Table 1 Suppl. A list of primers used in this study (F - forward, R - reverse).

Primer name	Accession No.	Primer sequence (5'-3')	Purpose
SikTrxh-qF	KC915015.1	AAGGTGGATGTGGATGAACTGG	quantitative PCR
SikTrxh-qR	KC915015.1	CAACCTTGTCCACTTCTTTTCCA	quantitative PCR
SikGAPDH-qF	KF563904.1	TTCAACATTATTCCCAGCAGCAC	quantitative PCR
SikGAPDH-qR	KF563904.1	TAAGTAGCCTTCTTCTCAAGTCTC	quantitative PCR
NtCAT-qF	U93244.1	AGGTACCGCTCATTCACACC	quantitative PCR
NtCAT-qR	U93244.1	AAGCAAGCTTTTGACCCAGA	quantitative PCR
NtAPX-qF	U15933.1	CAAATGTAAGAGGAAACTCAGAGG	quantitative PCR
NtAPX-qR	U15933.1	CAGCCTTGAGCCTCATGGTACCG	quantitative PCR
NtSOD-qF	AF053076.1	AGCTACATGACGCCATTTCC	quantitative PCR
NtSOD-qR	AF053076.1	CCCTGTAAAGCAGCACCTTC	quantitative PCR
NtLEA5-qF	AB093097.1	TTGAATCTGGGGTTTTGGTT	quantitative PCR
NtLEA5-qR	AB093097.1	GGAAGCATTGACGAGCTAGG	quantitative PCR
NtP5CS-qF	HM854026.1	ACATTAGGCGAAGAGTATTGT	quantitative PCR
NtP5CS-qR	HM854026.1	ACTTCACACACCCACTTACCT	quantitative PCR
NtUbiquitin-qF	U66264.1	TCCAGGACAAGGAGGGTAT	quantitative PCR
NtUbiquitin-qR	U66264.1	CATCAACAACAGGCAACCTAG	quantitative PCR
SikTrxh (*BamH* I)-F	KC915015.1	GAGCTCGGAAACACATAAGTTGCTG	cloning
SikTrxh-R(*Sac* I)-R	KC915015.1	GGATCCAAAATGGCGGAAGAAGGA	cloning
SikTrxh-F(*BamH* I)-F	KC915015.1	GAGCTCGGAAACACATAAGTTGCTG	subcellular localization
SikTrxh-R(*Xba* I)-R	KC915015.1	TCTAGATCGTCGATGTTGCCGACTTA	subcellular localization

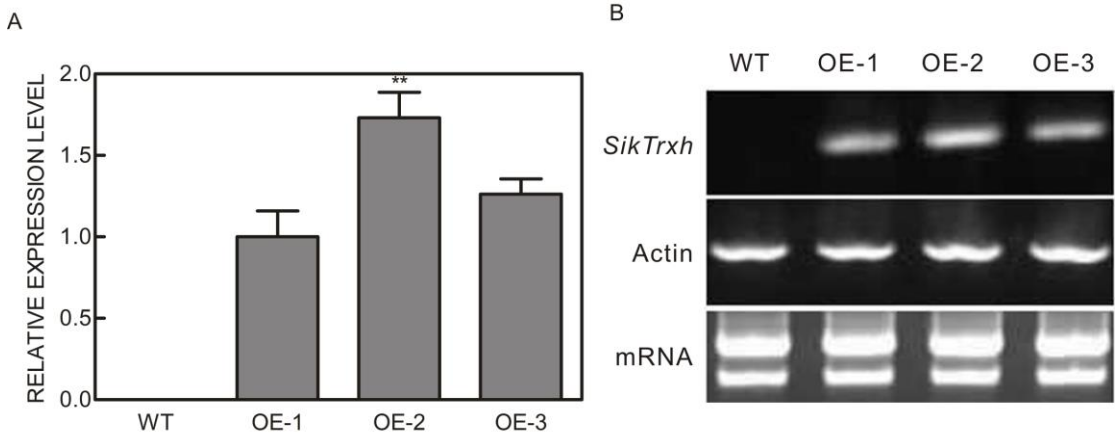

Fig. 1 Suppl. Expressions of *Saussurea involucrata thioredoxin-h* (*SikTrxh*) in wild-type (WT) and transgenic *SikTrxh* tobacco plant lines. *A* - identification of *SikTrxh* in tobacco plants by quantitative reverse transcription PCR. *B* - semi quantitative reverse transcription PCR in *SikTrxh* tobacco plants. Means ± SDs, $n = 3$; ** - significant differences between treatments at $P \leq 0.01$.

