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Supplemental Data**

**On Sharing Quantitative Trait GWAS Results in an Era of
Multiple-omics Data and the Limits of Genomic Privacy**

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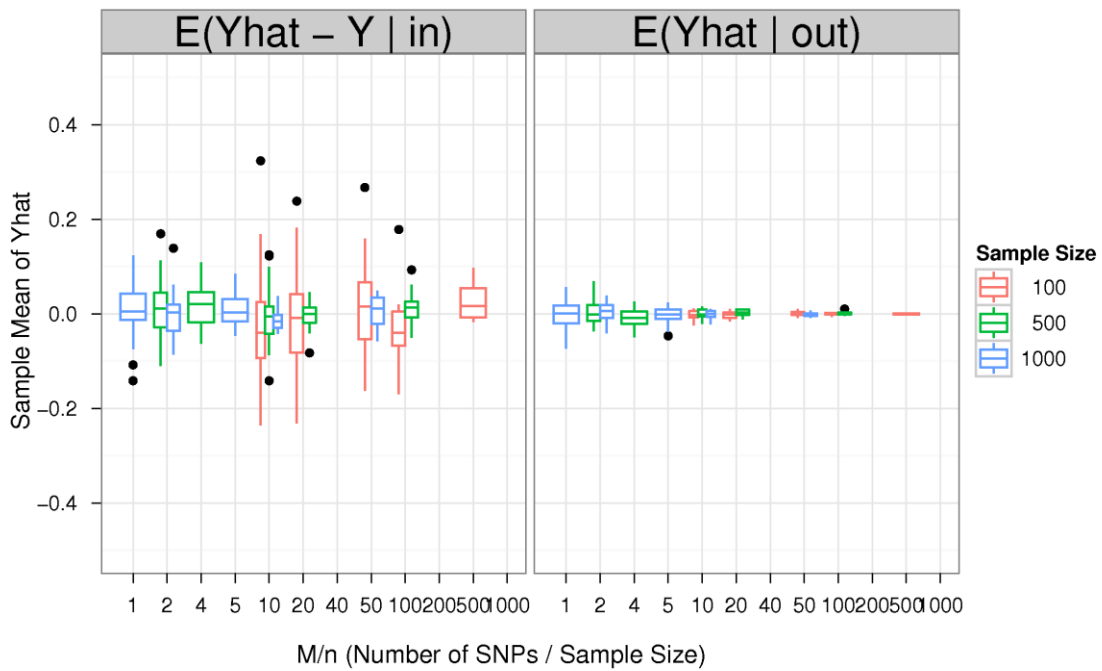


Figure S1. Simulated Sample Mean of \hat{Y} by Membership Status

This figure shows simulation results for twelve combinations of sample size and number of SNPs. Each simulation consisted of n test sample individuals ($n = 100, 500, 1000$) used to estimate regression coefficients and 1000 individuals as reference. For all simulations $\mu = 0$ and $\sigma = 1$. The left panel shows the average of $\hat{Y} - Y$ over all individuals in the test sample. Each box plot represents up to 50 independent simulations for given n and M . The right panel shows the average of \hat{Y} over all individuals in the reference sample. The box plots lie around zero consistent with what we would expect from the mean estimated in eq. 1.

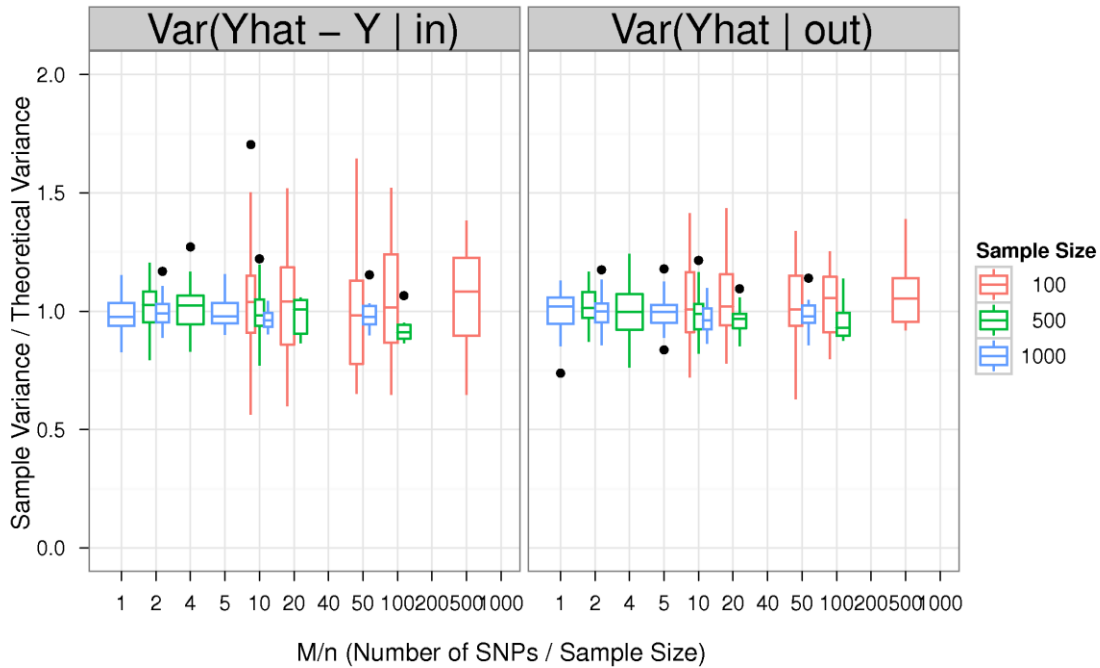


Figure S2. Sample Variance of \hat{Y} by Membership Status

For twelve combinations of sample size and number of SNPs we simulated genotypes and phenotypes. Each simulation consisted of n test sample individuals (100, 500, 1000) used to estimate regression coefficients and 1000 individuals as reference. This figure shows the sample variance of $\hat{Y} - Y$ (divided by the theoretical value) for individuals in the study and the sample variance of \hat{Y} (divided by the theoretical value) for reference individuals. The box-plots lie around 1 consistent with our calculations. Each box corresponds to an independent simulation. This figure shows simulation results for twelve combinations of sample size and number of SNPs. Each simulation consisted of n test sample individuals (100, 500, 1000) used to estimate regression coefficients and 1000 individuals as reference. For all simulations $\mu = 0$ and $\sigma = 1$. The left panel shows the sample variance of $\hat{Y} - Y$ (divided by the theoretical value) over all individuals in the test sample. The right panel shows the sample variance of \hat{Y} (divided by the theoretical value) over all reference individuals. The box plots lie around 1 consistent with our calculations in equation 1.