Figure S1_Ranftl_et_al.

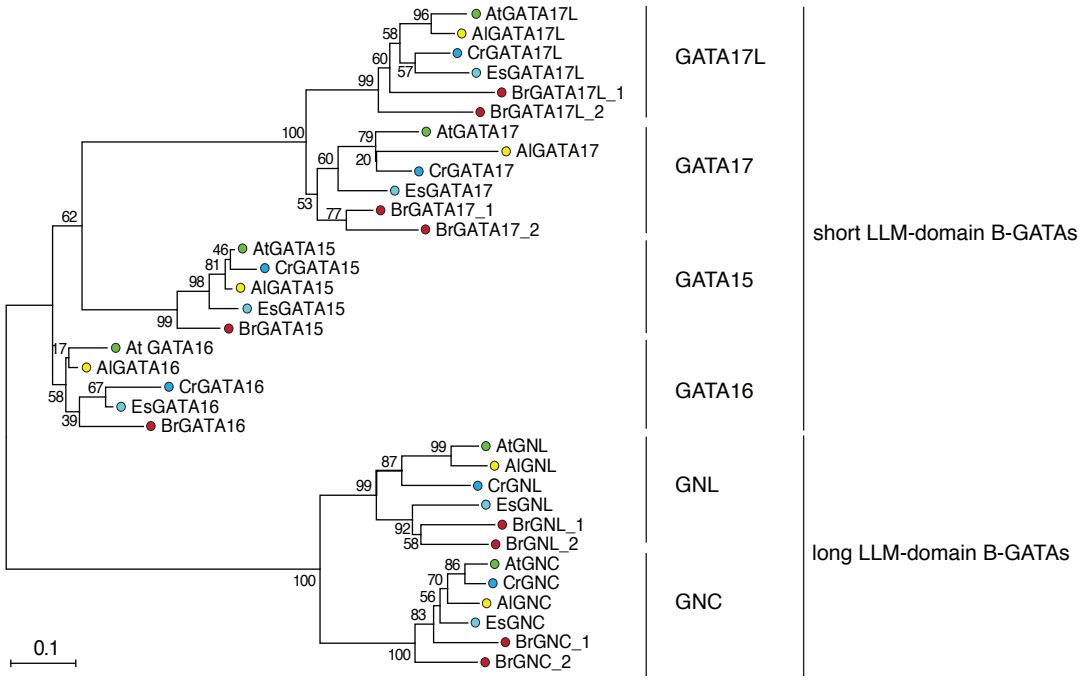

Figure S1: Evolutionary conservation of LLM-domain B-GATAs within the *Brassicaceae*. Phylogenetic tree of the LLM-domain B-GATAs from Brassicaceae species *Arabidopsis thaliana (At), Arabidopsis lyrata* (*Al*), *Capsella rubella* (*Cr*), *Eutrema salsugineum* (*Es*), and *Brassica rapa* (*Br*). The underlying alignment is shown in Fig. S2. Species identities are color-coded for ease of viewing; bootstrap values are shown at nodes. The tree is drawn to scale, with branch lengths in the same units as those of the evolutionary distances used to infer the phylogenetic tree. The evolutionary distances were computed using the JTT matrix-based method and are in the units of the number of amino acid substitutions per site.

