Supplemental figure 7

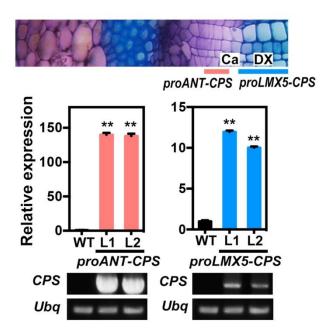


Figure S7. Expression analysis of the *CPS* gene in transgenic plants harboring *proANT-CPS* and *proLMX5-CPS* constructs.

Transgenic plants were grown in a greenhouse for three months. RNA was extracted from the third to eighth internodes of both wild-type (WT) and transgenic plants for quantitative and semi-quantitative RT-PCR analysis. The ubiquitin gene served as the reference gene. Error bars represent the standard deviation (\pm SD). Asterisks indicate statistically significant differences compared to the WT values, as determined by one-way ANOVA followed by Dunnett's test for pairwise comparisons: *, P < 0.05; **, P < 0.01.