

Figure S1. Identification of RcBBX family genes in Rosa chinensis

(A) Phylogenetic analysis of BBX family genes among Arabidopsis thaliana, *Rosa multiflora* and *Rosa chinensis*. Bootstrap values indicate the divergence of each branch. Different groups are classified and shown by different color.

(B) Numbers of BBX family genes among Arabidopsis thaliana, Rosa multiflora and Rosa chinensis.



Figure S2. Amino acid sequence comparison of *CO*, *COL4* and *COL5* across different species Alignment of amino acid sequences of *RcCO* (A), *RcCOL4* (B) and *RcCOL5* (C) with the counterparts from *Rosa chinensis* (Rc), *Rosa multiflora* (Rm), *Arabidopsis thaliana* (At), *Fragaria* × *ananassa* (Fa), *Prunus persica* (Pp), *Solanum tuberosum* (St), *Lagerstroemia indica* (Li), *Gossypium darwinii* (Gd), *Thespesia populneoides* (Tp), *Raphanus sativus* (Rs), *Fragaria vesca* (Fv), *Prunus avium* (Pa), *Ziziphus jujube* (Zj), *Theobroma cacao* (Tc), *Vigna angularis* (Va), *Prunus mume* (Pm), *Cucumis sativus* (Cs), *Cucumis melo* (Cm), *Malus domestica* (Md). Red lines indicate two B-box domains, green lines indicate VP motif and blue lines indicate CCT domain. The asterisks below the red lines indicate the Zn²⁺-ligating conserved Cys, His and Asp residues presented in the B-box.



Figure S3. Expression level of CO, COL4 and COL5 in three OF and three

CF roses under LD and SD condition.

(A) Relative expression of *CO* in three OF roses (*Rosa laevigata*, *Rosa multiflora* and *Rosa berberifolia*) and three CF roses (*Rosa chinensis* cv 'Sichun', *Rosa chinensis* cv 'Viridiflora' and *Rosa hybrida* cv 'Molde').

(B) Relative expression of *COL4* in three OF roses (*Rosa laevigata*, *Rosa multiflora* and *Rosa berberifolia*) and three CF roses (*Rosa chinensis* cv 'Sichun', *Rosa chinensis* cv 'Viridiflora' and *Rosa hybrida* cv 'Molde').

(C) Relative expression of *COL5* in three OF roses (*Rosa laevigata, Rosa multiflora* and *Rosa berberifolia*) and three CF roses (*Rosa chinensis* cv 'Sichun', *Rosa chinensis* cv 'Viridiflora' and *Rosa hybrida* cv 'Molde').

The bar above and below the graphs indicates the light conditions, with day and night denoted in white and black, respectively.



Figure S4. Flowering phenotype and gene expression levels of *RcCOL5*-silenced plants under LD and SD

(A), (B) Phenotypic characterization of TRV-*RcCOL5* plants under long day LD (A) and SD (B) conditions (Plants were photographed 44 days after transplanting).

(C), (D) Relative expression of *RcCOL5* in silenced plants under long day LD (C) and SD (D) conditions Error bars indicate \pm SD (n=10). Letters above the bars denote significant differences (*P* < 0.05).

(E) Flowering time of RcCOL5-silenced plants under LD and SD conditions. Error bars indicate ±SD

(n=10). Letters above the bars denote significant differences as determined Kruskal Wallis test (P < P

0.05).



15 mM 3-AT

Figure S5. *RcCO* not *RcCOL4* binds to the promoter of *pRcFT* in yeast one hybrid.

Yeast Y187 cells containing pGADT7-*RcCO*/pGADT7-*RcCOL4* and pHis2-*pFT* were incubated, and the binding activities were examined on SD medium lacking Tryptophan, Leucine and Histidine (SD/–Trp/–Leu/–His) with the proper concentration of 3-amino-1, 2, 4-triazole (15mM) to inhibit self-activation.

