

**Table S1.** Primers used for quantitative real-time RT-PCR. Sequences start at the 5' end.

Gene product	Gene name	Primer	Sequence	Anneal. Temp.
Actin 9	<i>NtAct9</i>	NtAct2A	CTATTCTCCGCTTTGGACTTGGC A	60 °C
		NtAct2B	AGGACCTCAGGACAACGGAAAC G	
Cytokinin oxidase/dehydrogenase	<i>AtCKX1</i>	fCKX1-510	CACCTTTGGCAATTCTACAT	60 °C
		rCKX1-510	TGTCCTTGAAGCGAGTGA	
Dehydrin	<i>NtERD10B</i>	DehF2	ATGGACAAGGCGGAAGAAG	58 °C
		DehR2	GTTGTTGCAGTTGAATGAGT	
1-pyrroline-5-carboxylate synthase	<i>NtP5CS A</i>	Nt P5CS_A_for1	CTGGAGGCTCGAGTGTAATG	60°C
		Nt P5CS_A_rev 1	TAGTTGTCCTGCCCTTGTC	

**Table S2.** The content of xanthophyll cycle pigments and DEPS during drought stress progression and subsequent recovery.

Pigments [mg cm <sup>-2</sup> ]		Control	1 d drought	6 d drought	11 d drought	Recovery
<b>V+A+Z</b>	<b>WT</b>	0.56± 0.041	0.73± 0.064	0.95± 0.067	1.06± 0.079	0.72± 0.041
	<b>W6:CKX</b>	0.53± 0.027	0.71± 0.081	0.90± 0.048	1.10± 0.082	0.77± 0.079
	<b>35S:CKX</b>	0.63± 0.033	0.78± 0.039	0.91± 0.081	1.13± 0.067	0.84± 0.036
<b>DEPS</b>	<b>WT</b>	0.23± 0.011	0.28± 0.039	0.36± 0.011	0.37± 0.014	0.26± 0.013
	<b>W6:CKX</b>	0.24± 0.022	0.30± 0.027	0.37± 0.017	0.40± 0.017	0.23± 0.012
	<b>35S:CKX</b>	0.22± 0.013	0.26± 0.012	0.30± 0.012	0.35± 0.018	0.21± 0.019

Xanthophyll cycle pigments (V, violaxanthin; A, antheraxanthin; and Z, zeaxanthin) were determined in wild-type and *CKX1* transgenic tobacco plants. DEPS represents the ratio of de-epoxidated xanthophyll cycle pigments to their total sum. WT, wild-type.

**Figure S1.** Photos of wild-type and *CKXI* transgenic tobacco plants under control (well-watered) conditions and after 10-day drought.

