

Figure S1 Interaction analysis of *BnCER1-2* promoter with BnaC9.DEWAX1 protein by yeast one-hybrid assay. (A) Nucleotide sequence of promoter region of *BnCER1-2* gene used in yeast one-hybrid assay, which is 100 bp upstream of the start codon of the *BnCER1-2* gene. Nucleotide in red indicated GCC-like motif. (B) Co-transfection verification for *BnCER1-2* promoter interaction with BnaC9.DEWAX1 protein. The prey and bait constructs were co-transformed to Y1H gold yeast competent cell. The prey construct contains the BnaC9.DEWAX1 gene driven by the CaMV 35S promoter. The bait construct consists of the AUR1-C antibiotic resistance gene driven by the *BnCER1-2* promoter linked with the yeast iso-1-cytochrome C minimal promoter.

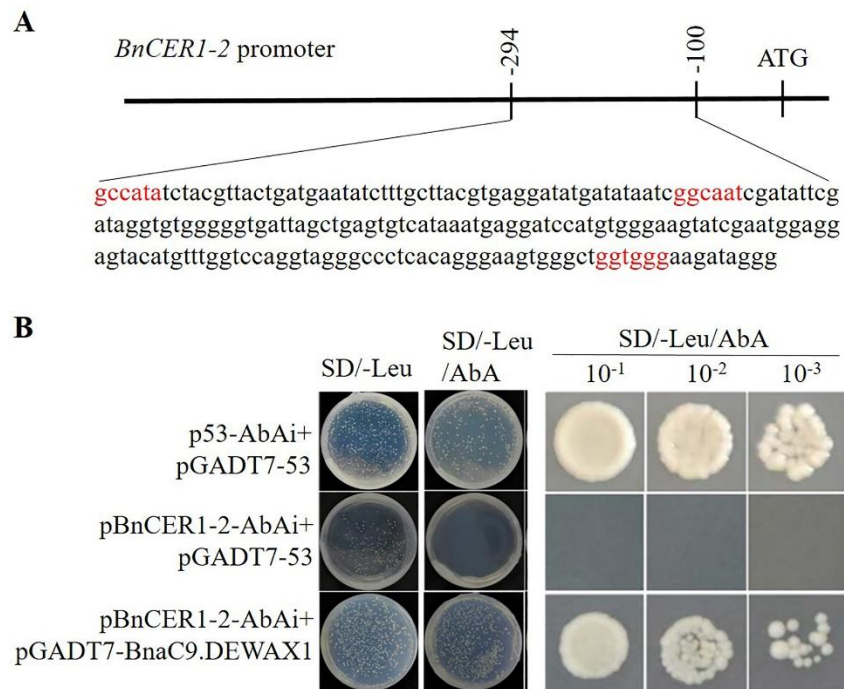


Figure S2 Nucleotide and amino acid sequences (A) and phylogenetic analysis (B) of BnaC9.DEWAX1. (A) The AP2/ERF DNA-binding domain is underlined, the putative nuclear localization signal (NLS) are double underlined, and the putative acidic domain is marked with dots below. (B) A phylogenetic tree constructed using BnaC9.DEWAX1 and other Arabidopsis ERF subfamily members (B-1~B-6). BnaC9.DEWAX1, indicated by the asterisk, was grouped with members of the ERF subfamily B-3, and sub-grouped with Arabidopsis DEWAX.

