



Figure S6 Frequency histograms of the deviations in the simulated true predictive accuracy $r_{g,\hat{g}}$ from the estimated predictive accuracy for the datasets with $\hat{r}_{g,\hat{g},o}$ (empty box and whiskers capped with brackets) and without $\hat{r}_{g,\hat{g}}$ (green boxes), outliers, regarded as the benchmark for each of the seven methods in Scenarios 1 to 3. All the scenarios are based on the same 1000 data sets simulated assuming 177 genotypes and a marker effect variance of 0.2019.