

**Supplemental data for Attaran et al.,
“Temporal dynamics of growth and photosynthesis suppression by jasmonate
signaling”**

Supplemental Figure 1. Design of experiments for analysis of growth, photosynthetic efficiency, and gene expression profiling.

Supplemental Figure 2. COR treatment does not have an immediate effect on Φ_{II} .

Supplemental Figure 3. Validation of RNA-seq data by qPCR.

Supplemental Figure 4. COR treatment decreases *PAG* transcript levels.

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Supplemental Figure 6. Coronatine treatment elevates nonphotochemical exciton quenching (NPQ) at dawn of the day after treatment.

Supplemental Figure 7. Effect of COR treatment on H₂O₂ production.

The following supplemental tables are available separately for download as individual Excel files:

Supplemental Table S1. Fine temporal resolution of gene expression after coronatine treatment of Arabidopsis.

Supplemental Table S2. Top 50 repressed and top 50 induced defense genes.

Supplemental Table S3. Primers used for qRT-PCR analysis.

Supplemental Table S4. List of photosynthesis- and defense-associated genes used in this study.

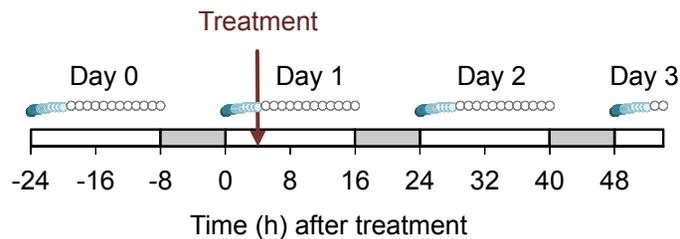
Phenometrics analysis

- intact plants grown on soil
- grown for 3-4 weeks, 7-10 rosette leaves
- 5 μ M coronatine or sterile water (mock) sprayed 3.5 h after dawn

- long-day photoperiod (LD 16:8)
- continuous monitoring of multiple plants
- one plant per replicate, at least two biological reps

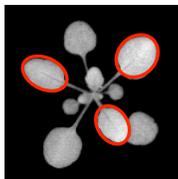
Imaging intervals

- 2 min • 5 min • 15 min • 30 min • 60 min

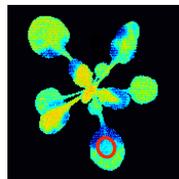


- determination of leaf area and Φ_{II} of 2-3 actively growing leaves from fluorescence images
- red outline denotes area used for measurement

Growth (leaf area)



Photosynthesis (Φ_{II})



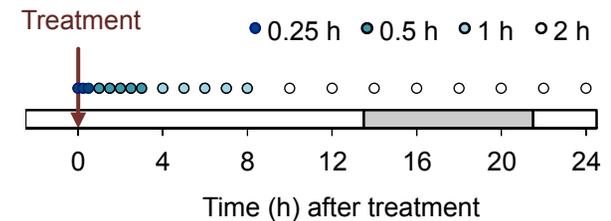
Gene expression analysis

- plants grown on plates (MS medium)
- grown for 20 d, 6-7 rosette leaves
- 5 μ M coronatine (COR) or sterile water (mock) sprayed 2.5-3 h after dawn

- long-day photoperiod (LD 16:8) maintained during sampling
- five plants pooled per sample, two biological replicates

