

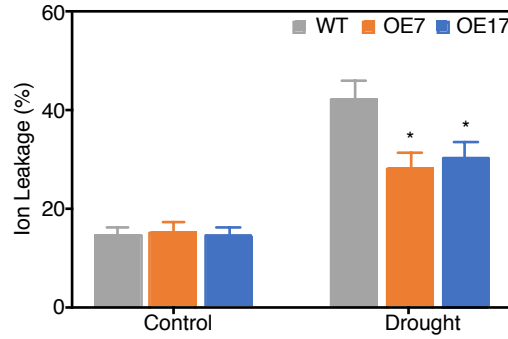
## Supplementary Material

### 1 Supplementary Figures and Tables

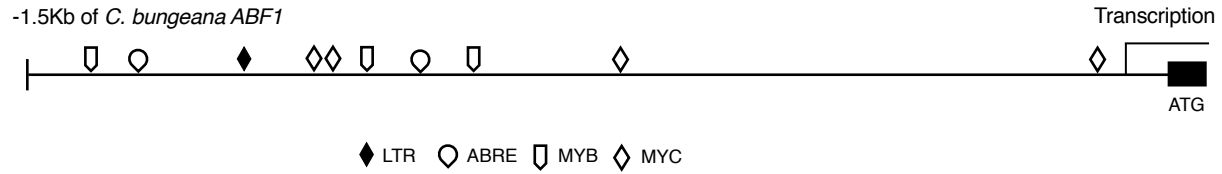
#### 1.1 Supplementary Figures

Majority	MDRPXVSGPMDLPI MHDS DRYEL VKDI GSGNFGVARL MRDKQSNEL VAVKYI ERGEKI DENVKREI I NHR	
	10 20 30 40 50 60 70	
Peptide 1-4	-----MHDS DRYEL VKDI GSGNFGVARL MRDKQSNEL VAVKYI ERGEKI DENVKREI I NHR	56
CbSnRK2.6	MDRPGVSGPMDLPI MHDS DRYEL VKDI GSGNFGVARL MRDKQSNEL VAVKYI ERGEKI DENVKREI I NHR	70
AtSnRK2.6	MDRPAVSGPMDLPI MHDS DRYEL VKDI GSGNFGVARL MRDKQSNEL VAVKYI ERGEKI DENVKREI I NHR	70
Majority	SLRHPNI VRFKEVI LTPHLAI VMEYASGGELFERI CNAGRFSEDEARFFFQQLI SGVSYCHDMQVCHRD	
	80 90 100 110 120 130 140	
Peptide 1-4	SLRHPNI VRFKEVI LTPHLAI VMEYASGGELFERI CNAGRFSEDEARFFFQQLI SGVSYCHDMQVCHRD	126
CbSnRK2.6	SLRHPNI VRFKEVI LTPHLAI VMEYASGGELFERI CNAGRFSEDEARFFFQQLI SGVSYCHDMQVCHRD	140
AtSnRK2.6	SLRHPNI VRFKEVI LTPHLAI VMEYASGGELFERI CNAGRFSEDEARFFFQQLI SGVSYCHAMQVCHRD	140
Majority	LKLENTLLDGSPAPRLKI CDFGYSKSSVL HSQPKSTVGTPAYI APEVLLKKEYDGKI ADVWSCGVTLYVM	
	150 160 170 180 190 200 210	
Peptide 1-4	LKLENTLLDGSPAPRLKI CDFGYSKSSVL HSQPKSTVGTPAYI APEVLLKKEYDGKI ADVWSCGVTLYVM	196
CbSnRK2.6	LKLENTLLDGSPAPRLKI CDFGYSKSSVL HSQPKSTVGTPAYI APEVLLKKEYDGKI ADVWSCGVTLYVM	210
AtSnRK2.6	LKLENTLLDGSPAPRLKI CDFGYSKSSVL HSQPKSTVGTPAYI APEVLLKKEYDGKI ADVWSCGVTLYVM	210
Majority	LVGAYPFEDPEEPKNFRKTI HRI LNVQYAI PDYVHI SPECRHLI SRI FVADPEKRI SI PEI RNHEWFLKN	
	220 230 240 250 260 270 280	
Peptide 1-4	LVGAYPFEDPEEPKNFRKTI HRI LNVQYAI PDYVHI SPECRHLI SRI FVADPEKRI SI PEI RNHEWFLKN	266
CbSnRK2.6	LVGAYPFEDPEEPKNFRKTI HRI LNVQYAI PDYVHI SPECRHLI SRI FVADPEKRI SI PEI RNHEWFLKN	280
AtSnRK2.6	LVGAYPFEDPEEPKNFRKTI HRI LNVQYAI PDYVHI SPECRHLI SRI FVADPAKRI SI PEI RNHEWFLKN	280
Majority	LPADLMNDNAMNSQFDES DQPGQSI EEI MQI I AEATVPPAGSQSL NHYLTGSLDI DDEMDDLESDLDDL	
	290 300 310 320 330 340 350	
Peptide 1-4	LPADLMNDNAMNSQFDES DQPGQSI EEI MQI I AEATVPPAGSQSL NHYLTGSLDI DDEMDDLESDLDDL	336
CbSnRK2.6	LPADLMNDNAMNSQFDES DQPGQSI EEI MQI I AEATVPPAGSQSL NHYLTGSLDI DDEMDDLESDLDDL	350
AtSnRK2.6	LPADLMNDNTMTTQFDES DQPGQSI EEI MQI I AEATVPPAGTQNL NHYLTGSLDI DDEMEELESDLDDL	350
Majority	DI DSSGEI VYAM	
	360	
Peptide 1-4	DI DSSGEI VYAM	348
CbSnRK2.6	DI DSSGEI VYAM	362
AtSnRK2.6	DI DSSGEI VYAM	362

**FIGURE S1 |** Alignment of the amino acid sequences of Peptide1-4, CbSnRK2.6, and AtSnRK2.6. Peptide1-4, the four positive clones by yeast two hybrid; CbSnRK2.6, *Chorispora bungeana* SnRK2.6/OST1 (QBA17182.1); AtSnRK2.6, *Arabidopsis thaliana* SnRK2.6/OST1 (NP\_567945.1).



