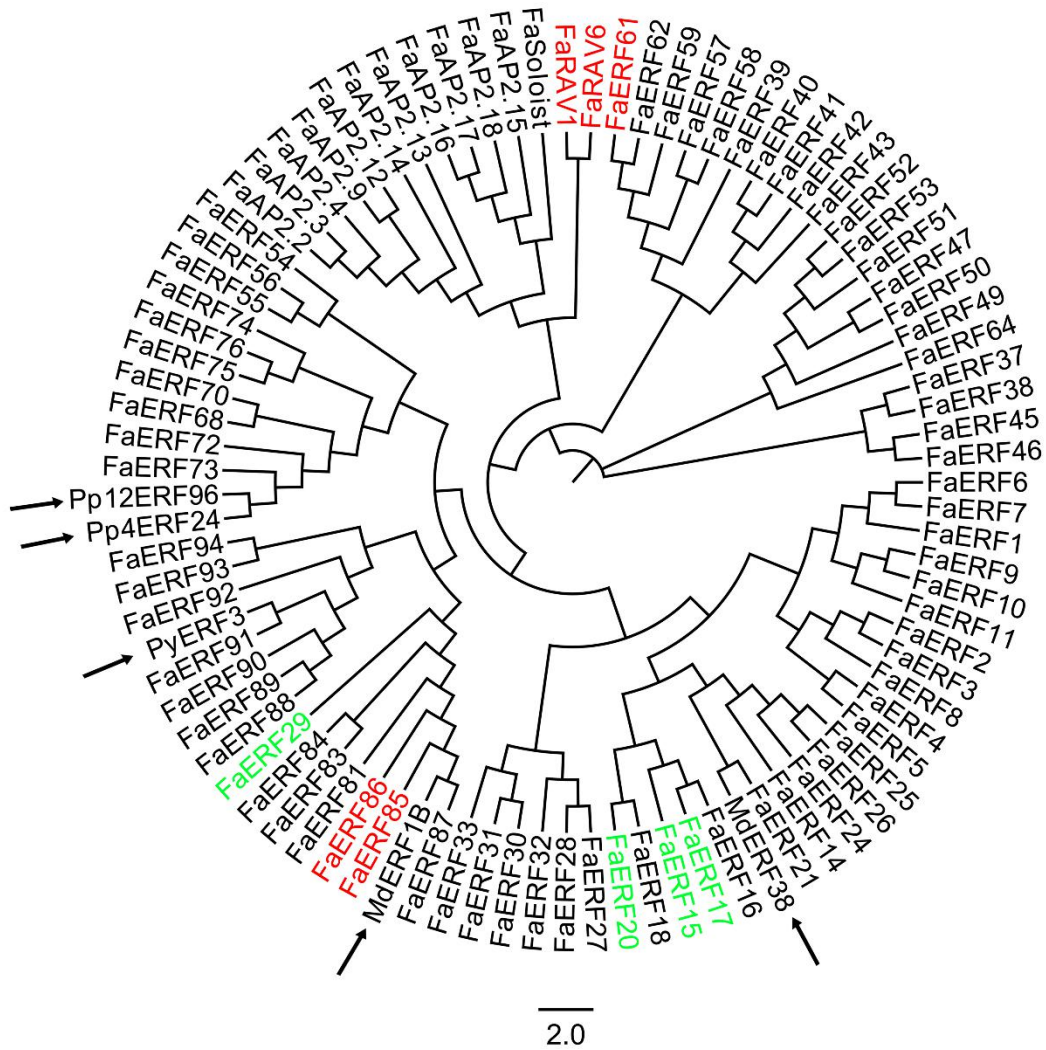
