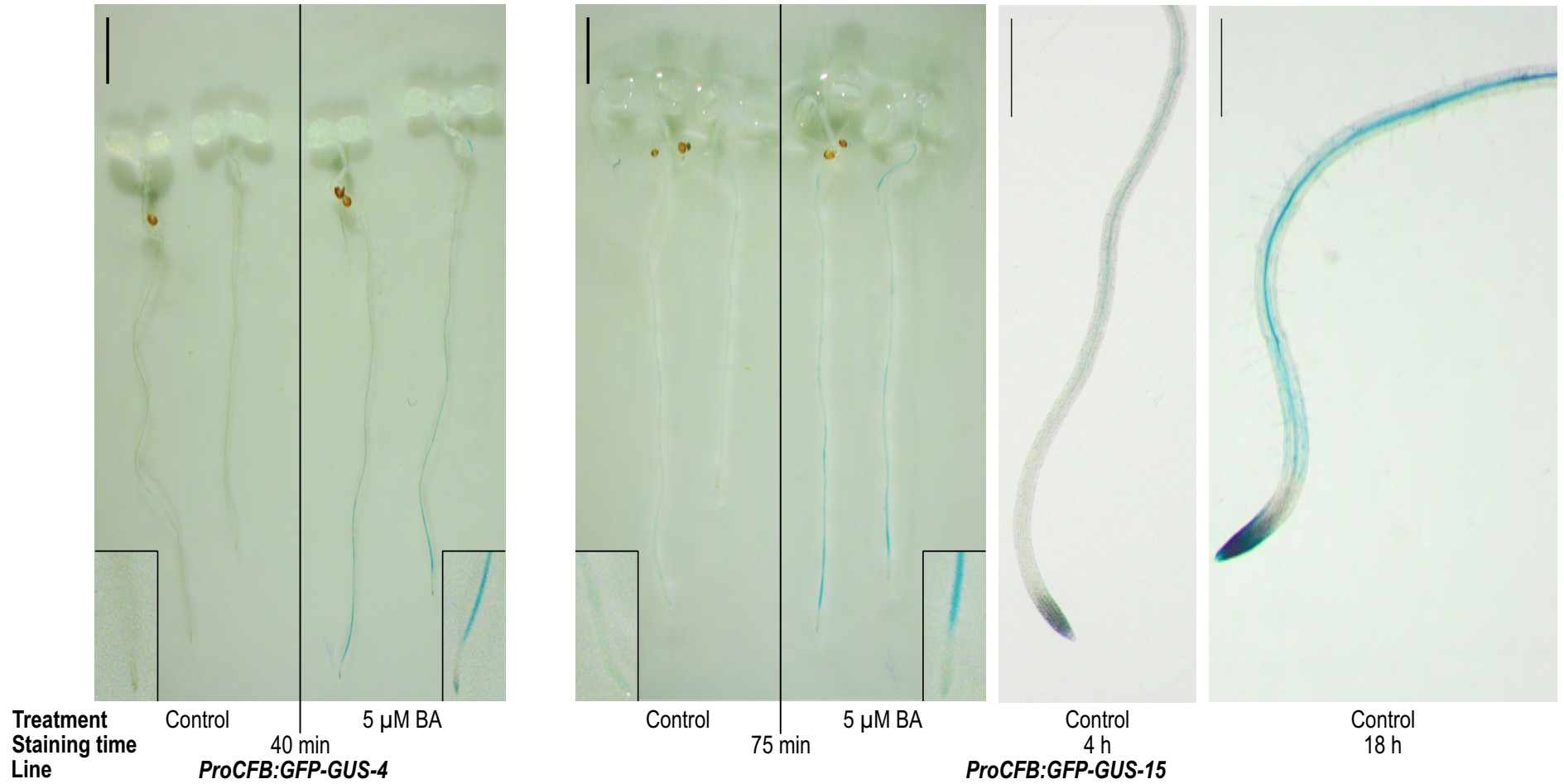

Figure S1. Histochemical staining of *CFB* promoter induction by cytokinin in two independent transgenic lines carrying a *ProCFB:GFP-GUS* reporter gene. 6-day-old seedlings were treated with 5 µM of the synthetic cytokinin 6-benzyladenine (BA) or a solvent control for the times indicated. Subsequently, the seedlings were stained according to Jefferson et al. (1987) for the times indicated, inspected and photographed as described in Materials and methods. The insets show magnifications of root tips. Scale bar = 5 mm.

