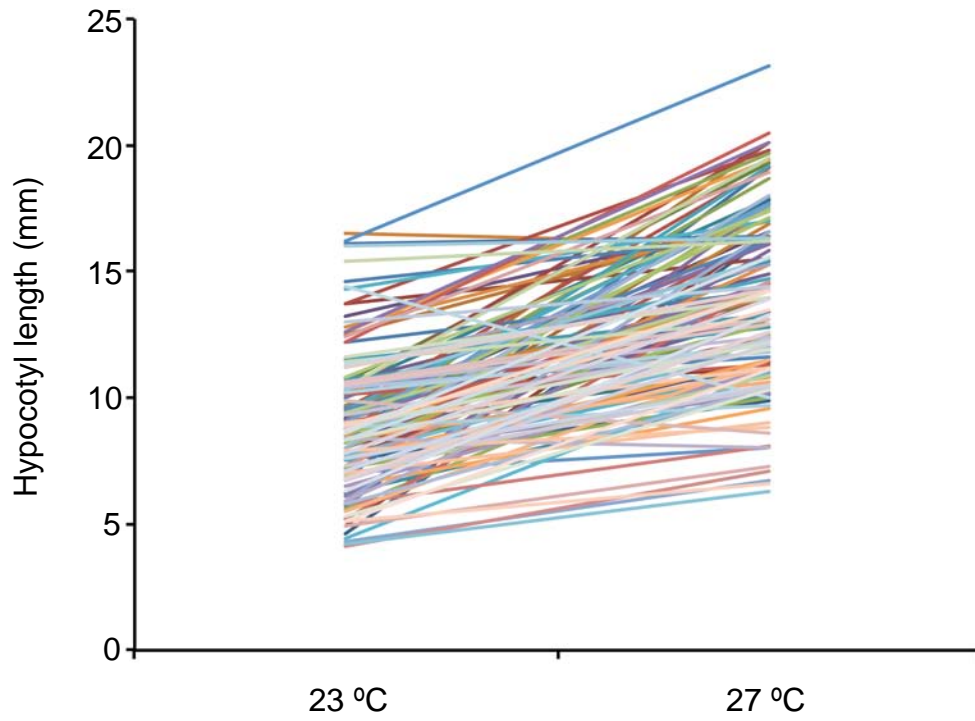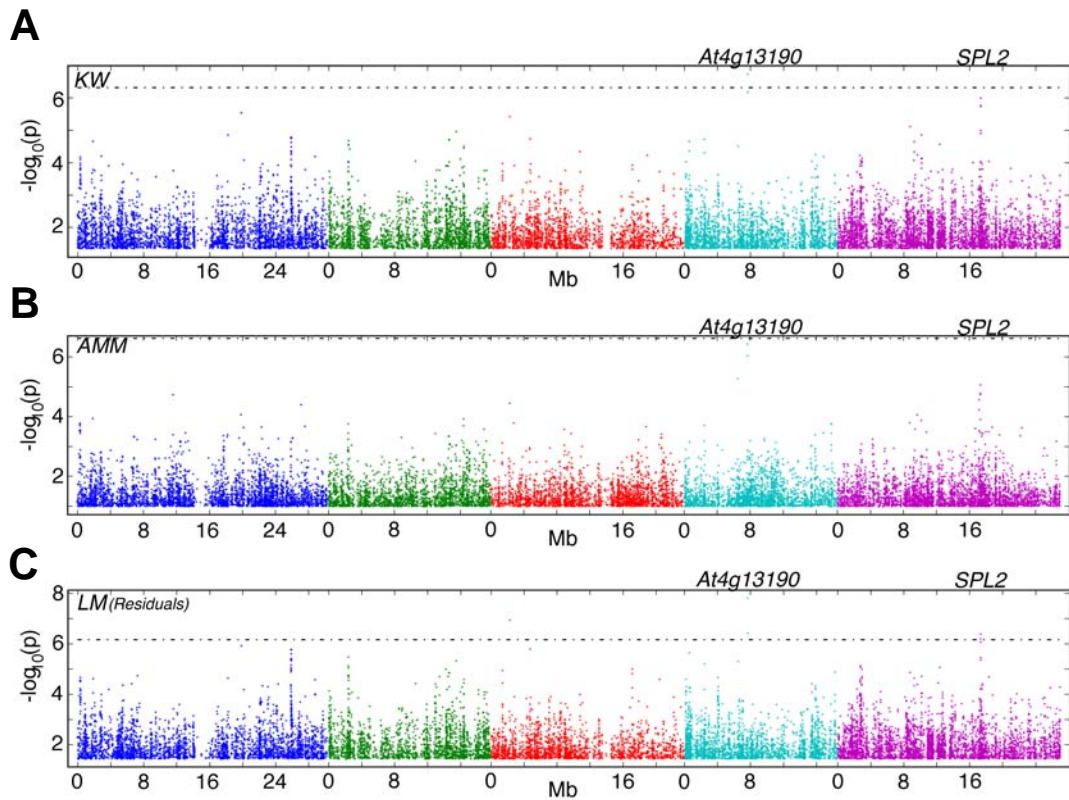# Supplementary Figure S1


