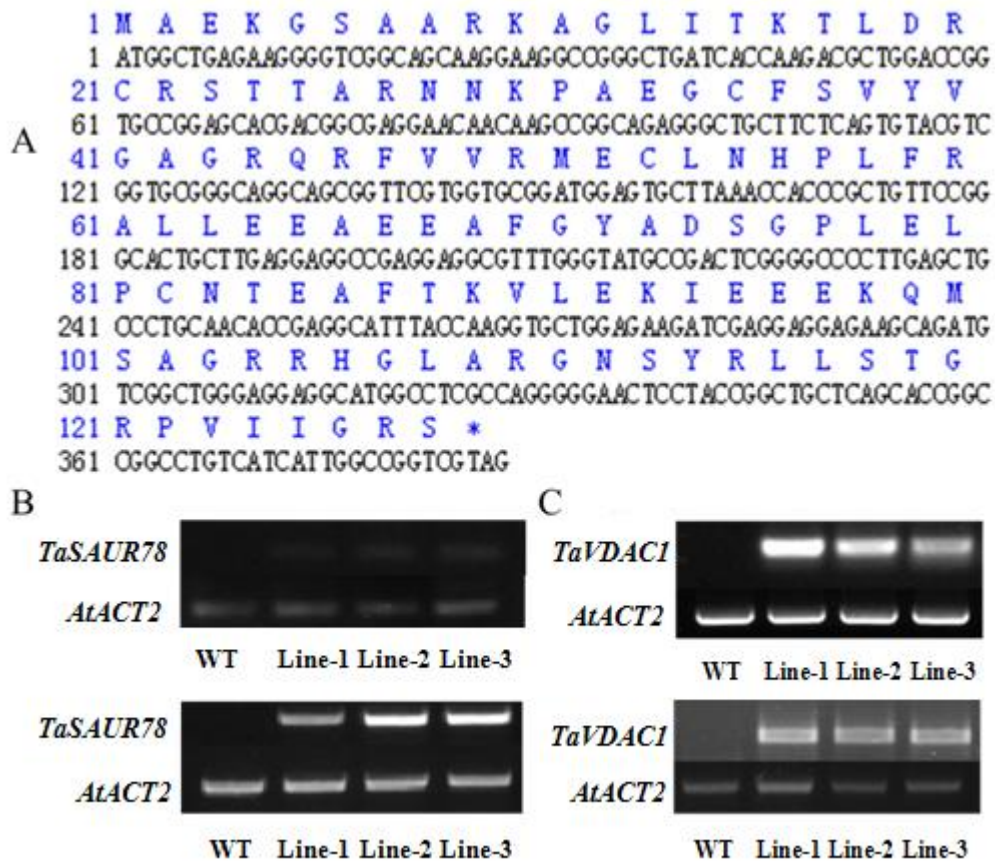


Appendix A Changes in the expression of candidate SAURs in the transcriptome analysis of wheat roots. Numbers in table are \log_2 of gene expression in Jimai 19 root under salt stress than that before salt stress.

Gene ID	Time after salt stress treatment					Annotation
	2 h	6 h	24 h	48 h	72 h	
Treas_5DL_32B83E57E		-3.11	-4.32	-5.53	-5.60	SAUR
Treas_5DL_677150034		-2.88	-3.70	-3.69	-5.76	SAUR
Treas_5BL_80B9C8E10				-4.62	-5.10	SAUR
Treas_4AL_0682CD14B				3.91	3.62	SAUR
Treas_7DL_17EE618FC					3.65	SAUR
Treas_7DL_E71974C9D					3.98	SAUR
Treas_1AL_13807565F		1.04				SAUR

