

Figure S1

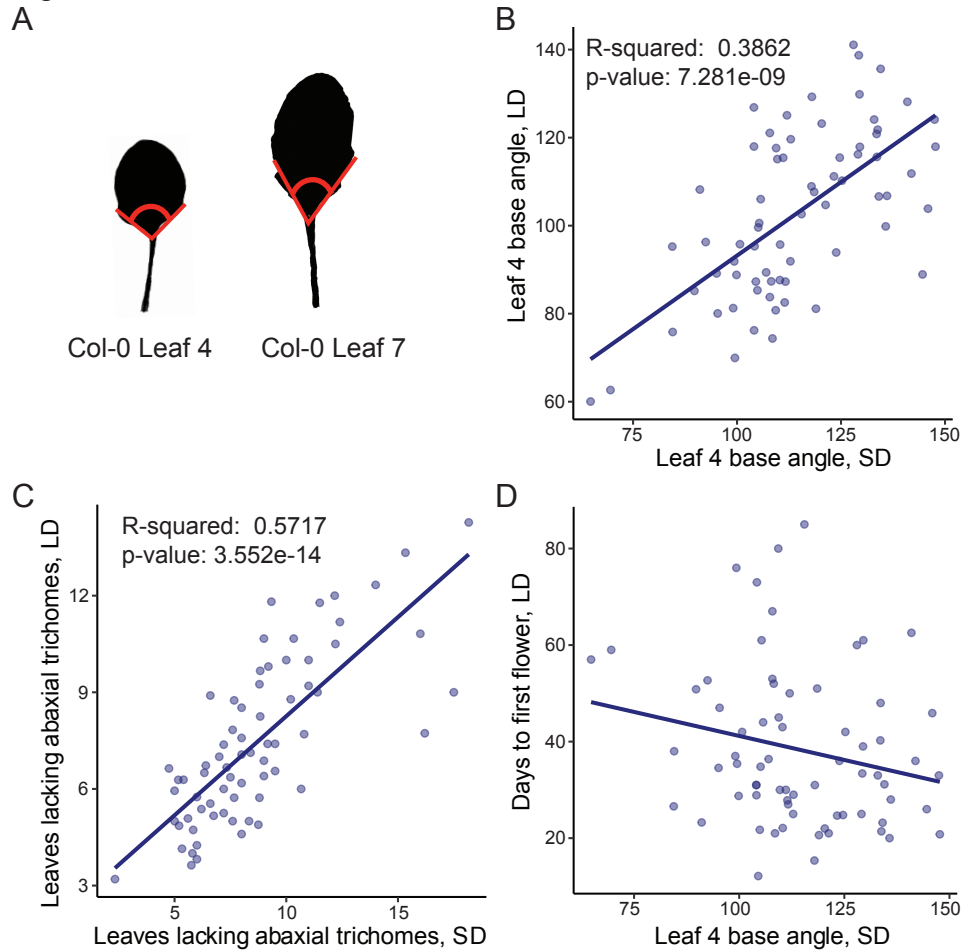


Fig. S1. Relationship between vegetative traits and flowering time in SD and LD.

(A) Leaves four and seven of the Col-0 accession, with measures of leaf base angle indicated in red.

(B) Correlation between leaf four base angle in LD and SD conditions.

(C) Correlation between leaves lacking abaxial trichomes in SD and leaves lacking abaxial trichomes in LD conditions.

(D) Correlation between leaf four base angle in SD and days to opening of first flower in LD conditions. Blue lines shown are linear regression model; R^2 and p -values from linear regression analysis displayed in upper right corner of each panel.