Supplementary Figure S1. Reaction norms that represent thermal response across all the analysed strains.
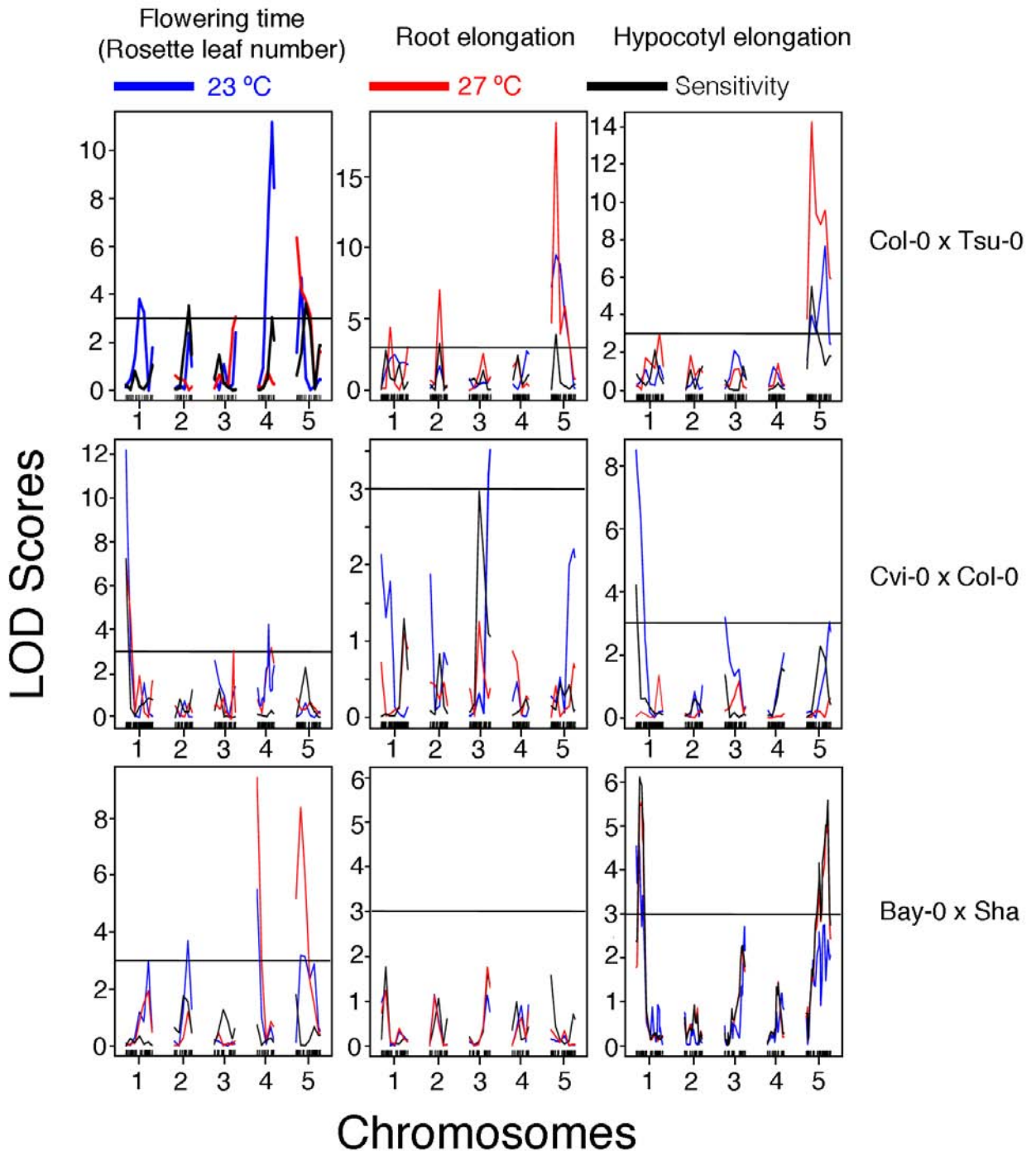
Supplementary Figure S2