Figure S2_Ranftl_et_al

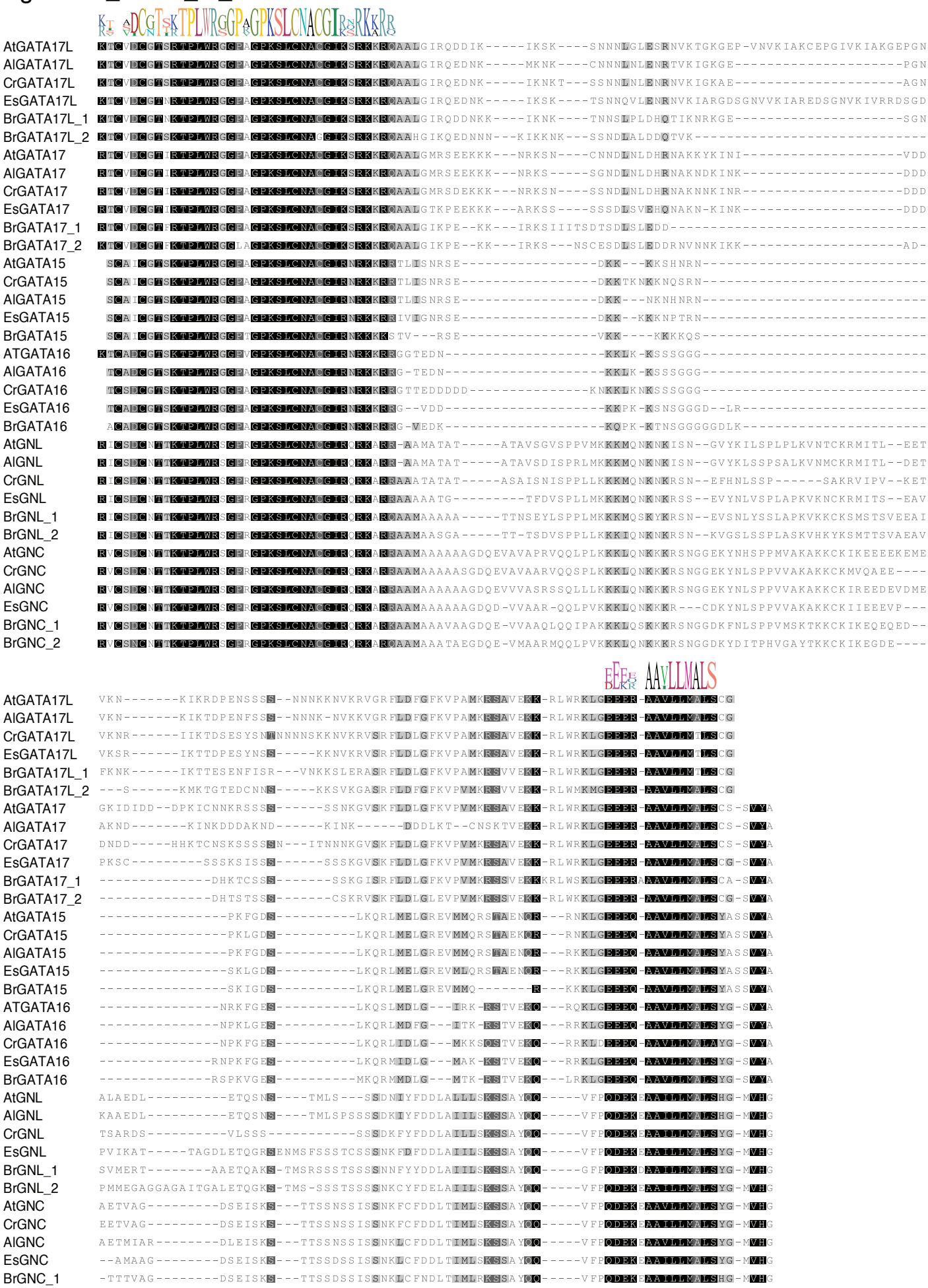

Figure S2: Sequence alignment of the GATA-domain and the LLM-domain. Pretty box sequence alignment (http://www.ebi.ac.uk/Tools/msa/clustalw2/) of the *Brassicaceae* GATA factors used for the phylogenetic analysis shown in Figure 1. Sequence conservation is represented by a sequence logo above the respective alignments. Black boxed residues indicate completely conserved amino acids, different shades of grey indicate residues that are highly conserved between the aligned sequences with darker grey reflecting a higher degree of conservation (dark grey: 80-100%; light grey: 60-80%; white: less than 60%).

Figure S3_Ranftl_et_al.