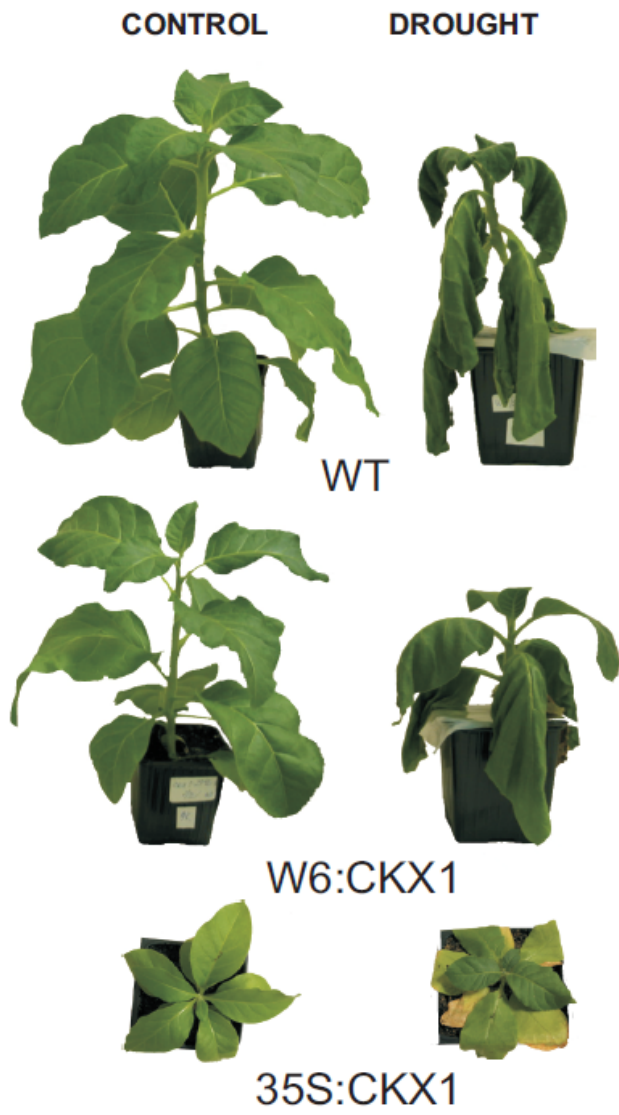
**Figure S2.** Content of cytokinin metabolites in leaves and roots of wild-type and *CKXI* transgenic tobacco plants. Control - control (hydrated) conditions; D - drought stress (10-d dehydration); D + HS – combined drought and heat stress (10 d dehydration + 40°C for 2 h), D recovery – 24 h recovery following rehydration; D+HS recovery – 24 h recovery after combined stress, 2 h HS - heat stress (40°C for 2 h); 6 h HS - heat stress (40°C for 6 h). Cytokinin metabolites were grouped according to their structure and function into 5 groups: P - cytokinin phosphates (*trans*-zeatin riboside-, isopentenyladenosine- and dihydrozeatin riboside phosphates), O-glc - cytokinin O-glucosides [*trans*-zeatin(riboside) O-glucoside and dihydrozeatin(riboside) O-glucoside], N-glc - cytokinin N-glucosides (7N- and 9N-glucosides of *trans*-zeatin, isopentenyladenine and dihydrozeatin), *cisZ*(MP,R) - *cis*-zeatin /riboside/phosphate, *cisZ* glc - *cisZ*-glucosides [*cis*-zeatin (riboside) O-glucoside and 7N- and 9N-glucoside]. WT, wild type. UL, upper leaves, LL, lower leaves, R, roots.

**Figure S3.** Transcript levels of the *P5CSA* gene in leaves and roots of wild-type and *CKXI* transgenic tobacco plants. Details for designation of individual variants are as described in Fig. 1. WT, wild-type.

**Figure S4.** Chlorophyll content of individual leaves of wild-type and *CKXI* transgenic tobacco plants under control (well-watered) conditions and after 6-day drought. The leaves were numbered from the bottom to the top. WT, wild-type.

**Figure S5.** Content of abscisic acid metabolites (phaseic acid, ABA-glucosylester, dihydrophaseic acid and neophaseic acid) in leaves and roots of wild-type and *CKXI* transgenic tobacco plants. Control - control (hydrated) conditions; D - drought stress (10-d dehydration); D + HS – combined drought and heat stress (10 d dehydration + 40°C for 2 h), D recovery – 24 h recovery following rehydration; D+HS recovery – 24 h recovery after combined stress, 2 h HS - heat stress (40°C for 2 h); 6 h HS - heat stress (40°C for 6 h). WT, wild type. UL, upper leaves, LL, lower leaves, R, roots.

**Figure S6.** Thermal images of tobacco wild-type and *CKX1* transgenic tobacco plants exposed 40°C. A - immediately after transfer to 40°C, B – after 10 min at 40°C, C - after 20 min at 40°C.



