

Figure S1. Molecular weight (kDa) vs. isoelectric point plots of TaBZR genes. The distinct round shape colors represent the *TaBZR* gene family members.

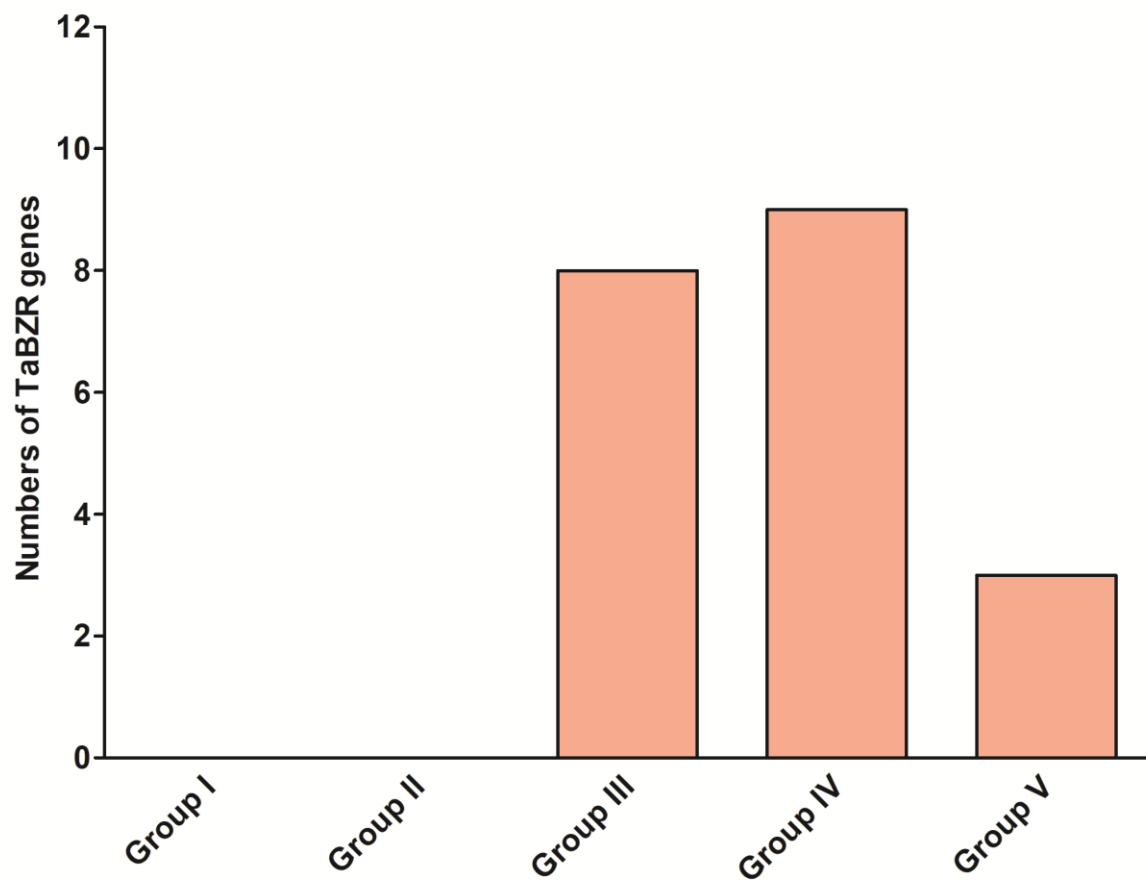


Figure S2. Distribution of *TaBZR* genes in a different group of the phylogenetic tree. The y-axis indicates the number of *TaBZR* genes and x-axis indicates the phylogenetic groups.

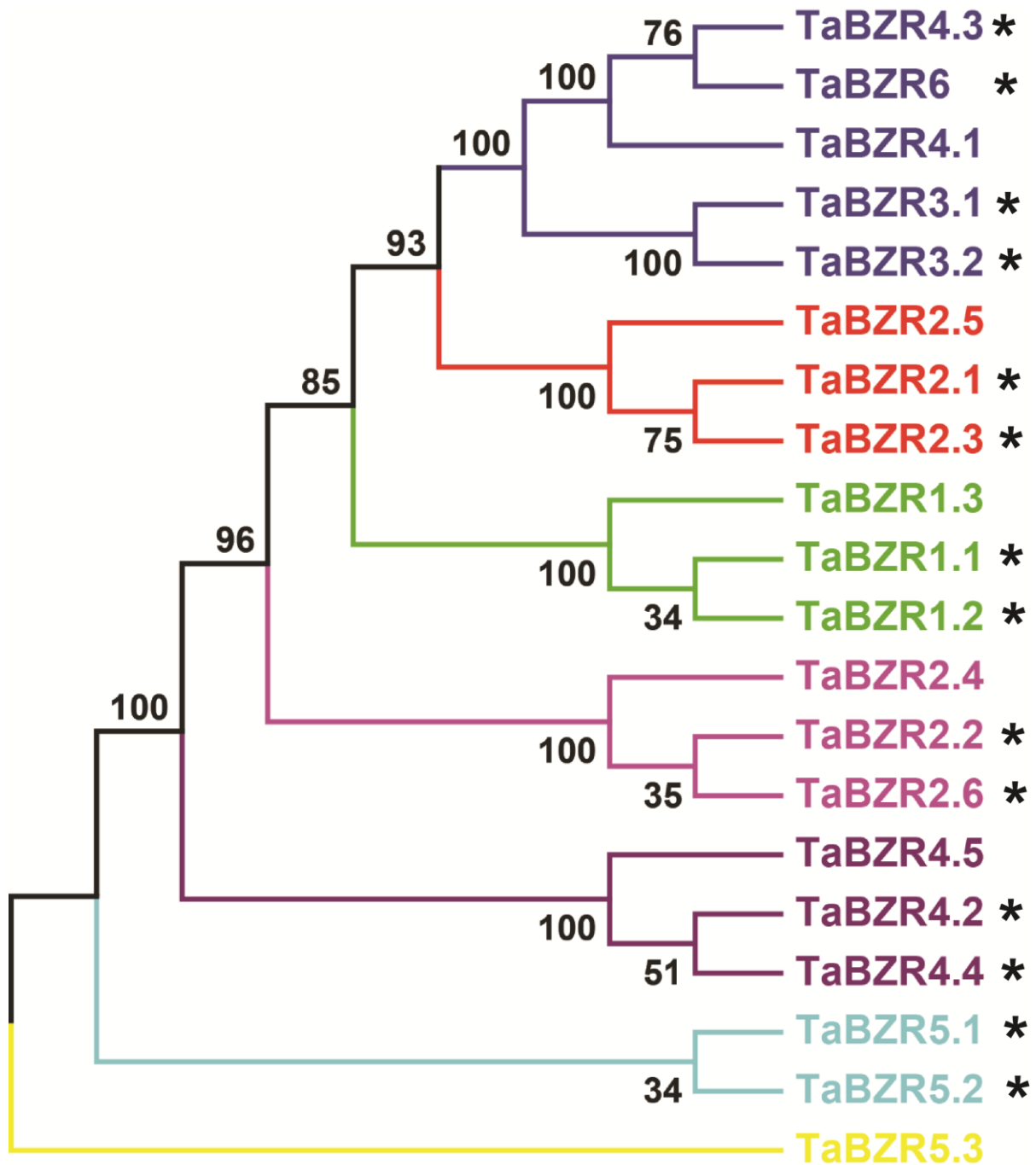


Figure S3. Phylogenetic analysis of *TaBZR* genes. A phylogenetic tree was constructed using MEGAX with the neighbor-joining (NJ) method and 1000 bootstrap replications. A black asterisk indicates the duplicated genes.