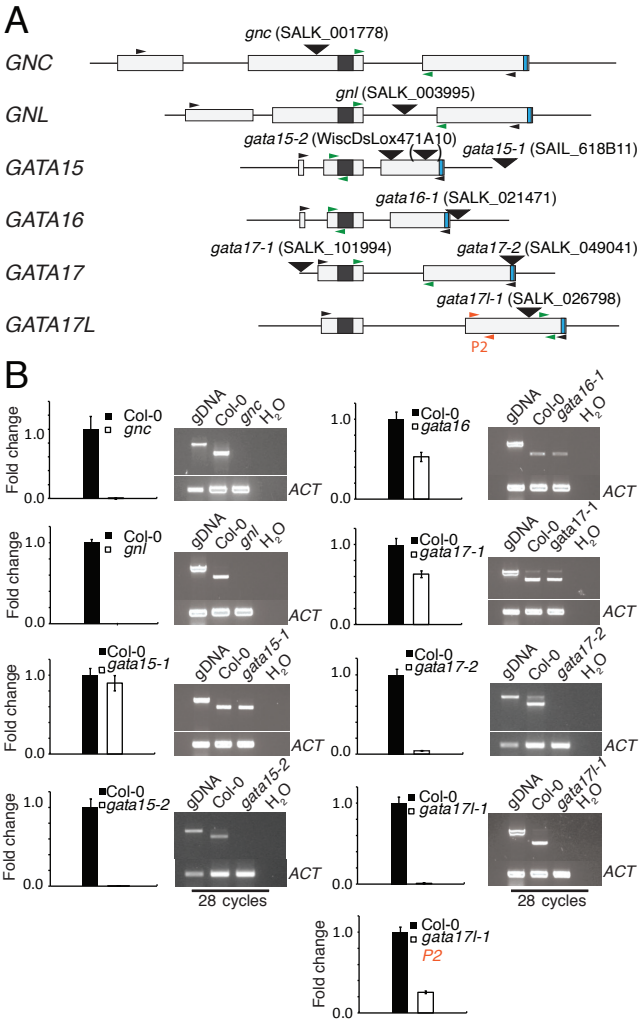

Figure S3: *GATA* insertion mutant analysis. A. Schematic representation of the gene models of the six Arabidopsis LLM-domain B-GATA genes with exons (boxes) and introns (lines). The sequences coding for the GATA DNA-binding domain and the LLM-domain are represented as black and blue boxes, respectively. The T-DNA insertion positions are shown. The position in brackets of the *GATA15* insertion refers to the original misannotation of this insertion (www.signal.salk.edu). The image is identical to the one shown in Figure 1C except that the positions of the primer pairs used for sqPCR (black arrowheads) and qRT-PCR (green and red arrowheads) were added. **B.** Results from qRT-PCR analyses (left panels, fold change refers to normalized fold change) and sqRT-PCR analyses (right panels) with RNA prepared from seven day-old Col-0 wild type seedlings and *gata* gene mutants. In the sqRT-PCR experiment, genomic DNA (gDNA) was used to control for contamination. A reaction mix with water (H_2O) was used to control for purity of the reaction components. The *ACTIN2* (*ACT2*) gene was used as a reference gene for the sqRT-PCR.

Figure S4_Ranftl_et_al.

