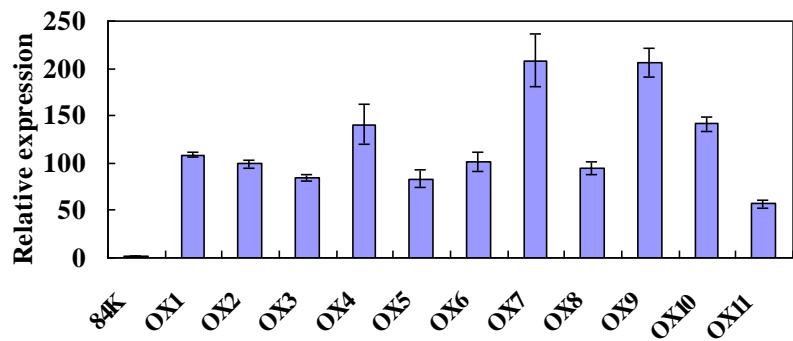
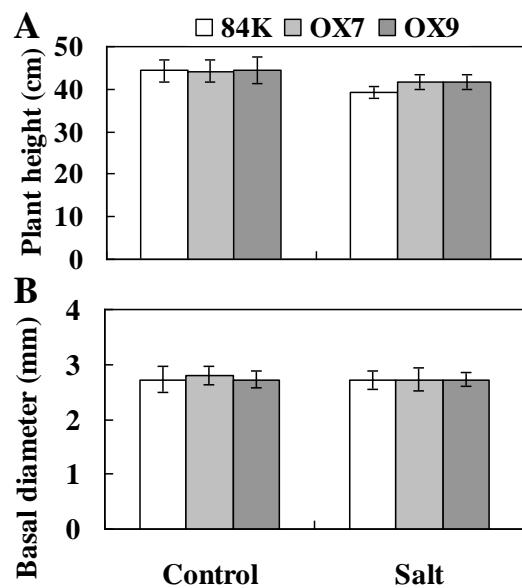


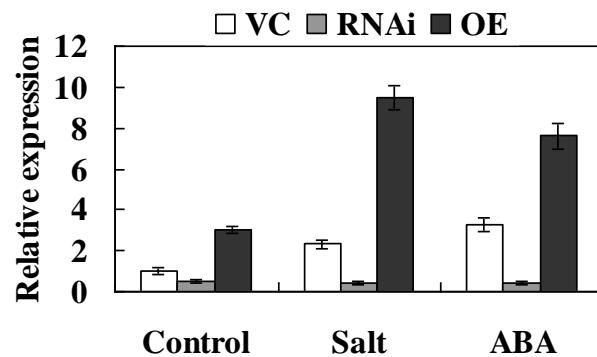
**Figure S1.** Sequence alignment and phylogenetic analyses of ThHSFA1 and other plant HSF proteins. (A) Alignment of the amino acid sequences of some HSF proteins. Identity within the same amino acid is indicated by shading. The homeobox domains include the DBD, HR-A/B, NLS region, and AHA. (B) A phylogenetic tree of HSFA proteins was constructed by MEGA 5.05 using the neighbor-joining method. The numbers beside each node represent bootstrap values based on 1000 replications.



**Figure S2.** Expression analysis of *ThHSFA1* in transgenic poplar by RT-qPCR. RT-qPCR results showing *ThHSFA1* expression in 11 transgenic overexpression poplar lines (OX). Parallel analysis of the *PagActin* gene was carried out for normalization to the amount of added template. The error bars represent  $\pm$  SD, which were calculated from multiple biological replicates.



**Figure S3.** Effects on the growth of transgenic poplar overexpressing *ThHSFA1*. Plant height and basal diameter of nontransgenic 84K and *ThHSFA1*-transformed poplars under control and salt stress conditions. Poplar plants were cultivated and subjected to salt treatment every 2 days for 10 days as described in Figure 4. The error bars represent  $\pm$  SD from multiple biological replicates.



**Figure S4.** RT-qPCR analysis of the expression of *ThHSFA1* in different transgenic *T. hispida* plants. The expression of *ThHSFA1* was determined under normal control conditions and treatment with 150 mM NaCl or 40 µM ABA for 24 h. The expression level of *ThHSFA1* in VC plants under control conditions was used as the calibrator (designed as 1). VC: the empty pROKII transformed *T. hispida* plants; RNAi: transiently RNAi-silencing *ThHSFA1* in *T. hispida* plants. OE: transiently overexpressing of *ThHSFA1* in *T. hispida* plants. The error bars represent ± SD, which were calculated from multiple biological replicates.

