Supplemental Data

Figure S1

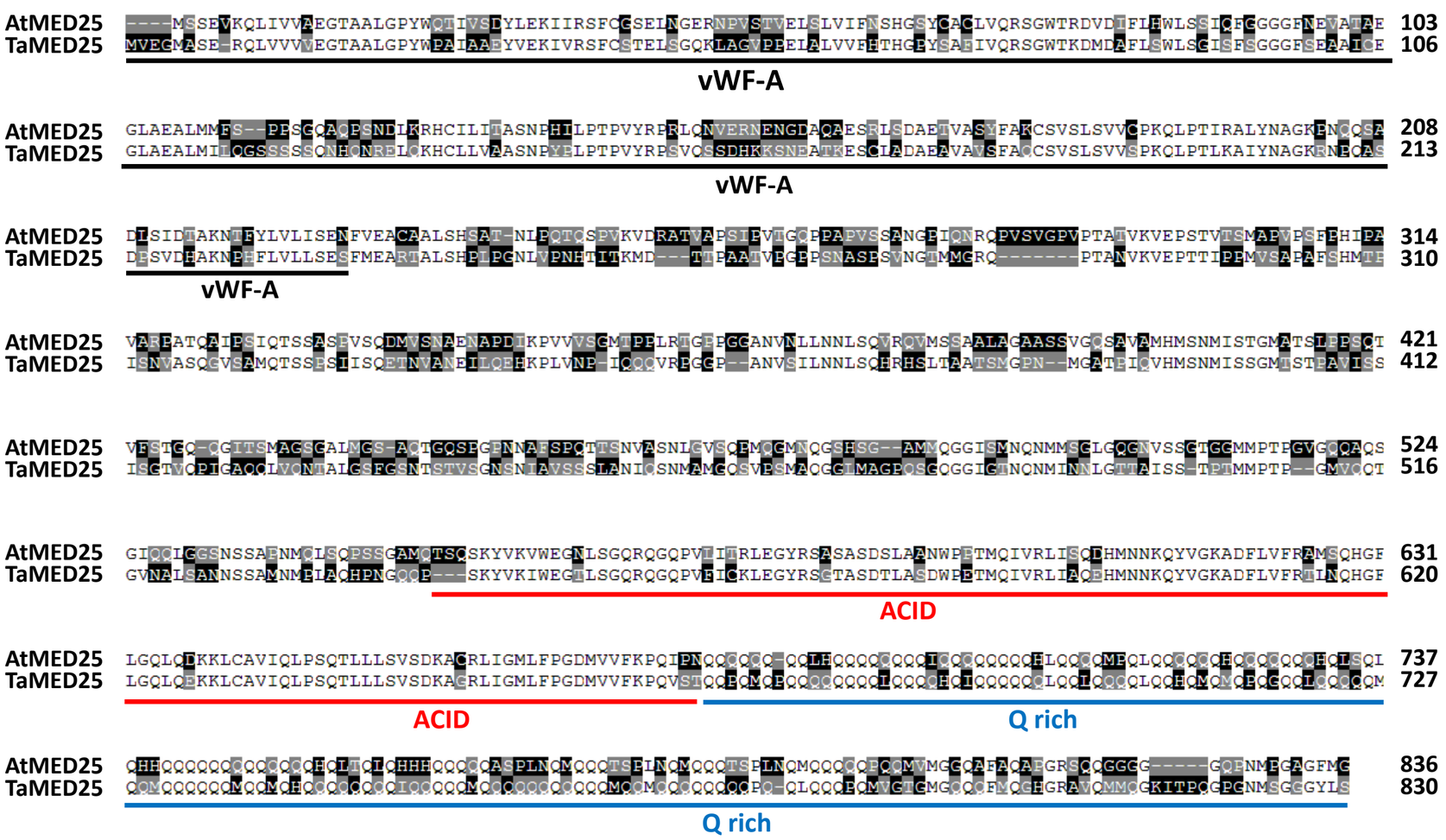

Figure S1. Sequence comparison of AtMED25 and TaMED25 proteins. TaMED25 is homologous to *Arabidopsis* AtMED25 (NP_173925) with 52% sequence identity. The conserved vWF-A, ACID and Q-rich domains are separately underlined by black, red and blue lines. Residues that are not identical between the two proteins are shaded in dark or gray.

Figure S2

Figure S2. Allelic variation at the *TaMED25-A*, *TaMED25-B* and *TaMED25-D* coding regions. *TaMED25-A*, *TaMED25-B* or *TaMED25-D* represents *TaMED25* CDS nucleotide sequences derived from wheat A, B or D genome; nucleotide variations among *TaMED25-A*, *TaMED25-B* and *TaMED25-D* are shaded in dark or gray.

Figure S3

Scaffold61769 from *Triticum urartu*:

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Scaffold61247 from *Aegilops tauschii*:

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GTCCAACCATTTGACCCCCTGACATCTTAGATGAGATCCTGATTTGCAATCATTTCAAATCCAGAAGCAACATTCTCTTTCATCTAAGCTTATTTTATGAATGTGTACTTTGTTTCTCTGGATCCAACATTCTGAA
TGAACCAGAGCATTGTTATTAGCTCCTTGAAGAATAGGTTTGGCTGAACCGGCCTGATTTCTAGCTGAGGCGAACATATCCAAGATATATAAAGGATTTGTTCCAAGAGGTTTAAATCAAAATAGAGATAGTGC
CCAATCTTCTGAAACCTGATTAATGCAAAGAGCACCAACTTAACTTCCTCCACGTCAAAAGCCTTACTCTCCAATCCTTGTGTTAACTTTGCCATGAAGTATTGTTGAAAAAAAAACTTACCATGCATTAAAAT
CTGCACCAAGATACTAGTACACTTTGTTTTTCTGAACCTACTGAAAATTTTGTGAAGCATGGAACAGAATATCGGTTTGTGCTGCCAATGCTCATTGTTTTCACGGCCTACACCTTCAAAGCTGAAACCAATTG
TTATACTTTCGGATTGTGTACTGTAATTTGCTATCCTCTTAAATATACCATACCATATTCTATCTTTGCAAAGCATTTCAATGTTGTATTTCTCATCTTATCATCTGTGTTGCAG**GGTTATAGGAGTGGAACAGCG**
TCTGACACGTAAGTCTTTAAACTGTTGCAATACTATTTTTGTGATCATTGAGATTAAGAAATTTTACAGCTAGCTGTTATTGTTGTTCTTTTTCTTGAAAATGTATCGTTTTAGCAGAAATATTGAATTTTTAGTG
GACACCTACACCTTGTTTGTGAAGTCATTCTCATCATACTATCTGTAATACATCCTGTGCATCCCGTAACTTATCTGAACACACCTATCAGCTATAGGATTATGGGATGCTAAGATTAGTTGCAAACCAACTAAAT
ACCAGTCGTTGTAGGTTGGTATGTCATATTTTGTTTCTTTGGCAGCACCTGCCAAATTTTGCTAGTGTACTGATTGCCAGATATATTCATGAATGTTTTCTTAGTGCAATATCTTACCTGCTGTTCAAGCGCAATT
TCAGTTGGAAACCTGACAATGTTTCTGAGTTCTAATATGATACACCCAGTGAAGAAGCTTGTTTTCCTGCACTTTGTTGGGCAACTTTGAATGCCATTTGCCTTGACTCAATAAAATCTATCATCGTGTCTTATT
TTTCTCCTTAAGTTTTACAACAGCGCTTTCATACAATCTGCAAATCATACCATCCCTAAAGAAACTGAAGCTGTACTTTTATATTCAGA**CTTGCTTCAGACTGGCCAGAAACGATGCAGATCGTGCGCCTC**
ATAGCCCAAGAGCATATGAACAACAAGTTTGTCGCTCAACTAGCCCATGCTTTTCCTTCTTAAAACCGCTGCCTTATTGTGTGTTCTTCCTAATATCATTCCTGCNTTATTGTGTGTTCTTCCTAATATCATTCC
TGCTCAACTTTGGTTGTTCGATCATGTAATTGTACAGG**CAGTATGTTGGCAAGGCGGACTTTCTAGTATTTCGGACATTGAATCAGCATGGGTTCCTCGGACAACTACAAGAGAAGAAACTG**GTGAG
TTGCTCAGTGCTTGTTTTAACCTTGTGGAATATTTATGATCTCAGTTTGAACTGCACTTAATTAAGCATCGTATCATACATTTACTTCTTTTAATGTTCAAGTGGTTCATTGCTTCAG**TGTGCAGTGATTCAGCT**
ACCTTCACAAACTTTGCTGTTGTCAGTGTCTGACAAAGCTGGGCGCCTCATAGGAATGCTGTTCCCAGGGGTATGTTTATAACTAATTGATTGATTACCGCAACTTGTCTCTTGTATTCATCTGAATCAA
CACTTCTCTGCCGAGTTTTCCCCAG**GATATGGTGGTATTCAAACCACAGGTCTCAACTCAGCAGCCACAGATGCAGCCACAGCAGCAGCAGCAGCAGCTACAACAGCAGCAGCACCAAATACAGC**
AGCAACAGCAGCAACTACAGCAACTGCAACAGCAGCAACTACAACAGCACCAAATGCAAATGCAGCCTCAAGGCCAGCAACTTCAGCAGCAGCAGCAGATGCAGCAAATGCAACAGCAACAA
CAACAGATGCAGCAAATGCAACACCAACAACAGCAGCAGCAGCAGCAGATTCAACAGCAGCAACAGATGCAGCAGCAGCAGCAGCAACAGCAACAACAACAGATGCAGCAAATGCAGCA
GCAGCAGCAGCAGCAGCAACAGCCTCAACAACTCCAGCAGCAGCCGCAGATGGTGGGTACAGGGATGGGTCAGCAACAATTCATGCAGGGGCATGGTCGGGCGGTGCAGATGATGCAAGGA
AAGATCACGCCACAGGGCCCAGGCAACATGTCTGGAGGAGGCTACCTATCTTGA

