

GeDiPNet Shared-Gene Disease Pairs

Similarity: Jaccard index on shared curated genes (disease_gdp). Significance: upper-tail hypergeometric test ($P(X \geq k)$), 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: 2026-10-10 03:00:13. Filters applied: disease name contains "normophosphatemic familial tumoral calcinosis" (5 matching pairs). · Rows: 5 · Generated: 2026-10-10 08:32:32

Disease A	Disease B	Shared Genes	Corroborated Shared Genes	Shared Gene Names	Similarity Score	Overlap Coefficient	P-value	FDR Q-value	Shared Cluster
Myelodysplastic syndrome	normophosphatemic familial tumoral calcinosis	1	1	SAMD9 (2)	0.02128	1.00000	2.987e-3	3.949e-3	
Intestinal disease	normophosphatemic familial tumoral calcinosis	1	1	SAMD9 (2)	0.06667	1.00000	9.092e-4	1.576e-3	
normophosphatemic familial tumoral calcinosis	Urogenital abnormalities	1	1	SAMD9 (2)	0.10000	1.00000	5.845e-4	1.156e-3	
normophosphatemic familial tumoral calcinosis	Tumoral calcinosis	1	1	SAMD9 (4)	0.20000	1.00000	2.598e-4	6.509e-4	
normophosphatemic familial tumoral calcinosis	Spectrum and myeloid neoplasm risk	1	1	SAMD9 (2)	0.33333	1.00000	1.299e-4	3.931e-4	