

Figure S1. The fraction of participants with more than one variant in their gene for each of the 99 genes in the 140 gene-trait combinations.

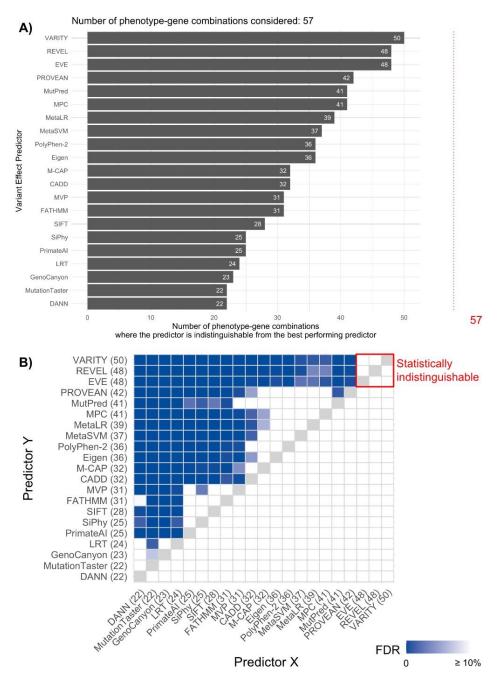


Figure S2. A) The number of gene-trait combinations for which each predictor is either best-performing or indistinguishable from best-performing. The red line highlights the maximum value based on the 57 combinations where all 20 predictors could make enough predictions. **B)** Comparisons between all pairs of computational predictors, determining if the performance of one predictor is significantly different than another. Variant effect predictors are ranked top-to-bottom and right-to-left based on decreasing number of gene-trait combinations where the predictor is among the best-performing predictors. Comparisons in which one predictor Y is significantly different from another predictor X (with FDR < 10%) are indicated in blue.

		Predictor:	VARITY_	_R; Variar	nt Type: n	nissense_	_andpro	tein_trun	cating; M	ode: rece	ssive
# of participants w/ qualifying variants	93-900	4.8	4.8	4.8	4.8	4.8	4.8	4.4	4.7	4.8	4.8
	56-92	4.8	4.8	4.8	4.8	4.8	4.8	4.6	4.7	4.8	4.8
	39-55	4.8	4.8	4.8	4.8	4.8	4.8	4.6	4.8	4.8	4.8
	30-38	4.8	4.8	4.8	4.8	4.8	4.8	4.7	4.8	4.7	4.7
	24-29	4.8	4.8	4.8	4.8	4.8	4.8	4.8	4.8	4.8	4.8
	20-23	4.7	4.7	4.7	4.7	4.7	4.7	4.7	4.7	4.7	4.7
	16-19	4.8	4.8	4.8	4.8	4.8	4.8	4.9	4.9	4.9	4.8
	14-15	4.6	4.7	4.7	4.7	4.7	4.7	4.8	4.7	4.7	4.7
	12-13	4.8	4.8	4.8	4.8	4.8	4.8	4.9	4.8	4.8	4.8
	10-11	4.5	4.5	4.5	4.5	4.5	4.5	4.7	4.6	4.5	4.5
		1000- 1300	1301- 1650	1651- 2200	2201- 3160 # 6	3161- 4730 of particin	4731- 9420 ants w/ t	9421- 11700	11701- 24500	24501- 40900	
# of participants w/ trait											

Figure S3. The number of gene-trait combinations in a 10-by-10 grid. Genes were divided into deciles based on the number of participants with a qualifying variant in that gene and traits were divided into deciles based on the number of participants with that trait.

of gene-trait combinations (log10 scale) 0 2 4 6