

Supporting Information

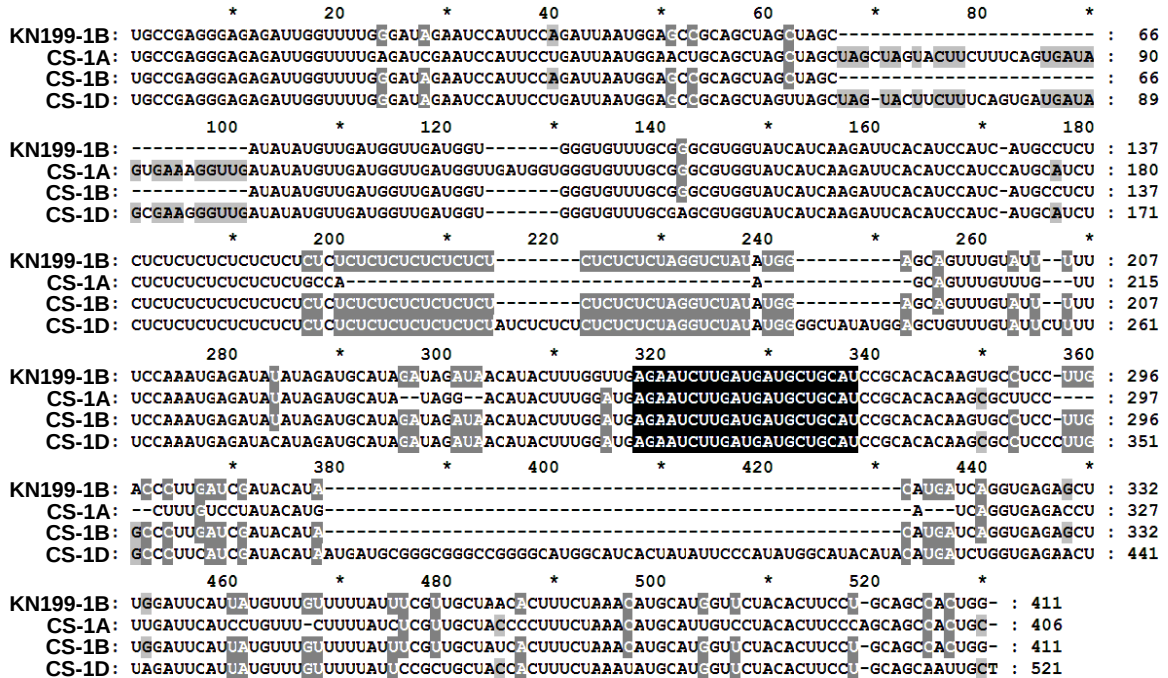
tae-MIR172

Figure S1. Sequence alignment of *tae-MIR172* precursors from chromosome 1B of Kenong199 (KN199) and chromosomes 1A, 1B and 1D of Chinese spring (CS). The mature *tae-miR172* sequences are represented by black shade boxes.

Figure S2

(a)



KN199 #1 #3 #4 #5
pUbi:tae-MIR172

(b)



KN199 #1 #3 #4 #5
pUbi:tae-MIR172

Figure S2. Morphological characters of the *pUbi:tae-MIR172* transgenic bread wheat plants. (a) Whole plant view of different *pUbi:tae-MIR172* transgenic lines. Bar = 20 cm. (b) The spike phenotypes of the *pUbi:tae-MIR172* transgenic lines. Bar = 2 cm. #1, #3, #4 and #5 represent independent transgenic lines.

