

# Supplementary Figures: The genomic basis for short-term evolution of environmental adaptation in maize

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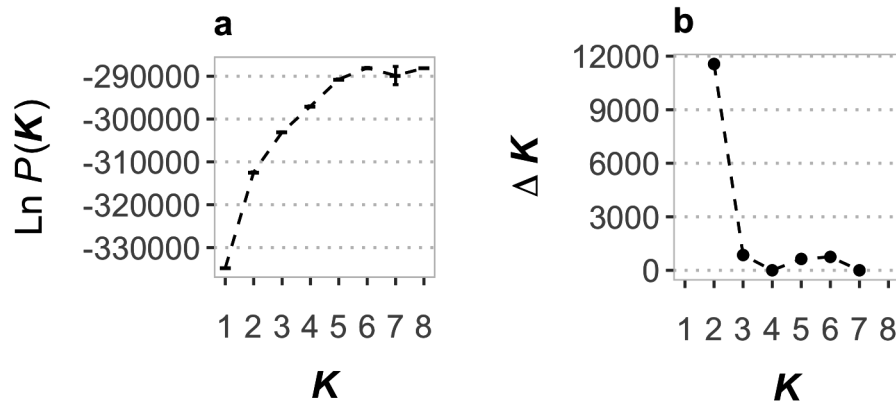


Figure S1: **Fit statistics for STRUCTURE across levels of  $K$ .** Values for  $\Delta K$  were estimated according to Evanno *et al.* (2005) Molecular Ecology 14:2611. The standard deviation from replicate runs is shown in (a).

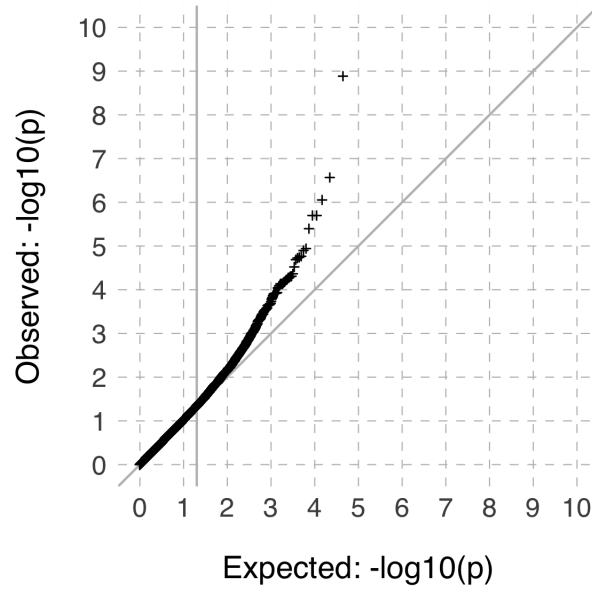


Figure S2: **QQ plot for GWA tests.**  $-\log_{10}(p)$  values for observed (y-axis) and expected (x-axis)  $p$ -values for K and K\_CHR based GWA methods. The vertical solid gray line corresponds to  $\alpha = 0.05$ .

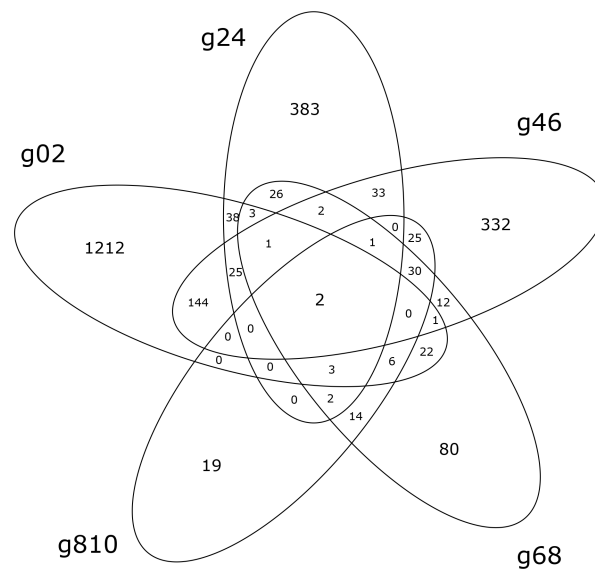


Figure S3: Venn diagram showing the number of shared SIM<sup>+</sup> markers detected in SIM tests between sequential pairs of generations.

