

Supplemental Figures

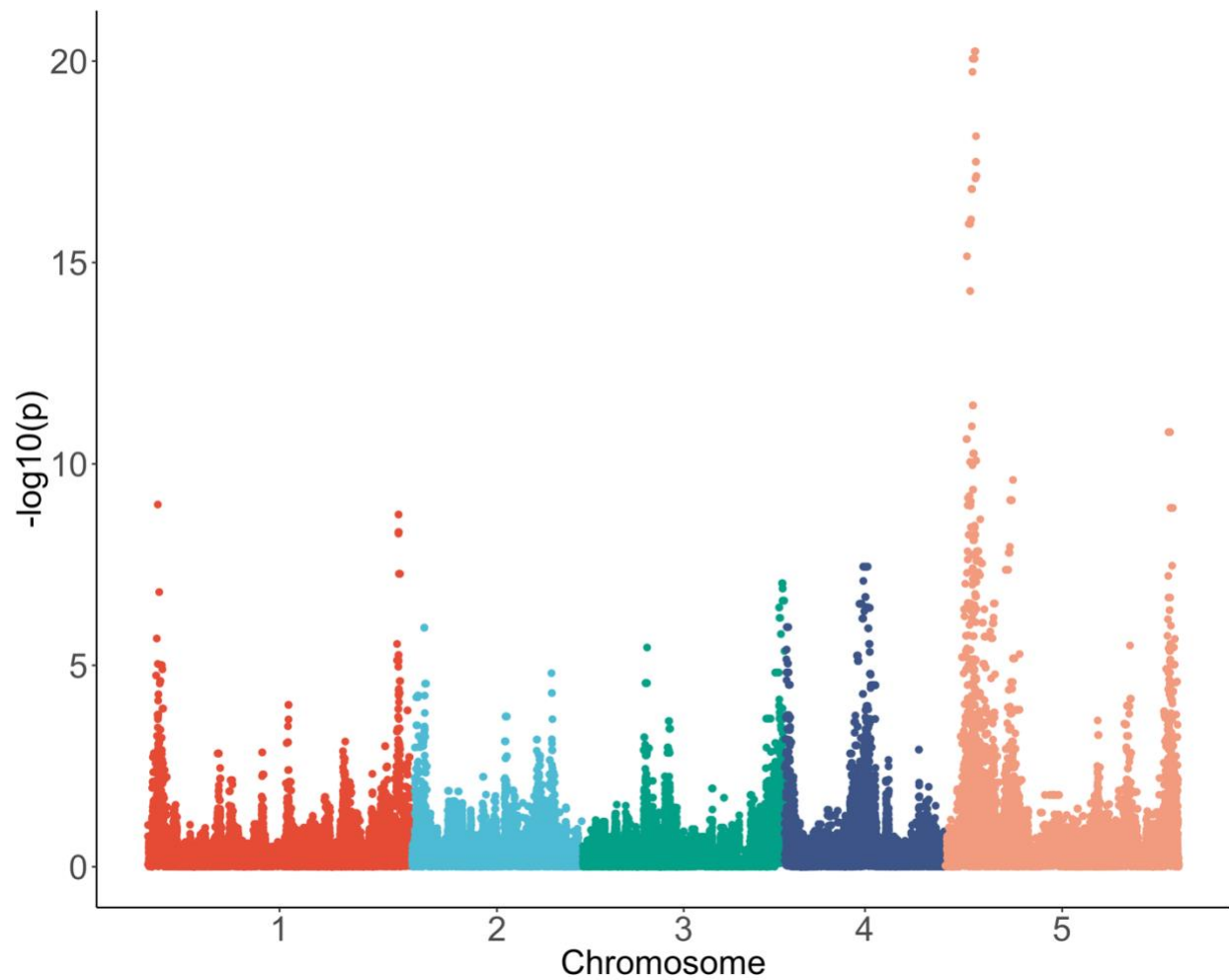


Figure S1: Manhattan plot of BD_SAR using the linear mixed model algorithm in GEMMA with a population covariate. Default settings for the linear mixed model method documented in the GEMMA manual were used.