Primer ID	Sequence of primers (5'-3')	Purpose
RcCO-F	caccATGTTGAAAGAAGAGAGAGCAATG	Cana alanina ta D TOPO
RcCO-R	GTATGAAGGAACAATGCCGTATC	Gene cioning to D-10PO
RcCOL4-F	caccATGTTTCACTCGGGGCAATC	Gene cloning to D-TOPO
RcCOL4-R	AAAAGAGGGAACGACGCCGTAGC	
pRcFT-F	caccATATCAGTTCTTCATGGCAATCAG	Promoter cloning to D-TOPO
pRcFT-R	TAACTAATTTTACACAGGCCACCT	
RcCO-F-EcoR I	GGAATTCATGTTGAAAGAAGAGAGAGA	For yeast one/two hybrid
RcCO-R-Xho I	CCTCGAGGTATGAAGGAACAATGCCGTAT	
RcCOL4-F-Nde I	CCATATGATGTTTCACTCGGGGCAATC	For yeast one/two hybrid
RcCOL4-R-Sal I	GGTCGACAAAAGAGGGAACGACGCC	
pFT-pHis-F	GGAATTCATATCAGTTCTTCATGGCAATCAG	For yeast one hybrid
pFT-pHis-R	GGAGCTCTAACTAATTTTACACAGGCCACCT	
RcCO-F-BamH I	GGAATTCATGTTGAAAGAAGAGAGAGA	Vectors for in vitro expression of protein
RcCO-R-Xho I	CCTCGAGGTATGAAGGAACAATGCCGTAT	
RcCOL4-F-BamH I	GGAATTCATGTTTCACTCGGGGCAATC	Vectors for in vitro expression of protein
RcCOL4-R-Xho I	CCTCGAGAAAAGAGGGAACGACGCCGTAGC	
NF-YB-F-BamH I	GGAATTCATGGCCGACTCGGACAACGACTC	Vectors for in vitro expression of protein
NF-YB-R-Xho I	CCTCGAGCCTTGACCTCACTGAAGCT	
NF-YC-F-BamH I	GGAATTCATGGATCAGCAAGGACATGGGCA	Vectors for in vitro expression
NF-YC-R-Xho I	CCTCGAGATGATCAGATGGTGACTGTTGCTG	of protein
RcCOL4-mu1-F	CTTTCCTCCGTAAACTGCGACACAAAGATCCACGC	For mutation of Cys-18
RcCOL4-mu1-R	CAGTTTACGGAGAGGAAAGCGGAGTCTGCTCGGCA	
RcCOL4-mu2-F	CGACTCTGTTCTCCCGAGCAGACTCCGCTTTCCTCT	For mutation of Cys-26
RcCOL4-mu2-R	TGCTCGGGAGAACAGAGTCGCCGTCGCCGATTTGCA	
RcCOL4-mu3-F	ACCCTCTCCGTCACGTGCGACCGAGAAATCCACTCT	For mutation of Cys-61
RcCOL4-mu3-R	CACGTGACGGAGAGGGTGGCGTCGTCGGCCTTGCA	
RcCOL4-mu4-F	ACGTCACGTCCAAGGCCGACGACGCCACCCTCT	For mutation of Cys-69
RcCOL4-mu4-R	GGCCTTGGACGTGACGTGGGCGGGAGCCTGCT	
RcCO-VIGS-F	TGAATCCGGTGAAGAACAGCAAC	VIGS vector construction
RcCO-VIGS-R	ACCTTCTCCATACTGAACTGGTAC	
RcCOL4-VIGS-F	GTTTCACTCGGGGCAATC	VIGS vector construction
RcCOL4-VIGS-R	TTG AGT CGT CCG AGT TGA GTG AG	
CORE-BOX(BJ)-F	GTTTATCTTTGAACAAAGATGAACCACAGAATGATCGATC	CORE motif probe
CORE-BOX(BJ)-R	ATGCTGCTGATCGATCATTCTGTGGTTCATCTTTGTTCAAAGATAAAC	
CORE-BOX-F	GTTTATCTTTGAACAAAGATGAACCACAGAATGATCGATC	Competitor probe
CORE-BOX-F	ATGCTGCTGATCGATCATTCTGTGGTTCATCTTTGTTCAAAGATAAAC	
RcGAPDH-F	GCTGGCAGGTATCCTTTCTG	q-PCR
RcGAPDH-R	GGCGACAATATCAGCCAAGT	
RcCO-O-F	GATACCACCGAGGACGGGTT	q-PCR
RcCO-O-R	CAGGACGCAGCCTCATCTTC	
RcCOL4-O-F	GGCTTCGATCTCCGCTTCTG	q-PCR
RcCOL4-O-R	TCAACTTCCTCGACGACCGA	
RcCOL5-O-F1	CGCCTCCCGGAAAGCCTATG	DCD
RcCOL5-O-R1	CCCGGCGCCGAGTTAAAGAT	-q-PCR
RcFT-Q-F	AGCTTGTGAGTTGTGGGTCT	non
RcFT-Q-R	ATTGGGAACCGCCCAAGAAA	-q-PCR
Actin2-F	GGTAACATTGTGCTCAGTGGTGG	RT-PCR
Actin2-R	AACGACCTTAATCTTCATGCTGC	
RcCO-RT-F	CTCCCCATCTCCGGCTTCCTC	RT-PCR
RcCO-RT-R	TCCATCCCCAACTGATG	
RcCOL4-RT-F	GTTCTGCCGAGCAGACTCCGC	RT-PCR
RcCOL4-RT-R	AGATCCAAATACGGATCCA	

Table S1. The primers used in this study.