Figure S3. Nucleotide sequences of scaffold61769 from *Triticum urartu* and scaffold61247 from *Aegilops tauschii* that contain *TaMED25* gene. Exons of *TaMED25* gene are marked by red color. ‘N’s in the sequences represent the sequence gaps that have yet to be identified.

Figure S4

Figure S4. Schematic diagram of *TaMED25* gene structure. Black boxes indicate exons, and black lines in the middle represent introns.

Figure S5

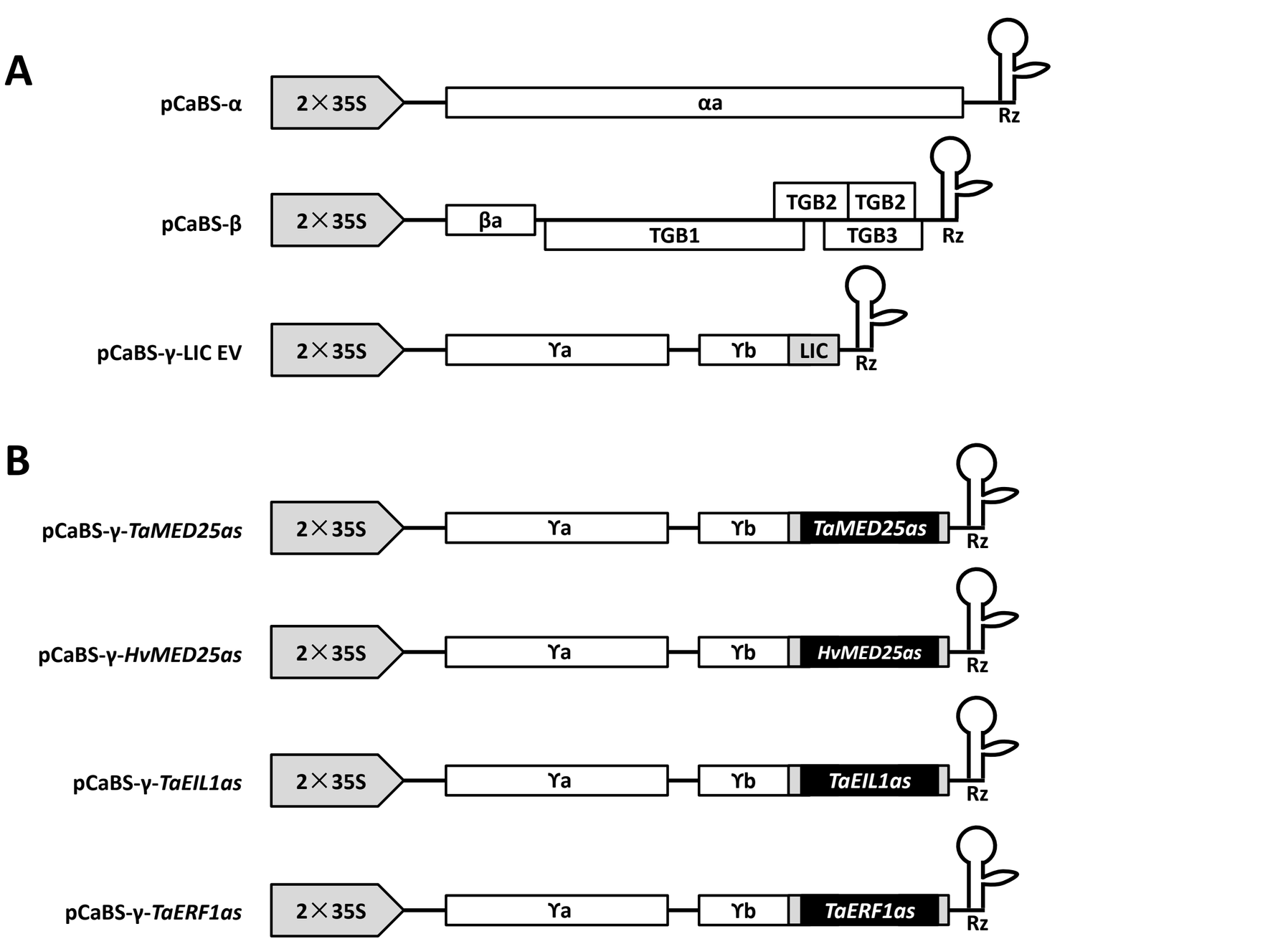

Figure S5. Constructions of BSMV-VIGS vectors. **(A)** Schematic representations of pCaBS-α, pCaBS-β and pCaBS-γ. (B) Construction of pCaBS-γ vectors for silencing of *TaMED25*, *HvMED25*, *TaEIL1* and *TaERF1*. The antisense fragments (about 300 bp in length) of *TaMED25*, *HvMED25*, *TaEIL1* and *TaERF1* (Shown in Supplemental Fig. S6 and Fig. S7) were PCR amplified and ligated into the LIC region of pCaBS-γ vector by using ligation independent cloning (LIC) strategy.