Sampling intervals

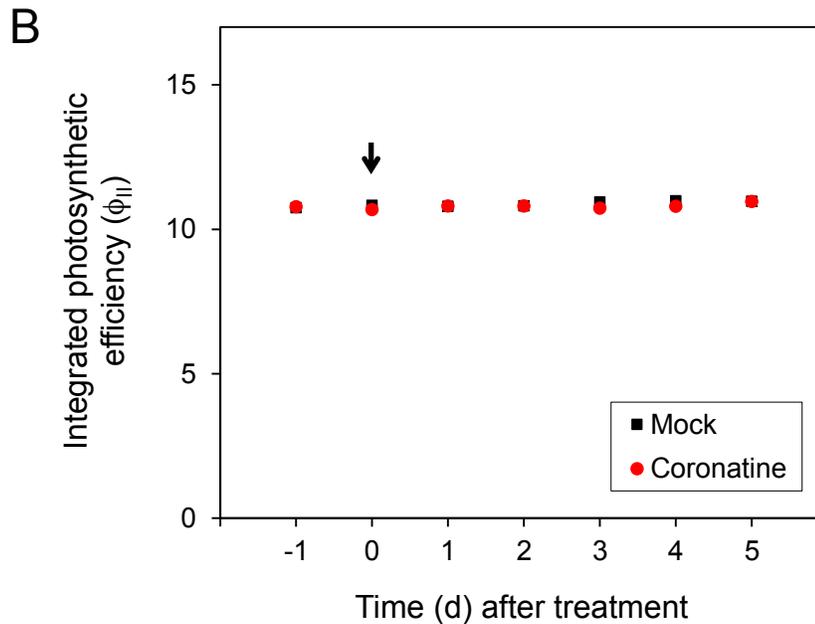
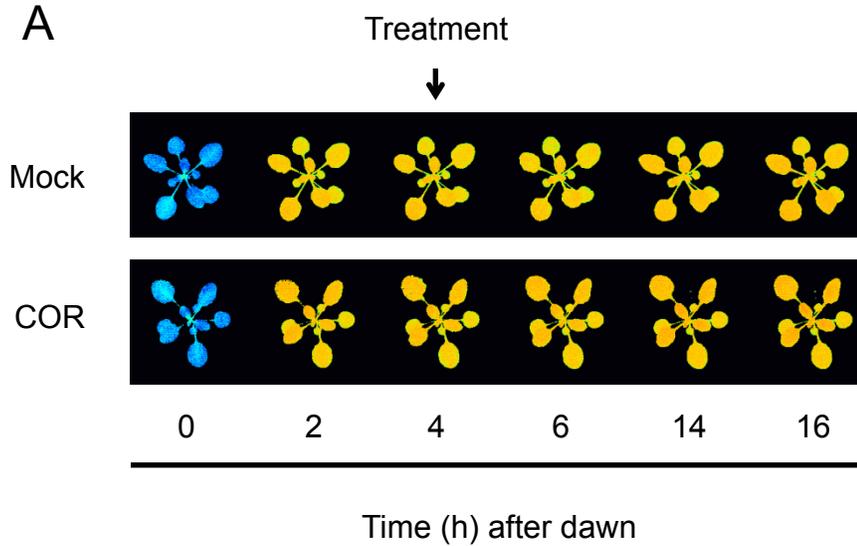
- 0.25 h • 0.5 h • 1 h • 2 h



Analysis

- RNA sequenced by Illumina Hi-Seq 2000
- reads mapped to TAIR10 transcripts using RSEM, data presented as transcripts per million (TPM)
- differential expression assessed by change in transcript level (COR – mock) and by fold change (COR / mock)

Supplemental Figure 1. Design of experiments for analysis of growth, photosynthetic efficiency, and gene expression profiling.

