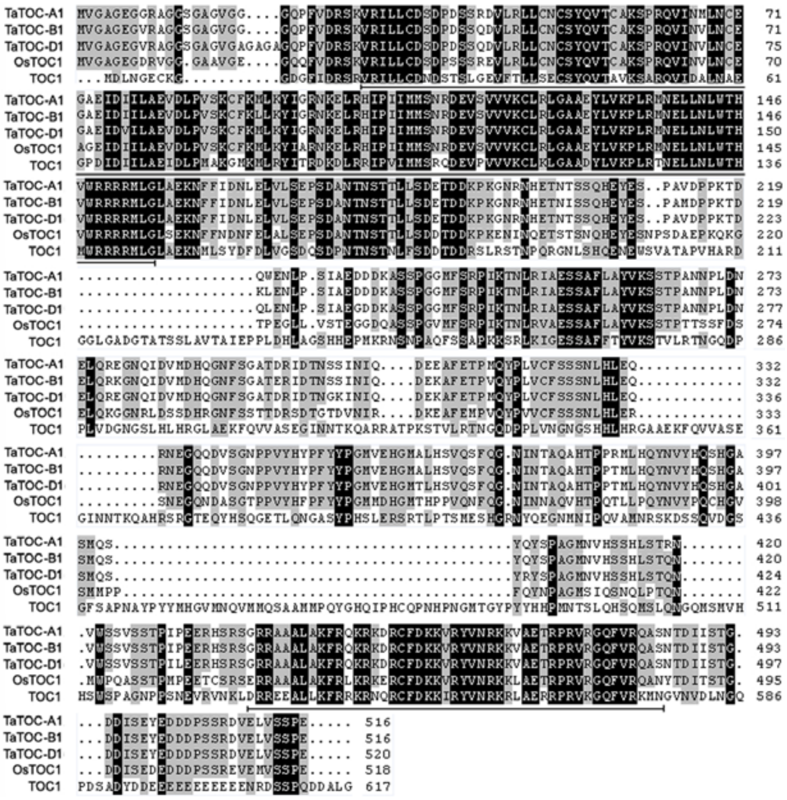
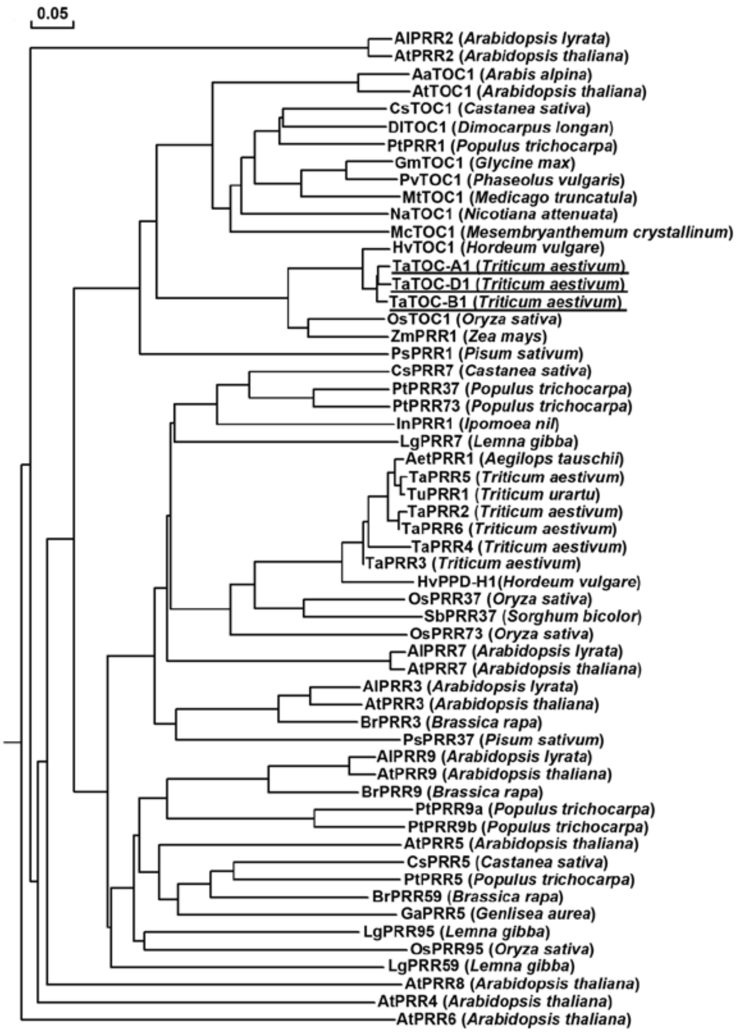