Figure S6

***TaMED25-D* CDS:**

ATGGTGGAGGGGATGGCTTCGGAGAGGCAGCTGGTGGTGGTCGTTGAGGGCACGGCGGCGCTGGGGCCGTACTGGCCCGCCATTGCGGCCGAGTACGTCGAGAAGATCGTTCGGAGTTTTTGTTCTACTG
AACTATCAGGGCAGAAGCTTGCAGGGGTACCACCTGAGCTTGCATTAGTTGTCTTCCATACCCACGGACCATACAGTGCCTTTATTGTACAACGCAGCGGTTGGACAAAAGATATGGATGCTTTTCTTTCATG
GTTATCAGGAATATCATTTAGTGGTGGAGGCTTCAGTGAAGCTGCTATTTGTGAAGGTCTTGCTGAAGCACTGATGATACTCCAAGGCAGTTCTAGTAGCAGCCAGAATCATCAAAATCGTGAACTTCAAAAG
CATTGCCTACTTGTTGCTGCAAGTAATCCTTACCCGCTGCCTACACCTGTCTACCGCCCTTCTGTTCAAAGTAGTGATCACAAAAAGAGCAACGAAGCAACAAAGGAATCATGTCTTGCTGATGCTGAGGCT
GTTGCAGTCTCATTTGCTCAGTGCTCTGTGTCATTGTCGGTGGTATCTCCTAAACAGCTACCAACACTGAAGGCAATATACAACGCGGGAAAGAGGAATCCTCAAGCTTCTGATCCATCAGTTGATCATGCCA
AAAATCCACATTTTCTTGTTTTGCTCTCTGAGAGTTTCATGGAGGCTCGAACAGCTCTAAGCCATCCTTTACCCGGGAACCTTGTCCCAAACCACACCATTACAAAAATGGATACCACACCTGCAGCTACTGT
GCCAGGACCACCTTCGAATGCCAGTCCCTCAGTGAATGGAACGATGATGGGACGGCAACCGACTGCAAATGTTAAAGTGGAGCCAACAACTATACCACCAATGGTTTCTGCACCTGCATTCTCTCATATGAC
ACCTATTTCAAATGTTGCTTCTCAAGGTGTATCAGCAATGCAAACTTCTTCACCATCGATTATTTCACAAGAAACAAATGTTGCAAATGAAATATTGCAAGAGCATAAGCCTTTAGTAAACCCTATCCAACAAC
AGGTTCGGCCTGGTGGCCCAGCAAATGTTAGCATCCTAAACAATCTTTCACAACATCGACACTCTTTAACAGCA**GCTACCTCAATGGGACCTAACATGGGGGCAACACCTATACAAGTGCACATGTCAA**
ACATGATATCGAGTGGCATGACATCGACTCCCGCTGTCATATCTTCTATATCTGGAACAGTACAGCCAATTGGTGCTCAACAGTTGGTACAGAACACAGCTCTCGGTTCTTTTGGGTCAAACACT
TCTACTGTATCTGGTAATTCAAATATTGCCGTATCTTCTTCTTTGGCTAACATACAAAGCAACATGGCCATGGGACAATCAGTGCCTTCTATGGCACAAGGTGGTCTGATGGCTGGTCCACAATCA
GGACAAGGTGGAATTGGTACGAACCAAAACATGATAAATAACCTTGGGACTACGGCTATCTCTTCTACGCCTACAATGATGCCAACACCAGGAATGGTCCAGCAAACAGGAGTAAACGCTCTTAGTGCGAA
CAACAGTTCTGCTATGAATATGCCTCTGGCACAACATCCTAATGGCCAGCAACCATCGAAGTATGTCAAAATTTGGGAGGGAACTTTGTCTGGGCAAAGGCAAGGACAACCTGTATTTATTTGTAAACTTGAA
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CGGACATTGAATCAGCATGGGTTCCTCGGACAACTACAAGAGAAGAAACTGTGTGCAGTGATTCAGCTACCTTCACAAACTTTGCTGTTGTCAGTGTCTGACAAAGCTGGGCGCCTCATAGGAATGCTGTTC
CCAGGGGATATGGTGGTATTCAAACCACAGGTCTCAACTCAGCAGCCACAGATGCAGCCACAGCAGCAGCAGCAGCAGCAGCAGCTACAACAGCAGCAGCACCAAATACAGCAGCAACAGCAGCAACTA
CAGCAACTGCAACAGCAGCAACTACAACAGCACCAAATGCAAATGCAGCCTCAAGGCCAGCAACTTCAGCAGCAGCAGCAGATGCAGCAAATGCAACAGCAACAACAACAGATGCAGCAAATGCAACA
CCAACAACAGCAGCAGCAGCAGCAGATTCAACAGCAGCAACAGATGCAGCAGCAGCAGCAGCAACAGCAACAACAACAGATGCAGCAAATGCAGCAGCAGCAGCAGCAGCAACAGCCTCAACAACTCC
AGCAGCAGCCGCAGATGGTGGGTACAGGGATGGGTCAGCAACAATTCATGCAGGGGCATGGTCGGGCGGTGCAGATGATGCAAGGAAAGATCACGCCACAGGGCCCAGGCAACATGTCTGGAGGAGGCT
ACCTATCTTGA

***TaEIL1* cDNA partial:**

CGGATAAAACTAGCAAGTGGGAGATCGACGCAGGTGAACACCACCACAGCTACAAGTAGAGGAAGTGGAATTTCTCTTGTGGAAAAAAGGGAGAGTTGCTTGAGTGGCCATGATGGGAGGTG
GGCTGCTCATGGATCAGGGCATGGCGTTCTCCGGCGTGCACAACTTCGTGGATCTGCTCCAGCAGAACGGCGCCGACAAGAACCTCGGCTTCGGCTCCCTTATGCCGCAGACTTCCTCCGGCG
ACCAGTGCGTCATGGGCGAGGGCGACCTCGTGGACCCCCCGACGGACAACTTCCCGGACGCCGGGGAGGACGACAGCGACGACGATGTGGATGACATCGAGGAGCTGGAGCGCCGCATGTGGCGCGACC
GCATGAAGCTCAAGCGCCTCAAGGAGCTGCAGCAGAGCCGCGGCAAAGAGCAGGCCGCCGCCGGCGGCGGCGTTGGCGACGGCTTGAAGCCGCGGCAGTCGCAGGAGCAGGCGCGCCGCAAGAAGAT
GTCGCGCGCGCAGGACGGCATCCTCAAGTACATGCTCAAGATGATGGAGGTGTGCCGCGCCCAGGGGTTCGTGTACGGCATCATTCCGGAGAAGGGCAAGCCCGTGAGCGGCGCCTCTGACAACCTCCGT
GCCTGGTGGAAGGAGAAGGTCCGCTTCGACCGGAACGGCCCGGCCGCCATCGCCAAGTACCAGGCGGACAACGCCGTGCCGGGCTCCGAGAGCGAGCTGGCTTCCGGCACCGCCAGCCCGCACTCGCTG
CAGGAGCTGCAGGACACCACGCTGGGCTCGCTCCTCTCGGCGCTCATGCAGCACTGCGATCCCCCGCAGCGAAGGTTCCCGCTCGAGAAGGGCATCTCTCCTCCATGGTGGCCGTCCGGCGACGAGGAGT
GGTGGCCGGAGCTTGGCATCCCCAAGGACCAGGGCCCGCCCCCGTACAAGAAGCCCCATGACCTCAAGAAGGCTTGGAAGGTGAGCGTGCTCACCGCTGTCATCAAGCACATGTCGCCGGACATCGAGAA
GATCCGGCGCCTCGTCCGCCAGTCCAAGTGCCTCCAGGACAAGATGACCGCCAAGGAGATCTCCACCTGGCTGGCCGTGGTGAAGCAGGAAGAGGAGCTGTTCATGAGGCTGCACCCGGGCGCTCGCCCT
CCAGCGTCTGCCGGCGGCATCGCCAGTGCCATATCATTCAACGCCAGCTCGAGTGAGTACGACGTTGACCTCGCCGACGACTGCAAGGGCGATGAGGCCGGCACCCACAAGATGGCCATGGCCGATCCAA
CCGCCTTCAACCTCGGCGTGGCCATCCTGAATGACAAGTTCCTGATGCAAGCGCCCATGAAAGAGGAGACCGCCGACATGGAGTATGTCCAGAAGAGGAGCGCGGTGGCCGCCGAGCCGGAGCTGATGCT
GAACAACCGCGTCTACACCTGCAACAACGTCCAGTGCCCGCACAGCGACTACGGGTACGGATTCCTTGACCGGAATGCGCGCAGCAGCCACCAGTACACCTGCAAGTACAATGATCCCCTCCCGCCAAGC
GCGGAGAACAAGGCAGCGCCACCTGCGCCGCCGCAAGTCTTCCCGGCGGCCTACAACCAGCAGAACCATGGGCTCAACAACCTGGATTTTGGCCTGCCCATGGATGGGCAGAGGTCCATCGCCGAGCTGA
TGAACATGTACGACACCGCCTTCCCGGCCACCAACAAGAACATGGGCAACGACGACGTCACCATTATAGAGAGGCCCAATGCCATCACCCCGGGAGCGCAGATGGACGAGGGTTTCTTTGGACAGGGCAA
TGGAATTGGAGGCAATGGCGACAGTATGTTCAGTGATGTCAGTAACATGATGCAGCAGCAGCAGCAGCAGCAAGCACAACAGCCACAGCAGCAGCAGGCCCCGGCGCAGCAGCAGTTCTTCATCCGTGAC
GACGCGCAGGCGCAGTTCGGGAACCAGATGGGCAGCATCTCCGGCGCATCGGATTTCAGGTTCGGCTCTGGCTTCAACATGTCTGGCACCGTCGACTACCCGCAGAAGAACGACGGCCCCAATTGGTACTA
CTGAATGAAGAATAAACTCGTAGGGTCATCATAAGC

