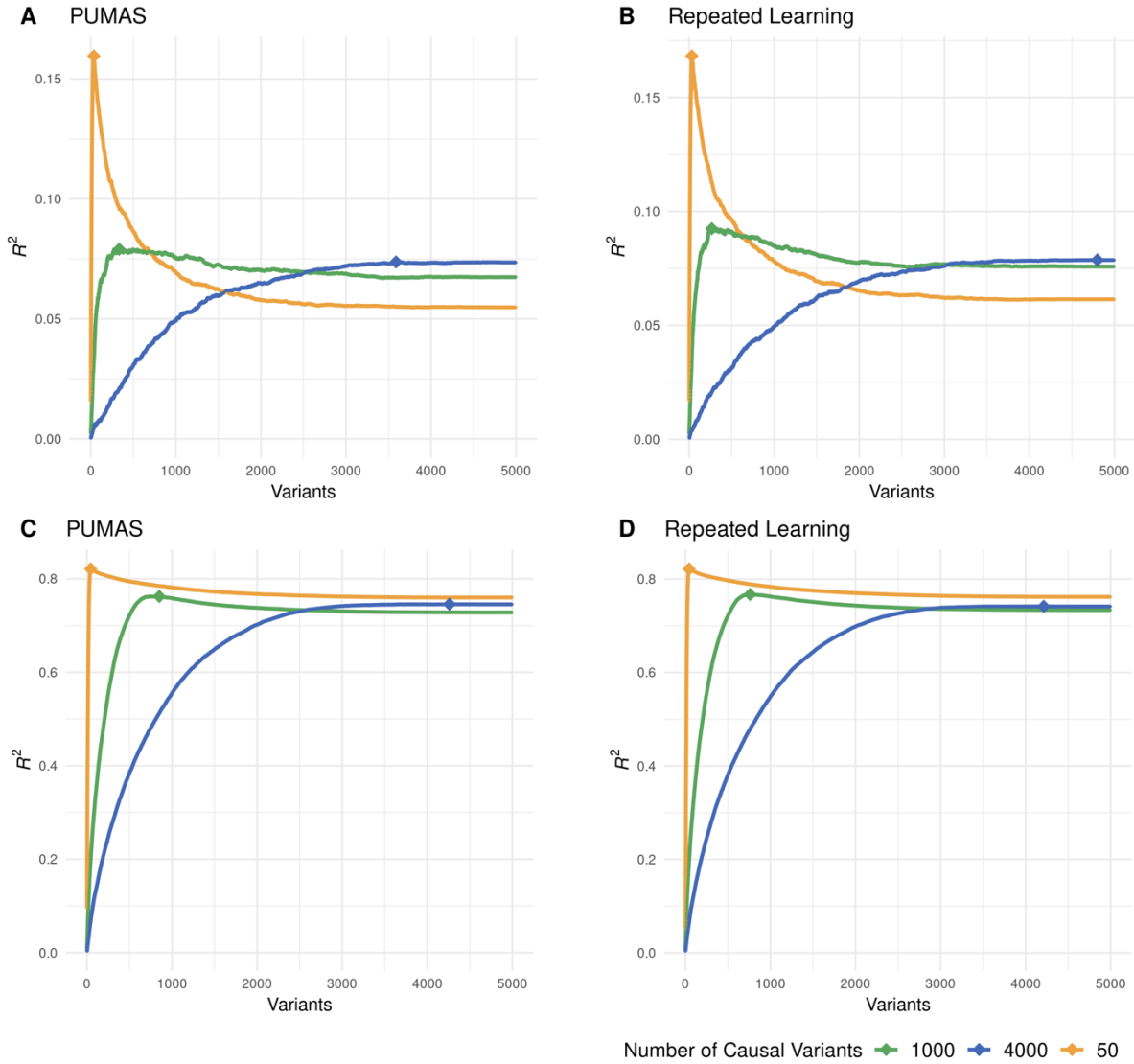
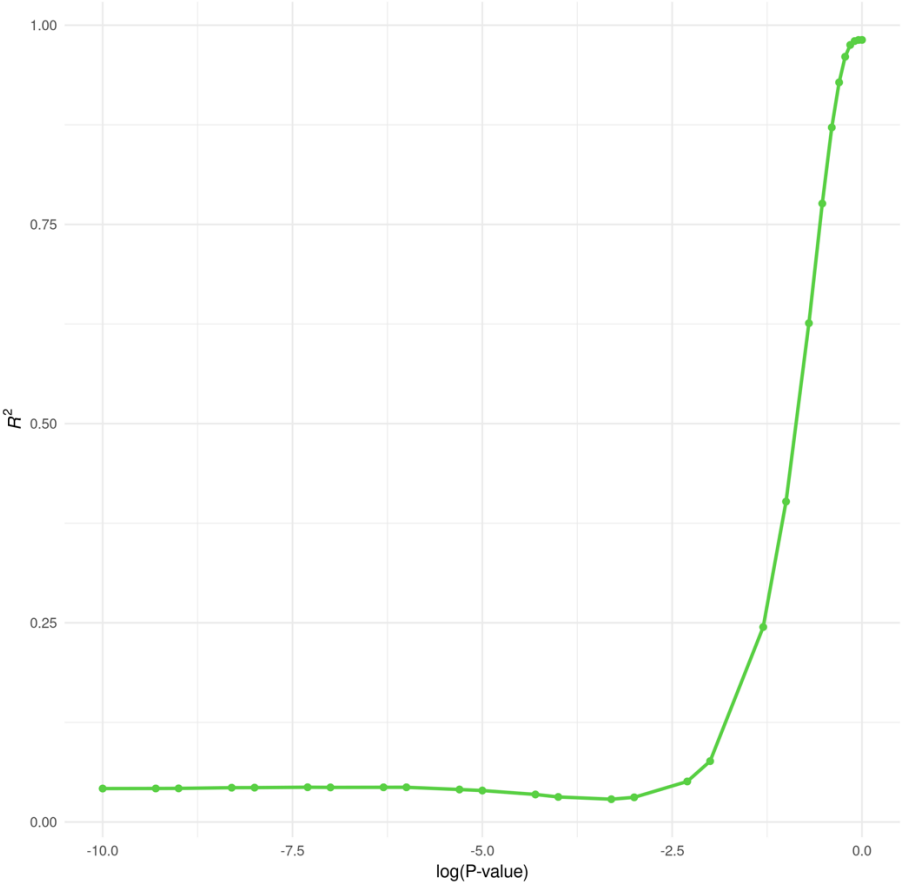