Supplemental Figure S2. Genome-wide association analysis of temperature sensitivity in hypocotyl elongation. Manhattan plots of GWAS results across world -wide collection of Arabidopsis accessions using the KW (A) or the AMM (B) methods. The sensitivity was calculated as the slope of the reaction norms. Alternatively, residuals of a regression analysis of hypocotyl lengths at 23 ºC and 27 ºC were also used as a measure of temperature sensitivity (C), which also identified the same loci. All the analysis was done using GWAPP.

Supplementary Figure S3
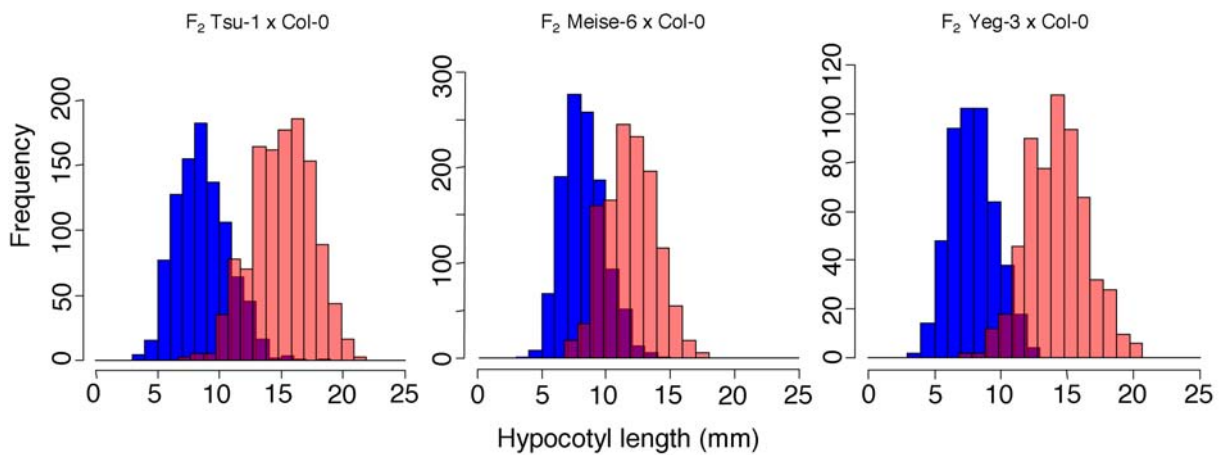
Supplemental Figure S3. Frequency distributions of hypocotyl lengths for F_2 populations derived from strains with reduced temperature sensitivity (Tsu-1, Meise-6 and Yeg-3) and Col-0. The measurements are from 9-day old F_2 seedlings grown at 23 ºC (blue) and 27 ºC (red).
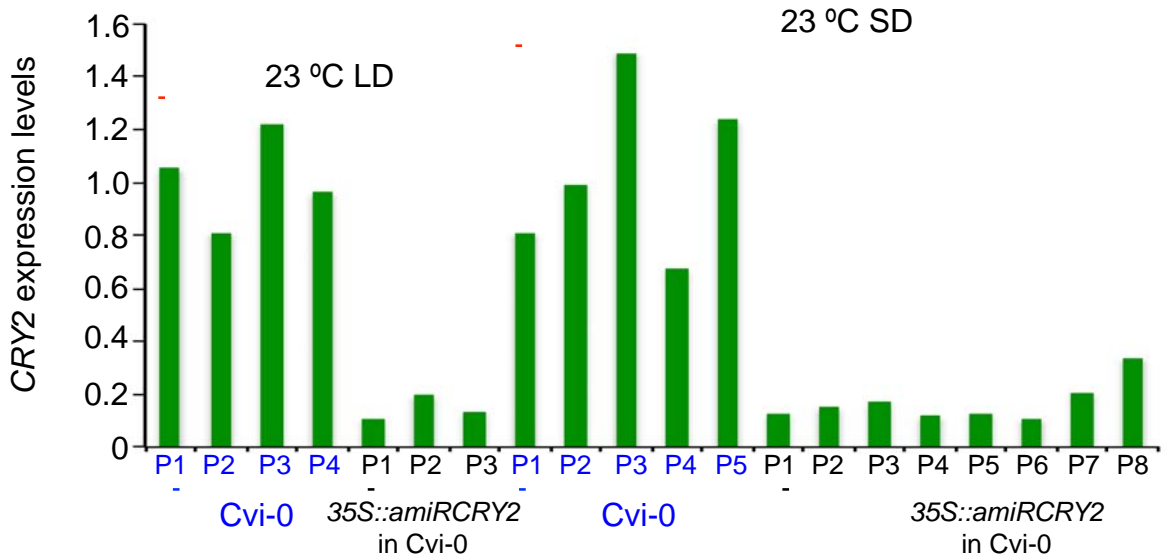
Supplementary Figure S4