***TaERF1* CDS:**

ATGTCTGATCCCAGCGCCAGCAGCACGGCCTCTTCTTCTCCGACTTCTTCATCTACGTCGCCCCGGCTCACCACCGGCG**TCGTCAACTTTCTGGCCCGTCGTGCGGTGACCACGCAGCAGAACCACCA**
CCTACCAGCAGCCGAAGCATTCCCGCTGCACTCGCCGGGCTCCTCCACCGGCTCCGCCGACTCCGCGCCCTGGCACCACCGCGCCCCGGCCACGCCGCCACCTGTTCTTCCGTTCGACCCCA
GCGACGCCGACGAGATGCTCCTGCTAGACATGCTCTCCCAGCACCACGAGGTCCAGCACGCCGCGGCCGCACCGACGACGGCGCCGGCGAAGCAAGAGGCCGACGAGGAGGGCAAGGTGGCA
CTAGGTGTGGGTCGCGCGTTCCGCGGAGTGCGGAAGCGACCGTGGGGCAAGTTCGCGGCCGAGATCCGGGACTCGACGCGCAACGGCGTGCGCGTGTGGCTGGGCACCTTCGACAGCCCAGAAGCTGCG
GCGCTGGCGTACGACCAGGCTGCGTTCGCCATCCGCGGCGGGGCCGCCGTTCTCAACTTTCCGGCCGATCAGGTCCGGCGCTCGCTCGAGGGCGCCGCTGACGACGCATGCGGCCGTGCCCATGGCTTGTC
GCCCGTGCTGGCGCTCAAGCGGCGGCATTGCATGCGGAGCCGGAAGGCCGCGGCGGCCGGCAGGGTGGCGAAGGCCGCCACCCGGGGGGTGCGGCCGGGGTGTGTGATGGAGCTTGAGGACCTCGGCG
CGGAGTACCTCGAGCAGCTGCTTGGCGCCTCCGAGGACACGGCGTCCATGAGTTCATGGTGCTGGAGCCACCAGTCCGTATGA

Figure S6. Nucleotide sequences from *TaMED25*, *TaEIL1* and *TaERF1* that were used for BSMV mediated silencing. The full length CDSs of *TaMED25*, *TaEIL1* and *TaERF1* are shown above, and the red color represents the selected sequences used for the generation of BSMV silencing constructs, as shown in Supplemental Fig. S5B.

Figure S7

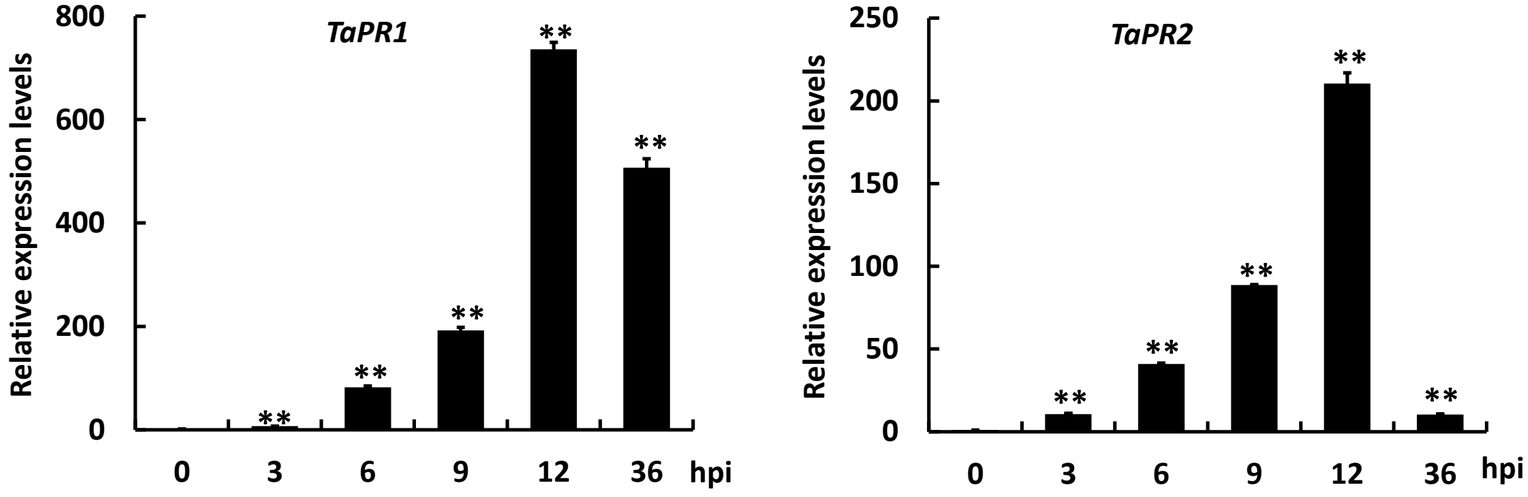

Figure S7. *TaPR* genes are induced by *Bgt* infection. The relative transcript levels of *TaPR1* and *TaPR2* in the *Bgt*-infected bread wheat leaves were determined by using qRT-PCR analyses. The amplification of the *TaGAPDH* gene was used as an internal control to normalize all the data. Error bars indicate SD among three independent replicates, and "**" above the bars represent significant differences of expression levels between control and each treatment at $p<0.01$ (Student's *t* test). All the experiments were performed three times with similar results.

Figure S8

***HvMED25* CDS:**

ATGGTGGAGGGGATGGCTTCGGAGAGGCAGCTGGTGGTGGTCGTCGAGGGCACGGCGGCGCTGGGGCCGTACTGGACCGCCATTGCGACCGAGTACGTCGAGAAGATCGTTCGGAGTTTTTGTTCAACTG
AACTATCAGGGCAGAAGCTTGCAGGGGTACCACCTGAGCTTGCATTAGTTGTCTTCCATACCCATGGACCTTACAGTGCCTTTGTTGTACAACGCAGCGGTTGGACAAAAGATATGGATGCTTTTCTTTCATG
GTTATCAGGAATATCATTTAGTGGTGGAGGCTTCAGTGGAGCTGCTATTTGTGAAGGTCTTGCTGAAGCACTGATGATACTCCAAGGCAGTCCTAGCAACAGCCAGAATCATCAAAATCGTGAACTTCAAAA
GCATTGCCTACTTGTTGCTGCAAGTAATCCTTACCCGCTGCCTACACCTGTCTATCGCCCTTCTGTTCAAAGTAGTGATCACAAAAAGAGCAATGAAGCAACAAAGGAATCATGTCTTGCTGATGCTGAGGCT
GTTGCAGTCTCATTTGCTCAGTGCTCTGTATCGTTGTCGGTGGTATCTCCTAAACAGCTACCAACACTGAAGGCAATATACAATGCGGGAAAGAGGAATCCTCAAGCTTCTGATCCATCAGTTGATCATGCCA
AAACCCCACATTTTCTTGTTTTGCTGTCTGAGAGTTTCATGGAGGCTCGAACCGCCCTAAGCCATCCTTTACCTGGGAACCTTGTCCCAAACCACACCATTACAAAAATGGATACCGCACCTGCAACTACTGT
GCCAGGACCACCTTCGAATGCCAGTCCCTCAGTGAATGGAACGATGATGGGACGTCAACCGACTGCAAATGTTAAAGTGGAGCCGACAACTATACCACCAATGGTTTCTCAACCTGCATTCTCTCATATGAC
ACCTATTTCAAATGTTGCTTCTCAAGGAATATCAGCAATGCAAACTTCTTCACCATTGATTATTTCACAAGAAACAAATGTTGCAAATGAAATATTGCAAGAGCATAAACCTTTAGTAAACCCTATCCAACAAC
AGGTTCGGCCTGGTGGCCCAGCAAATGGTAGCATCCTAAACAATCTGTCACAACATCGACACTCTTTAACAGCA**GCTACCTCAATGGGACCTAACATGGGAGCAACACCTATACAAGTGCACATGTCA**
AACATGTTATCAAGTGGCATGACATCAACCCCCGCTGTCATATCTTCTATATCTGGAACAGTACAGCCAATTGGTGCTCAACAGTTGGTACAGAACACAGCTCTCGGTTCTTTTGGGTCAAACAC
TTCTACTGTATCTGGTAATTCAAATATTGCCGTATCGTCTTCTTTGGCTAACATACAAAGCAACATGGCCATGGGACAATCAGTGCCTTCTATGGCACAAGGTGGTTTGATGGCTGGTTCACAATC
AGGACAAGGTGGAATTGGTACGAACCAGAACATGATAAATAACCTTGGCACTACAGCTATCTCTTCTACGCCTACAATGATGCCAACGCCAGGAATGGTCCAACAAACAGGAGTAAATGCTCTTAGTGTGAA
CAACAGTTCTGCTATGAATATGCCTATGCCTCAACATCCTAATGGCCAGCAACCATCGAAGTATGTCAAAATTTGGGAGGGAACTTTGTCTGGGCAAAGGCAAGGACAACCTGTATTTATTTGTAAACTTGAA
GGTTATAGGAGTGGAACAGCATCTGACGCGCTTGCTTCAGACTGGCCAGAAACAATGCAGATCGTGCGCCTCATAGCCCAAGAGCATATGAATAACAAGCAGTATGTTGGTAAGGCAGACTTTCTAGTATTT
CGGACATTGAATCAGCATGGGTTCCTCGGACAACTACAAGAGAAGAAACTGTGTGCAGTGATTCAGCTACCTTCACAAACTTTGCTGTTGTCAGTGTCTGACAAAGCTGGGCGCCTCATAGGAATGCTGTTC
CCAGGGGATATGGTGGTATTCAAACCACAGGTCTCGACTCAGCAGCCACAGATGCAGCCACAGCAGCAGCAGCAGCTGCAACAGCAGCAGCACCAAATACAGCAGCAACAGCAGCAACTACAGCAACTG
CAACAGCAGCAACTACAGCAGCACCAAATGCAAATGCAGCCTCAAGGCCAGCAACTTCAGCAGCAGCAGCAGATGCAGCAAATGCAACAGCAACAACAACAGATGCAGCAAATGCAACACCAACAACA
GCAGCAGCAGATTCAACAGCAGCAGCAGATGCAGCAGCAGCAGCAACAACAACAGCAACAGATGCAGCAGATGCAGCAGCAGCAGCAGCAACAGCCTCAACAACTCCAGCAGCAGCCCCAGATGGTGG
GTACAGGGATGGGTCAGCAACAATTCATGCAGGGGCATGGTCGGGCGGTGCAGATGATGCAAGGAAAGATCGCGCCACAGGGCCCAGGCAACATGTCTGGGGGAGGCTACCTATCTTGA

