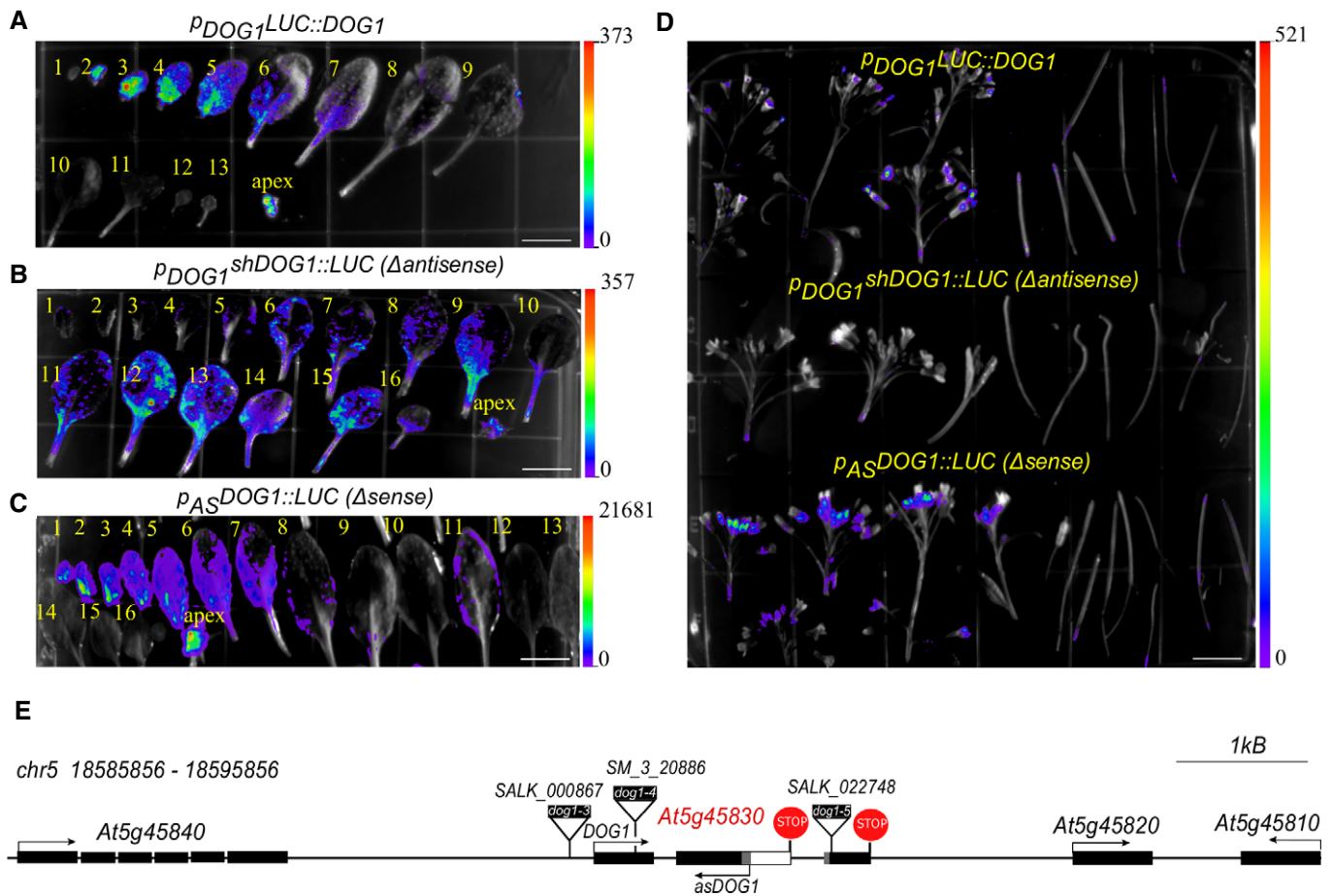