Figure S2

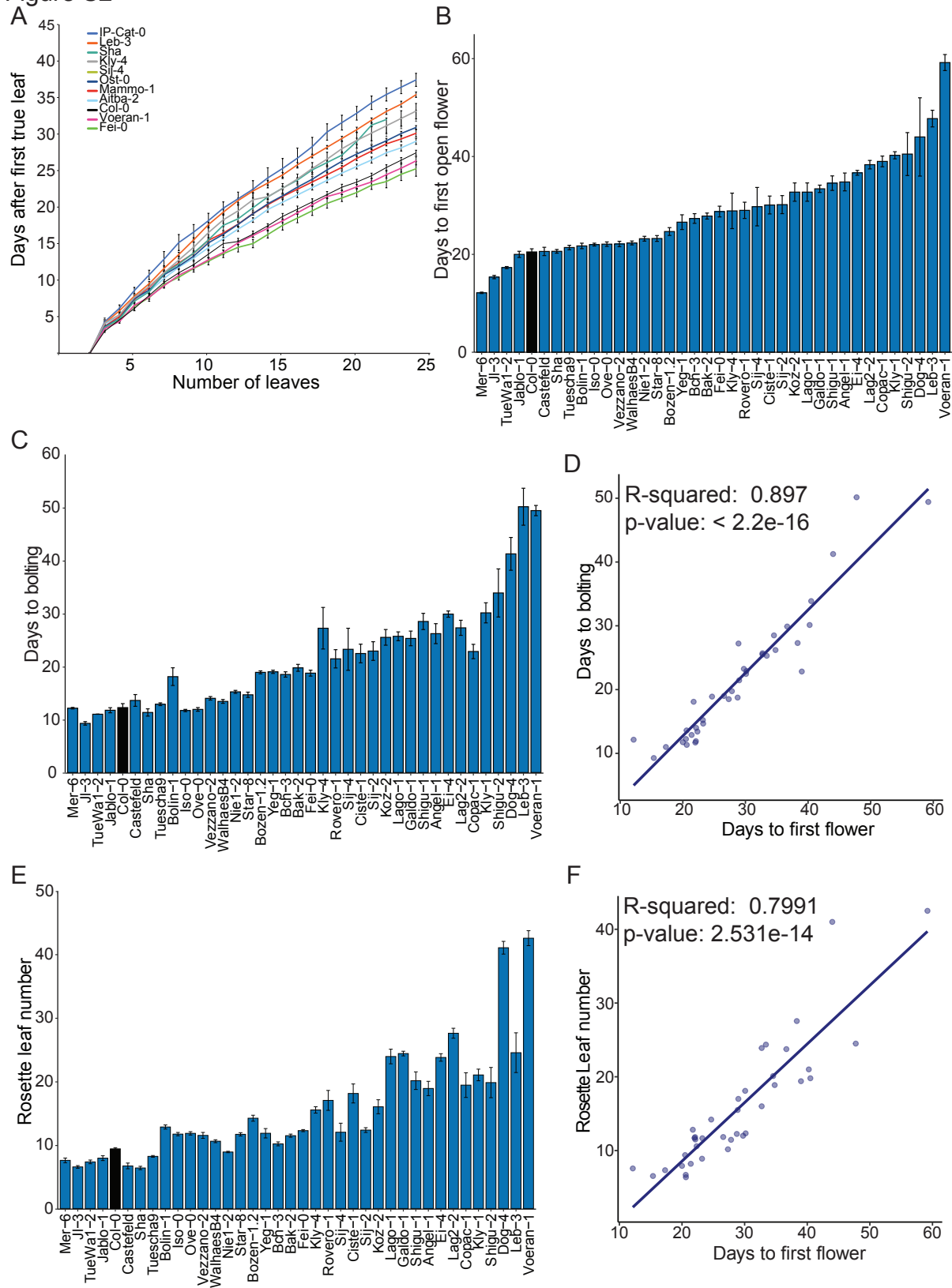


Fig. S2. Assessment of reproductive phase transition for scoring timing of timing of reproductive phase transition in natural accessions.

(A) Rate of leaf initiation in a group of selected accessions. Data show number of visible leaves and days after the appearance of first true leaves.

(B) Days to first open flower in a group of selected accessions.

(C) Days to bolting in a group of selected accessions, in same order as S2B.

(D) Correlation between days to opening of first flower and days to bolting in LD conditions. Blue lines shown are linear regression model; R^2 and p -values from linear regression analysis displayed in upper right corner of each panel.

(E) Rosette leaf number in a group of selected accessions, in same order as S2B.

(F) Correlation between rosette leaf number and days to opening of first flower. Blue lines shown are linear regression model; R^2 and p -values from linear regression analysis displayed in upper right corner of each panel.

