

Supplementary

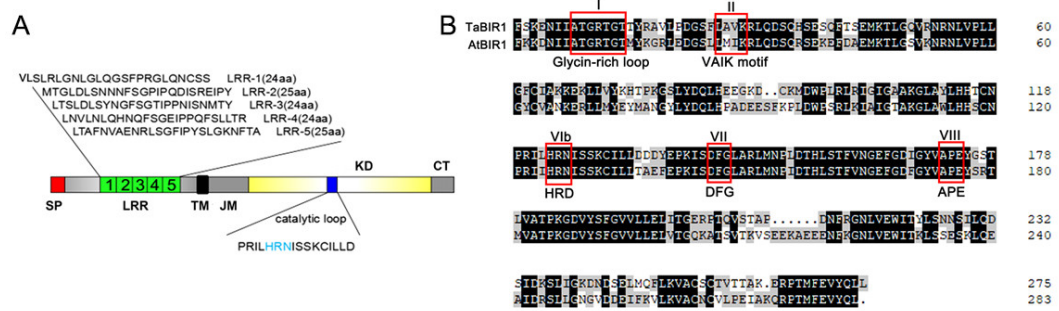


Figure S1. Bioinformatics analysis and sequence alignment for *TaBIR1*. (A) Schematic diagram of *TaBIR1* protein. SP, signal peptide; LRR, leucine-rich repeat motif; TM, transmembrane domain; JM, juxtamembrane domain; KD, kinase domain; CT, carboxyl-terminal. (B) Multiple alignment of intracellular kinase domains of *TaBIR1* and its homologue *AtBIR1* in Arabidopsis. The conserved subdomains were marked in red boxes.

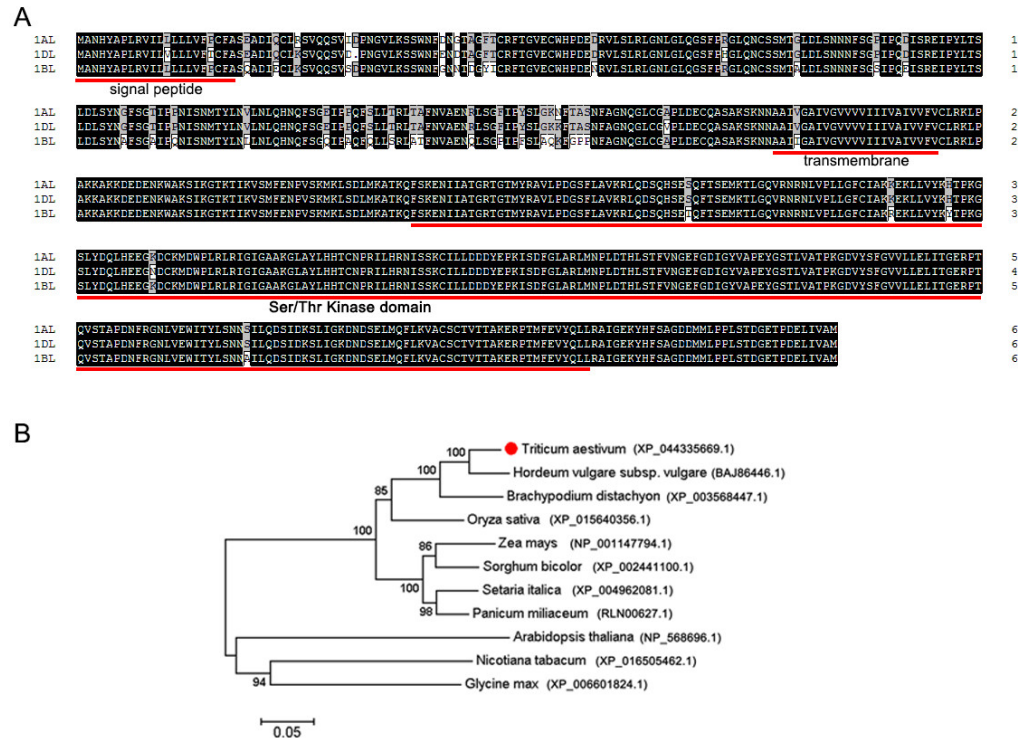


Figure S2. (A) Protein sequences alignment of the three homeologues of *TaBIR1* from wheat A/B/D subgenomes. The red lines indicated the signal peptide, transmembrane

domain and cytoplasmic serine/threonine kinase domain of TaBIR1. (B) Phylogenetic relationship of TaBIR1 and the homologous proteins. The tree was carried out with the MEGA7 software by the neighbour-joining method.

