

Table S1. Primer sequences of this study.

Name	Sequence (5'-3')	Usage
<i>PtoNF-YC5-F</i>	GCGT <u>TCGAC</u> ATGGAGCAAGG	Cloning
<i>PtoNF-YC5-R</i>	GG <u>ACTAGT</u> CTGAGGGCGACTG	
<i>PtoNF-YC6-F</i>	GCGT <u>TCGAC</u> ATGGATCAGCAAG	
<i>PtoNF-YC6-R</i>	GG <u>ACTAGT</u> CTACTGATCTGAGGGTGAC	
<i>PtoNF-YC7-F</i>	GCGT <u>TCGAC</u> ATGATGGGACCTT	
<i>PtoNF-YC7-R</i>	GG <u>ACTAGT</u> TCAGGAATCTTCAGGTGGC	
<i>PtoNF-YC8-F</i>	GCGT <u>TCGAC</u> ATGGACCAGCA	
<i>PtoNF-YC8-R</i>	GG <u>ACTAGT</u> TCAGGAATCTTCAGGTGGCT	
<i>PtoNF-YC5-F</i>	CGGTCTTGGAATCACACGGA	qRT-PCR
<i>PtoNF-YC5-R</i>	CCGACAGGCATTGTTCTCT	
<i>PtoNF-YC6-F</i>	GAACAATGCCTGTTGGAGGG	
<i>PtoNF-YC6-R</i>	TGTCACAGGCTTGCCCATTA	
<i>PtoNF-YC7-F</i>	AGTCCCGAGAGGGAGTCTTC	
<i>PtoNF-YC7-R</i>	TTTGCTGTGGCCAAATCTGC	
<i>PtoNF-YC8-F</i>	GGAAAGCCTGTGGTGGATCA	
<i>PtoNF-YC8-R</i>	AGGAATCTTCAGGTGGCTGC	
<i>AtCO-F</i>	CAGGCAAACAGTGTATGCACCAGG	
<i>AtCO-R</i>	CCGCAGCCACTCTCCCTCTG	
<i>AtSOC-F</i>	GGGATCTCATGAAAGCGAAGTTTG	
<i>AtSOC-R</i>	CTTGAAGAACAAGGTAACCCAATGAA	
<i>AtSVP-F</i>	GGAAAACTGTTTCGAGTTCTG	
<i>AtSVP-R</i>	TCTTTGTTTCAATCACACGC	
<i>AtFT-F</i>	AGAAGACTTTAGATGGCTTCTT	
<i>AtFT-R</i>	TTATCGCATCACACACTATATAAG	
<i>AGL-F</i>	GGCTGGAGAAACTACTTGAA	
<i>AGL-R</i>	TTTAAGCGTCGTCAGTTTTG	
<i>API-F</i>	CATGGGTGGTCTGTATCAAGAAGAT	
<i>API-R</i>	CATGCGGCGAAGCAGCCAAGGTT	
<i>AtSEP3-F</i>	CGGTCGTCATCATCATCAACA	
<i>AtSEP3-R</i>	GTCCTGCTCCCATTCCATCTT	
<i>PtACTIN-F</i>	CTCCATCATGAAATGCGATG	
<i>PtACTIN-R</i>	TTGGGGCTAGTGCTGAGATT	

<i>AtUBQ-F</i>	GGGCACTCAAGTATCTTGTTAGC	
<i>AtUBQ-R</i>	TGCTGCCCCAACATCAGGTT	
AD-PtCOL1-F	CGGAATTTCATGCCACGTGTCAC	
AD-PtCOL1-R	CGGGATCCGAATGATGGGACAAT	
AD-PtCOL2-F	CGGAATTTCATGTTGAAGCAAGAGAGTAGTGG	
AD-PtCOL2-R	CGGGATCCGAATGATGGGACAAT	Y2H vector
BD-PtNF-YC6-F	CGGAATTTCATGGATCAGCAAGGGTATGGG	construction
BD-PtNF-YC6-R	CGGGATCCCTGATCTGAGGGTGACTGCTG	
BD-PtNF-YC8-F	CGGAATTTCATGGACCAGCAAGGCCATG	
BD-PtNF-YC8-R	CGGGATCCGAATCTTCAGGTGGCTGCT	

Table S2. Comparison of similarity between PtoNF-YC5/6/7/8 protein and AtNF-YC3/9 protein.

Gene Members	PtoNF-YC5	PtoNF-YC6	PtoNF-YC7	PtoNF-YC8
AtNF-YC3	43.97%	55.00%	32.39%	46.51%
AtNF-YC9	51.74%	58.44%	36.06%	53.10%

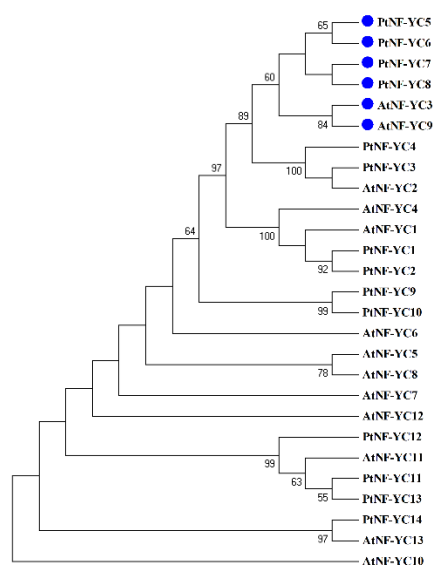


Figure S1. Phylogenetic trees constructed by NF-Y proteins from Arabidopsis and *Populus*.

