

Supplementary Material

Table S1. CAMTA genes of different genome assemblies in *Prunus persica*.

Peach varieties	<i>Prunus persica</i> Genome	Gene ID	Genome references
'Lovell'	Whole Genome Assembly v2.0	Prupe.1G108700.1	54, 55
		Prupe.8G060300.1	
		Prupe.6G187700.1	
		Prupe.1G224000.1	
		Prupe.1G122800.1	
'Chinese Cling'	Chinese Cling Genome V1.0	evm.model.contig279.973	56
		evm.model.contig125.12	
		evm.model.contig7.29	
		evm.model.contig275.159	
		evm.model.contig279.1102	
'Zhongyoutao 14'	Zhongyoutao 14 Genome v1.0	Pp01G011310.1	57
		Pp08G008580.1	
		Pp06G017540.1	
		Pp01G028410.1	
		Pp01G012670.1	
'124 Pan'	124 Pan Genome v1.0	P124PAN14929.1	58
		P124PAN03468.1	
		P124PAN21190.1	
		P124PAN16004.1	
		P124PAN15065.1	

References listed in the main text.

Table S2. Fruit CAMTA genes in *Rosaceae* family.

Fruit name	Organism	Genome source	Gene number	Gene ID	Length (aa)
Strawberry	<i>Fragaria x ananassa</i>	Genome v1.0	16	FxaC_13g22180.t2	1004
				FxaC_13g26730.t1	914
				FxaC_13g38580.t1	907
				FxaC_14g14610.t1	1005
				FxaC_14g18980.t1	928
				FxaC_15g15470.t1	1005
				FxaC_17g39580.t1	989
				FxaC_18g15530.t1	989
				FxaC_19g28040.t1	987
				FxaC_1g24361.t1	1074
				FxaC_20g31520.t1	987
				FxaC_2g28010.t1	1073
				FxaC_3g23640.t1	654
				FxaC_3g23862.t1	879
				FxaC_3g23863.t1	1074
				FxaC_4g16590.t1	1191
Apple	<i>Malus domestica</i>	Genome v1.0	8	MD01G1031100	1107
				MD05G1044600	1070
				MD10G1051700	1074
				MD13G1121200	977
				MD13G1144300	1004
				MD15G1318400	1108
				MD16G1121200	977
				MD16G1157900	910
				Ppy00g1083.1	1125
				Ppy01g0314.1	1111
Pear	<i>Pyrus pyrifolia</i>	Genome v1.0	10	Ppy05g0286.1	1075
				Ppy13g0414.1	1176
				Ppy13g1287.1	982
				Ppy13g1472.1	1010
				Ppy13g1558.1	916
				Ppy15g2682.1	1114
				Ppy16g0935.1	987
				Ppy16g1031.1	881
Sweet cherry	<i>Prunus avium</i>	Genome v1.0	5	Pav_sc0000028.1_g850.1.mk	1027
				Pav_sc0000091.1_g250.1.mk	1100
				Pav_sc0000334.1_g570.1.mk	1138
				Pav_sc0001031.1_g010.1.mk	914
				Pav_sc0010200.1_g030.1.mk	993
Apricot	<i>Prunus armeniaca</i>	Genome v1.0	4	PARG04349m01	1268
				PARG04567m01	898
				PARG05795m01	994
				PARG28696m01	1086

Almond	<i>Prunus dulcis</i>	Genome v2.0	5	Prudul26A007803	1131
				Prudul26A015191	914
				Prudul26A016773	1086
				Prudul26A019053	1085
				Prudul26A030701	894

Table S3. Primer sequences for 35S-*PpCAMTAs*-GFP vectors recombination.