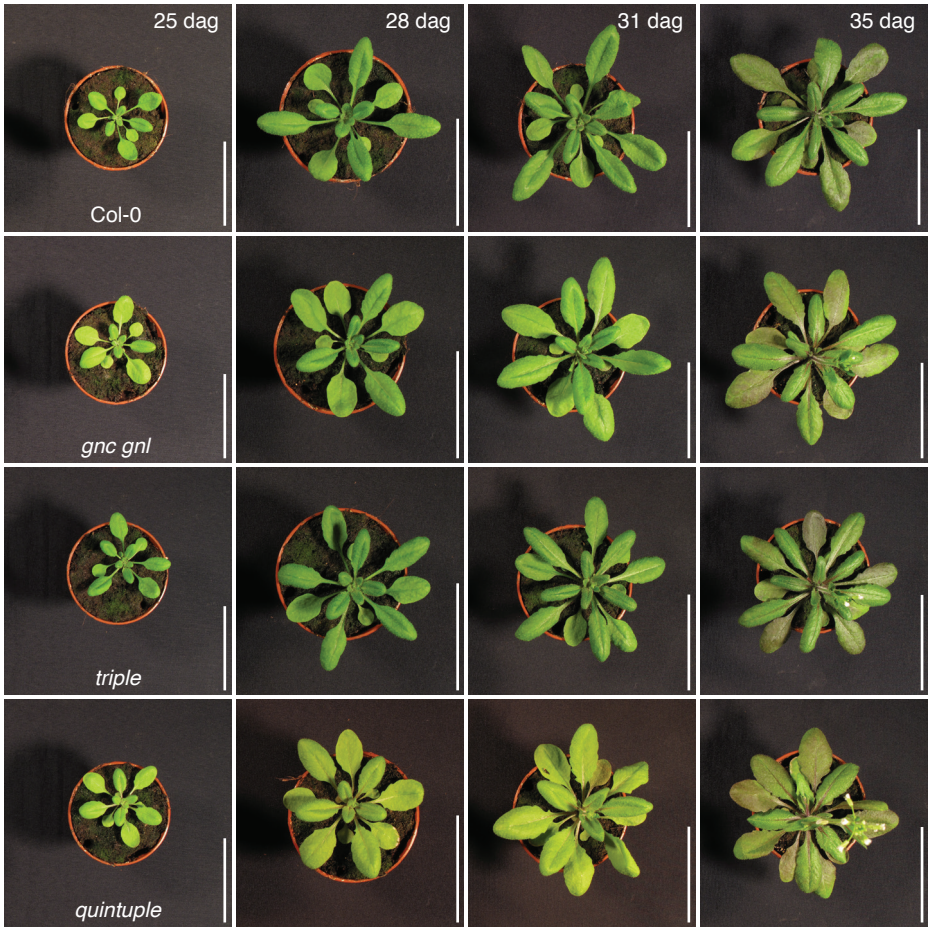

Figure S4: Mature plant phenotypes of *GATA* gene mutants. Representative photographs of Arabidopsis plants at 25 days after germination (dag), 28 dag, 31 dag, and 35 dag. Please note that the chlorophyll accumulation defect is maintained in the *quintuple* mutant but lost in the other mutants. Scale bar = 5 cm.

Figure S5_Ranftl_et_al.

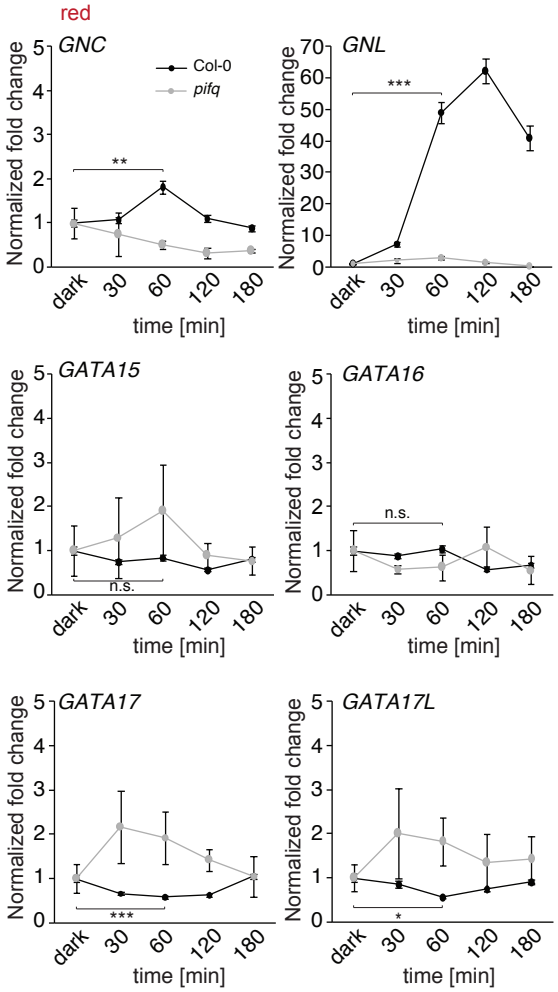

Figure S5: *GATA* gene expression in red light conditions is PIF-dependent. Averages and standard errors of three replicate qRT-PCR analyses of four day-old dark-grown wild type and *pifq* seedlings after transfer to red (7.2 µmol s^{-1} m^{-2}) light. Student's t-test for the 12 hr time point: *gnc gnl* vs. Col, * $p \leq 0.05$; *quintuple* vs. Col, ** $p \leq 0.01$; *triple* vs. Col, n.s. = not significant.