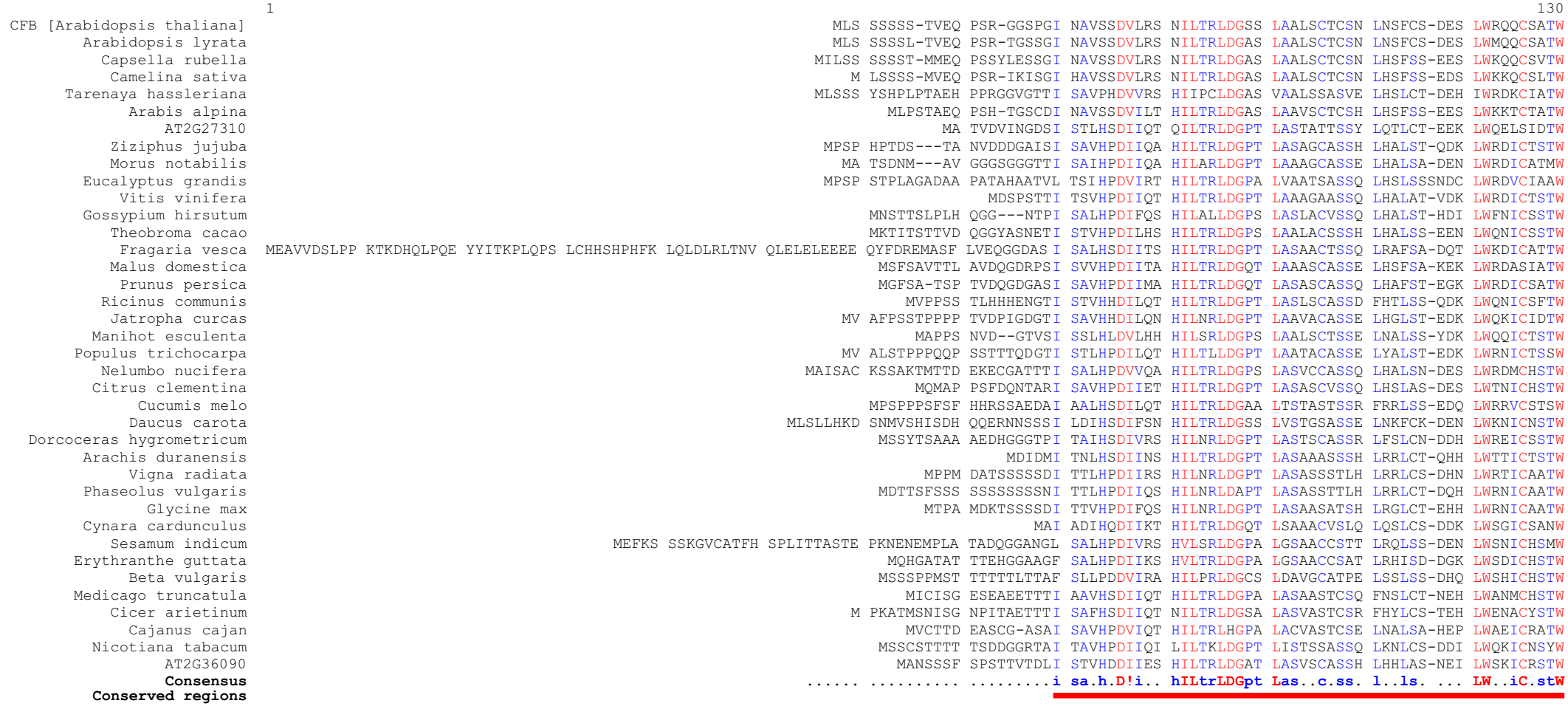

Figure S2. Multiple sequence alignment of Arabidopsis CFB, AT2G27310, and AT2G36090 and orthologs of other dicotyledoneous plant species. The alignment was carried out using MultAlin (http://multalin.toulouse.inra.fr/multalin/) with the standard settings (Corpet, 1988). The colored lines correspond to the conserved regions shown in Fig. 2A. Red and blue amino acid symbols denote highly (≥ 90 %), and less (≥ 50 % and < 90%) conserved residues, respectively. Symbols for amino acids other than letters in the consensus sequence: ! = I or V; $ = L or M; % = F or Y; # = N, D, Q, E, B, or Z.