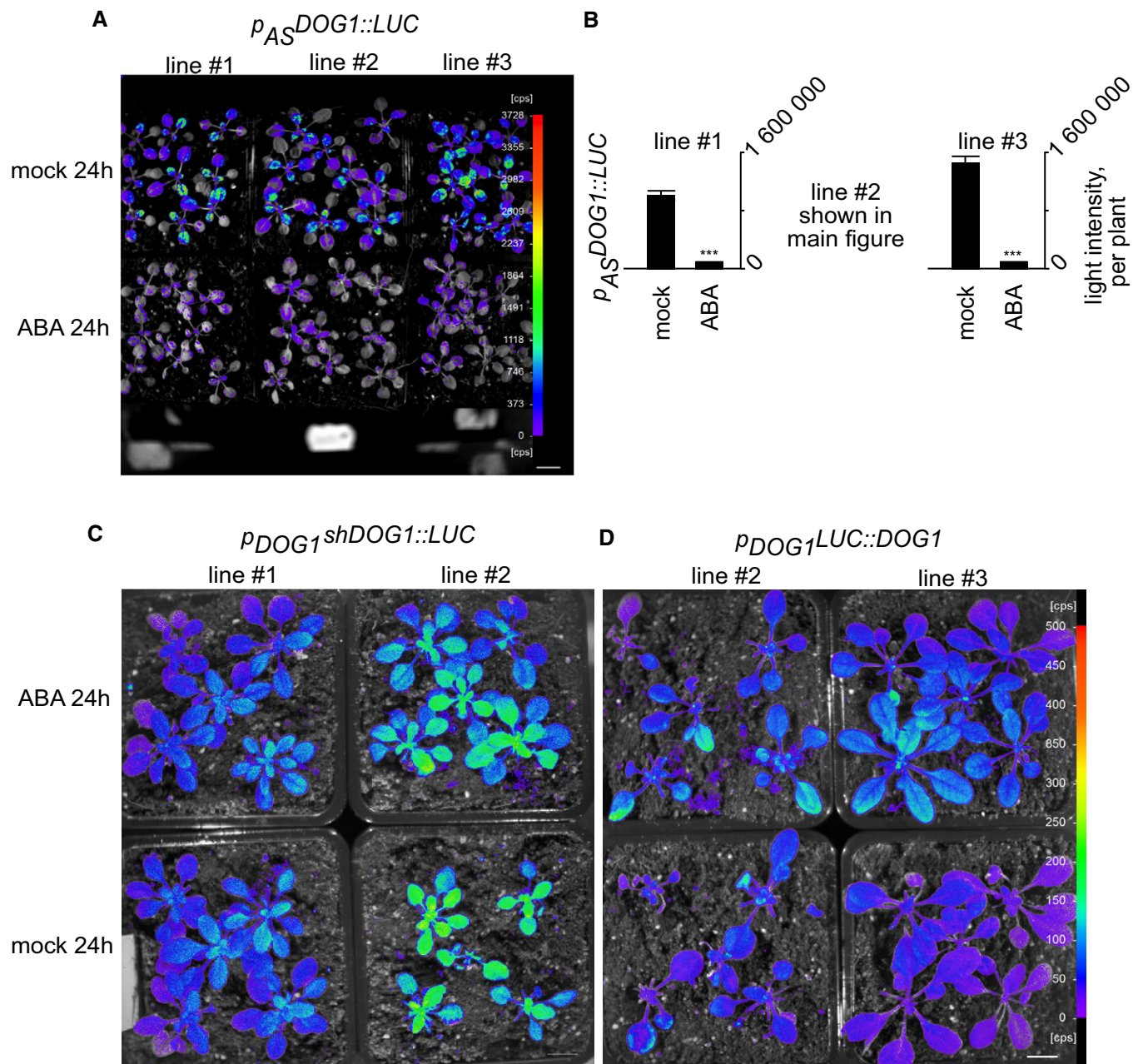