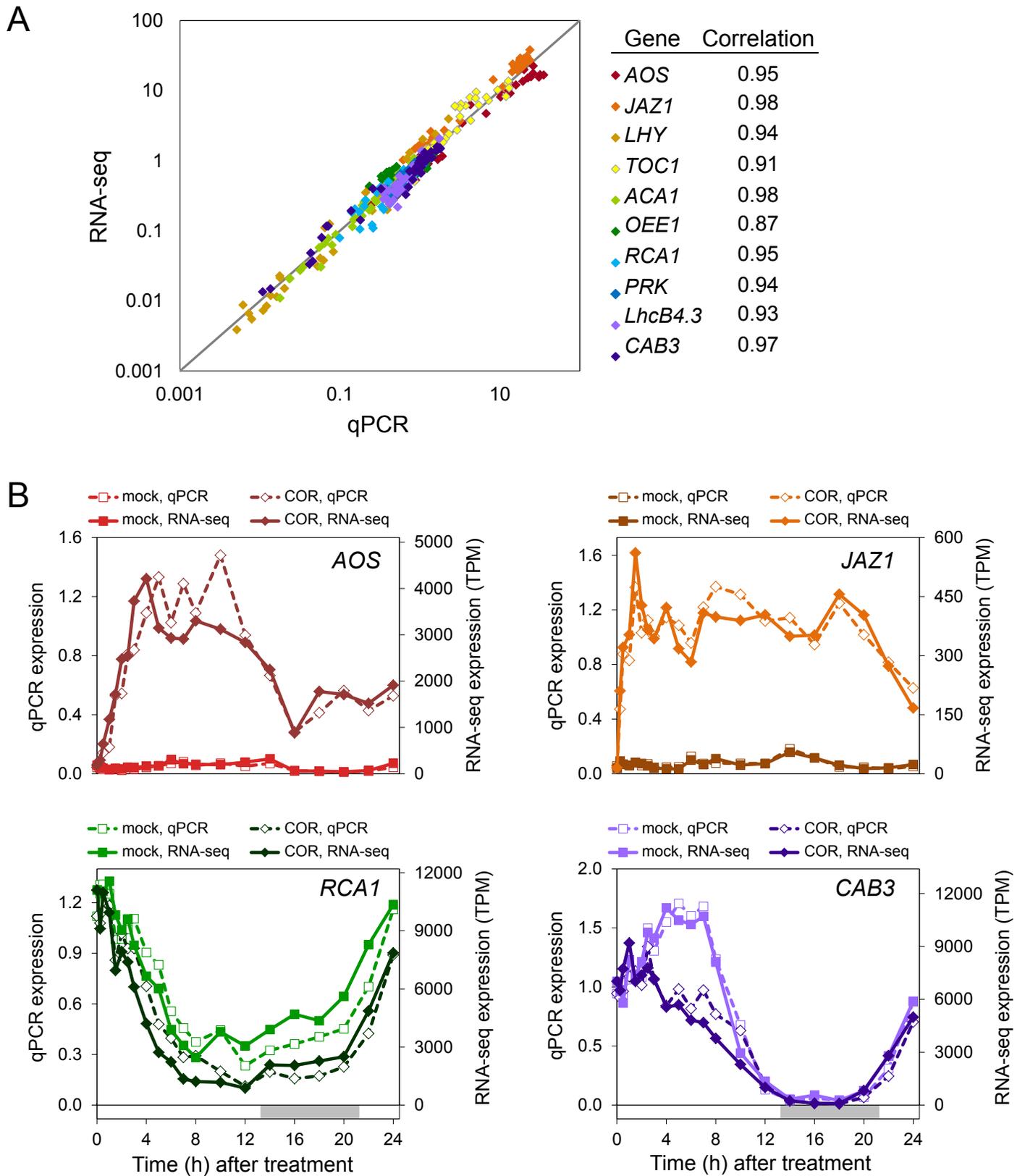


Supplemental Figure 2. COR treatment does not have an immediate effect on Φ_{II} .

Col-0 plants were treated with COR or a mock control as described in the legend to Figure 1.

A) False color images of Φ_{II} from representative plants were captured at the indicated times after dawn of the day of treatment. Images for the 0 h time point were taken 1 min after dawn (i.e., dark-light transition). Establishment of steady-state photosynthesis after the dark-light transition is shown by the change from blue (low Φ_{II}) to yellow (high Φ_{II}).

B) COR has a negligible effect on photosynthesis during a five-day period following treatment. Φ_{II} values were measured hourly and subsequently integrated over the course of the entire day for the five-day period following treatment. Values are the means \pm SD for two biological replicates.



Supplemental Figure 3. Validation of RNA-seq data by qPCR.