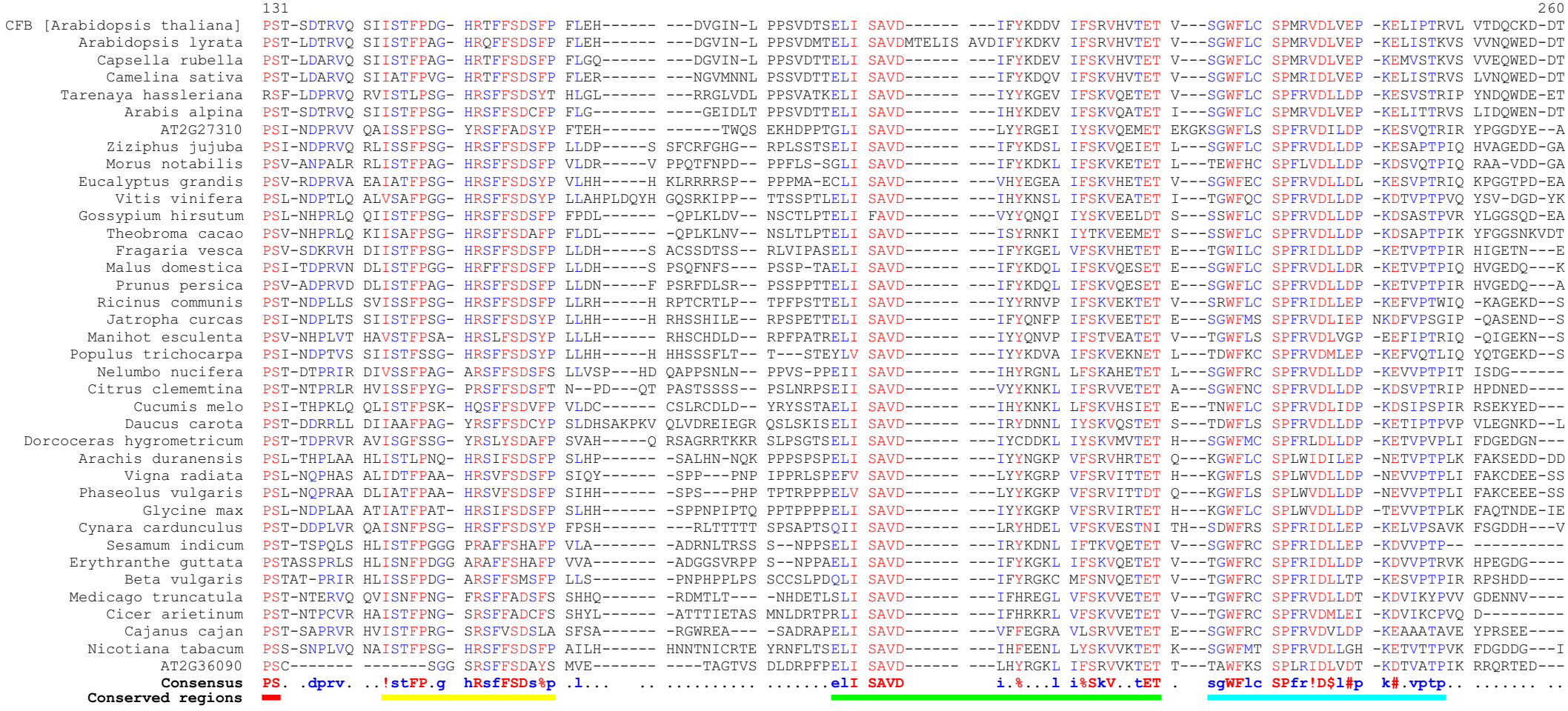

Figure S2. (continued)