Primers	Sequence (5'→3')
eGFP- <i>PpCAMTA1</i> -FP	ctgccaaattcgcgaccggtATGGCTGATACCAGAAAATACCTCC
eGFP- <i>PpCAMTA1</i> -RP	tcctttgctagtcataccggtTTGACCTTCGGTGAGTGCAAG
eGFP- <i>PpCAMTA2</i> -FP	ctgccaaattcgcgaccggtATGGCGGAACGCGTATCG
eGFP- <i>PpCAMTA2</i> -RP	tcctttgctagtcataccggtATCAAATGCTATAGACATGAAAGTGTCC
eGFP- <i>PpCAMTA3</i> -FP	ctgccaaattcgcgaccggtATGTATGAGATACAAGTTGGCTCTGG
eGFP- <i>PpCAMTA3</i> -RP	tcctttgctagtcataccggtTGGACCTGCTGTAGGCATGAA
eGFP- <i>PpCAMTA4</i> -FP	ctgccaaattcgcgaccggtATGATGCAATCAGGGTATAATATTAATG
eGFP- <i>PpCAMTA4</i> -RP	tcctttgctagtcataccggtGGGAACTGATACATATCAATGTCTTC
eGFP- <i>PpCAMTA5</i> -FP	ctgccaaattcgcgaccggtATGGAAAAGCAGCTTGGGG
eGFP- <i>PpCAMTA5</i> -RP	tcctttgctagtcataccggtACTATCCATGTTAGAGTCAGGATCCA

Lowercase letters indicate sequences on the vector.

Table S4. Primer sequences for RT-qPCR analysis.

Primers	Sequence (5'→3')
qPCR- <i>PpCAMTA1</i> -FP	ACCTAATTGCACGTCGTTCC
qPCR- <i>PpCAMTA1</i> -RP	TTCTTCCGAACCTGATGTCC
qPCR- <i>PpCAMTA2</i> -FP	AAATCCAGGCTCATGTACGG
qPCR- <i>PpCAMTA2</i> -RP	CAGTCCCCTTACGTCTCCAA
qPCR- <i>PpCAMTA3</i> -FP	CAGCCATTCTGGGGTGAAT
qPCR- <i>PpCAMTA3</i> -RP	CAGCCTCCCATAGCGAAGAG
qPCR- <i>AtICS1</i> -FP	TATCTCCGGCAGCCGCCACT
qPCR- <i>AtICS1</i> -RP	ACGCCGGAGGAAAACGACGG
qPCR- <i>AtEDS1</i> -FP	CGAGACACATCAACTGTTGCAA
qPCR- <i>AtEDS1</i> -RP	CGCCTCTGCGCTTCCA
qPCR- <i>AtSARD1</i> -FP	TCGAGTTGGATTCGTAGCCG
qPCR- <i>AtSARD1</i> -RP	TCGCTTCAGTCATCGCTTCA
qPCR- <i>AtCBP60g</i> -FP	TCGTGGACGCCACCACAAACA
qPCR- <i>AtCBP60g</i> -RP	TCAGCGTTCAGCGGCACGAG
qPCR- <i>AtPAD4</i> -FP	ATCTTCTCCGCCGTCATTCC
qPCR- <i>AtPAD4</i> -RP	CACGTGGCAGAAGTTGTGTG
qPCR- <i>AtPR1</i> -FP	CACATCCGAGTCTCACTGAC
qPCR- <i>AtPR1</i> -RP	CAGACTCATACACTCTGGTG
<i>AtEF1α</i> -FP	TGAGCACGCTCTTCTTGCTTTCA
<i>AtEF1α</i> -RP	GGTGGTGGCATCCATCTTGTTACA

Table S5. Primer sequences for *AtCAMTA3* pro::*PpCAMTA*-pBI121 vectors recombination.

Primers	Sequence (5'→3')
pBI121- <i>PpCAMTA1</i> -FP	cggagaaagcaatattctagaATGGCTGATACCAGAAAATA
pBI121- <i>PpCAMTA1</i> -RP	ggactgaccacccggggatccTTGACCTTCGGTGAGTGCAA
pBI121- <i>PpCAMTA2</i> -FP	cggagaaagcaatattctagaATGGCGGAACGCGTATCGTA
pBI121- <i>PpCAMTA2</i> -RP	ggactgaccacccggggatccATCAAATGCTATAGACATGA
pBI121- <i>PpCAMTA3</i> -FP	cggagaaagcaatattctagaATGTATGAGATACAAGTTGG
pBI121- <i>PpCAMTA3</i> -RP	ggactgaccacccggggatccTGGACCTGCTGTAGGCATGA
<i>AtCAMTA3</i> promoter-FP	CTTTTCCTTTTACTATCTTATTCTCTATCT
<i>AtCAMTA3</i> promoter-RP	GATATTGCTTTCTCCGATCTCAGAG

Lowercase letters indicate sequences on the vector.