Figure S6_Ranfl_et_al.

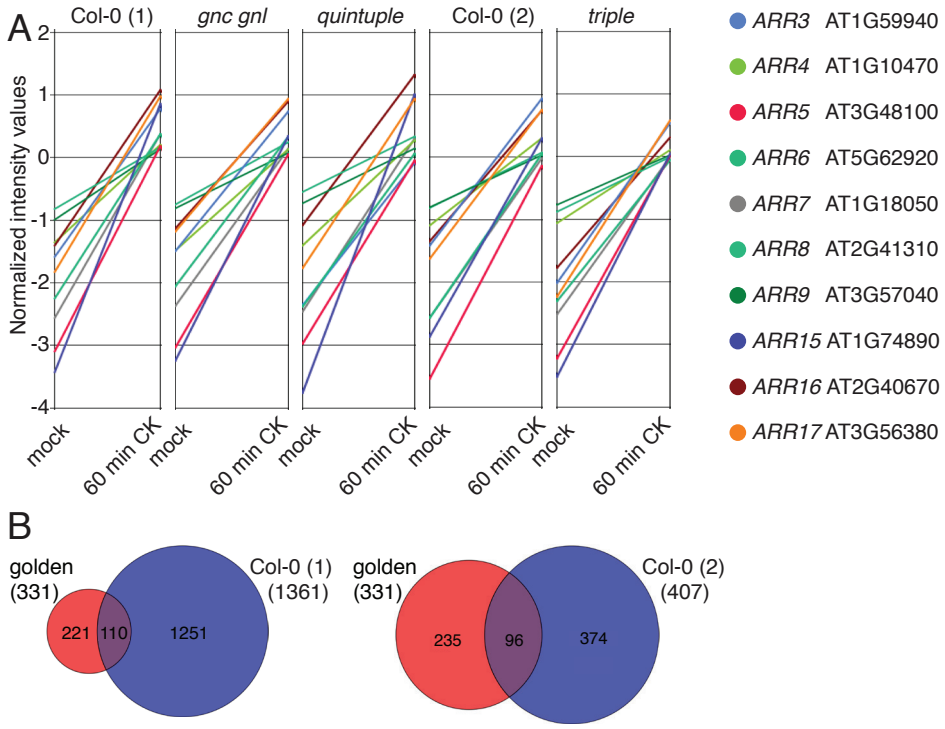

Figure S6: The effects of CK-induction in the two microarray data sets are comparable. A. Graphic representation of the CK-induction of *ARR* genes from *Arabidopsis thaliana* in the two microarray data sets reveals that CK-induction was comparable between the two Col-0 wild type controls as well as in the different *GATA* gene mutants. **B.** Venn diagrams comparing the CK-induction (two-fold induction) in the two wild type samples, Col-0 (1) and Col-0 (2) with the "golden list" of previously identified CK-regulated genes. See Supplemental Table S3 for a list of all CK-regulated genes from the "golden list".

Figure S7_Ranftl_et_al.

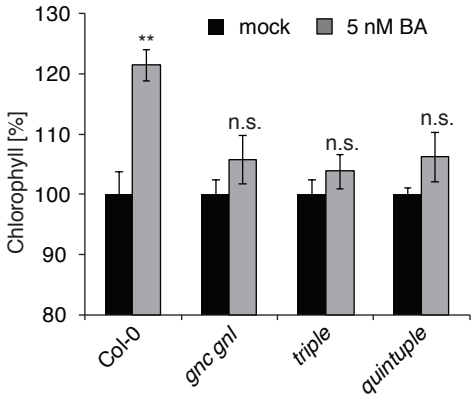

Figure S7: CK cannot efficiently induce greening in *GATA* gene mutants. Result of the quantification of chlorophyll A and B from 14 day-old wild type and different *gata* mutant plants grown in the absence and presence of 5 nM 6-BA. Student's t-tests: ** $p \leq 0.01$; n.s. = not significant.

Figure S8_Ranftl_et_al.

