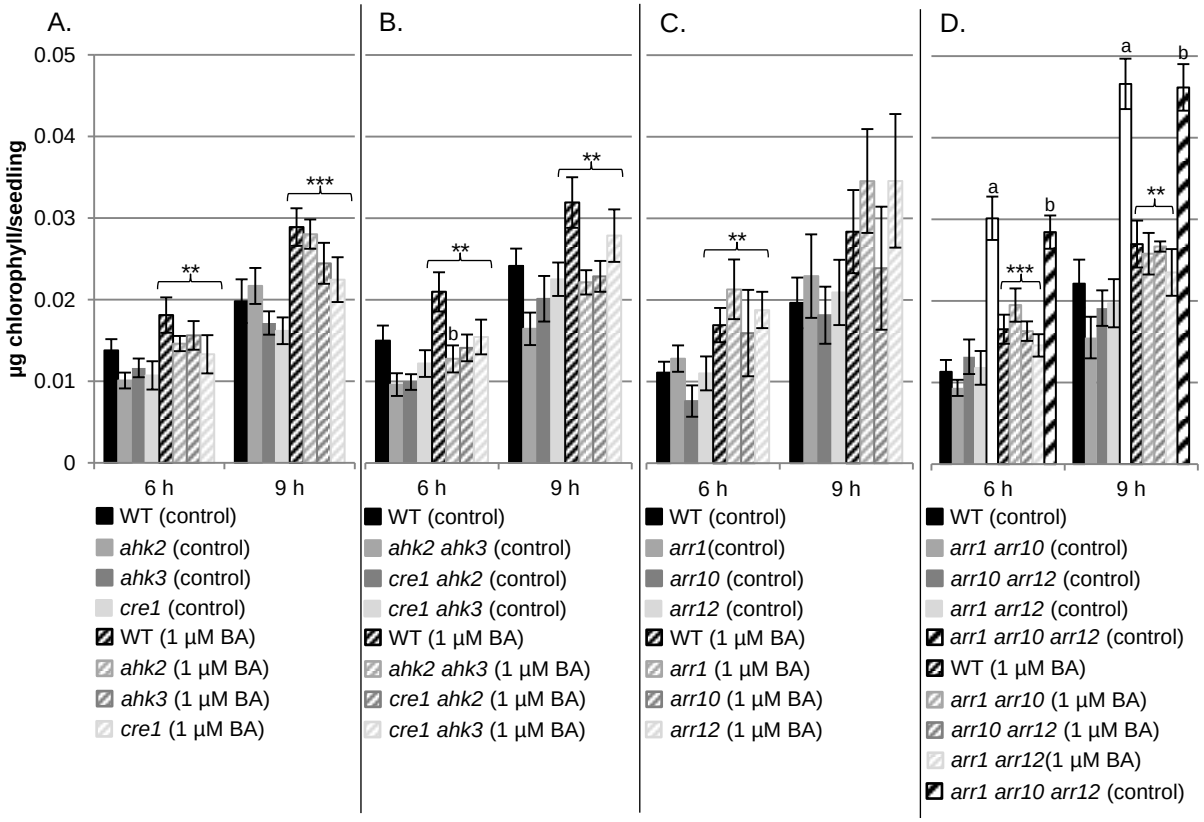

Figure S1. Greening rate in mutants of the cytokinin signaling pathway.
(A) Single (*ahk2, ahk3, cre1*), (B) double (*ahk2 ahk3, cre1 ahk2, cre1 ahk3*) cytokinin receptor mutants and (C) single (*arr1, arr10, arr12*) and (D) double and triple *arr* (*arr1 arr10, arr1 arr12, arr10 arr12, arr1 arr10 arr12*) mutants were grown for 3 days in dark on medium (MS, no sucrose) with or without 1 µM BA. Control conditions are visualized by solid bars; treatment with 1 µM BA with hatched bars. After exposure to light, chlorophyll content was measured at different time points. Diagrams shown are the average of at least 4 independent experiments each with 3 replicates per time point. One replicate consisted of 30 etiolated seedlings grown on one plate. Error bars represent SE ($n \geq 3$). Letters indicate significant differences between WT and the different genotypes under control conditions (a) and after BA treatment (b) ($P < 0.05$); asterisks above brackets indicate a significant cytokinin effect in the respective genotype (** $0.01 > P > 0.001$; *** $P < 0.001$). Additional time points can be found in Figure 2.