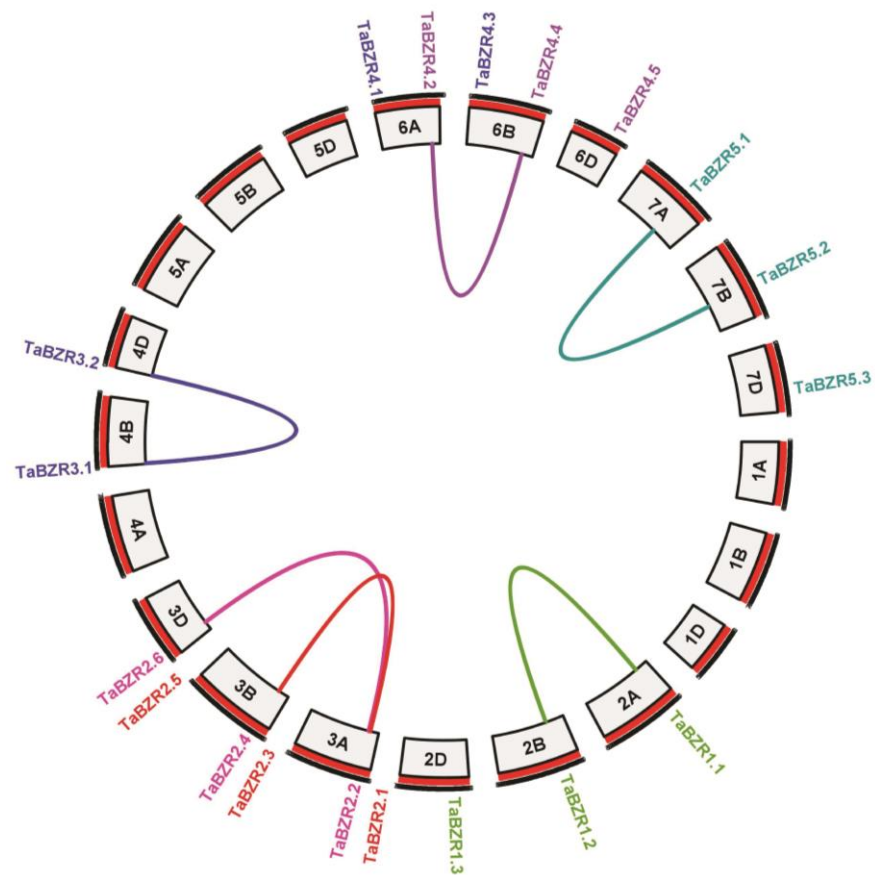


Figure S4. Chromosomal distribution and duplicated BZR gene pairs in wheat. Duplicated BZR gene pairs are connected with lines with distinct colors. The figure was generated using TB tools.

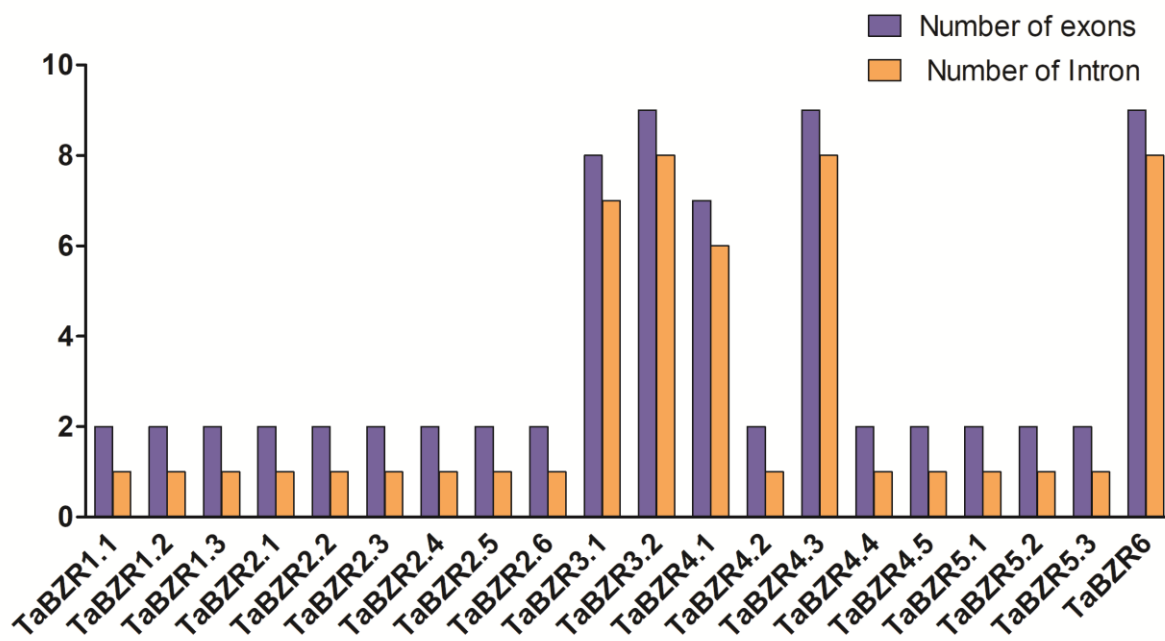


Figure S5. Distribution of exon and introns in *TaBZR*s gene family. The y-axis indicates the number of exon and introns and x-axis indicates the *TaBZR* genes. Exons and introns are represented by purple and orange boxes, respectively.

A

	*	20	*	40	*	60	
TaBZR1.1 :	-----	MTSGAARAA	-----	AAAEAEAGLGRTPIW	:	24	
TaBZR1.2 :	-----	MTSGAARAA	-----	AAAEADAGLGRTPIW	:	24	
TaBZR1.3 :	-----	MTSGAARAA	-----	AAAEADAGLGRTPIW	:	24	
TaBZR2.1 :	MEGVAKSVVAP--	MEVAAGAVGEEAMAVAVAAGRRGCIRSTRGFWTVRRQARGGAVKTSLRHPTP	:	63			
TaBZR2.2 :	-----	MATGGGGGG	-----	GAADFGAAGGAGGEMPTW	:	27	
TaBZR2.3 :	MEGVAKSIMAP--	MEVAG-AGREEAEAAEAVAGRRGCIRSTRGFWTVRRQARGGAVKTSLRHPTP	:	62			
TaBZR2.4 :	-----	MATGGGGGG	-----	ADFGAAGGAGGEMPTW	:	25	
TaBZR2.5 :	MEGVAKSIMAP--	MEVAG-AGEEEAMA--VAAGRRGCIRSTRGFWTVRRQARGGAVKTSLRHPTP	:	60			
TaBZR2.6 :	-----	MATGGGGGGGGGG	-----	ADFGAAGGAGGEMPTW	:	29	
TaBZR3.1 :	MLRLDPGEYDEETMGGAVKEED---	DSDEEGEEDDFIVA---	GDE--	PRPPEQQGRRRGRGRE	:	55	
TaBZR3.2 :	MLRLDP-----	MGGAVKEEDGEGEDSDEE-EEEDFIADAAAGDEQHARPE---	RRRGRGRE	:	54		
TaBZR4.1 :	MATKHP-----	HGDADPSTS---	PPPPPSRRPRGFASASTP-----	AAPPPPGRRRGERERE	:	49	
TaBZR4.2 :	-----	-----	-----	MASRVPTW	:	8	
TaBZR4.3 :	MATKHP-----	HGDADPSTS---	PPPPPSRRPRGFASASNP-----	FAPPPPGRRRGERERE	:	49	
TaBZR4.4 :	-----	-----	-----	MASRVPTW	:	8	
TaBZR4.5 :	-----	-----	-----	MASRVPTW	:	8	
TaBZR5.1 :	-----	-----	-----	MMHGFAGGS---	GGGGGHGLGGTRVPTW	:	25
TaBZR5.2 :	-----	-----	-----	MMHGFAGGS---	GGGGGHGLGGTRVPTW	:	25
TaBZR5.3 :	-----	-----	-----	MMHGFAGGS---	GGGGGHGLGGTRVPTW	:	25
TaBZR6 :	MATKHP-----	HGDADPSTS---	PPPPPSRRPRGFASASTP-----	AAPPPPGRRRGERERE	:	49	

