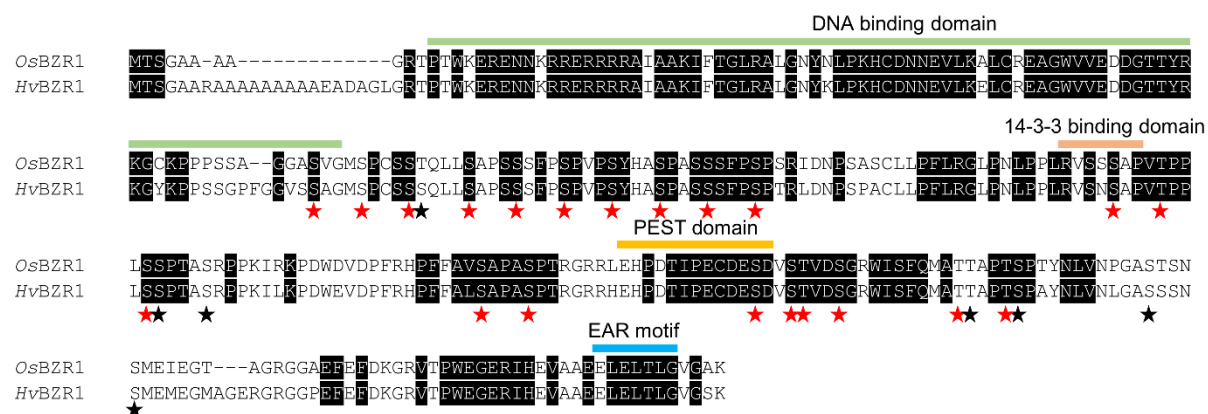


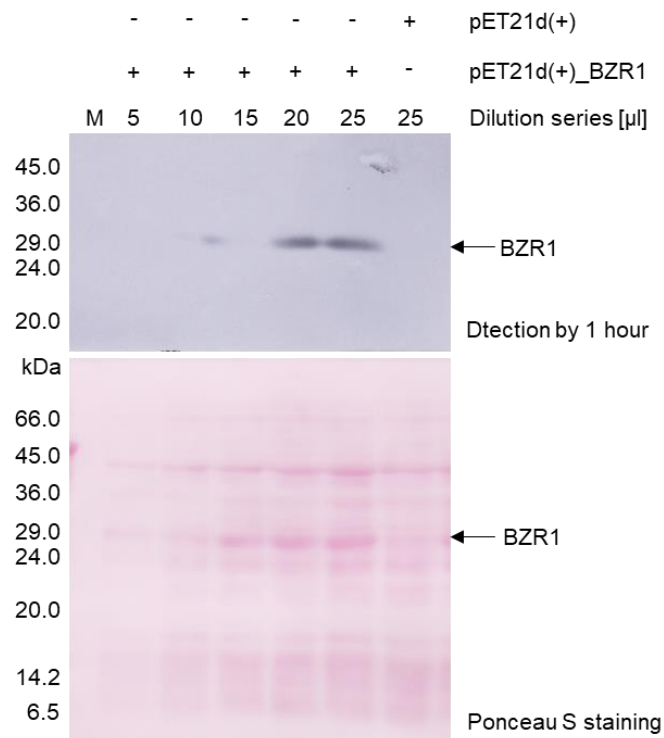
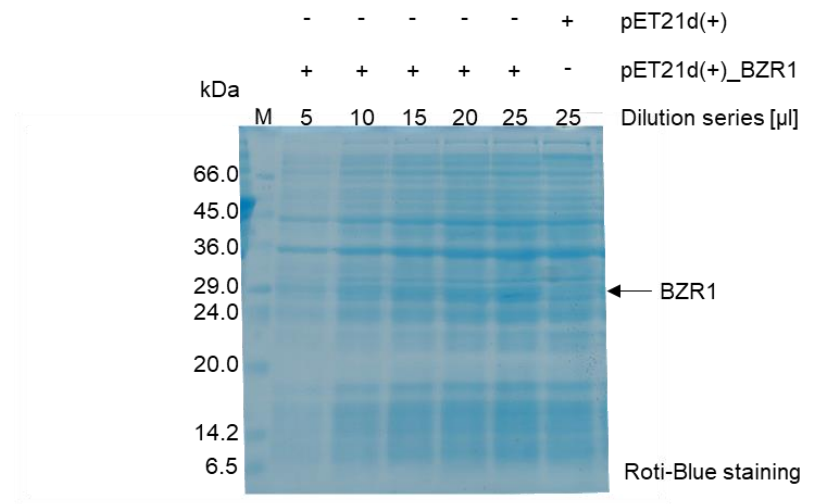
# Supplementary Material