**Figure S1**

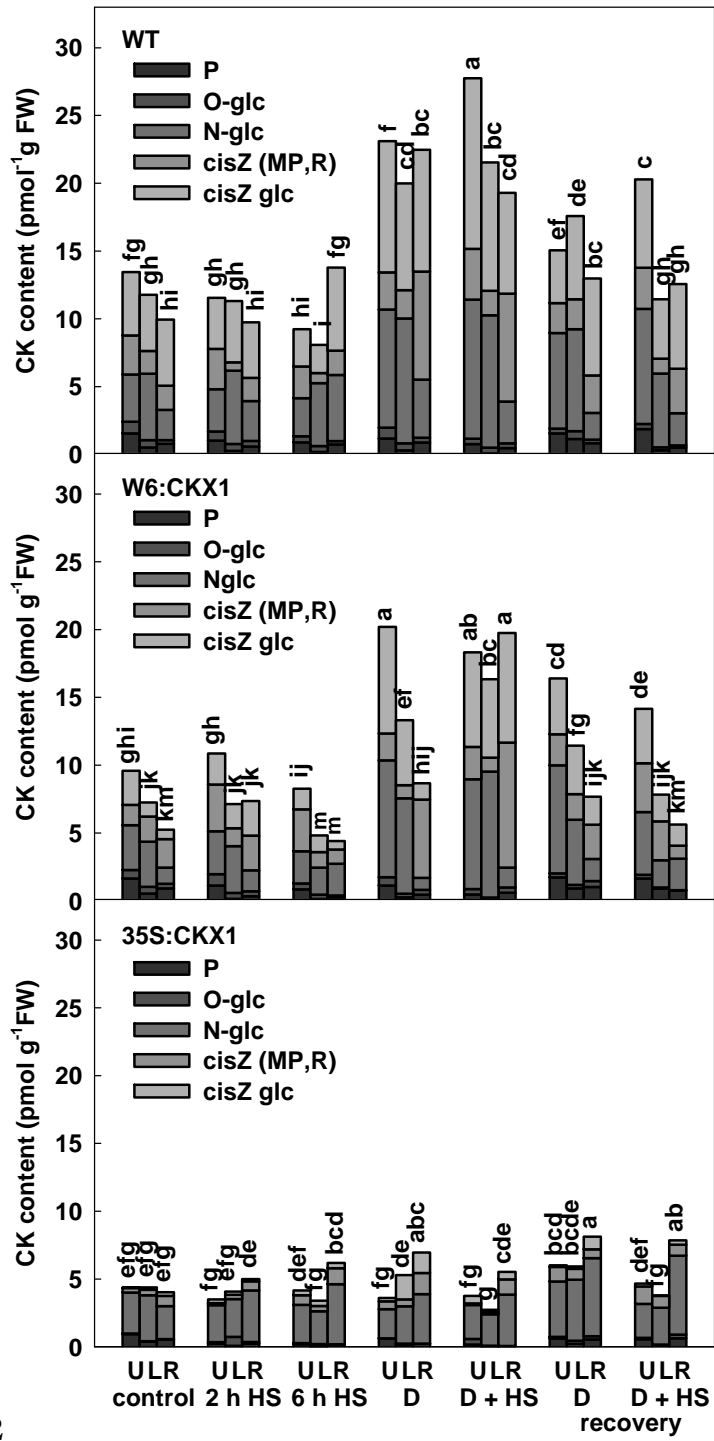


Figure S2