**Table S1. Primer sequences used in this study.**

Primers used for RT-qPCR				
Genes	GenBank number	Forward and reverse primers (5'-3')		Reference
<i>ThWRKY4</i>	JX416193	GCCTTCGTTATCTTGCCTGCTC	CGATCGGTGGGGCCTCTTC	Zheng et al., 2013 [7]
<i>ThHSFA1</i>	MW881195	AGCAATCAAGCGATAACC	AGGAGGAATGCCGTCAAG	
<i>Thtubulin</i>		CACCCACCCTTGTTCCAG	ACCGTCGTATCTTCACC	Zheng et al., 2013 [7]
<i>PagActin</i>		ACCCTCCAATCCAGACACTG	TTGCTGACCGTATGAGCAAG	
Primers used for ChIP-PCR				
<i>ProThWRKY4</i>		TAGATATCTATACTTTAATAC	TGTTTATGTTACGAATCTG	
<i>ProThtubulin</i>		TACCATACCGTATCCGTAC	ACCATACCCGTATCCATATC	
Constructs		Forward and reverse primers (5'-3')		
Specific primers used for genetic transformation of poplar				
pMD <sup>TM</sup> 19-T-ThHSFA1		ATGAGTAGCGTTCAAGAAC	TCACATCCTGTGTTCTCAGC	
		GGGGACAACCTTT-	GGCGGCCGCAACACTTT-	
pDONR207-ThHSFA1		GTACAAAAAAAGTTGGAATGAG-	GTACAAGAAAGTTGGG-	
		TAGCGTTCAAGAAC	TATCACATCCTGTGTTCTCAGC	
pROKII-ThHSFA1		CTCTAGAGGATCCCCGG-	TCGAGCTCGG-	
		GATGAGTAGCGTTCAAGAAC	TACCGGGTCACATCCTT-	
		ThHSFA1-Cis(AscI)-F:	GTGTTCTCAGC	
		TTGGCGCCCCCCAC-	ThHSFA1-Cis(SwaI)-R:	
pFGC5941-ThHSFA1		CGGCCTCCATGAAACC	CATGATTAAATCTCACCCCCAG-	
		ThHSFA1-Anti(PacI)-F:	CAGAACATCAG	
		CCTTAATTAACCAC-	ThHSFA1-Anti(XbaI)-R:	
		CGGCCTCCATGAAACC	TGCTCTAGACTCACCCCCAG-	
Genomic DNA PCR		GACGCACAATCCCACATATCC	CAGAACATCAG	
			TCACATCCTGTGTTCTCAGC	
Primers used for yeast one-hybrid assay				
pGADT7-Rec2-ThHSFA1		TGGCCATTATGGCCCCGG-	GACATTTTTTCCCGGGTCACAT	
		GATGAGTAGCGTTCAAGAAC	CCTTGTGTTCTCAGC	
pHIS2-3×HSE		AATTCCACGAAAATTCAA-	CCTTGAATTTTCGTGCTT-	
		GCACGAAAATTCAAGCAC-	GAATTTTCGTGG	
pHIS2-Pro <i>ThWRKY4</i>		GAAAATTCAAGGAGCT	GCAC-	
		ACTATAGGGCGAATTCTAGA-	GCGTGAGCTCTGTTTATGTTAC-	
		TATCTATACTTTAATAC	GAATCTG	
Primers used for dual-luciferase reporter assay				
pGreenII 62-SK-ThHSFA1		TCTAGAACTAGTG-	GCGTACCGAATTGGTAC-	
		GATCCATGAGTAGCGTTCAA-	CTCACATCCTGTGTTCTCAGC	
pGreenII		GAAG		
0800-Luc-Pro <i>ThWRKY4</i>		GACGGTATCGATAAGCTTTA-	TCTAGAACTAGTG-	
		GATATCTATACTTTAATAC	GATCCTGTTTATGTTACGAATCTG	
Primers used for subcellular localization and transcriptional activation assay				
pBI121-ThHSFA1-GFP		TCTAGACTGGTACCCGG-	CTAGTCAGTCGACCCGGG-	
		GATGAGTAGCGTTCAAGAAC	TACATCCTGTGTTCTCAGC	
pGBK7-ThHSFA1		CATGGAGGCCGAATTCATGAG-	GCAGGTCGAC-	
		TAGCGTTCAAGAAC	GGATCCTCACATCCTT-	
pGBK7-ThHSFA1-N		CATGGAGGCCGAATTCATGAG-	GTGTTCTCAGC	
		TAGCGTTCAAGAAC	GCAGGTCGAC-	
pGBK7-ThHSFA1-C		CATGGAGGCCGAATTCGTGAAGT	GGATCCAATCTGTCCATCTGATA-	
		ATCAGCCCTTAAT	TAG	
			GCAGGTCGAC-	
			GGATCCTCACATCCTT-	
			GTGTTCTCAGC	