**Figure S1.** The amino acid sequence of *HvBZR1* (BAJ85589.1) and *OsBZR1* (Q7XI96) contains DNA binding domain (green line), 14-3-3 binding domain (brown line), PEST domain (yellow line), and EAR motif (blue line). The red asterisk indicates serine and threonine residues which are phosphorylated in *Arabidopsis thaliana* and *Oryza sativa* (21 sites), the black asterisk indicates other serine and threonine residues which are phosphorylated in *O. sativa* (7 sites). The black background marks regions that are similar between *A. thaliana*, *O. sativa*, and *H. vulgare*.

<i>OsBZR1</i>	ATGACGTCCGGGGCGGCG--GCGGCG-----	18
<i>HvBZR1</i>	ATGACGTCCGGGGCTGCCGGGCGGCGGCGGCGGCGGCTGCGGAGGCGGACGCC	60
	***** ** *	
<i>OsBZR1</i>	-----GGGAGGACGCCGACGTGGAAGGAGAGGAGAGACAACAAGAGGCGGGAGCGGCGG	78
<i>HvBZR1</i>	GGGCTGGGGCGGACGCCGACGTGGAAGGAGCGGGAGACAACAAGCGCGCGAGCGGCGG	120
	*** *****	
<i>OsBZR1</i>	CGGCGTGCCATCGCCGCCAAGATCTTACGCGGCTCCGGGCGCTCGGGAACTACAACCTC	138
<i>HvBZR1</i>	CGCCGGGCCATCGCCGCCAAGATCTTACCGGCTCCGCGCGCTCGGCAACTACAAGCTC	180
	** ** ***** *	
<i>OsBZR1</i>	CCCAAGCACTGCGACAACAACGAGGTGCTCAAGGCGCTCTGCCGCGAGGCCGGCTGGGTT	198
<i>HvBZR1</i>	CCCAAGCACTGCGACAACAACGAGGTGCTCAAGGAGCTCTGCCGCGAGGCCGGATGGGTA	240
	*****	
<i>OsBZR1</i>	GTCGAGGACGACGGCACCACCTACCGCAAGGGATGTAAGCCGCGCCATCGT-----CG	252
<i>HvBZR1</i>	GTGGAGGACGACGGCACCACCTACCGCAAGGGATACAAGCCGCGCTCGTCCGGGCCGTTC	300
	** ***** *	
<i>OsBZR1</i>	GCTGGGGGAGCGTCGGTGGGGATGAGCCCTGCTCGTCAACGCAGCTGCTGAGCGCGCCG	312
<i>HvBZR1</i>	GGTGGGTCTCTCGGCGGGCATGAGCCCTGCTCGTCTCGAGCTGCTCAGCGCGCCG	360
	* *****	
<i>OsBZR1</i>	TCGTCTGCTGTTCCCGAGCCCGGTGCGCTGCTACACGCGAGCCGCGCTCGTCGAGCTTC	372
<i>HvBZR1</i>	TCGTCTGCTGTTCCCGAGCCCGGTGCTTCTTCTACACGCGAGCCGCGCTCGTCGAGCTTC	420
	***** *	
<i>OsBZR1</i>	CCGAGCCCCAGCCGGATCGACAACCCGAGCGCTCCTGCTCCTCCCGTTCTCCGGGGG	432
<i>HvBZR1</i>	CCGAGCCCCACGCGCCTCGACAACCCGAGCCCGCTGCTCCTCCCGTTCTCCGTGGC	480
	***** ** ***** *	