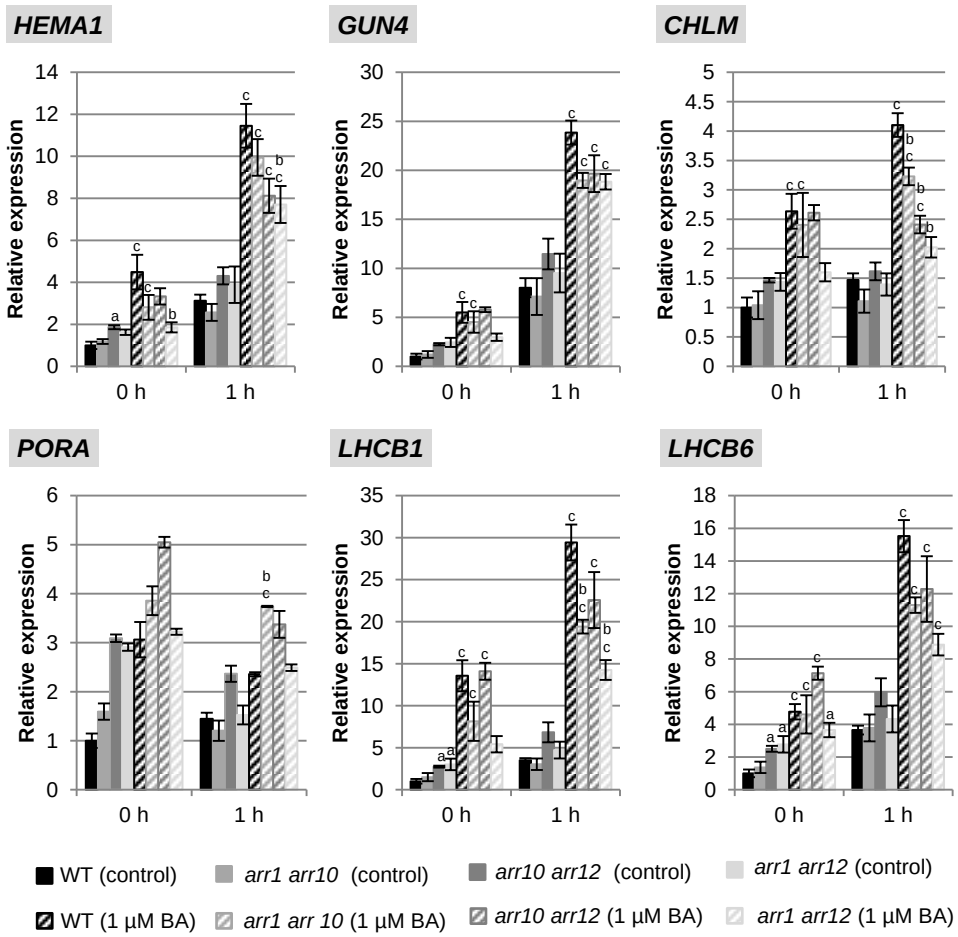

Figure S2. Effect of cytokinin on transcript level of genes encoding key steps in the chlorophyll biosynthesis pathway and of *LHCB* in *arr* double mutants.
Wild-type (WT) and *arr1 arr10, arr10 arr12* and *arr1 arr12* seedlings were grown for 3 days in dark on medium (MS, no sucrose) with or without 1 µM BA. A-I. Analysis of transcript levels by quantitative real-time PCR of *HEMA1* (A), *GUN4* (B), *GUN5* (C), *PORA* (D), *LHCB1* (E), *LHCB6* (F). Transcript levels of WT (control) in dark were set to 1 (n ≥ 3). Letters indicate significant differences between WT and the different genotypes under control condition (a) or after BA treatment (b) or between control and BA treatment for each genotype (c) ($P < 0.05$).

