Supplemental Table 1: The primers used in this paper.

Gene name	Primer sequences (5'-3')
The primers used to confirm the genes derived from the analysis of cDNA-AFLP	
actin(X63603)	CCACACAGGTGTGATGGTTG
	CACGTCGCACTTCATGATCG-
NtSAM1(AF127243)	CAGACCAATAAACAAGCTTCA'
	CCTGAAGGACTCTTTCA
TOBLT (D13952)	ACCGGAAGACTGCATGCA
	AACCATCCACCAAAGTTTCA
NtERD10C(AB049337)	GGAAGAAGAGAAGGCGGGTGA
	GGTCTTTGAGTGATATCCTGGTA
NtSPS (AF194022)	GAATTCAGGCGCTTCGTTGTCA
	ACCCCTAGTTTCTCCAGTGA
NtSOD (AB093097)	GACGGACCTTAGCAACAGG
	CTGTAAGTAGTATGCATGTTC
NtCA (AF454759)	CGCCTGTGGAGGTATCAAA
	GAGAAGGAGAAAGACCGAACT
NtRbohD(AJ309006)	ACCAGCACTGACCAAAGAA
	TAGCATCACAACCACAACTA
NtCAT1 (U93244)	TGGATCTCATACTGGTCTCA
	TTCCATTGTTTCAGTCATTCA
NtGPX(AB041518)	GGTTTGCACTCGCTTCAAG
	AGTAGTGGCAAAACAGGAAG
NtAPX1(AU15933)	GAGAAATATGCTGCGGATGA
	CGTCTAATAACAGCTGCCAA
NtAPX2(D85912)	GACAACTCATACTTTACGGA
	CTTCAGCAAATCCCAACTCA
NtRub-SS (X02353)	ATGGCTTCCTCAGTTCTTTC
	CATTGCACTCTTCCGCCGTT'
ChlGapA (M14417)	CATTGTTGCAAACCAGTGGA
	TGAGACTTCACAAGGTGGAA
CyGAP (M14419)	TAAGGATTTGATGCTGGTGA
	ACATTCCTCAAAGATAACACA
NtRCA342 (U35111)	AGAGGAAAAGAAGCACAACA
	AAAGCTCAACCAAATCTTGTA
The walking primers for isolating the promoter of *NtSOD*	
NtSOD-1	GCGGAACCCTAGCCCTGTT
NtSOD-2:	GGAGCGAAAAGGTCTGGAAG
NtSOD-3	CAGTGCTCCATAGTCGTAGG
NtSOD-4:	TGCATTATGTCACCGCTAATTG
The walking primers for isolating the promoter of *NtCA*	

NtCA-1 *NtCA*-2 *NtCA*-3: *NtCA*-4	AGGGGAGATA GTAAGGCAAC GCAACAGGACGAGTTGGTTT GGGAACAGAAGGAGAAGAAG CATTTGGCTC AAGAACTTCCT
Primers used to generate different length promoters of *NtCA*	
CA-P1-5' CA-P2-5' CA-P3-5' CA-P4-5' CA-P5-5' CA-P6-5' CA-P7-5' CA-mini-5' CA-3'	CGGCTGCAGAAGGTTAATTGATTTAGTTGAAG CGGCTGCAGAGATAAGAGGAGCCAAAAGTG CGGCTGCAGTTCAACATGTTAACAAAAGCAAT CGGCTGCAGAAAATATTTTTACACTATTCAGGC CGGCTGCAGAACGGAATTCAATTAAACTCTC CGGCTGCAGCATCTGTGATCAGCAATAATTG CGGCTGCAGAAGTAAATTAGTTCTGATCACTC CGGCTGCAGCAACGTACAAACCTCATCTAC CGGAGATCTACCATGGTTGGCTCAAGAACTTCCTTTT
Primers used to generate different length promoters of *NtSOD*	
SOD-f-5' SOD-p1-5' SOD-p2-5' SOD-mini-5' SOD-3'	CGGCTGCAGTTTGGTGTTGTGTTTCATTTTTG CGGCTGCAGGTGGGAAGAGCATTAGG CGGCTGCAGATCCGTTACAAATGCGA CGGCTGCAGTTTCCCTTCATTTTTCATTC CGGAGATCTACCATGGTTTTCAGATATTCCCAAAATGC
Primers used to generate the removal of GCC box or 39 bp fragment from NtSOD-f or NtCA-p1	
GCC box del-5' GCC box del-3' 39 bp-del-5' 39bp-del-3'	GTGGGAAGAGCATTAGG TCGCATTTGTAACGGAT CATCTGTGATCAGCAATAATTG GAGTGATCAGAACTAATTTACTT
Primers used to detect the expression of *JERF3* in transgenic tobacco and in tomato	
JERF3 (AY383630)	GAGGATGACCATTATGATTC GGTACCATAGTAACGGGGGT
The walking primers for isolating the promoter of tomato *JERF3*	
JERF3-1 *JERF3*-2 *JERF3*-3 *JERF3*-4	CCGTCAAAACTAAATCATGA GGTGGTTCTATAATCTCCG TCACCGCCGAGTTTCTATGG ATGGGGTCGTTTCGATCTCG

