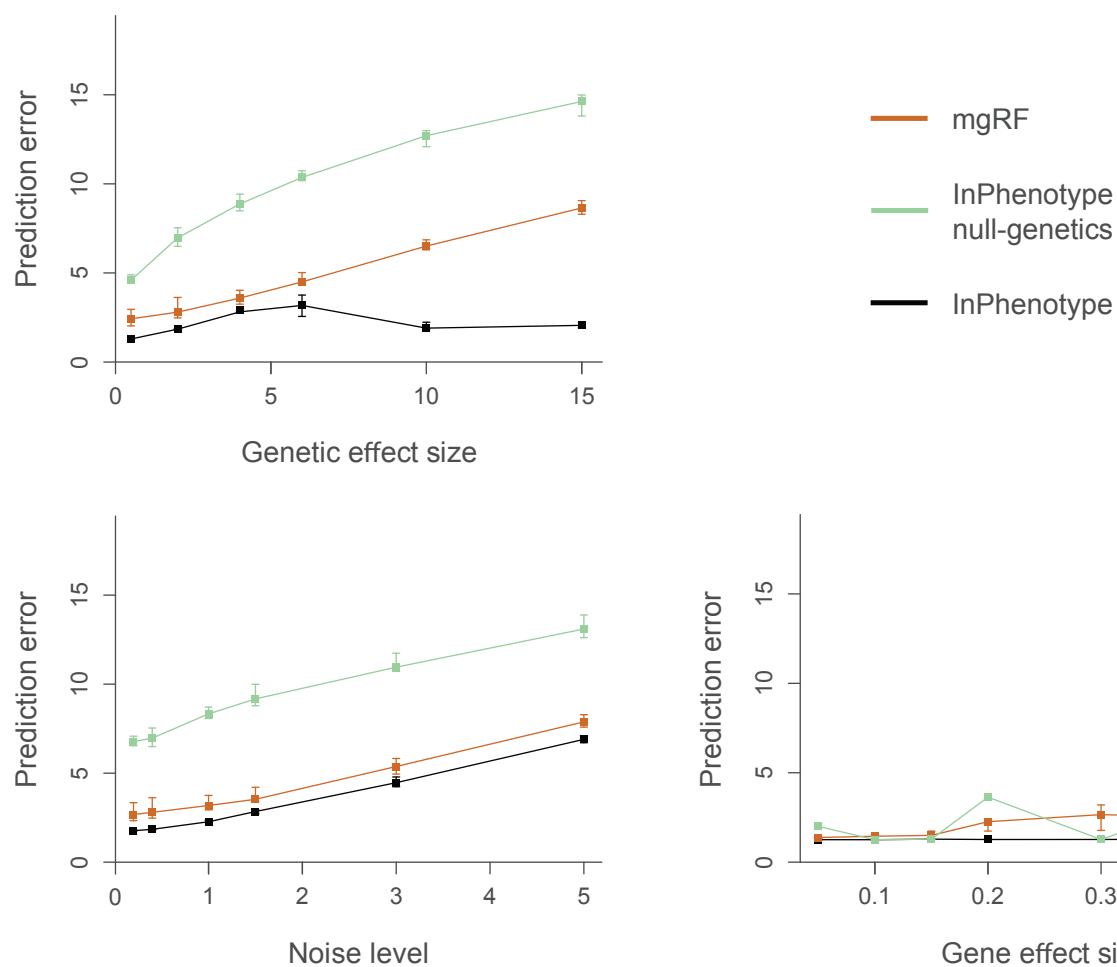
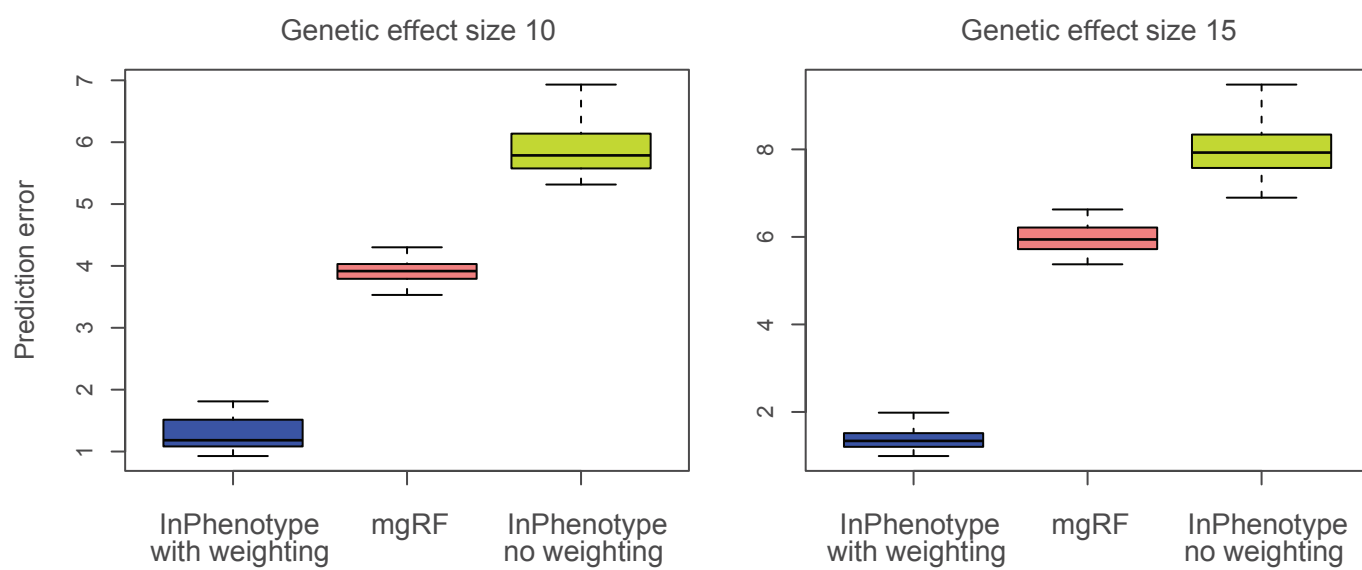


Figure S7

A



B



**Figure S7. (A) The contribution of genetic data.** Shown are prediction errors (y axis) that were calculated on different synthetic datasets of various data parameters (x axis). Prediction methods are: InPhenotype (black), InPhenotype in absence of genetic data ('null-genetics'; light blue), and mgRF (orange). In all cases, the default parameters are 200 individuals, gene-effect size 0.45, genetic-effect size 2, noise level 0.4, and a single causal SNP. The results indicate a substantial contribution of integrating genetic data within the InPhenotype forest. **(B) Performance of InPhenotype in the presence and absence of a weighting scheme.** Shown are box plots of prediction errors of different methods—InPhenotype (green), InPhenotype in the absence of a weighting scheme (blue), and mgRF (pink)—using genetic effect size of 10 (left) or 15 (right). Remaining parameters are: 200 individuals, gene-effect size 0.45, noise level 0.4, and a single causal SNP. The results indicate a substantial contribution of the weighting scheme to InPhenotype's performance.