<i>OsBZR1</i>	CTCCCCAACCTCCCGCCGCTCCGCGTCTCCAGCAGCGCGCCGTCACGCCGCCGCTCTCG	492
<i>HvBZR1</i>	CTCCCCAACCTGCCCCGCTCCGGGTCTCCAACAGCGCGCCAGTGACGCCGCCGCTCTCG	540
	***** ** ***** *	
<i>OsBZR1</i>	TCGCCGACGGCGTCGCGCCGCCAAGATCAGGAAGCCGACTGGGACGTCGACCCGTTTC	552
<i>HvBZR1</i>	TCGCCGACGGCGTCGCGCCGCCAAGATCCTGAAGCCGACTGGGAGGTCGACCCGTTTC	600
	***** *****	
<i>OsBZR1</i>	CGGCACCCCTTCTTCGCGGTCTCCGCGCGGCGAGCCCCACCCGCGGCGCGCCTCGAG	612
<i>HvBZR1</i>	CGGCACCCGTTCTTCGCGCTCTCCGCGCGGCGAGCCCCACCCGTGGCGCGGCGACGAG	660
	***** ***** *	
<i>OsBZR1</i>	CACCCGGACACGATACCGGAGTGCAGCAGTCCGACGTCTCCACGGTGGACTCCGGCCGG	672
<i>HvBZR1</i>	CATCCGACACGATACCGGAGTGCAGCAGTCCGACGTCTCCACGGTGGACTCTGGCCGG	720
	** *****	
<i>OsBZR1</i>	TGGATCAGCTTCCAGATGGCCACGACGCGCCGACGTGCGCCACCTACAACCTCGTCAAC	732
<i>HvBZR1</i>	TGGATCAGCTTCCAGATGGCCACGACGCGCCGACGTCCCGCGGTACAACCTCGTCAAC	780
	***** *** *	
<i>OsBZR1</i>	CCGGGCGCCTCCACCTCCAATCCATGGAGATAGAAGGGACGG-----CCGGCCGA	783
<i>HvBZR1</i>	CTAGGCGCTCCAGCTCAAATCCATGGAGATGGAGGAATGGCGGGGAGAGGGCCGA	840
	* ***** ** *	
<i>OsBZR1</i>	GGCGGCGCGGAGTTCGAGTTCGACAAGGGGAGGTTGACGCCATGGGAGGGCGAGAGGATC	843
<i>HvBZR1</i>	GGCGGCGCGGAATTCGAGTTCGACAAGGGGAGGTTGACGCCATGGGAAGGGGAAGGATC	900
	***** *****	
<i>OsBZR1</i>	CACGAGGTCGCCCGGAGGAGCTCGAGCTACGCTCGGCGTCGGCGCGAAATGA	897
<i>HvBZR1</i>	CATGAGTCGCCCGGAGGAGCTTGAGCTACGCTCGGCGTCGGCTCAAATGA	954
	** ***** *	

**Figure S2.** Alignment of the full-length coding sequences of the BZR1 gene for rice (*OsBZR1*, Os07t0580500-01) and barley (*HvBZR1*, AK354370). Asterisk indicates the same nucleotides between plant species.



**Figure S3.** Results of Roti-Blue (Roth) staining of polyacrylamide gel after SDS-PAGE. Results of dilution series *E. coli* BL21(DE3) cell lysate with recombinant protein of *HvBZR1* (pET21d(+)\_BZR1) compared to control (pET21d(+)\_empty). M, Sigma Marker wide range, Molecular Weight 6.5-200.0 in kDa (Sigma); red arrow, amplicon about appropriate length.

