



**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  $2\sigma_R$  ( $\sigma_R$  being the standard deviation of observed reliabilities over the 50 runs). Optimization of PEVmean and CDmean was made with  $h^2=0.95$ .