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: 2026-10-22 03:00:19. Filters applied: disease name contains "Mental retardation, autosomal dominant 51" (5 matching pairs). · Rows: 5 · Generated: 2026-10-21 22:12:37

Disease A	Disease B	Shared Genes	Corroborated Shared Genes	Shared Gene Names	Similarity Score	Overlap Coefficient	P-value	FDR Q-value	Shared Cluster
Intellectual developmental disorder dysmorphic hypotonia	Mental retardation, autosomal dominant 51	1	1	KMT5B (2)	0.50000	1.00000	6.457e-5	1.985e-4	
Intellectual developmental disorder, autosomal dominant 51	Mental retardation, autosomal dominant 51	1	0	KMT5B (1)	0.50000	1.00000	6.457e-5	1.985e-4	
Mental retardation, autosomal dominant 51	Neural tube defect	1	1	KMT5B (2)	0.01887	1.00000	3.357e-3	4.220e-3	
Complex neurodevelopmental disorder	Mental retardation, autosomal dominant 51	1	1	KMT5B (2)	0.00741	1.00000	8.652e-3	9.794e-3	
Mental retardation, autosomal dominant 51	Non-specific syndromic intellectual disability	1	1	KMT5B (2)	0.00271	1.00000	2.376e-2	2.528e-2	