

Supplemental Figures

Software for genome-wide association studies in autopolyploids and its application to potato

Rosyara et al.

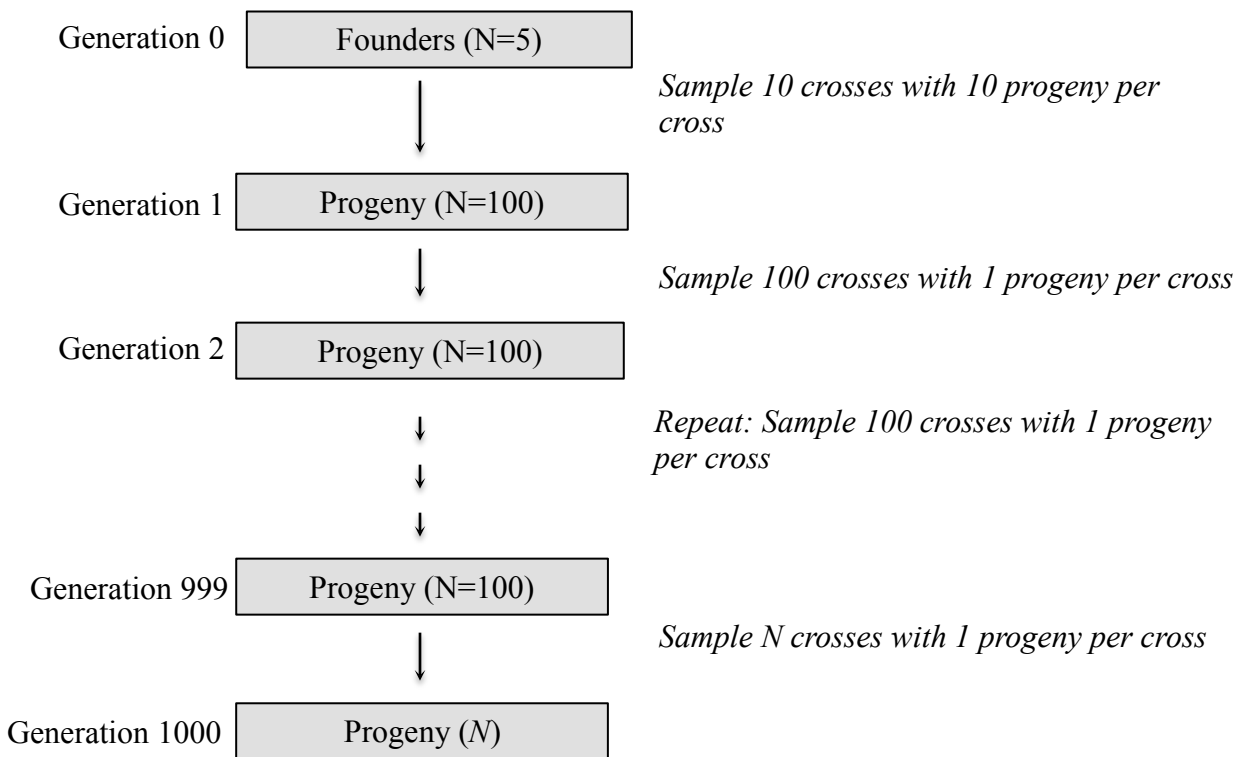


Figure S1. Scheme for generating simulated populations.

