

Supplementary Figures

Fully efficient, two-stage analysis of multi-environment trials with directional dominance and multi-trait genomic selection

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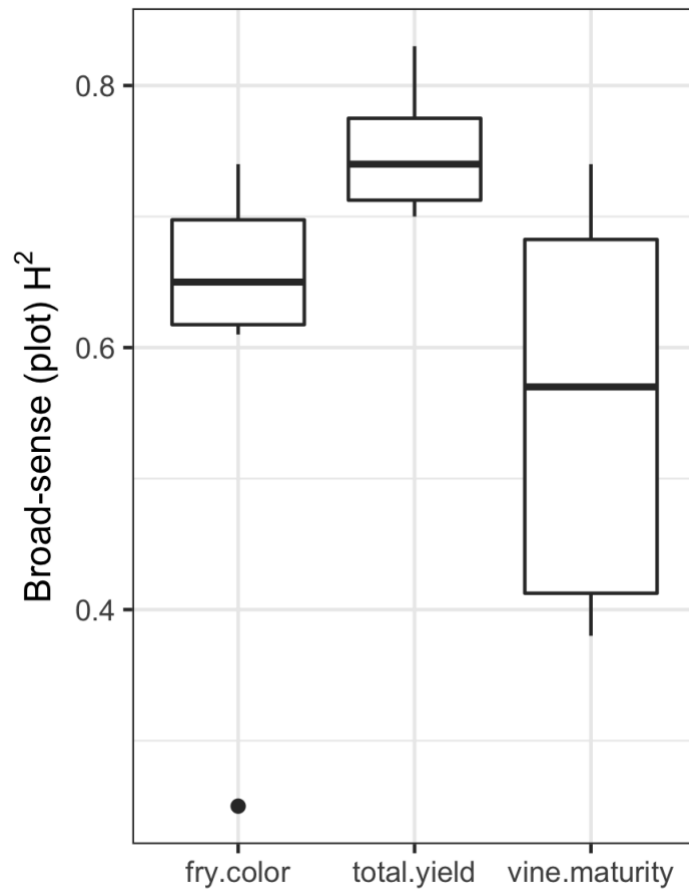


Figure S1. Distribution of the broad-sense heritability (plot basis) by year, from six years of potato yield trials at one location (Hancock, WI).

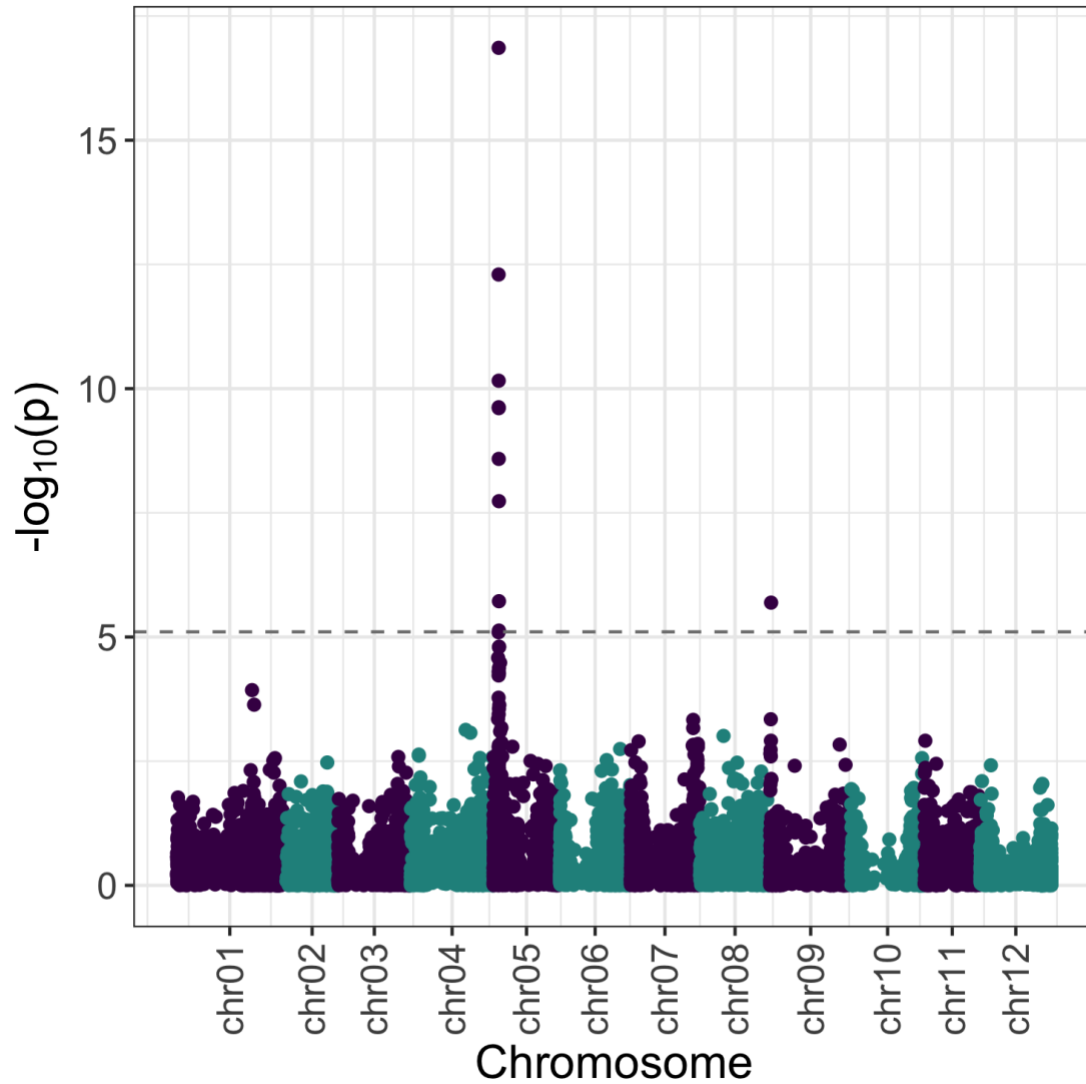


Figure S2. Genome-wide association results for potato vine maturity, using an additive model. The dashed line is the discovery threshold at significance level 0.05, corrected for multiple testing based on the effective number of markers.