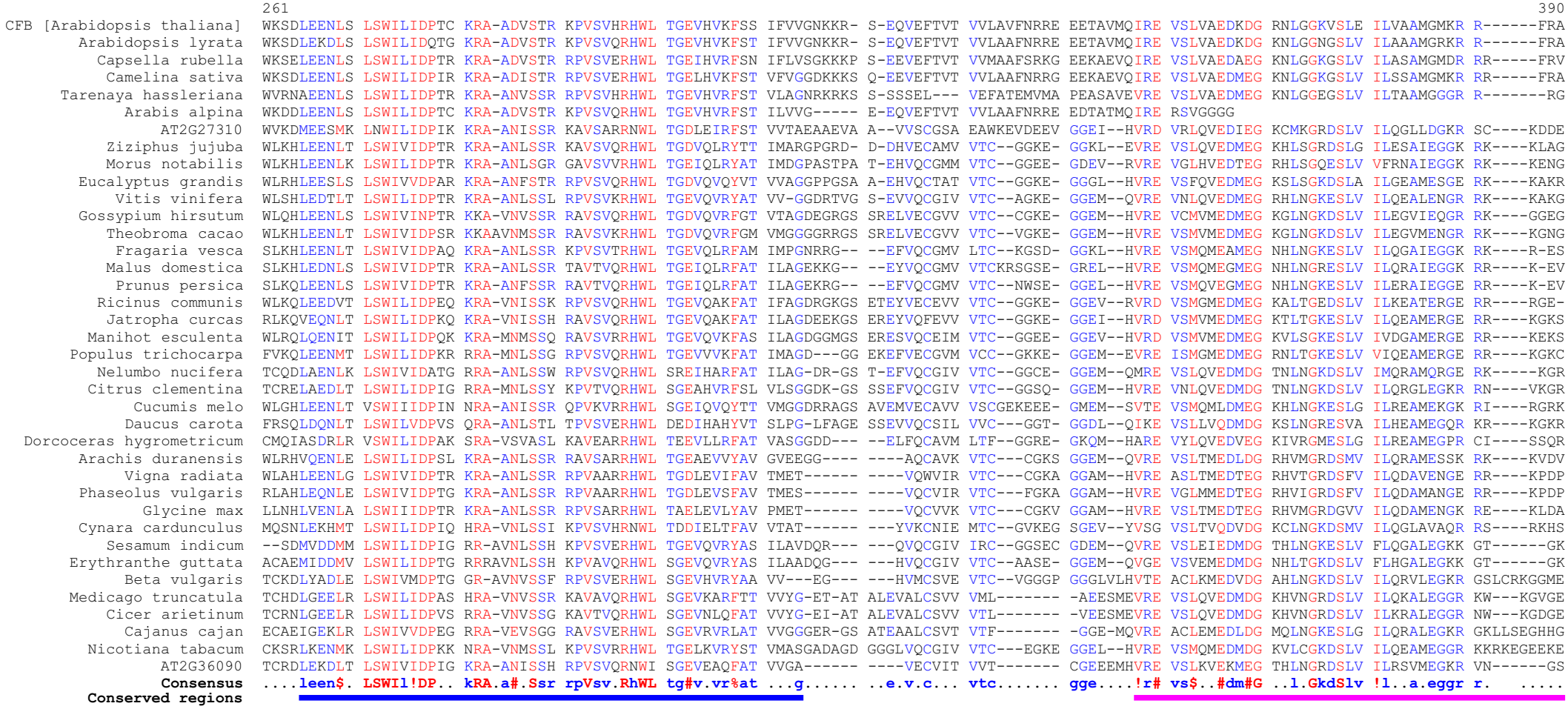

Figure S2. (continued)