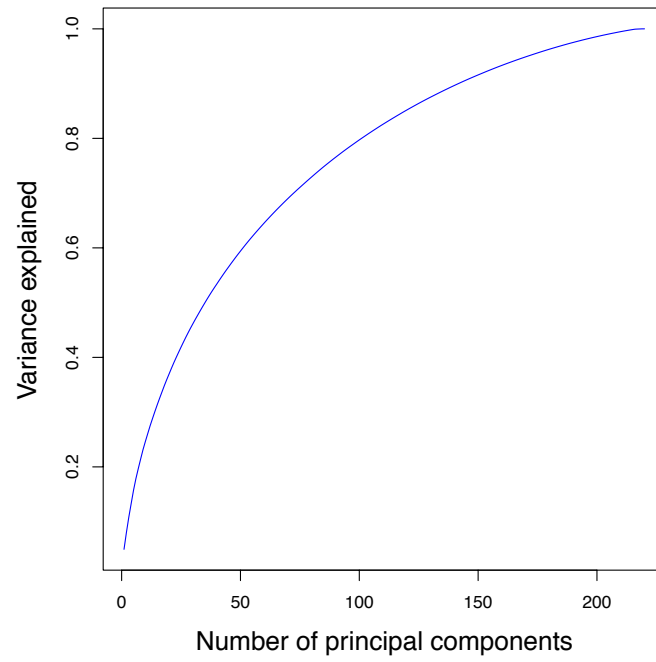


Figure S2. Cumulative proportion of variation for the SolCAP potato panel vs. number of principal components (PC).

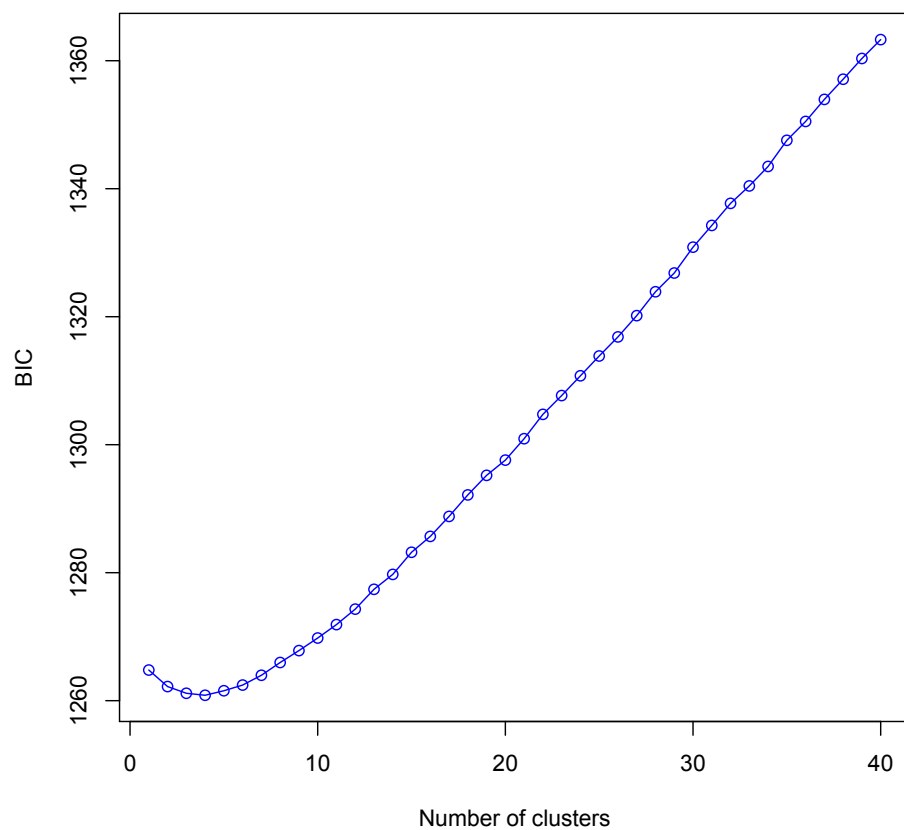


Figure S3. Bayesian Information Criteria (BIC) vs. number of clusters in k-means clustering.