Figure S3

5'-
ATGGTGCTGGATCTCAATGTGGAGTCGCCGGCGGACTCGGGCACGTCCAGCTCCTCCG
TGCTCAACTCCGCGGACGCCGGTGGCGGCGGCTTCCGGTTCGGCCTGCTCGGGAGCC
CTGATGATGACGACTGCTCCGGCGAGCCGGCGCCGGTTCGGGCCCCGGGTTCGTACGA
GGCAGCTCTTCCCCGCGTCGCCGCCCGGGCACGCGGGCGCGCCCCGGGGTGACGATG
GGGCAGCAGGCCCGGCGCCTGCGCCGATGGCGCCCGTGTGGCAGCCGCGGGCGCGC
CGAGGAGCTCCTCGTGGCGCAGCGGATGGCGCCCGCGAAGAAGACGCGGCGGGGCC
CGAGGTGCGCGCAGCTCGCAGTACAGGGGCGTCACCTTCTACCGCAGGACCGGCCGGT
GGGAGTCGCACATCTGGGATTGCGGGAAGCAGGTCTACTTGGGTGGTTTTCGACACTGC
GCACGCGGCCGCAAGGGCCTACGATCGCGCGGCGATCAAGTTCCGGGGGGCTGGAGGC
CGACATCAACTTCAATCTGAGCGACTACGAGGAGGATTTGAAGCAGATGAGGAACTGGA
CCAAGGAGGAGTTTCGTGCACATCCTCCGCCGCCAGAGCACGGGGTTTCGCCAGGGGGA
GCTCCAAGTACCGCGGCGTACGCTCCACAAGTGCGGCCGCTGGGAGGCAAGGATGG
GCCAGCTGCTCGGCAAGAAGTACATATATCTGGGCCTCTTTGACAGCGAAGTTGAAGCT
GCAAGGGCGTACGACAGGGCGGCGATTTCGCTTCAATGGGAGGGAAGCTGTGACTAACT
TTGAGAGCAGCTCCTACAATGGGGATGCTCCACCCGACGCCGAAAATGAGGCAATTGTT
GATGCTGATGCTCTTGACTTGATCTGCGGATGTCGCAACCCACCGCGCACGATCCCA
AGAGGGACAACATCATCGCCGGCCTTCAGTTAACTTTTGATTCCCCTGAATCGTCAACC
ACAATGATCTCTTCTCAGCCAATGAGCTCATCTTCGTCCCAGTGGCCTGTGCATCAACAT
GGCACGGCAGTAGCACCTCAGCAGCACCAGCGTTTGTACCCATCTGCTTGTGCATGGCTT
CTACCCGAACGTACAGGTGCAGGTGCAGGAGAGGCCCATGGAGGCAAGGCCCCCTGA
GCAGCCGTCGTCCTTCCCCGGCTGGGGGTGGCAAGCGCAAGCCATGCCGCCGGGGCTC
CTCCCACTCGCCGTTGCTTTACG**CTGCAGCATCATCAGGATTTT**CTACCGCCGCCGCC
GGCGCGAACCTCGCCCCGCCGCCGCGGTACCCGGACCACCACCGGTTCTACTTCCCC
CGCCCGCCGGACAACCTGA-3'

Figure S3 The coding sequence of *Q* from bread wheat cultivar **KN199**. The miR172-targeting site is highlighted in red.

Figure S4



Figure S4 The domestication-related traits of the spikes of *pUbi:tae-MIR172* transgenic lines.