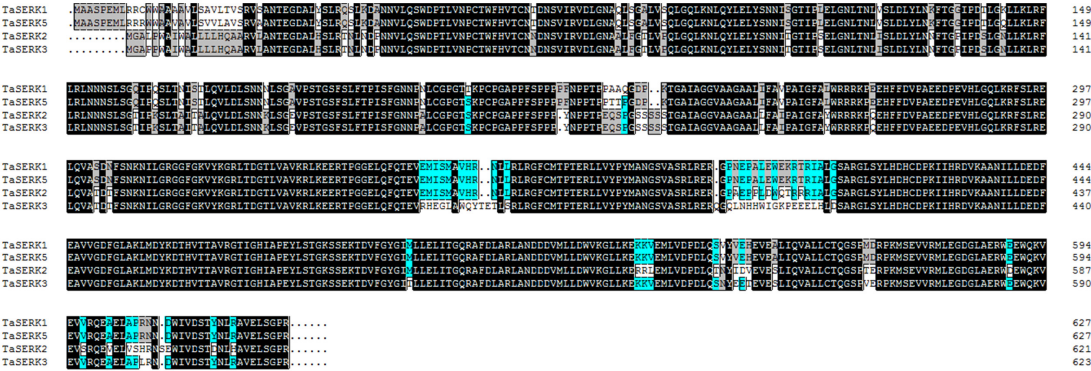


Figure S3. Sequences alignment of four wheat TaSERKs. The reference sequences were retrieved from Accession no. AK333001(*TaSERK1*); Accession no. AK333677.1(*TaSERK2*) ; Accession no. BT009223(*TaSERK3*); Accession no. BT009426 (*TaSERK5*) in NCBI database followed by a cDNA clone in wheat variety Su11. The protein sequences alignment were achieved by DNAMAN6.0 software.

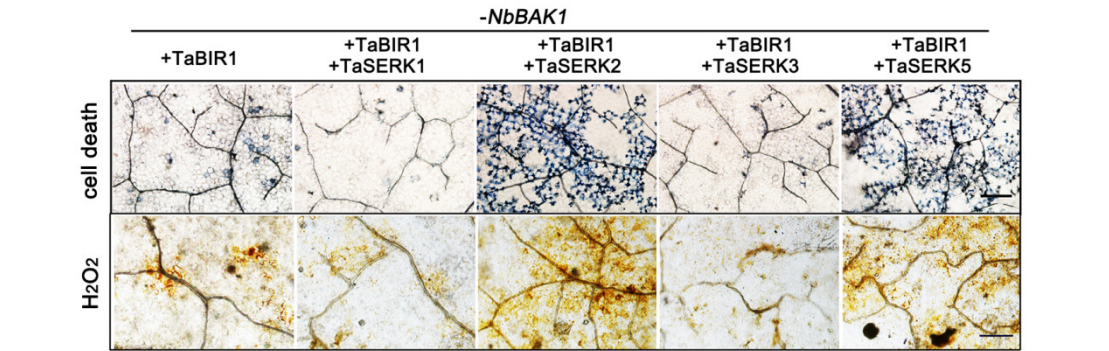


Figure S4. ROS accumulation and cell death in *NbBAK1* silencing plant leaves coexpressing TaBIR1 and TaSERKs. Two weeks after inoculation of TRV2:*NbBAK1*, *TaSERKs* and *TaBIR1* were co-expressed in the corresponding plant leaves. Forty-eight hours later, the leaves were collected for trypan blue staining and DAB staining for observations of cell death and H₂O₂. Similar results were obtained in three independent experiments. Bars, 100 μm.

Table S1. Primers used in this study.