**Table S1.** List of primers used in Real-Time PCR.

Gen Name	Orientation	5'–3' Sequence	Data Base ID	Literature
<i>HvDWF4</i>	Forward	CATCTCCTTGCCCCATCAATC	NCBI GenBank: DQ832258	Gruszka et al.2011
	Reverse	ATCGAAGTCGTGGACATGGT		
<i>HvBAK1</i>	Forward	TGCTGCCTTGCTATTTGCTA	NCBI GenBank: EF216861	Gruszka et al.2011
	Reverse	CTTGCCAAATCCACCTCTTC		
<i>HvBRI1</i>	Forward	GTCTCTGTCAAGCATTCCCCG	NCBI GenBank: AB088206	not published
	Reverse	AGCTTCCCAAGCCACGA		
<i>HvBSU1</i>	Forward	TGGCATCGCGTGAATAGGTT	NCBI GenBank: AK375108.1	not published
	Reverse	AACAACCTGAGCCTGCTTCCA		
<i>HvGSK1.1</i>	Forward	CCCTTCTTTGATGAGCTTCG	Ensemble Plants: HORVU3Hr1G034440.2	Groszyk et. al.2018
	Reverse	CAGGGGAAATGCTCACTTGT		
<i>HvGSK1.2</i>	Forward	TCTGGGCACACCTACAAGGG	Ensemble Plants: HORVU5Hr1G117030.1	Groszyk et. al.2018
	Reverse	TGGAGACCAGGTCCACTGCT		
<i>HvGSK1.3</i>	Forward	ACGAGATGGGCAATATGAG	Ensemble Plants: HORVU1Hr1G016490.9	Groszyk et. al.2018
	Reverse	GTTCCAAATGACCCATGACC		
<i>HvGSK2.1</i>	Forward	AGTGCTTGGGAGACTGGAGAGAC	Ensemble Plants: HORVU3Hr1G026020.1	Groszyk et. al.2018
	Reverse	GTGCTTCAGAGAGACGACATTG		
<i>HvGSK2.2</i>	Forward	CACCAACTCGGGAGGAAATA	Ensemble Plants: MLOC_68311.2	Groszyk et. al.2018
	Reverse	GCTCCCGTAGCTCATCAAAG		
<i>HvGSK3.1</i>	Forward	AAAGTGGCGTTGATCAGTTGG	Ensemble Plants: HORVU1Hr1G048580.7	Groszyk et. al.2018
	Reverse	CAGGGATGAGCTTTTATCTGAGG		
<i>HvGSK4.1</i>	Forward	GCGAGAAGGCAGAACCTGTT	Ensemble Plants: HORVU5Hr1G119790.18	Groszyk et. al.2018
	Reverse	TGTCACCCACCCACACAAAG		
<i>HvBZR1</i>	Forward	CCCGTTCTTCGCCCTCTC	NCBI GenBank: AJ508228	not published
	Reverse	ATCTGGAAGCTGATCCACCG		
<i>HvGAPDH</i>	Forward	TCAAGCAAGGACTGGAGAGG	NCBI GenBank: X60343	Gruszka et al.2011
	Reverse	ACACATCCACAGTGGGAACC		
<i>HvARF</i>	Forward	GCTCTCCAACAACATTGCCAAC	NCBI GenBank: AJ508228	Groszyk et. al.2018
	Reverse	GCTTCTGCCTGTACATACGC		
Groszyk J, Yanushevskaya Y, Zielezinski A, Nadolska-Orczyk A, Karlowski WM, Orczyk W (2018) Annotation and pro- filing of barley GLYCOGEN SYNTHASE3/Shaggy-like genes indicated shift in organ-preferential expression. PLoS One 13(6): e0199364				
Gruszka D, Szarejko I, Maluszynski M (2011) Identification of barley DWARF gene involved in brassinosteroid syn- thesis. Plant Growth Regulation 65(2): 343-358				