Figure S5

5'-

ATGTCTTCTCTCAGCCGGGAGCTCGTCTTCCTCATCCTGCAGTTCCTCGATGAGGAGAAGTTCAAGG
AGACCGTCCACAAGCTTGAGCAGGAGTCTGGCTTCTACTTCAACATGAAGTACTTCGAGGATGAGGT
GATCAATGGCAATTGGGATGAGGTGGAGCGCTACCTCGGGGGCTTCACCAAAGTCGACGACAACC
GCTACTCGATGAAGATATTCTTTGAGATCCGCAAGCAGAAGTATCTCGAGGCCCTCGACAAGCATGA
TCGGTCCAAGGCGGTTGAAATCTTGGTCAAGGACTTGAAGGTGTTTGCATCCTTTAATGAGGAGCTG
TTTAAGGAGATCACACAGCTATTGACTCTGGAGAAGTTTCAAGGAGAATGAGCAGCTCTCCAAGTATG
GTGATACAAAATCTGCAAGAGCAATAATGCTTGTTGAGCTGAAGAAGCTGATCGAAGCTAACCCCTT
ATTCCGTGACAAGCTTCAGTTTCCCAATCTGAAGAGTTCTAGATTACGGACACTTATCAATCAGAGCT
TAAACTGGCAGCACCAGCTTTGCAAAAATCCCAGGCCTAATCCTGACATCAAGACCCTCTTTGTTGA
TCATTCTTGTGGACAACCAAATGGTGCACGTGCTCCATCACCAGCAAACAATCCACTACTTGGATCT
ATACCTAAACCTGGTGGTTTCCCCCAATTGGGCGCCCATGGACCCTTTCAACCTGCACCAACACCTG
TCGCACCTCTGGCCGTTGGATGTCAAACCCTCCAGCAGTAACACATCCTGCTGTTTCTGGAGGTG
CTATTGGATTTGGTACTCCTACGAATCCTGCTGCTATGTTGAAGCATCCTAGGACACCCTCGGCTGC
TAACCCTTCTATGGACTATCCATCTGGAGATTCTGATCATGTGAGTAAGAGACCCAGGCCAGTTGGG
TTGTCTGAGGAGGTGAATCTTCCGGTGAATATGATGCCAGTAACTTATCCGCAGAGCCATAGCTACC
CGCAAGATGATTTCCATAAAGCTGTGCGACGGACATTGAGTCAAGGATCAGCTCCAATGAGCATGGA
TTTCCATCCAGTTCAACAACTCTTCTTCTTGGTACCAATGTTGGTGACATTGGATTGTGGGATG
TTGGCACCAAGGAGAGACTTGTGTAAGAACTTCAAGGTTTGGGAGCTTGGGAAATGTTCTATGGC
CCTCCAGGCAGCACTGGTTAAGGATCCTACCGTGTGAGTTAATCGCATAATTTGGAGTCCTGATGGA
ACCTTGTGTTGGTGTGCTTATTCAAGGCATATAGTACAGATTTATTCTTATCATGGTGGCGATGATATT
AGGCAACACTTGGAGATTGATGCACATGTTGGTGGCGTAAATGACATTGCATTGCCCCATCCAAATA
AGCAGCTGTGTATAATTACCTGTGGAGACGATAAGACGATAAAGGTGTGGGAGGCCACTAGTGGAA
CAAAACAATTTACCTTCGAAGGTCATGAAGCTCCTGTCTATTCTGTTTGTCCACATTACAAGGAAAAT
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CAGAGTTGACTATGATGCACCAGGTCATTGGTGCCTACGATGGCATATAGTGCGGATGGTTCAAGA
TTGTTTTCTTGCGGGACCAGCAAGGATGGTGAATCACACCTGGTGAATGGAATGAGAGTGAAGGT
GCGGTGAAGAGAACATACCAGGGATTTTCGTAAGCGATCTATGGGTGTTGTACAATTCGATACGACGC
GAAATAGGTTTTTGGCTGCTGGAGATGAATTCGTGATAAAGATTTGGGACATGGACAACACTAGTCT
TCTGACTACCATTGAAGCTGATGGTGGCCTACCTGCAAGCCCGCGTATCCGCTTTAACAAGGAGGG
TACTCTGTTGGCAGTCTCTACTGTTGATAATGGTATCAAAGTCTTAGCAAATGCTGATGGTGTTCGTT
TATTGCGCACACTGGAAAATCGTTCTTTTATGCTTTCACGTAGTGCATCTGAGACTGTAACAAAGCCT
CTAATAAACCCATTGACTGCTGCTGCTGCGGCAGCCGCCGCGCTGCCGCCGCTGCAACCAGTTCT
GGAAGTCTGCTCCATCACCTATAACTGCAATGAACGGGGACAACAGAAGCATGGTTGATGTAAAAC
CTAGAATAGCTGATGAGTCAATGGATAAGTCAAAGGTCTGGAAGCTTATGGAGATAACTGATACAGC
TCAGTGCAGATCATTAATACTAGGTGATAGTATTAGGACAGCTAAGATCTCGAGACTGATCTACACAA
ATTCAGGTGTTGCTATCTTGGCTTTAGCTTCAAATGCCGTCCATCTACTGTGGAAATGGCCACGTAAT
GAACGAAATTCAACTGGAAAGGCTACTGCTAGTGTCTCTCTCAATTATGGCAACCTCCAAGTGGCA
TTCTCATGACTAATGACACAATTGACAATAGTCTGATGAGGCCGTTCACTGCTTTGCTTTGTCAAAG
AATGATTCATATGTCATGTCAGCTTCAGGAGGGGAAAATCTCTCTATTCAACATGATGACTTTTAAGAC
GATGACGACGTTTATGCCTCCGCCACCAGCAGCTACTTTCCTCGCATTCCATCCTCAAGATAACAAC
ATAATTGCAATTGGAATGGATGATTCAACCATCCAAATTTACAACGTTCCGGATTGATGAGGTCAAAAG
TAAACTTAGAGGGCACTCTAAGAAAATTACAGGTCTTGCCTTTTCAAATGTGTTAAATGTTTTGGTATC
CTCTGGAGCTGATGCACAGATATGTGTTTGAACACTGATGGGTGGGAGAGGCAAAGGAGCAGATT
TTTGCAGATACCATCTGGTCGCCAACGTCCAACATCTTAGACACACGAGTTTCACTTCCACCAAGAT
CAACAGCATTGTCTTGTGTCATGAGACCCAGATTGCCATCTATGATGCCTCAAAATTAGAACCCGT
GAAGCAGTGGCCTCCTCGGGAGACATCTGCTCCTCCAATAACGCATGCTACATTCTCATGTGATAGT
CAACTGATTTATGCAAGCTTTCTAGATGCCACTGTCTGCATATTTAGCGCATCAAGTTTGAGACTTCA
ATGCCGAATTCTTCCAGCTTCTTATCTTCTCAAATATCAGTTCAAATGTTTCATCCAGTTGTGGTTGC
GGCACATCCTTCGGAAGCAAATCAGTTTGCTCTAGGCCTTACCGATGGCAGCGTTTATGTCATGGAA
CCGTTGGAATCTGAGAGAAAGTGGGGAATTCCTCCACCAGCGGAGAATGGATCGACGAGCAACATG
TCCACACCTCCTAATGGAGCTTCGAGTTCTGATCAACCAGAAAGATAA-3'