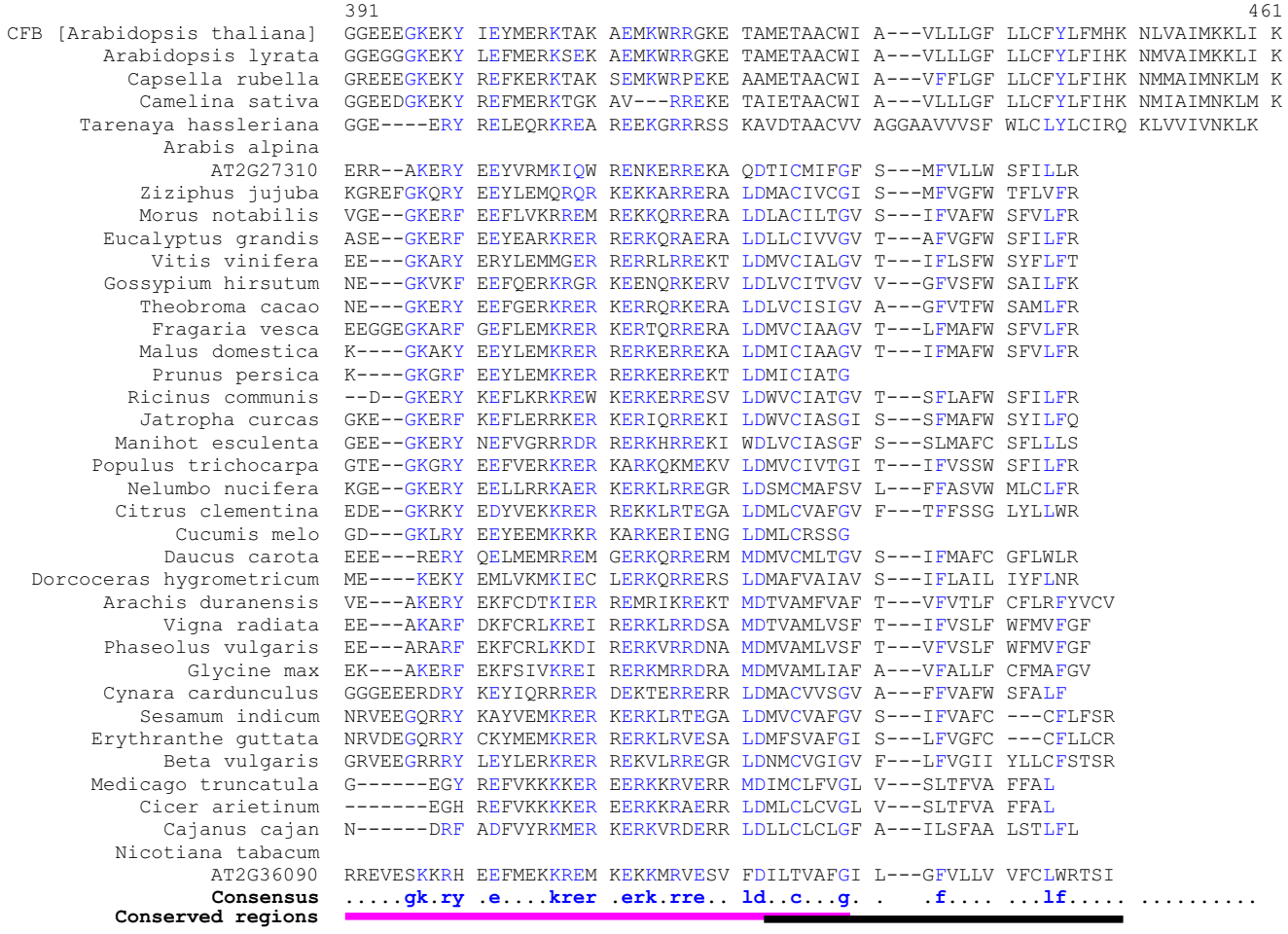

Figure S2. (continued)

Pro35S:CFB-GFP-52V

Figure S3. Phenotype of plants overexpressing a *CFB-GFP* fusion gene. Photograph of a transgenic plant harboring the *Pro35S:GFP-CFB* gene (individual 52V, see Figure 3) four weeks after germination showing the typical CFB overexpression phenotype with white inflorescence stem tips. The arrowhead indicates the onset of the white stem tissue. The inset shows the inflorescence of the same plant at a higher magnification.