Appendix B Primers used in this study

Primer name	Primer sequences	
	Forward	Rewards
<i>TaSAUR78</i> -cds	GTGCATCCTTCCAAAGATTCAACGA	TCCCAACCAACAAGGGTC
<i>TaVDAC1</i> -cds	GCCGATCCCAGCTCACCG	ATCCGAAACCGAGGAACACCC
<i>TaSAUR78</i> -GFPGUS	GCTCTAGAATGGCTGAGAAGGGGTC	GCTCTAGACTTCGACCGGCCAATGAT
<i>TaVDAC1</i> -GFPGUS	GCTCTAGAATGGGCGGCCCAGGCCTC	GCTCTAGATCAAGGCTTGAGAGCAAT
<i>TaSAUR78</i> -Y	CATATGGCCATGGAGGCCGATGGGCATGGCTGAGAAG	TATGCTAGTTATGCGGCCGCCTACGACCGGCCAAT
<i>TaVDAC1</i> -Y	GGAATTCATGGGCGGCCCAGGCCTC	CGGGATCCTCAAGGCTTGAGAGCAAT
<i>VDAC</i> -bifc	GCTCTAGAATGGGCGGCCCAGGCCTC	GGGGTACCAGGCTTGAGAGCAAT
<i>TaSAUR78</i> -bifc	GGGGTACCATGGCTGAGAAGGGGTC	GCTCTAGACTTCGACCGGCCAATGAT
<i>AtAct2</i>	TTCGTTTTGCGTTTTAGTCCC	GGGAACAAAAGGAATAAAGAGGC
<i>TaSAUR78</i>	GGTTCGTGGTGCGGATGGAGTGCTT	CCGACATCTGCTTCTCCTCCTCG
<i>TaVDAC1</i>	TCACCGGCGGCCATGGGCGG	CCCGAATGCATCCGAAACCGAGG
<i>TaTubulin</i>	GAGGCCTCGTGTGGTCGCTTTGT	GCCCAGTTGTTACCCGCACCAGA
<i>AtDREB</i>	CATCAGAGCCAAGACCAAAACC	TGTAGGACCATTGCCTCAGAAC
<i>AtRD26</i>	AATGGGTCGTCATCGTCT	GCATCGTAACCACCGTAA
<i>AtGOLS1</i>	GACGAGTCTCTTGATTACAAGAATGTT	AAACTGCTGAAGTGTCTGTTGC
<i>AtHSP70</i>	CTGACAGCGAGCGTCTCAT	GGATCACTGTATCTTCTCCGATT

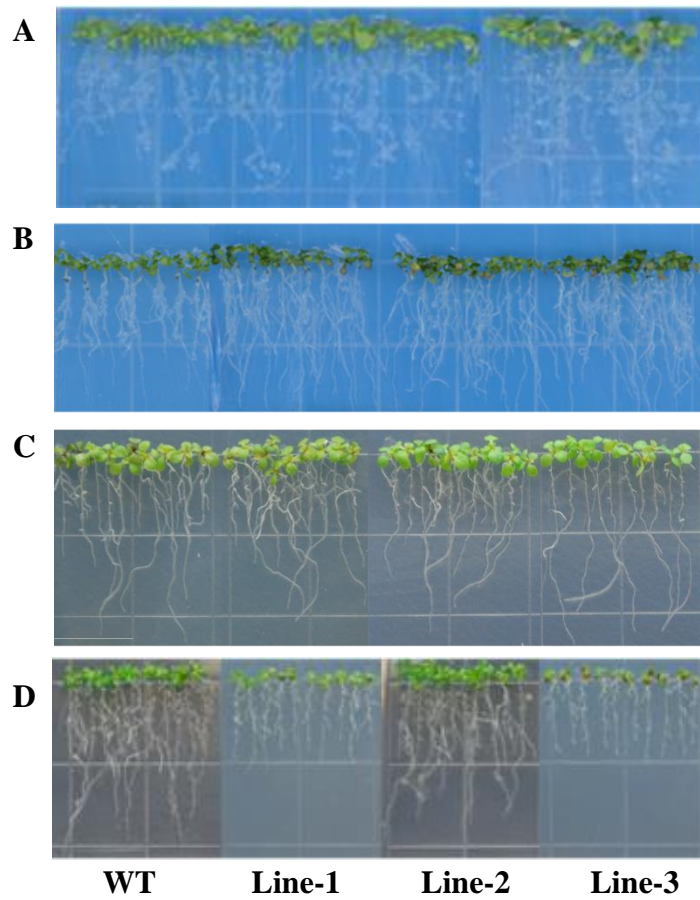


Appendix C *TaSAUR78* Cloning and confirmation transfection in *Arabidopsis*

A. cds and peptide sequence of *TaSAUR78*; B. Genomic DNA PCR (lower panel) and RT-PCR (upper panel) confirmation of *TaSAUR78* transfection in *Arabidopsis*; C. Genomic DNA PCR (lower panel) and RT-PCR (upper panel) confirmation of *TaVDAC1* transfection in *Arabidopsis*.

