

Table S1 PCR primers used in this study

Purpose	Accession number	Size of product	Forward primer (5' → 3')	Reverse primer (5' → 3')
<i>TaNF-YB2</i> location cassette	TraesCS2B02G199800	678 bp	tttaagcttatgccggactccgacaac	tttggatccacatgccctgtcttgctt
<i>TaNF-YB2</i> expression	TraesCS2B02G199800	923 bp	tgaccggagaaggaggaggttg	tagccatttacagtagcgagct
<i>Tatubulin</i> expression	U76558	364 bp	agaacactgtttaaggctcaac	gagctttactgctcgaacatgg
<i>TaGAPDH</i> expression	EU022331.1	432bp	ctgccttgctcctcttgctaa	cttgatggaaggaccagcaac
<i>TaNF-YB2</i> promoter	TraesCS2B02G199800	1798bp	gctgcctagatatggaggcg	ccggagtcgtgtgcggagtc
<i>TaNF-YB2-D1-GUS</i>	TraesCS2B02G199800	263bp	aaggtacctcgtcaagtctcaaa	ttccatggcatcgcccccgcgaag
<i>TaNF-YB2-D2-GUS</i>	TraesCS2B02G199800	591bp	ttggatcaccataatggaggcaagtgc	ttccatggcatcgcccccgcgaag
<i>TaNF-YB2-D3-GUS</i>	TraesCS2B02G199800	1112bp	ttggtaccgtgtttaaatttagac	ttccatggcatcgcccccgcgaag
<i>TaNF-YB2-D4-GUS</i>	TraesCS2B02G199800	1469bp	ttggtaccaagagaagtaaaactgc	ttccatggcatcgcccccgcgaag
<i>TaNF-YB2-D5-GUS</i>	TraesCS2B02G199800	1771bp	ttggtacatagatatggaggcggg	ttccatggcatcgcccccgcgaag
<i>TaNF-YB2</i> bait in two-hyb	tplb0013d06	678 bp	tttggatccatagccggactccgacaac	tttctgcaggtcatgccctgtcttgctt
<i>TaNF-YA7</i> bait in two-hyb	AK333451	621 bp	aaagaattcatgacttctgtgccgac	aaaggatccctcattcatggttccccga
<i>TaNF-YA2</i> prey in two-hyb	AK333603	630 bp	aaagaattcatgaagcgagctcgtgga	aaaggatcccttacctcatcatggaagc
<i>TaNF-YA3</i> prey in two-hyb	tplb0037n06	807 bp	aaagaattcatgagtggtcatgggatcgc	aaaggatccctcacgctgacggagatg
<i>TaNF-YA7</i> prey in two-hyb	AK333451	621 bp	aaagaattcatgacttctgtgccgac	aaaggatccctcattcatggttccccga
<i>TaNF-YC1</i> prey in two-hyb	AK331117	723 bp	aaagaattcgagaaccaccagctg	aaaggatccctcactcggagcttgaggg
<i>TaNF-YC2</i> prey in two-hyb	AK333406	772 bp	aaagaattcatggagccatcctcgag	aaaggatcccctagtttgaggagactgc
<i>TaNF-YC3</i> prey in two-hyb	AK333583	1468 bp	aaagaattcatggccgggaagaagagc	aaaggatcccctacggctccttcaccac
<i>TaNF-YC4</i> prey in two-hyb	tplb0006o07	600 bp	aaagaattcatggagcccaatccacca	aaaggatcccttactgctgctgggacgta
<i>TaNF-YC5</i> prey in two-hyb	tpl0008i06	1233 bp	aaagaattcatggccgggaagaagcaa	aaaggatcccctatggctccttcgccac
<i>TaNF-YC6</i> prey in two-hyb	tplb0009e11	555 pb	aaagaattcatggctccagatcgagg	aaaggatcccaccggatccctatggtga
<i>TaNFYC7</i> prey in two-hyb	KJ862216	768 bp	aaagaattcatggaaccgtcttcacaa	aaacctaggccgggggttgctcacia
<i>TaNFYC8</i> prey in two-hyb	KM078730	768 bp	aaaggatccgtatgaggaagaagctgggc	aaactgcagcctaactcattgtcgtga
<i>TaNF-YB2</i> prey in one-hyb	tplb0013d06	678 bp	tttgaattcatgccggactccgacaac	tttggatccatgccctgtcttgctt
<i>TaP5CS2</i> bait in one-hyb	KM523670	120 bp	aaacacgtgatggaggactgaacacc	aaaggatccttttctcgtcgccgca
<i>TaSOD1</i> bait in one-hyb	FJ890986	102 bp	aaacacgtgatgggtttctttctgctggttc	aaaggatccatacagtccttgct
<i>TaCAT5</i> bait in one-hyb	KP892532	153 bp	aaacacgtgatggatcctgctgaatctata	aaaggatccgtgggcgtacgtgtgctc
<i>TaPOD5</i> bait in one-hyb	AJ878510	122 bp	aaacacgtgatggacggagattagaaggca	aaaggatcctcgcagaagagagagac
<i>TaNF-YB2-cYFP</i>	TraesCS2B02G199800	678bp	aaatctagaatgccggactccgaca	aaaggatccgcatgccctgtcttgctt
<i>TaNF-YA7-nYFP</i>	AK333451	621bp	aaaggatccatgacttctgtgccgca	aaaggatccacattcatggttccccg
<i>TaNF-YC7-nYFP</i>	KJ862216	771bp	aaaggatccatggaaccgtcttcacaa	aaaggatccgccctccagattgatg
<i>TaNF-YC7-cYFP</i>	KJ862216	771bp	aaaggatccatggaaccgtcttcacaa	aaaggatccgccctccagattgatg