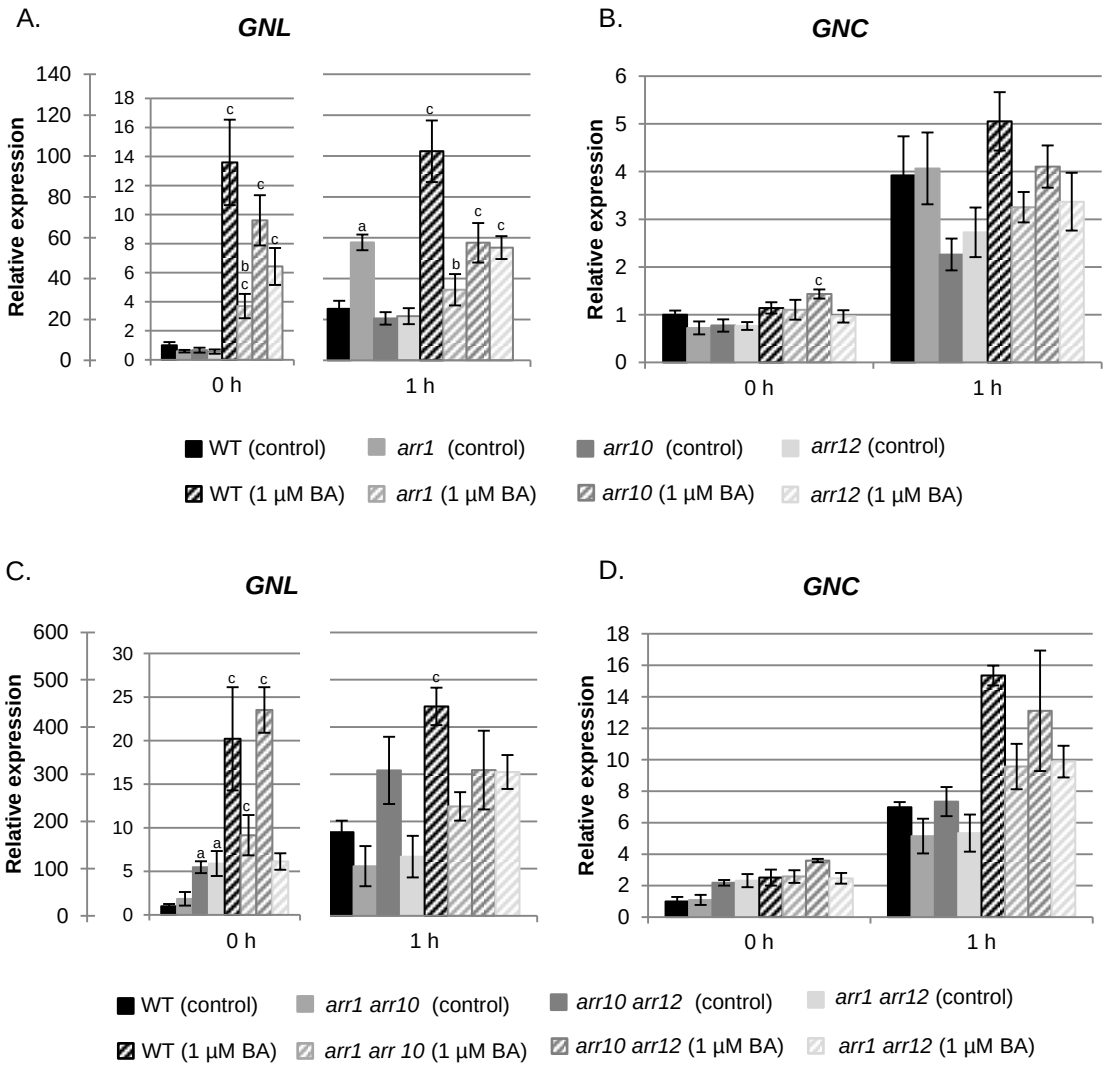

Figure S3. Interaction between cytokinin and the GATA transcription factor *GNL* during the greening response.

