

Expanded View Figures

Figure EV1. Nutrient availability determines *Arabidopsis thaliana* responses to *Bacillus amyloliquefaciens* GB03 (related to Fig 1).

- A Exposure to MVs from GB03, which was either grown on the nutrient-sufficient (0.5 MS) or grown on the nutrient-deficient (0.05 MS) medium, caused opposed impacts on plants grown in different medium. The petri dishes contain plastic partitions (red dotted lines) that separate different medium.
- B Quantification of fresh weight of seedlings grown under different treatment conditions. Values correspond to the means \pm SE of three biological replicates. Different letters denote significant differences at $P < 0.05$, Tukey's multiple comparison test within each group of the same DAT.
- C Anthocyanin accumulation levels in plants at 11 DAT. The boxplots show representative data from three independent experiments ($n = 9$). Whiskers represent the min to max data range, and the median is represented by the central horizontal line. The upper and lower limits of the box outline represent the first and third quartiles. Different letters denote significantly different means at $P < 0.05$, Tukey's multiple comparison test.
- D Relative gene expression levels of *Arabidopsis* *ELI3*, *MYB75*, *MDAR3*, and *GRXC11*, which are indicative of environmental stress conditions (Somssich *et al*, 1996; Teng *et al*, 2005; Li *et al*, 2010; Mehterova *et al*, 2012), in 5 DAT seedlings grown in 0.5 and 0.05 MS medium with or without exposure to GMVs. Values are means \pm SE of three biological replicates. Different letters denote significantly different means at $P < 0.05$, Tukey's multiple comparison test.
- E Gene Ontology (GO) comparative analysis of *Arabidopsis* genes that were repressed at 5 DAT by nutrient deficiency (0.05C vs. 0.5C) alone and that were repressed by the nutrient deficiency plus GMVs (0.05T vs. 0.5C). Diagrams are designed based on *VirtualPlant* platform. The size of circles represents the number of genes in each GO category. Scale color bar indicates the P -value cutoff of over-representation equal or less than the cutoff for each GO category. Darker color indicates higher possibility of each GO category. DEG lists for key terms are provided in Table EV3.

