

## GeDiPNet Cluster 267 -- Enriched Pathways

Pathway enrichment: KEGG + Reactome, upper-tail hypergeometric test, Benjamini-Hochberg FDR-corrected. Fold enrichment = (overlap / cluster gene count) / (pathway gene count / universe size). Top 15 pathways per cluster by q-value. See [scripts/build\\_cluster\\_enrichment.php](scripts/build_cluster_enrichment.php) on [gedipnet.bicnirrh.res.in](http://gedipnet.bicnirrh.res.in). Data as of: 2026-10-07 03:30:09. · Rows: 15 · Generated: 2026-10-07 17:48:30

| Pathway                                              | Source   | Overlap Genes | Overlap Gene Names  | Pathway Gene Count | Cluster Gene Count | Fold Enrichment | P-value  | FDR Q-value |
|------------------------------------------------------|----------|---------------|---------------------|--------------------|--------------------|-----------------|----------|-------------|
| NF-kappa B signaling pathway                         | KEGG     | 3             | BCL10, BIRC3, MALT1 | 105                | 6                  | 57.19           | 1.274e-5 | 4.111e-4    |
| Activation of NF-kappaB in B cells                   | Reactome | 2             | BCL10, MALT1        | 66                 | 6                  | 60.66           | 4.399e-4 | 7.210e-3    |
| FCERI mediated NF-kB activation                      | Reactome | 2             | BCL10, MALT1        | 79                 | 6                  | 50.68           | 6.300e-4 | 9.552e-3    |
| CLEC7A (Dectin-1) signaling                          | Reactome | 2             | BCL10, MALT1        | 79                 | 6                  | 50.68           | 6.300e-4 | 9.552e-3    |
| B cell receptor signaling pathway                    | KEGG     | 2             | BCL10, MALT1        | 91                 | 6                  | 43.99           | 8.351e-4 | 1.184e-2    |
| Downstream TCR signaling                             | Reactome | 2             | BCL10, MALT1        | 98                 | 6                  | 40.85           | 9.678e-4 | 1.323e-2    |
| C-type lectin receptor signaling pathway             | KEGG     | 2             | BCL10, MALT1        | 105                | 6                  | 38.13           | 1.110e-3 | 1.466e-2    |
| T cell receptor signaling pathway                    | KEGG     | 2             | BCL10, MALT1        | 122                | 6                  | 32.81           | 1.495e-3 | 1.844e-2    |
| CLEC7A/inflammasome pathway                          | Reactome | 1             | MALT1               | 6                  | 6                  | 333.61          | 2.994e-3 | 3.068e-2    |
| Tuberculosis                                         | KEGG     | 2             | BCL10, MALT1        | 181                | 6                  | 22.12           | 3.256e-3 | 3.261e-2    |
| Attachment of GPI anchor to uPAR                     | Reactome | 1             | PIGT                | 7                  | 6                  | 285.95          | 3.493e-3 | 3.425e-2    |
| Regulation of necroptotic cell death                 | Reactome | 1             | BIRC3               | 11                 | 6                  | 181.97          | 5.484e-3 | 4.649e-2    |
| Shigellosis                                          | KEGG     | 2             | BCL10, MALT1        | 250                | 6                  | 16.01           | 6.126e-3 | 5.006e-2    |
| RIPK1-mediated regulated necrosis                    | Reactome | 1             | BIRC3               | 16                 | 6                  | 125.10          | 7.968e-3 | 5.956e-2    |
| Transcriptional regulation of pluripotent stem cells | Reactome | 1             | FOXP1               | 17                 | 6                  | 117.75          | 8.465e-3 | 6.196e-2    |