

Supplementary Table S1. Primer used for TaATG8j analysis

<u>Name of Primers</u>	<u>Sequences (5'→3')</u>	<u>Amplified length (bp) /type of Oligonucleotides</u>	<u>Purpose</u>		
M13-F	TGTAAAACGACGGCCAGT	General primer	Checking		
M13-R	CAGGAAACAGCTATGACC				
PVX-F	CAATCACAGTGTGGCTTGC				
PVX-R	GACCCTATGGGCTGTGTTG	General primer	Checking		
pREP3x-S	CAGCGAAACTAAAAACCG	General primer	Checking		
pREP3x-AS	TCTAAAAGCGAAAAACAAAT				
Δ-as-seq-F	AAAGTGAGGTTAACGCAATACG	General primer	Checking		
Δ-as-seq-R	TCAGGCATCGTTTTCAAGTT				
TaATG8j-Clal-F	<u>ggcatcgat</u> ATGGCCAAGACTTGCTTCA	360	Expression in Tobacco		
TaATG8j-Sall-R	<u>catgtcgac</u> TTAGGCAGAGCCGAAAGT	360	Expression in Yeast		
TaATG8j-Sall-F	<u>catgtcgac</u> ATGGCCAAGACTTGCTTCA				
TaATG8j-Smal-R	<u>gtacccggg</u> TTAGGCAGAGCCGAAAGT				
TaATG8j-PB-F	<u>ctgtacaagggtacccccggg</u> ATGGCCAAGACTTGCTTCAA	357	Sub-cellular localization		
TaATG8j-PB-R:	<u>tctagtctcatctagaggatcctta</u> GGCAGAGCCGAAAGTGTT				
pBinGFP2-F	AAGACCCCAACGAGAAGC	General primer	Checking		
pBinGFP2-R	GAACCCCTAATTCCTTATCTG				
TaATG8j-PacI-F1	atattaattaaCTACGTGGTGCGGAAGAGG	104	VIGS-1		
TaATG8j-NotI-R1	tatgcgccgcTCATAGATGGCTGACATCAAC				
TaATG8j-PacI-F2	atattaattaaTCTGCCTAATCCATGTGCG	101	VIGS-2		
TaATG8j-NotI-R2	tatgcgccgcTGTGAGCAATCCACCAGCA				
TaATG8j-2AS: QT-F	CCATCTTCGTCTTTGTGAATAGC	177			
TaATG8j-2AS: QT-R	GCAACCTGAACATCCATTTATTT				
TaATG8j-2BS: QT-F	AATCTCGTCCCAGGCTGCG	167			
TaATG8j-2BS: QT-R	GAGGTGCGCAGGGACAAGG				
TaATG8j-2DS: QT-F	AACACTTTCGGCTCCGC	199			
TaATG8j-2DS: QT-R	TCTTATCTATTACTCTCGTCTGGTT				
TaEF-qRT-F	TGGTGTCAATCAAGCTTGGTATGGT	General primer			
TaEF-qRT-R	ACTCATGGTGCATCTCAACGGACT				
biomass-PstEF-F	TTCGCCGTCCGTGATATGAGACAA	General primer		Biomass assay	
biomass-PstEF-R	ATGCGTATCATGGTGGTGGAGTGA				
biomass-WEF-F	TGACCAGATCAACGAGCC	General primer			
biomass-WEF-R	CTCCAGGAGAGACTCATG				
TaPR1-S	GAGAATGCAGACGCCCAAGC	General primer		Pathogenesis Related	
TaPR1-AS	CTGGAGCTTGCACTCGTTGATC				
TaPR2-S	AGGATGTTGCTTCCATGTTTGCCG	General primer			
TaPR2-AS	AAGTAGATGCGCATGCCGTTGATG				
TaSOD-S	CCGAGGTCTGGAACCATCAC	General primer			
TaSOD-AS	AGCCGAAATCCTTCTCGATCT				

*The Uppercase letters indicate bases that match the initial template. Lowercase letters which are underlined in 5' extensions that indicates the restriction sites.

TaATG8j-2AS	GT GGCCT AT AGAGT TGT GCACGCAAT ACAACT AGACCCCAAGGGGT ACGGCAT AAGATT	0
TaATG8j-2BS		100
TaATG8j-2DS		41
TaATG8j-cDNA		0
TaATG8j-2AS		76
TaATG8j-2BS		199
TaATG8j-2DS		139
TaATG8j-cDNA		58
TaATG8j-2AS		176
TaATG8j-2BS		219
TaATG8j-2DS		219
TaATG8j-cDNA		138
TaATG8j-2AS		276
TaATG8j-2BS		319
TaATG8j-2DS		319
TaATG8j-cDNA		238
TaATG8j-2AS		376
TaATG8j-2BS		479
TaATG8j-2DS		419
TaATG8j-cDNA		338
TaATG8j-2AS		476
TaATG8j-2BS		579
TaATG8j-2DS		519
TaATG8j-cDNA		438
TaATG8j-2AS		570
TaATG8j-2BS		677
TaATG8j-2DS		616
TaATG8j-cDNA		534
TaATG8j-2AS		669
TaATG8j-2BS		759
TaATG8j-2DS		700
TaATG8j-cDNA		634
TaATG8j-2AS		731
TaATG8j-2BS		784
TaATG8j-2DS		800
TaATG8j-cDNA		695
TaATG8j-2AS		731
TaATG8j-2BS		784
TaATG8j-2DS		812
TaATG8j-cDNA		695

Figure S1. Alignment of the three subgenomic copies of *TaATG8j*, *TaATG8j* cDNA, the full-length cDNA sequence, was aligned from the wheat cultivar cv. Su11. The other cDNA sequences (*TaATG8j*-2AS, *TaATG8j*-2BS and *TaATG8j*-2DS) of *TaATG8j* were obtained from the Chinese Spring URGI genome database. The purple and red boxes indicate the start codon (ATG) and stop codon (TAA), respectively. Identical nucleotides are in black.