BES1_N/ DUF822 Domain

	*	80	*	100	*	120	*	
TaBZR1.1 :	FERENNNRRRRRRRAA	AKIFTSLALNKE	KKHCINNEVLKE	CREAGWVED	GGTTYRKG	:	89	
TaBZR1.2 :	FERENNNRRRRRRRAA	AKIFTSLALNKE	KKHCINNEVLKE	CREAGWVED	GGTTYRKG	:	89	
TaBZR1.3 :	FERENNNRRRRRRRAA	AKIFTSLALNKE	KKHCINNEVLKE	CREAGWVED	GGTTYRKG	:	89	
TaBZR2.1 :	FERENNNRRRRRRRAA	AKIFTSLALNKE	KKHCINNEVLKE	CREAGWVED	GGTTYRKG	:	89	
TaBZR2.2 :	FERENNNRRRRRRRAA	AKIFTSLALNKE	KKHCINNEVLKE	CREAGWVED	GGTTYRKG	:	92	
TaBZR2.3 :	FERENNNRRRRRRRAA	AKIFTSLALNKE	KKHCINNEVLKE	CREAGWVED	GGTTYRKG	:	90	
TaBZR2.4 :	FERENNNRRRRRRRAA	AKIFTSLALNKE	KKHCINNEVLKE	CREAGWVED	GGTTYRKG	:	90	
TaBZR2.5 :	FERENNNRRRRRRRAA	AKIFTSLALNKE	KKHCINNEVLKE	CREAGWVED	GGTTYRKG	:	94	
TaBZR2.6 :	FERENNNRRRRRRRAA	AKIFTSLALNKE	KKHCINNEVLKE	CREAGWVED	GGTTYRKG	:	94	
TaBZR3.1 :	FKERTILRRRRRRRAA	AKIFTSLALNKE	KKHCINNEVLKE	CREAGWVED	GGTTYRKG	:	115	
TaBZR3.2 :	FKERTILRRRRRRRAA	AKIFTSLALNKE	KKHCINNEVLKE	CREAGWVED	GGTTYRKG	:	118	
TaBZR4.1 :	FKERTILRRRRRRRAA	AKIFTSLALNKE	KKHCINNEVLKE	CREAGWVED	GGTTYRKG	:	114	
TaBZR4.2 :	FKERTILRRRRRRRAA	AKIFTSLALNKE	KKHCINNEVLKE	CREAGWVED	GGTTYRKG	:	73	
TaBZR4.3 :	FKERTILRRRRRRRAA	AKIFTSLALNKE	KKHCINNEVLKE	CREAGWVED	GGTTYRKG	:	114	
TaBZR4.4 :	FERENNNRRRRRRRAA	AKIFTSLALNKE	KKHCINNEVLKE	CREAGWVED	GGTTYRKG	:	73	
TaBZR4.5 :	FERENNNRRRRRRRAA	AKIFTSLALNKE	KKHCINNEVLKE	CREAGWVED	GGTTYRKG	:	73	
TaBZR5.1 :	FERENNNRRRRRRRAA	AKIFTSLALNKE	KKHCINNEVLKE	CREAGWVED	GGTTYRKG	:	90	
TaBZR5.2 :	FERENNNRRRRRRRAA	AKIFTSLALNKE	KKHCINNEVLKE	CREAGWVED	GGTTYRKG	:	90	
TaBZR5.3 :	FERENNNRRRRRRRAA	AKIFTSLALNKE	KKHCINNEVLKE	CREAGWVED	GGTTYRKG	:	90	
TaBZR6 :	FKERTILRRRRRRRAA	AKIFTSLALNKE	KKHCINNEVLKE	CREAGWVED	GGTTYRKG	:	114	

	140	*	160	*	180	*	
TaBZR1.1 :	P	-----					: 90
TaBZR1.2 :	P	-----					: 90
TaBZR1.3 :	P	-----					: 90
TaBZR2.1 :	E	-----					: 127
TaBZR2.2 :	P	-----					: 93
TaBZR2.3 :	E	-----					: 126
TaBZR2.4 :	P	-----					: 91
TaBZR2.5 :	E	-----					: 124
TaBZR2.6 :	P	-----					: 95
TaBZR3.1 :		-----SSSHP-----					: 120
TaBZR3.2 :	T	PRFAMLAFAISLSSPSAAAAALPTLLFVSSSSCAPGI	AVPPLAARPISRRAGCA	FALRTAAASS			: 183
TaBZR4.1 :	P	S-----LPPFAQFGAFQATSLET	FVFTNSINSYAIGT	PIDSQASALQTDDSL	SPSSILDSVVVAE		: 174
TaBZR4.2 :	P	-----					: 74
TaBZR4.3 :	P	P-----LPPFAQFGAFQATSLET	FVFTNSINSYAIGT	PLDSQASALQTDDSL	SPSSILDSVVVAE		: 174
TaBZR4.4 :	P	P-----					: 75
TaBZR4.5 :	P	-----					: 74
TaBZR5.1 :	P	-----					: 91
TaBZR5.2 :	P	-----					: 91
TaBZR5.3 :	P	-----					: 91
TaBZR6 :	P	P-----LPSEFAQFGAFQATSLET	FVFTNSINSYAIGT	PLDSQASALQTDDSL	SPSSILDSVVVAE		: 174

	200	*	220	*	240	*	260	
TaBZR1.1 :							PSSGPF	: 96
TaBZR1.2 :							PSSGPF	: 96
TaBZR1.3 :							PSSGPF	: 96
TaBZR2.1 :								: -
TaBZR2.2 :							AERMD	: 98
TaBZR2.3 :								: -
TaBZR2.4 :							AERMD	: 96
TaBZR2.5 :								: -
TaBZR2.6 :							AERMD	: 100
TaBZR3.1 :								: -
TaBZR3.2 :	P	FAVSRVPEGGFASPLLA	VFPDDEDADAAMDGGD	GGEQTGLATREAVAP	PRPPPERDFAGTPY			: 248
TaBZR4.1 :	Q	SIKNESYGNSSSANSIN	CMGSDQLLRASAVWAG	-----			DFTKTPY	: 215
TaBZR4.2 :							VTAEGTN	: 81
TaBZR4.3 :	Q	SIKNESYGNSSSANSIN	CMGSDQLLRASAVWAG	-----			DFTKTPY	: 215
TaBZR4.4 :							AAAEKAN	: 82
TaBZR4.5 :							IAAEKAN	: 81
TaBZR5.1 :							PPQARP	: 97
TaBZR5.2 :							PPQVRP	: 97
TaBZR5.3 :							PPQART	: 97
TaBZR6 :	Q	SIKNESYGNSSSANSIN	CMGSDQLLRASAVCAG	-----			DFTKTPY	: 215

		*	280	*	300	*	320	
TaBZR1.1	:	GGVSSAGMSPCSS	SQLLSAPS-----	SSFP	FVPSYHASFASS-----	SFPSPTRIDNPS	:	146
TaBZR1.2	:	GGVSSAGMSPCSS	SQLLSAPS-----	SSFP	FVPSYHASFASS-----	SFPSPTRIDNPS	:	146
TaBZR1.3	:	GGVSSAGMSPCSS	SQLLSAPS-----	SSFP	FVPSYHASFASS-----	SFPSPTRIDNPS	:	146
TaBZR2.1	:	--VSTDFGASCSS	GHL-----	QPS	SHSHSVATEATAG-----		:	157
TaBZR2.2	:	GIGCSVSPSPCSS	YQPSPRASYNASPTSS	SFP	GASSPFLPHSNN--MVNGVDATPILEWLQTFS		:	161
TaBZR2.3	:	--RSPGVGASGSS	DHL-----	QPS	SHSG--ATEATAG-----		:	154
TaBZR2.4	:	GIGCSVSPSPCSS	YQPSPRASYNASPTSS	SFP	GASSPFLPHSNN--MVNGVDATPILEWLQTFS		:	159
TaBZR2.5	:	--RSSGAGTGGSS	DHP-----	QPS	SHSG--ATEATAG-----		:	152
TaBZR2.6	:	GIGCSVSPSPCSS	YQPSPRASYNASPTSS	SFP	GASSPFLPHSNN--MVNGVDATPILEWLQTFS		:	163
TaBZR3.1	:	-----QLGVV	VKGEVAEAEDEIVAQLRVLKAAGVDGVMVDCWGWGVEAHRPQEYNWAGYKRLF				:	178
TaBZR3.2	:	VFVYVMLPLGVV	VKGEVAEAEDEIVAQLRVLKAAGVDGVMVDCWGWGVEAHRPQEYNWAGYKRLF				:	313
TaBZR4.1	:	IFVYASLSMGIINCYCQI	VDPEAVRAELRHLK	INVDGVVVD	CWGWGIVEAWTPQKYEWSGYRDLF		:	280
TaBZR4.2	:	FMVRSGPS	SPCSHQVSPRA-----	SFPT	SGTSSHTTLGGGR--GSCYEGGSLIFWLKNLS		:	135
TaBZR4.3	:	IFVYASLSMGIINCYCQI	VDPEAVRAELRHLK	INVDGVVVD	CWGWGIVEAWTPQKYEWSGYRDLF		:	280
TaBZR4.4	:	FVVRSGSR	SPCSHFVSPRAPYNPRAGPST	TFPT	SGTSSHTTLGGG---SSYIEGSSSFIWLNLS		:	144
TaBZR4.5	:	FMVRSGPS	SPCSHQVSPRA-----	SFPT	SGTSSHTTLGGGGSGSYIEGSSSFIWLNLS		:	137
TaBZR5.1	:	DEMRASAS	SPCSYQPSPRASYNPSFASS	SFP	SGSSSHITLGGGNNFIGGVEGSSLIWLNLS		:	162
TaBZR5.2	:	DEMRASAS	SPCSYQPSPRASYNPSFASS	SFP	SGSSSHITLGGGNNFIGGVEGSSLIWLNLS		:	162
TaBZR5.3	:	DEMRASAS	SPCSYQPSPRASYNPSFASS	SFP	SGSSSHITLGGGNNFIGGVEGSSLIWLNLS		:	162
TaBZR6	:	IFVYASLSMGIINCYCQI	VDPEAVRAELRHLK	INVDGVVVD	CWGWGIVEAWTPQKYEWSGYRDLF		:	280