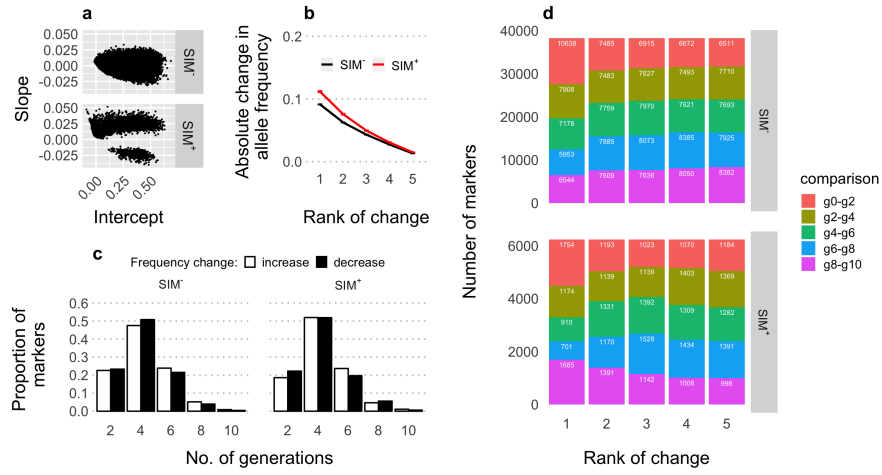


Figure S4: **Features of allele frequency change for SIM<sup>-</sup> and SIM<sup>+</sup> markers.** (a) Estimated slopes in allele frequency change across generations versus the corresponding intercept for the minor allele in  $g_0$ ; (b) Mean absolute change in allele frequency among the highest (rank 1) to lowest (rank 5) differences in allele frequency across sequential pairs of generations (i.e., independent of the generation pair, the mean among pairs of generations with the largest absolute allele frequency difference is shown at rank 1); (c) distribution for longest sequential generational runs of monotonic change in allele frequency; (d) number of markers in each pair of generations with the corresponding rank of change.