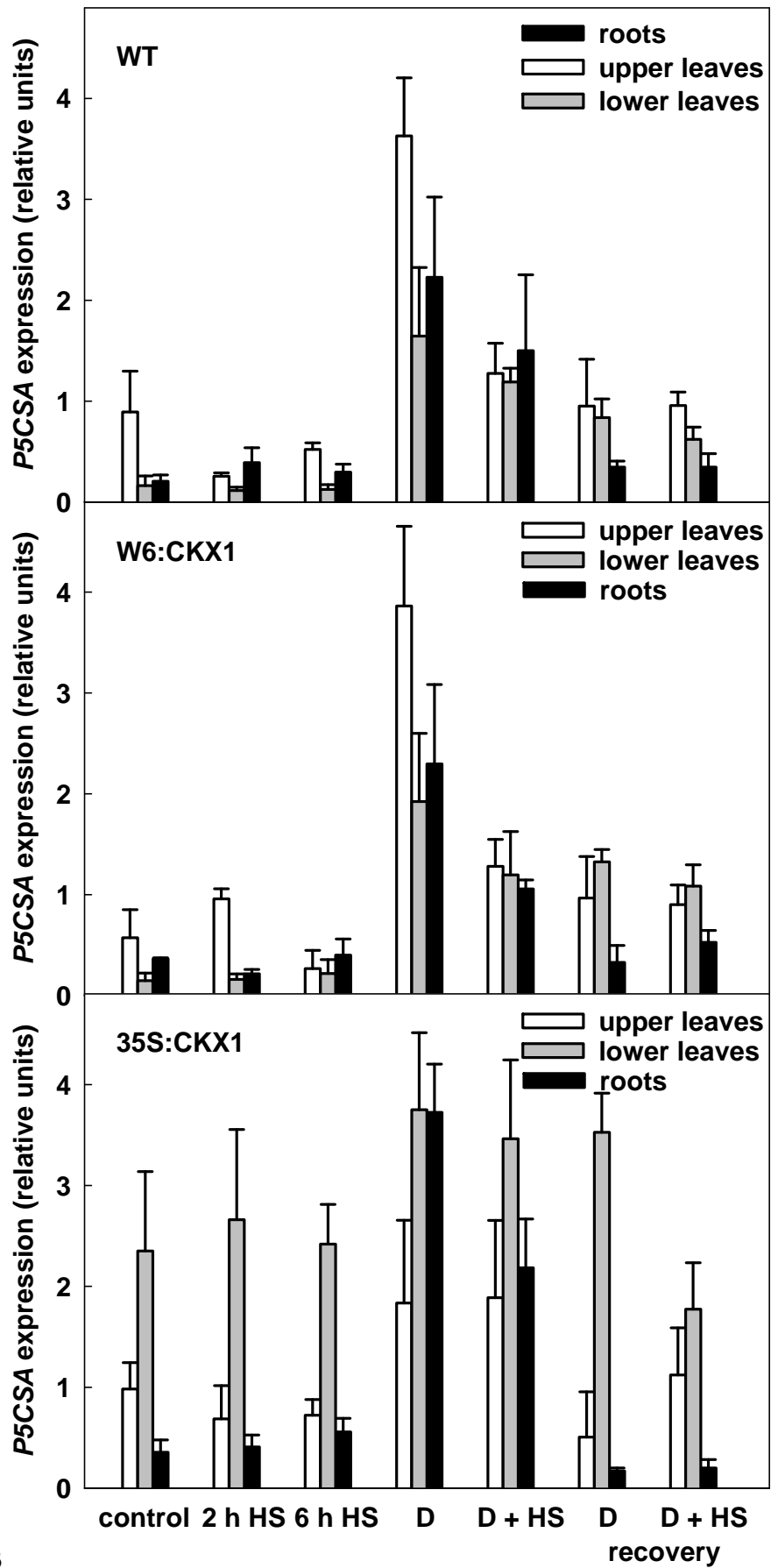


Figure S3

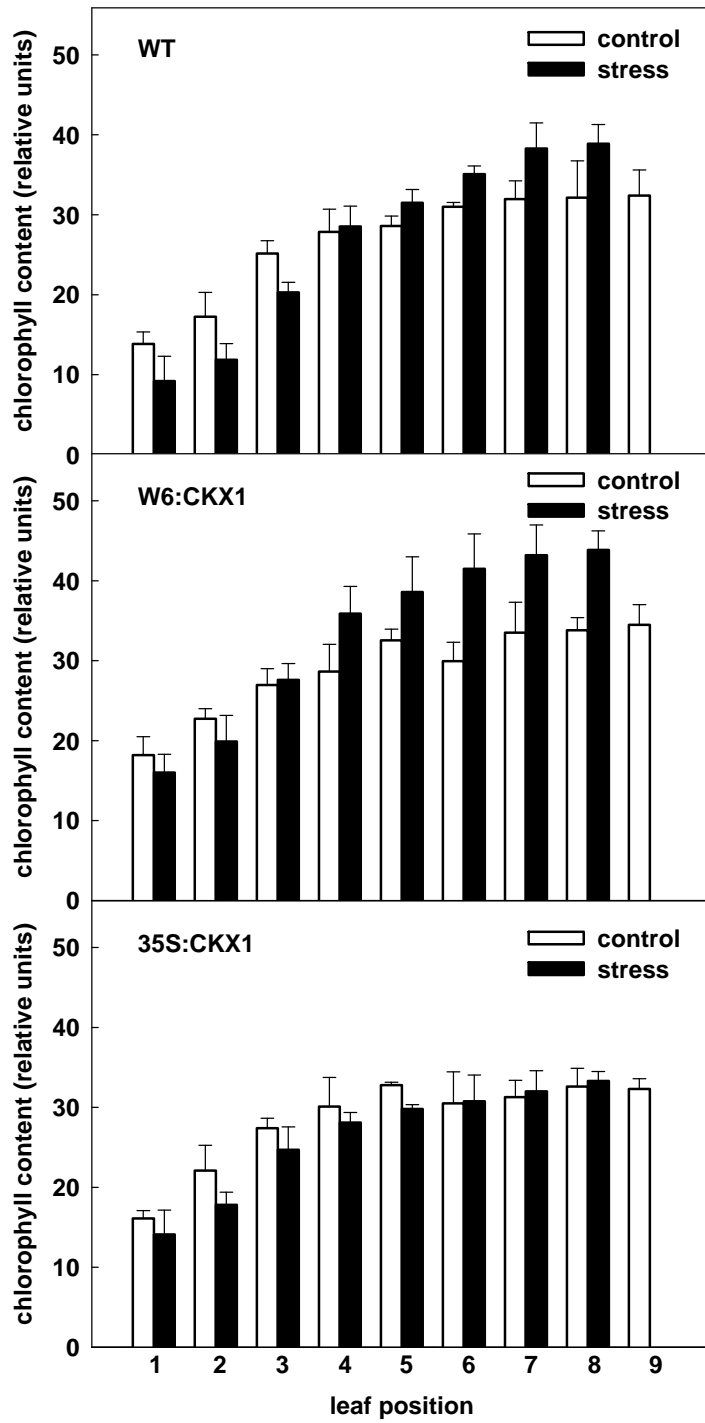


