Table S4

Table S4: : **Heritability estimates and confidence intervals, for two flowering traits from [3] and four traits measured in new experiments (trait abbreviations given in Table 1 of the main text).**

trait	replicates	means	broad-sense
LDV	0.829 (0.791,0.861)	0.631 (0.199,0.922)	0.858 (0.827,0.885)
LD	0.946 (0.933,0.957)	1.000 (0.000,1.000)	0.966 (0.958,0.973)
LA(S)	0.216 (0.153,0.297)	0.150 (0.040,0.424)	0.235 (0.167,0.306)
LA(H)	0.380 (0.319,0.445)	0.340 (0.090,0.729)	0.388 (0.327,0.451)
BT	0.948 (0.937,0.956)	1.000 (0.000,1.000)	0.956 (0.947,0.963)
LW	0.535 (0.473,0.596)	0.202 (0.029,0.682)	0.530 (0.468,0.589)

Three estimators were used: mixed model based on replicates ($\hat{h}^2_r$), mixed model based on genotypic means ($\hat{h}^2_m$), and the usual ANOVA-based broad-sense heritability estimator ($\hat{H}^2$). An LD-adjusted kinship matrix was used in the mixed model for $\hat{h}^2_r$ and $\hat{h}^2_m$.

The LD-adjusted kinship matrix was computed using version 2.0 of the LDAK-software [12], available at `http://dougspeed.com/ldak/`. We used sections of 1000 SNPs, with a buffer of 200. The maximum distance considered for LD was 250kb; the 'halflife' parameter (modeling LD-decay) was set to 20kb.