Figure S5 The coding sequence of *TaTPL* from the A genome of bread wheat cultivar KN199.

Figure S6

5'-
ATGTCTTCTCTCAGCCGGGAGCTCGTCTTCCTCATCCTGCAGTTCCTCGATGAGGAGAAGTTCAAGG
AGACCGTCCACAAGCTCGAGCAGGAGTCTGGTTTCTACTTCAACATGAAGTACTTTGAGGACGAGGT
GATCAATGGGAATTGGGATGAGGTGGAGCGCTACCTCGGGGGCTTCACCAAAGTCGACGACAACC
GCTACTCGATGAAGATATTCTTTGAGATCCGCAAGCAGAAGTATCTCGAGGGCCCTCGATAAGCATGA
TCGGTCCAAGGCGGTTGAAATCTTGGTCAAGGACTTGAAGGTGTTTGCATCCTTTAACGAGGAGCTG
TTTAAGGAGATAACACAGCTATTGACTCTGGAGAACTTCAGGGAGAATGAGCAGCTCTCCAAGTATG
GTGATACAAAATCTGCAAGAGCAATAATGCTTGTTGAGCTGAAGAAGCTGATCGAAGCTAACCCCTT
ATTCCGTGATAAGCTCCAGTTTCCCAATCTGAAGAGCTCTAGATTACGGACACTTATCAACCAGAGC
TTAAACTGGCAGCACCAGCTTTGCAAAAATCCTAGGCCTAATCCTGACATCAAGACCCTCTTTGTTGA
TCATTCTTGTGGACAACCAAATGGTGCACGTGCTCCATCACCAGCAAACAATCCACTACTTGGATCT
ATACCTAAACCTGGTGGTTTCCCCCAATTGGGCGCCCATGGACCCTTTCAACCTGCACCAACACCC
GTCGCACCTCTGGCCGGTTGGATGTCAAACCCTCCAGCAGTAACGCATCCTGCTGTTTCTGGAGGT
GCTATTGGATTTGGTACTCTACGAATCCTGCTGCTATGTTGAAGCATCCTAGGACACCCTCGGCTG
CTAACCTTTCTATGGATTATCCATCTGGAGATTCTGATCATGTCAAGTAAAGAGACCTAGGCCAGTTGG
GTTGTCTGAGGAGGTGAATCTTCCGGTGAATATGATGCCAGTAACTTATCCGCAGAGCCATAGCTAC
CCGCAAGATGATTTCCATAAAGCTGTCGCACGGACATTGAGTCAAGGATCAGCTCCAATGAGCATGG
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GTTGGCACCAAGGAGAGACTTGTGTAAGAACTTCAAGGTTTGGGAGCTTGGGAAATGTTCTATGG
CCCTCCAGGCTGCACTGGTTAAGGATCCTACCGTGTGAGTTAATCGCATAATATGGAGTCCTGATGG
AACCTTGTGGTGTGCTTATTCAAGGCATATAGTACAGATTTATTCTTATCATGGTGGCGATGATAT
TAGGCAACACTTGGAGATTGATGCACATGTTGGTGGCGTAAATGACATTGCATTGCCCCATCCAAAT
AAGCAGCTCTGTATAATTACCTGTGGAGACGATAAGACGATAAAGGTGTGGGAGGCCACCAGTGGA
ACAAAACAATTTACCTTTGAAGGTCATGAAGCTCCTGTCTATTCTGTTTGTCCACATTACAAGGAAAA
TATTCAGTTCATCTTTTCAACTGCTTTAGATGGAAAGATAAAGGCATGGCTCTATGATAATCTTGGGT
CCAGAGTTGACTATGATGCACCAGGTCAATTGGTGCACCTACGATGGCATATAGTGCGGATGGGTCAA
