

Supplementary Table S1. Primer used for TaATG8j analysis

Name of Primers	Sequences (5'→3')	Amplified length (bp) /type of Oligonucleotides	Purpose
M13-F	TGTAAAACGACGGCCAGT		
M13-R	CAGGAAACAGCTATGACC		General primer Checking
PVX-F	CAATCACAGTGGCTTGCG		
PVX-R	GACCCATGGGCTGTGTTG		General primer Checking
pREP3x-S	CAGCGAAACTAAAAACCG		
pREP3x-AS	TCTAAAAGCGAAAAACAAAT		General primer Checking
Δ-as-seq-F	AAAGT GAGGTTAACGCAATACG		
Δ-as-seq-R	TCAGGCATCGTTTCAAGTT		General primer Checking
TaATG8j-ClaI-F	<u>ggcatcgat</u> ATGGCCAAGACTTGCTTCA		
TaATG8j-SalI-R	<u>catgtcgac</u> TTAGGCAGAGCCGAAAGT	360	Expression in Tobacco
TaATG8j-SalI-F	<u>catgtcgac</u> ATGGCCAAGACTTGCTTCA		
TaATG8j-SmaI-R	<u>gtacccggg</u> TTAGGCAGAGCCGAAAGT	360	Expression in Yeast
TaATG8j-PB-F	<u>ctgtacaagggtaccccccggg</u> ATGGCCAAGACTTGCTTCAA		
TaATG8j-PB-R:	<u>tctagttcacatcagaggatccctt</u> GGCAGAGCCGAAAGTGTT	357	Sub-cellular localization
pBinGFP2-F	AAGACCCCAACGAGAAGC		
pBinGFP2-R	GAACCTTAATTCCCTTATCTG		General primer Checking
TaATG8j-PacI-F1	<u>atattaattaa</u> CTACGTGGTGCAGGAAGAGG		
TaATG8j-NotI-R1	<u>tatgcggccgc</u> TCATAGATGGCTGACATCAAC	104	VIGS-1
TaATG8j-PacI-F2	<u>atattaattaa</u> TCTGCCTAATCCATGTGCG		
TaATG8j-NotI-R2	<u>tatgcggccgc</u> TGTGAGCAATCCACCAGCA	101	
TaATG8j-2AS: QT-F	CCATCTCGTCTTGTGAATAGC		
TaATG8j-2AS: QT-R	GCAACCTGAACATCCATTATT	177	
TaATG8j-2BS: QT-F	AATCTCGTCCCAGGCTGCG		
TaATG8j-2BS: QT-R	GAGGTCGGCAGGGACAAGG	167	
TaATG8j-2DS: QT-F	AACACTTTGGCTCCGC		
TaATG8j-2DS: QT-R	TCTTATCTATTACTCTCGTCTGGTT	199	
TaEF-qRT-F	TGGTGTCACTCAAGCCTGGTATGGT		
TaEF-qRT-R	ACTCATGGTGCATCTCAACGGACT		General primer
biomass-PstEF-F	TTCGCCGTCCGTGATATGAGACAA		
biomass-PstEF-R	ATGCGTATCATGGTGGTGGAGTGA		General primer
biomass-WEF-F	TGACCAAGATCAACGAGGCC		
biomass-WEF-R	CTCCAGGAGAGACTCATG		General primer
TaPR1-S	GAGAATGCAGACGCCAAGC		
TaPR1-AS	CTGGAGCTTGCAGTCGTTGATC		General primer
TaPR2-S	AGGATGTTGCTTCCATGTTGCCG		
TaPR2-AS	AAGTAGATGCGCATGCCGTTGATG		General primer
TaSOD-S	CCGAGGTCTGGAACCACATCAC		
TaSOD-AS	AGCCGAAATCCTTCTCGATCT		General primer