<i>CaMV35S::TaNF-YB2</i>	TraesCS2B02G199800	1798bp	gctgcctagatatggaggcg	ccggagtcgtgttcggagtc
<i>CaMV35S_{pro}::TaNF-YB2</i> effector	TraesCS2B02G199800	678bp	ccatgccggactccgacaa	ggcttgcctgtcttgcct
<i>TaNF-YB2</i> overexpression cassette	TraesCS2B02G199800	730 bp	aaacatggcggactccgacaacg	aaaggttaccagtaaacagatac
<i>TaNF-YB2</i> knockdown cassette	TraesCS2B02G199800	867 bp	tttccatggataaaattgaccgat	tttggtgaccggagaaggaggaggt
<i>TaP5CS1</i> expression	AB193551	154 bp	gcacgtggacctgtgggtgttg	gttttcgcggaatccttaccacg
<i>TaP5CS2</i> expression	KM523670	120 bp	gctcttacgagggaagg	acttcagagggttttcgcgg
<i>TaP5CS3</i> expression	KT868850	78 bp	ctcttacgagggaaggcaa	tcattgcaagggaaggtc
<i>TaP5CS4</i> expression	KT218497	79 bp	caagttgataggtatttctgaa	aataaggtatctgtgcctcaa
<i>TaP5CS5</i> expression	AY888045	132 bp	tggtcactacagatgataaagt	tacttatgccacctcagcacc
<i>TaSOD1</i> expression	FJ890986	102 bp	gacgctgatgatcttggaagg	atcttagccctggagcccgatg
<i>TaSOD2</i> expression	FJ890987	117 bp	ccccatggactcaaaactcgt	gtcaagcttagctccacttgagt
<i>TaSOD3</i> expression	JQ613154	126 bp	tgcaagttgtgggagagcgt	gtcaggccaacaacaccacat
<i>TaSOD4</i> expression	AF092524	110 bp	gggcactattccactgtcgg	gcaacgcaggcacagtaacaa
<i>TaSOD5</i> expression	KR069092	120 bp	gtacggccagcgcacgtgt	gggttaaggttccttaggtg
<i>TaSOD6</i> expression	KC158224	141bp	caggaccctcttgacacaaa	atatttccagttaccaccttcc
<i>TaCAT1</i> expression	D86327	159 bp	gcgagaagatggatgcga	aggagagccagatggccttg
<i>TaCAT2</i> expression	X94352	150 bp	gcctcagctggcgtcgtac	acgcgctgacgacacccac
<i>TaCAT3</i> expression	GU984379	189 bp	caaggccatctggctctcct	tgtcagcctgcacgatccc
<i>TaCAT4</i> expression	HQ860268	170 bp	ggagaagacgaggatcaagaag	acttgagaggaagtcgatc
<i>TaCAT5</i> expression	KP892532	153 bp	ccagtggctcaccgcctcgg	acaccaactatcattgttcac
<i>TaCAT6</i> expression	KP892533	154 bp	gggcagaagctggcgtcgcgg	ttcatggctacaccacagag
<i>TaPOD1</i> expression	AF387866	124 bp	gcacacagaatgcaaaggca a	cgtagaagtacacttcatgcc
<i>TaPOD2</i> expression	AB518867	165 bp	cacgaagccagcgggacttc	tctgcacaaaggacggccac
<i>TaPOD3</i> expression	XM_044596808	119 bp	ggctcagctgctccaaggt	tggtatgataatcggtagtgg
<i>TaPOD4</i> expression	XM_044466229	132 bp	tacgagcagcagcaaatcat	gccctatgatctggacagag
<i>TaPOD5</i> expression	AJ878510	122 bp	acaggcgtgtccaggatc	aacacaccggcttaacggtc
<i>TaPOD6</i> expression	MW030685	149 bp	cttcaagacctcgacaccg a	cggcgaagaactcgtccttgaa
<i>TaPOD7</i> expression	MT166266	141 bp	ggaactcgtcaagctctacg	ttgtggtaacctcctgcag
<i>TaPOD8</i> expression	X56011	111 bp	agatcaggctcagctgtcc	attggccactggttctgtgg
<i>TaPOD9</i> expression	X53675	204 bp	ttgtacacggagtgaagatgtac	ccctgcacgtctaggattac
<i>TaP5CS2</i> knockdown cassette	KM523670	1128 bp	aaacatggctgtgtgagactctc	aaaggtaaccaggaaagatagcaa
<i>TaSOD1</i> knockdown cassette	FJ890986	456 bp	aaacatggcacagccttcacat	aaaggctcacttagccctggagccc
<i>TaCAT5</i> knockdown cassette	KP892532	792 bp	aaacatggatgcctgtgttttcac	aaagggtacctcatgaagcagaagg
<i>TaPOD5</i> knockdown cassette	AJ878510	1023 bp	aaacatggatggcgtccagagcagca	aaaggtaacctcacatgtggcggtac
<i>CaMV35S_{pro}::TaNF-YB2</i> effector	TraesCS2B02G199800	678 bp	aaagatcccatgccggactccgacaa	aaactgcagggtcttgcctgtcttgcct

<i>CaMV35S_{pro}::TaNF-YA7 effector</i>	AK333451	621bp	aaaaagcttcagactctgtcgccga	aaactgcagggctttcatgggtccccgact
<i>CaMV35S_{pro}::TaNF-YC7 effector</i>	KJ862216	771bp	aaaaagcttatggaaccgtttcacia	aaagaattctctgccgttccagattg
<i>CaMV35S_{pro}::LUC</i>	DI336552	63bp	gctctagataacttcgtata	atgtcagggtcagcaggaa
<i>TaP5CS2_{pro}::LUC</i>	KM523670	1903bp	tggaactgaacaccccccc	ttttcctcgtgccgca
<i>TaSOD1_{pro}::LUC</i>	FJ890986	1825bp	ttttctttcgtgcgttc	atacagtccttgcttcgt
<i>TaCAT5_{pro}::LUC</i>	KP892532	1761bp	atcctgcctgaatctata	gtgggcgtacgtgtgctc
<i>TaPOD5_{pro}::LUC</i>	AJ878510	1765bp	acggagatttagaaggca	tcgcagaaagagagac

Table S2 Information of the forty-five wheat cultivars examined for a field experiment

Cultivar name	Registration authorization and number		Registration date	Breeding organization	
BN 207	National	approval cultivar, 20200106	wheat	2020	Hebei Bo Genetic Technology Co., Ltd.
HN 085	HeBei	approval cultivar, 20190014	wheat	2019	Hebei Agricultural University
H 4399	HeBei	approval cultivar, 2008002	wheat	2008	Institute of Dryland Agriculture, Hebei Academy of Agriculture and Forestry Sciences
XM 13	National	approval cultivar, 2016021	wheat	2016	Xingtai Academy of Agricultural Sciences
JM 418	National	approval cultivar, 2016026	wheat	2016	Institute of Grain and Oil Crops, Hebei Academy of Agricultural Sciences
JM 691	National	approval cultivar, 20230157	wheat	2023	Institute of Grain and Oil Crops, Hebei Academy of Agricultural Sciences
SM 26	National	approval cultivar, 20180052	wheat	2018	Shijiazhuang Academy of Agricultural and Forestry Sciences, Hebei Wheat Engineering Technology Research Center
HM 26	National	approval cultivar, 20230153	wheat	2023	Handan Academy of Agricultural Sciences
ML-1	HeBei	approval cultivar, 20218011	wheat	2021	Hebei Dadi Seed Industry Co., Ltd., Shijiazhuang Academy of Agricultural and Forestry Sciences, Xinji Malan Farm
HN 8324	HeBei	approval cultivar, 20230006	wheat	2023	Hebei Agricultural University
JM 585	HeBei	approval cultivar, 2013004	wheat	2013	Institute of Grain and Oil Crops, Hebei Academy of Agricultural Sciences
S 4366	HeBei	approval cultivar, 20198019	wheat	2019	Shijiazhuang Academy of Agricultural and Forestry Sciences, Shijiazhuang Wanfeng Seed Industry Co., Ltd.
HN 6133	HeBei	approval cultivar, 20210020	wheat	2021	Hebei Agricultural University
SN 086	HeBei	approval cultivar, 20198017	wheat	2019	Hebei Dadi Seed Production Co., Ltd.
SM 32	National	approval cultivar, 20220092	wheat	2022	Shijiazhuang Academy of Agriculture and Forestry Sciences
SM 28	National	approval cultivar, 20180063	wheat	2018	Shijiazhuang Academy of Agricultural and Forestry Sciences, Hebei Wheat Engineering Technology Research Center
HG 35	Tianjin	approval cultivar, 2007003	wheat	2019	Institute of Dryland Agriculture, Hebei Academy of Agriculture and Forestry Sciences
SM 22	HeBei	approval cultivar, 2013002	wheat	2013	Shijiazhuang Academy of Agricultural and Forestry Sciences, Hebei Wheat Engineering Technology Research Center
JM 325	National	approval cultivar, 20210063	wheat	2021	Institute of Grain and Oil Crops, Hebei Academy of Agricultural Sciences
HM 19	National	approval cultivar, 20180049	wheat	2018	Handan Academy of Agricultural Sciences
DD 1912	National	approval cultivar, 20220085	wheat	2022	Hebei Dadi Seed Production Co., Ltd.
KN 1002	HeBei	approval cultivar, 20210012	wheat	2021	Genetics and Development, Chinese Academy of Sciences
HN 7008	HeBei	approval cultivar, 20210033	wheat	2021	Hebei Agricultural University
H 6172	National	approval cultivar, 2003036	wheat	2003	Handan Academy of Agricultural Sciences
J 5265	National	approval cultivar, 2009016	wheat	2009	Institute of Grain and Oil Crops, Hebei Academy of Agricultural Sciences