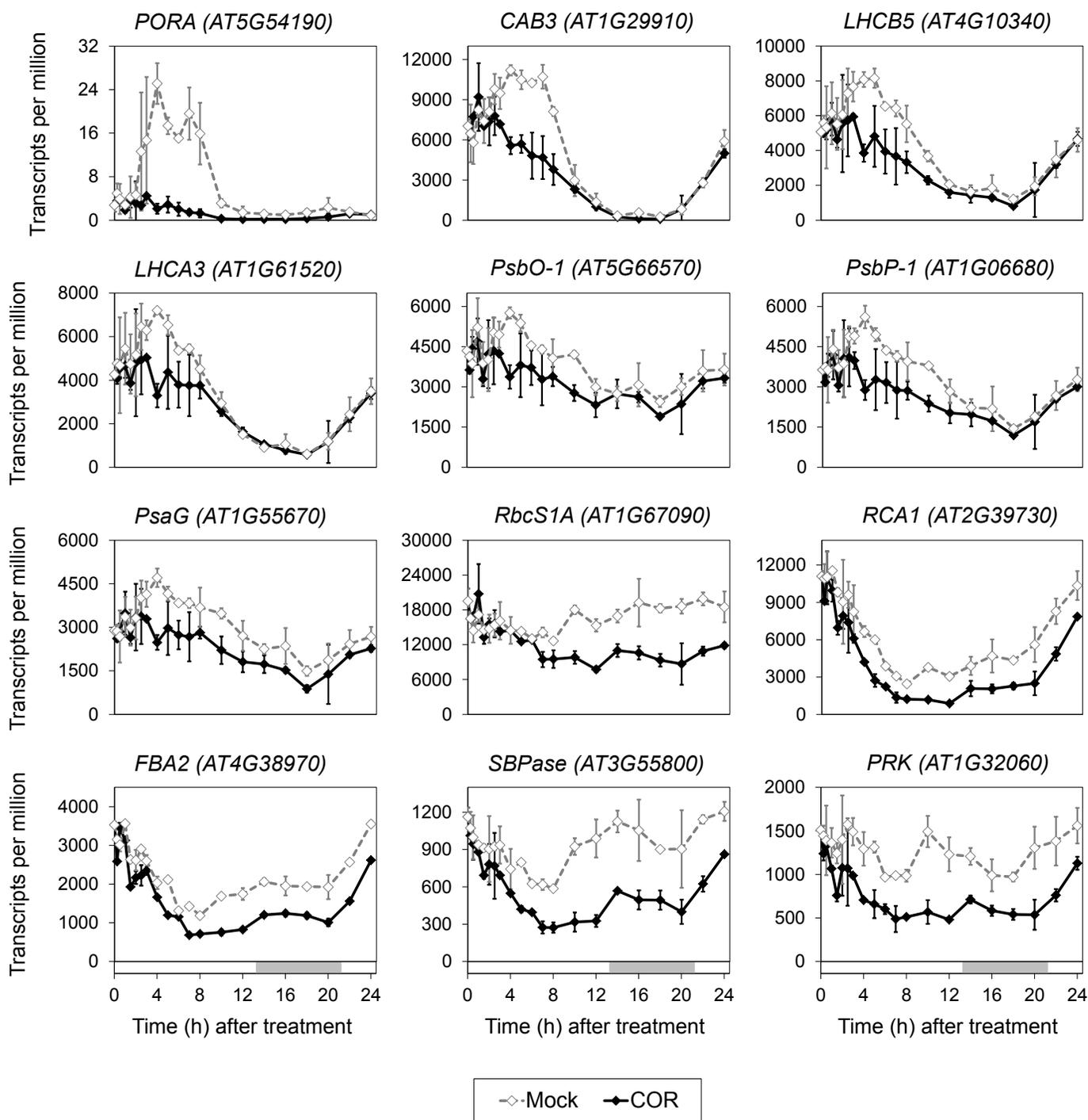
(legend on following page)

Supplemental Figure 3. Validation of RNA-seq data by qPCR.

Plants were treated with either COR or a mock control as described in the gene expression analysis section of Fig. S1. Gene expression levels at various times after treatment were measured by quantitative PCR (qPCR) or RNA-seq.