*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 GCCCT AT AGAGT TGT GCAC GCAAT ACAACT AGACCCC AAGGGGT AC GGCAT AAGATT	CCCCACAGG	AAGGT CCT CTT AAAT AGCC CGACACGCCAC	0	
TaATG8j-2BS		CCCCACAGG	AAGGT CCT CTT AAAT AGCC CGACACGCCAC	100	
TaATG8j-2DS		CCCCACAGG	AAGGT CCT CTT AAAT AGCC CGACACGCCAC	41	
TaATG8j- <i>c</i> DNA				0	
TaATG8j-2AS	TCACCAACAAACCCCTACCCCGGACTTCCCTCGGGTGGCGACTTCCCAATCCAGTC	CCCTCGATTCCGCCGGCCGATGCCCTCGAT	76		
TaATG8j-2BS	TCACCAACAAACCCCTACCCCGGACTTCCCTCGGGTGGCGACTTCCCAATCCAGTC	CCCTCGATTCCGCCGGCCGATGCCCTCGAT	139		
TaATG8j-2DS	TCACCAACAAACCCCTACCCCGGACTTCCCTCGGGTGGCGACTTCCCAATCCAGTC	CCCTCGATTCCGCCGGCCGATGCCCTCGAT	138		
TaATG8j- <i>c</i> DNA	TCACCAACAAACCCCTACCCCGGACTTCCCTCGGGTGGCGACTTCCCAATCCAGTC	CCCTCGATTCCGCCGGCCGATGCCCTCGAT	138		
TaATG8j-2AS	CAATCTCGTCCC[GCTGCGCCCT]CCGTC GAT T GT T CCATCGATCGA	GGTTGGAA	ATG	176	
TaATG8j-2BS	CAATCTCGTCCC[GCTGCGCCCT]CCGTC	GGTTGGAA	ATG	279	
TaATG8j-2DS	CAATCTCGTCCC[GCTGCGCCCT]CCGTC	GGTTGGAA	ATG	219	
TaATG8j- <i>c</i> DNA	CAATCTCGTCCC[GCTGCGCCCT]CCGTC	GGTTGGAA	ATG	138	
TaATG8j-2AS	AGGCAAGCTGAATCTGCTAGGATCCGTGAGAAAT	GCTGACAGAAATCCGGT	GATCGT	276	
TaATG8j-2BS	AGGCAAGCTGAATCTGCTAGGATCCGTGAGAAAT	GCTGACAGAAATCCGGT	GATCGT	379	
TaATG8j-2DS	AGGCAAGCTGAATCTGCTAGGATCCGTGAGAAAT	GCTGACAGAAATCCGGT	GATCGT	319	
TaATG8j- <i>c</i> DNA	AGGCAAGCTGAATCTGCTAGGATCCGTGAGAAAT	GCTGACAGAAATCCGGT	GATCGT	238	
TaATG8j-2AS	AGAAAGTA[CTTGTCCC[GCCGACCTC]ACTGTGGCCAGTTCCTCTCGCTTCTTG	AGCTACG	CTTGT	376	
TaATG8j-2BS	AGAAAGTA[CTTGTCCC[GCCGACCTC]ACTGTGGCCAGTTCCTCTCGCTTCTTG	AGCTACG	CTTGT	479	
TaATG8j-2DS	AGAAAGTA[CTTGTCCC[GCCGACCTC]ACTGTGGCCAGTTCCTCTCGCTTCTTG	AGCTACG	CTTGT	419	
TaATG8j- <i>c</i> DNA	AGAAAGTA[CTTGTCCC[GCCGACCTC]ACTGTGGCCAGTTCCTCTCGCTTCTTG	AGCTACG	CTTGT	338	
TaATG8j-2AS	GAATAGCACCTTGCCACCGACTGCTTCGTTGATGTCAGG	CATCT	GAAGAAAACAAGGACGAGGACGGCTT	CTCTGACATGACTTACA	476
TaATG8j-2BS	GAATAGCACCTTGCCACCGACTGCTTCGTTGATGTCAGG	CATCT	GAAGAAAACAAGGACGAGGACGGCTT	CTCTGACATGACTTACA	579
TaATG8j-2DS	GAATAGCACCTTGCCACCGACTGCTTCGTTGATGTCAGG	CATCT	GAAGAAAACAAGGACGAGGACGGCTT	CTCTGACATGACTTACA	519
TaATG8j- <i>c</i> DNA	GAATAGCACCTTGCCACCGACTGCTTCGTTGATGTCAGG	CATCT	GAAGAAAACAAGGACGAGGACGGCTT	CTCTGACATGACTTACA	438
TaATG8j-2AS	ACTTTCGGCTC[GCGTAA]CCATGTGCGCTGCCACTGTAAATAAAT	GGATGTTCAAGGT	TGCGACGTCTGT	ATGATCAT	570
TaATG8j-2BS	ACTTTCGGCTC[GCGTAA]CCATGTGCGCTGCCACTGTAAATAAAT	GGATGTTCAAGGT	TGCGACGTCTGT	ATGATCAT	677
TaATG8j-2DS	ACTTTCGGCTC[GCGTAA]CCATGTGCGCTGCCACTGTAAATAAAT	GGATGTTCAAGGT	TGCGACGTCTGT	ATGATCAT	616
TaATG8j- <i>c</i> DNA	ACTTTCGGCTC[GCGTAA]CCATGTGCGCTGCCACTGTAAATAAAT	GGATGTTCAAGGT	TGCGACGTCTGT	ATGATCAT	534
TaATG8j-2AS	3TGGATTGCGT[CGCTTAA]CATGGTTAATGC	TTTAAGTGTGGT	ATTTATCATCTGAATGTT	AGAACGGCCTGTAAAAC	669
TaATG8j-2BS	3TGGATTGCGT[CGCTTAA]CATGGTTAATGC	TTTAAGTGTGGT	ATTTATCATCTGAATGTT	AGAACGGCCTGTAAAAC	759
TaATG8j-2DS	3TGGATTGCGT[CGCTTAA]CATGGTTAATGC	TTTAAGTGTGGT	ATTTATCATCTGAATGTT	AGAACGGCCTGTAAAAC	700
TaATG8j- <i>c</i> DNA	3TGGATTGCGT[CGCTTAA]CATGGTTAATGC	TTTAAGTGTGGT	ATTTATCATCTGAATGTT	AGAACGGCCTGTAAAAC	694
TaATG8j-2AS	[AT]TCTCGCTCGTTAATGCTCTCATGCTCCTGGGATGTTCAATCGCAAATTA	GGCGAG			731
TaATG8j-2BS	[AT]TCTCGCTCGTTAATGCTCTCATGCTCCTGGGATGTTCAATCGCAAATTA	GGCGAG			784
TaATG8j-2DS	[AT]TCTCGCTCGTTAATGCTCTCATGCTCCTGGGATGTTCAATCGCAAATTA	GGCGAG			800
TaATG8j- <i>c</i> DNA	[AT]TCTCGCTCGTTAATGCTCTCATGCTCCTGGGATGTTCAATCGCAAATTA	GGCGAG			695
TaATG8j-2AS				731
TaATG8j-2BS	CCTTGTCCTTT				784
TaATG8j-2DS				812
TaATG8j- <i>c</i> DNA				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 URG1 genome database. The purple and red boxes indicate the start codon (ATG) and stop codon (TAA), respectively. Identical nucleotides are in black.