Serine rich phosphorylation sites

		*	340	*	360	*	380	*	
TaBZR1.1	:	FACLLPFLRGL	ENLPPLRV-----	NSA	VTTPPLSSE	TASRP-----	PKILKED	VEVDP	: 195
TaBZR1.2	:	FACLLPFLRGL	ENLPPLRV-----	NSA	VTTPPLSSE	TASRP-----	PKILKED	VEVDP	: 195
TaBZR1.3	:	FACLLPFLRGL	ENLPPLRV-----	NSA	VTTPPLSSE	TASRP-----	PKILKED	VEVDP	: 195
TaBZR2.1	:	-----	-----	GHQ	ALLEPEAE	-----	-----	-----	: 170
TaBZR2.2	:	NS---	TASNKRPHLPPLLI---	HGGS	ISA	VTTPPLSSE	TARTPRMKTW---	DESVIQ	PEFHGSN : 217
TaBZR2.3	:	-----	-----	DH	QALLEPEAE	-----	-----	-----	: 167
TaBZR2.4	:	NS---	TASNKRPHLPPLLI---	HGGS	ISA	VTTPPLSSE	TARTPRMKTW---	DESVIQ	PEFHGSN : 215
TaBZR2.5	:	-----	-----	DH	QEL--PEAE	-----	-----	-----	: 163
TaBZR2.6	:	NS---	TASNKRPHLPPLLI---	HGGS	ISA	VTTPPLSSE	TARTPRMKTW---	DESVIQ	PEFHGSN : 219
TaBZR3.1	:	HIIRD	LKLKLVVMSFHGCGGNVGDDV	SI	IP	EWVIEIGKSNPD	IYFTDREGRNTECL	SGIDK	: 243
TaBZR3.2	:	HIIRD	LKLKLVVMSFHGCGGNVGDDV	SI	IP	EWVIEIGKSNPD	IYFTDREGRNTECL	SGIDK	: 378
TaBZR4.1	:	GIIKEFKLKVQV	VSFHGSGECGSGGV	LIAL	PRWVLEIAQENQD	IYFTDREGRNTECL	SGIDK	: 345	
TaBZR4.2	:	SGSGF	ASSSKFPRYSPHSY-YFSGGS	ISA	VTTPSGSE	-RRMPCINAGWGEYPSAQV	QPF	FGAG : 198	
TaBZR4.3	:	GIIKEFKLKVQV	VSFHGSGECGSGGV	LIAL	PRWVLEIAQENQD	IYFTDREGRNTECL	SGIDK	: 345	
TaBZR4.4	:	SGSGF	ASSSKFPRYSPHSYDYFSGGS	ISA	VTTPSGSE	-RRMPCINAGWGEYPSVQV	QPF	FGAG : 208	
TaBZR4.5	:	SGSGF	PSSSKFPRYSPHSY--FSGGS	ISA	VTTPSCSE	-RRMPCINAGWGEYPSAQV	QPF	FGAG : 199	
TaBZR5.1	:	SNPSF	ASSSKLPQLH-HLY--FNGGS	ISA	VTTPSSSE	-THTPRMKTW---	ESQCVL	PEFAGAN : 220	
TaBZR5.2	:	SNPSF	ASSSKLPQLH-HLY--FNGGS	ISA	VTTPSSSE	-THTPRMKTW---	ESQCVL	PEFAGAN : 220	
TaBZR5.3	:	SNPSF	ASSSKLPQLH-HLY--FNGGS	ISA	VTTPSSSE	-THTPRMKTW---	ESQCVL	PEFAGAN : 220	
TaBZR6	:	GIIKEFKLKVQV	VSFHGSGECGSGGV	LIAL	PRWVLEIAQENQD	IYFTDREGRNTECL	SGIDK	: 345	

	400	*	420	*	440	*				
TaBZR1.1	: FR----	HPFFALSAFASPTRGRRHEH	PDTIPECDESD	STVDSGRWISFQMATT-----	A	:	246			
TaBZR1.2	: FR----	HPFFALSAFASPTRGRRHEH	PDTIPECDESD	STVDSGRWISFQMATT-----	A	:	246			
TaBZR1.3	: FR----	HPFFALSAFASPTRGRRHEH	PDTIPECDESD	STVDSGRWISFQMATT-----	A	:	246			
TaBZR2.1	:	-----	KHK	SLELTLSFSYM-----	:		185			
TaBZR2.2	:	-----	SPCVVNSTPPSP--G-RQMV	PDP-AWLAGIQSS	TPSSPTFSIMSSNP--FSVFKEAI	:	270			
TaBZR2.3	:	-----	KHK	SLELTLSFSYM-----	:		182			
TaBZR2.4	:	-----	SPCVVNSTPPSP--G-RQMV	PDP-AWLAGIQSS	TPSSPTFSIMSSNP--FSVFKEAI	:	268			
TaBZR2.5	:	-----	KHK	SLELTLSFTYM-----	:		178			
TaBZR2.6	:	-----	SPCVVNSTPPSP--G-RQMV	PDP-AWLAGIQSS	TPSSPTFSIMSSNP--FSVFKEAI	:	272			
TaBZR3.1	:	ERVLQGR	TA	VEVYFDFMRSFRVEFDEYFEDGI	ISEIE	GLGACGELRYPSYAANHGWKYPGIGEF	:	308		
TaBZR3.2	:	ERVLQGR	TA	VEVYFDFMRSFRVEFDEYFEDGI	ISEIE	GLGACGELRYPSYAANHGWKYPGIGEF	:	443		
TaBZR4.1	:	ERVLRGRTG	IEVYFDFMRSFHM	EFRLSEEG	LISAIE	GLGASGELRYPSCPEKMGWRYPGIGEF	:	410		
TaBZR4.2	:	GS	GYDDYASL	FNSTPSSPRGG-QGVG	PDEA	AWLSGFCSS	AGPSSPTY	SIMAPSNPFRVSGEMAA	:	262
TaBZR4.3	:	ERVLRGRTG	IEVYFDFMRSFHM	EFRLSEEG	LISAIE	GLGASGELRYPSCPEKMGWRYPGIGEF	:	410		
TaBZR4.4	:	GS	AYDDYASL	FNSTPSSPRGG-HGVG	PDP-AWLSGFCSS	AGPSSPTY	SIMAPSNPFRVSGEMAA	:	271	
TaBZR4.5	:	GS	GYDDYASL	FNSTPSSPRGGSHGVG	PDP-AWLSGFCSS	AGPSSPTY	SIMAPSSSRVFGEMAA	:	263	
TaBZR5.1	:	-----	YTS	LENSTPPSP--G-HHVA	PDP-AWLAGFQSS	AGPSSPTY	NLVSHN-----PFGI	:	268	
TaBZR5.2	:	-----	YTS	LENSTPPSP--G-HHVA	PDP-AWLAGFQSS	AGPSSPTY	NLVSHN-----PFGI	:	268	
TaBZR5.3	:	-----	YAS	LENSTPPSP--G-HHVA	PDP-AWLAGFQSS	AGPSSPTY	NLVSHN-----PFGI	:	268	
TaBZR6	:	ERVLRGRTG	IEVYFDFMRSFHM	EFRLSEEG	LISAIE	GLGASGELRYPSCPEKMGWRYPGIGEF	:	410		