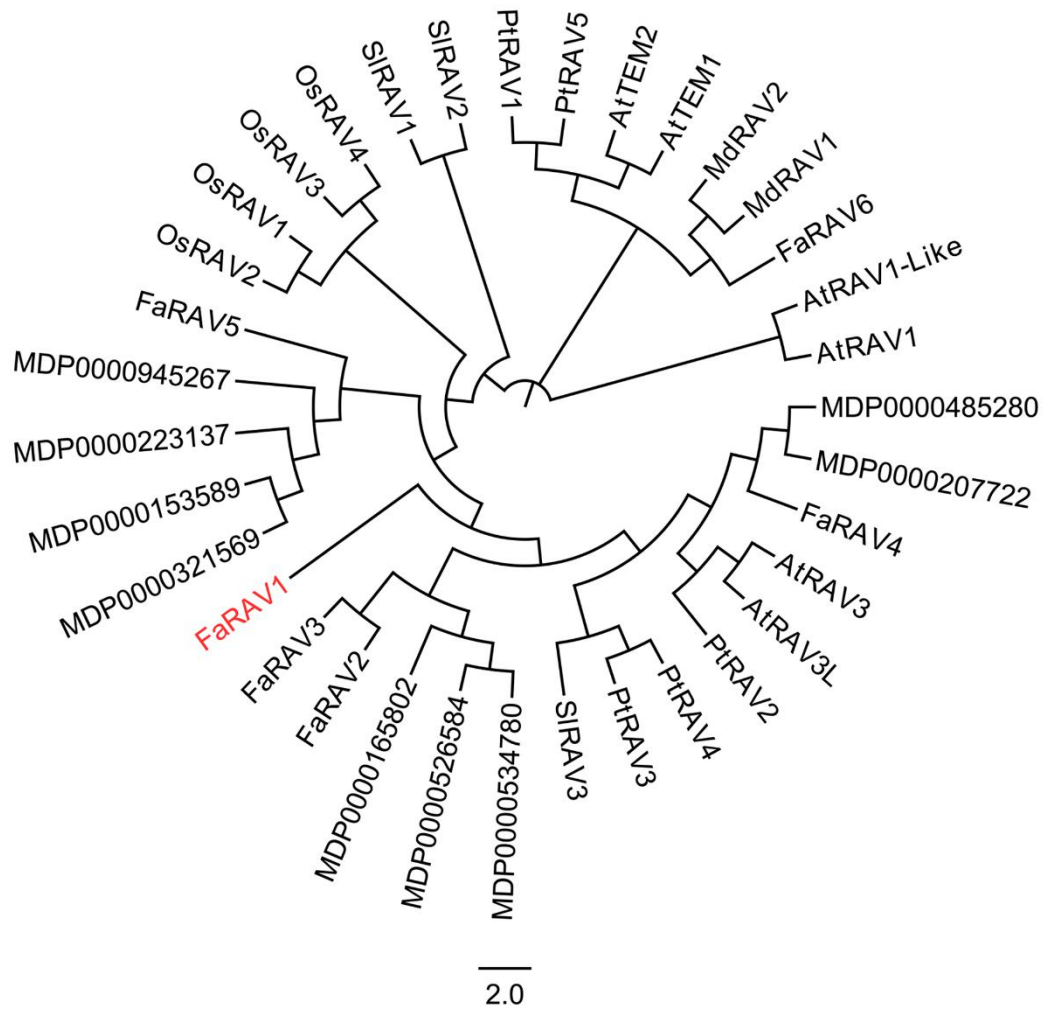