TaATG8j-2AS	VAKTCFKTEHPLERRQAES ARI REKYADRI PVI VEKADKS DVPEI DKKKYL VP ADLT VGQ	60
TaATG8j-2BS	MAKTCFKTEHPLERRQAES ARI REKYADRI PVI VEKADKS DVPEI DKKKYL VP ADLT VGQ	60
TaATG8j-2DS	VAKTCFKTEHPLERRQAES ARI REKYADRI PVI VEKADKS DVPEI DKKKYL VP ADLT VGQ	60
TaATG8j-cDNA	VAKTCFKTEHPLERRQAES ARI REKYADRI PVI VEKADKS DVPEI DKKKYL VP ADLT VGQ	60
TaATG8j-2AS	F VYVVRKRI KLSPEKAI F VF VNS TLPPTASLMS AI YEENKDEDGFL YMTYS GENTFGSA	119
TaATG8j-2BS	F VYVVRKRI KLSPEKAI F VF VNS TLPPTASLMS AI YEENKDEDGFL YMTYS GENTFGSA	119
TaATG8j-2DS	F VYVVRKRI KLSPEKAI F VF VNS TLPPTASLMS AI YEENKDEDGFL YMTYS GENTFGSA	119
TaATG8j-cDNA	F VYVVRKRI KLSPEKAI F VF VNS TLPPTASLMS AI YEENKDEDGFL YMTYS GENTFGSA	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.

