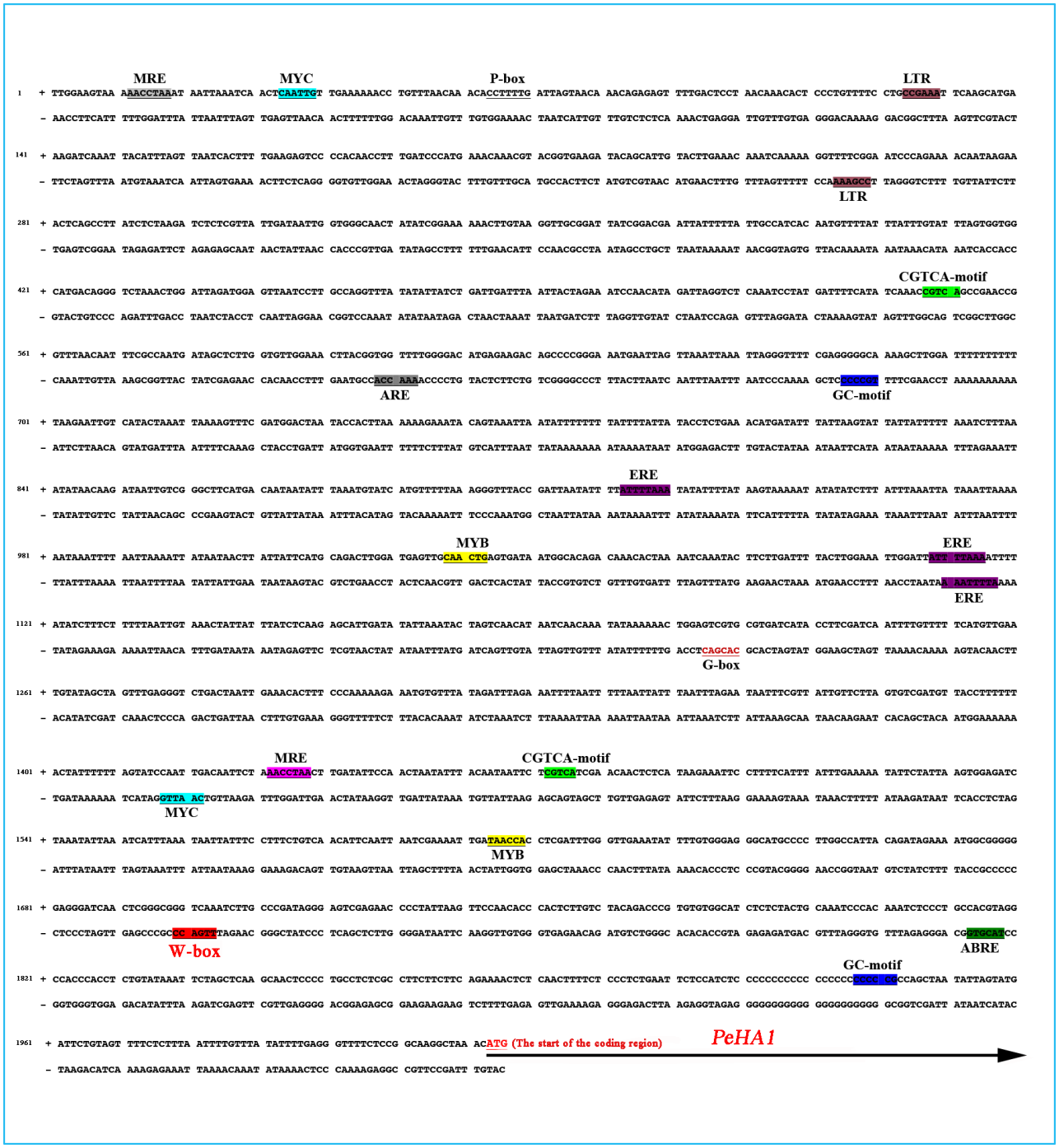
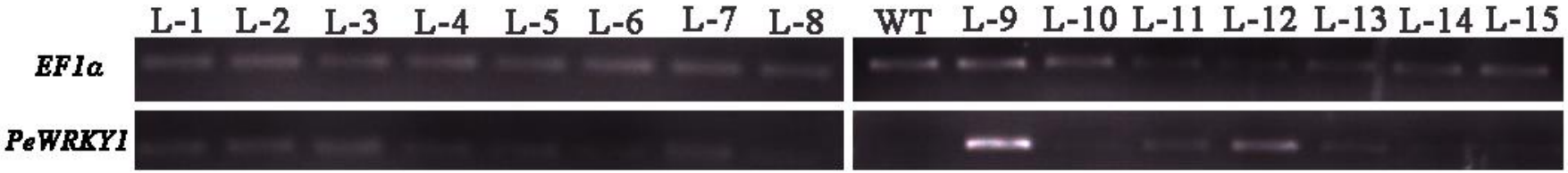