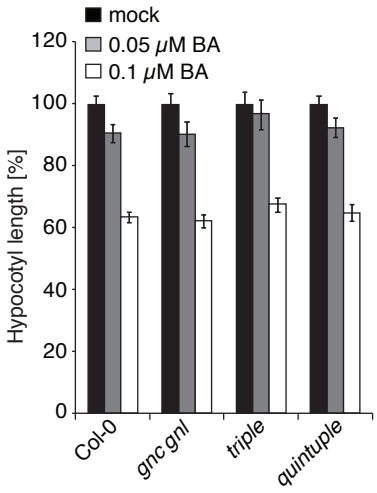

Figure S8: The effect of CK on hypocotyl elongation is not impaired in *GATA* gene mutants. Result from a hypocotyl elongation assay with five day-old dark-grown seedlings. Student's t-tests: not significant for all comparisons between different genotypes subjected to identical treatments (n > 25).

Figure S9_Ranftl_et_al.

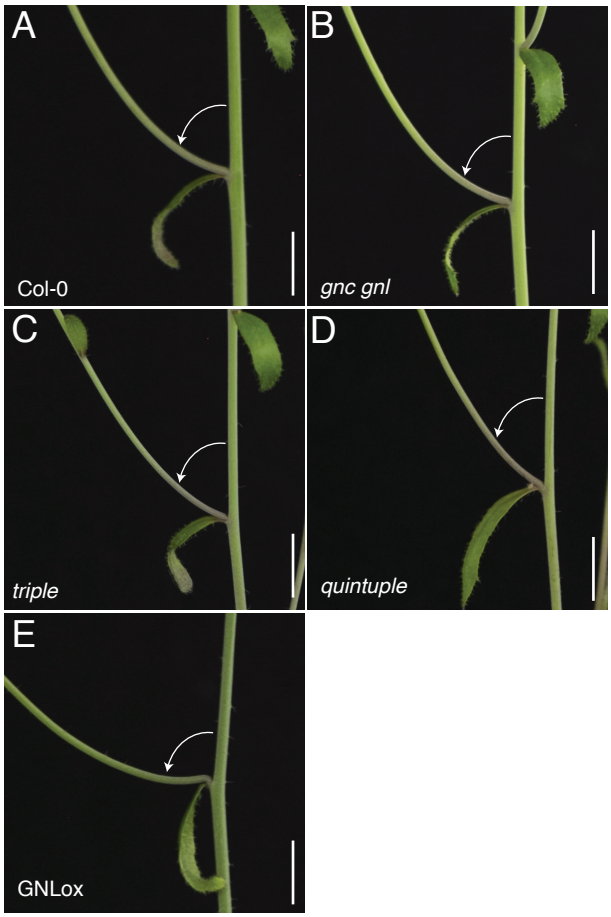

Figure S9: *GATA* gene dosage affects lateral inflorescence angles. Representative photographs of lateral branches branching off the primary inflorescences in the wild type, *GATA* gene mutants and overexpressors. Scale bar = 1 cm.

Figure S10_Ranftl_et_al.

A

Genotype	>4 sepals	>4 petals	n
Col-0	2.53%	2.22%	316
GATA15	2.51%	2.23%	359
gata16	1.33%	1.60%	376
gata17	3.66%	3.35%	328
gata17l	3.58%	3.28%	335
GATA15 gata16	1.72%	1.23%	408
gata17 gata17l	12.18%	10.38%	501
gnc gnl	1.88%	2.14%	373
gnc gnl GATA15 gata16	2.43%	4.00%	371
gnc gnl gata17 gata17l	9.14%	7.90%	405
triple	15.04%	13.37%	419
quintuple	14.54%	14.10%	454