Figure S4

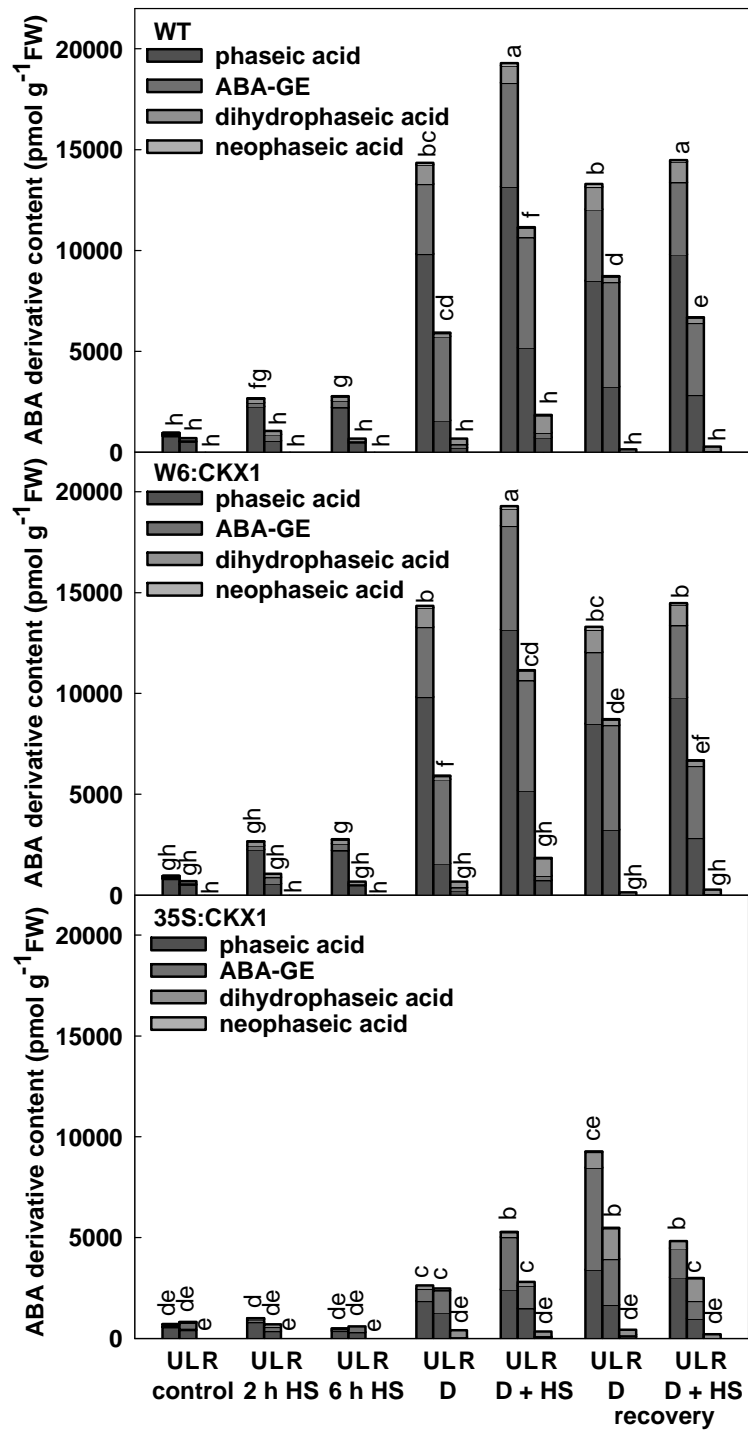
