Figure S1 Reliability of the predictions of Tass_GDD6 using different sampling algorithms on the Dent panel (A) and the Flint panel (B) using a λ value corresponding to an heritability of 0.5. The calibration sets were randomly sampled, or defined by: maximizing CDmean with a relationship matrix based on the IBS or weighted by the allelic frequencies; minimizing PEVmean with a relationship matrix weighted by the allelic frequencies; minimizing the mean (Amean) or the maximum (Amax) of the relationship coefficient between the reference individuals. The individuals that are not in the calibration set are in the validation set. As a consequence for each calibration set size the reliability is calculated with a different number of individuals. For each point, the vertical line indicates an interval of $2\sigma_R$ (σ_R being the standard deviation of observed reliabilities over the 50 runs).
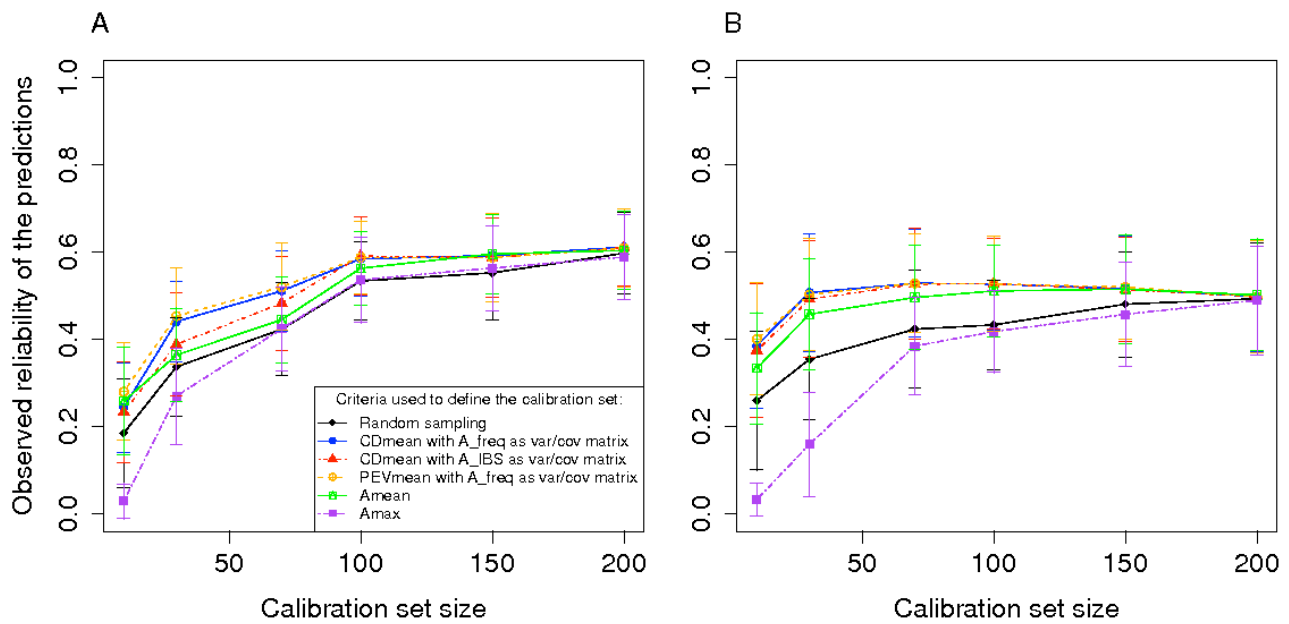
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Figure S2 Cross-validation on the predictions of flowering time using different sampling algorithms in the Dent panel (A) and the Flint panel (B). In a first step 30 individuals are randomly sampled to constitute the validation set. In a second step calibration sets are sampled from the remaining individuals using different approaches to optimize the prediction reliability of the validation set. These calibration sets were randomly sampled, or defined by: maximizing CDmean with a relationship matrix based on the IBS or weighted by the allelic frequencies; minimizing PEVmean with a relationship matrix weighted by the allelic frequencies; minimizing the mean (Amean) or the maximum (Amax) of the relationship coefficient between the reference individuals. For each point, the vertical line indicates an interval of $2\sigma_R$ (σ_R being the standard deviation of observed reliabilities over the 50 runs). Optimization of PEVmean and CDmean was made with $h^2=0.95$.

File S1   Genotype and Phenotypes of the Dent lines

&

File S2   Genotype and Phenotypes of the Flint lines

Available for download at http://www.genetics.org/lookup/suppl/doi:10.1534/genetics.112.141473/-/DC1.

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