Table S1. List of primers used in this study

Primer	Experiment	Sequence (5' -3')
PmCBFF1	Homology-based cloning of *PmCBF* genes	GAGACGAGGCACCCGGT
PmCBFR2	Homology-based cloning of *PmCBF* genes	AAACAHYTCCTCCTCATCC
5RaceF	Extension of 5' end of *PmCBFb*	AAGCAGTGGTATCAACGCAGAGTGG
3RaceR	Extension of 3' end of *PmCBFb*	ATTCTAGAGGCCGAGGCGGCCGACATG-d(T)30N-1N
PmCBFbrF1	Cloning of 3' end of cDNA *PmCBFb*	GACGTGGCGGCATTGGCTTTTAAAGG
PmCBFbrR1	Cloning of 5' end of cDNA PmCBFb	AGCATTGCGGTGGAGAAAGATGAAGC
PmCBFbZF	Cloning of full-length CDS of *PmCBFb*	CACACCTCTCTGAAACACCACTC
PmCBFbZR	Cloning of full-length CDS of *PmCBFb*	CACTAAACCCGAGAGACAGATTGACT
PmCBFcTF1	FPNI-PCR of 3' end of *PmCBFc*	CGGCATTGGCGTTTAGAGG
PmCBFcTF2	FPNI-PCR of 3' end of *PmCBFc*	GCGGAGTTTGGTGGATTGTGC
PmCBFcTF3	FPNI-PCR of 3' end of *PmCBFc*	GCAGTGATGAGAAGGAGAGAATGG
PmCBFcTR1	FPNI-PCR of 5' end of *PmCBFc*	CACCATTCTCTCCTTCTCATCACT
PmCBFcTR2	FPNI-PCR of 5' end of *PmCBFc*	TCCCTCTAAACGCCAATGCCG
PmCBFcTR3	FPNI-PCR of 5' end of *PmCBFc*	CTTGTTGGGCTCTCTCATTTCAC
PmCBFcZF	Cloning of full-length CDS of *PmCBFc*	CAGCTCAAGAAACTCAAAACAAGCTA
PmCBFcZR	Cloning of full-length CDS of *PmCBFc*	TGGTCGTCGAGTGACGTTAATCT
PmCBFaF1	Cloning of tandem array of *PmCBFab*	GACGTGGCGGCATTGGCTTTCAGAGG
PmCBFbR1	Cloning of tandem array of *PmCBFab*	TCATGGGCACGAGCAGCCAT
PmCBFcF1	Cloning of tandem array of *PmCBFca*	GAGAGAATGGTGGTGCAGGTGGAAG
PmCBFaR1	Cloning of tandem array of *PmCBFca*	TCCATATCCACGCTAAAAATCT
PmCBFbF1	Cloning of tandem array of *PmCBFbc*	GACCACCCTACGCACTTCGGAC
PmCBFcR1	Cloning of tandem array of *PmCBFbc*	CCCTTCTTGTTCTTCTCTTCCACCTG
M13F	Sequencing	AGCGGATAACAATTTCACACAGG
M13R	Sequencing	CGCCAGGGTTTTCCCAGTCACGAC
PmEF1αF	quantitative RT-PCR of *PmEF1α*	CGGATTCAATGTTAAGAATGTTGC
PmEF1αR	quantitative RT-PCR of *PmEF1α*	AGAACTGGAGCATATCCGTTACC
PmCBFaqF	quantitative RT-PCR of *PmCBFa*	GTGTCTTTTTCGTCGGATTCATCTC
PmCBFaqR	quantitative RT-PCR of *PmCBFa*	CTATTAGAGCCACAGTGACATGCTC
PmCBFbqF	quantitative RT-PCR of *PmCBFb*	GTCAATCTGTCTCTCGGGTTTAGTG
PmCBFbqR	quantitative RT-PCR of *PmCBFb*	CTAGAAACTAGACAAAGCACAGTACC
PmCBFcqF	quantitative RT-PCR of *PmCBFc*	CTCCATCGCAATGCTTAGGTG
PmCBFcqR	quantitative RT-PCR of *PmCBFc*	CGACTGACGTTAATCTTTTTCGTTAC

Table S2. The selected cis-elements predicted in the putative promoter of *PmCBFb*

Sort	Factor or site name	Signal sequence	Number
Tissue specific expression elements	DOFCOREZM	AAAG	19
	CACTFTPPCA1	YACT	12
	ROOTMOTIFTAPOX1	ATATT	6
	OSE2ROOTNODULE	CTCTT	5
	OSE1ROOTNODULE	AAAGAT	4
	TAAAGSTKST1	TAAAG	3
	GTGANTG10	GTGA	2
	POLLEN1LELAT52	AGAAA	1
Light response elements	INRNTPSADB	YTCANTYY	10
	-10PEHVPSBD	TATTCT	2
	SORLIP1AT	GCCAC	2
	SORLIP2AT	GGGCC	2
	GT1CONSENSUS	GRWAAW	1
	IBOXCORE	GATAA	1
Binding sites for MYB factors	MYBCORE	CNGTTR	5
	TATCCAOSAMY	TATCCA	3
	EECCRCAH1	GANTTNC	2
	MYBPLANT	MACCWAMC	1
	MYBST1	GGATA	1
Binding sites for MYC factors	MYCCONSENSUSAT	CANNTG	10
	T/GBOXATPIN2	AACGTG	1
Binding sites for WRKY factors	WRKY71OS	TGAC	7
	WBBOXPCWRKY1	TTTGACY	1
Binding sites for RAV factors	RAV1BAT	CACCTG	2
	RAV1AAT	CAACA	1
Abscisic acid related elements	ACGTABREMOTIFA2OSEM	ACGTGKC	4
	GADOWNAT	ACTGTGC	2
Heat shock	CCAATBOX1	CCAAT	3