GATTATTTTCTTGTGGGACCAGCAAGGATGGTGAATCACACCTGGTGGAAATGGAATGAGAGTGAAG
GTGCGGTGAAGAGAACATAACCAGGGATTTTCGTAAGCGATCGATGGGTGTTGTACAATTTGATACGAC
GCGAAATAGGTTTTTGGCTGCTGGAGATGAGTTCGTGATAAAGATTTGGGACATGGACAACACTAGT
CTTCTGACTACCATTGAAGCTGATGGTGGCCTACCTGCAAGCCCGCGTATCCGCTTTAACAAGGAG
GGTACTCTGTTGGCAGTCTCTACTGTTGATAATGGTATCAAAGTCTTAGCAAATGCTGATGGTGTTTCG
TTTATTGCGCACACTGGAAAATCGTTCTTTTGATGCTTCTCGTAGTGCATCTGAGACTGTAACAAAGC
CTCTTATAAACCCATTGACTGCTGCTGCCGCGGCAGCTGCCGCCGCCGCCGCTGCAACCAGTTCTG
GAACTGCTGCTCCATCATCTATAACTGCAATGAATGGGGACAACAGAAGCATGGTTGATGTAAACC
TAGAATAGCTGATGAGTCAATGGATAAGTCAAAGGTCTGGAAGCTTATGGAGATAACTGATACAGCT
CAGTGCAGATCACTAAACTAGGTGATAGTATTAGGACAGCTAAGATCTCGAGACTGATCTACACAA
ATTAGGTGTTGCTATCTTGGCTTTAGCTTCAAATGCCGTCCATCTACTGTGGAAATGGCCACGTAAT
GAACGAAATTCAACTGGAAAGGCTACTGCTAGTGTCTCTCTCAATTATGGCAACCTCCAAGTGGCA
TTCTCATGACTAATGACACAATTGACAATAGTCCTGATGAGGCCGTTCACTGCTTTGCTTTGTCAAAG
AATGATTCATATGTCATGTCAGCTTCAGGAGGGAAAATCTCTTATTCAACATGATGACTTTTAAGAC
GATGACAACGTTTATGCCTCCACCACCAGCAGCTACTTTCCTAGCATTCCATCCTCAAGATAACAACA
TAATTGCAATTGGAATGGATGATTCAACCATCCAAATTTACAACGTTCCGATTGATGAGGTCAAAAGC
AACTTAGAGGGCACTCTAAGAAAATTACAGGTCTCGCCTTTTCAAATGTGTTAAATGTTTTGGTATC
CTCTGGAGCTGATGCACAGATATGTGTTTGGAACTGATGGGTGGGAGAGGCAAAGGAGCAGATT
TTTGCAGATACCGTCTGGCCGCCAACGTCCAACATCTTAGACACACGAGTTCACTTCCACCAAGAT
CAACAGCATTGTCTTGTGTCCATGAGACCCAGATTGCCATCTATGATGCCTCAAACTAGAACCCG
TGAAGCAGTGGCCTCCTCGGGAGACCTCTGCTCCTCCAATAACGCATGCTACATTCTCATGTGATAG
TCAACTGATTTATGCAAGCTTTCTGGACGCCACTGTCTGCATATTTAGCGCATCAAGTTTGAGACTCC
AATGCCGAATTCTTCCAGCTTCTTATCTTCTCAAATATCAGTTCAAATGTTTCATCCAGTTGTGGTTG
CGGCACATCCTTCGGAGGCAAATCAGTTTGCTCTAGGCCTTACTGATGGCAGTGTTTATGTCATGGA
ACCGTTGGAATCTGAGAGAAAGTGGGGAATTCCTCCACCAGCGGAGAATGGATCGACGAGCAACAT
GTCCACACCTCCTAATGGAGCTTCGAGTTCTGATCAACCAGAAAGATAA-3'

Figure S6 The coding sequence of *TaTPL* from the D genome of KN199.