Analysis of transcript levels was done by quantitative real-time PCR of *GNL* and *GNC* in 3-days old etiolated seedlings exposed to light in wild type (WT) and *arr* single mutants (*arr1, arr10, arr12)* (A-B) and in *arr* double mutants (*arr1 arr10, arr10 arr12, arr1 arr12)* (C-D). Transcript levels of WT (control) in dark were set to 1. Error bars represent SE (n ≥ 3). Letters indicate significant differences between WT and the different genotypes under control condition (a) or after BA treatment (b) or between control and BA treatment for each genotype (c) ($P < 0.05$).

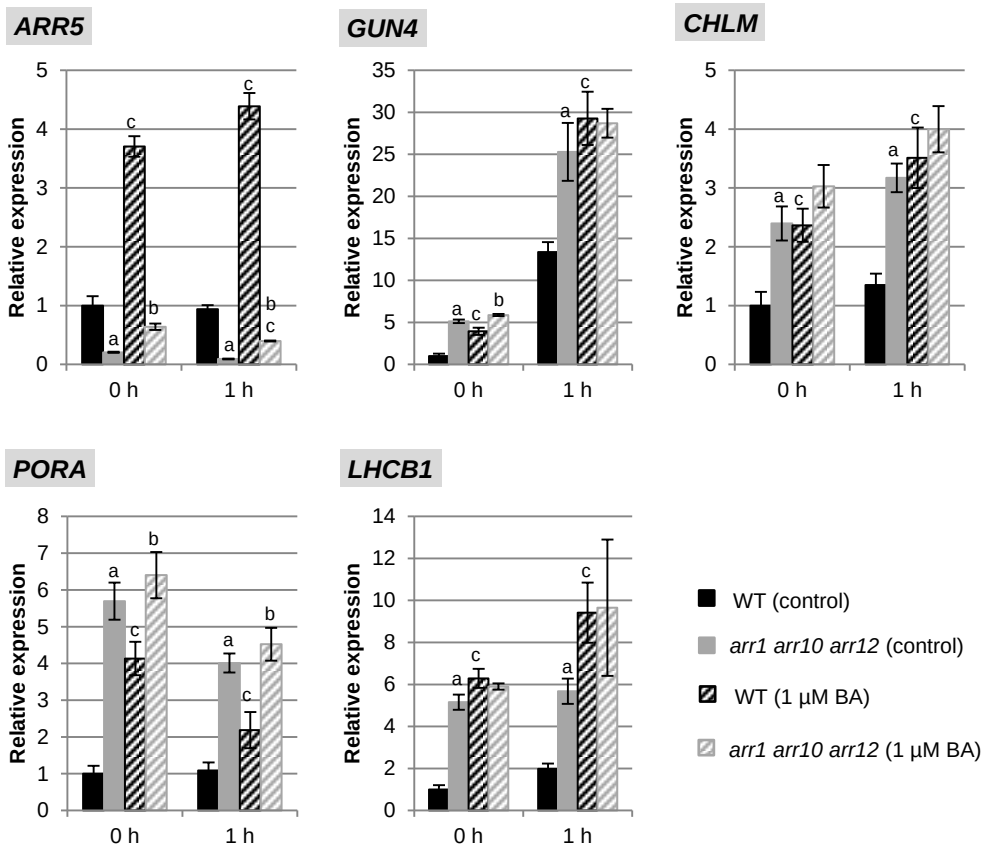

Figure S4. Effect of cytokinin on transcript level of genes encoding key steps in the chlorophyll biosynthesis pathway and of *ARR*5 and *LHCB1* in the *arr1 arr10 arr12* mutant during dark-to-light transition.

Seedlings were grown for 3 days in dark on medium (MS, no sucrose) with or without 1 µM BA prior to exposure to light. Analysis of transcript levels was done by quantitative real-time PCR of *ARR5, GUN4*, *GUN5*, *PORA* and *LHCB1*. Transcript levels of WT (control conditions) in dark were set to 1 (n ≥ 3). Letters indicate significant differences between WT and the different genotypes under control condition (a) or after BA treatment (b) or between control and BA treatment for each genotype (c) ($P < 0.05$). Analysis of additional genes can be found in Figure 6B.