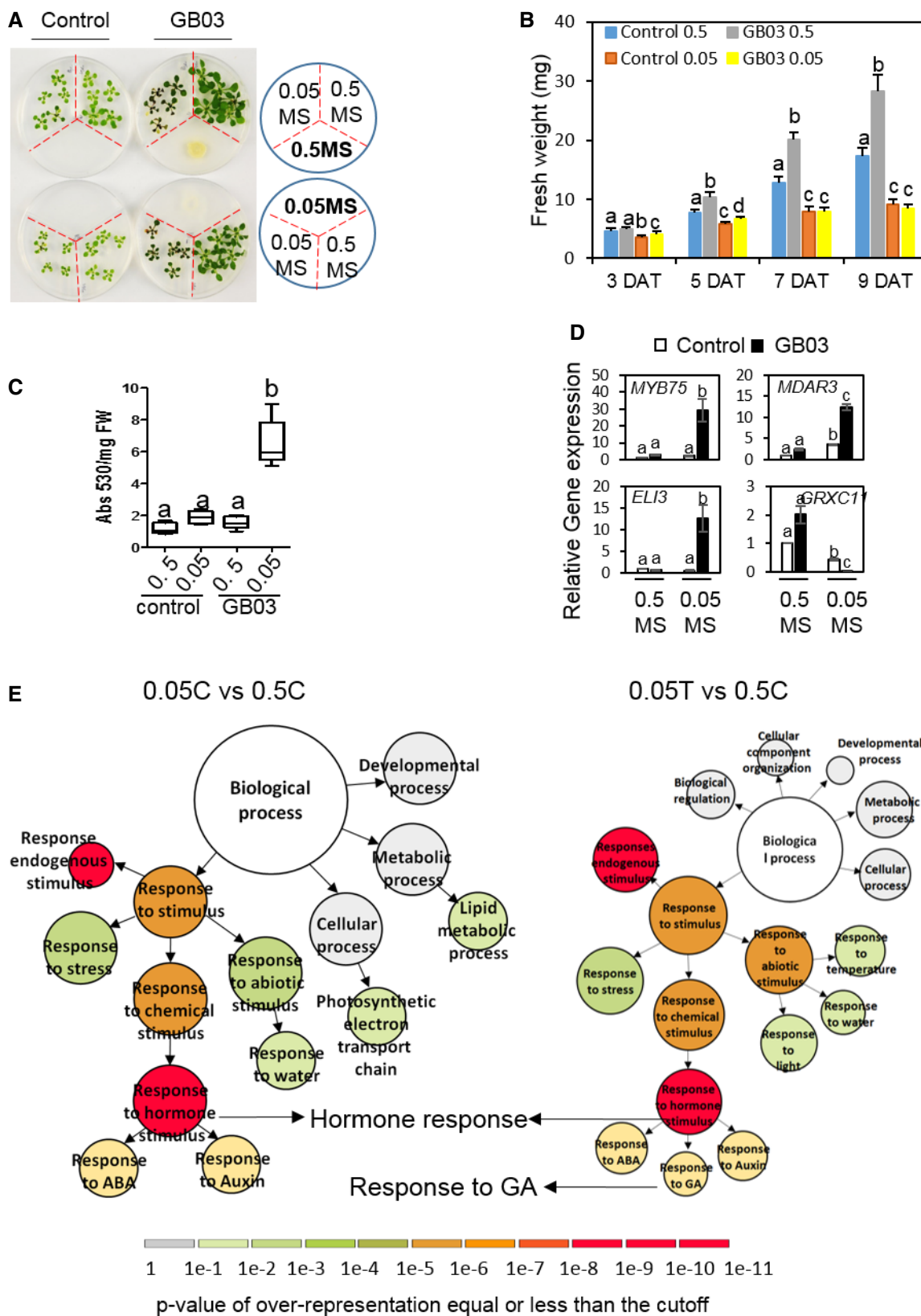


Figure EV1.

