Figure S1. Detection of silencing efficiency of *CaHsp18.1a* gene mediated by TRV2. **(A)** Plant phenotype of pTRV2:*CaPDS*、pTRV2:00 and pTRV2:*CaHsp18.1a;***(B)** Silencing efficiency of *CaHsp18.1a.*（C）Total chlorophyll content under the 42°C heat treatment for 24 h in TRV2:*CaHsp18.1a* and TRV2:00 plant phenotypes
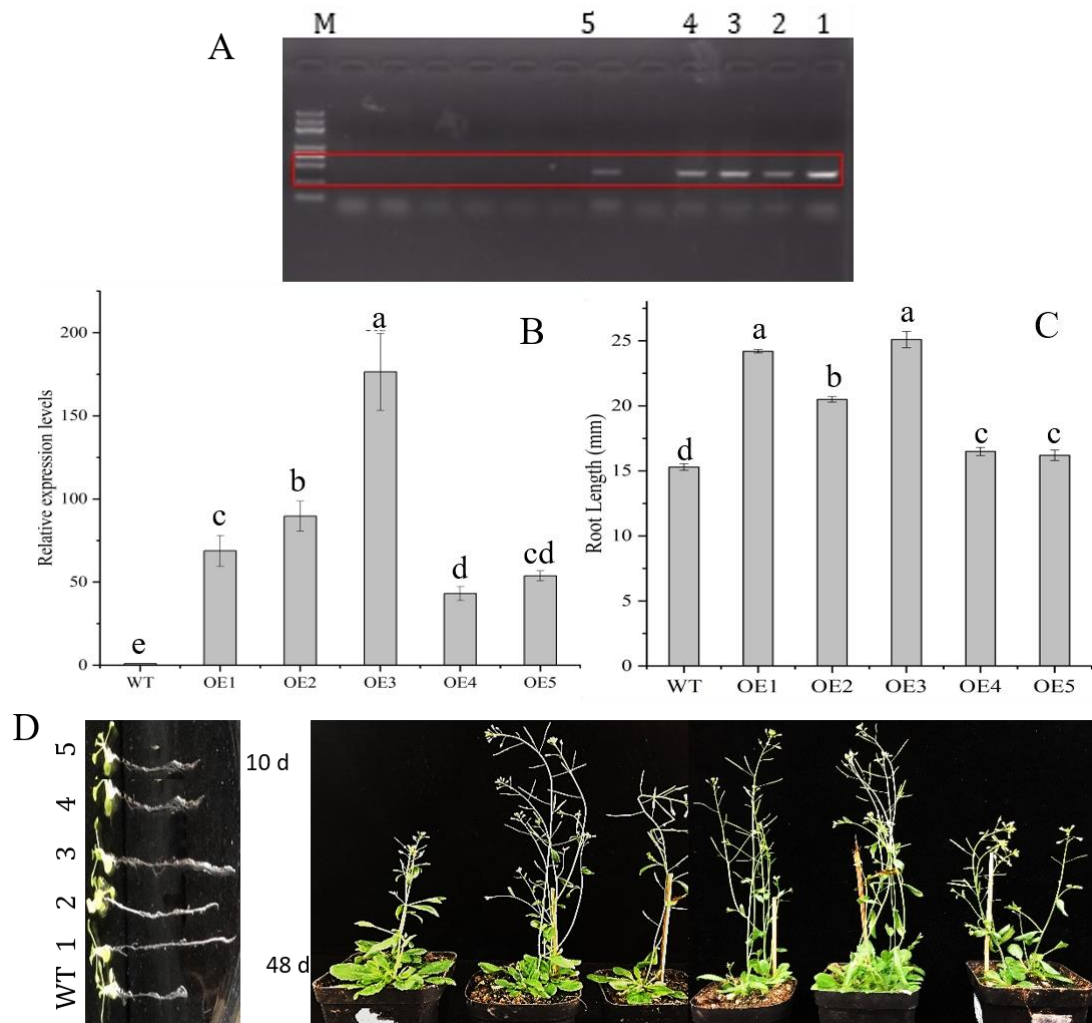
Figure S2. Validation and acquisition of homozygous strain of T3 generation of Arabidopsis with overexpression of *CaHsp18.1a*. **(A)** PCR analysis of the *CaHsp18.1a*gene in Arabidopsis; **(B)** Relative expression level of WT and *CaHsp18.1a*-OE Arabidopsis lines under normal conditions; **(C)** Root length of 10-days old *CaHsp18.1a*-OE Arabidopsis; **(D)** Root length and growth status of WT and *CaHsp18.1a*-OE Arabidopsis at 10 d and 48 d.
