Supplemental Figure 1: Phenotypic correlations between traits

Scatterplots of BLUEs demonstrate the positive correlation between traits, within populations. Pearson correlations are shown in the upper left.

Supplemental Figure 2: Haplotypes for six representative UW-SS-MAGIC lines

Lines in the top row are from Subset A, and each have 60 crossovers. Lines in the bottom row are from Subset B, and each have 103 crossovers. Genomic areas plotted in white did not have a founder probability rise above 50% in that region.

Supplemental Figure 3: QTL mapping and GWAS for flowering time

(A) Anthesis GDU QTL peaks and SNP association results in the *per se* population. (B) Silking GDU QTL peaks and SNP association results in the *per se* population.

Supplemental Figure 4: QTL mapping and GWAS for plant and ear height

(A) Plant height QTL peaks and SNP association results in the *per se* population. (B) Ear height QTL peaks and SNP association results in the *per se* population.

Supplemental Figure 5: All significant QTL identified for flowering time and plant height

Significant loci are plotted for flowering and height traits for the *per se* population, SS-3IIH6 hybrid population, and SS-PHJ89 hybrid populations. Previously characterized flowering and height loci are plotted as dashed vertical lines. To declare two significant loci under one large QTL peak, the LOD score was required to drop by at least five. Portions of the figure shaded in gray indicate the end of the chromosome, such that the physical distance of each chromosome is plotted on the white background.

Supplemental Figure 6: Founder plant height BLUP effects

QTL BLUP effects with +/- 2 standard errors at the most significant locus for SS-3IIH6 plant height in the *per se*, SS-3IIH6, and SS-PHJ89 populations on chromosomes six. This QTL was not significant in the *per se* or SS-PHJ89 populations.

Supplemental Figure 7: Observed vs predicted phenotypes and discard accuracy

(A) Scatterplot of observed vs predicted anthesis GDU for the *per se* population. To select for adaptation to Wisconsin, our breeding program discards the latest lines of a population. Lines in the top 15% of both observed and predicted anthesis values (i.e. flower the latest) are colored in green, lines that flower in the latest 15% of predicted values are plotted in pink, and lines that flower in the latest 15% of observed values are plotted in blue. Color is recorded for each DH line name. (B) Using the DH line color scheme from A, the hybrid phenotypes are plotted for SS-3IIH6 and SS-PHJ89. (C) Scatterplot of observed vs predicted plant height for the *per se* population. Our breeding program discards the tallest members of the population. Lines are colored in the same manner as Panel A. (D) Using the DH line color scheme from C, the hybrid phenotypes are plotted for SS-3IIH6 and SS-PHJ89.

Supplemental Figure 8: Box plots for each *per se* digenic class for two flowering time loci

The study of epistasis is difficult due to low sample sizes of each digenic class. Each panel represents a digenic class for the two most significant *per se* anthesis GDU loci on chromosomes three and eight. The population wide mean is plotted as a red dot on each panel. Sample size for each class is in the lower left corner.

Supplemental Figure 9: Bar plots for each SS-3IIH6 digenic class for two plant height loci

The study of epistasis is difficult due to low sample sizes of each digenic class. Each panel represents a digenic class for two significant SS-3IIH6 plant height loci on chromosomes one and six. The population wide mean is plotted as a red dot on each panel. Sample size for each class is in the lower left corner. Some digenic classes have no observed individuals.