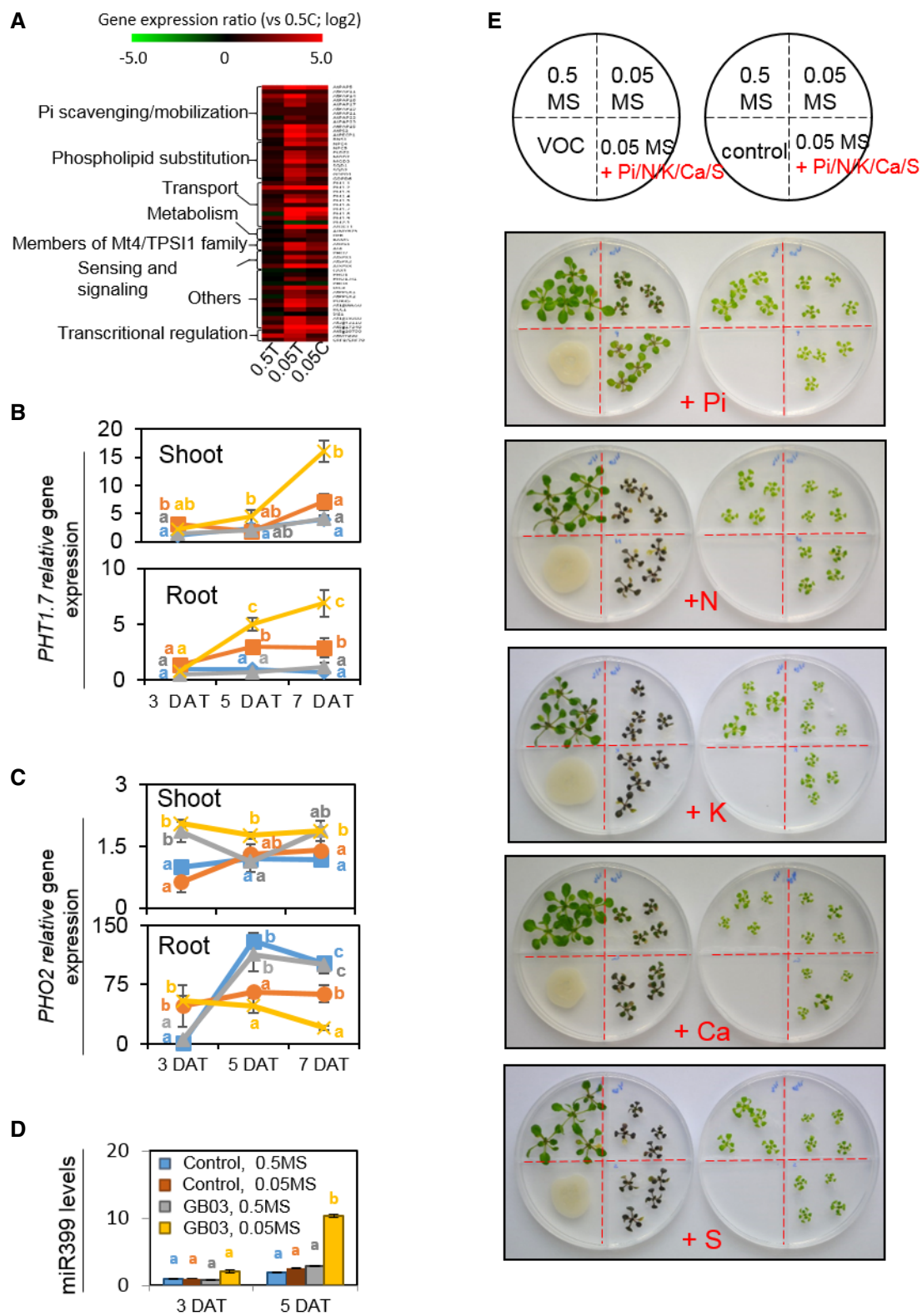


Figure EV2.

◀ **Figure EV2. Phosphate availability determines *Arabidopsis* responses to GMVs (related to Fig 2).**

- A A heatmap of RNAseq results showing the expression levels of Pi homeostasis genes in *Arabidopsis* grown under different conditions, including 0.5T (0.5 MS medium with GMV treatment), 0.05T (0.05 MS medium with GMV treatment), and 0.05C (0.05 MS medium without GMV treatment). Color scale indicates fold changes (\log_2) compared with gene expression in plants grown in 0.5C (0.5 MS medium without GMV treatment). DEG lists are provided in Table EV5.
- B, C GMVs caused plant hyper-sensitivity to Pi deficiency, as shown by GMV-dependent hyper-induction of PHT1.7 (B) and hyper-suppression of PHO2. (C) Data points indicate mean \pm SE ($n = 3$). Different letters denote significantly different means at $P < 0.05$, Tukey's multiple comparison test within each group of the same DAT.
- D The accumulation level of miR399 was strongly elevated by GMVs in nutrient-deficient plants. Values are means \pm SE of three biological replicates. Different letters denote significantly different means at $P < 0.05$, Tukey's multiple comparison test within each group of the same DAT.
- E Different macronutrients including phosphorus (P), nitrogen (N), potassium (K), calcium (Ca), and sulfur (S) were supplemented individually to the 0.05 MS medium, in order to bring the corresponding nutrient content to a level that is equal to that in the 0.5 MS medium. The petri dishes contain plastic partitions (red dotted lines) that separate different medium. A scheme showing medium partitions is shown on the top right corner.

Figure EV3. Deleterious effects caused by DA are due to an activation of immunity in Pi-deficient plants (related to Fig 4). ▶

- A DA induces genes involved in JA biosynthesis and signaling in *Arabidopsis* grown with Pi deficiency.
- B DA elevates JA accumulation levels in Pi-deficient *Arabidopsis*. Means \pm SE of three biological replicates.
- C Images of plants grown with different treatments using DA (9.7 $\mu\text{g/ml}$ free space) or MeJA (25 μM in plant growth medium).
- D, E Exogenous application of MeJA mimics DA-induced anthocyanin accumulation (D) and PS2 gene induction (E) patterns in Pi-deficient plants.
- F, G Compared with the wild-type plants, the JA-insensitive *coi1* mutant plants showed altered responses to DA under Pi-deficiency condition, as shown by plant images (F) and quantification of anthocyanin accumulation levels (G).

Data information: The boxplots show representative data from three independent experiments ($n = 6$). Whiskers represent the min to max data range, and the median is represented by the central horizontal line. The upper and lower limits of the box outline represent the first and third quartiles. qPCR results show values of means \pm SE ($n = 3$), and two biological replicates were analyzed with similar results. Different letters denote significantly different means at $P < 0.05$, Tukey's multiple comparison test.