Primer name	Sequence(5'-3')	Purpose
TaBIR1-qRT-F	GTAATCAAGGGCTATGTGG	qRT-PCR analysis in

TaBIR1-qRT-R	TCCTTTTTTGCTTTCTTGGC	wheat (also for VIGS efficiency)
TaBIR1(VI GS-1)- γ -F	TTAGCTAGCTGATTAATTAATCAGCAGTCAGTGAT TGACCC	vectors construction for wheat VIGS
TaBIR1(VI GS-1)- γ -R	TCCGTTGCTAGCTGAGCGGCCGCTACAATTCTGA AGACCGCGA	
TaBIR1(VI GS-2)- γ -F	TTAGCTAGCTGATTAATTAATCATTCTCGGCCGG GGACG	
TaBIR1(VI GS-2)- γ -R	TCCGTTGCTAGCTGAGCGGCCGCTGCAGCGTACC GCTACTCCAC	
GFP-VIGS- γ -F	TTAGCTAGCTGATTAATTAATGATATAGACGTTGT GGCTGTTGT	
GFP-VIGS- γ -R	TCCGTTGCTAGCTGAGCGGCCGCGACGACGACTTC TTCAAGTCCGCCAT	
qRT-TaEF-F	TGGTGTCATCAAGCCTGGTATGGT	qRT-PCR analysis of PTI genes in wheat VIGS
qRT-TaEF-R	ACTCATGGTGCATCTCAACGGACT	
qRT-PsEF-F	TTCGCCGTCCGTGATATGAGACAA	
qRT-PsEF-R	ATGCGTATCATGGTGGTGGAGTGA	
qRT-TaPR1-F	AAACAACATCCATCAAAACCA	
qRT-TaPR1-R	ATTACCAGGTGGATCATAGTTACA	
qRT-TaPR2-F	AGGATGTTGCTTCCATGTTTGCCG	
qRT-TaPR2-R	AAGTAGATGCCCATGCCGTTGATG	
Biomass-PstEF-F	TTCGCCGTCCGTGATATGAGACAA	Biomass detection in wheat VIGS
Biomass-PstEF-R	ATGCGTATCATGGTGGTGGAGTGA	
Biomass-WheatEF-F	TGACCAGATCAACGAGCC	
Biomass-WheatEF-R	CTCCAGGAGAGACTCATG	
TaBIR1full - 16318GFP	AGAGGACAGCCCAAGCTTATGGCAAATCATTATG CTCCT	vector construction for subcellular

-F		localization in wheat
TaBIR1full - 16318GFP -R	GCCCTTGCTCACCATGGATCCCATGGCGACAATG AGCTC	
TaBIR1full - pCAMBI A1302GFP -F	CATGGTAGATCTGACTAGTATGGCAAATCATTATG CTCCT	vector construction for subcellular localization in <i>N. benthamiana</i>
TaBIR1full - pCAMBI A1302GFP -R	GCCCTTGCTCACCATCCTAGGCATGGCGACAATG AGCT	
TaBIR1- GFP-F	CTGTACAAGGGTACCCCCGGGATGGCAAATCATT ATGCTCCT	vectors construction for TaBIR1 overexpression in <i>N. benthamiana</i>
TaBIR1- GFP-R	TCTAGTTCATCTAGAGGATCCTTACATGGCGACAA TGAGCT	
qRT- NbActin-F	TGGTCGTACCACCGGTATTGTGTT	qRT-PCR analysis of PTI gene in <i>N. benthamiana</i>
qRT- NbActin- R	TCACTTGCCCATCAGGAAGCTCAT	
qRT- NbPR1-F	CCGCCTTCCCTCAACTCAAC	
qRT- NbPR1-R	GCACAACCAAGACGTACTGAG	
qRT- NbPR2-F	AGGTGTTTGCTATGGAATGC	
qRT- NbPR2-R	TCTGTACCCACCATCTTGC	
TaBIR1full -(LUC-N)- F	AACACGGGGGACGAGCTCGGTACCATGGCAAAT CATTATGCTCCT	vectors construction for interaction of luciferase complementation assay
TaBIR1full -(LUC-N)- R	TCCTTGTAGTCCATTTGTTGGATCCCGCATGGCGA CAATGAGCTC	
TaBIR1full -(LUC-C)- F	AGAGAACACGGGGGACGAGCTCATGGCAAATCA TTATGCTCCT	
TaBIR1full	GTTTACATAACCGGACATGAGCTCCATGGCGACA	