## Expanded View Figures



**Figure EV1. Tissue-specific expression of *DOG1* sense and antisense.**

- A *DOG1* sense mRNA expression driven by the genomic construct. Numbers represent consecutive leaf number, from young to old. Scale bar: 2 cm.
- B *DOG1* sense mRNA expression driven by *DOG1* genomic construct with antisense promoter removed. Numbers represent consecutive leaf number, from young to old. Scale bar, 2 cm.
- C *DOG1* antisense expression analysis. Numbers represent consecutive leaf number, from young to old. Scale bar, 2 cm.
- D LUC expression analysis in flowers and siliques of plants expressing  $p_{DOG1}LUC::DOG1$ ,  $p_{DOG1}shDOG1::LUC$  and  $p_{AS}DOG1::LUC$ . Scale bar: 2 cm.
- E Schematic diagram of the *DOG1* gene at genomic scale: black boxes, exon sequences; grey boxes, alternative exonic regions; white box region included in alternatively polyadenylated *DOG1* short transcript; arrows show the sense and antisense transcripts TSS and expression direction of *DOG1*; red circles indicate TTS for short and long mRNA of *DOG1*, correspondingly. The positions of T-DNA insertions are indicated by black rectangles: *dog1-3* (SALK\_000867), *dog1-4* (SM\_3\_20886) and *dog1-5* (SALK\_022749).