**Supplemental Figure S4. QTL maps for multiple traits in different RIL populations.** LOD scores (y-axis) from R-QTL using the Multiple QTL Modeling (MQM) approach are plotted against the 5 Arabidopsis chromosomes (x-axis). QTL results from rosette leaf number, root elongation and hypocotyl elongation are shown in 3 different RILs. Horizontal bars correspond to the LOD threshold of 3 in each of the maps.
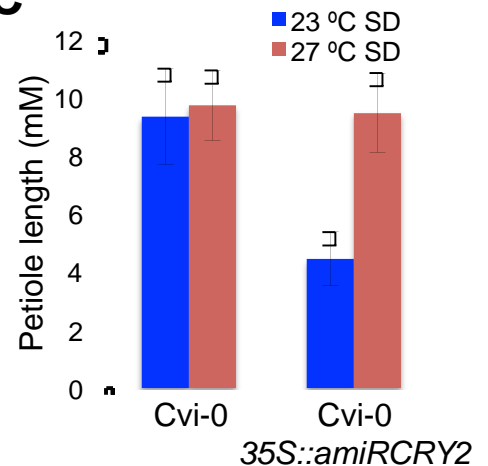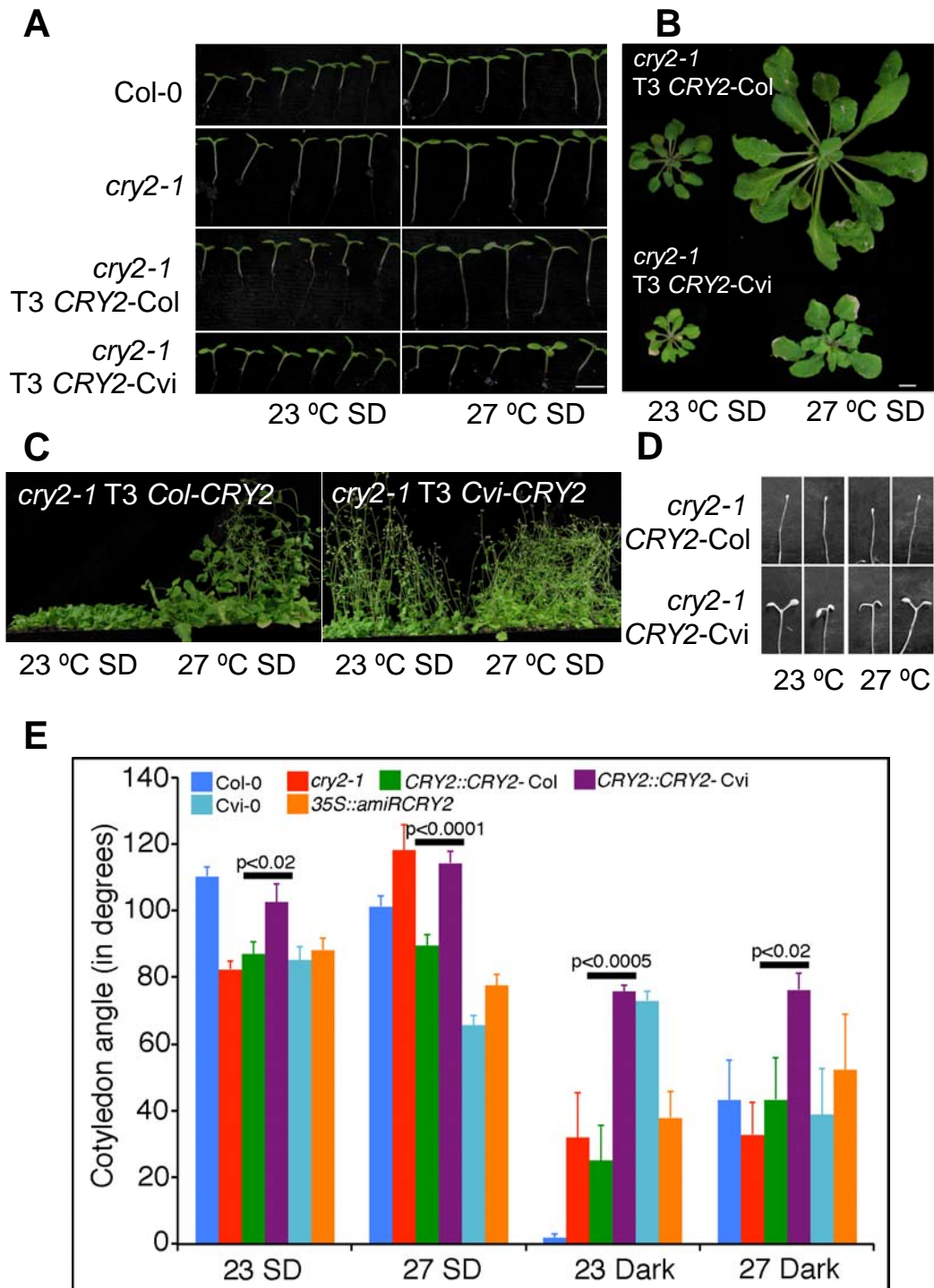
Supplementary Figure S5