Supplemental Figure 1. Alignment of the Amino Acid Sequences of TaTOC-A1, TaTOC-B1, TaTOC-D1, TOC1 (*Arabidopsis thaliana*, NP_200946), and OsTOC1 (*Oryza sativa*, BAD38854).

Identical amino acid residues are shaded in black, and similar amino acid residues are shaded in gray. Dots denote gaps introduced by the DNAman program. Two conserved regions, the pseudo-receiver domain at the N-terminal region and CCT (CO, COL, and TOC1) domain at the C-terminus, are underlined.



Supplemental Figure 2. Phylogenetic tree of deduced amino acid sequences of PRR in Some Plant Species.

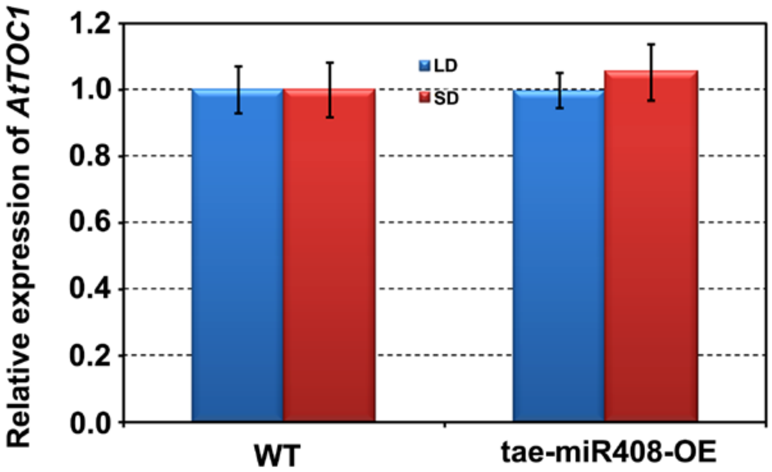
The proteins analyzed were as follows: TaTOC-A1 (underlined) (*Triticum aestivum*), TaTOC-B1 (underlined) (*Triticum aestivum*), TaTOC-D1 (underlined) (*Triticum aestivum*), AaTOC1 (*Arabis alpina*, KFK27896), AetPRR1 (*Aegilops tauschii*, ABL09481), AlPRR2 (*Arabidopsis lyrata subsp. Lyrata*, XP_002868017), AlPRR3 (*Arabidopsis lyrata subsp. Lyrata*, XP_002866368), AlPRR7 (*Arabidopsis lyrata subsp. Lyrata*,XP_002873067), AlPRR9 (*Arabidopsis lyrata subsp. Lyrata*, XP_002880264), AtPRR2 (*Arabidopsis thaliana* NP_567548), AtPRR3 (*Arabidopsis thaliana*,BAB13744), AtPRR4 (*Arabidopsis thaliana*, NP_199735), AtPRR5 (*Arabidopsis thaliana*,BAB13743), AtPRR6 (*Arabidopsis thaliana*, NP_176988), AtPRR7 (*Arabidopsis thaliana*, BAB13742), AtPRR8 (*Arabidopsis thaliana*, O23100), AtPRR9 (*Arabidopsis thaliana* ,BAB13741);