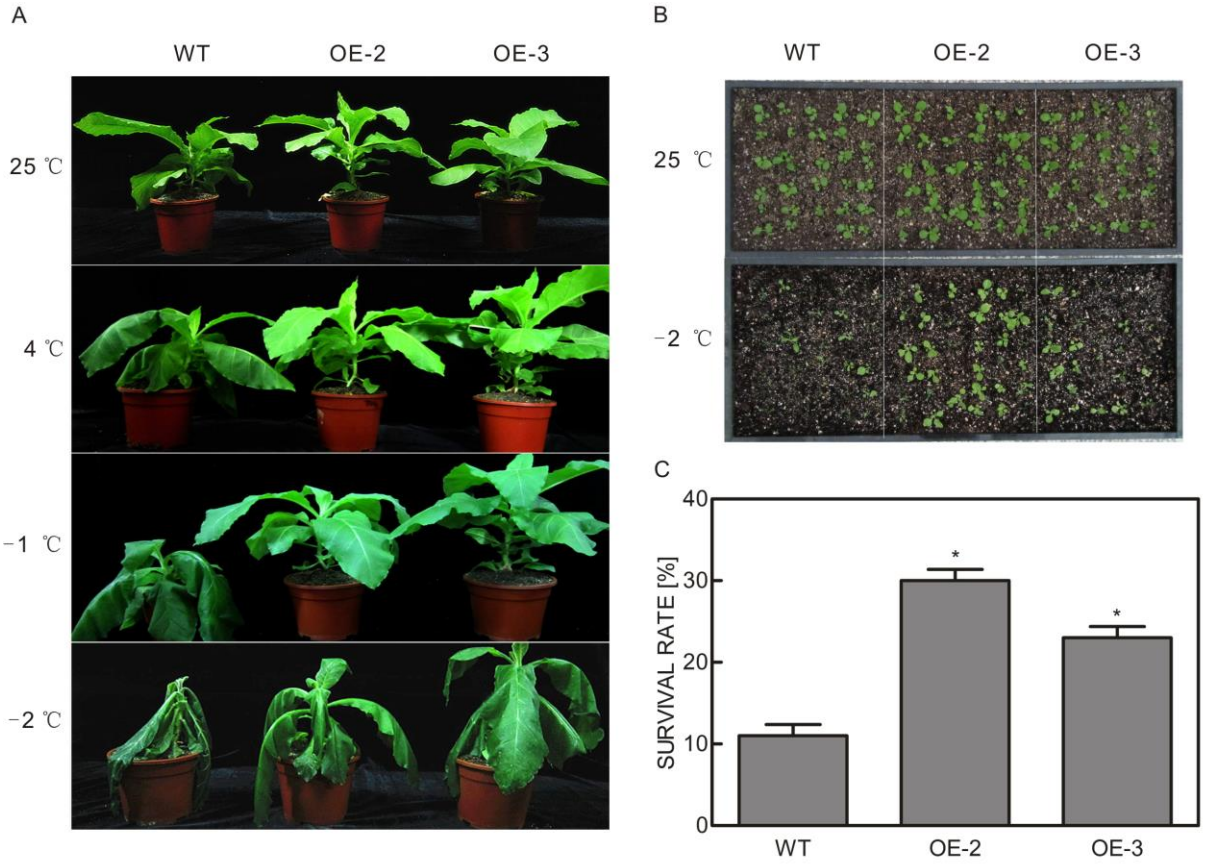

Fig. 2 Suppl. *A* - phenotypes of 6-week-old wild-type (WT) and transgenic *Saussurea involucrata thioredoxin-h* (OE-2 and OE-3) tobacco plants subjected to cold stress (4, -1, and -2 °C) for 2 h. Photographs were taken 2 h after the start of the stress treatments. *B* - tobacco phenotype observation at seedling stage. *C* - survival rate of tobacco seedlings after low temperature treatment. Means ± SDs, $n = 3$; * - significant differences between treatments at $P \leq 0.05$.

