

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: 2026-10-13 03:00:13. Filters applied: disease name contains "Chromosome 16p11.2 deletion syndrome" (5 matching pairs). · Rows: 5 · Generated: 2026-10-13 09:12:16

Disease A	Disease B	Shared Genes	Corroborated Shared Genes	Shared Gene Names	Similarity Score	Overlap Coefficient	P-value	FDR Q-value	Shared Cluster
Chromosome 16p11.2 deletion syndrome	interstitial lung disease 1	1	1	SFTPA1 (2)	0.33333	1.00000	1.299e-4	3.931e-4	
Chromosome 16p11.2 deletion syndrome	Chromosome 16p11.2 microdeletion syndrome	1	1	SH2B1 (2)	0.33333	1.00000	1.299e-4	3.931e-4	
Bronchopulmonary dysplasia	Chromosome 16p11.2 deletion syndrome	1	0	SFTPA1 (1)	0.02128	0.50000	5.837e-3	7.049e-3	
Chromosome 16p11.2 deletion syndrome	Interstitial lung disease	1	1	SFTPA1 (5)	0.01471	0.50000	8.554e-3	9.897e-3	
Chromosome 16p11.2 deletion syndrome	Idiopathic pulmonary fibrosis	1	1	SFTPA1 (2)	0.01190	0.50000	1.062e-2	1.199e-2	