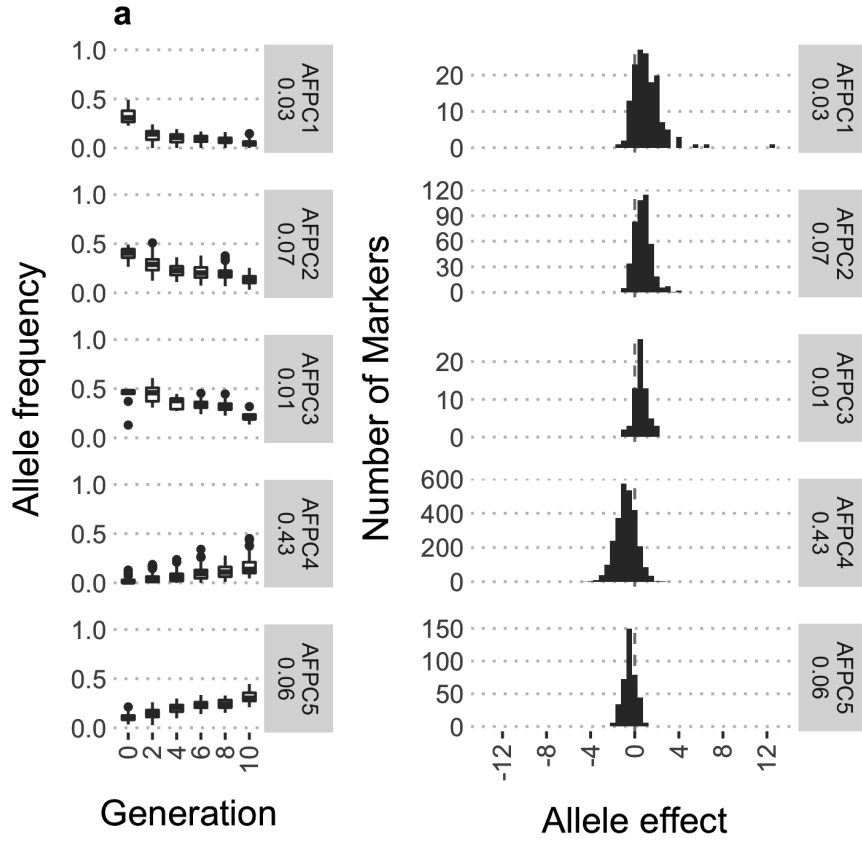


Figure S5: **Allele frequency profile clusters and corresponding distributions of additive allele effects.** (a) AFPCs 1 – 5; (b) AFPCs 6 – 10; (c) AFPCs 11 – 15. The left panels show box plots of allele frequencies per generation for  $\text{SIM}^+$  markers in the corresponding cluster. The right panels show histograms of additive allele effects for  $\text{SIM}^+$  in the corresponding cluster. Facet labels in indicate the AFPC identifier and the proportion of  $\text{SIM}^+$  markers belonging to the cluster.