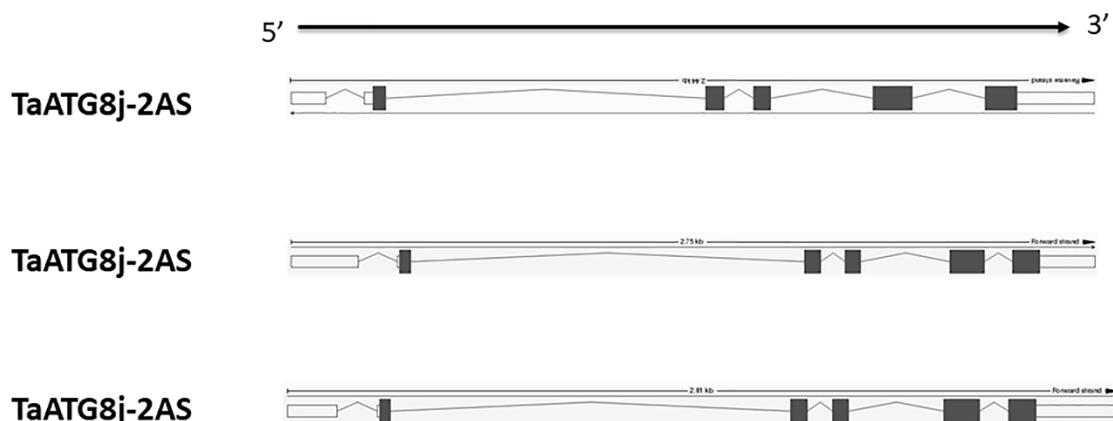


Figure S3. Diagram showing the three subgenomic copies of *TaATG8j* from the wheat cv. Chinese Spring URG1 genome database. Solid rectangles indicate exons, and zigzags indicate introns. The lengths of the three copies were *TaATG8j- 2AS*, 2.44 kb; *TaATG8j-2BS*, 2.75 kb; and *TaATG8j-2DS*, 2.81 kb.

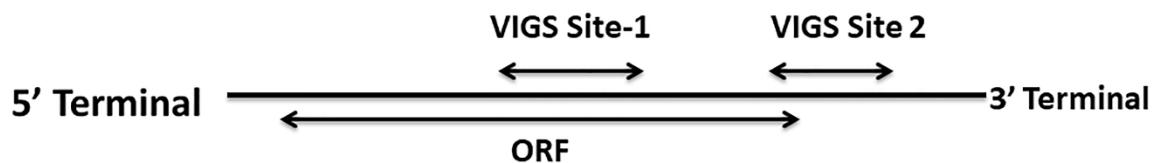


Figure S4. Virus-induced gene silencing fragments. Two fragments were considered from the open reading frame (ORF) and the ORF plus the 3' noncoding region of the *TaATG8j* gene for specific knockdown. ORF: open reading frame. VIGS Site -1: *TaATG8j* -1s. VIGS Site -2: *TaATG8j*-2s.