Genetic control of maize shoot apical meristem architecture

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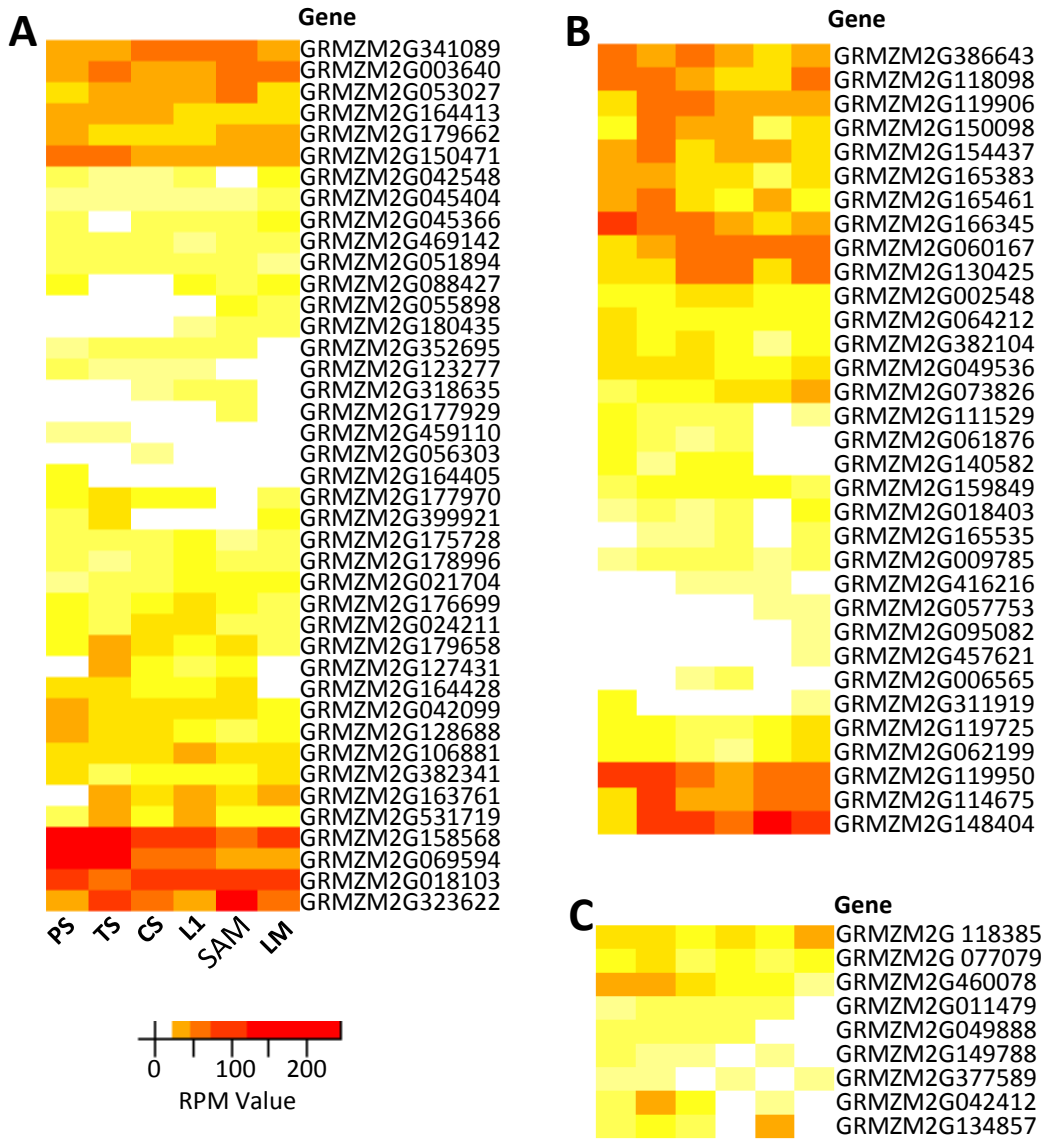