Table S1. Prediction of putative target genes of tae-miR172 in bread wheat. UPE, maximum energy to un-pair.

Target accession number	E-value	UPE	Target aligned fragment	Target description
CA609410	0.5	12.522	UGCAGCAUCAU CAGGAUUCU	weakly similar to UniRef100_Q0DL60 Cluster: Os05g0121600 protein; n=1; Oryza sativa Japonica Group Rep: Os05g0121600 protein - Oryza sativa subsp. japonica (Rice), partial (11%)
CA626451	0.5	21.238	UGCAGCAUCAU CAGGAUUCU	UniRef100_A6NAX8 Cluster: AP2 domain transcription factor; n=1; Zea mays Rep: AP2 domain transcription factor - Zea mays (Maize), partial (25%)
CA652598	0.5	13.558	UGCAGCAUCAU CAGGAUUCU	similar to UniRef100_Q0DL60 Cluster: Os05g0121600 protein; n=1; Oryza sativa Japonica Group Rep: Os05g0121600 protein - Oryza sativa subsp. japonica (Rice), partial (10%)
CA486144	0.5	11.277	UGCAGCAUCAU CAGGAUUCU	similar to UniRef100_Q2TQ34 Cluster: Transcription factor AP2D23-like; n=2; Oryza sativa Rep: Transcription factor AP2D23-like - Oryza sativa subsp. japonica (Rice), partial (18%)
TC438982	0.5	13.048	UGCAGCAUCAU CAGGAUUCU	similar to UniRef100_Q0DL60 Cluster: Os05g0121600 protein; n=1; Oryza sativa Japonica Group Rep: Os05g0121600 protein - Oryza sativa subsp. japonica (Rice), partial (9%)
TC427232	0.5	12.864	UGCAGCAUCAU CAGGAUUCU	weakly similar to UniRef100_Q0DL60 Cluster: Os05g0121600 protein; n=1; Oryza sativa Japonica Group Rep: Os05g0121600 protein - Oryza sativa subsp. japonica (Rice), partial (10%)
TC392280	0.5	13.048	UGCAGCAUCAU CAGGAUUCU	weakly similar to UniRef100_Q0DL60 Cluster: Os05g0121600 protein; n=1; Oryza sativa Japonica Group Rep: Os05g0121600 protein - Oryza sativa subsp. japonica (Rice), partial (18%)
TC401083	0.5	13.215	UGCAGCAUCAU CAGGAUUCU	similar to UniRef100_Q2TQ34 Cluster: Transcription factor AP2D23-like; n=2; Oryza sativa Rep: Transcription factor AP2D23-like - Oryza sativa subsp. japonica (Rice), partial (62%)
TC374382	0.5	13.215	UGCAGCAUCAU CAGGAUUCU	similar to UniRef100_Q2TQ34 Cluster: Transcription factor AP2D23-like; n=2; Oryza sativa Rep: Transcription factor AP2D23-like - Oryza sativa subsp. japonica (Rice), partial (76%)
CA648892	1	16.893	UGCAGCAUCAU CAGGAUUUU	UniRef100_Q5Y165 Cluster: Floral homeotic protein; n=3; Triticum Rep: Floral homeotic protein - Triticum turgidum subsp. dicoccon, partial (13%)
TC405024	1	17.371	UGCAGCAUCAU CAGGAUUUU	UniRef100_Q5Y165 Cluster: Floral homeotic protein; n=3; Triticum Rep: Floral homeotic protein - Triticum turgidum subsp. dicoccon, partial (15%)
TC400547	1	17.371	UGCAGCAUCAU CAGGAUUUU	UniRef100_Q5Y383 Cluster: Floral homeotic protein; n=1; Triticum turgidum subsp. carthlicum Rep: Floral homeotic protein - Triticum turgidum subsp. carthlicum, partial (49%)
TC381895	1	17.371	UGCAGCAUCAU CAGGAUUUU	UniRef100_Q5Y383 Cluster: Floral homeotic protein; n=1; Triticum turgidum subsp. carthlicum Rep: Floral homeotic protein - Triticum turgidum subsp. carthlicum, partial (36%)
TC368660	1	17.371	UGCAGCAUCAU CAGGAUUUU	UniRef100_Q5Y386 Cluster: Floral homeotic protein; n=5; Triticum Rep: Floral homeotic protein - Triticum aestivum (Wheat), complete
NP9350139	1.5	17.562	GGCAGCAUCAU CAGGAUUCU	GB AY714341.1 AAU94918.1 floral homeotic protein; AP2-like transcription factor; Q protein
GH725141	2.5	20.811	GGCAGCAUCAU CAAGAUCCU	similar to UniRef100_Q2PYW7 Cluster: Succinyl CoA ligase beta subunit-like protein; n=1; Solanum tuberosum Rep: Succinyl CoA ligase beta subunit-like protein - Solanum tuberosum (Potato), partial (11%)
TC404380	2.5	18.186	UGCAGCAUCAU CACGAUUC	similar to UniRef100_Q0J9J3 Cluster: Os04g0649100 protein; n=1; Oryza sativa Japonica Group Rep: Os04g0649100 protein - Oryza sativa subsp. japonica (Rice), partial (26%)
CA644318	2.5	20.726	AAGCUGCAUCA UCAAGAUUUU	
CA727182	3	11.11	AGUAGUAUUAU CAAGAUUUU	
TC438028	3	22.883	AUGCGCAAUCA UCAAGAUUUU	
TC420199	3	21.72	UGUGGUAACAU UAAGAUUCU	homologue to UniRef100_Q7XYC9 Cluster: 60s ribosomal protein L21; n=1; Triticum aestivum Rep: 60s ribosomal protein L21 - Triticum aestivum (Wheat), partial (97%)
DR731547	3	14.115	UUCAGCCUUAU UAAGAUUCU	