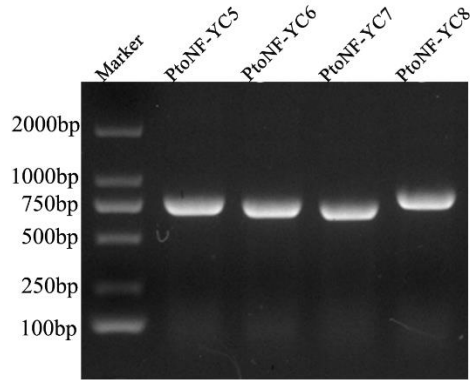


Figure S2. Amplification of the CDS of *PtoNF-YC5/6/7/8*.

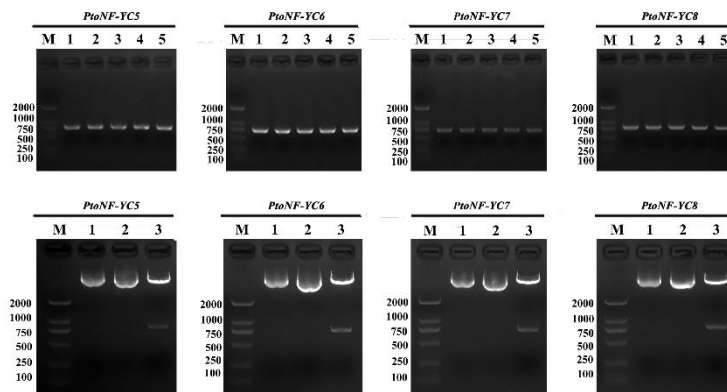


Figure S3. pSuper1300-GFP-PtoNF-YC5/6/7/8 bacterial liquid PCR and plasmid double enzyme digestion identification. M: 2000 DNA Maker, (below) 1: pSuper1300-GFP empty vector, 2: pSuper1300-GFP-PtoNF-YC5/6/7/8 vector, 3: pSuper1300-GFP-PtoNF-YC5/6/7/8 plasmid double restriction digestion identification.

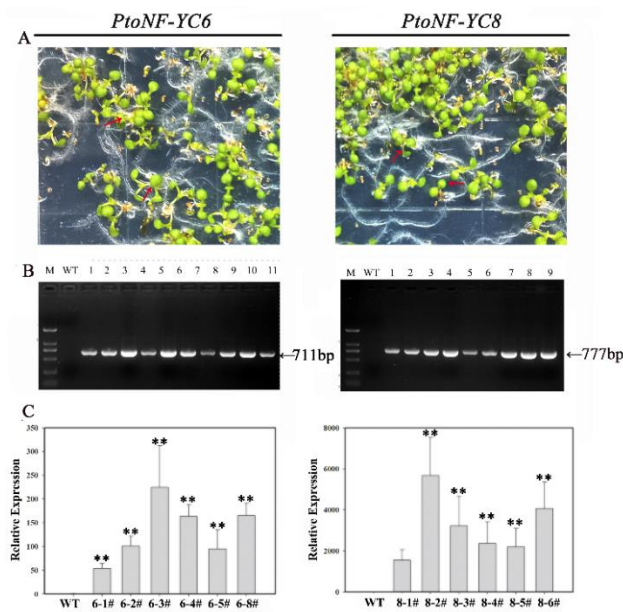


Figure S4. Identification of *PtoNF-YC6* and *PtoNF-YC8* transgenic Arabidopsis. (A) Hygromycin screening of transgenic Arabidopsis. (B) DNA level identification the transgenic Arabidopsis. (C) Transcription level analysis. ** $p < 0.01$.