A

B
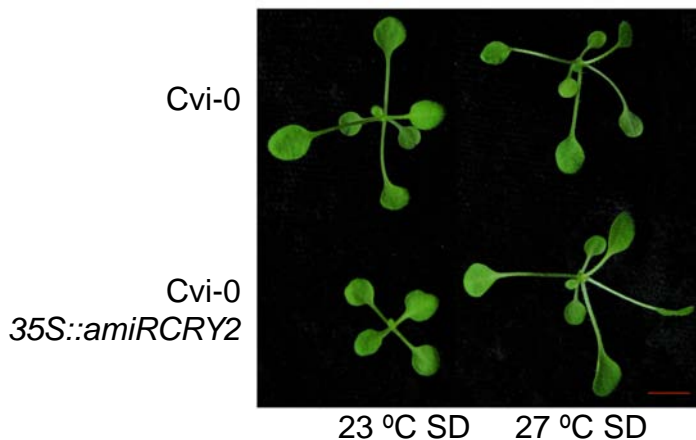
C

Supplementary Figure S5. Cvi-0 plants in which *CRY2* function is compromised display temperature-sensitivity in petiole elongation. A) Expression levels of CRY2 is reduced in *35S::amiRCRY2* lines in the Cvi-0 background. Plants representing independent T2 transgenic lines are analysed and thus no standard deviation is shown. **B)** Architecture of the *35S::amiRCRY2* plants in the Cvi-0 background compared with Cvi-0 in different temperature regimes. Scale bar = 5mm. **C)** Temperature-induced petiole elongation response in *35S::amiRCRY2* plants in the Cvi-0 background compared with Cvi-0.

Supplementary Figure S6

**Supplementary Figure S6. Allelic variation at *CRY2* confers variation in temperature associated architectural phenotypes. A)** Representative examples for hypocotyl elongation in plants with different *CRY2* genotypes grown at two different thermal regimes. Scale bar = 5mm. **B)** Representative pictures for *cry2-1* mutant plants transformed with *CRY2*-Col-0 or *CRY2*-Cvi-0 at 23 ºC or 27 ºC. Scale bar = 5mm. **C)** Temperature sensitivity in flowering time in plants carrying the *CRY2*-Col-0 allele in the *cry2-1* background compared with plants carrying the *CRY2*-Cvi-0 allele in the *cry2-1* background. **D)** Differences in the cotyledon opening phenotype conferred by *CRY2*-Col-0 and *CRY2*-Cvi-0 alleles in the *cry2-1* background at different temperatures. **E)** Cotyledon opening measured across different genotypes in multiple conditions. 23 and 27 represent 23 ºC and 27 ºC respectively. SD and Dark represent short day or continuous dark light conditions. p-values for the difference between the *CRY2*-Col-0 and *CRY2*-Cvi-0 alleles is shown above.