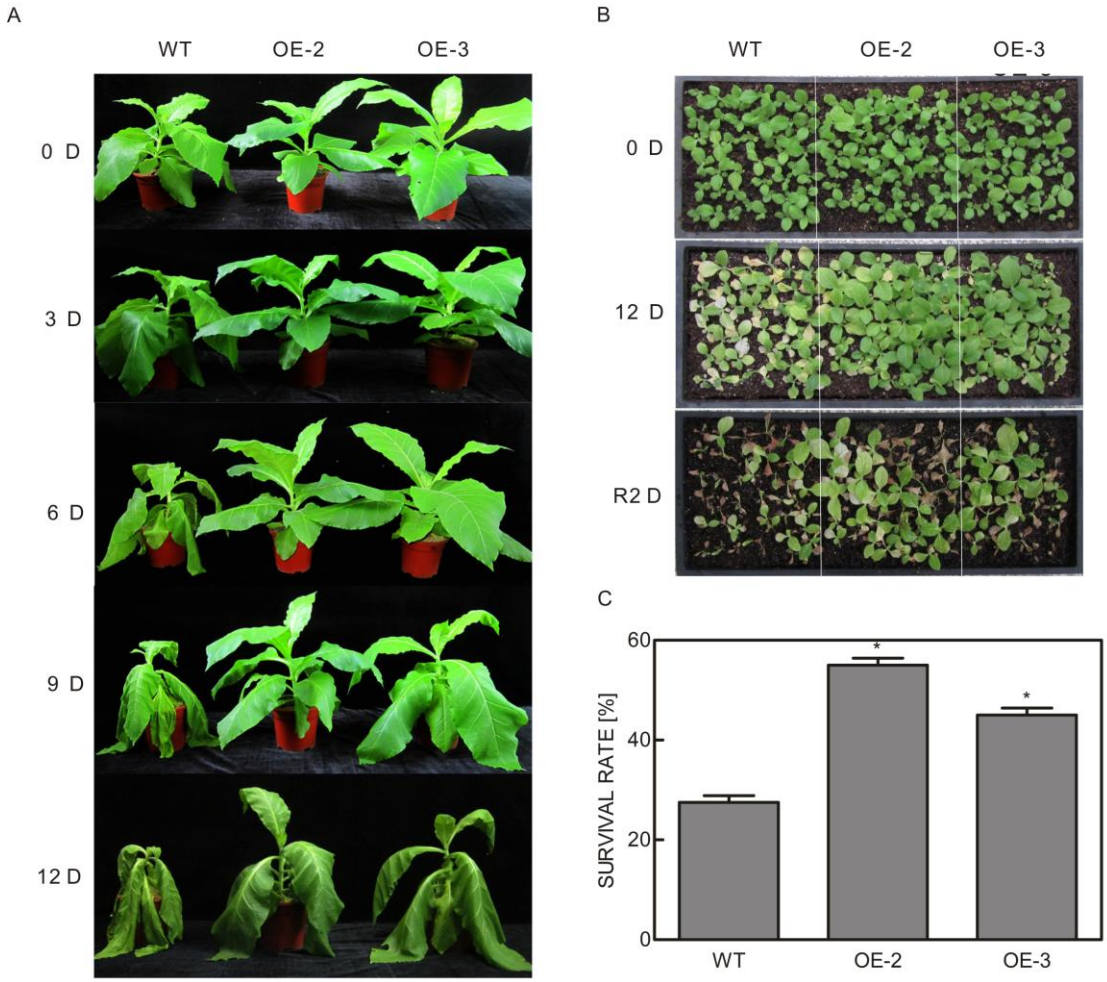

Fig. 3 Suppl. *A* - phenotypes of 6-week-old wild-type (WT) and transgenic *Saussurea involucrata thioredoxin-h* (OE-2 and OE-3) tobacco plants subjected to drought stress for 12 d. Photographs were taken 0, 3, 6, 9, and 12 d after the start of the stress treatments. *B* - tobacco phenotypes at the seedling stage. *C* - survival rate of tobacco seedlings after drought treatment. Means ± SDs, $n = 3$; * - significant differences between treatments at $P \leq 0.05$.