A

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ATGACAACCTTTTGGAGAAAAGCTCTGATGTGGAGGTTATACACAAGTATCTCTTTGAGGAC 60
M T T F E K S S D V E V I H K Y L F E D 20
TTGATGATCCCTGATTGCTTCATGGAAGATTTTGTCTTTGATGATGCTGCTTTTGTCTCA 120
L M I P D C F M E D F V F D D A A F V S 40
GGACTCTTGTCTCTAGAACCCTTTAACCAGTTTCCTAAACAAGAGCCTAGTTCACCGGTT 180
G L L S L E P F N P V P K Q E P S S P V 60
CTTGATCCAGATTCTGTGTCCAAGAGTTTCTACAAATTGAAGCAGAATCATCATCATCG 240
L D P D S C V Q E F L Q I E A E S S S S 80
TCAACAACCTACAACATCACCTGAGGCTGAGACAGTCTCAAACCGAAAAAGACCAAGGAGG 300
S T T T T S P E A E T V S N R K R P R R 100
GTCGAAGAGACGAGACACTACAGAGGCGTGAGAAGGAGACCATGGGGGAAATTTGCAGCA 360
V E E T R H Y R G V R R R P W G K F A A 120
GAGATTCGAGATCCGGCCAAGAAAGGATCTAGGATGTGGCTAGGCACATTGAGACTGAT 420
E I R D P A K K G S R M W L G T F E T D 140
ATTGATGCTGCAAGAGCTTATGACTACACAGCTTTTAAGCTCAGGGGAAGAAAAGCTGTG 480
I D A A R A Y D Y T A F K L R G R K A V 160
CTCAACTTTCTTTGGATGCTGGTAAGTATGATGCTCCGATCAATTCTTGCCGGAAGAGG 540
L N F P L D A G K Y D A P I N S C R K R 180
AGAAGAAACGATGTACCGGAGCCTCAAGGAATAACTACTAGTACTACATCATCTTCATCA 600
R R N D V P E P Q G I T T S T T S S S S 200
AACTAA 606
N * 201

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B

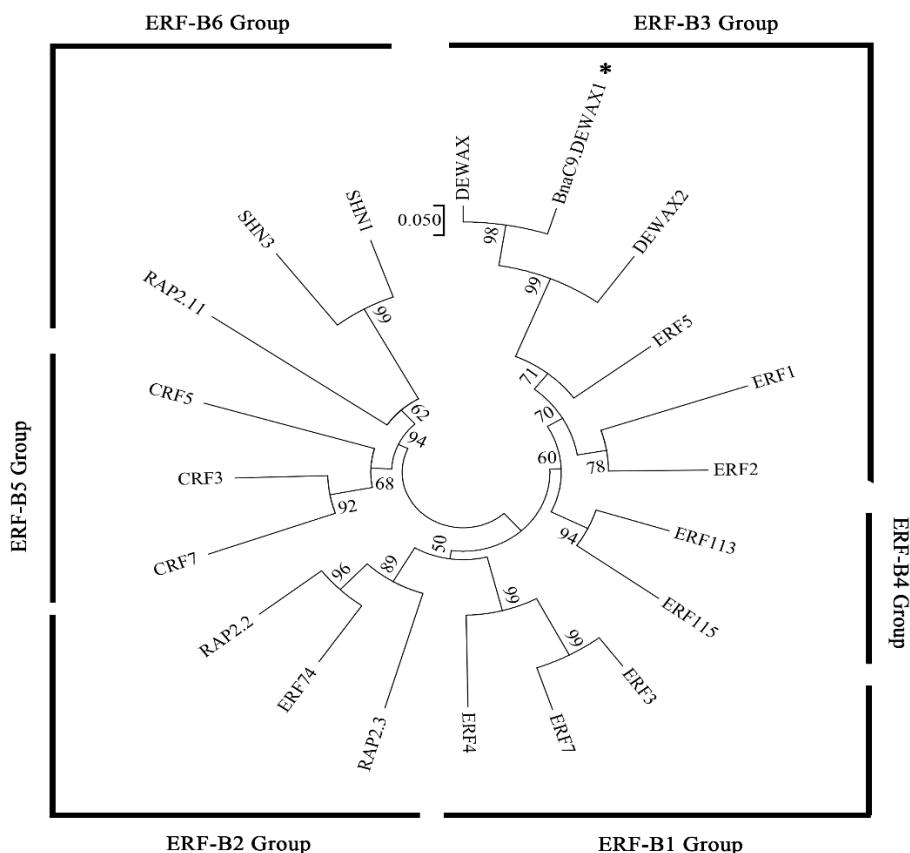


Table S1 Nucleotide sequence in *BnCER1-2* and *CER1* promoter regions regulated by BnaC9.DEWAX1.