-(LUC-C)- R	ATGAGCTC	
TaSERK1- (LUC-N)- F	AACACGGGGGACGAGCTCGGTACCATGGCTGCGT CGCCGGAGATG	
TaSERK1- (LUC-N)- R	TCCTTG TAGTCCATTTGTTGGATCCCCTCGGGCCG GACAGCT	
TaSERK2- (LUC-N)- F	AACACGGGGGACGAGCTCGGTACCATGGGGGCG CTGCCGTGGG	
TaSERK2- (LUC-N)- R	TCCTTG TAGTCCATTTGTTGGATCCCCTTGGCCCTG ATAGCT	
TaSERK3- (LUC-N)- F	AACACGGGGGACGAGCTCGGTACCATGGGGGCG CCGCCGT	
TaSERK3- (LUC-N)- R	TCCTTG TAGTCCATTTGTTGGATCCTCTTGGGCCAG ACAGTT	
TaSERK5- (LUC-N)- F	AACACGGGGGACGAGCTCGGTACCATGGCTGCGT CGCCGGAGA	
TaSERK5- (LUC-N)- R	TCCTTG TAGTCCATTTGTTGGATCCCCTCGGGCCG GACAGCT	
TaSERK1- ICD(FLA G-HA)- PICH-F	TACAATTATCGATACAATGGATTACAAGGATGACG ACGATAAGCGGCGACGTAAACCTG	vectors construction for Co-IP interaction
TaSERK1- ICD(FLA G-HA)- PICH-R	TAAAGCAGGACAAGCttaAGCGTAGTCTGGGACGT CGTATGGGTACCTCGGGCCCGACA	
TaSERK2- ICD(FLA G-HA)- PICH-F	TACAATTATCGATACAATGGATTACAAGGATGACG ACGATAAGCGCCGCAGGAAACCGC	
TaSERK2- ICD(FLA G-HA)- PICH-R	TAAAGCAGGACAAGCttaAGCGTAGTCTGGGACGT CGTATGGGTACCTTGGCCCTGATA	
TaSERK3- ICD(FLA	TACAATTATCGATACAATGGATTACAAGGATGACG ACGATAAGCGCCGCAGGAAACCGC	

G-HA)- PICH-F		
TaSERK3- ICD(FLA G-HA)- PICH-R	TAAAGCAGGACAAGCttaAGCGTAGTCTGGGACGT CGTATGGGTATCTTGGGCCAGACA	
TaSERK5- ICD(FLA G-HA)- PICH-F	TACAATTATCGATACAATGGATTACAAGGATGACG ACGATAAGCGGCGACGTAAACCTG	
TaSERK5- ICD(FLA G-HA)- PICH-R	TAAAGCAGGACAAGCttaAGCGTAGTCTGGGACGT CGTATGGGTACCTCGGGCCGACA	
TaBIR1- ICD- pBinGFP- F	CTGTACAAGGGTACCCCCGGGATGTGTCTGCGGA AATTACCAGC	
TaBIR1- ICD- pBinGFP- R	TCTAGTTCATCTAGAGGATCCTTACATGGCGACAA TGAGCTC	
TaBIR1full -PICH- HA-F	TTACAATTATCGATACAATGTACCCATACGACGTC CCAGACTACGCTATGGCAAATCATTATGCTCCT	HA-tagged vector construction for TaBIR1 expression of VIGS in <i>N. benthamiana</i>
TaBIR1full -PICH- HA-R	CTCATTAAAGCAGGACAAGCTTACATGGCGACAA TGAGCT	
qRT- NbActin-F	TGGTCGTACCACCGGTATTGTGTT	qRT-PCR analysis of VIGS in <i>N. benthamiana</i>
qRT- NbActin- R	TCACTTGCCCATCAGGAAGCTCAT	
qRT- NbBAK1- F	GAGGTGGGAGGAATGGCAAA	
qRT- NbBAK1- R	TTGGCCCCGACAATTCATCT	
qRT- NbSOBIR 1-F	CCAGCAAGTCACAGAAGGGA	
qRT-	CCAACACCACACCAAAGCTG	

NbSOBIR 1-R		
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