Supplementary Figure S7
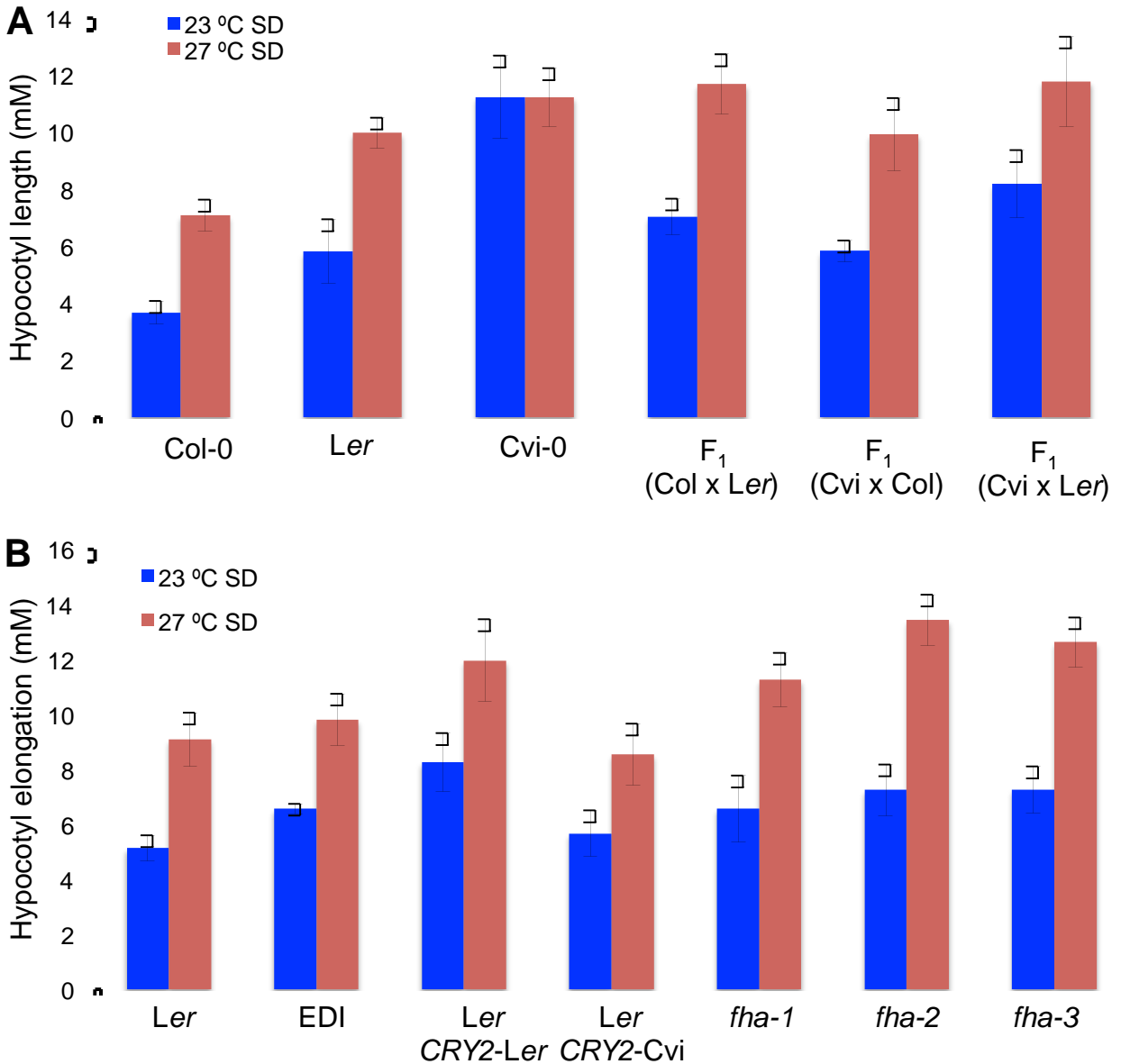
Supplementary Figure S7. The effect of the *CRY2*-Cvi-0 allele is dependent on the genetic background. A) Temperature response in hypocotyl elongation in different genotypes. **B)** Temperature response in L*er, EDI*-NIL, and L*er* transformed with *35S::CRY2*-Col-0 or *35S::CRY2*-Cvi-0. The *fha* mutants, which carry mutations in *CRY2* in the L*er* background, are shown.