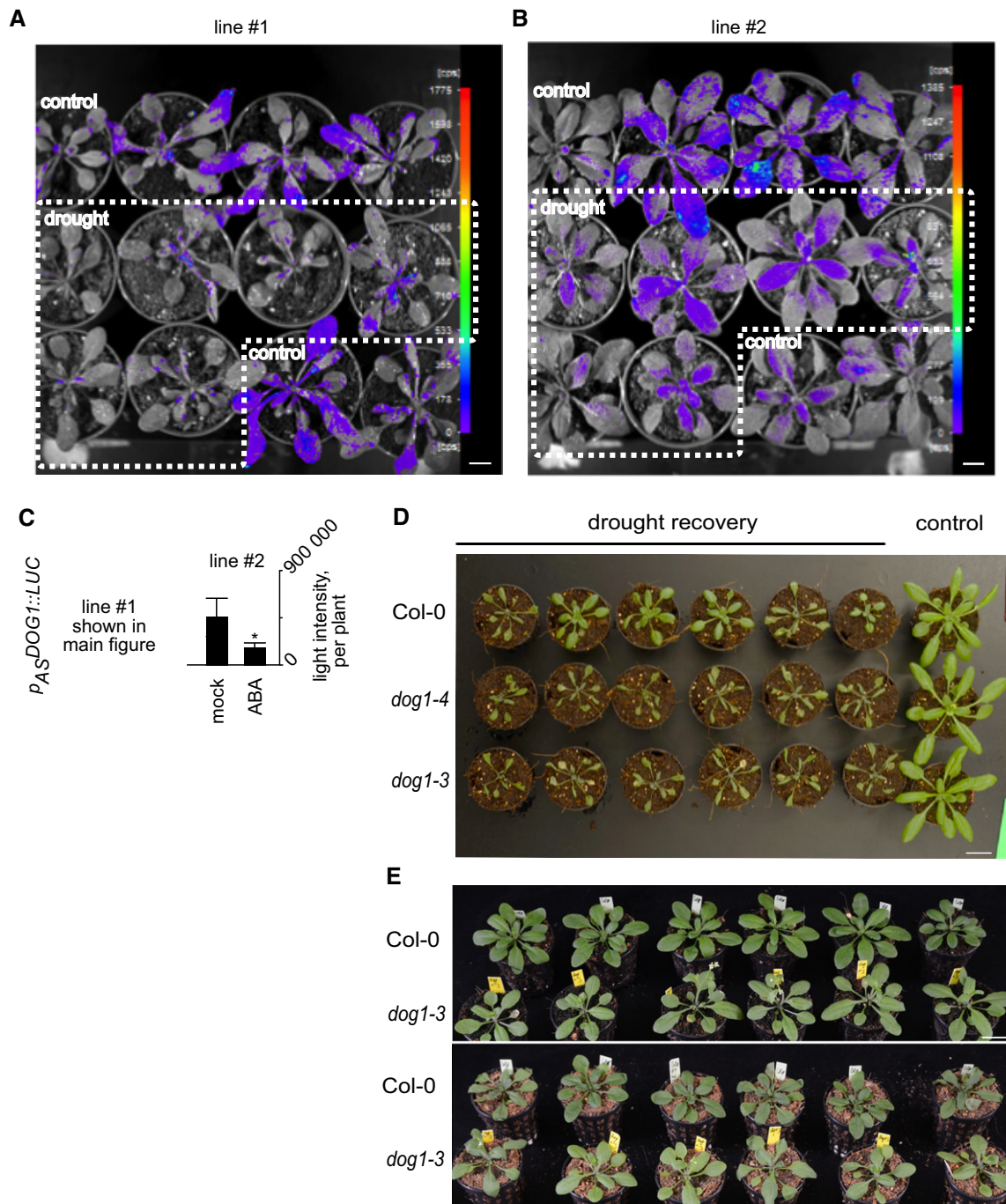


**Figure EV2.** ABA response of 20-day-old transgenic lines expressing  $p_{AS}^{DOG1}::LUC$ .

A, B LUC pictures taken after 24 h of treatment and LUC quantification per seedlings of 20-day-old transgenic lines expressing  $p_{AS}^{DOG1}::LUC$ . Scale bar, 2 cm. \*\*\* $t$ -test-derived  $P$ -value < 0.001. Error bars represent standard deviation,  $n = 9$  for each of three independent lines.

C LUC pictures of 40-day-old transgenic *Arabidopsis* lines expressing  $p_{DOG1}^{shDOG1}::LUC$ . Scale bar, 2 cm.

D  $p_{DOG1}^{LUC}::DOG1$  constructs after mock and ABA treatments. Scale bar, 2 cm.



**Figure EV3. Analysis of drought responses in  $p_{ASDOG1::LUC}$  transgenic plants and *dog1* mutants.**

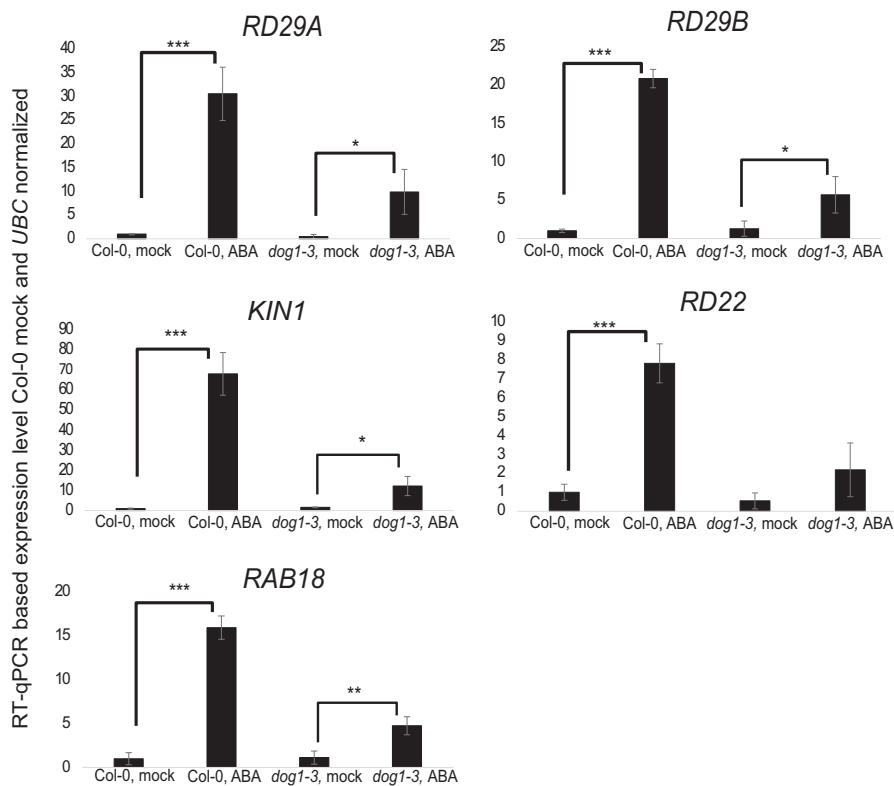
A, B Downregulation of antisense transcription by drought of two independent  $p_{ASDOG1::LUC}$  lines. Scale bar, 1 cm.