AtTOC1 (*Arabidopsis thaliana*, NP_200946), BrPRR3 (*Brassica rapa*, NP_001288859), BrPRR9 (*Brassica rapa*, NP_001288875), CsPRR5 (*Castanea sativa*, ABV53464), CsPRR7 (*Castanea sativa*, ABV53463), CsTOC1 (*Castanea sativa*, AAU20772); DlTOC1 (*Dimocarpus longan*, AIT56195), GaPRR5 (*Genlisea aurea*, EPS67215), GmTOC1 (*Glycine max,*ABW87010), HvPpd-H1 (*Hordeum vulgare*, AAY42111); HvTOC1 (*Hordeum vulgare*, BAK01373), InPRR1 *(Ipomoea nil*, BAO57288), LgPRR37 (*Lemna gibba*, BAE72700), LgPRR59 (*Lemna gibba*, BAE72701), LgPRR95 (*Lemna gibba* ,BAE72702); McTOC1 (*Mesembryanthemum crystallinum*, AAQ73525); MtTOC1 (*Medicago truncatula*, KEH33445), NaTOC1 (*Nicotiana attenuate*, AFA35965), OsPRR37 (*Oryza sativa*,BAD38855), OsPRR73 (*Oryza sativa*,BAD38856), OsPRR95 (*Oryza sativa*,BAD38857); OsTOC1 (*Oryza sativa*, BAD38854), PsPRR1 (*Pinus sylvestris*, AFV78751), PsPRR37 (*Pinus sylvestris*, ACU42263), PsPRR59 (*Pinus sylvestris*, ACU42265), PtPRR1 (*Populus trichocarpa*, AID51407), PtPRR5 (*Populus trichocarpa*, XP_002321349), PtPRR5a (*Populus trichocarpa*, AID51409), PtPRR5b (*Populus trichocarpa*, AID51410), PtPRR9a (Populus trichocarpa, AID51412), PtPRR9b (*Populus trichocarpa*, XP_002320232), PtPRR37 (*Populus trichocarpa*, AID51408), PtPRR73 (*Populus trichocarpa*, AID51411), PvTOC1 (*Phaseolus vulgaris*, AEA92684), SbPRR37 (*Sorghum bicolor*, AGN92441), TaPRR2 (*Triticum aestivum*, ABL09470), TaPRR3 (*Triticum aestivum,* BAL63649), TaPRR4 (*Triticum aestivum*, BAM31260), TaPRR5 (*Triticum aestivum,* ABL09464), TaPRR6 (*Triticum aestivum*, ABL09468), TuPRR1 (*Triticum urartu*, BAM93402), ZmPRR1 (*Zea mays*, ADU60098). The phylogenetic tree was constructed using MEGA4.0 software. The length of the branch line indicates the extent of the difference according to the scale on the upper left.

Supplemental Figure 3. Predication of miR408 Targets in a Number of Plant Species.