Figure S3

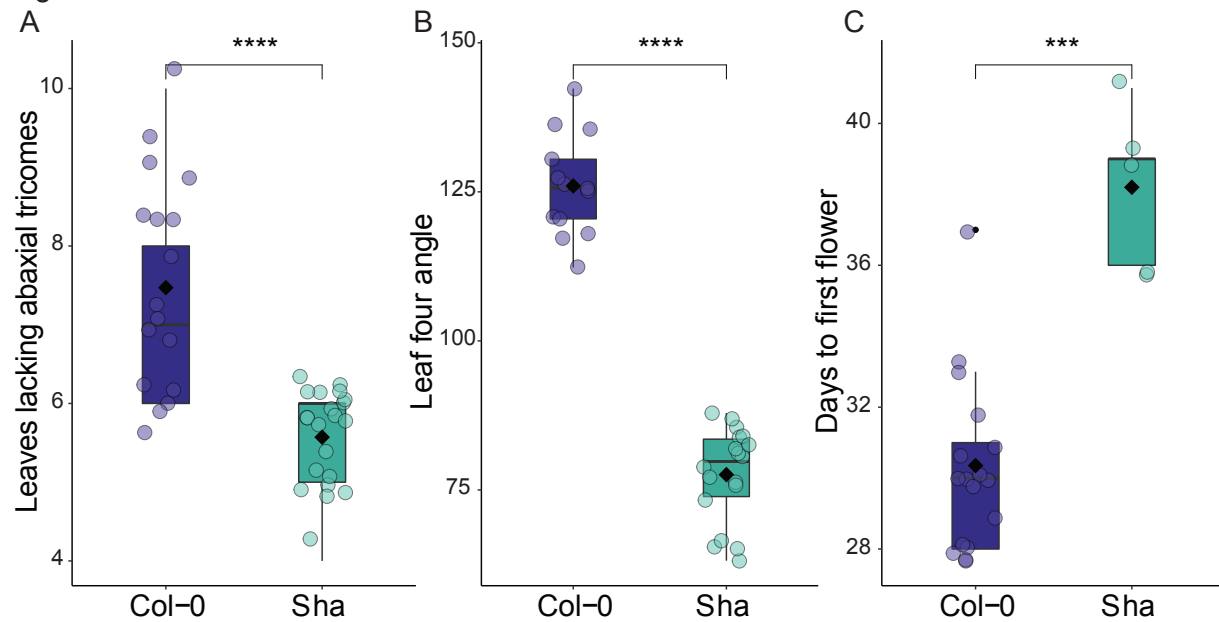


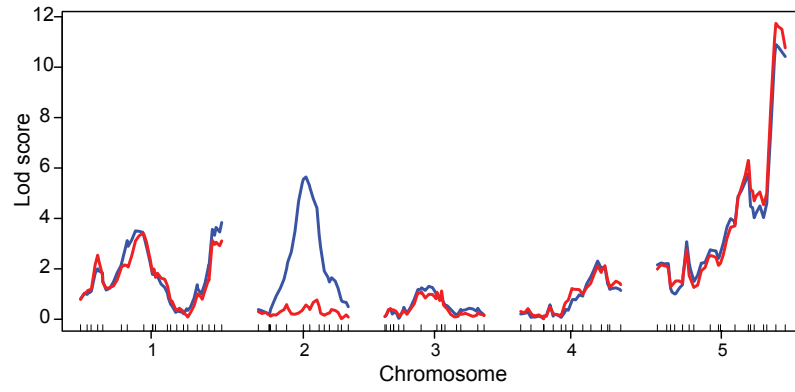
Fig. S3. Timing of vegetative phase change of Sha and Col-0 in non-vernalized conditions.

(A-D) The number of leaves lacking abaxial trichomes (A), leaf four base angle (B), and days to first open flower (C) in non-vernalized LD conditions. Significance was determined by two-tailed Student's *t*-test (** $p < 0.001$, **** $p < 0.0001$).

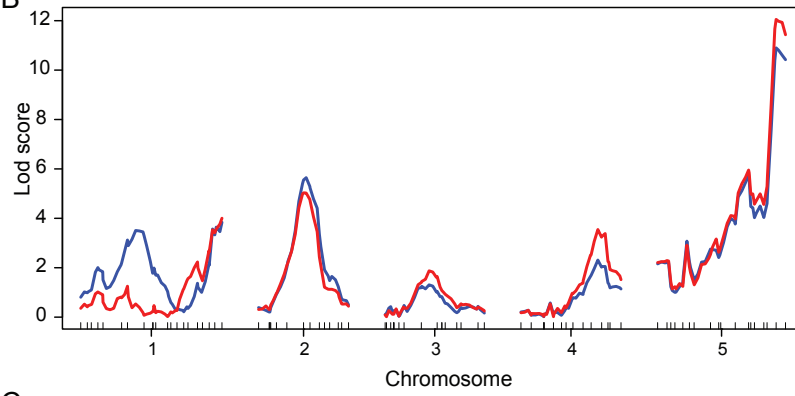
Blue/green dots indicate biological replicates; black dot indicate outliers; center line marks the median value; boxes outline the first and third quartiles, whiskers mark minimum and maximum values.

Figure S4

A



B



C

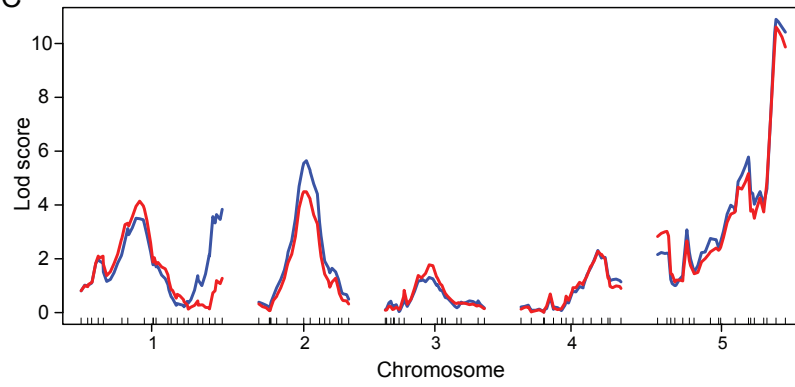


Fig. S4. Covariate analysis of leaves lacking abaxial trichomes and QTLs in Sha X Col-0 RILs.

