

1 **SUPPLEMENTARY MATERIAL OF:**

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3 **A *PLENA*-like gene of peach is involved in carpel formation and**
4 **subsequent transformation into a fleshy fruit.**

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13 **Running title:** Characterisation of a *PLENA*-like gene from peach.

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1 **Legend to supplementary figures**

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3 **Supplementary fig. 1.** Structural comparison of some C-type MADS-box genes.
4 Rectangles represent exons while the lines among blocks represent introns. In red are
5 depicted the coding sequences, while the non-coding part of the transcribed regions (5'
6 and 3' UTRs) are in grey. Peach genes (*PpFAR* and *PpPLE*) are highlighted by a peach
7 background. Other gene structures are: *AmFAR* and *AmPLE*: *Antirrhinum majus*
8 *FARINELLI* and *PLENA*, respectively; *AG*, *SHP1* and *SHP2*: *Arabidopsis AGAMOUS*,
9 *SHATTERPROOF1* and *SHATTERPROOF2*, respectively.

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12 **Legend to supplementary tables**

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14 **Supplementary Table 1:** sequences of the oligonucleotides used in qRT-PCR
15 experiments. All the considered genes are tomato-specific but for the last two that are
16 the peach C-type MADS-box described in this paper. Acronyms are as in Figures. In the
17 last column the GenBank accession numbers are reported.

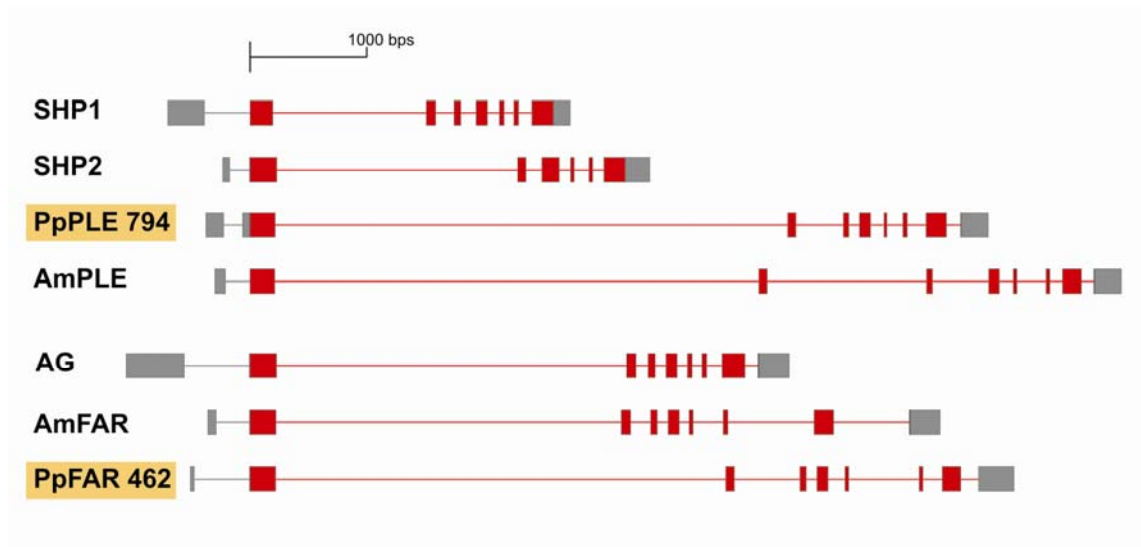
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19 **Supplementary Table 2.** Table showing the amino acid sequence identities among C-
20 type MADS-box transcription factors from *Arabidopsis* (*AG*, *SHP1* and *SHP2*:
21 *AGAMOUS*, *SHATTERPROOF1* and *SHATTERPROOF2*, respectively), **snapdragon**
22 (*AmFAR* and *AmPLE*: *FARINELLI* and *PLENA*), **tomato** (*TAG1* and *TAGL1*) and
23 **peach** (*PpFAR* and *PpPLE*). Sequences of the *AGAMOUS/FARINELLI* clade have been
24 highlighted in green, those belonging to the *PLENA* group in yellow while the two
25 *SHATTERPROOF* genes have been left in white. Data have been obtained from a