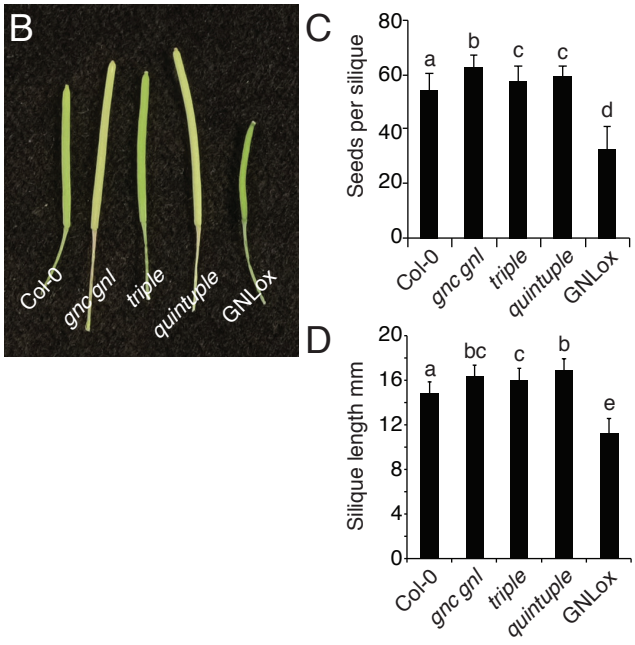

Figure S10: Floral morphology and silique parameters are influenced in *GATA* gene mutations. A. Quantitative phenotypic analysis of sepal and petal numbers in the wild type and the *GATA* gene mutant backgrounds. **B.** Photographs of representative mature siliques from the different genetic backgrounds. **C.** and **D.** Quantitative analysis of seed number per silique (C) and silique length (D). Datasets with no statistical difference fall in one group and were labeled accordingly ($n \geq 57$).

Figure S11_Ranftl_et_al.