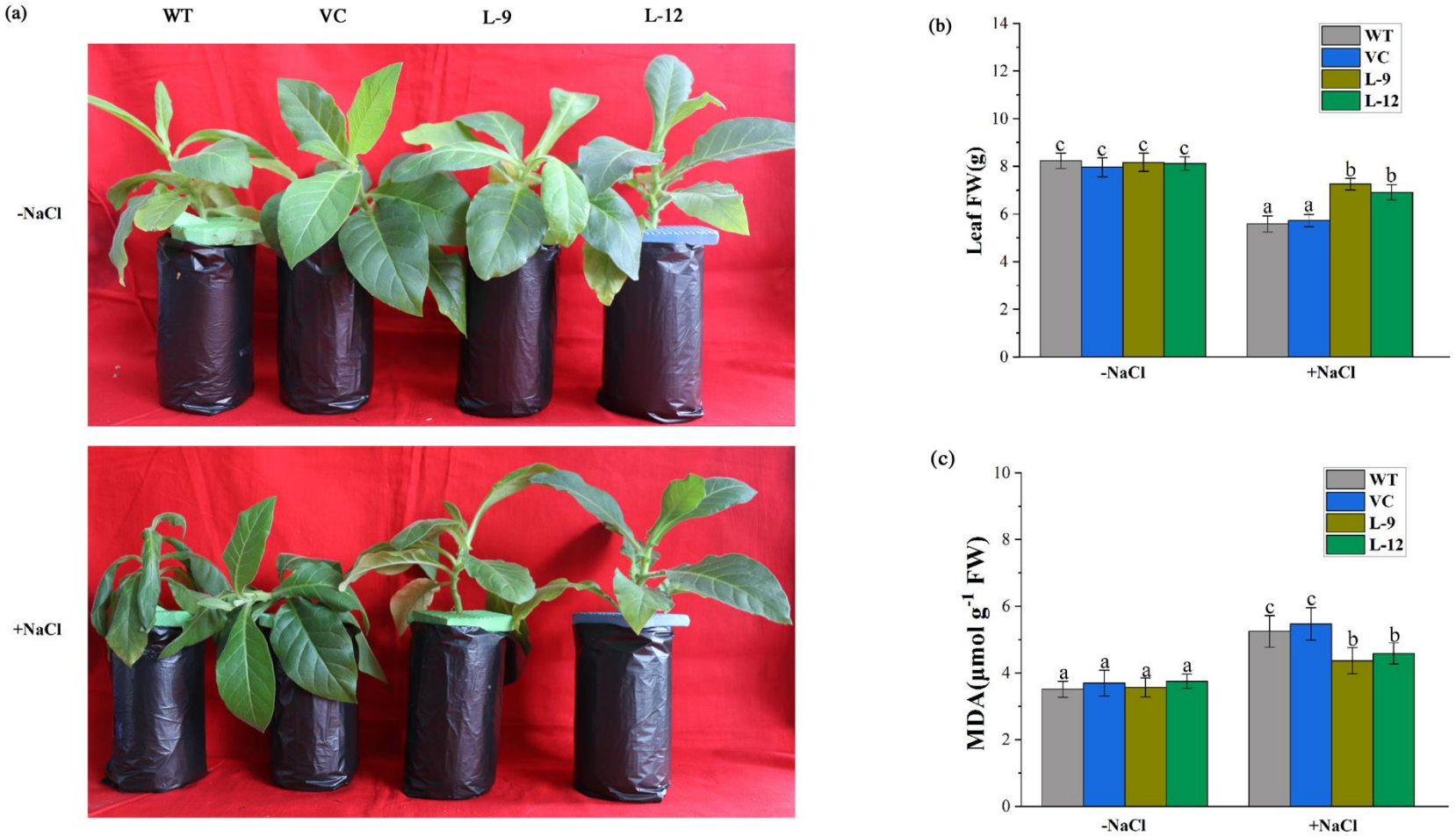