Table S2. Constructs used in this study.

Construct name	Vector	Description
<i>pUbi:tae-MIR172</i>	<i>pUbi:cas</i>	For gene transformation
<i>p35S:tae-MIR172</i>	<i>pGreen0800</i>	For transient expression assay in <i>N. benthamiana</i>
<i>p35S:Q-Myc</i>	<i>PGWB17</i>	For transient expression assay in <i>N. benthamiana</i>
<i>p35S:mQ-Myc</i>	<i>PGWB17</i>	For transient expression assay in <i>N. benthamiana</i>
<i>p35S:Q-GFP</i>	<i>PGWB5</i>	For subcellular localization analysis in <i>N. benthamiana</i>
<i>BD-Q</i>	<i>pGBKT7</i>	For luciferase transient expression assay
<i>p35S:GAL4-BD-Q</i>	<i>P2GW7</i>	For luciferase transient expression assay
<i>AD-Q</i>	<i>pGADT7</i>	For Y2H assay
<i>BD-TaTPL</i>	<i>pGBKT7</i>	For Y2H assay
<i>nYFP-TaTPL</i>	<i>pEarly201</i>	For BiFC assay in <i>N. benthamiana</i>
<i>nYFP-Q</i>	<i>pEarly202</i>	For BiFC assay in <i>N. benthamiana</i>
<i>nLUC-Q</i>	<i>p1300-35S-nLUC</i>	For LCI assay in <i>N. benthamiana</i>
<i>nLUC-Q^{mEAR1}</i>	<i>p1300-35S-nLUC</i>	For LCI assay in <i>N. benthamiana</i>
<i>nLUC-Q-N</i>	<i>p1300-35S-nLUC</i>	For LCI assay in <i>N. benthamiana</i>
<i>nLUC-Q-M</i>	<i>p1300-35S-nLUC</i>	For LCI assay in <i>N. benthamiana</i>
<i>nLUC-Q-C</i>	<i>p1300-35S-nLUC</i>	For LCI assay in <i>N. benthamiana</i>
<i>cLUC-TaTPL</i>	<i>p1300-35S-cLUC</i>	For LCI assay in <i>N. benthamiana</i>
<i>cLUC-TaTPL-N</i>	<i>p1300-35S-cLUC</i>	For LCI assay in <i>N. benthamiana</i>
<i>cLUC-TaTPL-NΔCTHL</i>	<i>p1300-35S-cLUC</i>	For LCI assay in <i>N. benthamiana</i>
<i>cLUC-TaTPL-C</i>	<i>p1300-35S-cLUC</i>	For LCI assay in <i>N. benthamiana</i>

Table S3. Primers used in this study.