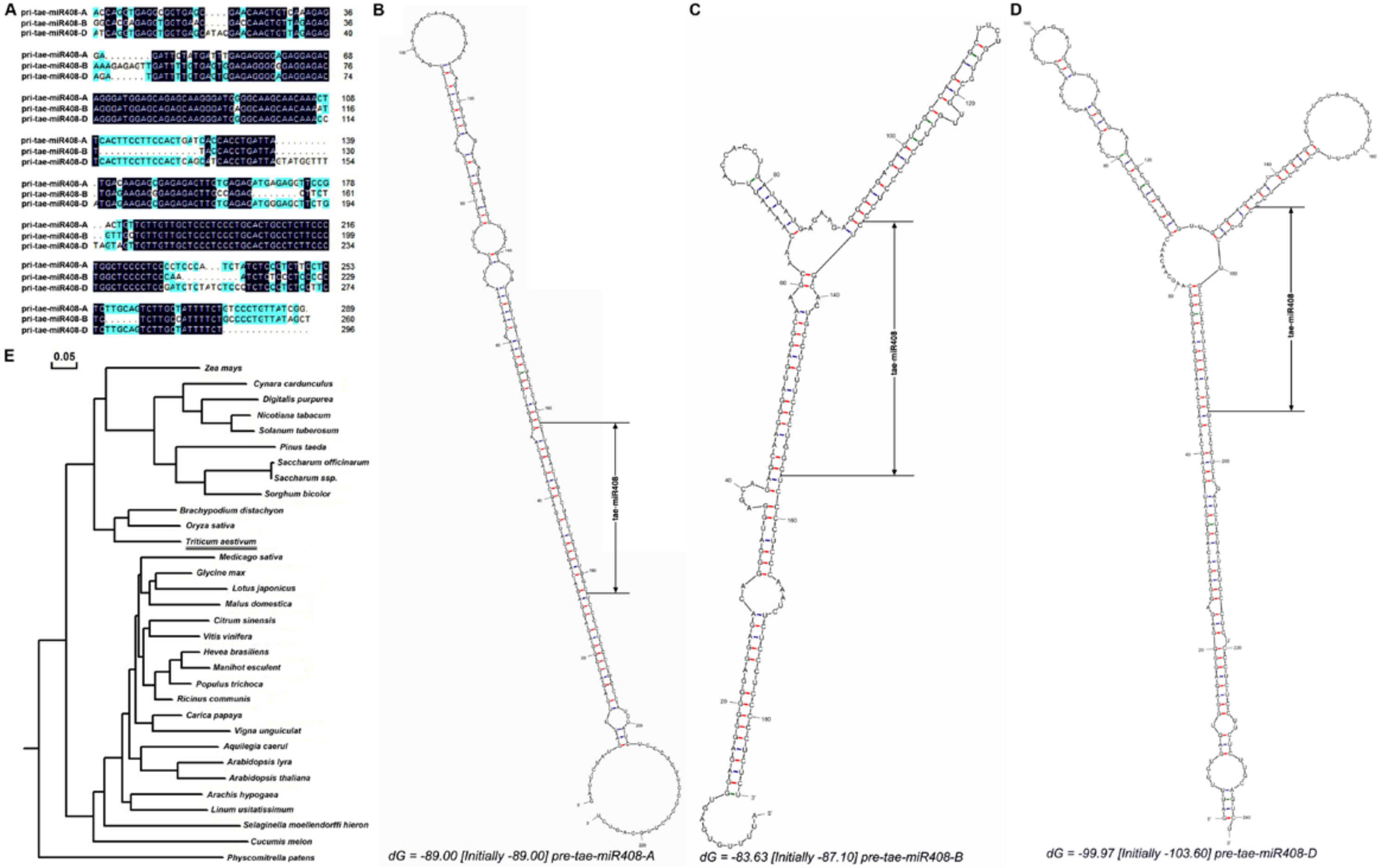
These plants include *Aarabidopsis thaliana* (At), *Brachypodium distachyon* (Bd), *Glycine max* (Gm), *Hordeum vulgare* (Hv), *Oryza sativa* (Os), and *Zea mays* (Zm).

Supplemental Figure 4. Mutation in *TaTOC-A1*, *TaTOC-B1*, and *TaTOC-D1*. Arrowheads indicate the mutated nucleotides.



Supplemental Figure 5. Expression of *AtTOC1* in Transgenic *Arabidopsis* Overexpressing tae-miR408 (tae-miR408-OE).

LD, long days; SD, short days; WT, wild type.