Genes	Position (relative to ATG)	Nucleotide sequences of promoter regions (5'-3')
<i>BnCER1-2</i>	-294 ~ -100	gccata tctacgttactgatgaatatctttgcttacgtgaggatatgatataatc ggcaat cgatattcgat aggtgtgggggtgattagctgagtgataaatgaggatccatgtgggaagtatcgaatggaggagt acatgtttggtccaggtaggggccctcacagggaagtgggct ggtggg aagatagg
<i>CER1</i>	-317 ~ -153	gaagccatccatcaacc ggtgca tttcctcaa ggcatg gatgatgatcagaacatcgatga ggtgg g agggggaattagctgagtgataaatgaggatccatgtggagatcatcgaatggtagtagtacat gtttggtcttagct ggcccc accacaag

Red indicated GCC-like motif.

Table S2 Primers used in this study.

Name	Sequence (5'-3')	
For qRT-PCR		
BnDEWAX1-Fq	GTTCTTGATCCAGATTCCTGT	
BnDEWAX1-Rq	GTGATGTTGTAGTTGTTGACG	
BnACT7-Fq	GTGACAATGGAAGTGAATGGTGA	
BnACT7-Rq	GTGCCTAGGACGACCAACAATACTC	
CER1-Fq	AGGTCGACAGGGAGACCAAC	
CER1-Rq	ATAAGCGCTGCCATCAACAC	
AtEF1a-qF	TCGTTATGATCGACTCTCTTATGG	
AtEF1-qR	CCAAAAAGGAGGGAGAGAGAAAG	
For subcellular localization		
BnDEWAX1-Fs	<u>GGAATTC</u> ATGACAACCTTTTGAGAAAAGCTCTG	<i>EcoRI</i>
BnDEWAX1-Rs	CG <u>GATCC</u> TTAGTTTGATGAAGATGATGTAGTA	<i>BamHI</i>
For overexpression/complementation transgenic arabidopsis		
BnDEWAX1-Fo	CATTTGGAGAGGACACTAGT <u>GATCC</u> ATGACAACCTTTTGAGAAAAGCTCTG	<i>BamHI</i>
BnDEWAX1-Ro	GCAGGGTCGACGGTATCGATA <u>AAGCTT</u> TTAGTTTGATGAAGATGATGTAGTA	<i>HindIII</i>
Hpt-F	CTGAACTCACCGCGACGTCTGTC	
Hpt-R	GCCTCCGCTCGAAGTAGCGC	
Yeast one-hybrid assays		
BnDEWAX1-Fy	CG <u>GATCC</u> ATGACAACCTTTTGAGAAAAGCTCTG	<i>BamHI</i>
BnDEWAX1-Ry	CCG <u>CTCGAGT</u> TAGTTTGATGAAGATGATGTAGTACTAGTAG	<i>XhoI</i>
BnCER1-2P-Fy	CCC <u>AAGCTT</u> GCCATATCTACGTTACTGATGAATATC	<i>HindIII</i>
BnCER1-2P-Ry	CCG <u>CTCGAGC</u> CCCTATCTTCCCACCAGCC	<i>XhoI</i>
For transcriptional activity assay		
BnDEWAX1-Fra	CCGTCTAGAACTAGT <u>GATCC</u> ATGACAACCTTTTGAGAAAAGCTCTG	<i>BamHI</i>
BnDEWAX1-Rra	TTTGCGGAGTACCCG <u>GATCC</u> TTAGTTTGATGAAGATGATGTAGTA	<i>KpnI</i>
For Transient dual-LUC assay		
BnDEWAX1-Ftr	<u>GGAATTC</u> ATGACAACCTTTTGAGAAAAGCTCTG	<i>EcoRI</i>
BnDEWAX1-Rtr	CCG <u>CTCGAGT</u> TAGTTTGATGAAGATGATGTAGTACTAGTAG	<i>XhoI</i>
BnCER1-2P-Ftr	GTCGACGGTATCGATA <u>AAGCTT</u> GCCATATCTACGTTACTGATGAATATC	<i>HindIII</i>
BnCER1-2P-Rtr	AGAACTAGTGGATCCCCG <u>GATCC</u> CCCTATCTTCCCACCAGCC	<i>SmaI</i>
For prokaryotic expression		
BnDEWAX1-Fgex	CCGCGTGATCCCCG <u>GATCC</u> ATGACAACCTTTTGAGAAAAGCTCTG	<i>EcoRI</i>
BnDEWAX1-Rgex	GTCACGATGCGGCCG <u>CTCGAGC</u> TACTGAGGAGGATTCATCTCCGGT	<i>XhoI</i>

The underlined indicates the site of restriction enzyme.