H 444	HeBei approval cultivar, 2012002	wheat	2012	Institute of Dryland Agriculture, Hebei Academy of Agriculture and Forestry Sciences
ND 399	HeBei approval cultivar, 2012004	wheat	2012	College of Agronomy and Biotechnology, China Agricultural University, Hebei Jincheng Seed Industry Co., Ltd.
SM 25	HeBei approval cultivar, 2016013	wheat	2016	Shijiazhuang Academy of Agricultural and Forestry Sciences, Hebei Wheat Engineering Technology Research Center
S 4185	National approval cultivar, 990007	wheat	1999	Shijiazhuang Academy of Agricultural and Forestry Sciences
HN 9204	National approval cultivar, 20220051	wheat	2022	Hebei Agricultural University
ZM 155	HeBei approval cultivar, 2012005	wheat	2012	Institute of Crop Sciences, Chinese Academy of Agricultural Sciences
HN 6426	HeBei approval cultivar, 20190018	wheat	2019	Hebei Agricultural University
SN 956	HeBei approval cultivar, 2016016	wheat	2016	Shijiazhuang Dadi Seed Industry Co., Ltd., Shijiazhuang New Wheat Variety New Technology Research Institute
JM 22	National approval cultivar, 2006018	wheat	2006	Crop Research Institute of Shandong Academy of Agricultural Sciences
GY 2018	HeBei approval cultivar, 2008007	wheat	2008	Gaocheng Institute of Agricultural Sciences
GY 5818	HeBei approval cultivar, 20190010	wheat	2019	Gaocheng District Institute of Agricultural Sciences, Shijiazhuang City
HN 5102	HeBei approval cultivar, 20190022	wheat	2019	Hebei Agricultural University
JM 120	HeBei approval cultivar, 2016019	wheat	2016	Institute of Grain and Oil Crops, Hebei Academy of Agricultural Sciences
GY 5766	HeBei approval cultivar, 2014002	wheat	2014	Gaocheng Institute of Agricultural Sciences
SL 02-1	National approval cultivar, 2007016	wheat	2007	Hebei Normal University, Luancheng County Seed Farm
GY 5218	HeBei approval cultivar, 2015005	wheat	2015	Gaocheng District Institute of Agricultural Sciences, Shijiazhuang City
H 6172	National approval cultivar, 2003036	wheat	2003	Handan Academy of Agricultural Sciences, Hebei Province
SY 20	National approval cultivar, 2011011	wheat	2011	Shijiazhuang Academy of Agriculture and Forestry Sciences
ZXM 99	National approval cultivar, 20180053	wheat	2018	Hebei Zhongxin Seed Technology Co., Ltd.
SN 952	HeBei approval cultivar, 20208017	wheat	2020	Hebei Dadi Seed Production Co., Ltd.

Table S3 *cis*-acting regulatory elements situated in the *TaNF-YB2* promoter

Element	Distance from ATG (± strand)	Motif sequence	Function
A-box	384- 286+	CCGTCC CCGTCC	<i>cis</i> -acting regulatory element
TATA-box	975- 815- 815- 815-	TATA TATATAA TATATA TATA	core promoter element around –30 of transcription start
CAAT-box	849- 690- 623- 145-	CCAAT CAAAT CCAAT CAAT	common <i>cis</i> -acting element in promoter and enhancer regions
ABRE	1395- 473+ 507- 333- 1002+ 330+ 487- 323- 1351+ 1004+	GACACGTGGC ACGTG ACGTG ACGTG GCAACGTGTC CGCACGTGTC ACGTG ACGTG ACGTG ACGTG	ABA, drought responsive element
ABRE3a	486-	TACGTG	ABA, drought responsive element
ABRE4	486+	CACGTA	ABA, drought responsive element
MYB	657- 88-	CAACCA CAACCA	ABA ,drought responsive element
MYB recognition site	544-	CCGTTG	drought responsive element
MYC	1739+ 763-	CATTG CATTG	drought and salt stress responsive element
AAGAA-motif	1036-	GAAAGAA	<i>cis</i> -acting element involved in the abscisic acid responsiveness
CCGTCC-box	384- 286+	CCGTCC CCGTCC	<i>cis</i> -acting regulatory element related to meristem expression
CAT-box	1399+ 663+ 1289- 213+	GCCACT GCCACT GCCACT GCCACT	<i>cis</i> -acting regulatory element related to meristem expression
CCAAT-box	544+	CAACGG	MYBHv1 binding site
CGTCA-motif	1215- 142- 321+ 505+ 252+	CGTCA CGTCA CGTCA CGTCA CGTCA	<i>cis</i> -acting regulatory element involved in the MeJA-responsiveness
TGACG-motif	1215+ 142+ 321- 505- 252-	TGACG TGACG TGACG TGACG TGACG	<i>cis</i> -acting regulatory element involved in the MeJA-responsiveness

Table S4 Drought-related *cis*-acting elements situated in *TaP5CS2*, *TaSOD1*, *TaCAT5* and *TaPOD5* promoters

Gene Name	Site Name	Sequence	Position	Strand	Organism	Function
<i>TaP5CS2</i>	CAAT-box	CAAT	274	4 (-)	<i>Nicotiana glutinosa</i>	common cis-acting element in promoter and enhancer regions
		CAAT	385	4 (-)	<i>Nicotiana glutinosa</i>	
		CAAT	467	4 (+)	<i>Nicotiana glutinosa</i>	
		CAAT	664	4 (-)	<i>Nicotiana glutinosa</i>	
		CAAT	776	4 (+)	<i>Nicotiana glutinosa</i>	
		CAAAT	1058	5 (-)	<i>Pisum sativum</i>	
		CAAT	1050	4 (+)	<i>Nicotiana glutinosa</i>	
		CAAT	1167	4 (-)	<i>Nicotiana glutinosa</i>	
		CAAT	1191	4 (-)	<i>Nicotiana glutinosa</i>	
		CAAT	1200	4 (+)	<i>Nicotiana glutinosa</i>	
		CAAT	1327	4 (+)	<i>Nicotiana glutinosa</i>	
		CAAAT	1408	5 (+)	<i>Pisum sativum</i>	
	TATA-box	TATA	261	4 (+)	<i>Arabidopsis thaliana</i>	core promoter element around -30 of transcription start
		TATA	1392	4 (-)		
		TATA	1573	4 (-)		
	ABRE	ACGTG	516	5 (+)	<i>Arabidopsis thaliana</i>	cis-acting element involved in the abscisic acid responsiveness
		TACGGTC	797	7 (-)		
		ACGTG	839	5 (-)		
		TACGGTC	1348	7 (-)		
		ACGTG	1644	5 (+)		
	DRE core	GCCGAC	1292	6 (+)	<i>Arabidopsis thaliana</i>	
		GCCGAC	1331	6 (-)		
	MBS	CAACTG	280	6 (-)	<i>Arabidopsis thaliana</i>	MYB binding site involved in drought-inducibility
		CAACTG	562	6 (-)		
		CAACTG	943	6 (-)		
	MYB	CAACCA	618	6 (+)	<i>Arabidopsis thaliana</i>	ABA ,drought responsive element
	MYB recognition site	CCGTTG	1749	6 (-)	<i>Arabidopsis thaliana</i>	drought responsive element
	MYC	TCTCTTA	1922	7 (-)	<i>Arabidopsis thaliana</i>	drought and salt stress responsive element
<i>TaSOD1</i>	CAAT-box	CCAAT	250	5 (+)	<i>Arabidopsis thaliana</i>	common cis-acting element in promoter and enhancer regions
		CAAT	251	4 (+)	<i>Nicotiana glutinosa</i>	
		CAAT	301	4 (-)	<i>Nicotiana glutinosa</i>	
		CAAAT	569	5 (-)	<i>Pisum sativum</i>	
		CAAT	596	4 (+)	<i>Nicotiana glutinosa</i>	
		CAAT	617	4 (-)	<i>Nicotiana glutinosa</i>	
		CAAT	635	4 (+)	<i>Nicotiana glutinosa</i>	
		CAAAT	658	5 (+)	<i>Pisum sativum</i>	
		CAAAT	706	5 (+)	<i>Pisum sativum</i>	
		CAAT	720	4 (-)	<i>Nicotiana glutinosa</i>	
		CAAAT	736	5 (+)	<i>Pisum sativum</i>	
		CAAAT	1390	5 (-)	<i>Pisum sativum</i>	
		CAAT	1451	4 (+)	<i>Nicotiana glutinosa</i>	
		CAAT	1555	4 (-)	<i>Nicotiana glutinosa</i>	
		CAAAT	1618	5 (-)	<i>Pisum sativum</i>	