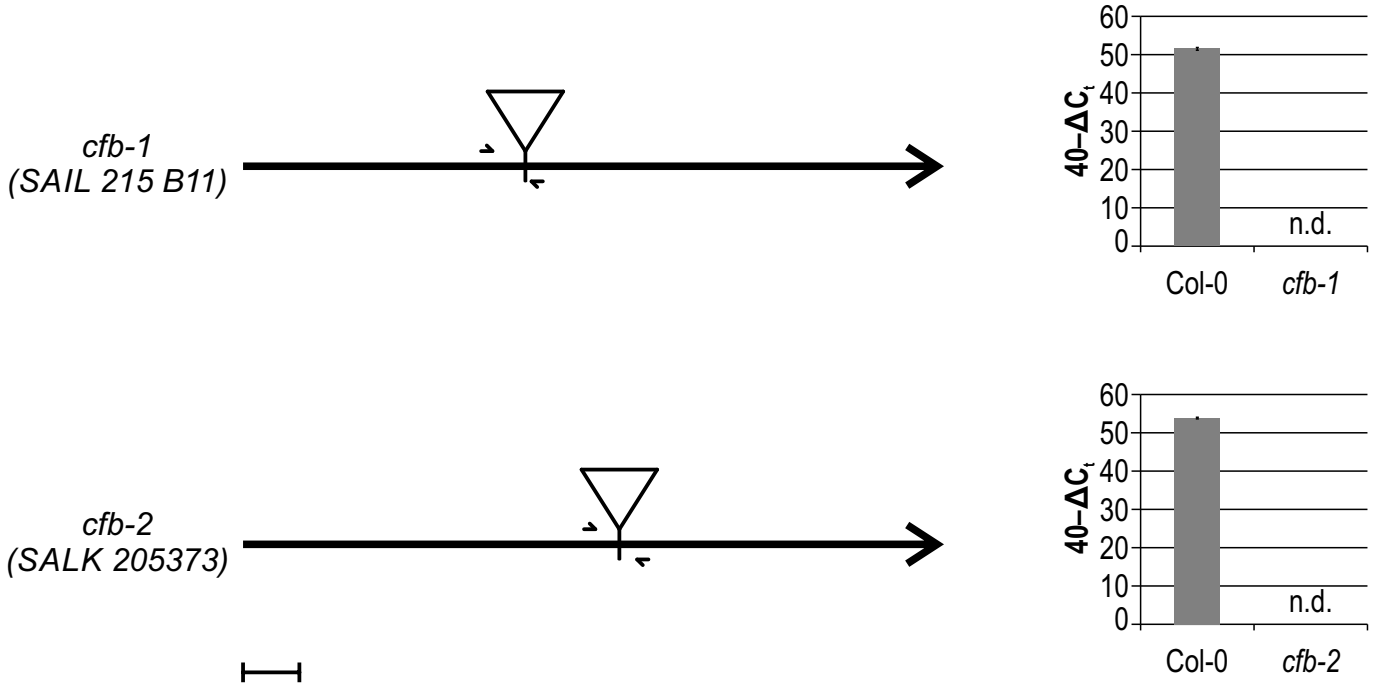

Figure S4. Analysis of the *CFB* transcript in *cfb-1* and *cfb-2* mutants. The position of the T-DNA insertions relative to the cDNA of *CFB* (represented by a bold arrow) is marked by triangles, the position of the primers used for quantitative real-time RT-PCR by half arrows. Transcript abundance was measured by 40 cycles of quantitative real-time RT-PCR in leaves of wild-type (Col-0), *cfb-1*, and *cfb-2* mutant plants. *AT3G25800* (*PP2AA2*) was used as a reference gene. Primer sequences are listed in Table S2. Error bars = SD (n = 3). n.d.: not detected. Scale bar = 100 bp.