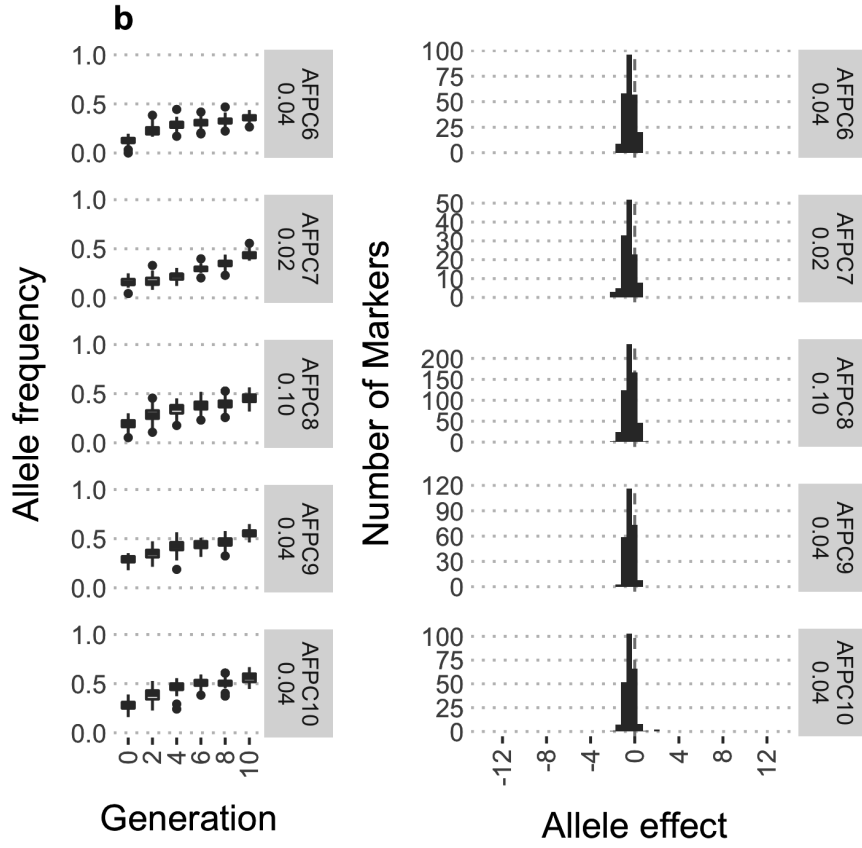


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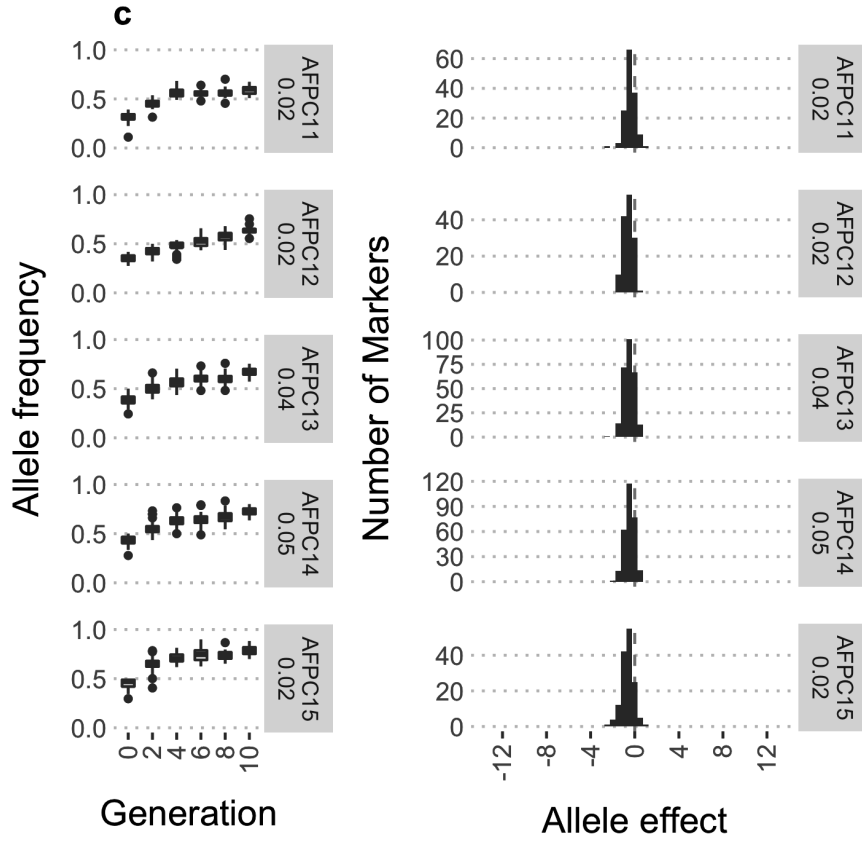