Gene Name	Site Name	Sequence	Position	Strand	Organism	Function
<i>TaSOD1</i>	CAAT-box	CAAAT	1625	5 (-)	Pisum sativum	common cis-acting element in promoter and enhancer regions
		CAAAT	1642	5 (-)	Pisum sativum	
		CAAAT	1791	5 (-)	Pisum sativum	
		CAAT	1844	4 (-)	Nicotiana glutinosa	
		CAAAT	1929	5 (+)	Pisum sativum	
		CAAT	1934	4 (+)	Nicotiana glutinosa	
		CAAT	1981	4 (-)	Nicotiana glutinosa	
	DRE core	GCCGAC	802	6 (-)	Arabidopsis thaliana	
		GCCGAC	1324	6 (+)		
	MYB	CAACCA	301	6 (+)	Arabidopsis thaliana	ABA ,drought responsive element
		CAACCA	456	6 (+)		
		CAACCA	618	6 (+)		
		TAACCA	702	6 (+)		
		CAACAG	1534	6 (-)		
		TAACCA	1800	6 (+)		
	MYC	CATTTG	568	6 (+)	Arabidopsis thaliana	drought and salt stress responsive element
		CATTTG	706	6 (-)		
	MYB-binding site	CAACAG	1534	6 (-)	Nicotiana tabacum	drought responsive element
<i>TaCAT5</i>	CAAT-box	CAAAT	181	5 (-)	Pisum sativum	common cis-acting element in promoter and enhancer regions
		CAAAT	299	5 (+)	Pisum sativum	
		CAAAT	325	5 (-)	Pisum sativum	
		CAAT	342	4 (+)	Nicotiana glutinosa	
		CCAAT	349	5 (-)	Arabidopsis thaliana	
		CAAT	858	4 (-)	Nicotiana glutinosa	
		CCAAT	1028	5 (+)	Arabidopsis thaliana	
		CAAT	1029	4 (+)	Nicotiana glutinosa	
		CAAT	1049	4 (+)	Nicotiana glutinosa	
		CAAT	1083	4 (-)	Nicotiana glutinosa	
		CAAAT	1157	5 (+)	Pisum sativum	
		CCAAT	1315	5 (-)	Arabidopsis thaliana	
		CAAAT	1349	5 (+)	Pisum sativum	
	TATA-box	TATAAAA	153	7 (-)	Pisum sativum	core promoter element around -30 of transcription start
		TATAA	155	5 (-)	Arabidopsis thaliana	
		TATA	156	4 (+)	Arabidopsis thaliana	
		TATACA	629	6 (-)	Helianthus annuus	
		TATA	631	4 (+)	Arabidopsis thaliana	
		TATA	763	4 (+)	Arabidopsis thaliana	
		TATA	1043	4 (-)	Arabidopsis thaliana	
		TATATA	1373	6 (-)	Arabidopsis thaliana	
		ATATAT	1374	6 (-)	Brassica napus	
		TATA	1375	4 (-)	Arabidopsis thaliana	
	DRE core	GCCGAC	1057	6 (+)	Arabidopsis thaliana	
		GCCGAC	1579	6 (+)		
	DRE1	ACCGAGA	652	7 (-)	Zea mays	
	MYB	TAACCA	840	6 (+)	Arabidopsis thaliana	ABA ,drought responsive element
		TAACCA	1211	6 (+)		
		CAACCA	1601	6 (+)	Arabidopsis thaliana	

Gene Name	Site Name	Sequence	Position	Strand	Organism	Function
<i>TaPOD5</i>		CAACCA	1626	6 (+)		
		TAACCA	1706	6 (+)		
		CAACCA	1745	6 (+)		
	MYB recognition site	CCGTTG	1131	6 (+)	Arabidopsis thaliana	drought responsive element
	ABRE	ACGTG	492	5 (+)	Arabidopsis thaliana	cis-acting element involved in the abscisic acid responsiveness
		TACGGTC	521	7 (-)		
		ACGTG	839	5 (-)		
	MYC	CATTTG	180	6 (+)	Arabidopsis thaliana	drought and salt stress responsive element
		CATGTG	299	6 (-)		
		CATGTG	618	6 (+)		
		CATTTG	1157	6 (-)		
		CATTTG	1244	6 (+)		
	CAAT-box	CAAAT	1064	5 (-)	Pisum sativum	common cis-acting element in promoter and enhancer regions
		CAAAT	1110	5 (+)	Pisum sativum	
		CAAT	1410	4 (+)	Nicotiana glutinosa	
		CAAAT	1506	5 (+)	Pisum sativum	
		CAAAT	1514	5 (+)	Pisum sativum	
		CAAT	1535	4 (+)	Nicotiana glutinosa	
		CAAT	1547	4 (+)	Nicotiana glutinosa	
		CAAAT	1760	5 (-)	Pisum sativum	
		CAAT	1765	4 (+)	Nicotiana glutinosa	
	TATA-box	TATAA	1495	5 (-)	Arabidopsis thaliana	core promoter element around -30 of transcription start
		TATA	1496	4 (-)	Arabidopsis thaliana	
		ATATAT	1572	6 (-)	Brassica napus	
		TATATA	1573	6 (-)	Arabidopsis thaliana	
		TATA	1575	4 (-)	Arabidopsis thaliana	
		TATA	1580	4 (-)	Arabidopsis thaliana	
		TATA	1588	4 (-)	Arabidopsis thaliana	
		TATACA	1887	6 (-)	Helianthus annuus	
		TATA	1889	4 (-)	Arabidopsis thaliana	
	MBS	CAACTG	1466	6 (+)	Arabidopsis thaliana	MYB binding site involved in drought-inducibility
		CAACTG	1702	6 (-)	Arabidopsis thaliana	
	MYB	TAACCA	731	6 (+)	Arabidopsis thaliana	ABA ,drought responsive element
		TAACCA	1731	6 (+)		
	MYB recognition site	CCGTTG	540	6 (+)	Arabidopsis thaliana	drought responsive element
	ABRE	TACGGTC	516	7 (-)	Arabidopsis thaliana	cis-acting element involved in the abscisic acid responsiveness
		ACGTG	517	5 (+)		
		ACGTG	589	5 (+)		
		ACGTG	816	5 (+)		
		TACGGTC	817	7 (-)		
		ACGTG	923	5 (-)		

