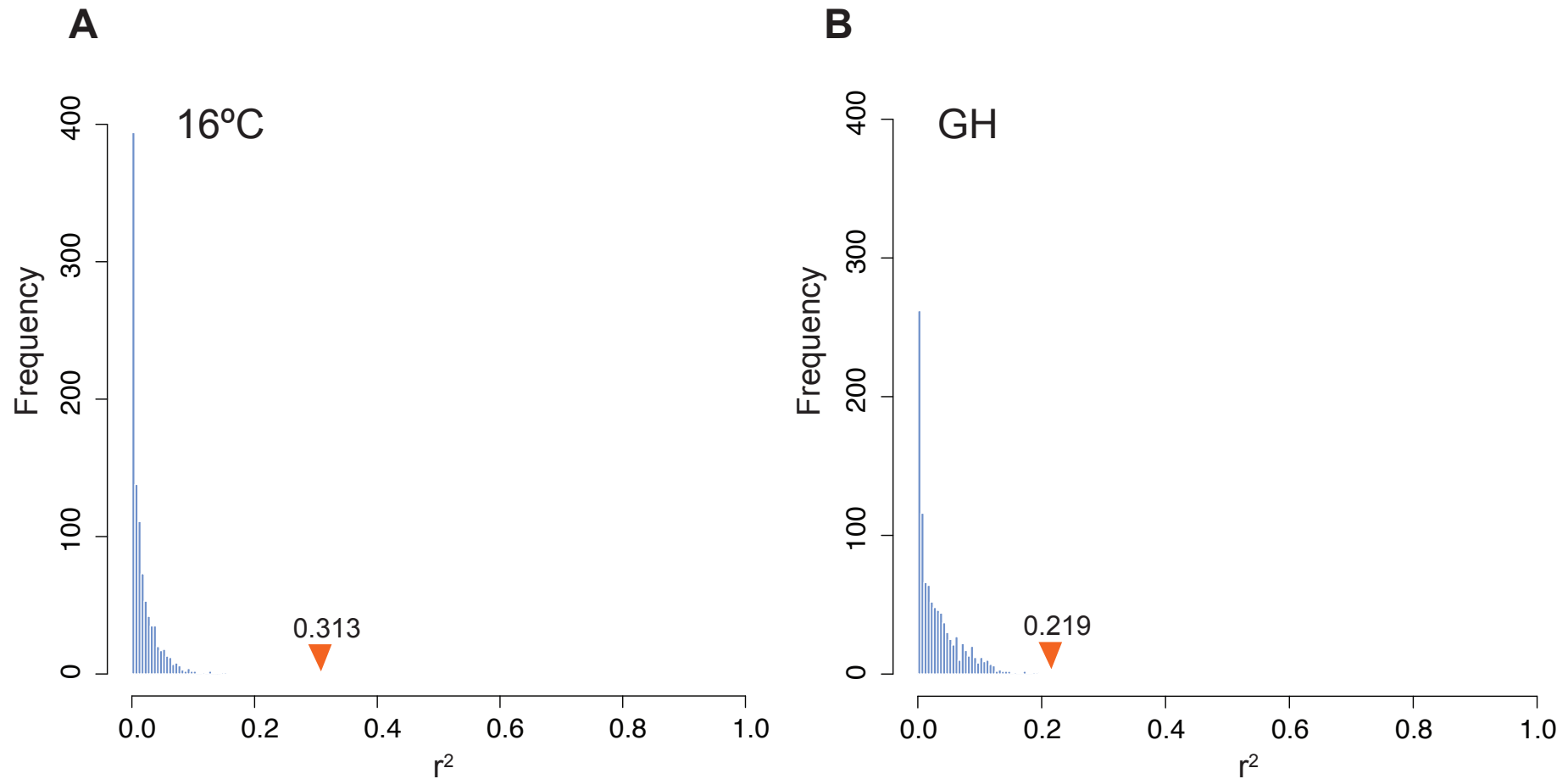


Supplemental figure 1. GWAS and QQ plots for flowering time and the *FLC* expression at 16°C and greenhouse. The single-trait models for flowering time (A, C) and *FLC* expression (B, D). A-B are 16°C, and C-D are a greenhouse. Gray horizontal lines show threshold (p -value < 0.05 with Bonferroni collection) and orange arrows in A and C show *a priori* flowering time genes identified in the previous study (Sasaki et al., 2015). The arrows in B and D are corresponding to A and C, respectively.



Supplemental figure 2. Permutation test for the predictions of flowering time under 16°C and a greenhouse. Orange arrows show r^2 that was estimated by observed flowering time (BLUE) and the predicted flowering time. For permutation tests, the flowering time phenotypes were randomized and transformed to BLUE with keeping genetic background effects using the IBS matrices (1000 times).