	460	*	480	*	500	*	520	
TaBZR1.1	: PTSFAYNIVNLG	ASSNSMEMEG-----	MAGERGRSGPE	EDDKG-----	:		286	
TaBZR1.2	: PTSFAYNIVNLG	ASSNSMEMLDG-----	MAGERGRSGPE	EDDKG-----	:		286	
TaBZR1.3	: PTSFAYNIVNLG	ASSNSMEMDG-----	MAGERGRSGPE	EDDKG-----	:		286	
TaBZR2.1	:	-----	-----	-----	-----	-----	-	
TaBZR2.2	:	P	GGGSSRMCTPGQSGTCSFV	IPG-MARHPDVHMDV--VSDE	AFGSSTNGGA-----	:	320	
TaBZR2.3	:	-----	-----	-----	-----	-----	-	
TaBZR2.4	:	P	GGGSSRMCTPGQSGTCSFV	IPG-MARHPDVHMDV--VSDE	AFGSSTNGGA-----	:	318	
TaBZR2.5	:	-----	-----	-----	-----	-----	-	
TaBZR2.6	:	P	GGGSSRMCTPGQSGTCSFV	IPG-MARHPDVHMDV--VSDE	AFGSSTNGGA-----	:	322	
TaBZR3.1	:	QCYDRYLQKNLR	RFAAEARGHAMWAKSPDNAGHYNSEFNNTGF	CDGGDYDSYYGRFFINWYAQVL	:		373	
TaBZR3.2	:	QCYDRYLQKNLR	RFAAEARGHAMWAKSPDNAGHYNSEFNNTGF	CDGGDYDSYYGRFFINWYAQVL	:		508	
TaBZR4.1	:	QCYDRYMQKNLR	QSALTRGHLFWARGPDNAGYYNSRS	SHETGFCDGGDYDSYYGRFFINWYSGIL	:		475	
TaBZR4.2	:	ATASSSRMRTPC	QSGTCSFVA---IAVHGDVQMGAR--AEDD	AFGSG-----	:		305	
TaBZR4.3	:	QCYDRYMQKNLR	QSALTRGHLFWARGPDNAGYYNSRS	SHETGFCDGGDYDSYYGRFFINWYSGIL	:		475	
TaBZR4.4	:	ATASSSRMRTPC	QSGTCSFVA---IAAHGDVQMEHR--EADD	AFGSG-----	:		314	
TaBZR4.5	:	ATAGSSRMCTFA	QSGTCSFVM---IAVHGDVQMGAR--AEDD	AFGSG-----	:		306	
TaBZR5.1	:	ALASSSR	ACTPGQSGTCSFVMGDHAF	FAHHDVQMEMADGAPDDAFGSNSNG-----	:		319	
TaBZR5.2	:	ALASSSR	ACTPGQSGTCSFVMGDHAF	FAHHDVQMEMVEGAADDAFGSNSNG-----	:		319	
TaBZR5.3	:	ALASSSR	VCTPGQSGTCSFAMGDHAF	FAHHDVQMEMVEGAADDAFGSNSNG-----	:		319	
TaBZR6	:	QCYDRYMQKNLR	QSALARGHLFWARGPDNAGYYNSRS	SHETGFCDGGDYDSYYGRFFINWYSGIL	:		475	

	*	540	*	560	*	580	
TaBZR1.1 :	-----	RVTFW EG ER I HEVA-----	AEE--	LE LT LG V GSK-----			: 313
TaBZR1.2 :	-----	RVTFW EG ER I HEVA-----	AEE--	LE LT LG V GSK-----			: 313
TaBZR1.3 :	-----	RVTFW EG ER I HEVA-----	AEE--	LE LT LG V GSK-----			: 313
TaBZR2.1 :	-----						: -
TaBZR2.2 :	---	QCATAGLVR AW EG ER I H EDS-----	GSD--	ELE LT L-----	GSSRT RS -----		: 356
TaBZR2.3 :	---						: -
TaBZR2.4 :	---	QCATAGLVR AW EG ER I H EDS-----	GSD--	ELE LT L-----	GSSRT RS -----		: 354
TaBZR2.5 :	---						: -
TaBZR2.6 :	---	QCATAGLVR AW EG ER I H EDS-----	GSD--	ELE LT L-----	GSSRT RS -----		: 358
TaBZR3.1 :	LDHADRVLM	LARI A EG S A I AVKVSGIHWWYK T ASHAA E L T AGFYNPCN R DGYAPIA Q VLKKHGA					: 438
TaBZR3.2 :	LDHADRVLM	LARI A EG S A I AVKVSGIHWWYK T ASHAA E L T AGFYNPCN R DGYAPIA Q VLKKHGA					: 573
TaBZR4.1 :	IDHVDQVLS	LATIA E DCAA I VVKIPSIYWWR T ASHAA E L T AGFYNP T N R DGYSFVFRMLKKHSI					: 540
TaBZR4.2 :	-----	GRFVS V N AW EG ER I H EV C -----	ASDEPE	L DT LGL G SSN T FRASALN-----			: 347
TaBZR4.3 :	IDHVDQVLS	LATIA E DCAA I VVKIPSIYWWR T ASHAA E L T AGFYNP T N R DGYSFVFRMLKKHSI					: 540
TaBZR4.4 :	-----	GRFVL V N AW EG ER I H EV C -----	ASDEHE	L DT LGL G SSK T FRAGAVN-----			: 356
TaBZR4.5 :	-----	GRFVS V N AW EG ER I H EV C -----	ASDEPE	L DT LGL G SSK T FRAGAVN-----			: 348
TaBZR5.1 :	---	NNGSPGLV K A W EG ER I H EE C -----	ASD--	ELE LT L-----	GSSRT R GEQPF-----		: 359
TaBZR5.2 :	---	NNGSPGLV K A W EG ER I H EE C -----	ASD--	ELE LT L-----	GSSRT R GEPPF-----		: 359
TaBZR5.3 :	---	NNGSPGLV K A W EG ER I H EE C -----	ASD--	ELE LT L-----	GSSRT R GEPPF-----		: 359
TaBZR6 :	IDHVDQVLS	LATIA E DCAA I VVKIPSIYWWR T ASHAA E L T AGFYNP T N R DGYSFVFRMLKKHSI					: 540

C-terminal domain

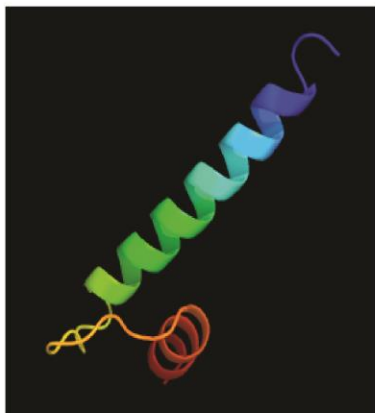
	*	600	*	620	*	640	*	
TaBZR1.1 :	-----							: -
TaBZR1.2 :	-----							: -
TaBZR1.3 :	-----							: -
TaBZR2.1 :	-----							: -
TaBZR2.2 :	-----							: -
TaBZR2.3 :	-----							: -
TaBZR2.4 :	-----							: -
TaBZR2.5 :	-----							: -
TaBZR2.6 :	-----							: -
TaBZR3.1 :	AINFTCVEL	RTMDQHEVYPEALADPEGLVWQ V INA A WDAGIQ V ASENALPCYDRDGFNKTLEN A K						: 503
TaBZR3.2 :	AINFTCVEL	RTMDQHEVYPEALADPEGLVWQ V INA A WDAGIQ V ASENALPCYDRDGFNKTLEN A K						: 638
TaBZR4.1 :	ILKVVCYG	PEFTVQEND--EAFADPEGLTWQ V MNA A WDHGLSVSVESALPCLD V DMYSRILD T AK						: 603
TaBZR4.2 :	-----							: -
TaBZR4.3 :	ILKVVCYG	PEFTVQENG--EAFADPEGLTWQ V MNA A WDHGLSVSVESL P CLD V DMYSRILD T AK						: 603
TaBZR4.4 :	-----							: -
TaBZR4.5 :	-----							: -
TaBZR5.1 :	-----							: -
TaBZR5.2 :	-----							: -
TaBZR5.3 :	-----							: -
TaBZR6 :	ILKVVCYG	PEFTVQEND--EAFADPEGLTWQ V MNA A WDHGLSVSVESALPCLD V DMYSRILD T AK						: 603

