRAS, TGFB1                          | 55              | 32                 | 42.47           | 2.271e-6 | 1.593e-4    |
| positive regulation of miRNA transcription                           | GO:1902895 | 4             | SMAD4, EGFR, TGFB1, TERT                           | 56              | 32                 | 41.71           | 2.443e-6 | 1.690e-4    |
| cellular response to hypoxia                                         | GO:0071456 | 5             | ATF4, PTGS2, TGFB1, TERT, AQP3                     | 139             | 32                 | 21.01           | 3.630e-6 | 2.322e-4    |
| cell population proliferation                                        | GO:0008283 | 6             | ERBB2, SMAD4, CCND1, EGFR, ODC1, TGFB1             | 263             | 32                 | 13.32           | 4.892e-6 | 2.950e-4    |
| cellular response to growth factor stimulus                          | GO:0071363 | 4             | ERBB2, SMAD4, EGFR, TGFB1                          | 76              | 32                 | 30.74           | 8.332e-6 | 4.528e-4    |
| cellular response to gamma radiation                                 | GO:0071480 | 3             | CDKN1A, HRAS, CRYAB                                | 28              | 32                 | 62.57           | 1.451e-5 | 6.986e-4    |
| response to UV-A                                                     | GO:0070141 | 2             | CCND1, EGFR                                        | 4               | 32                 | 291.98          | 1.701e-5 | 7.908e-4    |
| positive regulation of vascular endothelial growth factor production | GO:0010575 | 3             | ATF4, PTGS2, TGFB1                                 | 32              | 32                 | 54.75           | 2.187e-5 | 9.631e-4    |
| positive regulation of cell population proliferation                 | GO:0008284 | 7             | CCND1, CDKN1A, EGFR, HRAS, ODC1, TGFA, TGFB1       | 532             | 32                 | 7.68            | 2.641e-5 | 1.110e-3    |
| cell surface receptor signaling pathway                              | GO:0007166 | 6             | BAG1, CD274, ERBB2, EGFR, HRAS, TGFA               | 373             | 32                 | 9.39            | 3.549e-5 | 1.391e-3    |