Figure S8. The coding sequence of *HvMED25*. The full length CDS of *HvMED25* is shown above, and the red color represents the selected sequence for the generation of BSMV silencing construct, as shown in Supplemental Fig. S5B.

Figure S9

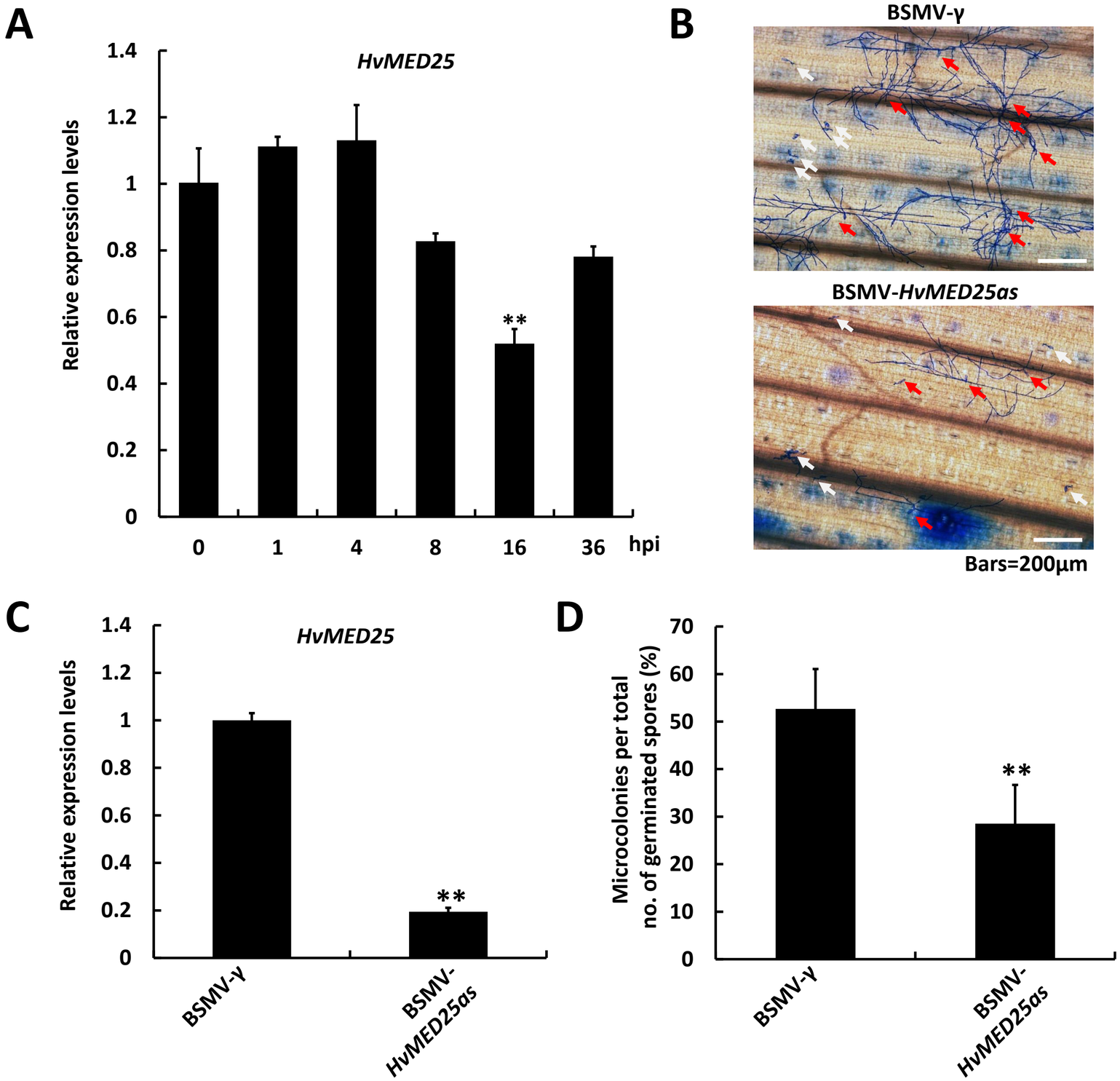

Figure S9. Knockdown of barley *MED25* reduces barley susceptibility to *Blumeria graminis* f. sp. *hordei* (*Bgh*) fungus. **(A)** qRT-PCR analysis of *HvMED25* relative expression levels in *Bgh*-infected barley leaves. Leaf samples of *Bgh* K1-infected barley cultivar 'Golden Promise' were collected at 0, 1, 4, 8, 16 and 36 hpi, and the expression level of *HvMED25* was normalized to the internal control gene *HvActin1*. **(B)** *B. graminis* microcolony formation on BSMV-γ- or BSMV-*HvMED25as*-infected barley leaves. Barley (*Hordeum vulgare*) cultivar 'Golden Promise' was infected with BSMV-*HvMED25as* that harboring antisense fragment of *HvMED25*, or BSMV-γ empty vector constructs. After typical BSMV symptoms appeared, the leaves were challenged with the spores of *Bgh* isolate K1 at a low density. Leaf samples were collected at 72 hpi for staining, and the microcolonies were microscopically observed and analyzed. Red arrows indicate successfully colonized spores, and white arrows represent spores germinated but failed to form colony. Bars = 200 μm. **(C)** Relative transcript levels of *HvMED25* in BSMV-mediated *HvMED25* silencing barley leaves. The expression levels of *HvMED25* in BSMV-γ and BSMV-*HvMED25as* BSMV-VIGS barley leaves were determined by qRT-PCR, and its expression levels were normalized against *HvActin1*. **(D)** Statistical analysis of *B. graminis* microcolony formation index on barley BSMV-γ or BSMV-*HvMED25as* lines. For each treatment, 10-15 leaves (4-5cm in length) were independently collected (the third and fourth leaves from 10-15 BSMV-infected barley plants). The successfully colonized *B. graminis* and the spores without forming colony were then separately counted. The *B. graminis* microcolony formation index represents the percentage of successfully colonized *B. graminis* out of all analyzed spores. The experiments above were independently replicated for three times to calculate the mean and standard deviation. "**" above the bars represent groups with significant differences at $p<0.01$ (Student's *t* test).