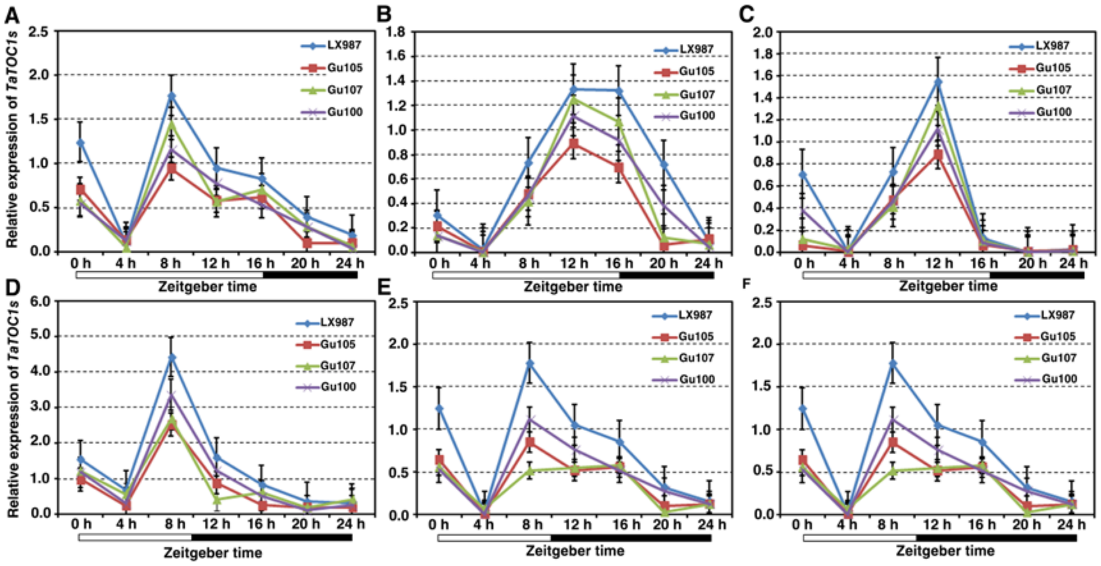


Supplemental Figure 6. Identification of tae-miR408 and Phylogenetic Analysis among miR408s in Various Species.

(A) Alignment of the primary transcripte sequences of pri-tae-miR408a, pri-tae-miR408b, and pri-tae-miR408d. Identical nucleotide bases are shaded in black, and similar ones are shaded in blue. Dots denote gaps introduced by the DNAman program.

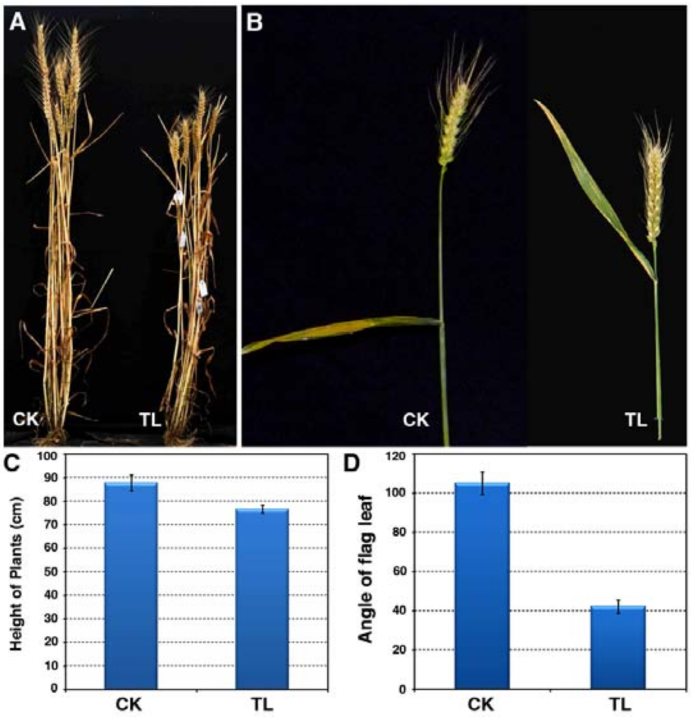
(B)-(D) Stem-loop structure of three tae-miR408 precursors predicted using the mfold web server (http://mfold.rna.albany.edu/?q=mfold).

(E) Phylogenetic tree of tae-miR408 (double underlined) with miR408 from other plants species. The miR408 sequences from 32 species were aligned using DNAMAN software (version 7), and the phylogenetic tree was constructed using the maximum likelihood (ML) method, with 1000 bootstrap replicates.



Supplemental Figure 7. Expression of *TaTOC-A1*(A and D), *TaTOC-B1*(B and E), and *TaTOC-D1*(C and F) in Transgenic Wheat Overexpressing tae-miR408.

