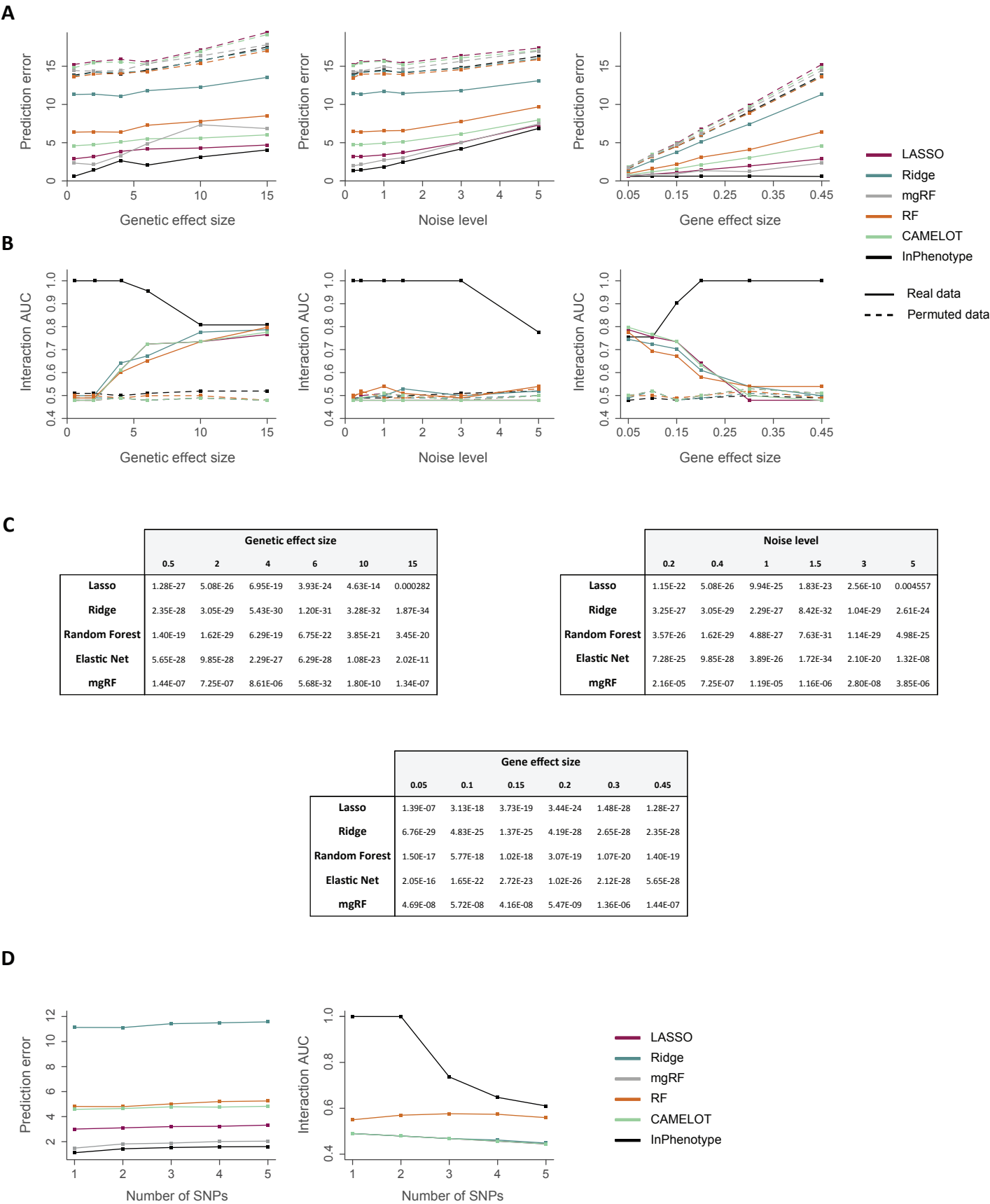


Figure S9



**Figure S9. (A,B) InPhenotype outperforms existing methods in prediction errors and in accuracy of predicting gene-locus interactions in the case of two causal SNPs.** Shown as in **Figure 2** but for the case of two causal SNPs. **(C)** Shown are P-values of paired *t*-tests when comparing prediction errors of InPhenotype to prediction errors of other methods (rows) using two informative SNP. Each column refers to a different genetic effect size (**top left**), noise level (**top right**) and gene effect size (**bottom**). **(D)** Shown is the prediction error and interaction AUCs for various numbers of causal SNPs.