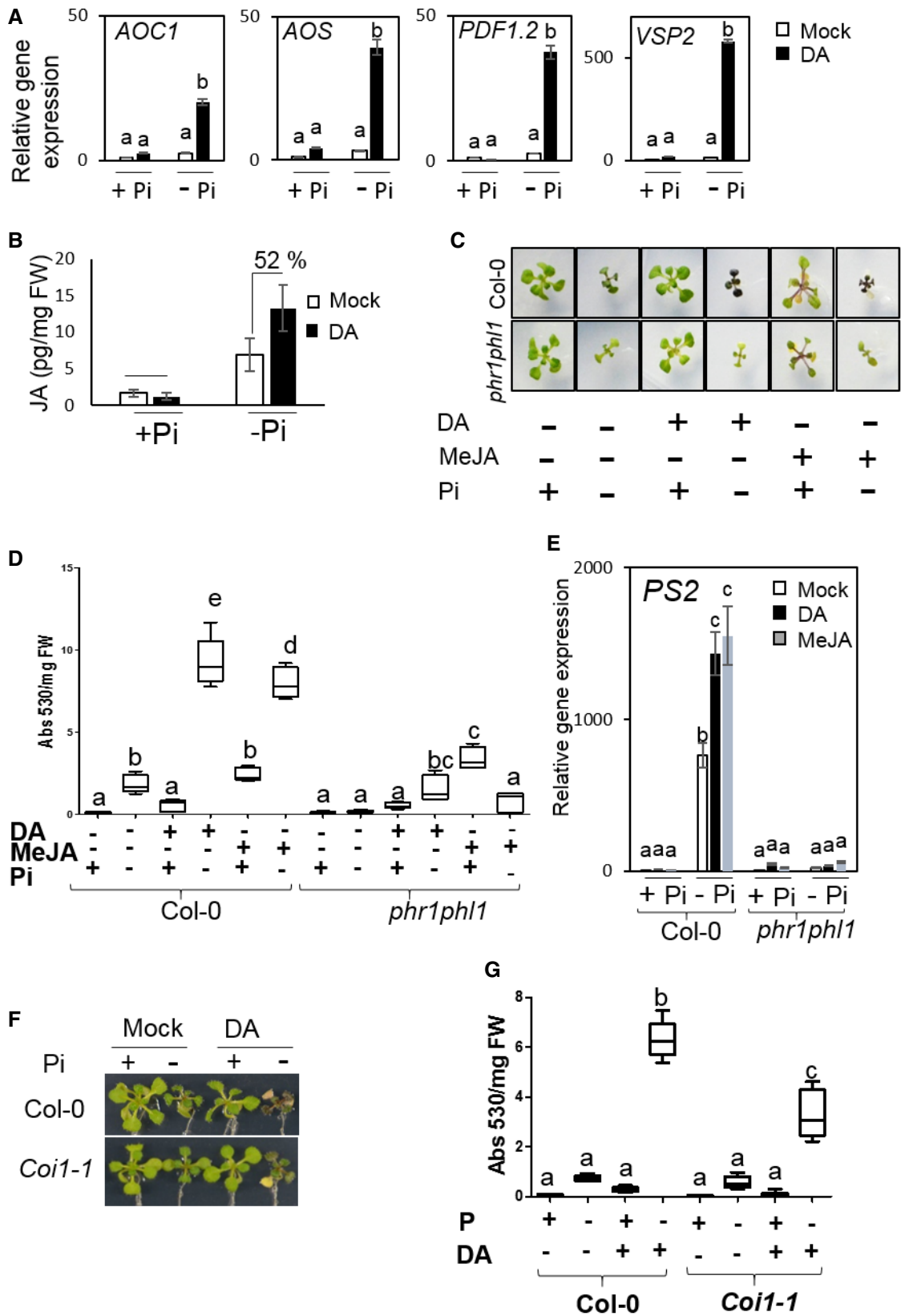


Figure EV3.

Figure EV4. DA suppresses plant ROS burst but not PTI gene expression in response to flg22 (related to Fig 5).

- A Fresh weights measured in plants grown with or without DA treatments. Different letters denote significantly different means at $P < 0.05$, Tukey's multiple comparison test. The boxplots show representative data from three independent experiments ($n = 15$). Whiskers represent the min to max data range, and the median is represented by the central horizontal line. The upper and lower limits of the box outline represent the first and third quartiles.
- B Transcriptional suppression of some immune response-related genes by DA. qPCR results show values of means \pm SE ($n = 3$), and two biological replicates were analyzed with similar results. Different letters denote significantly different means at $P < 0.05$, Tukey's multiple comparison test.
- C DA suppresses plant ROS burst induced by flg22 or elf18. ROS accumulation was represented in relative luminescence units (RLU). Data point indicates mean \pm SE ($n = 24$). Three independent experiments were performed, and similar results were observed. $**P < 0.01$, Student's t -test.
- D DA, but not 2,3-butanediol (BTDL) or acetoin (ATN), suppresses plant ROS burst induced by flg22 or elf18. Three independent experiments were performed with similar results. Data bar indicates mean \pm SE ($n = 24$) for 60 min. Different letters denote significantly different means at $P < 0.05$, Tukey's multiple comparison test.
- E DA suppresses plant ROS burst induced by flg22 in P-deficient grown plants. Data bar indicates mean \pm SE ($n = 24$) for 60 min. Three independent experiments were performed with similar results. $**P < 0.01$, Student's t -test.
- F DA induces gene expression of *AZ11* in P-deficient grown *Arabidopsis* plant. Different letters denote significantly different means at $P < 0.05$, Tukey's multiple comparison test. qPCR data indicate mean \pm SE ($n = 3$), and two biological replicates were analyzed with similar results.