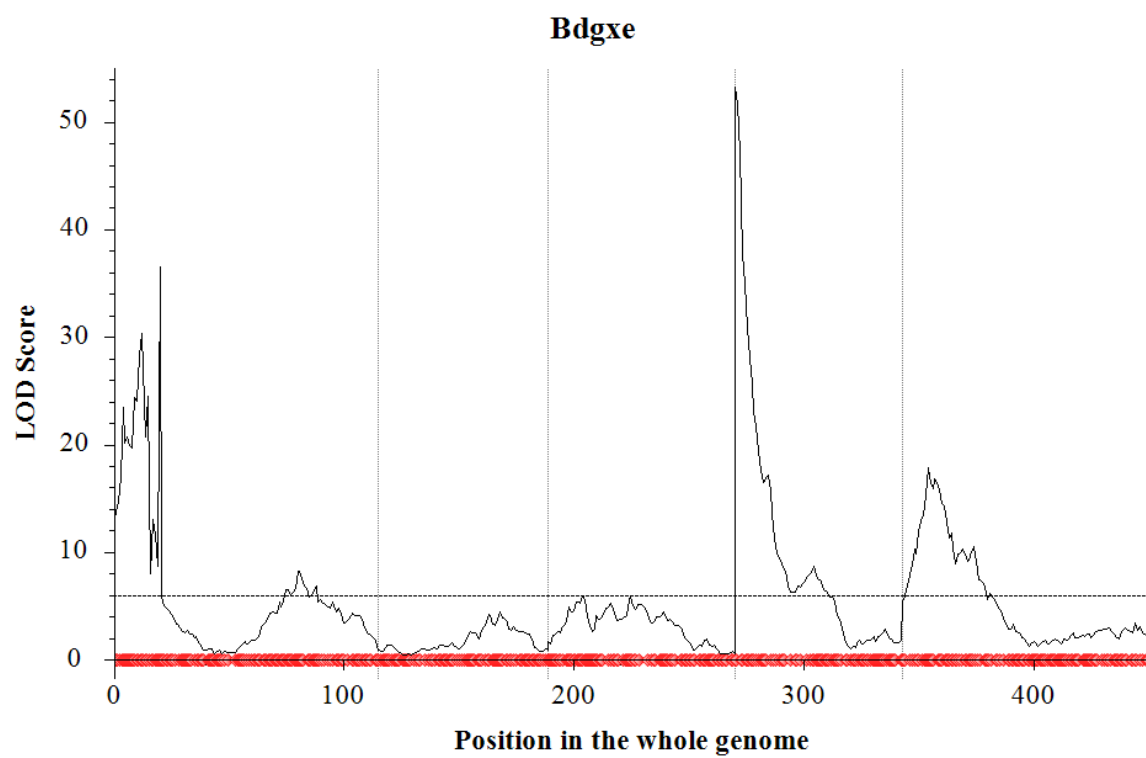


Figure S2: LOD plot of BD_SAR using the JICIM method in QTL IciMapping. We used the default settings for the JICIM method, with 1000 permutations to determine QTL significance.

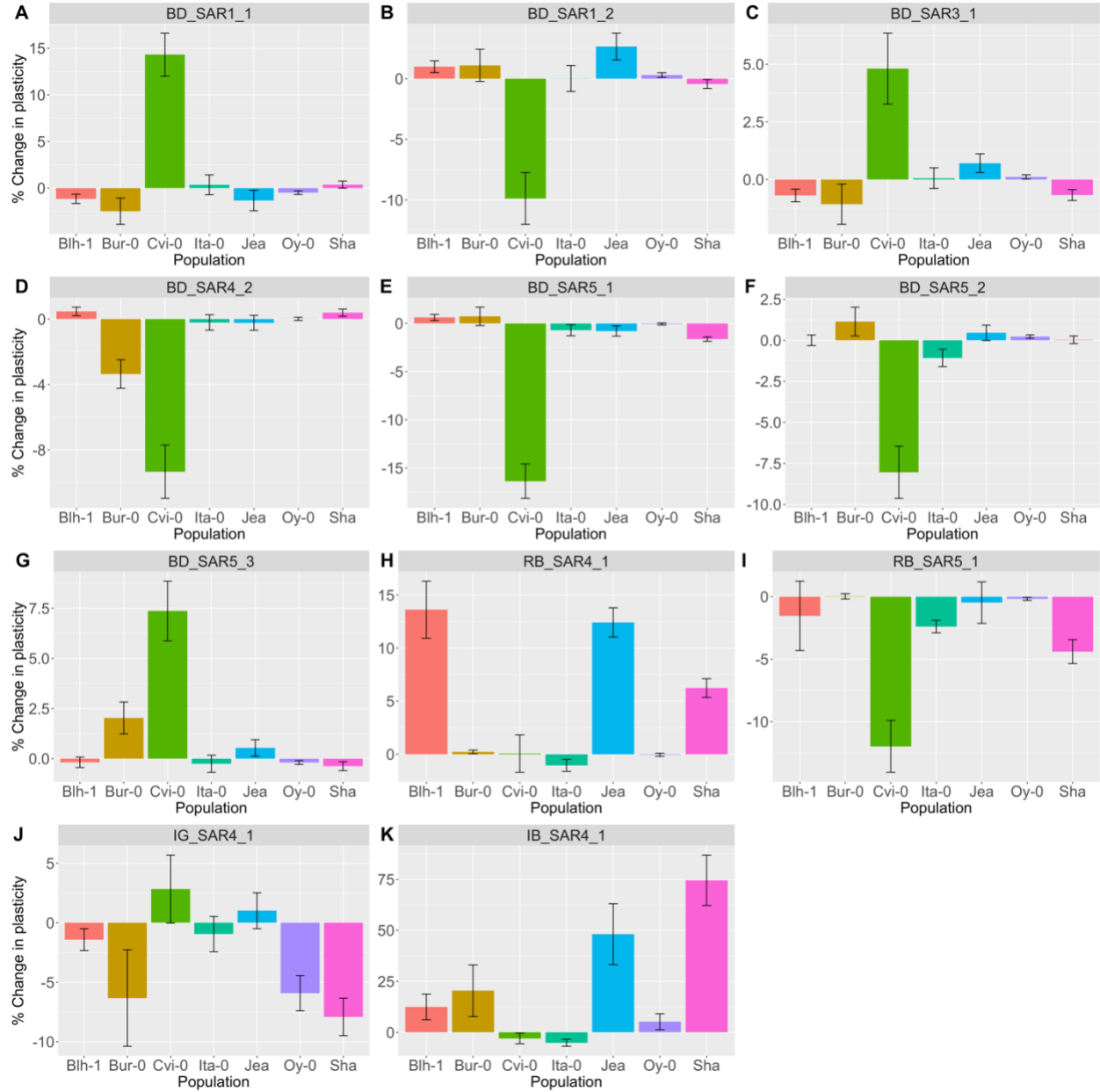


Figure S3: Allelic series among additional SAR QTL. The % change in plasticity relative to the Col-0 allele (allelic specific change in plasticity / average plasticity) are plotted for SAR QTL. Each panel represents a different SAR QTL (panel title). Bars represent one standard error of the estimated allelic substitution effect.