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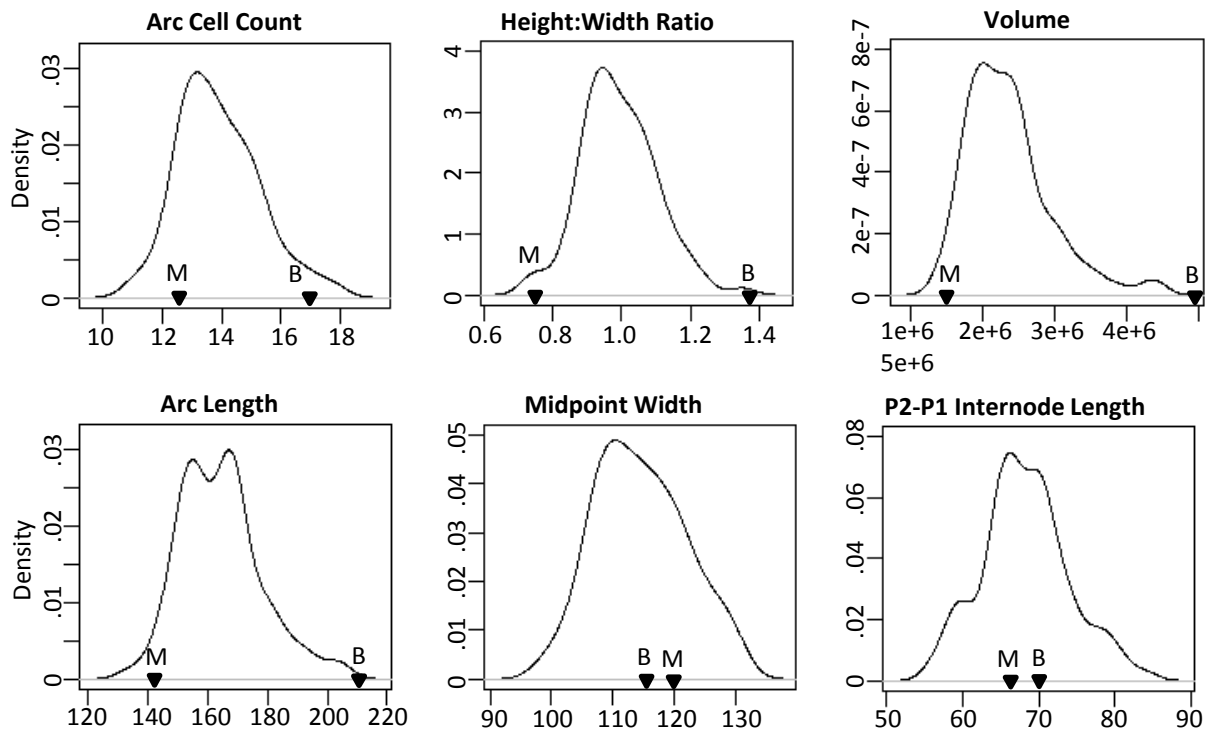
Figure S1   Density distributions of remaining SAM traits in the IBMRIL population. B73 and Mo17 are indicated as B and M, respectively.

Figure S2 Patterns of expression in candidate genes. Gene expression across SAM ontogeny for genes expressed in the B73 SAM and IBMRIL apices located under QTL with expression significantly correlated with SAM architecture (see Figure 5) for SAM height (**A**), width (**B**), and PIL (**C**). PS=Proembryo stage SAM, TS=Transition stage SAM, CS=Coleoptile stage SAM, L1=L1 SAM of 14-day seedling, SAM=SAM of 14-day seedling, LM=Lateral Meristem of 14-day seedling. Annotations, locations, and RPM values of genes are listed in Table S4.

Table S1   Genotypes used for IBM subset and NILs.

Table S2   SAM measurements for time course experiment

Table S3   Correlation values for SAM traits.

Table S4   SAM measurements for IBM RILs examined

Table S5   All QTL for SAM traits.

Table S6   SAM data for NILs examined

Table S7   Annotations, locations, and RPM values of genes in Figure S2.