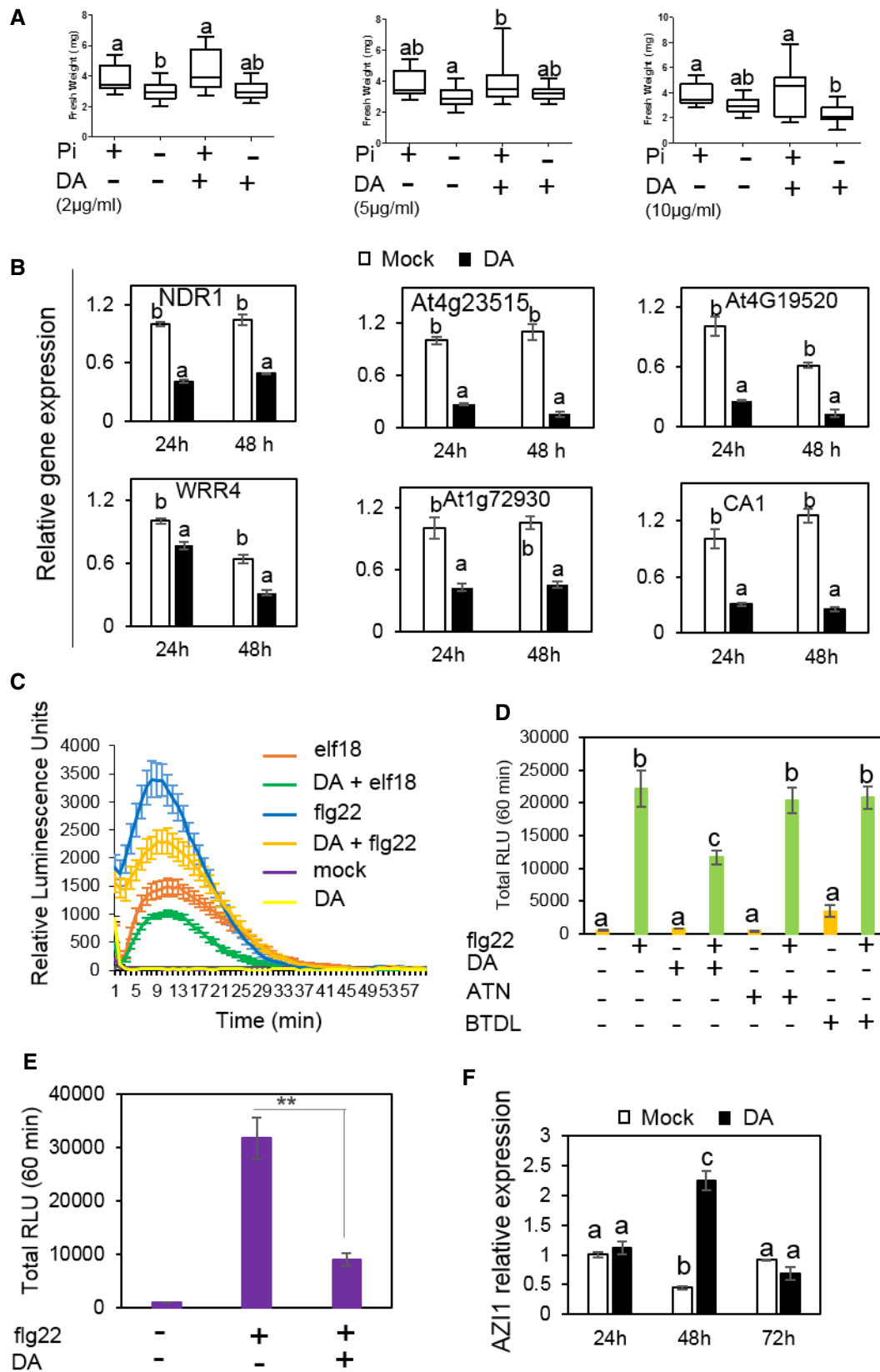


Figure EV4.