

## GeDiPNet Cluster 450 -- 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 00:03:13

| Pathway                                 | Source   | Overlap Genes | Overlap Gene Names              | Pathway Gene Count | Cluster Gene Count | Fold Enrichment | P-value  | FDR Q-value |
|-----------------------------------------|----------|---------------|---------------------------------|--------------------|--------------------|-----------------|----------|-------------|
| Non-small cell lung cancer              | KEGG     | 4             | MET, TP53, PIK3CA, JAK3         | 73                 | 6                  | 109.68          | 1.867e-8 | 1.284e-6    |
| Gastric cancer                          | KEGG     | 4             | MET, TP53, PIK3CA, TGFBR2       | 150                | 6                  | 53.38           | 3.440e-7 | 1.648e-5    |
| Hepatitis B                             | KEGG     | 4             | TP53, PIK3CA, TGFBR2, JAK3      | 163                | 6                  | 49.12           | 4.803e-7 | 2.207e-5    |
| Hepatocellular carcinoma                | KEGG     | 4             | MET, TP53, PIK3CA, TGFBR2       | 170                | 6                  | 47.10           | 5.686e-7 | 2.547e-5    |
| Pathways in cancer                      | KEGG     | 5             | MET, TP53, PIK3CA, TGFBR2, JAK3 | 533                | 6                  | 18.78           | 9.773e-7 | 4.085e-5    |
| Human T-cell leukemia virus 1 infection | KEGG     | 4             | TP53, PIK3CA, TGFBR2, JAK3      | 224                | 6                  | 35.74           | 1.716e-6 | 6.661e-5    |
| MET activates PI3K/AKT signaling        | Reactome | 2             | MET, PIK3CA                     | 6                  | 6                  | 667.22          | 3.117e-6 | 1.102e-4    |
| Central carbon metabolism in cancer     | KEGG     | 3             | MET, TP53, PIK3CA               | 71                 | 6                  | 84.58           | 3.910e-6 | 1.338e-4    |
| Melanoma                                | KEGG     | 3             | MET, TP53, PIK3CA               | 73                 | 6                  | 82.26           | 4.253e-6 | 1.436e-4    |
| Pancreatic cancer                       | KEGG     | 3             | TP53, PIK3CA, TGFBR2            | 77                 | 6                  | 77.99           | 4.999e-6 | 1.641e-4    |
| Chronic myeloid leukemia                | KEGG     | 3             | TP53, PIK3CA, TGFBR2            | 77                 | 6                  | 77.99           | 4.999e-6 | 1.641e-4    |
| Colorectal cancer                       | KEGG     | 3             | TP53, PIK3CA, TGFBR2            | 87                 | 6                  | 69.02           | 7.229e-6 | 2.233e-4    |
| PI3K-Akt signaling pathway              | KEGG     | 4             | MET, TP53, PIK3CA, JAK3         | 361                | 6                  | 22.18           | 1.148e-5 | 3.261e-4    |
| Measles                                 | KEGG     | 3             | TP53, PIK3CA, JAK3              | 139                | 6                  | 43.20           | 2.958e-5 | 7.162e-4    |
| Cellular senescence                     | KEGG     | 3             | TP53, PIK3CA, TGFBR2            | 157                | 6                  | 38.25           | 4.259e-5 | 9.636e-4    |