1	ATG	CCGGACTCCGACAACGACTCCGGCGGGCCGAGCAACGCGGACTTCTCGTCGCCCAAG
1	M	P D S D N D S G G P S N A D F S S P K
61		GAGCAGGACAGGTTCTGCGGATCGCCAACGTGAGCCGGATCATGAAGAAGGCGCTGCCG
21		E Q D R F L P I A N V S R I M K K A L P
121		GCCAACGCCAAGATCTCCAAGGACGCCAAGGAGACGGTGCAGGAGTGCCTGTCGAGTTC
41		A N A K I S K D A K E T V Q E C V S E F
181		ATCTCCTTCATACCGGCGAGGCCCTCCGACAAGTGCCAGCGCGAGAAGCGCAAGACCATC
61		I S F I T G E A S D K C Q R E K R K T I
241		AACGGCGACGACCTGCTCTGGGCCATGACCACGCTCGGCTTCGAGGACTACATGGAGCCG
81		N G D D L L W A M T T L G F E D Y M E P
301		CTCAGGCTCTACCTCCACAAGTTCCGCGAGCTCGAGGGCGAGAAGGCCGTCGGCGCCGGC
101		L R L Y L H K F R E L E G E K A V G A G
361		GGCGTTGGCGGTTACCTCCCCCGNCGGGTCAGGCTCGCAGCAGAGGGAGTCGACGCCA
121		G V G A L P S P X G S G S Q Q R E S T P
421		AGGAACAATGGCGGAGGCGGTGAGGCCGCGCGCTACGGCGGCATGTACGGTGGCGCCGGG
141		R N N G G G G E A G G Y G G M Y G G A G
481		GCAGGAGGAGGCGGCGGCGCATGTTTCATGATGATGGGGCAGCCCATGTACGGGTCCCCG
161		A G G G G G G M F M M M G Q P M Y G S P
541		CCGGCGGACAGGTACCAACATCCGCAGCATCACCACCAGATGATGACGGGCGGGCAAGGC
181		P A A G Y Q H P Q H H H Q M M T G G Q G
601		GGGTACGGCTACGGCGACGCCGCGCCGGCGGGGCTTTCGTCGTCCTCAGGGTTCGGC
201		G Y G Y G D A G A G G G S S S S S G F G
661		AGGCAAGACAGGGCATGA
221		R Q D R A *

Fig. S1 The open reading frame of *TaNF-YB2* and its corresponding translated amino acids.

The translation start codon ATG and termination codon TAG of *TaNF-YB2* are highlighted using boxes. The functional domain specified by the NF-YB proteins in plant species is underlined.

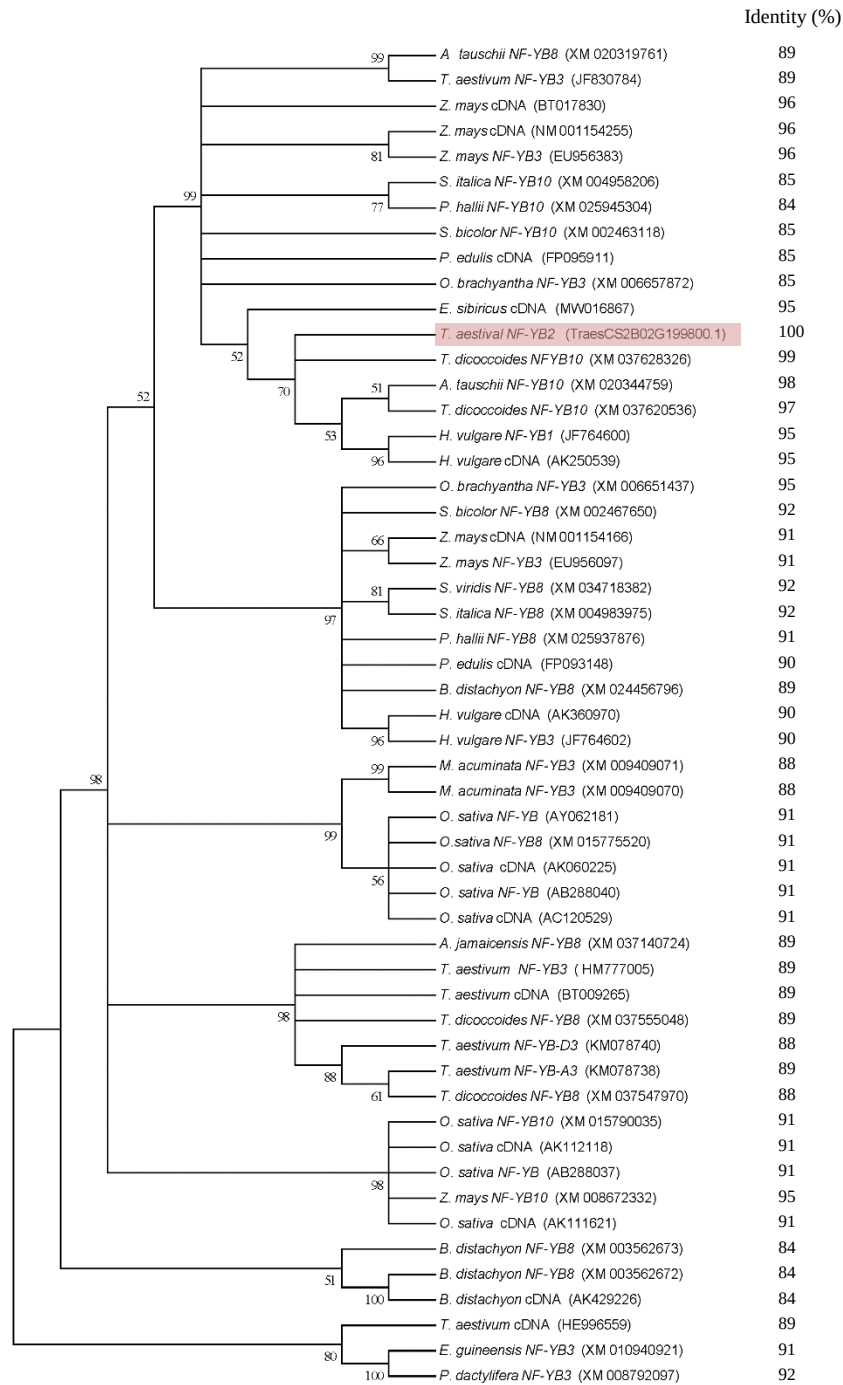
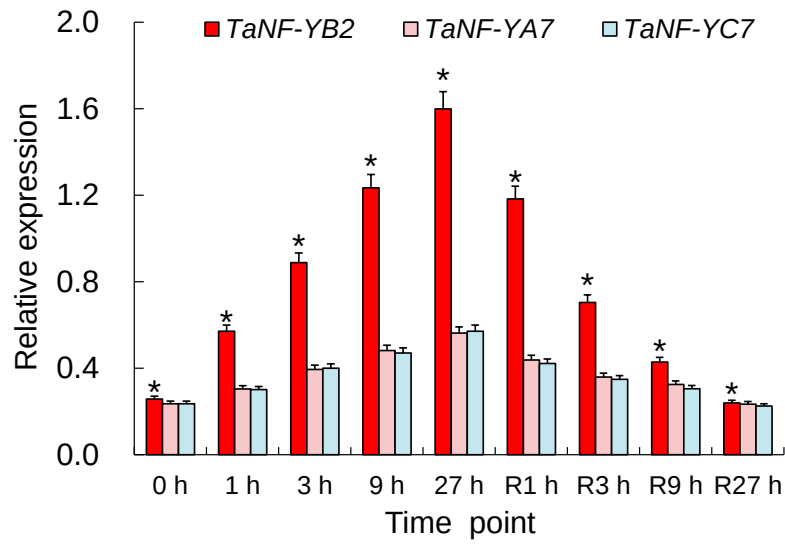