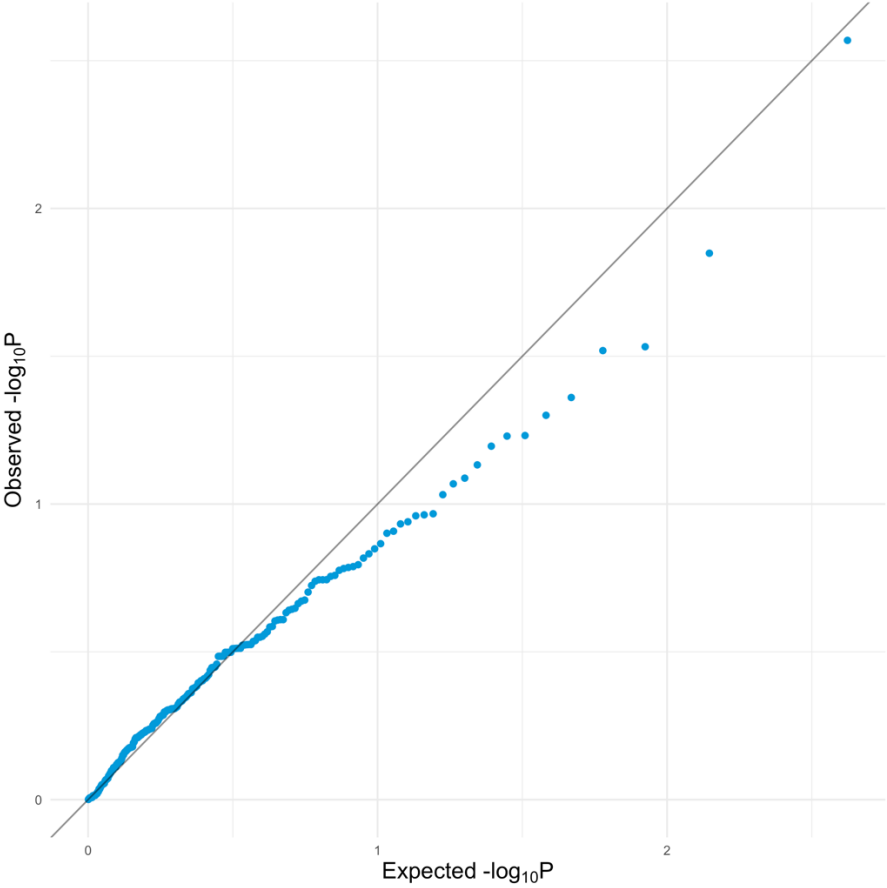
Supplementary Figure 1. Comparing the performance of two model-tuning strategies in more simulation settings. (A) our newly proposed method using summary statistics as input with sample size of 20,000 and heritability of 0.2 (B) a traditional repeated learning approach applied to individual-level data with sample size of 20,000 and heritability of 0.2 (C) our newly proposed method using summary statistics as input with sample size of 100,000 and heritability of 0.8 (D) a traditional repeated learning approach applied to individual-level data with sample size of 100,000 and heritability of 0.8. The X-axis shows the value of tuning parameter (i.e. number of variants in the model). The Y-axis shows the predictive performance quantified by R^2 . The three curves in each panel represent three different levels of sparsity and genetic architecture.



Supplementary Figure 2. PUMAS result using clumped IGAP 2013 AD GWAS as input.



Supplementary Figure 3. QQ plot for p-values of LDSC intercept estimates between non-imaging AD-proxy GWAS and UK Biobank imaging traits.



Supplementary Figure 4. QQ plot for associations between breast cancer and UK Biobank imaging traits.