TaATG8j-2AS	MAKT	CFKTEHPLERRQAES	ARI	REKYADRI	PVI	VEKADKS	DVPEI	DKKKYL	VPADL	TVGQ	60
TaATG8j-2BS	MAKT	CFKTEHPLERRQAES	ARI	REKYADRI	PVI	VEKADKS	DVPEI	DKKKYL	VPADL	TVGQ	60
TaATG8j-2DS	MAKT	CFKTEHPLERRQAES	ARI	REKYADRI	PVI	VEKADKS	DVPEI	DKKKYL	VPADL	TVGQ	60
TaATG8j-cDNA	MAKT	CFKTEHPLERRQAES	ARI	REKYADRI	PVI	VEKADKS	DVPEI	DKKKYL	VPADL	TVGQ	60
TaATG8j-2AS	FVYVVRKRI	KLSPEKAI	FVFVNS	TLPTASLMS	AI	YEENKDEDGFL	YMTYS	GENTFGS	A		119
TaATG8j-2BS	FVYVVRKRI	KLSPEKAI	FVFVNS	TLPTASLMS	AI	YEENKDEDGFL	YMTYS	GENTFGS	A		119
TaATG8j-2DS	FVYVVRKRI	KLSPEKAI	FVFVNS	TLPTASLMS	AI	YEENKDEDGFL	YMTYS	GENTFGS	A		119
TaATG8j-cDNA	FVYVVRKRI	KLSPEKAI	FVFVNS	TLPTASLMS	AI	YEENKDEDGFL	YMTYS	GENTFGS	A		119

Figure S2. Multiple alignment of the TaATG8j proteins of wheat cv. Su 11 with three copies of the Chinese Spring Wheat Genomic Database. Identical amino acid residues are in black.

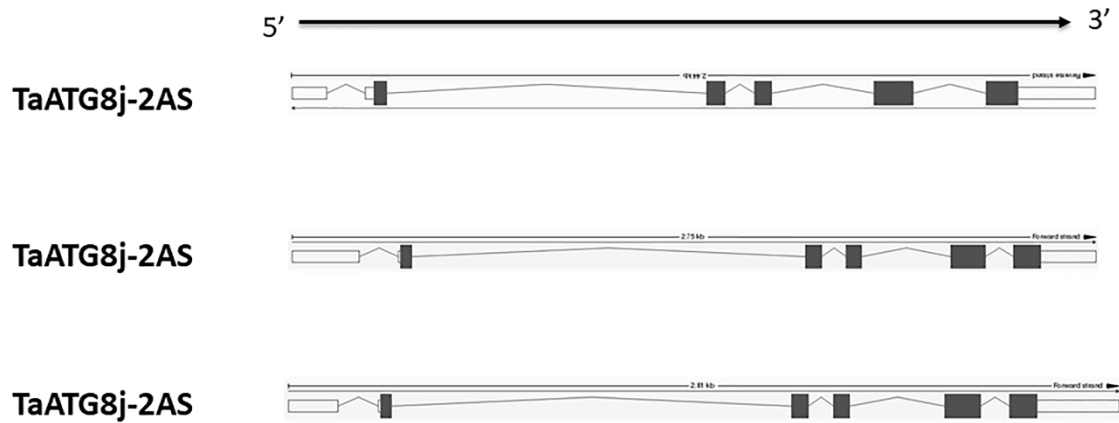


Figure S3. Diagram showing the three subgenomic copies of *TaATG8j* from the wheat cv. Chinese Spring URGI genome database. Solid rectangles indicate exons, and zigzags indicate introns. The lengths of the three copies were *TaATG8j*-2AS, 2.44 kb; *TaATG8j*-2BS, 2.75 kb; and *TaATG8j*-2DS, 2.81 kb.

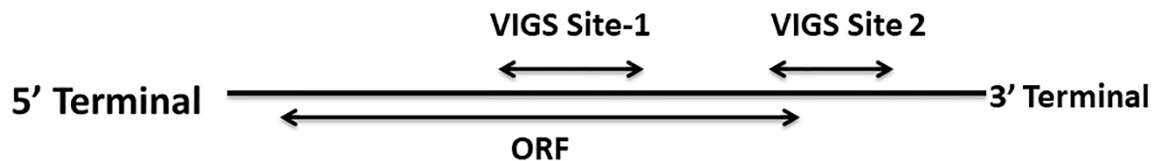


Figure S4. Virus-induced gene silencing fragments. Two fragments were considered from the open reading frame (ORF) and the ORF plus the 3' noncoding region of the *TaATG8j* gene for specific knockdown. ORF: open reading frame. VIGS Site -1: *TaATG8j* -1s. VIGS Site -2: *TaATG8j* -2s.