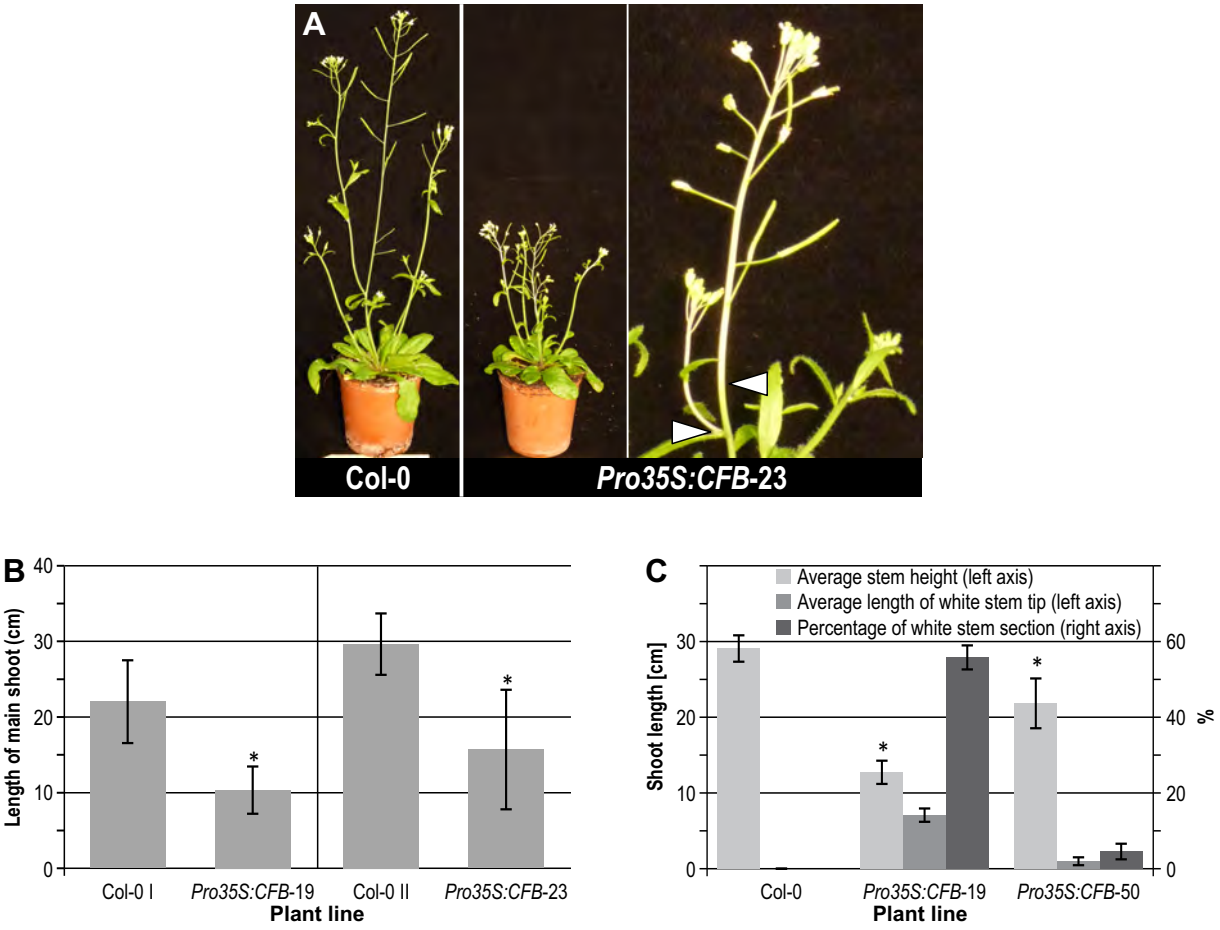

Figure S5. Comparison of independent *CFB* overexpressing lines to the reference line *Pro35S:CFB*-19 and wild type. A, Comparison of line *Pro35S:CFB*-23 to wild type at the flowering stage. The onset of albinotic tissue formation is indicated with arrowheads. B, Comparison of inflorescence stem length between the wild type (Col-0) and the *CFB* overexpressing lines 19 and 23, respectively. Stem lengths of plants grown on soil in the greenhouse were measured 30 (line 19) or 38 (line 23) days after sowing. C, Lengths of the main stems and percentage of the white upper portion of the stems of lines 19 and 50 in comparison to the wild type. Stem lengths of plants grown on soil in the greenhouse were measured 38 days after sowing. Error bars = SD (n ≥ 8). Asterisks indicate a *p* value < 0.01 (Student's *t*-test; comparison transgenic lines vs. wild type).

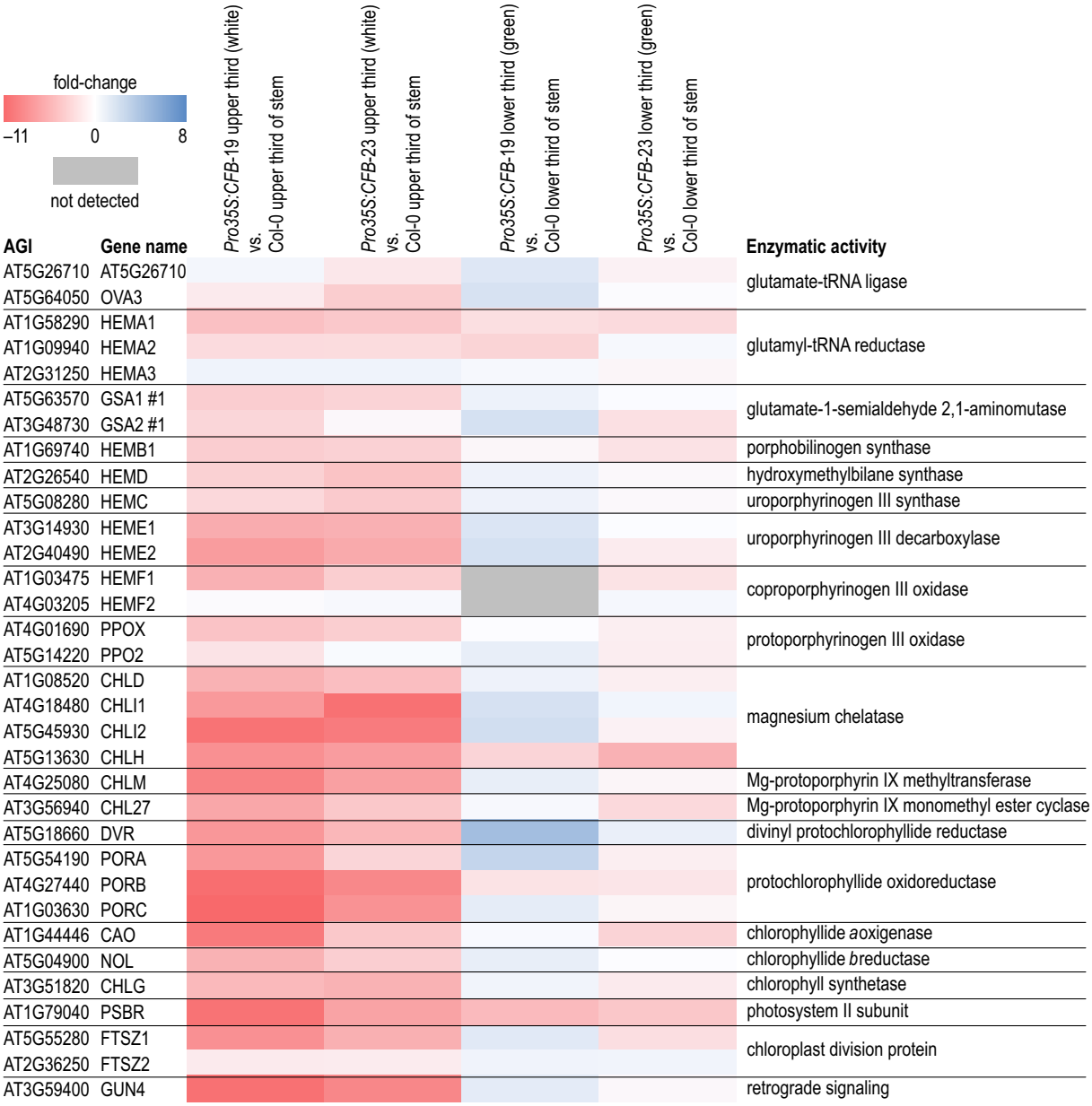

Figure S6. Expression of chlorophyll biosynthesis and other chloroplast-related genes in green and white stem sections of two *CFB* overexpressing lines, *ProCFB35S:CFB*-19 and *Pro35S:CFB*-23. The upper and lower third of the stems of flowering plants were pooled from twenty plants of wild type and the two *CFB* overexpressing lines each. Transcript levels were quantified by qRT-PCR. The fold-changes between the samples indicated were calculated and shown as a heat map.