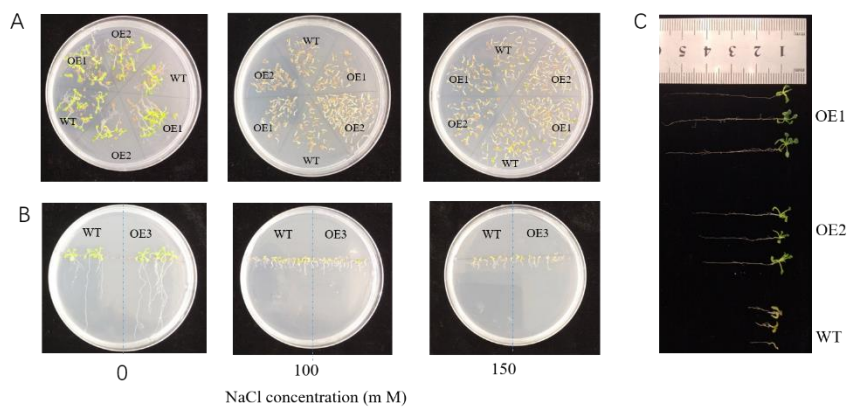
Figure S3. Germination of the transgenic Arabidopsis under salt stress. **(A)** Germination of WT and *CaHsp18.1a*-OE Arabidopsis seedlings grown on MS medium contain 0, 100 and 150mM NaCl for 7 days, respectively; **(B)** Root growth of WT and *CaHsp18.1a*-OE Arabidopsis lines grown on MS medium containing 0, 100 and 150mM NaCl for 10 days; **(C)** Root length of WT and *CaHsp18.1a*-OE Arabidopsis lines under salt stress

Table S1 The main primers sequence used in this research

Primer Name	Forward Primer	Reverse Primer
qAtHsfB4	5' CCGGAGTTTGCTCGTGATCT 3'	5' GGTGGTGTGACATGAACGGA 3'
qAtHsfA8	5' GGCAGTATCAGGAGGTGACG 3'	5' CCGATGGTGGCTGGTATGTT 3'
qAtHsfA2	5' TGGTGTGCTTGTAGCTGAGG 3'	5' CTCCGTTTCCTCCCCACATC 3'
qAtHsfA7A	5' TCTTCACCAAGCCATGACGC 3'	5' CGAAGGACTCTGCATTGCTC 3'
qAtHsf1	5' CGTTAAGTTACGCCAGCAGC 3'	5' TCCGCTTCTTATTGGCCTCG 3'
qAtHsfA3	5' GATGACCCGACTCTTGACCC 3'	5' GACCCTTGGCTTTGGCTAGT 3'
qAtHsp70	5' CAGCGTCAAGCGACTAAGGA 3'	5' ACCAGCAGTTGCCTTGACTT 3'
qAtHsp101	5' ACCAGAGCTCTTGAACAGGC 3'	5' TGTGAAGAGACTTACCGGGTC 3'
qAtHspC300	5' CGCTGTTCAAGCAGATTGGG 3'	5' AAGGATTTGCTGTCGCGGTA 3'
qAtAPX1	5' TGCTACCAAGGGTTGTGACC 3'	5' ACAGGGTCGTCCAATAGTGC 3'
qAtAPX2	5' GAGCTAGCCCATGATGCCAA 3'	5' CAAGGTGTGTCCACCAGACA 3'
qAtSOD1	5' GGTCCACATTTCAACCCCGA 3'	5' GGACAACAACAGCCCTACCA 3'
qAtCAT	5' CAGAGACACCGTCTTGGACC 3'	5' GCCTGTCTGAATCCCAGGAC 3'
qAtP5CS1	5' GCAGCTTTGCGGATCTTCAG 3'	5' GATATGGGGCTCTTCGGGTG 3'
qAtMYB124	5' CGGTATCAGTACACCGCGAA 3'	5' TCTGCGCCAAGGAGCTTAAA 3'
qAtRD29a	5' TATTCGCCGGAATCTGACGG 3'	5' GATGCCTCACCGTATCCAGG 3'
qAtNCED3	5' CAGAGACACCGTCTTGGACC 3'	5' GCCTGTCTGAATCCCAGGAC 3'
qAtRab18	5' AGCTCGGAGGATGATGGACA 3'	5' AGCCACCAGCATCATATCCG 3'
pCaHsp18.1a-TRV2	5'-AAGGTTACCGAATTCTCTAGA ATGTCTCTGATTCCAAGC–3'	5'-GAGACGCGTGAGCTCGGTACC ACTTTCACTTCCTCTCTC-3'
pCaHsp18.1a-2307	5'-GAGAACACGGGGGACTCTAGA ATGTCTCTGATTCCAAGCTTCT-3'	5'-GGGAAATTCGAGCTCGGTACC TTAACCAGATATGTCAATTGCC-3'
pCaHsp18.1a-2307-G	5'-GAGAACACGGGGGACTCTAGA ATGTCTCTGATTCCAAGCTTCT-3'	5'-TCCCTTACCCATGGTACC ACCAGATATGTCAATTGCCTTG-3'