**FIGURE S2** | Ion leakage of WT and transgenic lines after drought stress. Four-week-old wild type (WT) and transgenic tobacco lines OE7 and OE17 (*35S:CbABF1*) were drought stressed by withholding water for 12 d, and the leaves were detached for ion leakage assay. Error bars represent SD (n = 18). Two-way ANOVA (Tukey test) was performed, and statistically significant differences are indicated by asterisks (\*  $P < 0.05$ ). Values shown are derived from experiments that were performed three times with similar results, and representative data from one repetition are presented.



**FIGURE S3** | Distribution of major stress-related *cis*-elements in the promoter region of *CbABF1*.

## 1.2 Supplementary Tables

**TABLE S1** | List of primers used in present study.

Genes	Purpose	Primers	Sequences (5'-3')
<i>CbABF1</i>	5' RACE	5TR	AGGCGATGGATGCTCCTTCGAC
	3' RACE	3TR	AGGCTGAAATTATGAAAACCCATAATAACGAGG
<i>CbABF1</i>	q-PCR	AQ-F	AACACATTAGGTGAGCCAGG
		AQ-R	AGCAGGAACAGAACCACTAATAG
<i>CbABF1</i>	Full-length <i>ABF1</i> amplification	YH1	AATGCATATGATGGGTACTCAAATCGACTTCAACAACAC
		YH393	TCCAGTCGACTTACCAAGGACCCGTAAGCGTTC

<i>CbABF1</i>	Truncated <i>ABF1Δ1</i> amplification	YH1	AATGCATATGATGGGTACTCAAATCGACTTCAACAACAC
		YH89	TCCAGTCGACACTAATAGGTTGTGCTGGGGCTGC
<i>CbABF1</i>	Truncated <i>ABF1Δ2</i> amplification	YH90	AATGCATATGGGTTCTGTTCTGCTGGTGAG
		YH393	TCCAGTCGACTTACCAAGGACCCGTAAGCGTTC
<i>CbABF1</i>	To construct <i>ABF1Δ2</i> effector	DL90	CGGGATCCGGTTCTGTTCTGCTGGTGAG
		YH393	TCCAGTCGACTTACCAAGGACCCGTAAGCGTTC
<i>CbABF1</i>	To construct <i>ABF1</i> effector	DL1	CGGGATCCATGGGTACTCAAATCGACTTCAACAACAC
		YH393	TCCAGTCGACTTACCAAGGACCCGTAAGCGTTC
<i>CbSnRK2.6</i>	To construct <i>CbSnRK2.6</i> effector	DLS1	CGGGATCCATGGATCGGCCAGGAGTGAGTGGTC
		DLS362	TCCAGTCGACTCACATTGCATACACAATCTCTCC
<i>CbABF1</i>	PD-F		<u>GGGGACAAGTTTGTACAAAAAAGCAGGCTT</u> CATGGGTACTCAAATCGACTTCAAC
	Gateway	PD-R	<u>GGGGACCACTTTGTACAAGAAAGCTGGGT</u> CCCAGGACCCGTAAGCGTTC
<i>CbACTIN</i>	qRT-PCR	AC-F	GGATGCTTACGTTGGTGACGA
		AC-R	TCTCCATGTCATCCCAGTTGC
<i>CbSnRK2.6</i>	3' RACE	3TR	TTCTAAGTCTTCGGTGTTACATTTCGC
	5' RACE	5TR	TAACATACAGAGTTACCCACAAGACC
<i>NtLEA5</i>	qRT-PCR	LE-F	TTGAATCTGGGGTTTGGTT
		LE-R	GGAAGCATTGACGAGCTAGG
<i>NtERD10C</i>	qRT-PCR	ER-F	AACGTGGAGGCTACAGATCG
		ER-R	GTTCTCTTGGGCATGAGTT
<i>NtLTP1</i>	qRT-PCR	LT-F	GCAGAAGCCATAACCTGTGG
		LT-R	CAGTGGAAGGGCTGATCTTG
<i>NtPOX</i>	qRT-PCR	POX-F	TTAGCTGCTCGTGATGCTGT
		POX-R	AGTTGAGCTCTGAGGGTCCA
<i>NtSOD</i>	qRT-PCR	SOD-F	CTCCTACCGTCGCCAAAT
		SOD-R	GCCCAACCAAGAGAACCC
<i>NtCAT1</i>	qRT-PCR	CAT-F	AGCCGGTGGGAAGATTAGTT
		CAT-R	AAGCAAGCTTTTGACCCAGA
<i>NtEF1-α</i>	qRT-PCR	EF1-F	TGAGATGCACCACGAAGCTC
		EF1-R	CCAACATTGTCACCAGGAAGTG

Note: The underlined fragments are attB1 and attB2 sequences according to the gateway system.