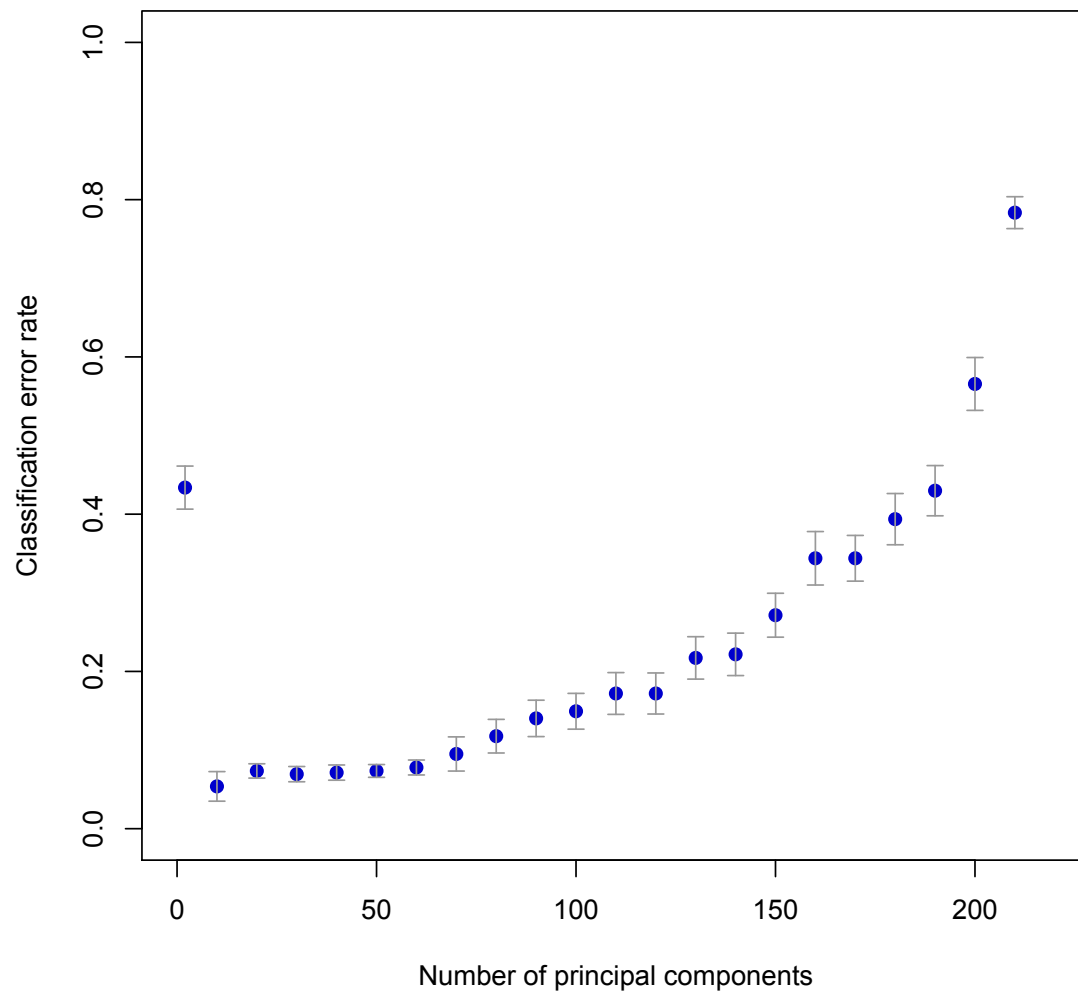


Figure S4. Classification error by LDA vs. number of principal of components (PC) for the potato diversity panel. The mean and ± 1 standard error based on 100 replicates are shown.

