**Supplementary Table S1. Primer used for TaATG8j analysis**

<table>
<thead>
<tr>
<th>Name of Primers</th>
<th>Sequences (5′→3′)</th>
<th>Amplified length (bp) /type of Oligonucleotides</th>
<th>Purpose</th>
</tr>
</thead>
<tbody>
<tr>
<td>M13-F</td>
<td>TGTAAAACGACGGCCAGT</td>
<td>General primer</td>
<td>Checking</td>
</tr>
<tr>
<td>M13-R</td>
<td>CAGGAAAACTATGACC</td>
<td>General primer</td>
<td>Checking</td>
</tr>
<tr>
<td>PVX-F</td>
<td>CAATCAGAGTGTTGCTTG</td>
<td>General primer</td>
<td>Checking</td>
</tr>
<tr>
<td>PVX-R</td>
<td>GACCCCTATGGGCTGTTG</td>
<td>General primer</td>
<td>Checking</td>
</tr>
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<td>pREP3x-S</td>
<td>CGCGAAGACTAAACCG</td>
<td>General primer</td>
<td>Checking</td>
</tr>
<tr>
<td>pREP3x-AS</td>
<td>TCCTAAGGCAAAAAACAAAT</td>
<td>General primer</td>
<td>Checking</td>
</tr>
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<td>'A-as-seq-F</td>
<td>AAAGTGAGGTTAAACGAAAC</td>
<td>General primer</td>
<td>Checking</td>
</tr>
<tr>
<td>'A-as-seq-R</td>
<td>TCGAGCATCCTGTTCAAGT</td>
<td>General primer</td>
<td>Checking</td>
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<td>TaATG8j-Clai-F</td>
<td>ggatgcggtAGGCCAAGACTTGCTTCA</td>
<td>Expression in Tobacco</td>
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<tr>
<td>TaATG8j-Clai-R</td>
<td>CAGGAAACAGCTATGACC</td>
<td>Expression in Yeast</td>
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<td>TaATG8j-Sall-F</td>
<td>CAACTGCTATATCCATGGCTTGCTTCA</td>
<td>Sub-cellular localization</td>
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<td>AAGACCCCAACGGAAGC</td>
<td>General primer</td>
<td>Checking</td>
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<tr>
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<tr>
<td>TaATG8j-2AS: QT-R</td>
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<td>TaATG8j-2BS: QT-F</td>
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<td>TaATG8j-2DS: QT-F</td>
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<td>TaATG8j-2DS: QT-R</td>
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<tr>
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<td>General primer</td>
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<tr>
<td>TaEF-qRT-R</td>
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<td>General primer</td>
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<td>Biomass assay</td>
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<td>biomass-PstEF-R</td>
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<tr>
<td>biomass-WEF-F</td>
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<td>General primer</td>
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</tr>
<tr>
<td>biomass-WEF-R</td>
<td>CTCCAGGAGAGTCATCAGT</td>
<td>General primer</td>
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</tr>
<tr>
<td>TaPR1-S</td>
<td>CAGAATGCGAGCCAGCCACAACG</td>
<td>General primer</td>
<td>Pathogenesis Related</td>
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<tr>
<td>TaPR1-AS</td>
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<td>TaPR2-S</td>
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<td>TaPR2-AS</td>
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<td>TaSOD-S</td>
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<td>General primer</td>
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<tr>
<td>TaSOD-AS</td>
<td>ACTCCAGGAGGAAACCTTCTCTGATC</td>
<td>General primer</td>
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</tbody>
</table>

*The Uppercase letters indicate bases that match the initial template. Lowercase letters which are underlined in 5′ extensions that indicates the restriction sites.*
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 URG genome database. The purple and red boxes indicate the start codon (ATG) and stop codon (TAA), respectively. Identical nucleotides are in black.
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.