Table S14. for each cross-validation scheme and model, shown is the percentage of genes (with test R^2 >= 0.05) where the model had the best predictive power

	KNN	Elastic-Net	Combined	Single-SNP
Cross-pop	9%	39%	16%	34%
Mixed-pop	3%	37%	18%	41%
Intra-pop	3%	47%	22%	26%