

Figure S5

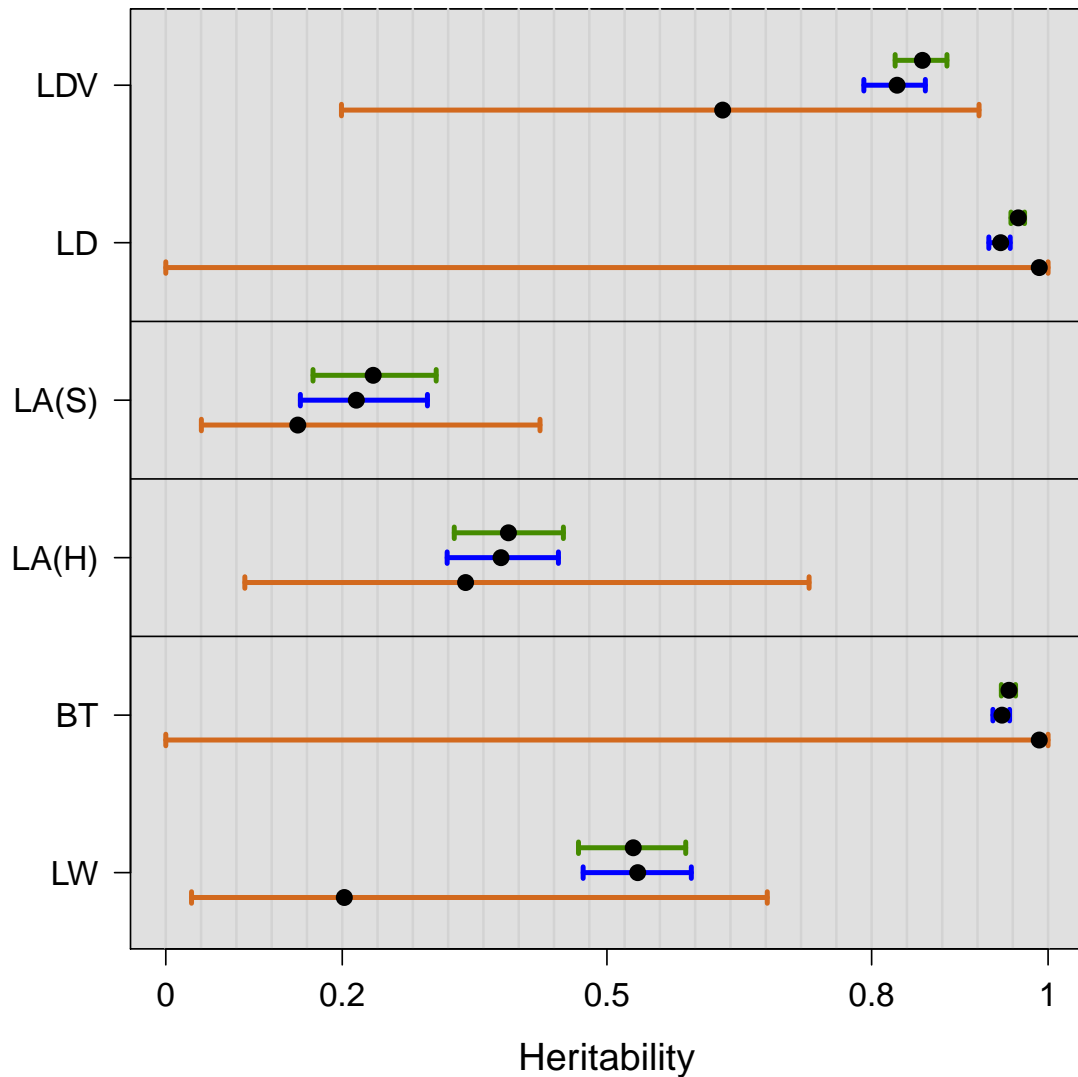


Figure S5 : **Heritability estimates and confidence intervals for two flowering traits from [3] (LDV and LD), and 4 traits from new experiments.** Three estimators were used: the ANOVA-based estimator of broad-sense heritability ( $\hat{H}^2$ , green), the marker-based estimator using individual plant data ( $\hat{h}_r^2$ , blue) and the marker-based estimator using genotypic means ( $\hat{h}_m^2$ , brown). Traits from different experiments are separated by the black horizontal lines. Trait abbreviations are given in Table 1 of the main text. The LD-adjusted kinship matrix was computed using version 2.0 of the LDAK-software [12]. We used sections of 1000 SNPs, with a buffer of 200. The maximum distance considered for LD was 250kb; the 'half-life' parameter (modeling LD-decay) was set to 20kb.