Table S6. Transcription levels for SA-related genes after 1 day infected with *Pst* DC3000. Means and standard errors were calculated from three replicates, different letters represent significant differences ($P < 0.05$).

Gene Name	WT	<i>camta2,3</i>	OE- <i>PpCAMTA1</i>		
			#5	#6	#13
<i>AtEDS1</i>	0.033±0.002a	0.042±0.003a	0.035±0.003a	0.038±0.004a	0.047±0.009a
<i>AtPAD4</i>	0.038±0.005b	0.078±0.009a	0.058±0.004ab	0.051±0.002b	0.060±0.003ab
<i>AtSARD1</i>	0.043±0.007b	0.117±0.013a	0.071±0.006ab	0.070±0.017ab	0.099±0.020ab
<i>AtCBP60g</i>	0.017±0.003a	0.036±0.006a	0.032±0.004a	0.025±0.005a	0.029±0.006a
<i>AtICS1</i>	0.016±0.004a	0.031±0.004a	0.021±0.002a	0.028±0.008a	0.029±0.005a

Figure S1. Conserved motifs in CAMTAs were identified using MEME suite program. Each motif is displayed with a specific color.

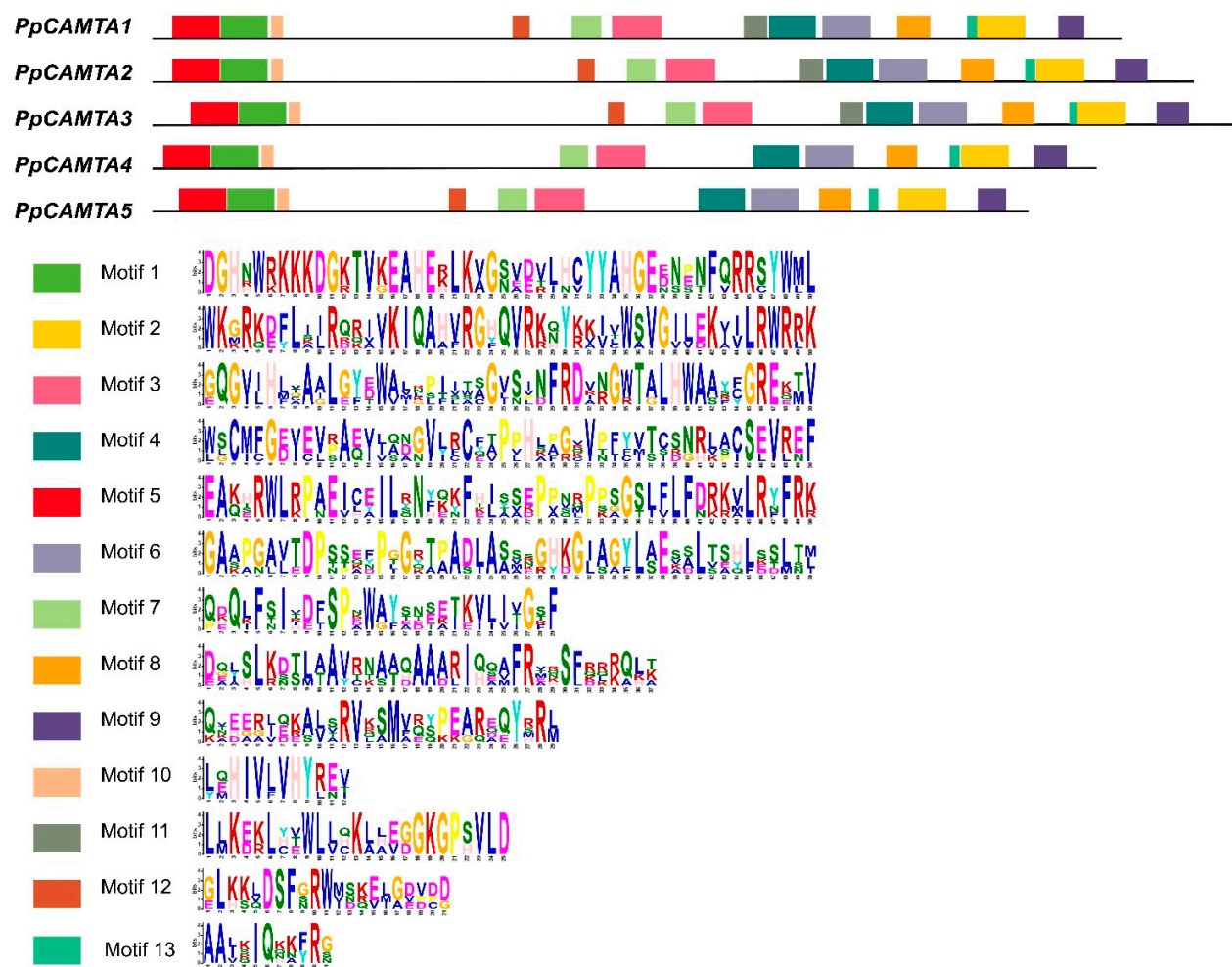


Figure S2. Transcript levels of CAMTA genes in response to UV-B and MeJA. (A) UV-B treatment. (B) MeJA treatment. Error bars represent SE (n=3). * $P<0.05$, ** $P<0.01$, *** $P<0.001$.

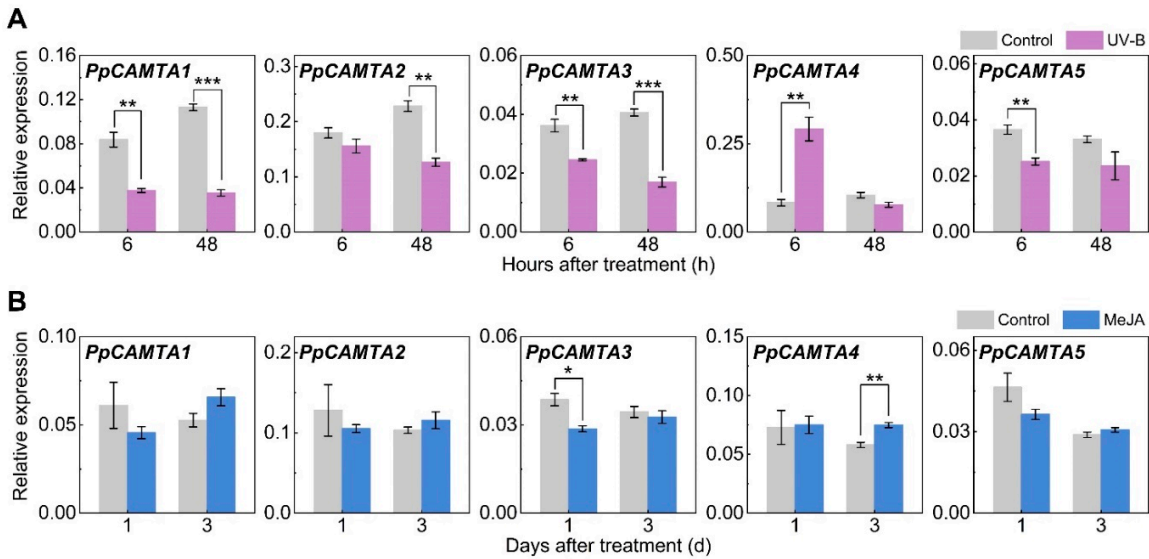


Figure S3. Expression levels of *PpCAMTA1*, *PpCAMTA2* and *PpCAMTA3* in OE-*PpCAMTA*s transgenic lines. Error bars indicate SE calculated from three biological replicates. N.D., not detected.

