

**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	GCTGACAGAA	CTCCGGT	276
TaATG8j-2BS	AGGCAAGCTGAATCTGCTAGGATCCGTGAGAAAT	GCTGACAGAA	CTCCGGT	379
TaATG8j-2DS	AGGCAAGCTGAATCTGCTAGGATCCGTGAGAAAT	GCTGACAGAA	CTCCGGT	319
TaATG8j- <i>c</i> DNA	AGGCAAGCTGAATCTGCTAGGATCCGTGAGAAAT	GCTGACAGAA	CTCCGGT	238
TaATG8j-2AS	AGGAAGTA[CTTGTCCC[GCCGACCTCACTGTTGGCAGT]TTCAGCTACGTGGTGGCCAGGCTACTGTTGGCAGTTGCTGATCGTACGTGGCTTGT	GGCCAGA	GGCCAGA	376
TaATG8j-2BS	AGGAAGTA[CTTGTCCC[GCCGACCTCACTGTTGGCAGT]TTCAGCTACGTGGTGGCCAGGCTACTGTTGGCAGTTGCTGATCGTACGTGGCTTGT	GGCCAGA	GGCCAGA	479
TaATG8j-2DS	AGGAAGTA[CTTGTCCC[GCCGACCTCACTGTTGGCAGT]TTCAGCTACGTGGTGGCCAGGCTACTGTTGGCAGTTGCTGATCGTACGTGGCTTGT	GGCCAGA	GGCCAGA	419
TaATG8j- <i>c</i> DNA	AGGAAGTA[CTTGTCCC[GCCGACCTCACTGTTGGCAGT]TTCAGCTACGTGGTGGCCAGGCTACTGTTGGCAGTTGCTGATCGTACGTGGCTTGT	GGCCAGA	GGCCAGA	338
TaATG8j-2AS	GAATAGC ACCTTGCCACCGACTGCTTCGTTGATGTCAGCGATCTATGAAGAAAACAAGGACGAGGAGCGCTTCTGTACATGACTTACATGGCGAGAAC	GGATGTCAGGTTGCGACGTCTGTGTACATACAT	ATGGCGAGAAC	476
TaATG8j-2BS	GAATAGC ACCTTGCCACCGACTGCTTCGTTGATGTCAGCGATCTATGAAGAAAACAAGGACGAGGAGCGCTTCTGTACATGACTTACATGGCGAGAAC	GGATGTCAGGTTGCGACGTCTGTGTACATACAT	ATGGCGAGAAC	579
TaATG8j-2DS	GAATAGC ACCTTGCCACCGACTGCTTCGTTGATGTCAGCGATCTATGAAGAAAACAAGGACGAGGAGCGCTTCTGTACATGACTTACATGGCGAGAAC	GGATGTCAGGTTGCGACGTCTGTGTACATACAT	ATGGCGAGAAC	519
TaATG8j- <i>c</i> DNA	GAATAGC ACCTTGCCACCGACTGCTTCGTTGATGTCAGCGATCTATGAAGAAAACAAGGACGAGGAGCGCTTCTGTACATGACTTACATGGCGAGAAC	GGATGTCAGGTTGCGACGTCTGTGTACATACAT	ATGGCGAGAAC	438
TaATG8j-2AS	ACTTTCGGCTCTGCCTAAACCATGTCGCGTGCCTACTGTAAATAAAT	GGATGTCAGGTTGCGACGTCTGTGTACATACAT	ATCAGTATGCTG	570
TaATG8j-2BS	ACTTTCGGCTCTGCCTAAACCATGTCGCGTGCCTACTGTAAATAAAT	GGATGTCAGGTTGCGACGTCTGTGTACATACAT	ATCAGTATGCTG	677
TaATG8j-2DS	ACTTTCGGCTCTGCCTAAACCATGTCGCGTGCCTACTGTAAATAAAT	GGATGTCAGGTTGCGACGTCTGTGTACATACAT	ATCAGTATGCTG	616
TaATG8j- <i>c</i> DNA	ACTTTCGGCTCTGCCTAAACCATGTCGCGTGCCTACTGTAAATAAAT	GGATGTCAGGTTGCGACGTCTGTGTACATACAT	ATCAGTATGCTG	534
TaATG8j-2AS	3TGGATTGCTC[CATGGTTAATGC]TTAAAGTGTGGTATTTATCATCTGAATGTTAGAACGGCTGTAAAACCTGATTTACGGTCCAAGATTCAG	ATTCAG	669	
TaATG8j-2BS	3TGGATTGCTC[CATGGTTAATGC]TTAAAGTGTGGTATTTATCATCTGAATGTTAGAACGGCTGTAAAACCTGATTTACGGTCCAAGATTCAG	ATTCAG	759	
TaATG8j-2DS	3TGGATTGCTC[CATGGTTAATGC]TTAAAGTGTGGTATTTATCATCTGAATGTTAGAACGGCTGTAAAACCTGATTTACGGTCCAAGATTCAG	ATTCAG	700	
TaATG8j- <i>c</i> DNA	3TGGATTGCTC[CATGGTTAATGC]TTAAAGTGTGGTATTTATCATCTGAATGTTAGAACGGCTGTAAAACCTGATTTACGGTCCAAGATTCAG	ATTCAG	694	
TaATG8j-2AS	[AT]TCTCGCTCGGTTAATGCTCTCATGCTCCTGGGATGTTCAATCGCAAATTAATGGCG	GGCGAG		731
TaATG8j-2BS	[AT]TCTCGCTCGGTTAATGCTCTCATGCTCCTGGGATGTTCAATCGCAAATTAATGGCG	GGCGAG		784
TaATG8j-2DS	[AT]TCTCGCTCGGTTAATGCTCTCATGCTCCTGGGATGTTCAATCGCAAATTAATGGCG	GGCGAG		800
TaATG8j- <i>c</i> DNA	[AT]TCTCGCTCGGTTAATGCTCTCATGCTCCTGGGATGTTCAATCGCAAATTAATGGCG	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.

