CIRCADIAN CLOCK ASSOCIATED 1 and ATAF2 differentially suppress cytochrome P450-mediated brassinosteroid inactivation

Hao Peng and Michael M. Neff*

Department of Crop and Soil Sciences, Washington State University, Pullman, WA 99164, USA

Table S1. Sequences of *ATAF2* promoter fragment used for targeted Y1H. The CCA1 binding site (CBS) is underlined.

Name	Sequence
p*ATAF2*-CBS	ATAAAAAAGTAGTGGCTGCTGAGATTTTTCTTTTTAA ATCTTAGTGGTAAATCTTAGTGGTAA

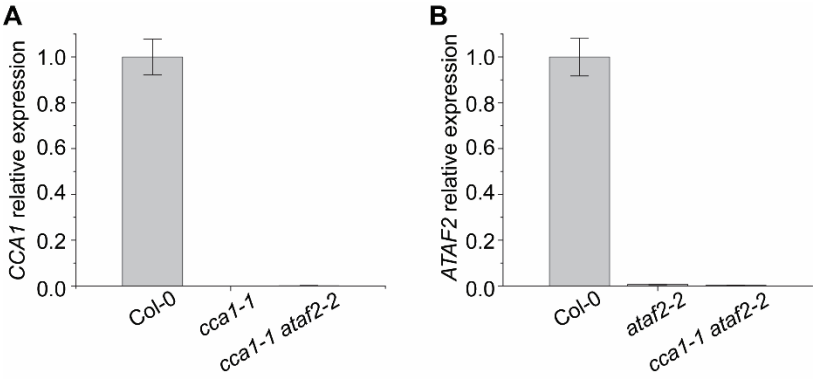

Fig. S1. qRT-PCR assays on *CCA1* (A) and *ATAF2* (B) transcript accumulations demonstrate that *cca1-1*, *ataf2-2* and *cca1-1 ataf2-2* are all gene knock-out mutants. Four-day-old seedlings grown at 25 °C in 80 μmol m^{-2} s^{-1} continuous white light were used for RNA extraction. Each qRT-PCR value is the mean of results from three biological replicates. Error bars denote the s.e.m.

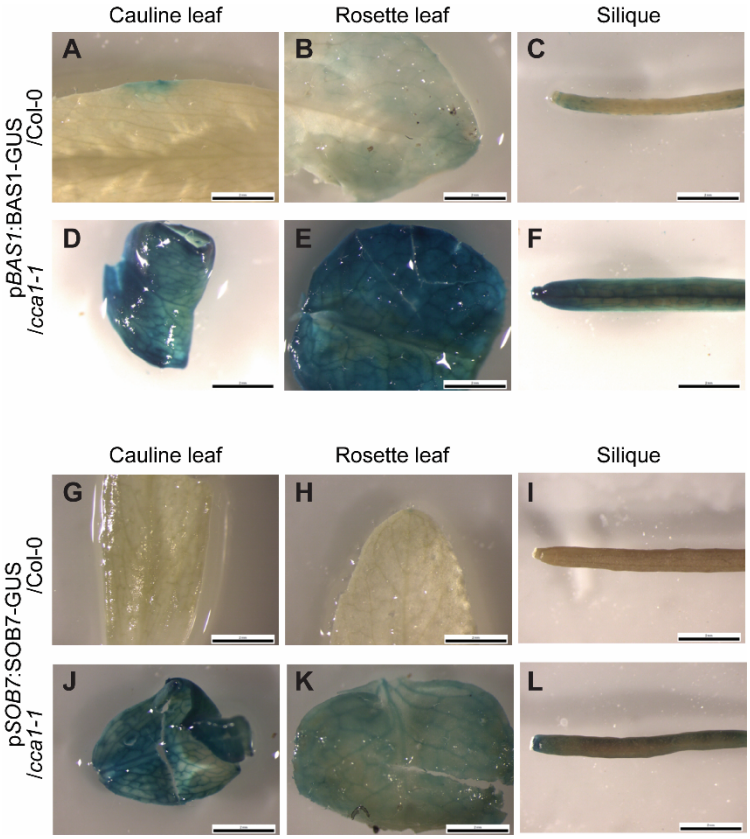

Fig. S2. CCA1 modulates the tissue-specific expression patterns of BAS1 and SOB7 in leaves and siliques. The role of CCA1 in restricting BAS1 and SOB7 expression within cauline leaf, rosette leaf and silique was demonstrated by GUS analysis on F3 homozygous segregants of p*BAS1*:BAS1-GUS/Col-0 (A-C), p*BAS1*:BAS1-GUS/*cca1-1* (D-F), p*SOB7*:SOB7-GUS/Col-0 (G-I), and p*SOB7*:SOB7-GUS/*cca1-1* (J-L). Scale bars: 2 cm.

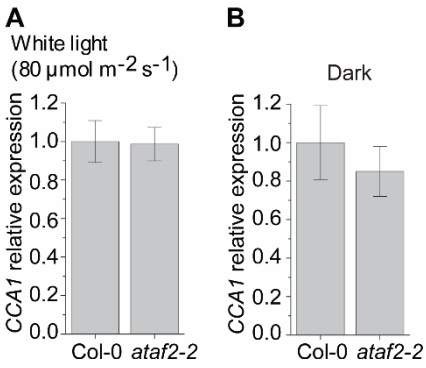

Fig. S3. Compared to Col-0, *ataf2-2* seedlings did not show significant changes of *CCA1* expression in either continuous light (A) or darkness (B). Each qRT-PCR value is the mean of results from three biological replicates × three technical replicates (n=9). Error bars denote the s.e.m.