Primer name	Sequence (5'-3')
pUbi:tae-MIR172-F	CGCGGATCCTGCCGAGGGAGAGATTGGTT
pUbi:tae-MIR172-R	CGGGGTACCCCACTGGCTGCAGGAAGTGTAG
Q-F1	AGGAGTGCCTTTTATTCGGTCCCGG
Q-R1	CCACCGCCGTCTGGTCACAACG
Q-F	ATGGTGCTGGATCTCAATGTGGAGTCGC
Q-R(-stop)	GTTGTCCGGCGGGGCGGGGGAA
SOE-mQ-F	GTCTTATTGCCCTGCACTGCCGTGCCG
SOE-mQ-R	GCGCTACGGTTGACGGCACGGCAGTGCA
35S:tae-MIR172-F	CTTCGGTACCTGCCGAGGGAGAGATTGGTT
35S:tae-MIR172-R	CTTCGGATCCCCAGTGGCTGCAGGAAGTGTAG
TaTPL-outer-F	CAGGCTAGGTTTACGGCCAGG
TaTPL-outer-R	CTGAGATGGATACCTTGTTAGTG
TaTPL-F	ATGTCTTCTCTCAGCCGGGAGC
TaTPL-R	TTATCTTTCTGGTTGATCAGAACTCGA
TaTPL-R(-stop)	TCTTTCTGGTTGATCAGAACTCGA
AD-Q-F	GGAATTCCATATGATGGTGCTGGATCTCAATGTGGAG
AD-Q-R(-stop)	CGGAATTCGTTGTCCGGCGGGGCGGGGGAA
BD-TaTPL-F	AGGAGGACCTGCATATGATGTCTTCTCTCAGCCGGGAGC
BD-TaTPL-R	ACGGATCCCCGGGAATTCTTTTCTGGTTGATCAGAACTCGA
TaTPL- Δ CTHL-F	GTTTCTACTTCCGGTTGAAATCTTGGTCAAGGACTT
TaTPL- Δ CTHL-R	ATTTCAACCGGAAGTAGAAACCAGACTCCTGCTCG
nLUC-Q-F	GGGGTACCATGGTGCTGGATCTCAATGTGGAGTCG
nLUC-Q-R	GCGTCGACGTTGTCCGGCGGGGCGGGG
nLUC-Q-N-R	GCGTCGACCCCATTTGTAGGAGCTGCTCTCA
nLUC-Q-C-F	GGGGTACCGATGCTCCACCCGACGCC
Q ^{mEAR1} -F	ATGGTGGCCGCTGCCGCTGTGGAGTCGCCGGCGGACTCG
nLUC-Q ^{mEAR1} -F	GGGGTACCATGGTGCCGCTGCCGCTGTG
cLUC-TaTPL-F	ACGCGTCCCGGGGCGGTACCATGTCTTCTCTCAGCCGGGAGC
cLUC-TaTPL-R	GTTGCTGCAGGTGCACTTATCTTTCTGGTTGATCAGAACTCGA
cLUC-TaTPL-N-R	GTTGCTGCAGGTGCACTTAGAAATCATCTTGCGGGTAGCTATG
cLUC-TaTPL-C-F	ACGCGTCCCGGGGCGGTACCCATAAAGCTGTCGCACGGAC
BD-Q-F	AGGAGGACCTGCATATGATGGTGCTGGATCTCAATGTGGAG
BD-Q-R(-stop)	ACGGATCCCCGGGAATTCGTTGTCCGGCGGGGCGGGGGAA
BD-F	ATGAAGCTACTGTCTTCTATCGAACAAGC
5'RACE-Q-outer-R	TCGACCGCGCGCACCCACCGC
5'RACE-Q-inner-R	CACCCACCGCCGTCTGGTCACAA
tae-miR172-RT	GTCGTATCCAGTGCAGGGTCCGAGGTATTCGCACTGGATACGACATGCAG
Real-Q-F	GCACCTCAGCAGCACCAGCGTTT
Real-Q-R	GCGGGCGGGGGAAGTAGAACC
Real-tae-miR172-F	CGGGCTAGAATCTTGATGATGC