Fig. S2 Phylogenetic relationships among *TaNF-YB2* and its homologous genes across various plant species.

a



b

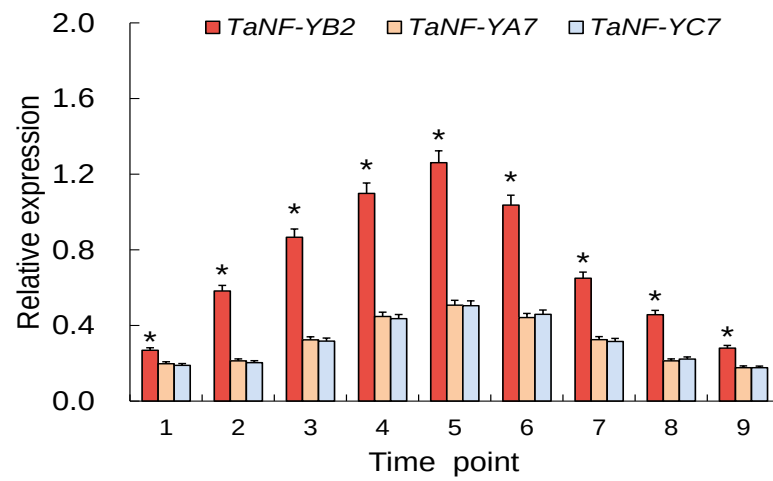


Fig. S3 The expression of *TaNF-YB2*, *TaNF-YA7*, and *TaNF-YC7* under drought stress conditions.

(a) Expression patterns of *TaNF-YB2*, *TaNF-YA7*, and *TaNF-YC7* in roots. (b) Expression patterns of *TaNF-YB2*, *TaNF-YA7*, and *TaNF-YC7* in leaves.

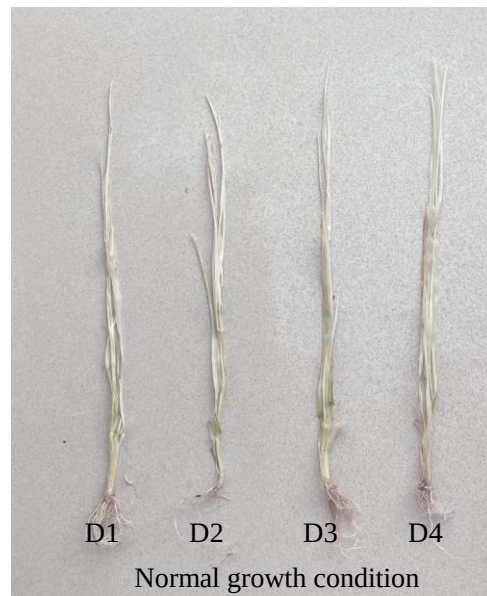


Fig. S4 GUS histochemical staining results in which reporter gene was driven by different length of *TaNF-YB2* promoters under normal growth condition

AD	BD	SD-TL			SD-TLH		
		1	10 ⁻¹	10 ⁻²	1	10 ⁻¹	10 ⁻²
TaNF-YB2	TaNF-YA2						
TaNF-YB2	TaNF-YA3						
TaNF-YB2	TaNF-YC1						
TaNF-YB2	TaNF-YC2						
TaNF-YB2	TaNF-YC3						
TaNF-YB2	TaNF-YC4						
TaNF-YB2	TaNF-YC5						
TaNF-YB2	TaNF-YC6						
TaNF-YB2	TaNF-YC8						
TaNF-YA7	TaNF-YC1						
TaNF-YA7	TaNF-YC2						
TaNF-YA7	TaNF-YC3						
TaNF-YA7	TaNF-YC4						
TaNF-YA7	TaNF-YC5						
TaNF-YA7	TaNF-YC6						
TaNF-YA7	TaNF-YC8						

Fig. S5 Yeast two-hybrid assay results between the TaNF-YB2 protein and the members in subfamilies of NF-YA and NF-YC in *T. aestivum*.

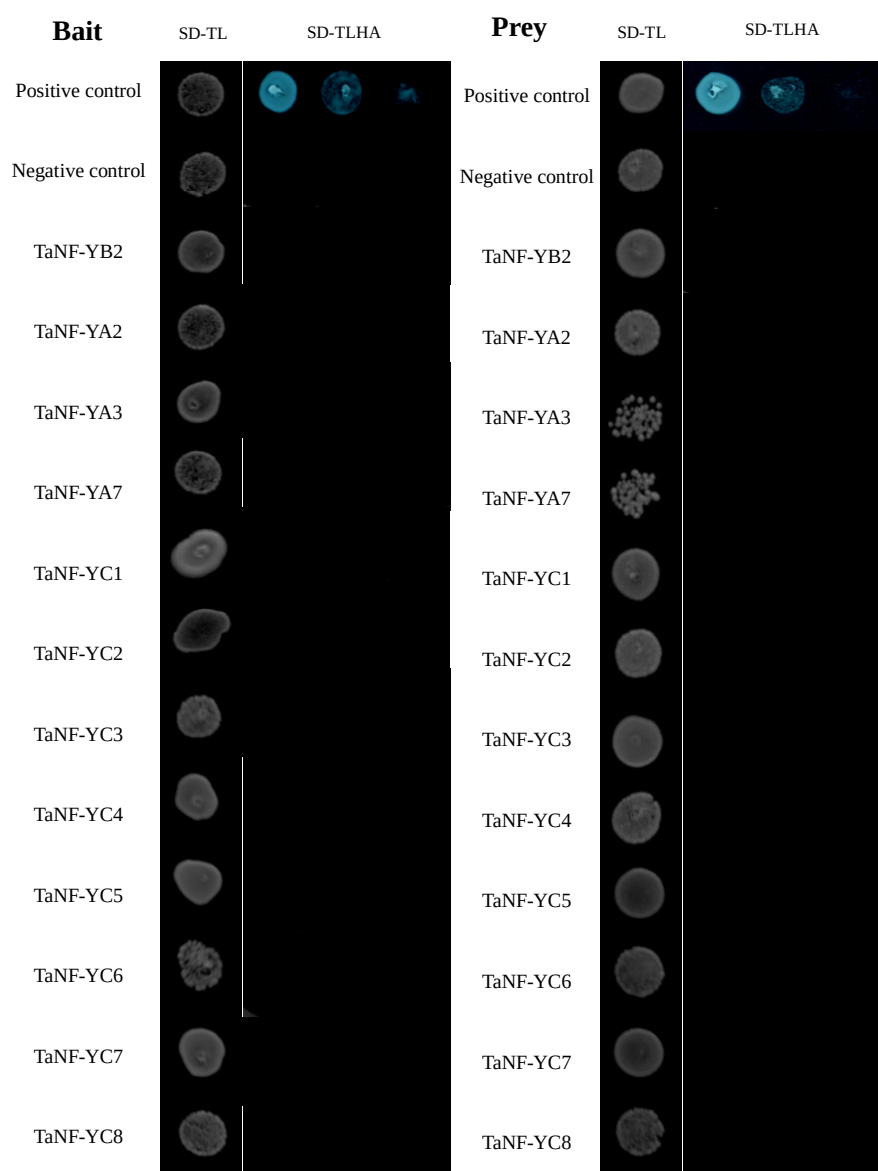


Fig. S6 Auto-activation detection of NF-Y candidate proteins in yeast cells.

