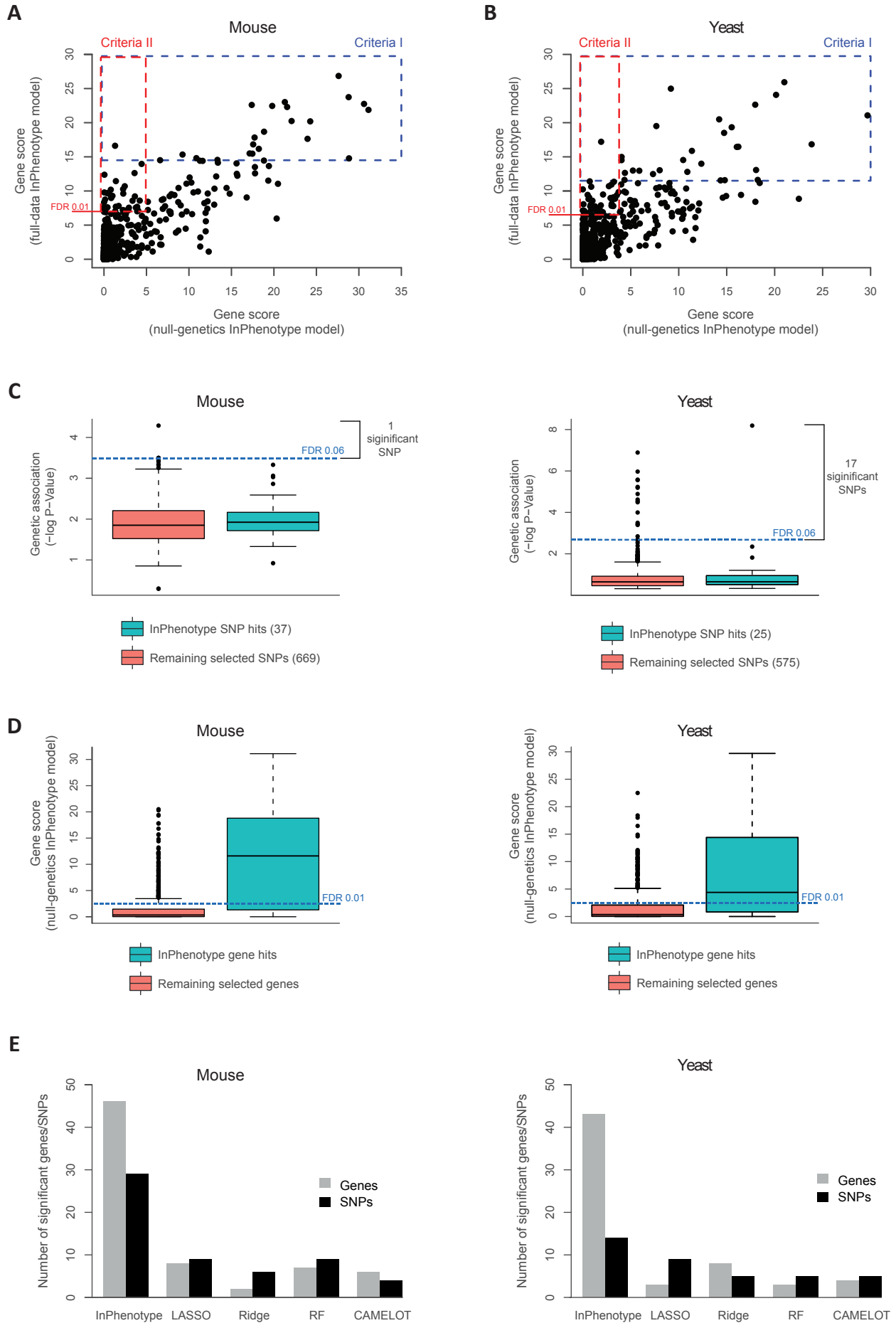


Figure S3



**Figure S3. Application of Inphenotype on real data in yeast and mouse. (A,B) Selection of genes based on their gene scores.** A scatter plot of gene scores that were calculated using a full-data InPhenotype model (y axis) and a null-genetics InPhenotype model (x axis) in the murine (A) and yeast (B) data. Selection based on criteria I and II are presented in blue and red rectangles, respectively. **(C) Standard GWAS scores.** Distributions of standard genetic association scores ( $-\log P$ -value of association, ANOVA test) are shown across all loci that were identified by InPhenotype (turquoise) and across all remaining loci that were selected in a pre-processing step, which were given as input to the InPhenotype method (peach), in the murine (**left**) and yeast (**right**) datasets. **(D) Identification of genes in the absence of genotyping data.** Plots are shown as in C but for  $-\log P$ -values that were obtained by InPhenotype in the absence of genotyping. **(E) Identification of significant genes and SNPs.** Shown are the numbers of genes that attained permutation-based significance of  $FDR < 0.01$  (gray) and numbers of SNPs that attained permutation-based significance with  $FDR < 0.06$  (black), when applying InPhenotype and alternative methods on the murine (**left**) and yeast (**right**) datasets.