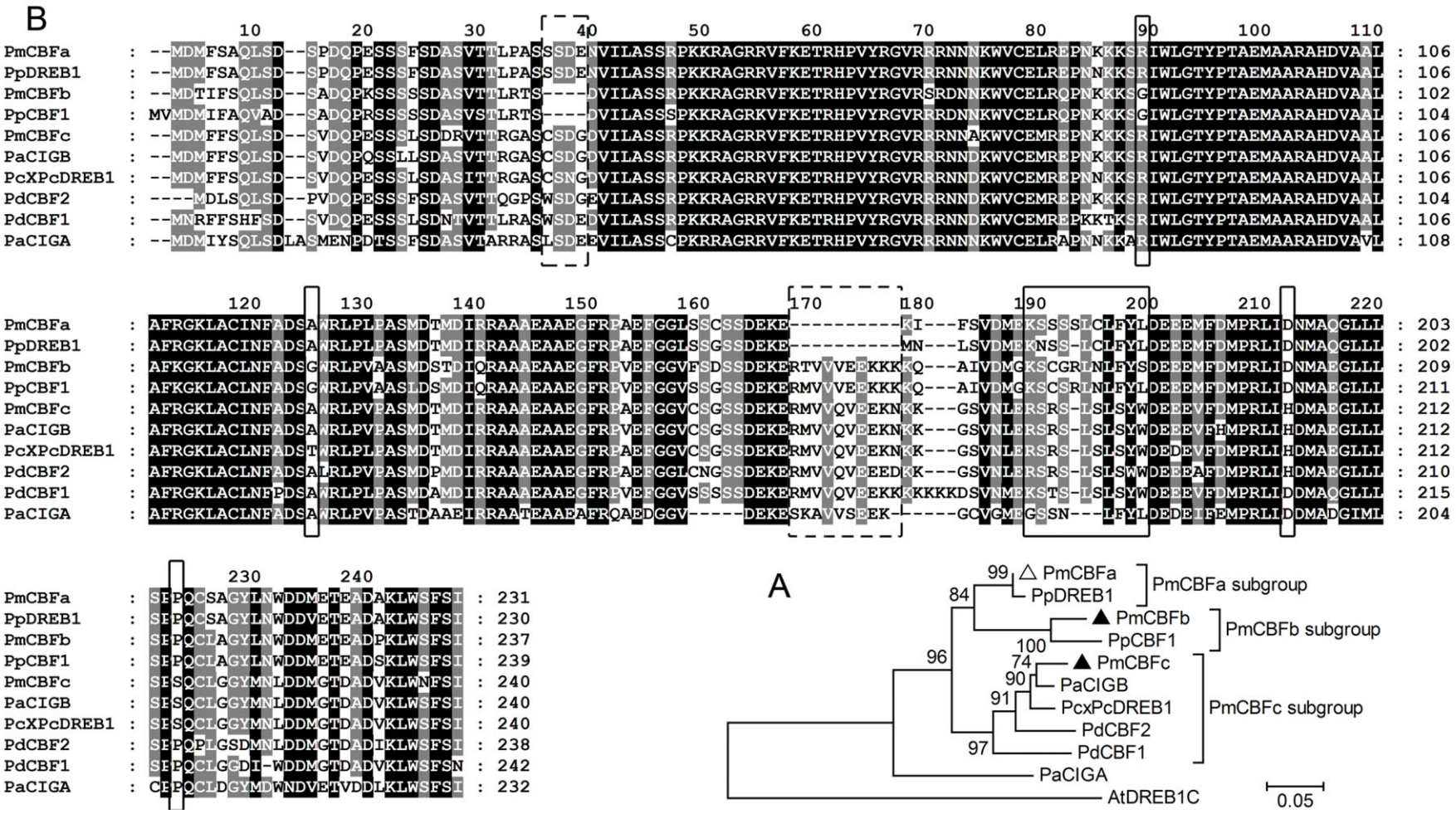

Fig. S1. Sequence analysis of CBF proteins in *Prunus*. *A* - Phylogenetic analysis of CBF/DREB1 proteins from *Prunus* spp. using the Neighbor-Joining method, with bootstrap analysis with 1000 replications. The AtDREB1C is used as an outgroup for better calculation. The sequences used in these analyses are as follows: PmCBFa (ADF43033.1), PmCBFb (ADF43034.1), and PmCBFc (ADF43035.1) from *Prunus mume*; PpDREB1 (ABR19831.1) and PpCBF1 (ADU03762.1) from *P. persica*; PaCIGA (BAC20183.1), and PaCIGB (BAC20184.1) from *P. avium*; PdCBF1 (AFL48190.1) and PdCBF2 (AFL48191.1) from *P. dulcis*; Pc×PcDREB1 (ACF94686.1) from *P. canescens*× *P. cerasus*; AtDREB1C (NP_567719.1) from *Arabidopsis thaliana*. *B* - Multiple alignment of the sequences from *Prunus* spp. Diversity in conserved regions and non-conserved regions are indicated by *solid* and *dashed boxes*, respectively.