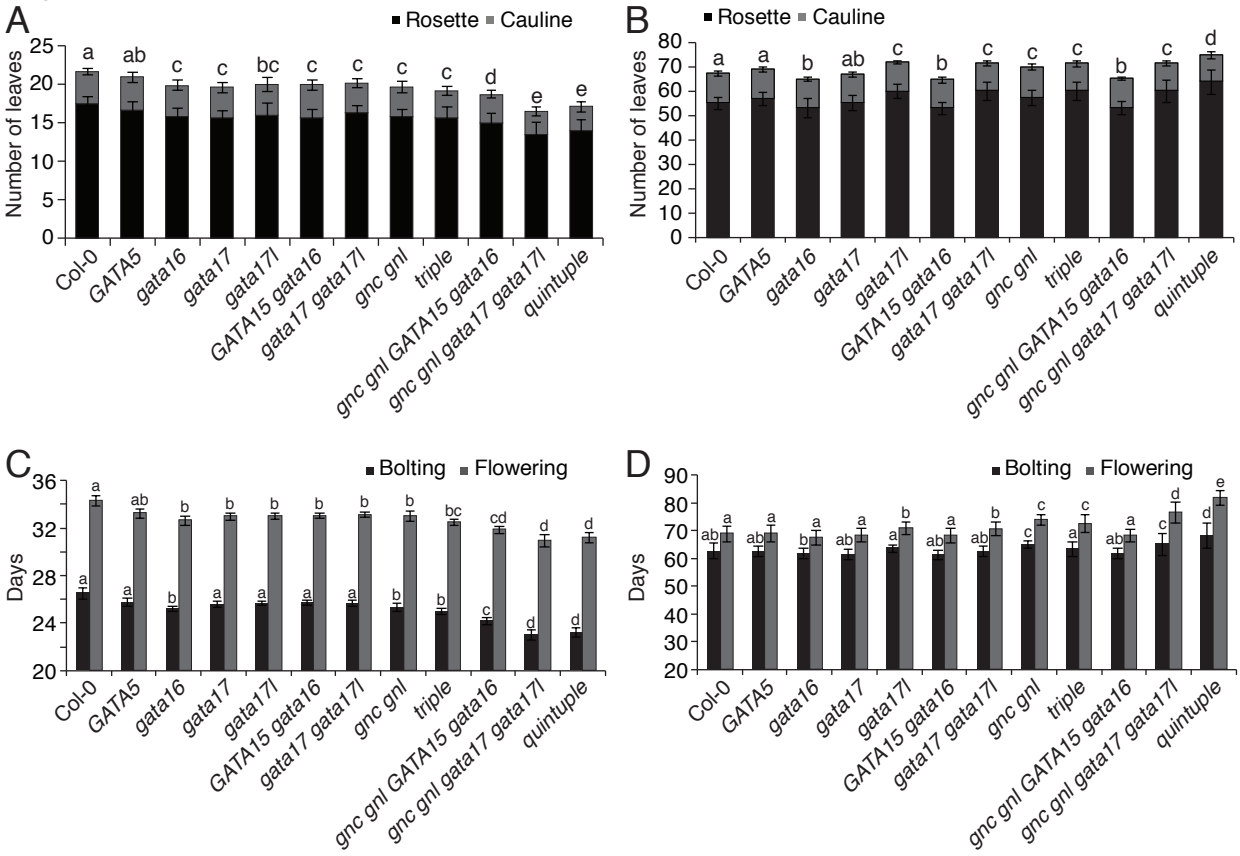

Figure S11: Quantitative analysis of flowering time in long and short day-conditions. A. - D. Quantitative analysis of flowering based on leaf number counts or days to bolting of the long day and short day-grown plants as shown in Figure 10B and C. n = 20. Student's t-test: datasets with no statistical difference fall in one group and were labeled accordingly.

Figure S12_Ranftl_et_al.

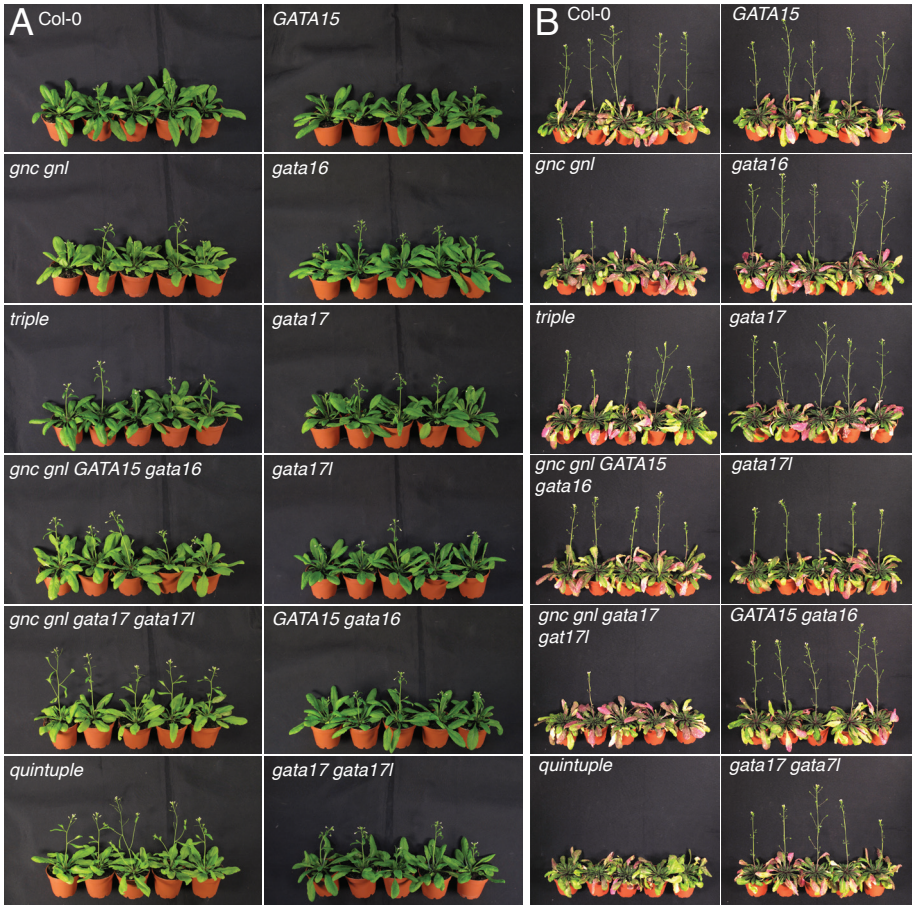

Figure S12: ***GATA*** **gene mutations alter flowering in long day and short day conditions.** Representative photographs of **A.** five week-old plants grown in long day conditions or **B.** ten week-old plants grown in short day-conditions to demonstrate the acceleration of flowering in long day-grown mutant plants and the delay in flowering in mutants grown in short days.