The white and black boxes at the bottom of each graph represent light and dark periods, respectively. Data are the mean ± s.e.m.



Supplemental Figure 8. Comparison of the Plant Heights (A and C) and Flage Leaf Angle (B and D) between the Transgenic Wheat Overexpressing tae-miR408 (TL) and Controls (CK).

Error bars indicate standard errors of the means (n=10).

Supplemental Table 1. Comparison of cDNA Sequence Identity (%) of *TaTOC-A1*, *TaTOC-B1*, and *TaTOC-D1*

cDNA identity (%)	*TaTOC-A1*	*TaTOC-B1*	*TaTOC-D1*
TaTOC-A1	---	96.0	93.8
TaTOC-B1	96.0	---	94.3
TaTOC-D1	93.8	94.3	---

Supplemental Table 2. Main Regulatory Motifs Found within the Promoter Sequences of the Three *TaTOC1* Genes (about 1000bp Upstream of the ATG Initiation Codon of Each Homoeolog)

Motif Name	Motif Functions	Motif Number		
		TaTOC-A1	*TaTOC-B1*	*TaTOC-D1*
ABRE	Abscisic acid responsiveness	4	6	4
ACE	Light responsiveness	0	1	0
CAAT-box	Common cis-acting element in promoter and enhancer regions	6	3	5
EE	Essential for circadian rhythmicity	1	1	1
G-box	Light responsiveness	1	3	1
MBS	MYB binding site	1	1	1
Motif IIb	Abscisic acid responsiveness	1	1	1
Sp1	Light responsive element	7	6	7
TATA-box	Core promoter element around -30 of transcription start	0	1	0

Supplemental Table 3. Primers Used in This Study

Primer Name	Primer Sequence (5′-3′)	Objective
TaTRNi-F	GGGGTACCACTAGTTGCAGTATCCTTTGGTA *Kpn*I *Spe*I	For RNA interference vector construction, southern blotting and In situ hybridization
TaTRNi-R	CGGGATCCGAGCTCGCAACTTTCTTCCGATT *Bam*HI *Sac*I	For RNA interference vector construction, southern blotting, In situ hybridization and transgenic wheat detection
tae-MIR408b-F1	CTGGATCCGAGAGAAAGAGAGTTGATTTTGTGAG *Bam*HI	For overexpression vector construction and wheat transformation
tae-MIR408b-R1	TTGGTACCCTATAACAGGGGCAGAAAATGG *Kpn*I	
TaTOC-A1F1	ATGGTGGGCGCCGGC	For the amplification of the full length TaTOC-A1 cDNA and Arabidopsis overexpression vector construction
TaTOC-A1R1	TTCTGGTGAAGAAACCAACTCAAC	

TaTOC-B1F1	ATGGTGGGCGCCGG	For the amplification of the full length TaTOC-B1 cDNA and Arabidopsis overexpression vector construction
TaTOC-B1R1	CTCTGGTGAAGAAACCAACTCAAC	
TaTOC-D1F1	ATGGTGGGCGCCGGCGAGG	For the amplification of the full length TaTOC-D1 cDNA and Arabidopsis overexpression vector construction
TaTOC-D1R1	CTCTGGTGAAGAAACCAACTCAACGTC	
tae-MIR408b-F2	GAGAGAAAGAGAGTTGATTTTGTGAG	For overexpression vector construction, Arabidopsis transformation
tae-MIR408b-R2	CTATAACAGGGGCAGAAAATGG	
pTCK303-F	CTCTAACCTTGAGTACCTATC	For transgenic plants detection
pTCK303-D	CTATGACACGGCTGTTTCGAG	For transgenic plants detection
TaTOC-A1F2	ACCGACAGAATCGACACTAATG	For *TaTOC-A1* expression analysis with RT-PCR
TaTOC-A1R2	GGATGGATCATCGTCTTCG	