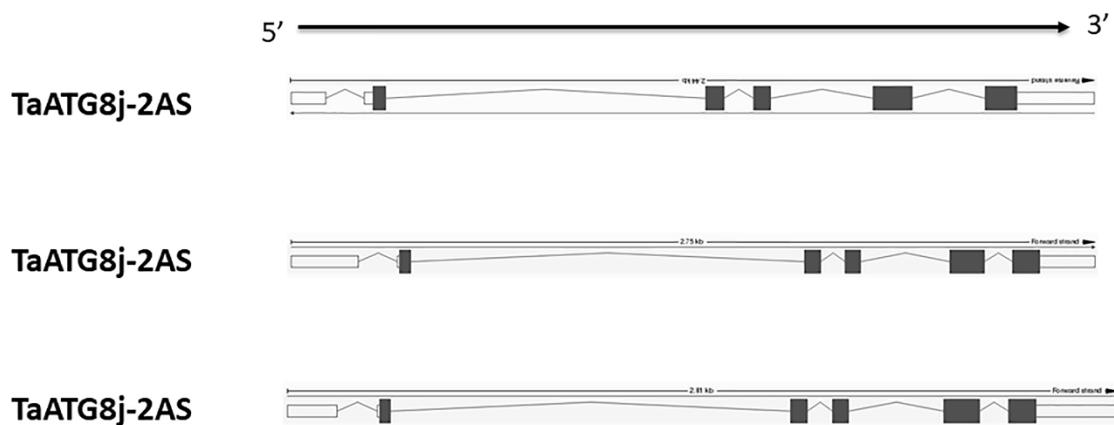


Figure S3. Diagram showing the three subgenomic copies of *TaATG8j* from the wheat cv. Chinese Spring URG1 genome database. Solid rectangles indicate exons, and zigzags indicate introns. The lengths of the three copies were *TaATG8j- 2AS*, 2.44 kb; *TaATG8j-2BS*, 2.75 kb; and *TaATG8j-2DS*, 2.81 kb.

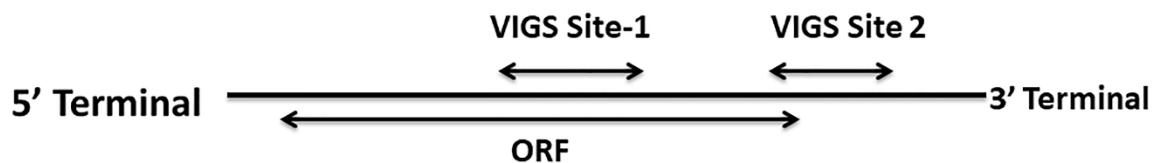


Figure S4. Virus-induced gene silencing fragments. Two fragments were considered from the open reading frame (ORF) and the ORF plus the 3' noncoding region of the *TaATG8j* gene for specific knockdown. ORF: open reading frame. VIGS Site -1: *TaATG8j* -1s. VIGS Site -2: *TaATG8j*-2s.