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. (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 of FDR < 0.01 (gray) and numbers of SNPs that attained murine (left) and yeast (right) datasets.