Col-0 *Pro35S:CFB*-19 Col-0 *Pro35S:CFB*-19

long day **short day**

Figure S7. Formation of the albinotic stem tip of *CFB* overexpressing plants grown under long-day (16 h light/8 h dark) and short-day (8 h light/16 h dark) conditions. Arrowheads mark the onset of albinotic tissue formation.

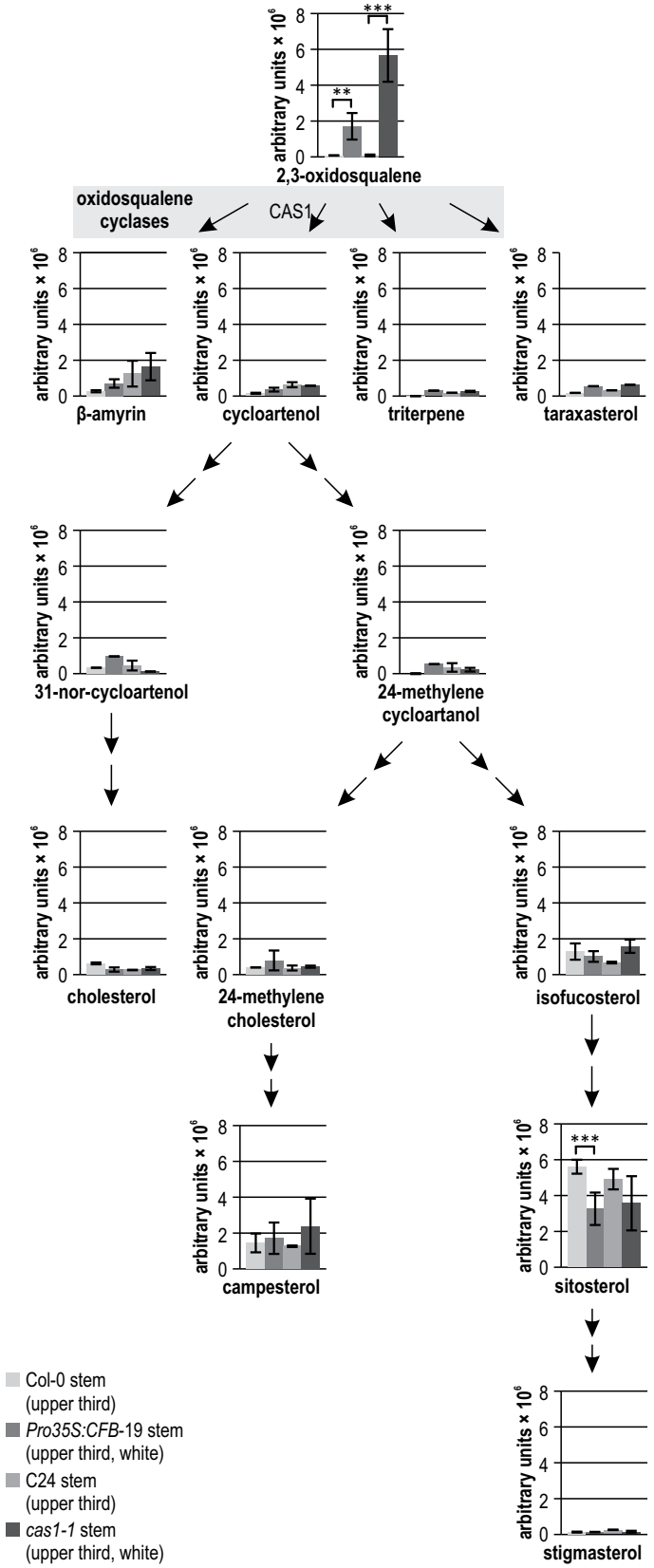

Figure S8. Relative concentrations of sterol metabolites in different genotypes and tissues. Sterol metabolites were measured in the upper thirds of the inflorescence stems of wild-type, *CFB* overexpressing (Col-0 background), and *cas1-1* (C24 background) mutant plants. In the two latter plants, the upper third of the stem contained only albinotic tissue. Units of the y axis are mass spectrometry peak heights normalized to the internal control × 10^6. Significance codes: **: $p < 0.01$; ***: $p < 0.001$. Error bars = SD of two to four biological replicates