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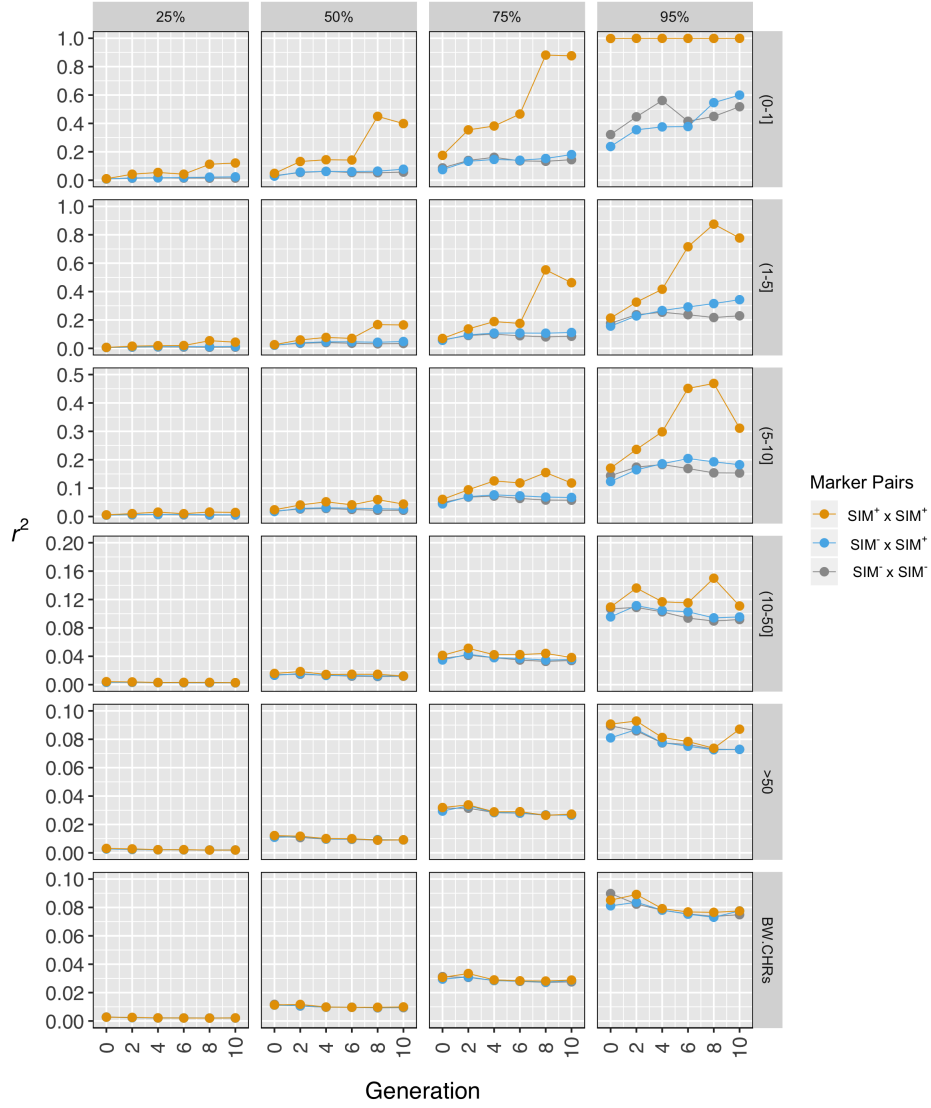