Figure S10

***TaERF1*$_{pro}$:**

GTGTTCTGACTGGCACCCCATTCTGGTCAGAATGGATTATTCGGTCAAAATTAGAATTTGTCATGAGTGACGTCACATTGGAATAGAATGTGACAAGTCAAGATGGAGTAGAAGGTTGCCATGTCTGAAATGG
ATAAGGAAAGTTTCGAGGTCCTTCCTAATTAATTAAGGCATTTGGGCAATACCAAATAGAAGCCAGACGTACTTGTCCTAGCTATATGTCAAATGCTAGAGTGCAATTTTCTTGAGTAAATAGCTACTTCCTCTT
GTCCATAATATAAGATGTTTTTTTTTGAAATGATATAAGATGTTTTTTTAATACTACACTAGTGTCACAAAACGTCTTACATTATGCGGGCGGAGGGATTAGCTAGCTAGCCAGCCAGGGGTATGTGGCTTGTGG
TCGTAACATGTGCACACAAGTAGCTAGAACAAGCAGCTAGTCACCAGCCTCTCGAAGTCGCTGTCTGCTGCTAATTGCGGGTCCGATAGGCACAACTGAATGTGTAGCAAAGCTGTATCCAAATTTCCGTGT
TTTTTTCAAAGACAATCAGAATTTATTATAAAAGTTCACCGTAAGTTCAAAGAACCATAGACGTAATAAAAATTATATCGAGGTCTCTAGGCTACTACATAATAAAAATTATATCGAGGTTTCTAAGCTACTACG
TAATAAAAATTATATCAAGGTCTCTAGGCTGCTACCATTGCCAAAAAAAAAACTTGAGTCATAGTTGAACCATTGAAACGACCTAAAGCATCTATCATCATATCTCG**CCATATCACATGCACCACAAGAGGT**
CCTAACCCCGTCGTCCCAAAGGACGGCAGAAATGTACATCGGAGCTCCGTTGACTCAGTCTGTCCGGACATACTCATGGAAATCGAAACTTGAAAGACCAACTCGAAGAAGAGACACCATCAT
CCATCCAAACACCGCTCTGTGAGAAGTAACAAACGAAGCCGAGGCAGTAGGATCTCATCGGCTCATCGGTGGAGCCTTGAGGGAAGAATTTGACCCAACCACAGCTTACGAGGAATGGAAGAA
AATTGACCTATGAAATTTGCACGGATGATAAGCTTCCCGCAAAAAAAAAAATGCTACGCGTGCTGGCGCCATTCGGTCTTGGAGACTTTGCCTACAACTTGACCAAGGAAAAAGAGTATATCTAGA
GTTCTATAGACTACGACGCTCCTGGCTAAGCACAAGTTACCATTCTTTCCACCTTTCTGTCTGGAAGCGGACCCAACGAACGCATGGACGACAAATTAATCGCAGATACAATGTATCACATGTTTTT
GTGCCAGTGGAGGGTTACATTCTTCTAATCTAATCCAATTGTCCATGGAAGACTCGATCAGGGTGAGTGAGTGACACACACCTAGCTACTTAACAAACACGTGGTGGTCGCCGGACGGCTCCACTTGACACT
ATGTCCACTTGATCATAACCAAATAAGCTACCCAGATGCAATTATTCTTATTATTATTTTT**GCAGGTGCAATTAATTTTATTGGTACTACTATGAATTTCCCATGATCGATCAAATATCCTAATATGCTCTTT**
TGCTCCCGATCTCCCATGATCTACCATGAATTCAAATCTTTGTGAATTATTTCGCTATATTTGTTATAGTTTAGTCTTCATATGGGTGCAGATAAGCTTGGGAGCCAAAACTCCAGGCCGTGACGA
ATTCTTGTTGCCTTTCACAGTCACCACTAGTGCCCGCAAATTTCTAATTTTTTGGATCTTAAATTTCATAATCCATATTCTTTTTATTTATTTTTCCTATATTTTGCTTGAATTGGCATCTCGGTTTCT
AGGACTATCTCAACCTACAATTAGTACTCATGTCAAAACGAATGTGCCCCAGCAACAGCACGTTGCCAAGCAGAGCATTTTCCCAGTAATTCCAAATCTACCCTCCGCTGCATCATTCTCACCTCTGCTC
AACCAACTCCCGCCACCGGTATAAATTCCCATGGAGCCGCGCCTCCATCCGTTCCAGCTTCCAACCGACATCCCACGAGAAAAACTCC

Figure S10. Promoter sequence of *TaERF1* used for yeast one-hybrid analysis and transactivation assay. P1 and P2 regions of *TaERF1*$_{pro}$ are marked in red and blue, respectively.

Figure S11

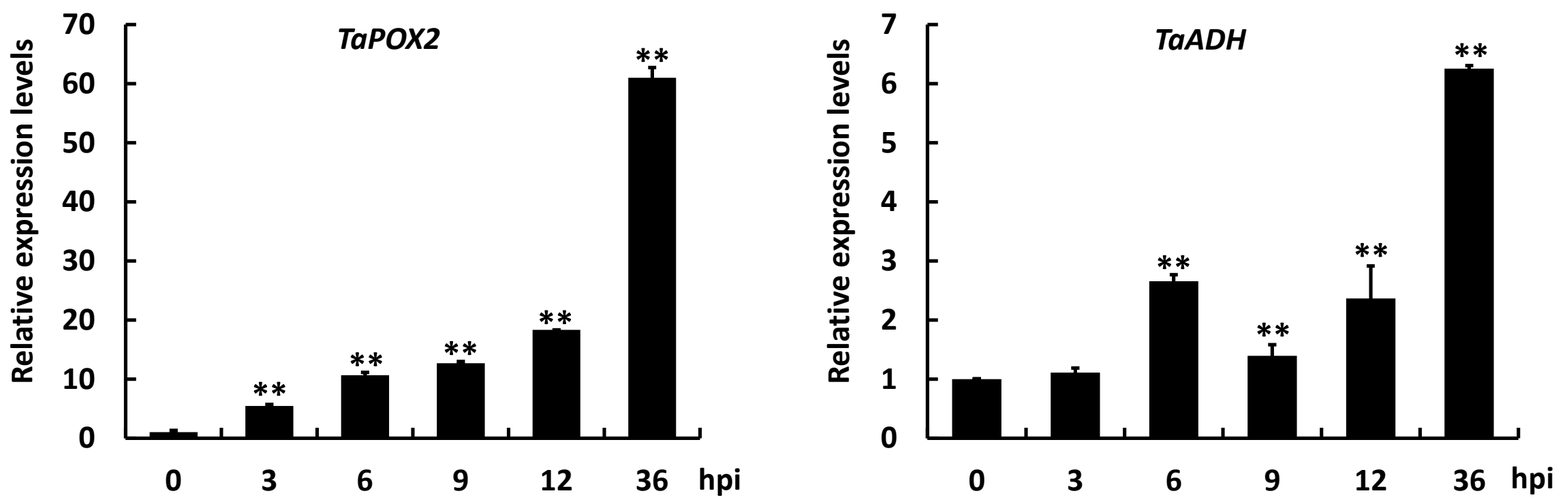

Figure S11. TaERF1 targeting genes *TaPOX2* and *TaADH* are induced by *Bgt* infection. Bread wheat first leaves were collected at different time points after the inoculation of *Bgt*, and the relative transcript levels of *TaPOX2* and *TaADH* were quantified by qRT-PCR. The amplification of the *TaGAPDH* gene was used as an internal control to normalize all the data. Error bars indicate SD, and "**" above the bars represent significant differences of expression levels between control and each treatment at $p<0.01$ (Student's *t* test).

Table S1. Statistical analysis of *B. graminis* microcolony formation index on the BSMV-VIGS bread wheat lines. The successfully colonized *B. graminis* and the spores without forming colony were separately counted, and the *B. graminis* microcolony formation index represents the percentage of successfully colonized *B. graminis* out of all analyzed spores. Numbers before and after "±" separately represent the means and SD of each replication. Three independent replications were conducted, and the significant difference level of microcolony formation indexes between BSMV-γ control and each treatment was analyzed by Student's *t* test. "**" in the table represent significant differences at $p<0.01$ level. "-", not analyzed.

Sample name	*B. graminis* microcolony formation index (%)			Significant difference level compared with BSMV-γ
	Replication 1	Replication 2	Replication 3	
BSMV-γ	35.45 ± 13.83	35.73 ± 15.35	41.08 ± 21.72	-
BSMV-*TaMED25as*	5.87 ± 4.20	8.55 ± 0.50	13.68 ± 4.68	**
BSMV-*TaEIL1as*	21.68 ± 17.58	17.01 ± 5.81	21.14 ± 3.65	**
BSMV-*TaERF1as*	15.98 ± 4.63	14.33 ± 2.36	18.50 ± 2.36	**

Table S2. Statistical analysis of *B. graminis* microcolony formation index on the BSMV-VIGS barley lines. The barley cultivar 'Golden Promise' was used for the analysis, and was infected by the *Bgh* isolate K1. The successfully colonized *B. graminis* together with the spores without forming colony were separately counted, and the *B. graminis* microcolony formation index represents the percentage of successfully colonized *B. graminis* out of all analyzed spores. Numbers before and after "±" represent the means and SD of each replication, respectively. Three independent replications were conducted, and the significant difference level of microcolony formation indexes between BSMV-γ control and each treatment was analyzed by Student's *t* test. "**" in the table mean the significant differences at $p<0.01$ level. "-", not analyzed.