- 1 multiple alignment performed using the ClustalW algorithm with a Gonnet 250 protein
- 2 weight matrix.
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1 Supplementary figure 1

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1 Supplementary table 1

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Gene name	oligo for name	sequence of oligo for	oligo rev name	sequence of oligo rev	GenBank Acc. Nos.
ACT: actin	ACT_FOR	AGGCACCCCTTAATCCCAAG	ACT_REV	AAGCACAGCCTGGATAGCAAC	AB199316
ACO1: ACC-oxidase	ACO1_FOR	TCATACAGACGCAGGAGGCA	ACO1_REV	GCATGGGAGGAACATCGATC	X04792
CAB4: major chlorophyll a/b binding protein	CAB_FOR	GCACTGTAAAAGCGCTCCTCAA	CAB_REV	GTCCAGCAGTGTCCCATCCGTAAT	M14443
EXP: expansin	EXP_FOR	ATTACGCGTTGCCAAATGACA	EXP_REV	AGCGCGGTAAGGCAAGTT	U82123
β -GAL 4: β -galactosidase	β -GAL_FOR	CTACTGCGAAGGGTTCCGTC	β -GAL_REV	TTTGAGGAATTGGACCACCG	AF020390
XET: xyloglucan endo-transglycosylases	XET_FOR	CACGAAAAGCTTGGTGTTC	XET_REV	TTCACTCGCCCTCCTTGTGT	X82685
PG: endo-polygalacturonase	PG_FOR	GAGGAACTATCAATGGCAATGGA	PG_REV	CCAGAAGGTTAAGGCCGTTG	X04583
PL: pectate lyase	PL_FOR	ATCGTGTGGTACCGGAAATCC	PL_REV	TCCCAAATCCAATTGCACAGT	BT012714
PME: pectin methyl esterases	PME_FOR	CCCTCTGGTGGTTCGCCTA	PME_REV	GATTGCATGGTGGCCTCATC	Les.7241
PSY1: phytoene synthase	PSY1_FOR	CGTTTTTTTGTTCATCGAGGC	PSY1_REV	CGTACAGAAAATTTCCGTCCATT	M84744
RIN: ripening inhibitor	RIN_FOR	AAACATCATGGCATTGTGGTGAGC	RIN_REV	ATGGTGCTGCATTTTCGGGTTGTA	AF448522
TAG1: agamous	TAG1_FOR	AAGGAACTAGGAAGGGGAAAAT	TAG1_REV	AACCAAAGCAACCTCAGCATCACA	AY098733
TAGL1: agamous like	TAGL1_FOR	TCAGCCAAATTACGAAGATGC	TAGL1_REV	AAGCTGGAGAGGAGTTTGGTCA	AY098735
NOR: non ripening	NOR_FOR	ACGATGCATGGAGTTTGTATTG	NOR_REV	TTAAGTCCATCGTCTCGTTGTTC	AY573802
CNR: colorless non ripening	CNR_FOR	AACAAATGGGAAGGGAAGAGAAGC	CNR_REV	GCACTGATCGACCTGGCAAGAA	DQ672601
PpFAR (MADS462)	TF 12	AGCTGGTTGTTGTTATGC	TF 43	TGGGCGAGTCAATGAGTTCTAT	Ppe.1710
PpPLE (MADS794)	TF 54	GGCACAACAGCAGCAAACAA	TF 55	CGCCTCCAAGATTACAGGGA	Ppe.2689

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1 Supplementary table 2

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	PpPLE	PpFAR	Ple	Far	TAG1	TAGL1	AG	SHP1	SHP2
PpPLE		70.6	75.9	68.4	70.9	72.0	66.4	73.0	70.0
PpFAR			69.7	72.5	73.8	65.8	72.3	68.2	64.2
Ple				69.4	68.9	73.1	65.5	68.5	65.4
Far					80.4	66.8	70.4	66.7	65.3
TAG1						65.7	72.5	65.7	62.3
TAGL1							64.2	66.7	64.5
AG								63.5	59.4
SHP1									85.8
SHP2									

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