	660	*	680	*	700	*		
TaBZR1.1 :	-----						:	-
TaBZR1.2 :	-----						:	-
TaBZR1.3 :	-----						:	-
TaBZR2.1 :	-----						:	-
TaBZR2.2 :	-----						:	-
TaBZR2.3 :	-----						:	-
TaBZR2.4 :	-----						:	-
TaBZR2.5 :	-----						:	-
TaBZR2.6 :	-----						:	-
TaBZR3.1 :	PRNDPDGRHLFGFTYLRLCSTLFE-GENLPEFERFVKRMHGEAVHDLRA-----						:	551
TaBZR3.2 :	PRNDPDGRHLFGFTYLRLCSTLFE-GENLPEFERFVKRMHGEAVHDLRA-----						:	686
TaBZR4.1 :	PRNDPDRHHLSTFFAYRQRTPFLLQRDVCFSELETFVKCMHGEATQNFVD-----						:	652
TaBZR4.2 :	-----						:	-
TaBZR4.3 :	PRNDPDRHHLSTFFAYRQRTPFLLQRDAFSELETFVKCMHELCLTYCSLRSANFRIPFVAIARL						:	668
TaBZR4.4 :	-----						:	-
TaBZR4.5 :	-----						:	-
TaBZR5.1 :	-----						:	-
TaBZR5.2 :	-----						:	-
TaBZR5.3 :	-----						:	-
TaBZR6 :	PRNDPDRHHLSTFFAYRQRTPFLLQRDVCFSELETFVKCMHGEATQNFVD-----						:	652

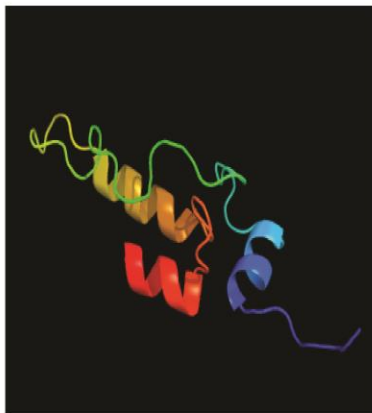
TaBZR1.1 :	----	:	-
TaBZR1.2 :	----	:	-
TaBZR1.3 :	----	:	-
TaBZR2.1 :	----	:	-
TaBZR2.2 :	----	:	-
TaBZR2.3 :	----	:	-
TaBZR2.4 :	----	:	-
TaBZR2.5 :	----	:	-
TaBZR2.6 :	----	:	-
TaBZR3.1 :	----	:	-
TaBZR3.2 :	----	:	-
TaBZR4.1 :	----	:	-
TaBZR4.2 :	----	:	-
TaBZR4.3 :	NSYC :	672	
TaBZR4.4 :	----	:	-
TaBZR4.5 :	----	:	-
TaBZR5.1 :	----	:	-
TaBZR5.2 :	----	:	-
TaBZR5.3 :	----	:	-
TaBZR6 :	----	:	-

