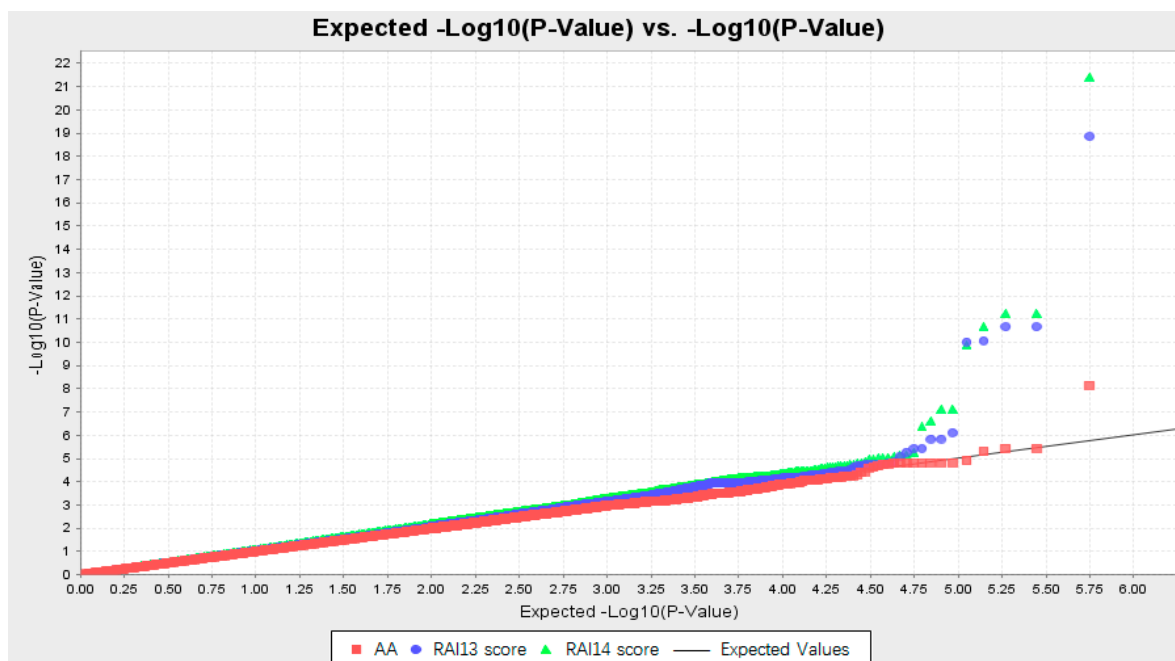
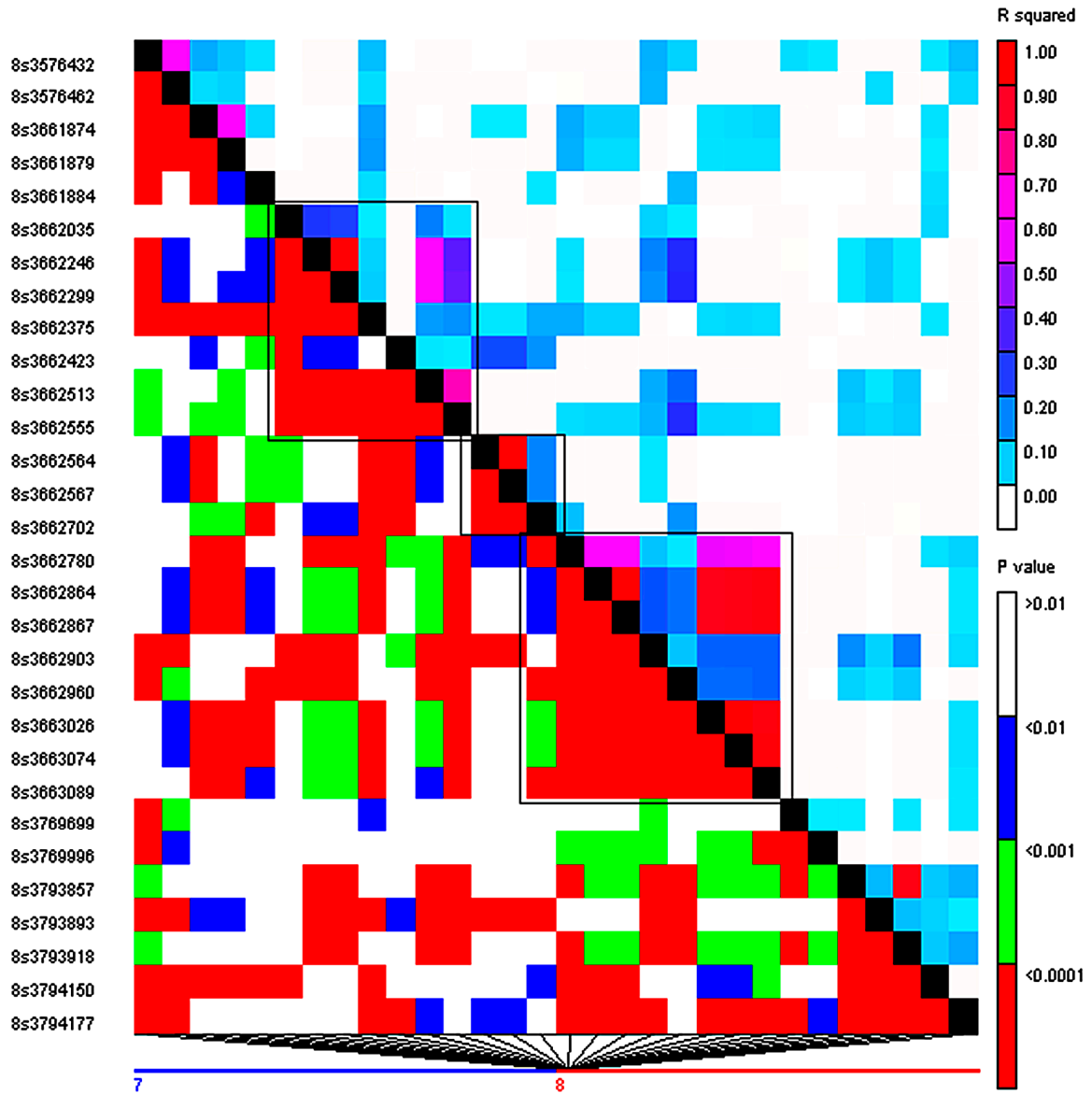