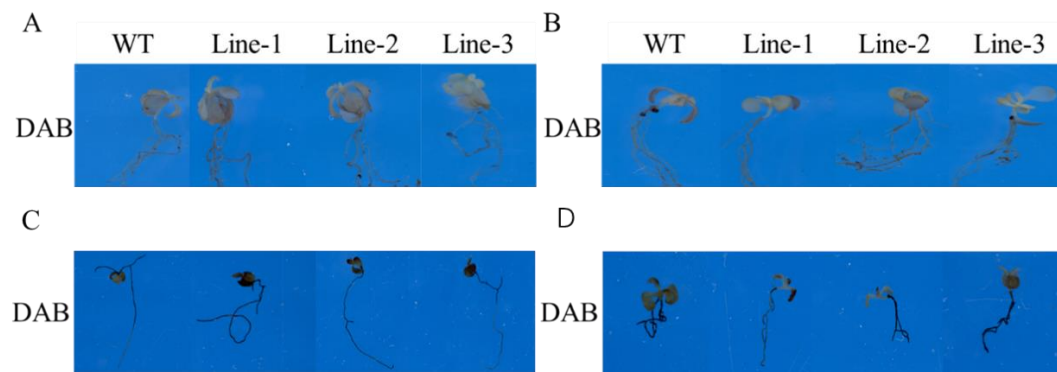
Appendix D Y2H screening results

Candidates	Reads
<i>Triticum aestivum</i> C2 domain-containing protein	8
<i>Triticum aestivum</i> SGT1 mRNA	7
<i>Triticum aestivum</i> TaSAG6 mRNA for seed imbibition protein	2
<i>Triticum aestivum</i> VDAC 1 mRNA	1
<i>Triticum aestivum</i> cultivar Iris (H9) S-adenosyl methionine decarboxylase mRNA, complete cds	1
<i>Triticum aestivum</i> polyubiquitin (WubiG) mRNA, partial cds	1



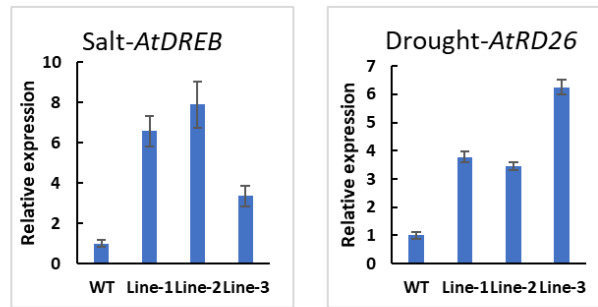
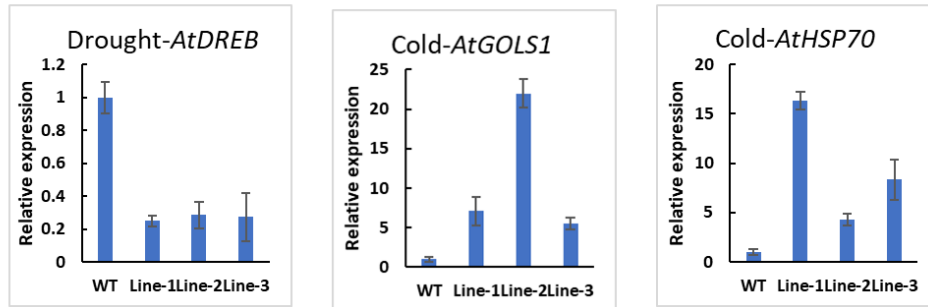
Appendix E Root length of overexpression lines and wild-type plants

TaSAUR78 Overexpression lines and wild-type plants grown erectly on MS media with 100mM NaCl (A) and 300mM mannitol (B). *TaVDAC1* Overexpression lines and wild-type plants grown erectly on MS media with 100mM NaCl (C) and 300mM mannitol (D).



Appendix F ROS accumulation in WT and overexpression lines under stress treatment

The Wild type (WT) and overexpression lines (Line-1, 2, 3) were stained with DAB. A-B: ROS accumulation in WT and *35S:TaSAUR78* overexpression lines under salt (A) and drought stress (B). C-D: ROS accumulation in WT and *35S:TaVDAC1* overexpression lines under salt (C) and drought stress (D).

A**B**

Appendix G The relative transcript levels of stress responsive genes in *35S:TaSAUR78* (A) and *35S:TaVDAC1* (B) lines under abiotic stress.

Salt-AtDREB, *Drought-AtRD26*, *Drought-AtDREB*, *Cold-AtGOLS1* and *Cold-AtHSP70* indicate respectively that the relative expression level of genes *AtDREB*, *AtRD26*, *AtDREB*, *AtGOLS1* and *AtHSP70* in wild type (WT) and 3 overexpression lines (line-1, 2, 3) under the salt, drought, drought, cold and cold stresses.