TaTOC-B1F2	GGTGCGACCGAGAGAATA	For *TaTOC-B1* expression analysis with RT-PCR
TaTOC-B1R2	CTAGATCATCCGCACACCAT	
TaTOC-D1F2	ACACTGCTCAAGCTCATACG	For *TaTOC-D1* expression analysis with RT-PCR
TaTOC-D1R2	TCATCCGCACACCACTC	
TaActin-F	AGTCGAGAACGATACCAGTAGTACGA	Used as internal reference
TaActin-R	GCCATGTACGTCGCAATTCA	
TaTOC1-a	GCAGCACTTGCAAAATTCAG	For three *TaTOC1s* expression analysis with qRT-PCR
TaTOC1-b	GTGCTAATTATATCTGTGTTGCTTGC	
TaTOC-A1F3	CCCCCAAAACAGACCAATG	For *TaTOC-A1* expression analysis with qRT-PCR
TaTOC-A1R3	CATAGGCGTCTCAAAAGCTTC	
TaTOC-B1F3	CAATTCCCGAGGAAAGACAC	For *TaTOC-B1* expression analysis with qRT-PCR
TaTOC-B1R3	AATGATCATCCGCACACCAT	

TaTOC-D1F3	GGTATCGAGCACACCAATTCT	For *TaTOC-D1* expression analysis with qRT-PCR
TaTOC-A1F3	GCAATGATCATCCTCACTCCC	
tae-MIR408b-F3	GGATGGAGCAGAGCAAGG	For *TaemiR408* expression analysis with qRT-PCR
tae-MIR408b-R3	TGGCAACTCTCTCCCTCTTCTC	
TaCO1-F	CAGACACCAATTCACTTCAGC	For *TaCO1* expression analysis with qRT-PCR
TaCO1-R	TCCACTTCCATGTCTGCAT	
TaFT1-F	GTCGTTCGGGCAGGAG	For *TaFT1* expression analysis with qRT-PCR
TaFT1-R	TGGAAGAGTACGAGCACGA	
Tubulin2-F	ATCCGTGAAGAGTACCCAGAT	Used as internal reference
Tubulin2-R	AAGAACCATGCACTCATCAGC	
AtTOC1 F	TCACCATGAGCCAATGAAAA	For *AtTOC1* expression analysis with qRT-PCR
AtTOC1 R	TTGAAACTTCTCCGCCAAAC	

LAD1-4	ACGATGGACTCCAGAG(G/C/T)(G/A/T)N(G/C/T)NNNCGGT	For hiTAIL-PCR
AC1	ACGATGGACTCCAGAG	
TP-0	CTTGGTAGGAGCAGTTGCAGAGGAGG	
TP-1	ACGATGGACTCCAGTCCGGGAGGAGGCGAAGCACATCCYGTGAGC	
TP-2	CCGGCGCCCACCATACCCAA	
AAP	GGCCACGCGTCGACTAGTACGGGIIGGGIIGGGIIG	For 5′ RACE
AUAP	GGCCACGCGTCGACTAGTAC	
GSP1	CWATCTGATTACCCT	
GSP2	CGAAAGGAGTGTGGTGCTATTG	
GSP3	CATCCGTCTYCTTCGCCAS	
tae-MIR408b-F4	TATCTAGAGAGAGAAAGAGAGTTGATTTTGTGAGTG *Xba*I	For tobacco leaf co-transformation assays of the tae-miR408 and *TaTOC1* genes

tae-MIR408b-R4	ATCCCGGGCTATAACAGGGGCAGAAAATGGC *Sma*I
TaTOC-A1F4	TATCTAGAATGGTGGGCGCCGGC *Xba*I
TaTOC-A1R4	ATCCCGGGTTCTGGTGAAGAAACCAACTCAAC *Sma*I
TaTOC-B1F4	TATCTAGAATGGTGGGCGCCGG *Xba*I
TaTOC-B1R4	ATCCCGGGCTCTGGTGAAGAAACCAACTCAAC *Sma*I
TaTOC-D1F4	TATCTAGAATGGTGGGCGCCGGCGAGG *Xba*I
TaTOC-D1R4	ATCCCGGGCTCTGGTGAAGAAACCAACTCAACGTC *Sma*I