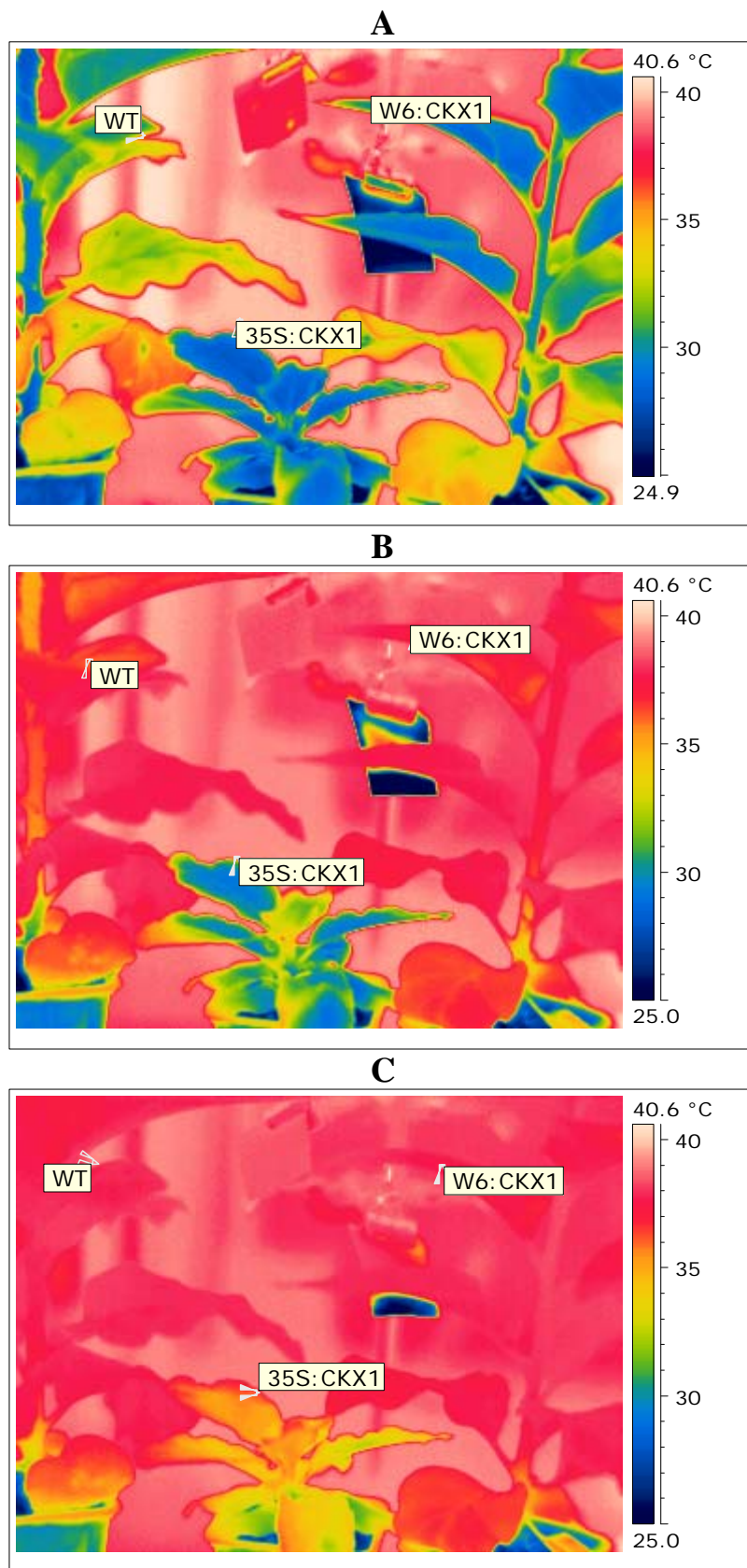


Figure S5





**Figure S6**