

Table S1: Primers RT-PCR and ChIP analyses

Primer sequences used for expression and ChIP analyses. Oligonucleotides were designed, for expression RT-PCR, on primary transcript corresponding to target gene sequences, including the housekeeping genes, and close to annotated genomic TSS (from <http://phytozome.jgi.doe.gov>) for single loci for the ChIP investigation. All the sequences are reported in a 5'-3' orientation, grouped according to main categories.

qPCR analyses			ChIP analyses	
<i>P. persica</i> ID	TAIR	Primer sequence 5'>3'	Primer sequence 5'>3'	ChIP Primers coordinates compared to TSS
Target genes				
Prupe.3G075200_CYCA2/3 related	CYCA2;3	Fw: AGGCTGTGCGAACAAATCCA Rev: CAGCAAGCATTTGGTCACATCC	Fw: AACATCTTGAAATGAGCCCACTTCGACATG Rev: GTCCCAAATAATCTTTCTGAGCAAACCTCCC	TSS +612bp (Fw) +779bp (Rev) (5'UTR)
Prupe.1G428100_CYCA related	CYCA3;1	Fw: CCAAAGCCAAAGGCGAAGAAA Rev: AATCATAAATGTCACGAGCATAAGG	Fw: GAAGCAATTCAAAGCAGGGAACCAAAATGG Rev: CCCTAGCGAATCTGTGAGTGTGAGAGG	-56bp (Fw) TSS +137 (Rev) (5'UTR)
Prupe.2G084600_CDKA-type	CDK2	Fw: CGTGGTTTACAAGGCTCGTG Rev: GCCTGACAATGTTGCCATGTT	Fw: GCTGGATGTACCCGCTGGAGCTG Rev: CTGTACACAAACAGTACCTGACCGC	-47bp (Fw) TSS +185 bp (Rev) (5'UTR)
Prupe.6G299900_CDKB-type	CDKB1	Fw: CCTCGACACCGATCTCAAGAA Rev: CCCTTGACAGTTGGTAGAGGA	Fw: GACATTGATGTACCATTATTACGTTGC Rev: CGTGTCCCGCGCTTGCCCTCACG	-104 bp (Fw) TSS +200bp (Rev) (5'UTR)
Prupe.1G006300_CKI	KRP3	Fw: CATCGCTTACCTGTCAACC Rev: GCCTCGAAGTCGCCCTAGAA	Fw: GGCTCTAGAGGCTGCCACTTACTAC Rev: CCTCATGTACTTGCCCATTTCTTGCTC	-9bp TSS +16bp (Fw) +242bp (Rev) (5'UTR and coding sequence)
Prupe.8G256300_WEE1-like protein	WEE1	Fw: GCTTGCTGACTTTGGATGTGC Rev: TGGCAACTCCCAAGGAGAAGA	Fw: CTGCTCTGATGTGATTTATGCCC Rev: GACAATTGGTGGCTTTCACCTAGC	-0 (Fw) TSS +221 bp (Rev) (coding sequence)
Prupe.5G131900_NST1	NST1	Fw: ACGGCCAGTCTCAAGTTCCTCCG Rev: CGAATACATCAAGATCAATCCTCTC	Fw: GTGGTTGGCTCTTCTCAAGGGATGG Rev: CGGTGAGAGAATGGAATTGAAGGAGCTAG	-86bp (Fw) TSS +108 bp (Rev) (coding sequence)
Prupe.5G117500_CABP-like	CABP-like	Fw: CCCGCGACCGCCATACTCTTAC Rev: TCAACGGAACGGACTCGCTGTG	Fw: CACCACCAACCGCTCATCTTCTCC Rev: CGTTGGTTTCTTCTCGGGTAGATCGG	-15 bp TSS +9bp (Fw) +122bp (Rev) (coding sequence)
Prupe.8G232200_Aux/IAA	AUX_IAA	Fw: CCAAGACCAACAAGGACAACA Rev: CATGCTCACCTTCACCA	Fw: TGTCCAGAGAGTGCAGTGTCCACG Rev: GGGCTGCGTCGGTATTAATATGCG	-24 bp (Fw) TSS +168 bp (Rev) (5'UTR)
Prupe.4G186800_NAC	NAC	Fw: CGAACCTTCACGCAAAATGGCAGCT Rev: CGGTCGTCAATATCCGGGAGC		
Housekeeping genes:				
Prupe.1G364800_TUB	TUB	Fw: CCGAGAATTGTGACTGCCTTCAAG Rev: AGCATCATCTGTCTGGGATTCC		
Prupe.4G204900_UBQ10	UBQ10	Fw: AAGGCTAAGATCCAAGACAAAGAG Rev: CCACGAAGACGAAGCACTAAG		
Prupe.8G137600_PPN1	PPN1	Fw: CCAGGAGAATCGGTGAGCAGAAAA Rev: TCGAGGGTGGAGGACTTGAGAATG		