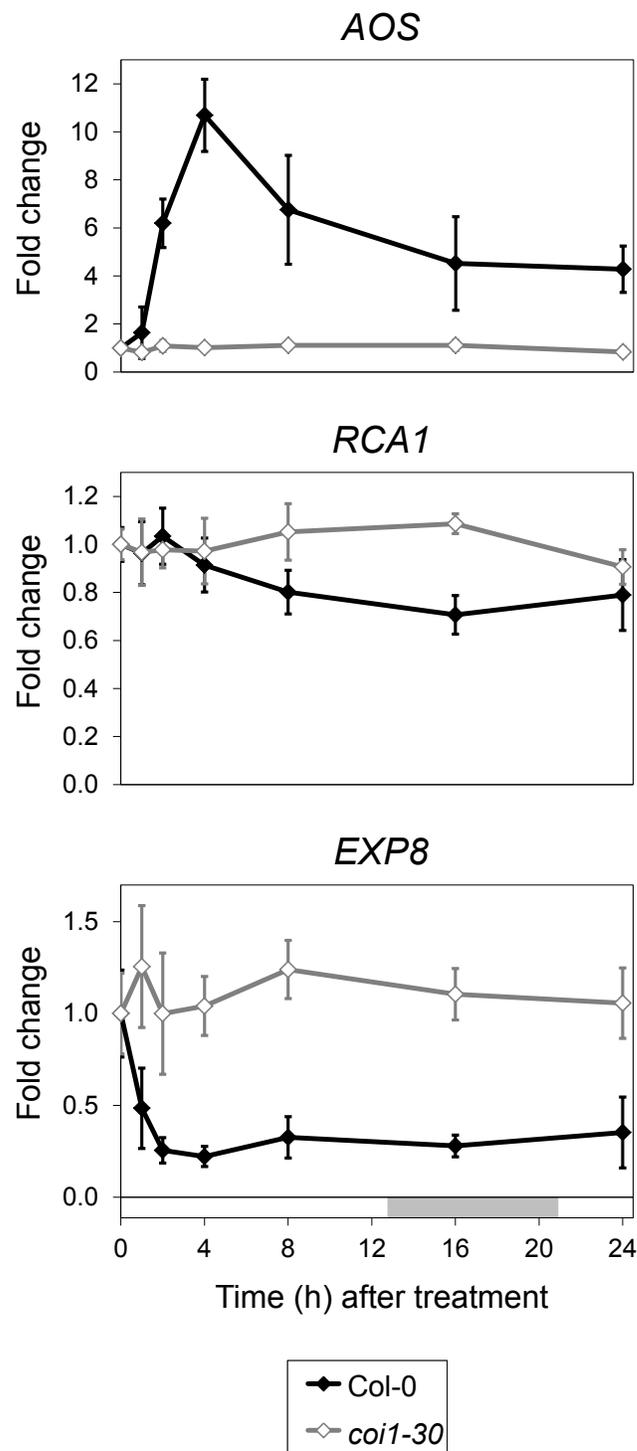
Correlation of fold change in the expression of the indicated genes measured by qPCR (x-axis) and RNA-seq (y-axis). Multiple data points for each gene correspond to each time point after treatment.

For each of the four genes shown (*AOS*, *JAZ1*, *RCA1*, and *CAB3*), the detailed time course of expression was determined with qPCR and RNA-seq. Photoperiod is denoted above the x-axis.



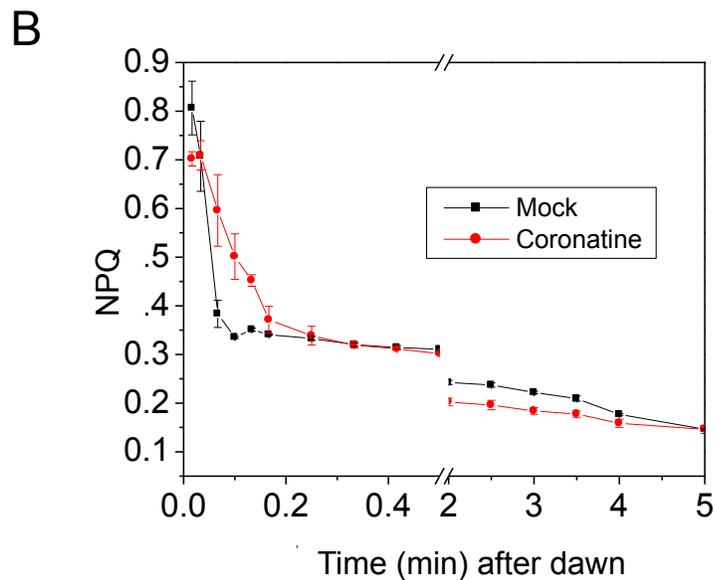
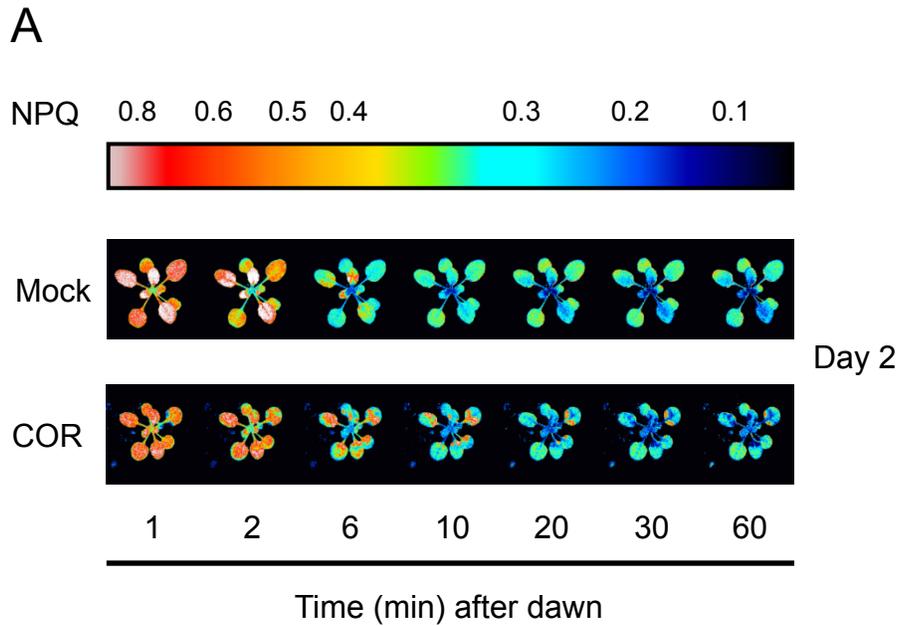
Supplemental Figure 4. COR treatment decreases *PAG* transcript levels.