Supplementary Figure S8
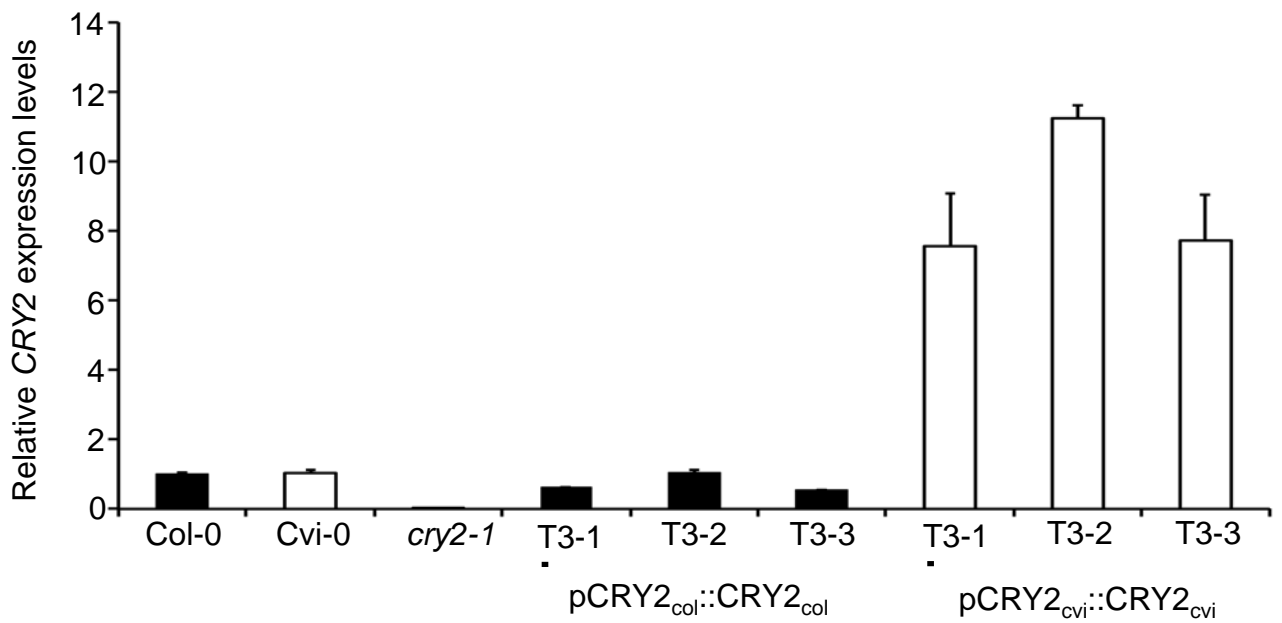
Supplementary Figure S8. Comparision of expression levels in transgenic lines. Expression levels of *CRY2* in three independent T3 transgenic lines carrying the *CRY2*-Col-0 or the *CRY2*-Cvi-0 allele in the *cry2-1* mutant background is shown along with the expression levels in Col-0 and Cvi-0.
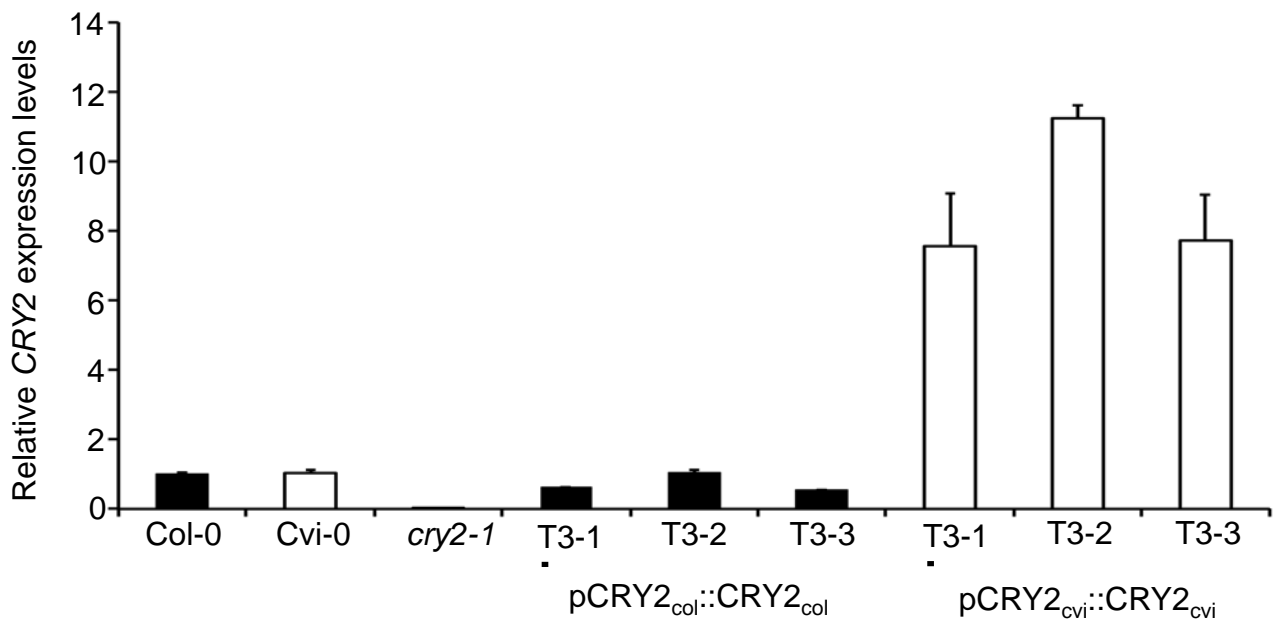
Supplementary Figure S8