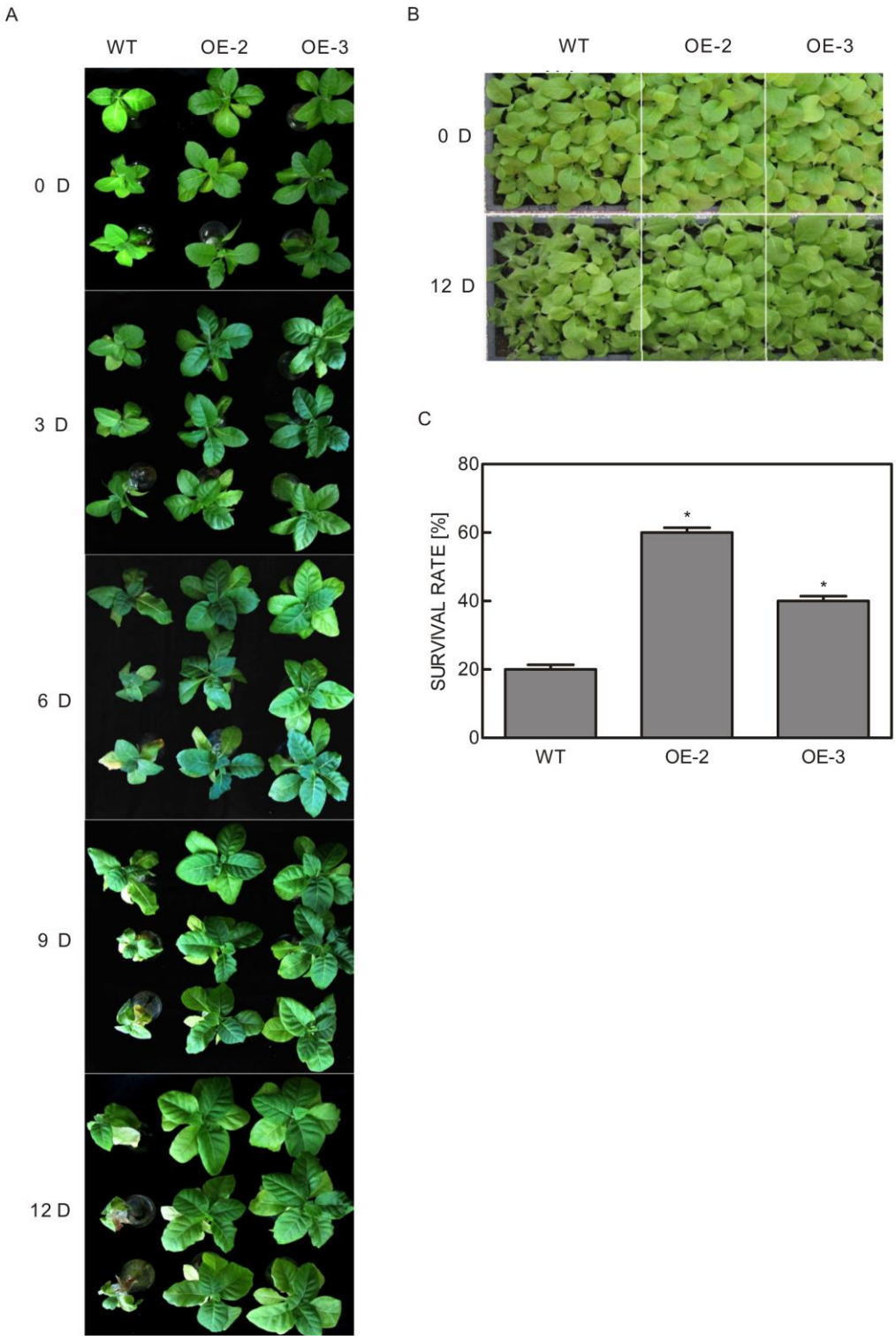

Fig. 4 Suppl. *A* - phenotypes of 6-week-old wild-type (WT) and transgenic *Saussurea involucrata thioredoxin-h* (OE-2 and OE-3) tobacco plants under salt (NaCl) stress. Samples were taken after 3, 6, 9, and 12 d; samples taken from the 25 °C tobacco were used as a control group. *B* - tobacco phenotype observation at seedling stage. *C* - survival rate of tobacco seedlings after salt treatment. Means ± SDs, $n = 3$, * - significant differences between treatments at $P \leq 0.05$.