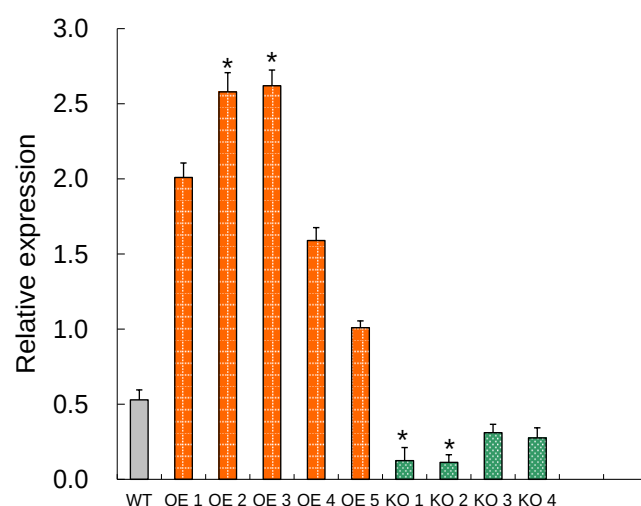


Fig. S7 Expression levels of the target genes in transgenic wheat lines of *TaNF-YB2*.

Expression levels of target gene in *TaNF-YB2* transgenic lines. Data shown are means $\pm$ standard deviation ($n = 3$). The expression values of target genes were normalized by *Tatubulin* and *TaGAPDH*, two constitutive genes in *T. aestivum* species, whose expression levels were set as 1.

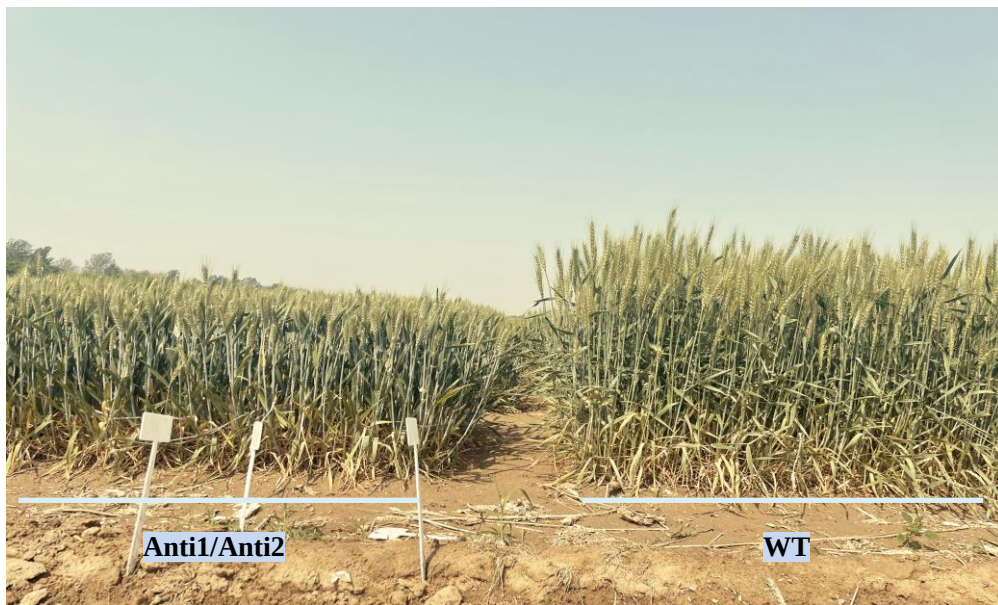
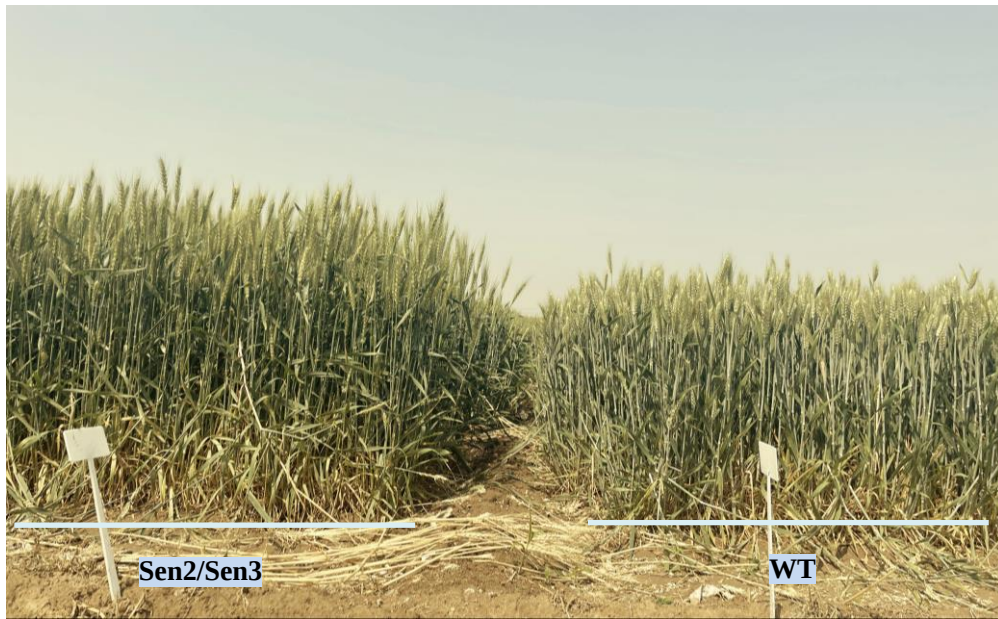


Fig. S8 Phenotypes of TaNF-YB2 transgenic lines at seed filling stage.

