Supplemental Fig. 1. Graphical display of population substructure for 627 lines with restricted phenology at variable population numbers (n=2, 3, 4, 5, 6, 7, 8, 9, and 10). There are 411 genotypes unique to this diversity panel and 216 from the Goodman-Buckler Diversity Set included in this diversity panel that have genotypic data. Population substructure was determined using STRUCTURE (Pritchard et al., 2000) with 511 unbiased SNP markers.

Supplemental Table 1. Maturity grouping, population substructure grouping, and pedigree information for 1411 diverse inbred lines. Population substructure was determined using STRUCTURE (Pritchard et al., 2000) with 511 unbiased SNP markers. 627 of these inbred lines were included in this diversity panel. The reason for discarding for the remaining 784 lines is provided.

Supplemental Table 2. Genetic and pedigree relationship matrix for 689 diverse inbred lines. There are 411 genotypes unique to this diversity panel, 216 from the Goodman-Buckler Diversity Set included in this diversity panel and 62 lines from the Goodman-Buckler Diversity Set not included in this diversity panel. Genetic relationships are above the diagonal and pedigree relationships are below the diagonal. Genetic relatedness was calculated as 1 minus the pair-wise Rogers dissimilarity distance (Rogers, 1972) based on 511 unbiased SNP markers. Pedigree relationships were calculated using a modified tabular method for calculating coefficients of coancestry that takes into account full inbreeding of individuals and unequal parental contributions. If lines were derived from sources of unknown origin or open pollinated populations, the parental contribution from that source was considered zero.