

## GeDiPNet Cluster 584 -- 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: 2026-10-20 03:30:09. · Rows: 15 · Generated: 2026-10-20 00:03:17

| Pathway                              | Source   | Overlap Genes | Overlap Gene Names         | Pathway Gene Count | Cluster Gene Count | Fold Enrichment | P-value  | FDR Q-value |
|--------------------------------------|----------|---------------|----------------------------|--------------------|--------------------|-----------------|----------|-------------|
| Endocrine resistance                 | KEGG     | 4             | TP53, CDKN2A, KRAS, GNAS   | 99                 | 11                 | 44.11           | 1.371e-6 | 5.491e-5    |
| Bladder cancer                       | KEGG     | 3             | TP53, CDKN2A, KRAS         | 41                 | 11                 | 79.89           | 5.979e-6 | 1.906e-4    |
| Cellular senescence                  | KEGG     | 4             | TP53, CDKN2A, RRAS2, KRAS  | 157                | 11                 | 27.82           | 8.636e-6 | 2.585e-4    |
| Hepatocellular carcinoma             | KEGG     | 4             | TP53, ARID1A, CDKN2A, KRAS | 170                | 11                 | 25.69           | 1.183e-5 | 3.346e-4    |
| Proteoglycans in cancer              | KEGG     | 4             | TP53, ANK1, RRAS2, KRAS    | 204                | 11                 | 21.41           | 2.429e-5 | 6.122e-4    |
| Melanoma                             | KEGG     | 3             | TP53, CDKN2A, KRAS         | 73                 | 11                 | 44.87           | 3.433e-5 | 8.103e-4    |
| Non-small cell lung cancer           | KEGG     | 3             | TP53, CDKN2A, KRAS         | 73                 | 11                 | 44.87           | 3.433e-5 | 8.103e-4    |
| Human cytomegalovirus infection      | KEGG     | 4             | TP53, CDKN2A, KRAS, GNAS   | 226                | 11                 | 19.32           | 3.632e-5 | 8.462e-4    |
| Glioma                               | KEGG     | 3             | TP53, CDKN2A, KRAS         | 76                 | 11                 | 43.10           | 3.874e-5 | 8.916e-4    |
| Pancreatic cancer                    | KEGG     | 3             | TP53, CDKN2A, KRAS         | 77                 | 11                 | 42.54           | 4.029e-5 | 9.199e-4    |
| Chronic myeloid leukemia             | KEGG     | 3             | TP53, CDKN2A, KRAS         | 77                 | 11                 | 42.54           | 4.029e-5 | 9.199e-4    |
| Stabilization of p53                 | Reactome | 2             | TP53, CDKN2A               | 11                 | 11                 | 198.51          | 4.176e-5 | 9.469e-4    |
| Longevity regulating pathway         | KEGG     | 3             | TP53, IRS4, KRAS           | 90                 | 11                 | 36.39           | 6.429e-5 | 1.333e-3    |
| Mitophagy - animal                   | KEGG     | 3             | TP53, RRAS2, KRAS          | 105                | 11                 | 31.19           | 1.018e-4 | 1.923e-3    |
| SUMOylation of transcription factors | Reactome | 2             | TP53, CDKN2A               | 18                 | 11                 | 121.31          | 1.158e-4 | 2.128e-3    |