Supplemental Legends:

Supplemental Figure 1: Expression of *JERF3* in tobacco has no effect on the growth at normal growth conditions.

(A) Different expression of *JERF3* in 5 independent OE lines and WT in 4 week old tobacco seedlings. (B) Phenotypes of 10 week old seedling development. (C) Phenotypes of flowering stage.

Supplemental Figure 2: Expression of *NtSPS* in response to cold.

4 week old tobacco seedlings in pots under 4℃ were used to extract RNA. The expression of *NtSPS* in tobacco was detected by Q-PCR. The actin transcripts were used as internal control, and the expression level of *NtSPS* was standardized as 100 at time "0". The assay was repeated three times. The bars represent (±) SE.

Supplemental Figure 3: LeEIL1 interacts with the promoter of *JERF3 i*n transient expression assays.

LeEIL1 interacts of with the promoter of *JERF3 in vivo*. Sequence of the *JERF3* promoter was cloned to replace the promoter of 35S in pBI121, upstream of the GUS reporter gene. LeEIL1 indicates the constitutive expression of full length *LeEIL1*; None, as the negative control of the effector, indicates the empty vector plasmid. Agrobacteria containing the reporter vector and effector vector were co-infiltrated into tobacco leaves. The relative GUS activity is the ratio of GUS reporter expression (35S:LeEIL1/empty vector). The assay was repeated three times. Error bars indicate ±SE.

Supplemental procedures

Plant materials and Growth conditions

All plants were grown in growth chambers at 25°C with a 16-hr light regime with illumination from cool white fluorescent lights of about 150 μmol m^{-2} s^{-1}. For the observation of tobacco growth, all plants of 5 independent OE lines and WT were put in pots. For root phenotypes, 10 week old seedlings in pots were gently washed with water,

and then photographed. For the cold treatment, 4 week old wild type tobacco (*Nicotiana tabacum* cv NC89) plants were treated at a temperature of 4°C for the time indicated in supplemental Figure 2.

RT-PCR and Real time Q-PCR assays

Total RNA was extracted using Trizol (Invitrogen, USA) according to the manufacturer's recommendations. 1 μg of total RNA was used to synthesize cDNA using 200 units of M-MLV reverse transcriptase (Promega, USA) following the manufacturer's instructions. After reverse transcription, RT-PCR or real time quantitative polymerase chain reactions (Q-PCR) were performed, the latter using an ABI Prism 7000 system (Applied Biosystems, USA). The mRNA levels detected with ethidium bromide staining were recorded by Molecular Imager® FX (Bio-Rad). The relative transcript abundance for each gene is relative to the *actins* transcript levels measured in the same sample. The primers used in this paper for RT-PCR or Q-PCR are listed in Supplemental Table 1.