# GeDiPNet Shared-Gene Disease Pairs

Similarity: Jaccard index on shared curated genes (disease_gdp). Significance: upper-tail hypergeometric test (P(X>=k)), Benjamini-Hochberg FDR-corrected across all tested pairs. Corroborated Shared Genes: count of shared genes backed by >=2 distinct disease_gdp.main_source values combined across both diseases (e.g. GWAS-backed for one, ClinVar-backed for the other still counts); Shared Gene Names lists each gene's own source count in parentheses. Overlap Coefficient: shared genes / MIN(each disease's own total gene count) -- complements the Jaccard-based Similarity Score by showing how much of the SMALLER disease's entire known gene-set is covered by this pair, which Jaccard (dividing by the union) can understate. Shared Cluster: cluster id if both diseases fall in the same label-propagation cluster (scripts/build_disease_clusters.php), blank otherwise. See scripts/build_related.php on gedipnet.bicnirrh.res.in. Data as of: 2026-10-20 03:00:20. Filters applied: disease name contains "Thyroid hormonogenesis defect" (5 matching pairs). · Rows: 5 · Generated: 2026-10-20 03:39:12

| Disease A | Disease B | Shared Genes | Corroborated Shared Genes | Shared Gene Names | Similarity Score | Overlap Coefficient | P-value | FDR Q-value | Shared Cluster |
|---|---|---|---|---|---|---|---|---|---|
| Cholangiocarcinoma | Thyroid hormonogenesis defect | 1 | 1 | SLC5A5 (2) | 0.02703 | 1.00000 | 2.324e-3 | 3.054e-3 | |
| Congenital hypothyroidism | Thyroid hormonogenesis defect | 1 | 1 | SLC5A5 (2) | 0.05263 | 1.00000 | 1.162e-3 | 1.729e-3 | |
| Thyroid dyshormonogenesis | Thyroid hormonogenesis defect | 1 | 1 | SLC5A5 (7) | 0.12500 | 1.00000 | 4.520e-4 | 8.260e-4 | |
| Goitre | Thyroid hormonogenesis defect | 1 | 0 | SLC5A5 (1) | 0.25000 | 1.00000 | 1.937e-4 | 4.414e-4 | |
| Follicular thyroid adenoma | Thyroid hormonogenesis defect | 1 | 0 | SLC5A5 (1) | 0.50000 | 1.00000 | 6.457e-5 | 1.985e-4 | |