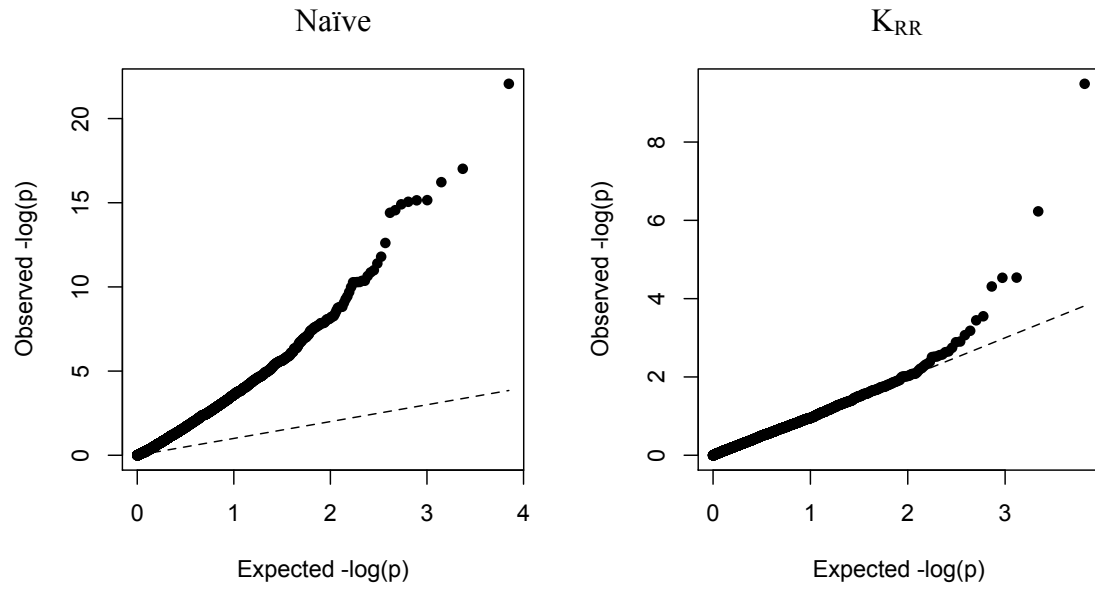


Figure S5. QQ plots comparing the inflation of p-values for the Naïve vs. K_{RR} model, using the additive marker model and the trait tuber shape in the SolCAP panel.

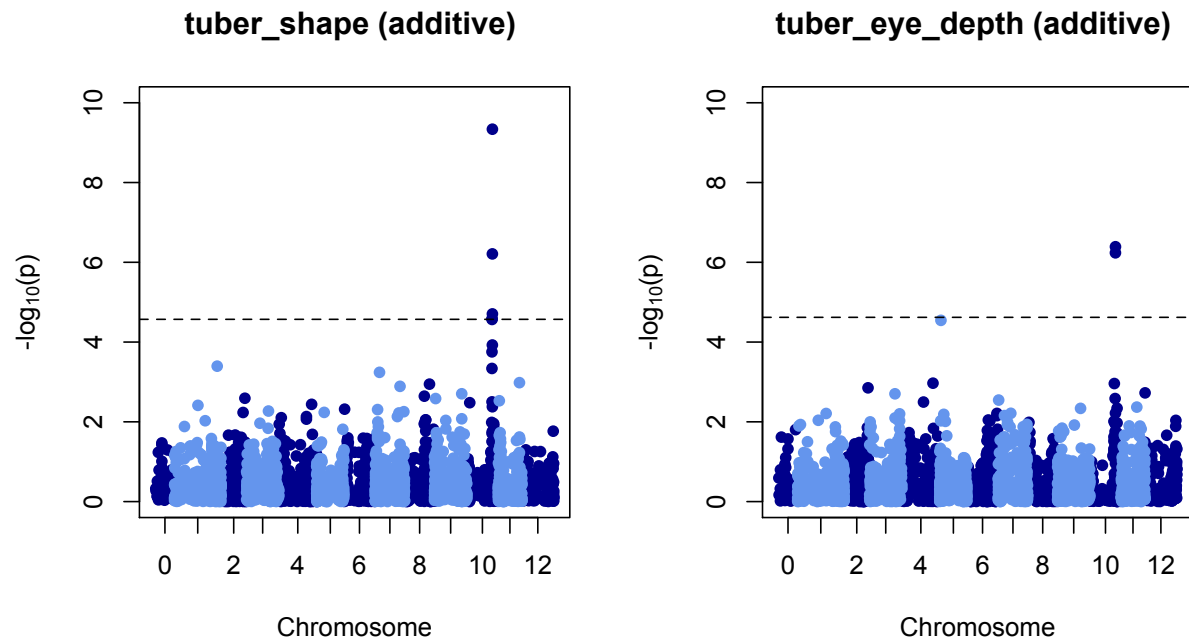


Figure S6. Manhattan plots for tuber shape and eye depth using the $Q_{DAPC} + K_{RR}$ model. Detection threshold (dashed line) is based on the permutation test (1000 replications).