# Supplementary Materials: Confirmation and Fine Mapping of a Major QTL for Aflatoxin Resistance in Maize Using a Combination of Linkage and Association Mapping

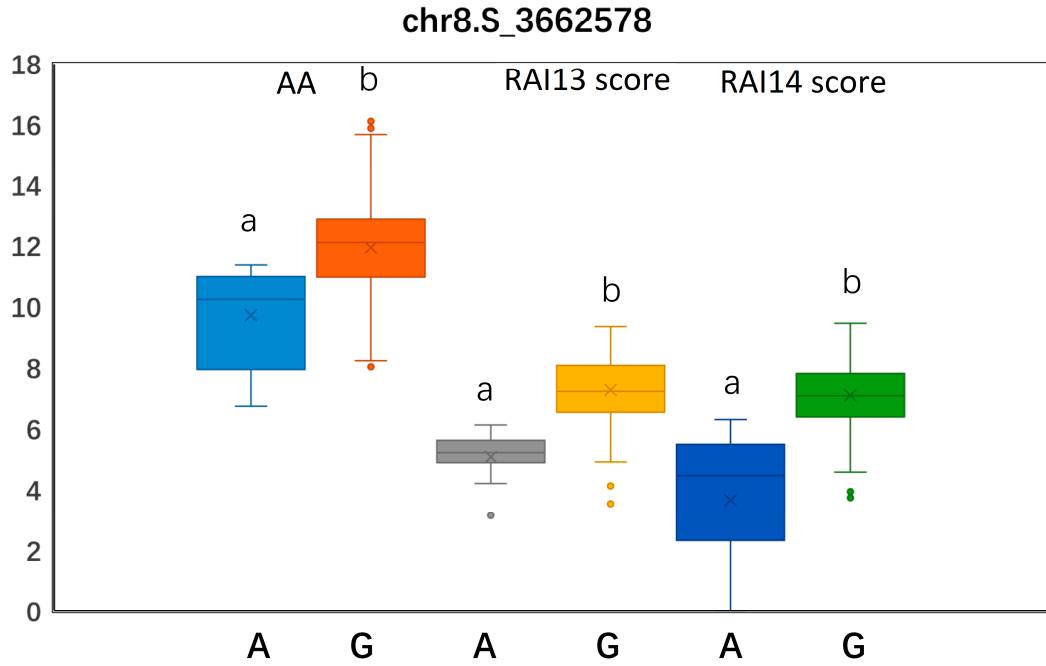
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**Figure S1.** Quantile-quantile (Q-Q) plots of estimated  $-\log_{10}(P)$ . Q-Q plots for the marker-trait association analysis for the AA and RAI score were generated using the GLM + Q method. The black line is the expected line under a null distribution. The observed  $P$  values for the AA and RAI score are represented by the indicated colours.



**Figure S2.** Linkage disequilibrium (LD) analysis using the  $r^2$  correlation between each marker within the association hot spots. Solid black lines represent the LD blocks.



**Figure S3.** The association between chr8.S\_3662578 marker allele polymorphisms and the AA and RAI score. Box plots for the AA (first two columns), RAI13 score (middle two columns) and RAI14 score (last two columns) in A-type and G-type maize inbred lines. The AA and RAI score of the G-type accessions were significantly higher than those of the A-type accessions (*t*-test:  $p = 7.73 \times 10^{-10}$ ,  $1.65 \times 10^{-21}$ , and  $2.97 \times 10^{-25}$  for AA, RAI13 score and RAI14 score, respectively).