S3 Table

Randomly added phenotypes (8522 total)		
Top rank	**3547**	**41.62%**
Top 10	**4315**	**50.63%**
Randomly removed phenotypes (8522 total) with p=$\frac{1}{3}$		
Top rank	**3963**	**46.50%**
Top 10	**4921**	**57.74%**
Double pathogenic variants on D1 (8522 total)		
Top rank	**5316**	**62.38%**
Top 10	**7602**	**89.20%**
Double pathogenic variants on D2 (8522 total)		
Top rank	**1309**	**15.36%**
Top 10	**3612**	**42.38%**
Double pathogenic variants on both (8522 total)		
D1 Variant		
Top rank	**3116**	**36.56%**
Top 10	**5428**	**63.69%**
D2 Variant		
Top rank	**3171**	**37.21%**
Top 10	**5468**	**64.16%**

Experiments when adding noise to phenotypes associated with 8,522 synthetic whole exome sequences. Each WES contains a single causative variant v_1 and is associated with phenotypes P_1. First, we randomly add the complete set of phenotypes from a randomly chosen disease to P_1 and record how well we recover v_1. Second, we randomly remove each phenotype in P_1 with a probability of $\frac{1}{3}$ and record how well v_1 is recovered. In the third experiment, we add another causative variant v_2 to the WES (which is causative for the disease that is phenotypically most similar to P_1, and is itself associated with phenotypes P_2), and use P_1 to recover v_1. We record how often we identify v_1 and v_2 at the first or top 10 ranks. Finally, we perform the same experiment using as phenotypes $P_1 \cup P_2$.