Supplementary Figure S1 Promoter sequence analysis of *Populus euphratica PeHA1*. The *PeHA1* promoter was isolated via genomic walking with a series of PCR amplifications. The primer sequences used for *PeHA1* promoter isolation are shown in Table S2. The double-stranded 2022-bp DNA sequence was analyzed using the PLACE and Plant-CARE databases. The following putative cis-acting elements are shown: MRE, MYB binding site involved in light responsiveness; MYC, cis-acting element response to drought and ABA; P-box, gibberellin-responsive element; LTR, cis-acting element involved in low-temperature responsiveness; CGTCA-motif, cis-acting

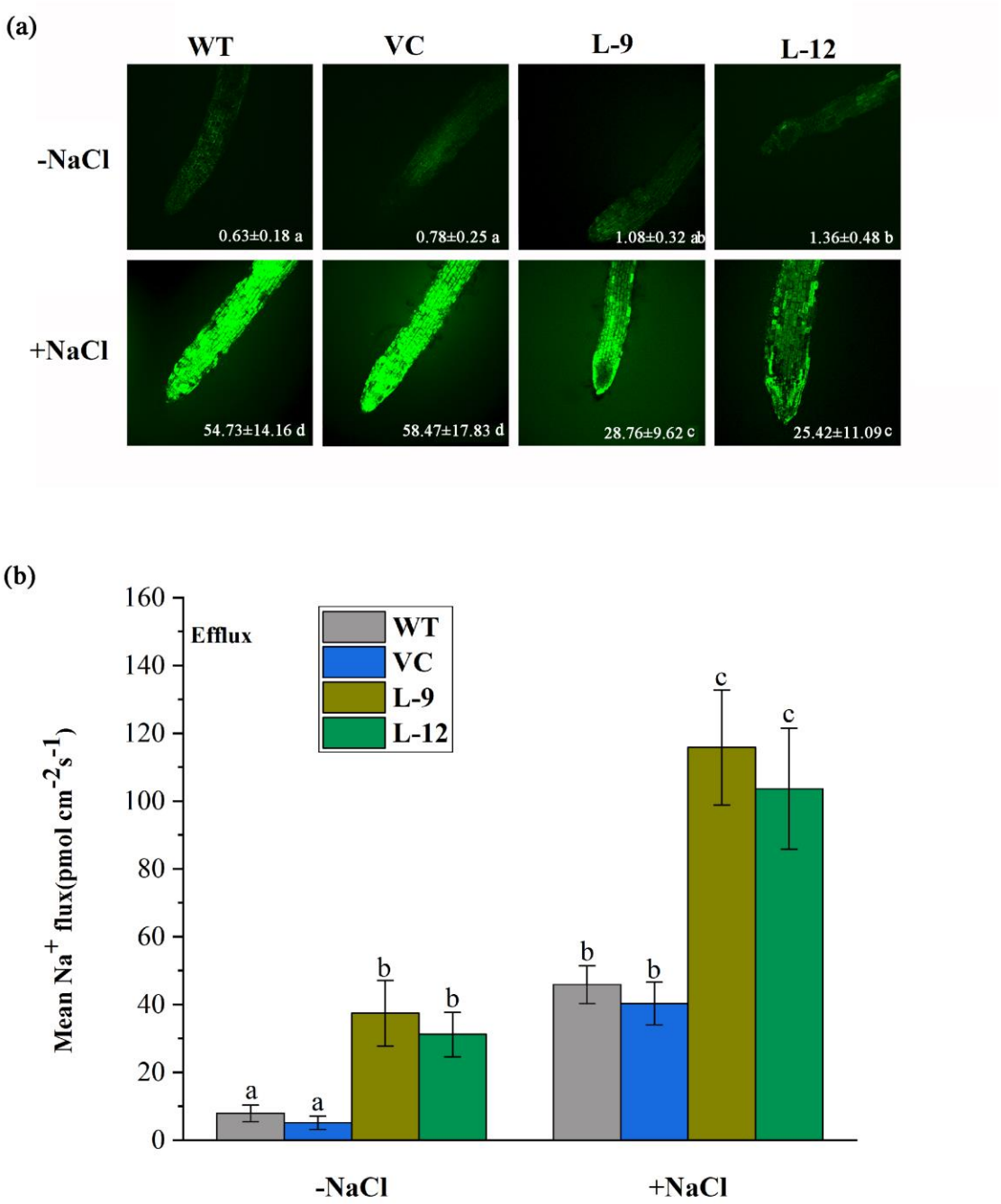
regulatory element involved in the MeJA-responsiveness; ARE, cis-acting regulatory element essential for the anaerobic induction; GC-motif, enhancer-like element involved in anoxic-specific inducibility; MYB, gene element involved in response to drought and ABA signals; G-box, cis-acting regulatory element involved in light responsiveness; W-box, the binding site for the WRKY family of transcription factors; ABRE, transcription factor involved in abscisic acid responsiveness; ATG, start codon of *PeHA1*. The start of the coding region of the *PeHA1* sequence is underlined.