Sample name	*B. graminis* microcolony formation index (%)			Significant difference level compared with BSMV-γ
	Replication 1	Replication 2	Replication 3	
BSMV-γ	56.20 ± 7.06	51.12 ± 10.88	50.32 ± 7.38	-
BSMV-*HvMED25as*	26.35 ± 12.19	29.55 ± 4.78	30.01 ± 6.70	**

Table S3. BiFC assay showing the interaction of TaMED25 and TaEIL1 in bread wheat protoplasts. The indicated combinations of constructs were cotransfected into bread wheat protoplasts, and YFP signal was observed by fluorescence microscope 24 h after transformation. In each replicate, more than 40 protoplast cells were analyzed, and the numbers of cells with or without YFP signal were statistically counted. Three replicates were independently performed.

Replication	Item	nYFP cYFP	TaMED25-nYFP cYFP	nYFP TaEIL1-cYFP	TaMED25-nYFP TaEIL1-cYFP
1	Cell number with YFP signal	0	0	0	50
	Cells without YFP signal	52	42	44	7
	Total cell number	52	42	44	57
2	Cell number with YFP signal	0	0	0	49
	Cells without YFP signal	43	40	40	2
	Total cell number	43	40	40	51
3	Cell number with YFP signal	0	0	0	40
	Cells without YFP signal	40	40	40	6
	Total cell number	40	40	40	46

Table S4. CFP fluorescence decay frequency within ROI in FLIM-FRET experiment to detect the interaction of TaEIL1 and TaMED25. Six independent cell nuclei were quantified by confocal microscope in each treatment. ROI: Region of interest. "**" in the table represents the significant differences at $p<0.01$ by Student's *t* test.

Sample name	Average fluorescence lifetime τ [ns]						
	Cell 1 ROI	Cell 2 ROI	Cell 3 ROI	Cell 4 ROI	Cell 5 ROI	Cell 6 ROI	Mean
TaEIL1-CFP/mYFP	3.15	3.06	2.96	3.09	2.98	2.94	3.03 ± 0.08
TaEIL1-CFP/TaMED25-mYFP	1.93	1.98	1.79	1.83	1.58	1.82	1.82 ± 0.14 **

Table S5. Statistical analysis of H_2O_2 accumulation index in *Bgt*-infected bread wheat epidermal cells. Two types of *Bgt*-infected bread wheat epidermal cells with differentially accumulated H_2O_2 (type I: cells without H_2O_2 production, type II: cells with highly accumulated H_2O_2, as shown in Fig. 9B and 9C) in BSMV-VIGS bread wheat leaves were microscopically counted, and H_2O_2 accumulation index represents the percentage of type II cells out of all *Bgt*-infected epidermal cells. In each treatment, at least 10 independent bread wheat leaves (3-4cm in length) were DAB-stained, and all the germinated *Bgt* spores on these leaves were microscopically analyzed. Three independent replications were conducted, and the significant difference level of microcolony formation indexes between BSMV-γ control and each treatment was analyzed by Student's *t* test. Numbers before and after "±" represent the means and SD of each replication, respectively. "**" and "*" in the table represent the significant differences at $p<0.01$ and $p<0.05$ levels, respectively. "-", not analyzed.

Sample name	H_2O_2 accumulation index (%)			Significant difference level compared with BSMV-γ
	Replication 1	Replication 2	Replication 3	
BSMV-γ	3.54 ± 1.99	6.17 ± 0.68	8.49 ± 3.17	-
BSMV-*TaMED25as*	21.68 ± 3.03	18.74 ± 1.60	21.70 ± 3.10	**
BSMV-*TaEIL1as*	16.05 ± 1.84	17.64 ± 1.94	16.44 ± 2.56	*
BSMV-*TaERF1as*	16.07 ± 2.63	20.46 ± 2.56	19.96 ± 4.02	*

Table S6. DNA constructs in this study.

Construct name	vector	Description
pCaBS-γ-TaMED25as	pCaBS-γ-LIC	For BSMV mediated silencing of *TaMED25*
pCaBS-γ-HvMED25as	pCaBS-γ-LIC	For BSMV mediated silencing of *HvMED25*
pCaBS-γ-TaEIL1as	pCaBS-γ-LIC	For BSMV mediated silencing of *TaEIL1*
pCaBS-γ-TaERF1as	pCaBS-γ-LIC	For BSMV mediated silencing of *TaERF1*
GAL4-AD-TaEIL1	pDEST22	For Y2H analysis
GAL4-BD-TaMED25	pDEST32	For Y2H analysis
GAL4-BD-TaEIL1	pDEST32	For transcriptional activity assay
GAL4-BD-TaEIL1-NT	pDEST32	For transcriptional activity assay
GAL4-BD-TaEIL1-MD	pDEST32	For transcriptional activity assay
GAL4-BD-TaEIL1-CT	pDEST32	For transcriptional activity assay
pHIS2-TaPIEpro-P1	pHIS2(-Leu)	For Y1H analysis
pHIS2-TaPIEpro-P2	pHIS2(-Leu)	For Y1H analysis
TaMED25-nLUC	p1300-35S-nLUC	For LCI assay
TaMED25-vWF-A-nLUC	p1300-35S-nLUC	For LCI assay
TaMED25-MD/ACID-nLUC	p1300-35S-nLUC	For LCI assay
TaMED25-MD-nLUC	p1300-35S-nLUC	For LCI assay
TaMED25-ACID-nLUC	p1300-35S-nLUC	For LCI assay
TaMED25-Q-rich-nLUC	p1300-35S-nLUC	For LCI assay
TaMED25-ΔACID-nLUC	p1300-35S-nLUC	For LCI assay
cLUC-TaEIL1	p1300-35S-cLUC	For LCI assay
cLUC-TaEIL1-NT	p1300-35S-cLUC	For LCI assay
cLUC-TaEIL1-MD	p1300-35S-cLUC	For LCI assay
cLUC-TaEIL1-CT	p1300-35S-cLUC	For LCI assay
HBT-TaEIL1-GFP	HBT	For subcellular localization analysis in wheat
HBT-TaMED25-RFP	HBT	For subcellular localization analysis in wheat
HBT-TaMED25-nYFP	HBT	For BiFC assay in wheat
HBT-TaEIL1-cYFP	HBT	For BiFC assay in wheat
HBT-TaEIL1-CFP	HBT	For FLIM-FRET assay in wheat
HBT-TaMED25-mYFP	HBT	For FLIM-FRET assay in wheat
p35S:TaEIL1-Myc	pGWB17	For LUC activity assay
p35S:TaMED25-Myc	pGWB17	For LUC activity assay
TaERF1pro:LUC	pGWB35	For LUC activity assay

Table S7. Primers used in this study.