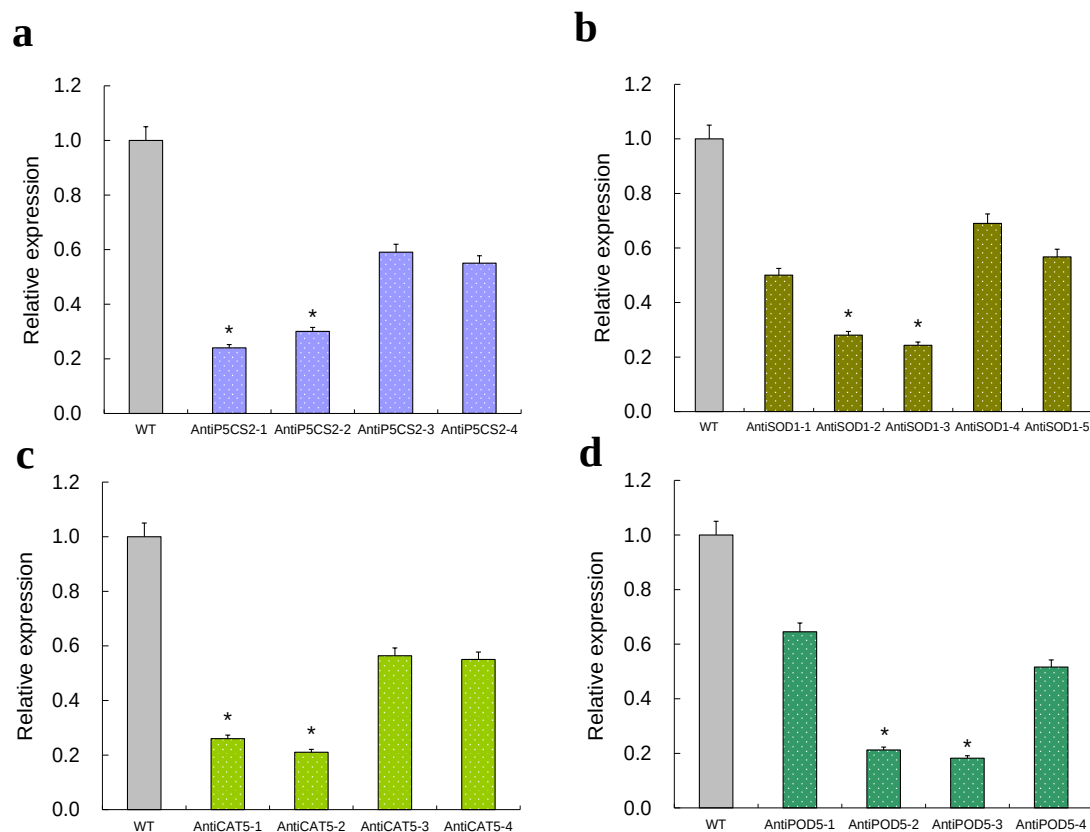


Fig. S9 Expression levels of the target genes in transgenic lines with knockdown expression of distinct osmotic stress responsive-associated genes.

(a) Expression levels of target gene for *TaP5CS2* transgenic lines. (b) Expression levels of target gene for *TaSOD1* transgenic lines. (c) Expression levels of target gene for *TaCAT5* transgenic lines. (d) Expression levels of target gene for *TaPOD5* transgenic lines. In (a) AntiP5CS2-1 to AntiP5CS2-4, four lines with *TaP5CS2* knockdown expression. In (b) AntiSOD1-1 to AntiSOD1-5, five lines with *TaSOD1* knockdown expression. In (c) AntiCAT5-1 to AntiCAT5-4, four lines with *TaCAT5* knockdown expression. In (d) AntiPOD5-1 to AntiPOD5-4, four lines with *TaPOD5* knockdown expression. In (a)-(d) WT, wild type. Data shown are means $\pm$ standard deviation ($n = 3$). The expression values of target genes were normalized by *Tatubulin* and *TaGAPDH*, two constitutive genes in *T. aestivum* species, whose expression levels were set as 1.

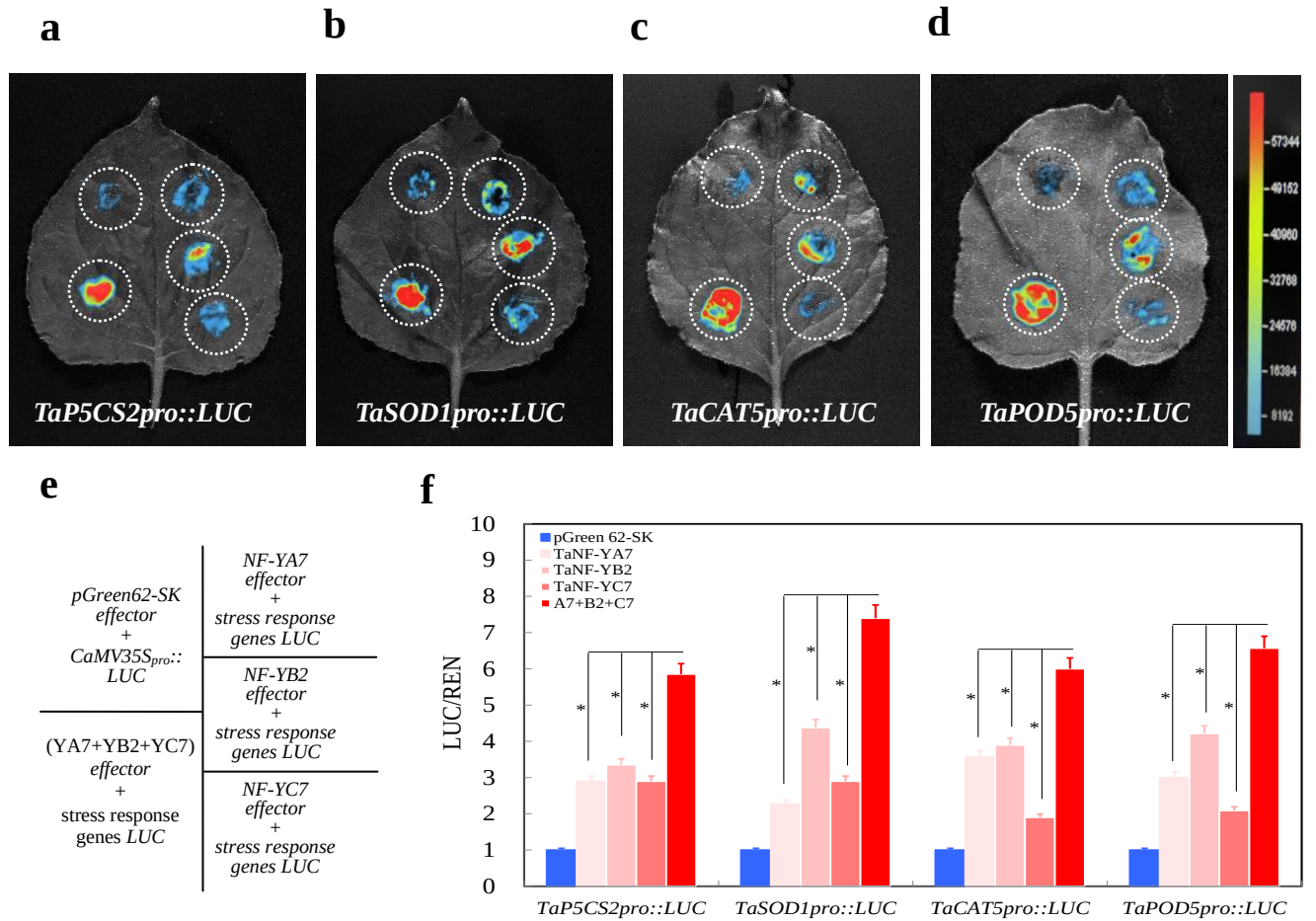


Fig. S10 Transcriptional activation assay results for distinct osmotic stress-associated genes regulated by TaNF-YB2, TaNF-YA7, and TaNF-YC7 Complexes.

(a)-(e) Dual-luciferase assays demonstrate that TaNF-YB2, TaNF-YA7, TaNF-YC7, and TaNF-YB2+TaNF-YA7+TaNF-YC7 transcriptionally activates *TaP5CS2*, *TaSOD1*, *TaCAT5*, and *TaPOD5*. (f) Cooperative and additive effects with TaNF-YB2, TaNF-YA7, TaNF-YC7 in driving *TaP5CS2*, *TaSOD1*, *TaCAT5*, *TaPOD5* expression. Luciferase activity is shown as LUC/REN ratio, using tobacco leaves co-transformed with the effector and the reporters. In (f) data presented are means $\pm$ standard deviation ($n = 3$). Student's *t*-test was used to test the statistical significance (* $p < 0.05$) between epidermal cells transformed with empty vector and cassette combinations.