Supplementary Figure S2 Semi-quantitative RT-PCR analysis of *PeWRKY1* in wild-type (WT) tobacco and transgenic lines L1–L15. The housekeeping gene elongation factor *1α* (*NtEF1α*) served as the internal control. The forward and reverse primers of *PeWRKY1* and *NtEF1α* are shown in Supplementary Table S1.

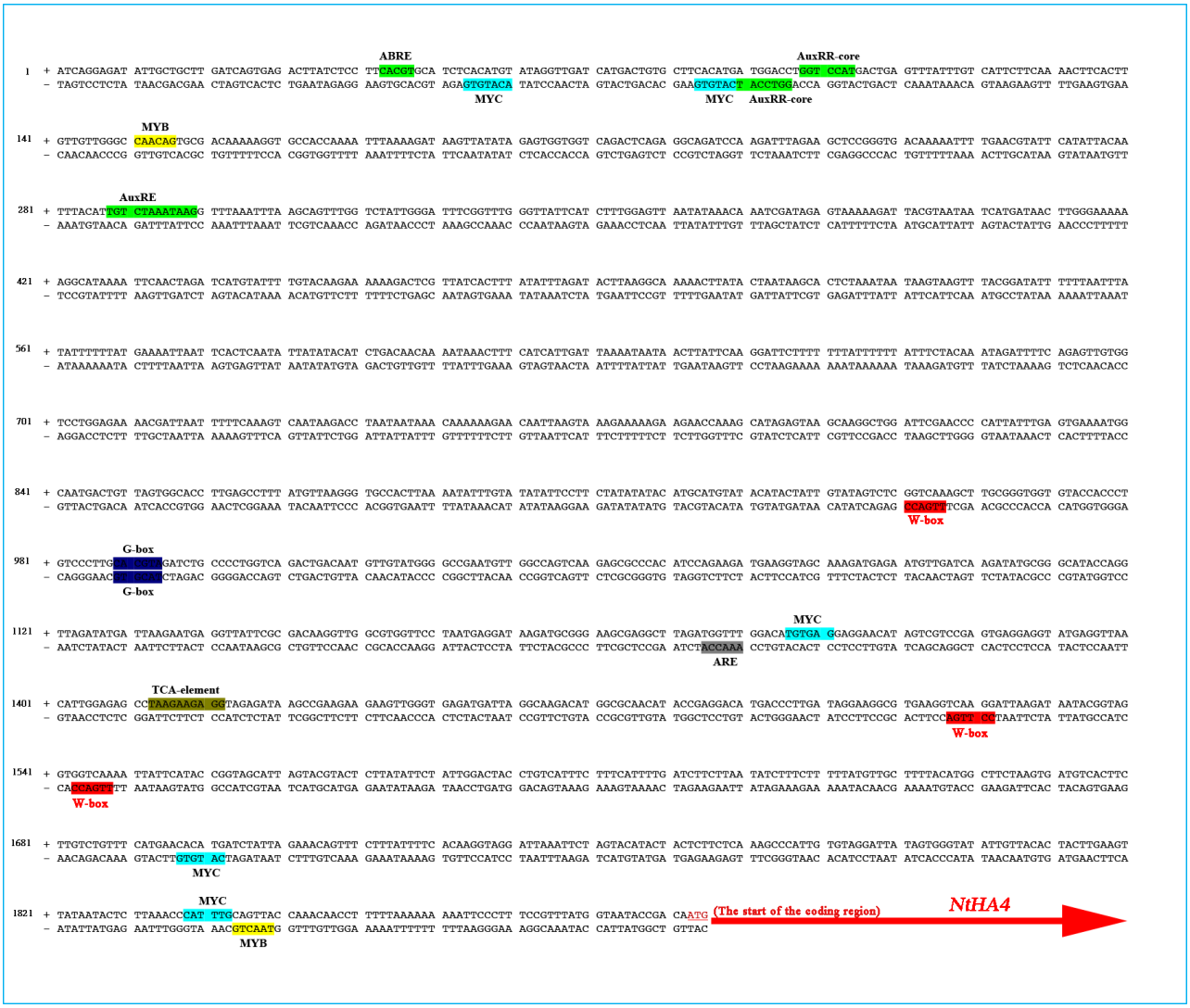

(a)
WT
VC
L-9
L-12
-NaCl
+NaCl
(b)
Leaf FW(g)
WT
VC
L-9
L-12
-NaCl
+NaCl
(c)
MDA(μmol g-1 FW)
WT
VC
L-9
L-12
-NaCl
+NaCl

Supplementary Figure S3 Phenotype tests of wild-type (WT) tobacco and *PeWRKY1*-transgenic plants. Four-week-old seedlings of WT, vector control (VC), and two transgenic lines L-9 and L-12 were exposed to 0 or 200 mM NaCl in MS nutrient solution for 3 days, and then leaf fresh weight and malondialdehyde (MDA) content were examined. (a) Representative images of salt-stressed plants. (b) Leaf fresh weight. (c) MDA content. Each column shows the mean of three independent experiments. Bars represent the standard error of the mean. Columns labeled with different letters show significant differences ($P < 0.05$) between the WT and *PeWRKY1*-transgenic lines.



Supplementary Figure S4 Na^+ concentrations and fluxes in roots of wild-type (WT) tobacco and *PeWRKY1*-transgenic plants. (a) Na^+ concentrations in root cells. Four-week-old seedlings of WT, vector control (VC), and transgenic lines L-9 and L-12 were exposed to 0 or 200 mM NaCl for 24 h. CoroNa-Green AM was used to detect the concentration of Na^+ in tobacco roots. Scale bar = 1.0 cm. (b) Na^+ fluxes at the root tip. Steady-state Na^+ fluxes were measured at the apical zones (200 μm from the root tip) in control and salinized plants. Each column shows the mean of three independent experiments. Bars represent the standard error

of the mean. Columns labeled with different letters show significant differences ($P < 0.05$) between the WT and *PeWRKY1*-transgenic lines.



Supplementary Figure S5 Promoter sequence analysis of tobacco *NtHA4*. The *NtHA4* promoter was isolated by genomic walking and a series of PCR amplifications. The double-stranded 1912-bp DNA sequence was analyzed using the PLACE and Plant-CARE databases. The primer sequences for *NtHA4* promoter isolation are shown in Table S2. The following putative cis-acting elements are shown: ABRE, abscisic acid responsiveness element; AuxRR-core, cis-acting regulatory element involved in auxin responsiveness; MYC, cis-acting element response to drought and ABA; AuxRE, cis-acting regulatory element involved in auxin responsiveness; W-box, the binding site for the WRKY family of transcription factors; G-box, cis-acting regulatory element involved in light responsiveness; ARE, cis-acting regulatory element essential for anaerobic induction; TCA element, salicylic acid responsiveness element; MYB, gene element involved in response to drought and ABA signals; ATG, start codon of *NtHA4*. The start of the coding region of the *NtHA4* sequence is underlined.