B

TaBZR1.1



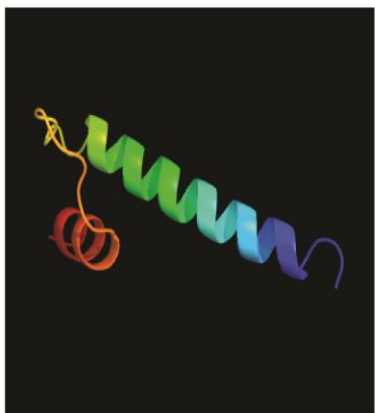
TaBZR1.2



TaBZR2.1



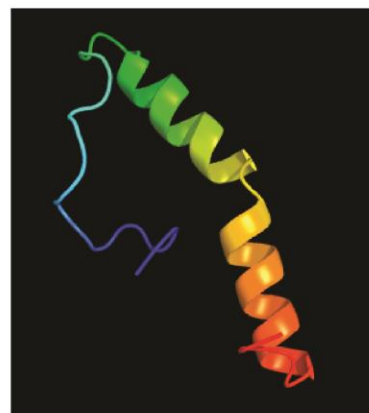
TaBZR2.2



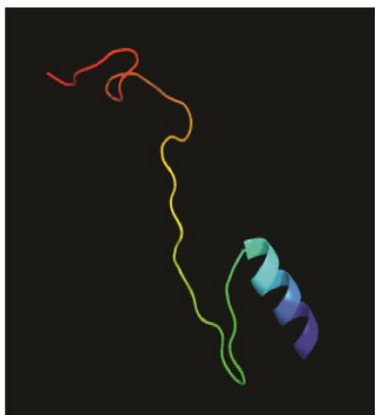
TaBZR2.3



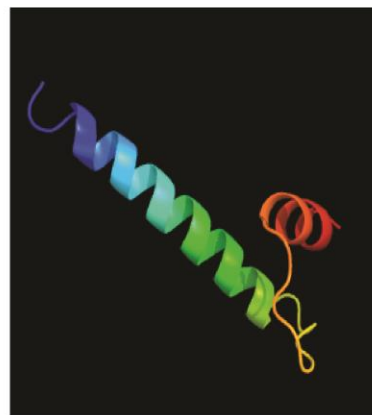
TaBZR2.4



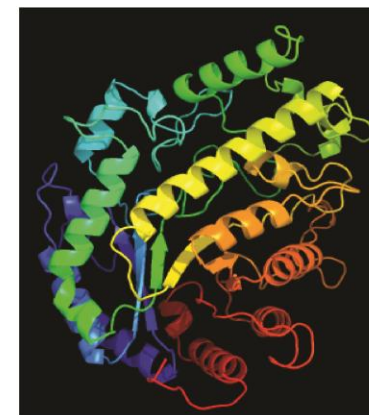
TaBZR2.5



TaBZR2.6



TaBZR3.1



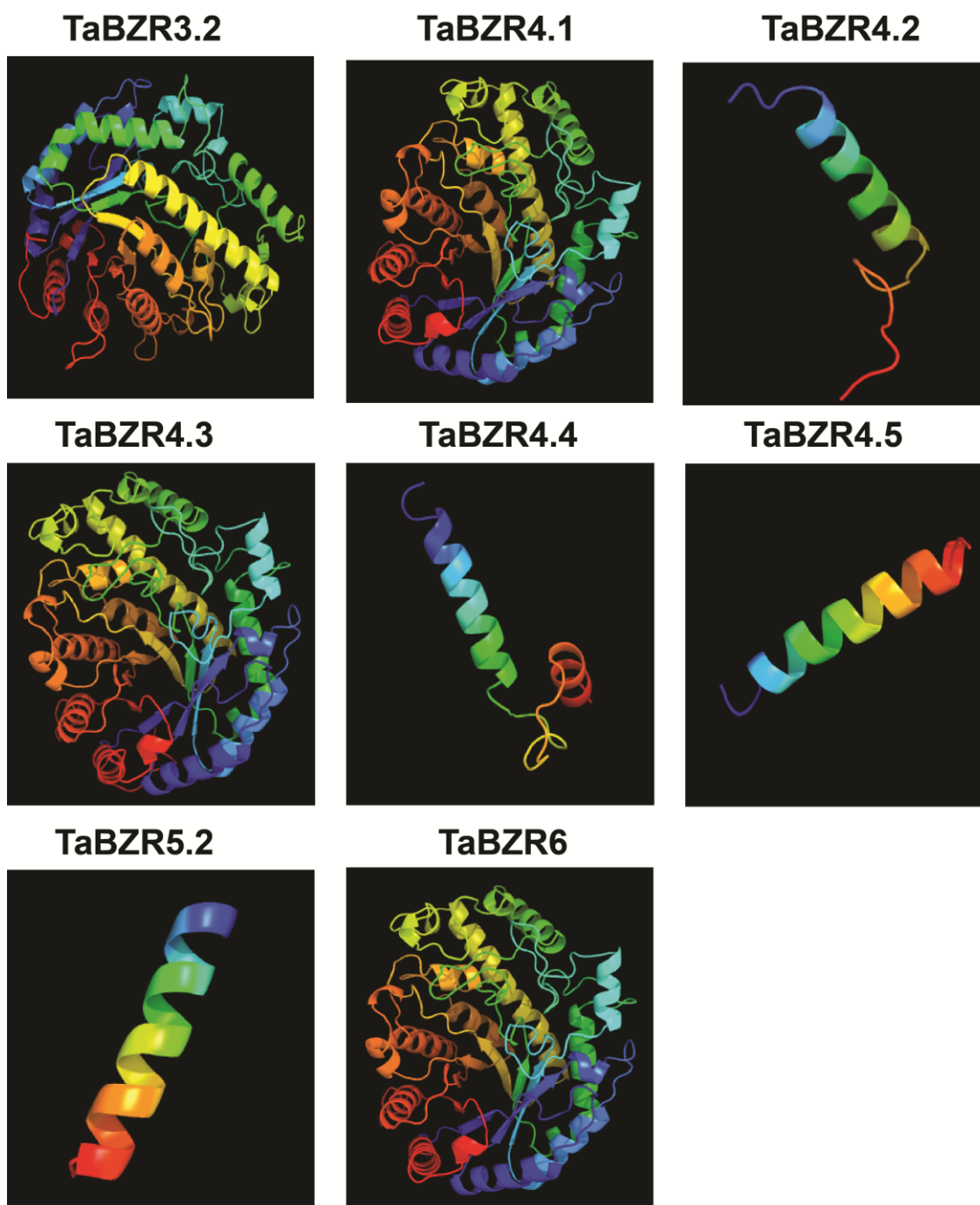
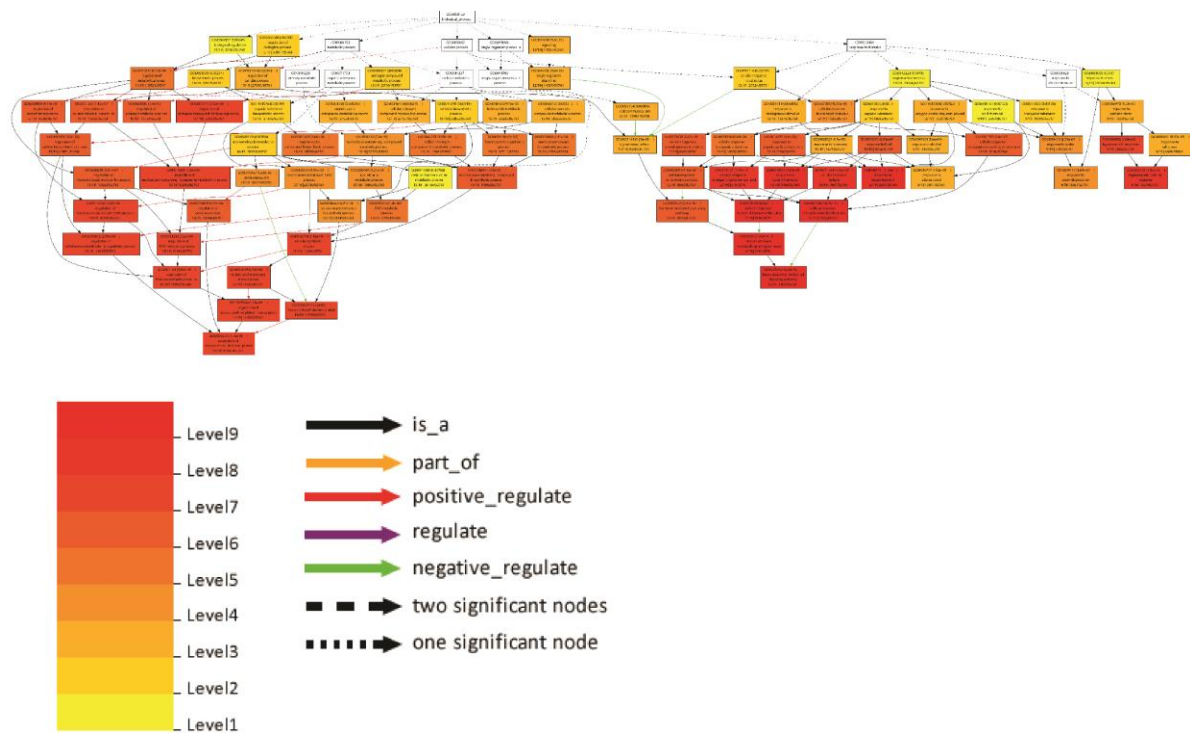
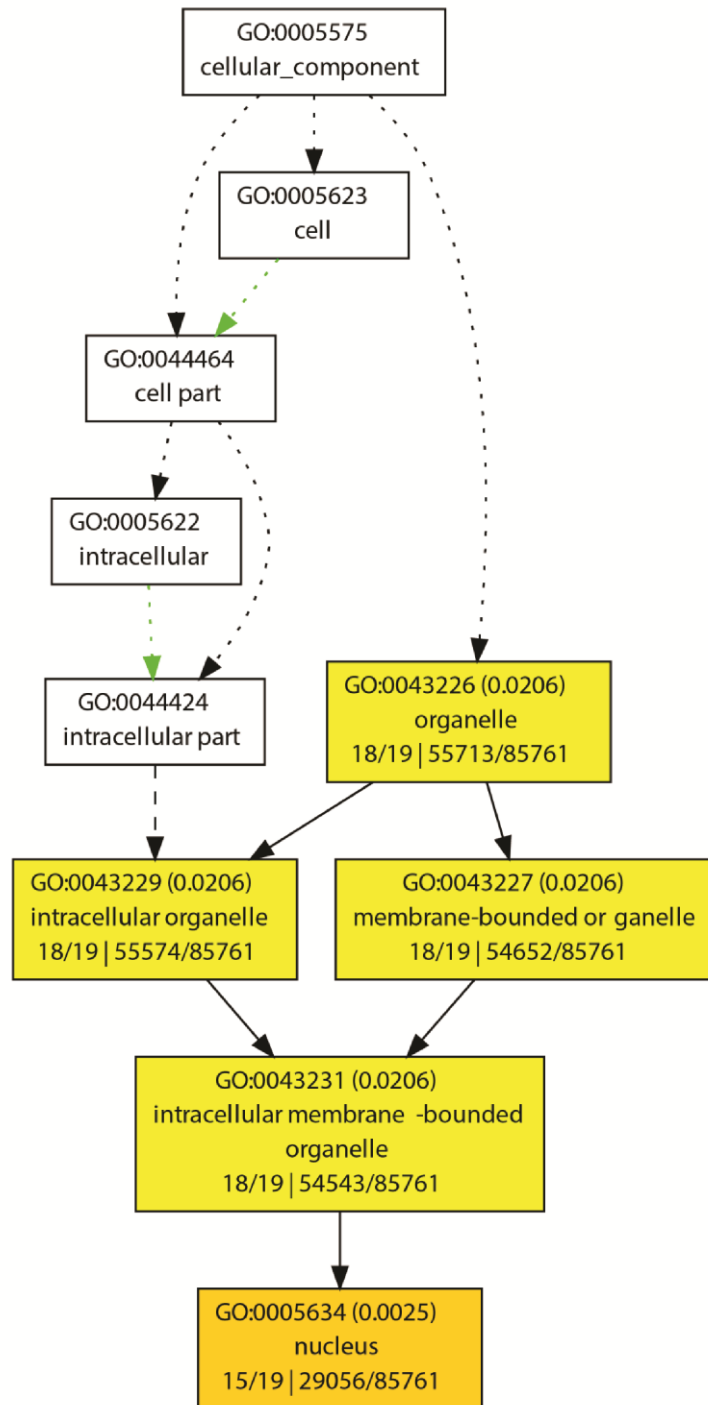


Figure S6. Alignment and 3-dimensional structure of the TaBZR protein sequences. **A.** The conserved BES_N1/DUF822 domain is boxed with red color. Red lines indicate serine-rich phosphorylation sites and the C-terminal domain. Colored and shaded amino acids are chemically similar residues. Dashes indicate gaps introduced to maximize the alignment of the homologous region. **B.** Predicted 3D structures TaBZR proteins.