Primer name	Sequence	Annotation
TaMED25-F1	5'GGGGGTTGTGGGTGGTGG3'	First round nested PCR for TaMED25 CDS cloning, forward (F) primer
TaMED25-R1	5'GCTCTGTACATAAGCACAAAACCAC3'	First round nested PCR for TaMED25 CDS cloning, reverse (R) primer
TaMED25-F	5'CCAAGGGGATTCGTGGAGGTT3'	Second round nested PCR for TaMED25 CDS cloning, F primer
TaMED25-R	5'GCCAAATCTCCAAGGAGCCTC3'	Second round nested PCR for TaMED25 CDS cloning, R primer
BSMV-TaMED25-F	5'AACCACCACCACCGTGCTACCTCAATGGGACCTAA3'	Construction of pCaBS-*TaMED25as* for BSMV silencing of *TaMED25*, F primer
BSMV-TaMED25-R	5'AAGGAAGTTTAATGGACCAGCCATCAGACC3'	Construction of pCaBS-*TaMED25as* for BSMV silencing of *TaMED25*, R primer
BSMV-HvMED25-F	Same with the primer 'BSMV-TaMED25-F'	Construction of pCaBS-*HvMED25as* for BSMV silencing of *HvMED25*, F primer
BSMV-HvMED25-R	5'AAGGAAGTTTAATGAACCAGCCATCAAACC3'	Construction of pCaBS-*HvMED25as* for BSMV silencing of *HvMED25*, R primer
BSMV-TaEIL1-F	5'AACCACCACCACCGTCGGATAAAACTAGCAAGTGGGA3'	Construction of pCaBS-*TaEIL1as* for BSMV silencing of *TaEIL1*, F primer
BSMV-TaEIL1-R	5'AAGGAAGTTTAAGGAAGTCTGCGGCATAAGG3'	Construction of pCaBS-*TaEIL1as* for BSMV silencing of *TaEIL1*, R primer
BSMV-TaERF1-F	5'AACCACCACCACCGTTCGTCAACTTTCTGGCCCGTCGT3'	Construction of pCaBS-*TaERF1as* for BSMV silencing of *TaERF1*, F primer
BSMV-TaERF1-R	5'AAGGAAGTTTAACTCTTGCTTCGCCGGCGCCGT3'	Construction of pCaBS-*TaERF1as* for BSMV silencing of *TaERF1*, R primer
ENTRY-TaMED25-F	5'GGGGACAAGTTTGTACAAAAAAGCAGGCTTCATGGTGGAGGGGATGGCTTC 3'	For pENTRY-TaMED25 construction, F primer
ENTRY-TaMED25-R	5'GGGGACCACTTTGTACAAGAAAGCTGGGTCAGATAGGTAGCCTCCTCCAGAC3'	For pENTRY-TaMED25 construction, R primer
ENTRY-EIL1-F	5'GGGGACAAGTTTGTACAAAAAAGCAGGCTTCATGATGGGAGGTGGGCTGCT3'	For pENTRY-TaEIL1 and pENTRY-TaEIL1-NT constructions, F primer
ENTRY-EIL1-R	5'GGGGACCACTTTGTACAAGAAAGCTGGGTCGTAGTACCAATTGGGGCCGTC3'	For pENTRY-TaEIL1 and pENTRY-TaEIL1-CT constructions, R primer
ENTRY-EIL1NT-R	5'GGGGACCACTTTGTACAAGAAAGCTGGGTCCAAGCCGTCGCCAACGCCGC3'	For pENTRY-TaEIL1-NT construction, R primer
ENTRY-EIL1MD-F	5'GGGGACAAGTTTGTACAAAAAAGCAGGCTTCATGAAGCCGCGGCAGTCGCAGG3'	For pENTRY-TaEIL1-MD construction, F primer
ENTRY-EIL1MD-R	5'GGGGACCACTTTGTACAAGAAAGCTGGGTCGGCGGCCACCGCGCTCCTCT3'	For pENTRY-TaEIL1-MD construction, R primer
ENTRY-EIL1CT-F	5'GGGGACAAGTTTGTACAAAAAAGCAGGCTTCATGGAGCCGGAGCTGATGCTGAA3'	For pENTRY-TaEIL1-CT construction, F primer
EIL1-CLuc-F	5'CGCGGATCCAATGATGGGAGGTGGGCTGCT3'	For cLuc-TaEIL1 construction, F primer
EIL1-CLuc-R	5'ACGCGTCGACTCAGTAGTACCAATTGGGGCCGTC3'	For cLuc-TaEIL1 construction, R primer
MED25-NLuc-F	5'CGCGGATCCAATGGTGGAGGGGATGGCTTC3'	For TaMED25-nLuc and TaMED25-vWF-A-nLuc constructions, F primer
MED25-NLuc-R	5'ACGCGTCGACAGATAGGTAGCCTCCTCCAGACAT3'	For TaMED25-nLuc and TaMED25-Q-rich-nLuc constructions, R primer
MEDΔN-Nluc-F(Uni)	5'CGCGGATCCAATGTTCATGGAGGCTCGAACAGC3'	For TaMED25-MD-nLuc, TaMED25-MD/ACID-nLuc and TaMED25-ACID-nLuc constructions, F primer
MEDΔC-Nluc-R(Uni)	5'ACGCGTCGACAGTTGAGACCTGTGGTTTGA3'	For TaMED25-MD/ACID-nLuc and TaMED25-ACID-nLuc constructions, R primer
MED-ACID-Nluc-F(Uni)	5'CACGGGGGACGAGCTCGGTACCATGTCGAAGTATGTCAAAATTTGGG3'	For TaMED25-ACID-nLuc construction, F primer
MEDΔACID-SOE-F	5'AATGGCCAGCAACCACAGCAGCCACAGATGCAGCC3'	For TaMED25ΔACID-nLuc construction, F primer
MEDΔACID-SOE-R	5'CATCTGTGGCTGCTGTGGTTGCTGGCCATTAGGATG3'	For TaMED25ΔACID-nLuc construction, R primer
EIL1-N-CLuc-F(Uni)	5'CGCGGATCCAATGATGGGAGGTGGGCTGCT3'	For cLuc-TaEIL1-NT construction, F primer
EIL1-N-CLuc-R(Uni)	5'ACGCGTCGACTCACAAGCCGTCGCCAACGCCGC3'	For cLuc-TaEIL1-NT construction, R primer
EIL1-MD-CLuc-F(Uni)	5'CGCGGATCCACGCATGTGGCGCGACCGCAT3'	For cLuc-TaEIL1-MD construction, F primer
EIL1-MD-CLuc-R(Uni)	5'ACGCGTCGACTCAGGCGGCCACCGCGCTCCTCT3'	For cLuc-TaEIL1-MD construction, R primer
EIL1-C-CLuc-F(Uni)	5'CGCGGATCCAATGGAGCCGGAGCTGATGCTGAA3'	For cLuc-TaEIL1-CT construction, F primer
EIL1-C-CLuc-R(Uni)	5'ACGCGTCGACTCAGTAGTACCAATTGGGGC3'	For cLuc-TaEIL1-CT construction, R primer
TaGAPDH-F	5'TTAGACTTGCGAAGCCAGCA3'	qRT-PCR primer for internal control gene *TaGAPDH*, F primer
TaGAPDH-R	5'AAATGCCCTTGAGGTTTCCC3'	qRT-PCR primer for internal control gene *TaGAPDH*, R primer
HvActin1-F	5'TGGCACCCGAGGAGCACC3'	qRT-PCR primer for internal control gene *HvActin1*, F primer
HvActin1-R	5'GTAACCTCTCTCGGTGAG3'	qRT-PCR primer for internal control gene *HvActin1*, R primer
real-TaMED25-F	5'TTTCTGCACCTGCATTCTCTC3'	qRT-PCR assay for *TaMED25*, F primer
real-TaMED25-R	5'ACCTGTTGTTGGATAGGGTTTACT3'	qRT-PCR assay for *TaMED25*, R primer
real-HvMED25-F	5'TTTCTCAACCTGCATTCTCTC3'	qRT-PCR assay for *HvMED25*, F primer
real-HvMED25-R	Same with the primer 'real-TaMED25-R'	qRT-PCR assay for *HvMED25*, R primer
real-EIL1-F	5'GTGCTCACCGCTGTCATCAAG3'	qRT-PCR assay for *TaEIL1*, F primer
real-EIL1-R	5'GCGAGGTCAACGTCGTACTCA3'	qRT-PCR assay for *TaEIL1*, R primer
real-ERF1-F	5'GGAGCCACCAGTCCGTATGA3'	qRT-PCR assay for *TaERF1*, F primer
real-ERF1-R	5'CACCCGGCAGAGGTATTCAA3'	qRT-PCR assay for *TaERF1*, R primer
real-TaPOX2-F	5'AGGGGCTTCGGCGTCATC3'	qRT-PCR assay for *TaPOX2*, F primer
real-TaPOX2-R	5'TTGGGCGTCGTCGTGTCC3'	qRT-PCR assay for *TaPOX2*, R primer
real-TaADH-F	5'AGCCAAGGGTCAAACTCC3'	qRT-PCR assay for *TaADH*, F primer
real-TaADH-R	5'GATGGTGAAGCGAGACTGC3'	qRT-PCR assay for *TaADH*, R primer
real-TaPR1-F	5'GAGAATGCAGACGCCCAAGC3'	qRT-PCR assay for *TaPR1*, F primer
real-TaPR1-R	5'CTGGAGCTTGCAGTCGTTGATC3'	qRT-PCR assay for *TaPR1*, R primer
real-TaPR2-F	5'AGGATGTTGCTTCCATGTTTGCCG3'	qRT-PCR assay for *TaPR2*, F primer
real-TaPR2-R	5'AAGTAGATGCGCATGCCGTTGATG3'	qRT-PCR assay for *TaPR2*, R primer
HIS2-TaERF1pro-P1-F	5'GGGCGAATTCCGGGGAGCTCGCAGGTGCAATTAATTTTATT3'	For pHIS2-TaERF1pro-P1 construction, F primer
HIS2-TaERF1pro-P1-R	5'TAATGCCAGGAATTTCTAGAGGGGCACATTCGTTTTGACATG3'	For pHIS2-TaERF1pro-P1 construction, R primer
HIS2-TaERF1pro-P2-F	5'GGGCGAATTCCGGGGAGCTCCCATATCACATGCACCAC3'	For pHIS2-TaERF1pro-P2 construction, F primer
HIS2-TaERF1pro-P2-R	5'TAATGCCAGGAATTTCTAGATGTCGTCCATGCGTTCGTTG3'	For pHIS2-TaERF1pro-P2 construction, R primer