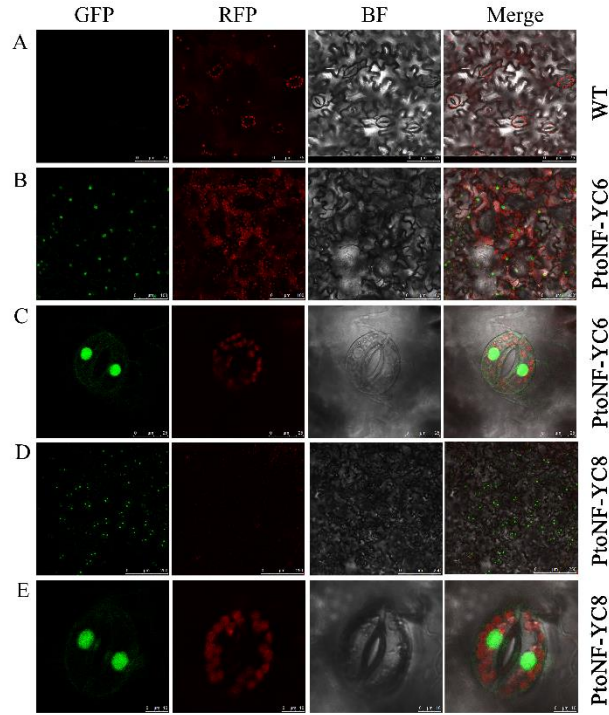


Figure S5. *PtoNF-YC6* and *PtoNF-YC8* visualized under fluorescence microscopy in transgenic Arabidopsis. (A) Leaf fluorescence signal of wild-type seedlings. (B,D). Leaf fluorescence signal of transgenic *PtoNF-YC6* and *PtoNF-YC8* plants, bar 100μm. (C,E). Fluorescence signal of *PtoNF-YC6* and *PtoNF-YC8* transgenic leaf guard cells, bar 25 μm.

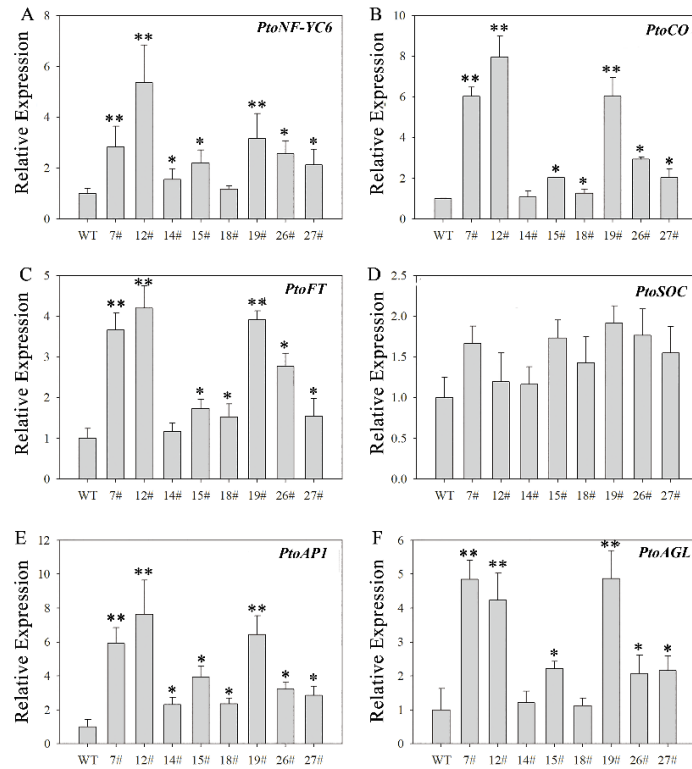


Figure S6. Expression analysis of *PtoNF-YC6* and endogenous flowering genes of *P. tomentosa* (A–F). * $p < 0.05$, ** $p < 0.01$.

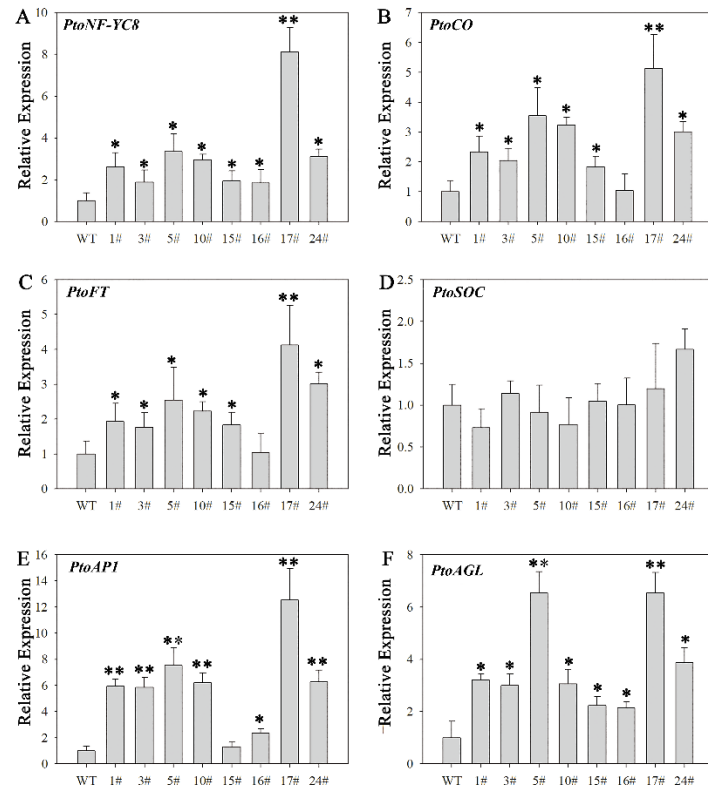


Figure S7. Expression analysis of *PtoNF-YC8* and endogenous flowering genes of *P. tomentosa* (A–F). * $p < 0.05$, ** $p < 0.01$.