(A) Covariate analysis using the peak coordinate of the QTL on chromosome two. Red lines are LOD scores based on leaves lacking abaxial trichomes using maximum likelihood via the EM algorithm. Blue lines are the LOD score based on a genome scan for number of leaves lacking abaxial trichomes with the effects of each QTL peak on chromosome five incorporated as an interacting covariate.

(B-C) Covariate analysis using the peak coordinates of the QTLs on chromosome one. Red lines are LOD scores based on leaves lacking abaxial trichomes using maximum likelihood via the EM algorithm. Blue lines are the LOD score based on a genome scan for number of leaves lacking abaxial trichomes with the effects of each QTL peak on chromosome five incorporated as an interacting covariate.

Table S1. Catalog numbers and phenotypic data of natural accessions used in this study

[Click here to download Table S1](#)

Table S2. Phenotypic and genotypic data of RIL lines used in this study

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Table S3. Primers used in this study

smRNA RT-qPCR		
Name	Use	Sequence (5'-3')
miR156 RT	miR156 reverse transcription	GTCGTATCCAGTGCAGGGTCCGAGGTATTTCGCACTGGA TACGACGTGCTC
miR172 RT	miR172 reverse transcription	GTCGTATCCAGTGCAGGGTCCGAGGTATTTCGCACTGGA TACGACATGCAG
miR156 F	miR156 qPCR	GCGGCGGTGACAGAAGAGAGT
miR172 F	miR172 qPCR	CGGCGGAGAATCTTGATGATGC
Universal R	miRNA qPCR	GTGCAGGGTCCGAGGT
SnoR101 F	SnoR101 qPCR	CTTCACAGGTAAGTTCGCTTG
SnoR101 R	SnoR101 RT and qPCR	AGCATCAGCAGACCAGTAGTT
mRNA RT-qPCR		
Name	Use	Sequence (5'-3')
oligo dT	Reverse transcription	TTTTTTTTTTTTTTTTTTTTTTTT
ACT2-F	qPCR	GCACCTGTCTTCTTACCG
ACT2-R	qPCR	AACCCTCGTAGATTGGCACA
SPL2-F	qPCR	TTTCCGATACCGAGCACAATAG
SPL2-F	qPCR	TACGGGTTGGAGGTTGCTTGAGG
SPL3-F	qPCR	ATGAGTATGAGAAGAAGCAAAGCG
SPL3-R	qPCR	TCCACTACTACTTGTAGCTTTACCT
SPL9-F	qPCR	GGAATTTGACCTAGAGAAAAGGAGTT
SPL9-R	qPCR	GCATCACCATTTTCGTAAAGCGAAG
SPL10-F	qPCR	CAGACAAAGGTGTGGGAGAATGCTC
SPL10-R	qPCR	TAGGGAAAGTGCCAAATATTGGCG
SPL13-F	qPCR	GGGTTTTCAAGGTAGCAAATTGCT
SPL13-R	qPCR	ACCAACAACATAGCTCTGGCTCTG
SPL11-F	qPCR	AGTCCAAGTTTCAACTTCATGGCG
SPL11-F	qPCR	GAACAGAGTAGAGAAAATGGCTGC
SPL15-F	qPCR	TGAATGTTTTATCACATGGAAGCTC
SPL15-R	qPCR	TCATCGAGTCGAAACCAGAAGATG
miR156C-F	qPCR	AAAAGCCTCAGATCTAACTCCAACAC
miR156C-R	qPCR	GCGTTTCTCTTAAAATTTGTCCCAAAACT
miR156A-F	qPCR	CTTCGTTCTCTATGTCTCAATCTCTC
miR156A-R	qPCR	TGATTAAAGGCTAAAGGTCTCCTC
TOE1-F	qPCR	CGAGTTATAATAATCCCGCCGAG
TOE1-R	qPCR	TTAAGGGTGTGGATAAAAGT
TOE2-F	qPCR	ATGGAGAACCACATGGCTGC
TOE2-R	qPCR	GGTGCTGTAGCTGCTACGGC
TOE3-F	qPCR	CTCACCCGATCATCACGAAG
TOE3-R	qPCR	TATTGAAACCGGACCAACGA

Table S4. DESeq and SNPEff results for Sha QTLs

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