Plants were treated with COR (black) or mock control (grey) as described in the gene expression analysis section of Fig. S1. Transcript levels for each of the indicated *PAGs* was determined by RNA-seq. Data points show mean expression level \pm SD of two biological replicates. Photoperiod is denoted above the x-axis.



Supplemental Figure 5. COR-induced changes in gene expression are dependent on COI1.

Wild-type (*Col-0*) and *coi1-30* plants were treated with either COR or mock control as described in the gene expression analysis section of Figure S1. The expression level of marker genes involved in JA biosynthesis (*AOS*), photosynthesis (*RCA1*), and cell expansion (*EXP8*) was determined by qPCR. Data show the mean \pm SD of the fold-change in gene expression (COR/Mock) of three biological replicates. Photoperiod is denoted above the x-axis.

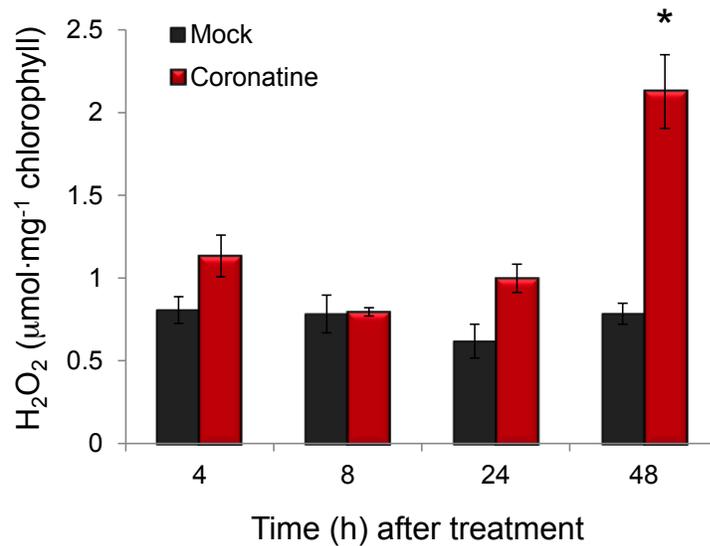


Supplemental Figure 6. Coronatine treatment elevates nonphotochemical exciton quenching (NPQ) at dawn of the day after treatment.

Col-0 plants were acclimated in the imaging chamber for 36 h and, 4 h after dawn of the following day (Day 1), were treated with either water (mock) or COR.

A) Representative false color images of NPQ (scale at top) taken at the indicated times after dawn of the day after treatment (Day 2).

B) NPQ values (mean \pm SD, n = 3 replicates) were calculated from chlorophyll fluorescence images taken at the indicated times after the onset of dawn (dark-light transition) of the day (Day 2) after treatment. For each replicate, NPQ was quantified for two to three actively growing leaves per plant.



Supplemental Figure 7. Effect of COR treatment on foliar H₂O₂ production.

Amplex Red assays were used to measure H₂O₂ accumulation in seedlings that were treated for the indicated times with COR or water as a mock control. Data show the mean ± SE of four biological replicates ($n = 4$) in one representative experiment. Asterisk denotes a significant difference ($P < 0.05$, two-tailed T-test) between the mock- and COR-treated samples.