

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: 2026-10-11 03:00:14. Filters applied: disease name contains "Epidermodysplasia verruciformis" (5 matching pairs). · Rows: 5 · Generated: 2026-10-11 10:10:18

Disease A	Disease B	Shared Genes	Corroborated Shared Genes	Shared Gene Names	Similarity Score	Overlap Coefficient	P-value	FDR Q-value	Shared Cluster
Combined immunodeficiency disease	Epidermodysplasia verruciformis	1	0	MST1 (1)	0.01961	0.14286	1.984e-2	2.161e-2	
Cholangitis	Epidermodysplasia verruciformis	1	1	MST1 (3)	0.04762	0.14286	6.348e-3	7.619e-3	
Epidermodysplasia verruciformis	Thyroid gland neoplasms	1	1	RHOH (4)	0.05000	0.14286	5.896e-3	7.109e-3	
Epidermodysplasia verruciformis	severe combined immunodeficiency due to CORO1A deficiency	1	1	CORO1A (2)	0.12500	1.00000	4.546e-4	9.726e-4	
Epidermodysplasia verruciformis	Immunodeficiency	4	4	RHOH (5), CORO1A (3), MST1 (2), IL7 (3)	0.02797	0.57143	2.180e-7	1.443e-6	