

Supplementary Information

Genome-wide variation in DNA methylation predicts variation in leaf traits in a foundational oak species

Figure S1

Results of separate principal component analyses (PCA) for SNP and methylation data in the CG, CHG, and CHH contexts. Shown are the first two principal components with the percentage of variance explained. Each label indicates an individual sample, with individuals coming from the same family represented by the same color. The sample labels indicate the provenance location, maternal tree ID, and progeny ID separated by periods.

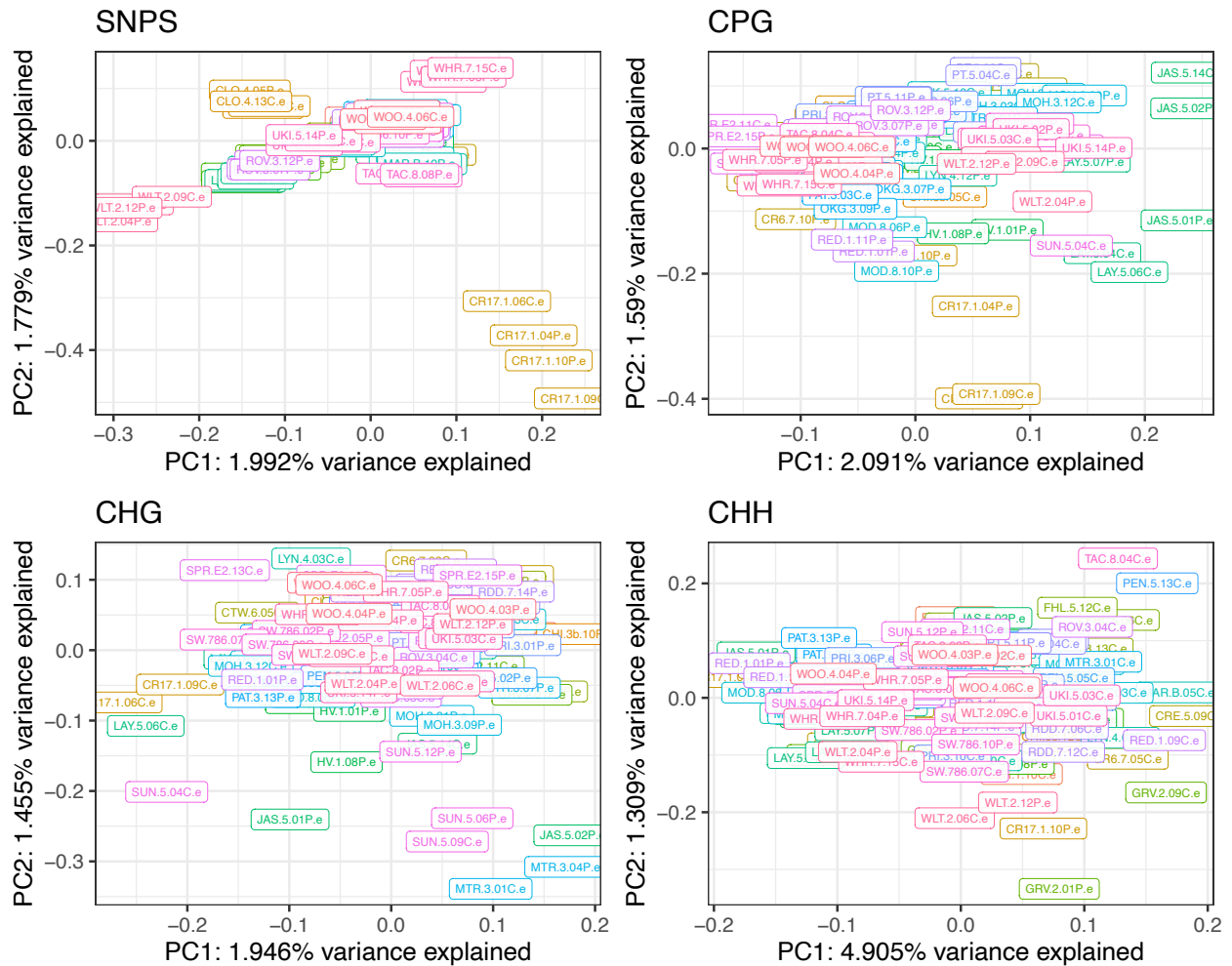


Figure S2

Estimated proportion of variance explained between simulated DNA methylation and simulated phenotypic data based on varying sample sizes and varying the true amount of variance explained by methylation and the true amount of variance explained by SNPs. At low sample sizes, there is large variation in the estimates of explained variance. Horizontal line shows the level of true variation explained by methylation.