Figure S6: **Linkage disequilibrium within and between chromosomes.** Top facet labels indicate the percentile of the distribution for  $r^2$ . Right facet labels indicate the genetic distance interval for pairwise LD between markers within chromosomes, while "BW.CHRS" corresponds to pairwise LD between markers on different chromosomes.



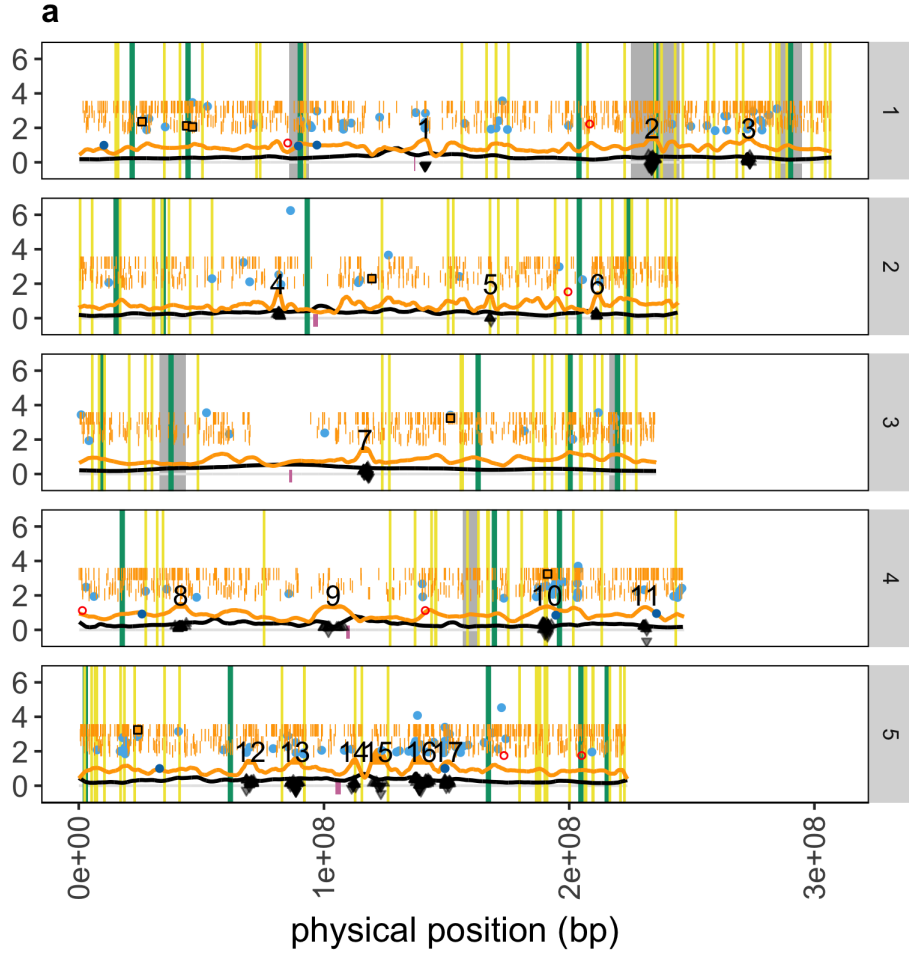


Figure S7: **Synthesis map.** Chromosomes (a) 1 – 5 and (b) 6 – 10. Multiple results are plotted on the physical map of each chromosome, with the y-axis corresponding to values for each of the following metrics: (i) kernel regression estimate of  $r^2$  for LD between sequential pairs of markers (black line); (ii) kernel regression estimate of  $-\log_{10}(q)$  for the SIM test (orange line: delimited  $\text{SIM}^+_{\text{regions}}$  are enumerated and encompass the orange shaded areas); (iii)  $-\log_{10}(q)$  value for  $\text{SIM}^+$  markers (orange vertical lines); (iv)  $-\log_{10}(q)$  value for complete-sweep  $\text{SIM}^+$  markers (orange filled box); (v) difference in observed heterozygosity between  $g_0$  and  $g_{10}$  for  $\text{SIM}^+$  markers in  $\text{SIM}^+_{\text{regions}}$  (black-filled triangles: pointing up if the change was positive and down if the change was negative); (vi)  $\log_{10}(\text{Bayes factor})$  values for  $\text{Bayenv}^+$  markers (cyan-filled points); (vii) bootstrap values for  $\text{FITR}^+$  markers (blue-filled points); (viii)  $-\log_{10}(q)$  value for  $\text{GWA}^+$  markers (red-outlined points); (ix) QTL previously identified for photoperiod sensitivity (gray shaded areas corresponding to QTL intervals) and flowering time per se (green vertical lines corresponding to QTL peaks); (x) candidate genes for flowering time (yellow vertical lines and labels); and (xi) centromeres (lilac-colored boxes).

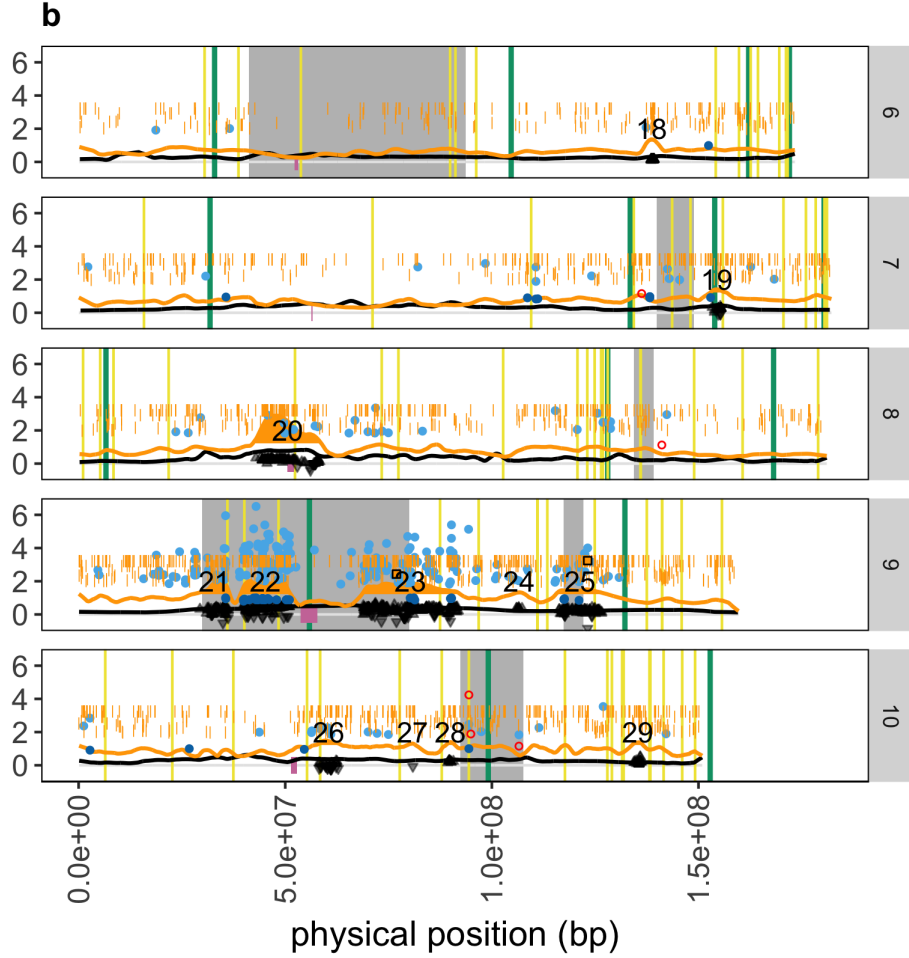


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