C Graph represents quantification of light intensity per plant. Error bars represent standard deviation. \**t*-test-derived *P*-value < 0.05, *n* = 12 for each of two lines.

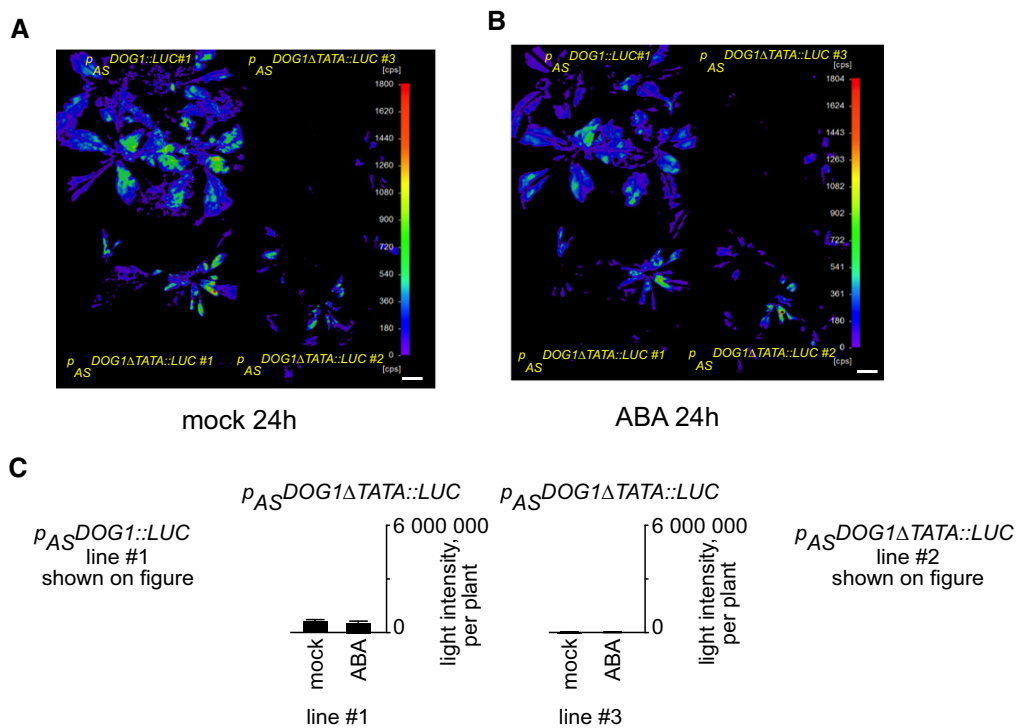
D Drought susceptibility of *dog1-3* and *dog1-4* mutants in comparison with Col-0 (WT) plants after 5 days of treatment, independent repeat. Scale bar, 2 cm.

E Growth phenotype of Col-0 (WT) and *dog1-3* mutant plants used for RT-qPCR analysis of *DOG1* sense/antisense and marker genes at 3 days of drought. Scale bar, 2 cm.





**Figure EV4.** RT-qPCR analysis of selected marker gene expression in Col-0 (WT) and *dog1-3* mutant after 10 h of 100 μM ABA spray-inoculation. Error bars represent standard deviation. \*, \*\* and \*\*\* represent t-test P-values of < 0.05, < 0.01 and < 0.001, respectively, n = 4.



**Figure EV5. Bioluminescence analysis of transgenic lines expressing  $p_{AS}^{DOG1::LUC}$  and  $p_{AS}^{DOG1::LUC\Delta TATA}$  lines after 24 h.**

A, B Plants were mock treated and imaged after 24 h, subsequently sprayed with 100 mM ABA and imaged 24 h later. Scale bar, 2 cm.

C Quantification of LUC pictures as relative light intensity per plant. Error bars represent standard deviation,  $n = 8$  for each of three lines.