Supplementary Figure S8. Comparision of expression levels in transgenic lines. Expression levels of *CRY2* in three independent T3 transgenic lines carrying the *CRY2*-Col-0 or the *CRY2*-Cvi-0 allele in the *cry2-1* mutant background is shown along with the expression levels in Col-0 and Cvi-0.

Legends for supplementary tables

1. Supplementary Table S1. Description and the phenotypes of the accessions used in the GWAS analysis. ABRC code – Stock centre identification numbers; Accessions ID – Unique identification number of the accession as per the 1001 genome project for using in GWAPP; HL23 – Hypocotyl length at 23 ºC; HL27 – Hypocotyl length at 27 ºC; SensHL – Temperature sensitivity in hypocotyl elongation; VarTemp- Percentage of variance explained by temperature; RLN23, RLN27 – Rosette leaf number at 23 ºC or 27 ºC; SensFT – Temperature sensitivity in flowering time; Location, country of origin and the Latitude is given as well for reference.

2. Supplementary Table S2. Summary statistics for accessions and the recombinant inbred lines. CT: Col-0 x Tsu-0; BS – Bay-0 x Sha; CvC – Cvi-0 x Col-0; RLN – rosette leaf number; CLN- Cauline leaf number; TLN- Total leaf number; RL- root length; HL- Hypocotyl length; SD-short days.

3. Supplementary Table S3. Phenotypic data from the Col-0 x Tsu-0 RIL population. RIL- line number of the population; RLN- rosette leaf number; RL- root length; HL- hypocotyl length; Sens-Sensitivity for the associated trait.

4. Supplementary Table S4 Phenotypic data from the Col-0 x Cvi-0 RIL population. RIL- line number of the population; RLN- rosette leaf number; RL- root length; HL- hypocotyl length; Sens-Sensitivity for the associated trait.

5. Supplementary Table S5. Phenotypic data from the Bay-0 x Sha RIL population. RIL- line number of the population; RLN- rosette leaf number; RL- root length; HL- hypocotyl length; Sens-Sensitivity for the associated trait.

6. Supplementary Table S6. Genetic correlations between various traits. CT- Col-0 x Tsu-0; BS – Bay-0 x Sha; CvC – Cvi-0 x Col-0; RLN – rosette leaf number; RL – root length; HL – Hypocotyl length.

7. Supplementary Table S7. QTL identified in this work using different RILs. For each detected QTL by the multiple QTL modeling, the closest marker (QTL(marker), the physical position in Mb is given within brackets), chromosome

30   (Chr), maximum LOD score (LOD), LOD-support interval (Int), percentage of
31   variance explained by the QTL (% var) and additive effect (AE) are shown.

32   **8. Supplementary Table S3. Oligos used in this study.**

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