A



B



C

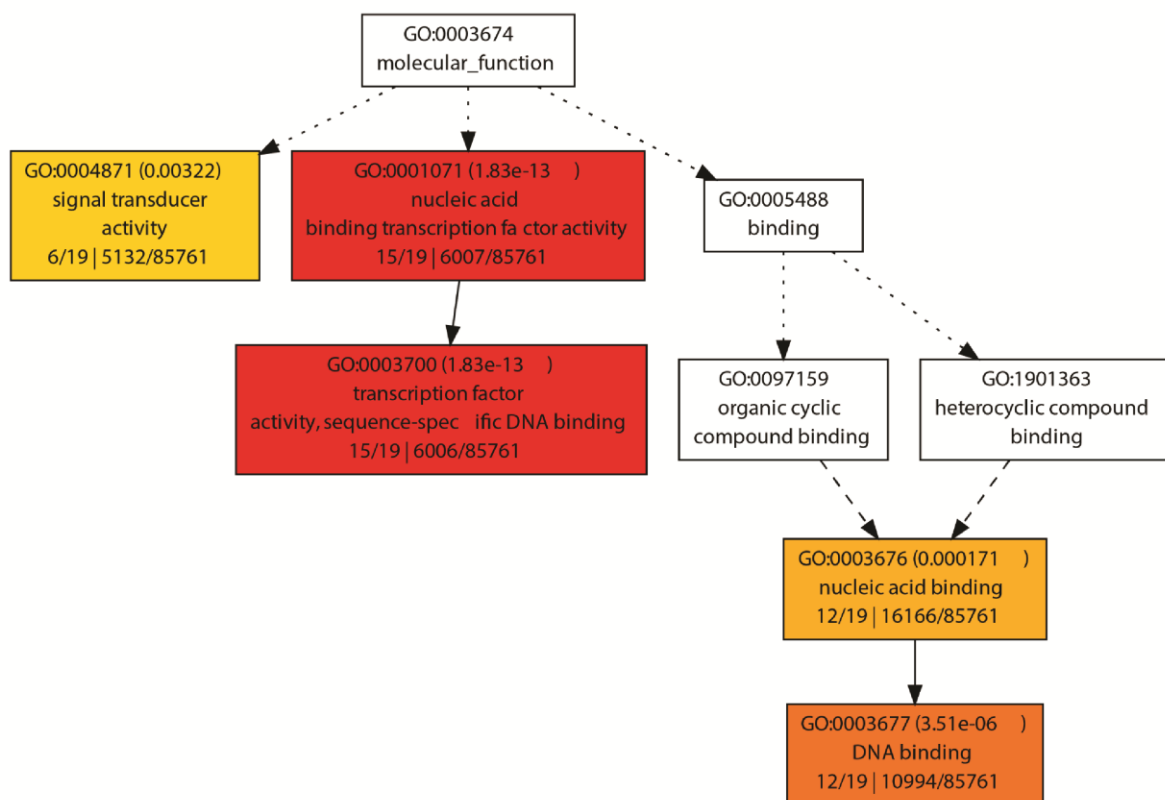


Figure S7. Gene ontology term distribution *TaBZR* gene family predicted using AgriGO A. Biological Process. B. Cellular component. C. Molecular function.

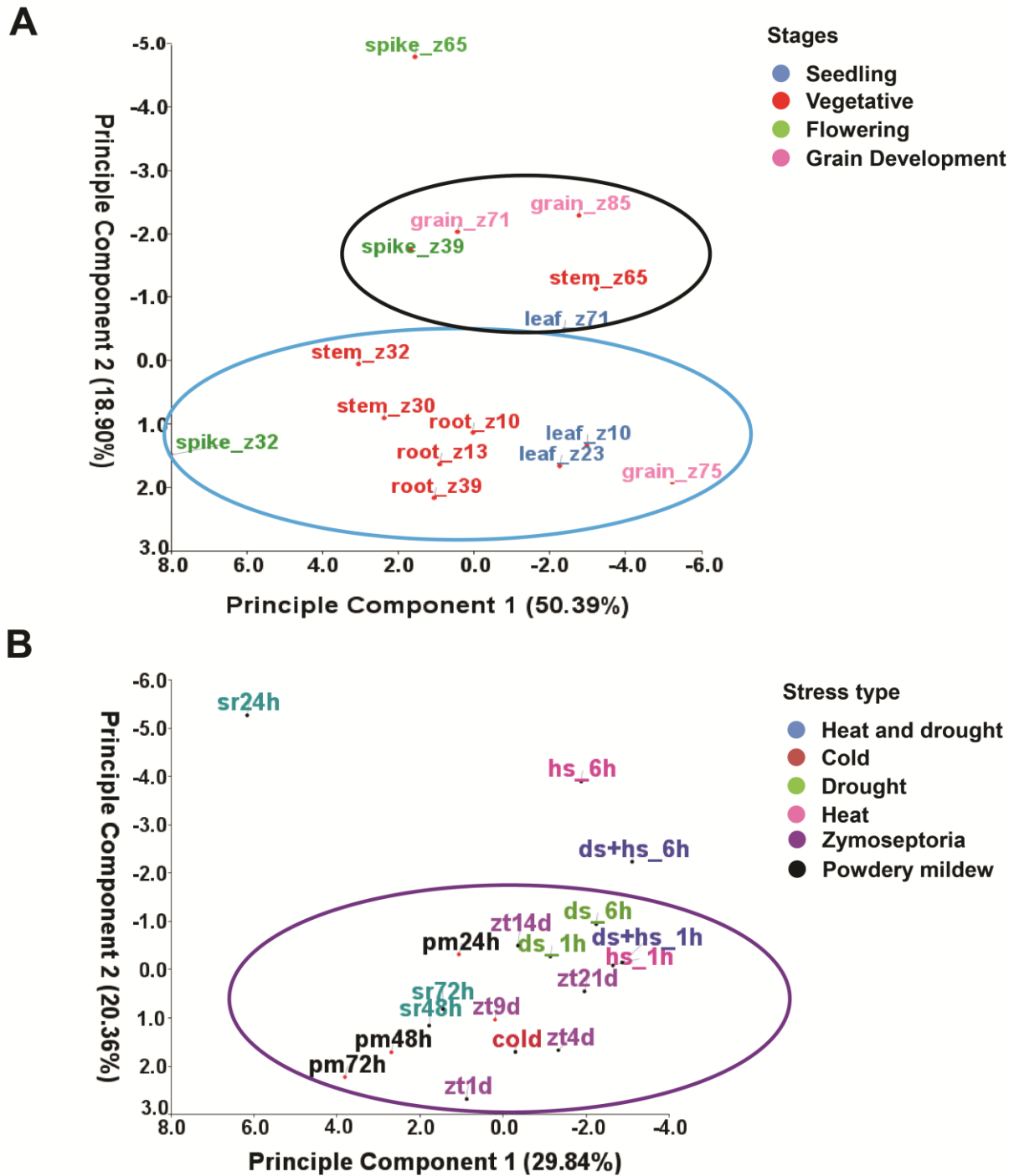


Figure S8. PCA plots displaying grouping of different A. Developmental stages B. Biotic and abiotic stress conditions based on the *TaBZR* expression pattern. DS: Drought stress, HS: Heat stress, Zt: *Zymoseptoria tritici*, PM: Powdery mildew; SR: Stripe rust, h: hour and d: days.