Supplementary Figure S6 Promoter sequence analysis of tobacco *NtHA2*. The *NtHA2* promoter was isolated by genomic walking and a series of PCR amplifications. The double-stranded 1963-bp DNA sequence was analyzed using the PLACE and Plant-CARE databases. The primer sequences for *NtHA2* promoter isolation are shown in Table S2. The following putative cis-acting elements are shown: MYB, gene element involved in response to drought and ABA signals; ERE, ethylene responsive element; MRE, MYB binding site involved in light responsiveness; MYC, cis-acting element response to drought and ABA; GC-motif, enhancer-like element involved in anoxic-specific inducibility; MBS, MYB binding site involved in drought-inducibility; ABRE, abscisic acid responsiveness element; ATG, start codon of *NtHA2*. The start of the coding region of the *NtHA2* sequence is underlined.

Supplementary Table S1. Primer sets used for quantitative real-time PCR.

Gene Name	Accession	Primer sets	Primer sets
PeACT7	XM_011034907	Forward Primer	CACACTGGAGTGATGGTTGG
		Reverse Primer	ATTGGCCTTGGGGTTAAGAG
PeWRKY1	XM_011034907	Forward Primer	GTGGTGATGACTTGGATGA
		Reverse Primer	CTTGGTTCTCTTACTGTTCTG
PeHA1	XM_011046711	Forward Primer	TGTGGTACTTGGTGGTGT
		Reverse Primer	CCTAAATGACGGAACAAT
NtEF1α	NM_001326165	Forward Primer	GCTGTGAGGGACATGCGTCAAA
		Reverse Primer	GTAGTAGATATCGCGAGTACCACCA
NtHA2	XM_016602228	Forward Primer	TCGTAGTGCTTCTGACATTG
		Reverse Primer	TACCGTCATTGAGGATTGC
NtHA4	XM_016619330	Forward Primer	TTTCCCGAGCACAAGTATGA
		Reverse Primer	GGTAACCTCCAAGAACAACAC

Supplementary Table S2. Primers used for cloning the promoters of *Populus euphratica PeHA1* and *Nicotiana tabacum* L. *NtHA2* and *NtHA4*.

Gene Name	Primer sets	Primer sets
PeHA1 Pro **（2022bp）**	**Forward Primer**	**CACCGACCAGCTGATAAAAGAAGG**
	Reverse Primer	**TTAACTCTAGCCGAGAAACC**
PeHA1 Pro **（1266bp）**	**Forward Primer**	**TGCGCTGTTCCGAAGATTGAATT**
	Reverse Primer	**TTAACTCTAGCCGAGAAACC**
NtHA2 pro **（1963bp）**	**Forward Primer**	**TTACTACTATATTTAGAT**
	Reverse Primer	**AAATCCACAAAGAGTGTGG**
NtHA4 pro **（1912bp）**	**Forward Primer**	**ATCAGGAGATATTGCTGCTT**
	Reverse Primer	**TGTCGGTATTACCATAAAC**

Table S3. PeWRKY1 DAP-seq peaks located upstream of the transcription start site (TSS) of the *PeHA1* gene.

Name	Merged-NW_011499985.1-371816-2
Chromosome	NW_011499985.1
Start	371584
End	372038
Strand	+
Stat	0
Parent files	WRKY_1_peaks.filter.narrowPeak|WRKY_2_peaks.filter.narrowPeak
Total	2
Subpeaks	
Peak1	WRKY_1_peak_38234
Peak2	WRKY_2_peak_39059
Region	up
Strand	+
GeneID	LOC105140044
Description	gi|743903334|ref|XP_011045013.1|/0.0e+00/PREDICTED: plasma membrane ATPase 4 isoform X2 [Populus euphratica] gi|743903333|ref|XM_011046711.1|/0.0/PREDICTED: Populus euphratica plasma membrane ATPase 4 (LOC105140044), transcript variant X2, mRNA sp|Q03194|PMA4_NICPL/0.0e+00/Plasma membrane ATPase 4 OS=Nicotiana plumbaginifolia GN=PMA4 PE=1 SV=1 PF00690.26/1.8e-14/Cation transporter/ATPase, N-terminus