1 **FaRAV1 positively regulates anthocyanin accumulation**  
 2 **Supplemental Data**



3  
 4 **Supplemental Figure S1.** Phylogenetic tree analysis of strawberry AP2/ERF proteins  
 5 and related AP2/ERF TFs from apple and pear. Those ERFs that activated *FaMYB10*  
 6 promoter are denoted in red, which repressed *FaMYB10* promoter are denoted in  
 7 green. Arrows indicated that the five ERFs which have been characterized in  
 8 anthocyanin biosynthesis in apple and pear. NCBI accession numbers of related  
 9 AP2/ERF TFs in apple and pear are as follows: MdERF1B (XM\_008342898.2),  
 10 MdERF38 (XM\_029104540.1), PyERF3 (MF489220), Pp4ERF24 (XM\_009335420.2)  
 11 and Pp12ERF96 (XM\_009370895.2).  
 12



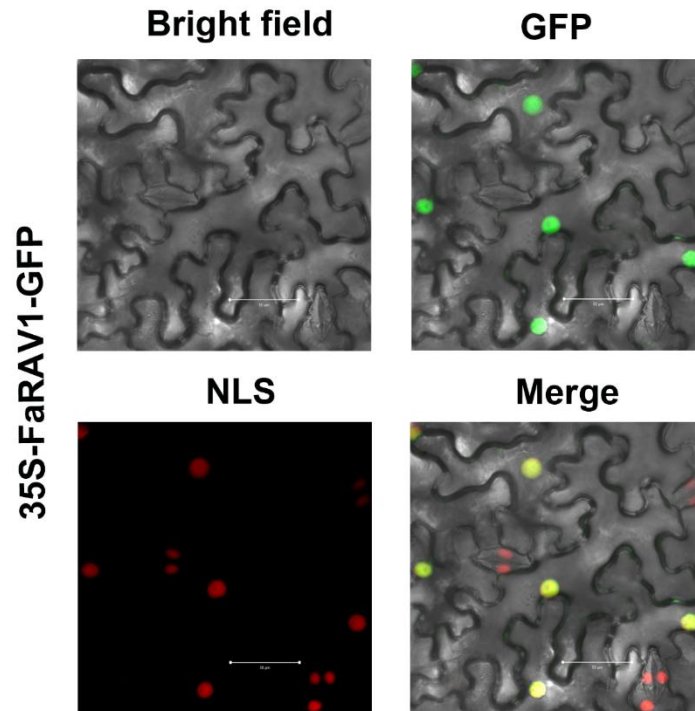
13

14 **Supplemental Figure S2.** Phylogenetic analysis of FaRAV1 and 34 other RAV  
 15 proteins. All the sequences were obtained from the NCBI database. FaRAV1 is  
 16 denoted in red. NCBI accession numbers: *Fragaria × ananassa* FaRAV1  
 17 (XM\_011466945.1), FaRAV2 (XM\_004309888.2), FaRAV3 (XM\_004301388.2),  
 18 FaRAV4 (XM\_004296255.2), FaRAV5 (XM\_011469524.1), FaRAV6  
 19 (XM\_004297092.2), *Arabidopsis thaliana* AtRAV1 (At1g13260), AtRAV1-like  
 20 (At3g25730), AtTEM1 (At1g25560), AtTEM2 (At1g68840), AtRAV3 (At1g50680),  
 21 AtRAV3L (At1g51120), *Solanum lycopersicum* SIRAV1 (XM\_004236951.3),  
 22 SIRAV2 (XM\_001320461.1), SIRAV3 (XM\_010319814.1), *Malus × domestica*  
 23 MdRAV1 (MDP0000939633), MdRAV2 (MDP0000128924), MDP0000945267,  
 24 MDP0000321569, MDP0000223137, MDP0000153589, MDP0000165802,  
 25 MDP0000534780, MDP0000526584, MDP0000485280, MDP0000207722, *Oryza*  
 26 *sativa* OsRAV1 (Os01g04800.1), OsRAV2 (Os01g04750.1), OsRAV3

27 (Os05g47650.1), OsRAV4 (Os01g49830.1), *Populus trichocarpa* PtRAV1  
28 (XP\_002315958.2), PtRAV2 (XP\_002304025.1), PtRAV3 (XP\_024446356.1),  
29 PtRAV4 (XP\_024458800.1), PtRAV5 (XP\_002311438.2).

30

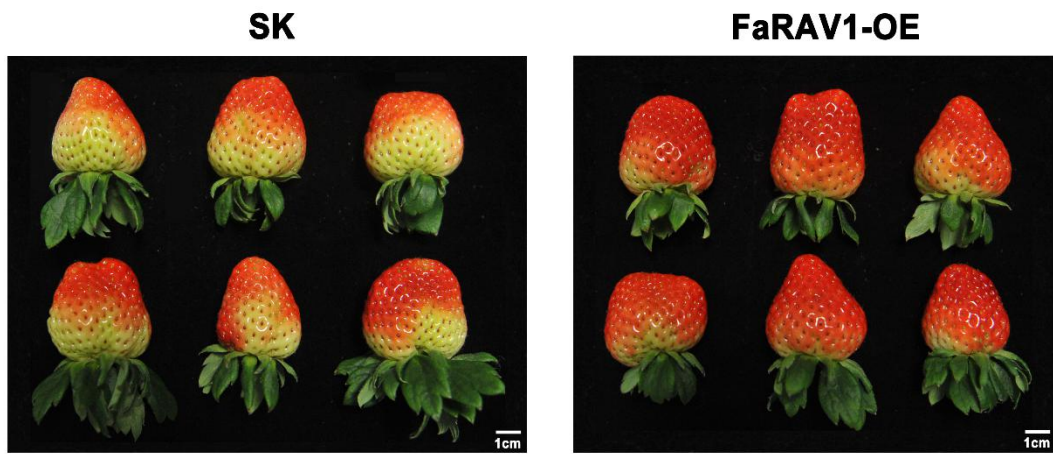
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32

33 **Supplemental Figure S3.** Subcellular localization of FaRAV1. *FaRAV1* was inserted  
34 into the pCAMBIA1300-sGFP vector and transiently expressed in tobacco leaves. The  
35 GFP fluorescence indicated the localization of *FaRAV1*. The tobacco was stably  
36 transformed with a specific nucleus-localized red fluorescent protein, mCherry and  
37 the red fluorescence indicated the nucleus-localized signal (NLS). Bars = 50  $\mu\text{m}$ .

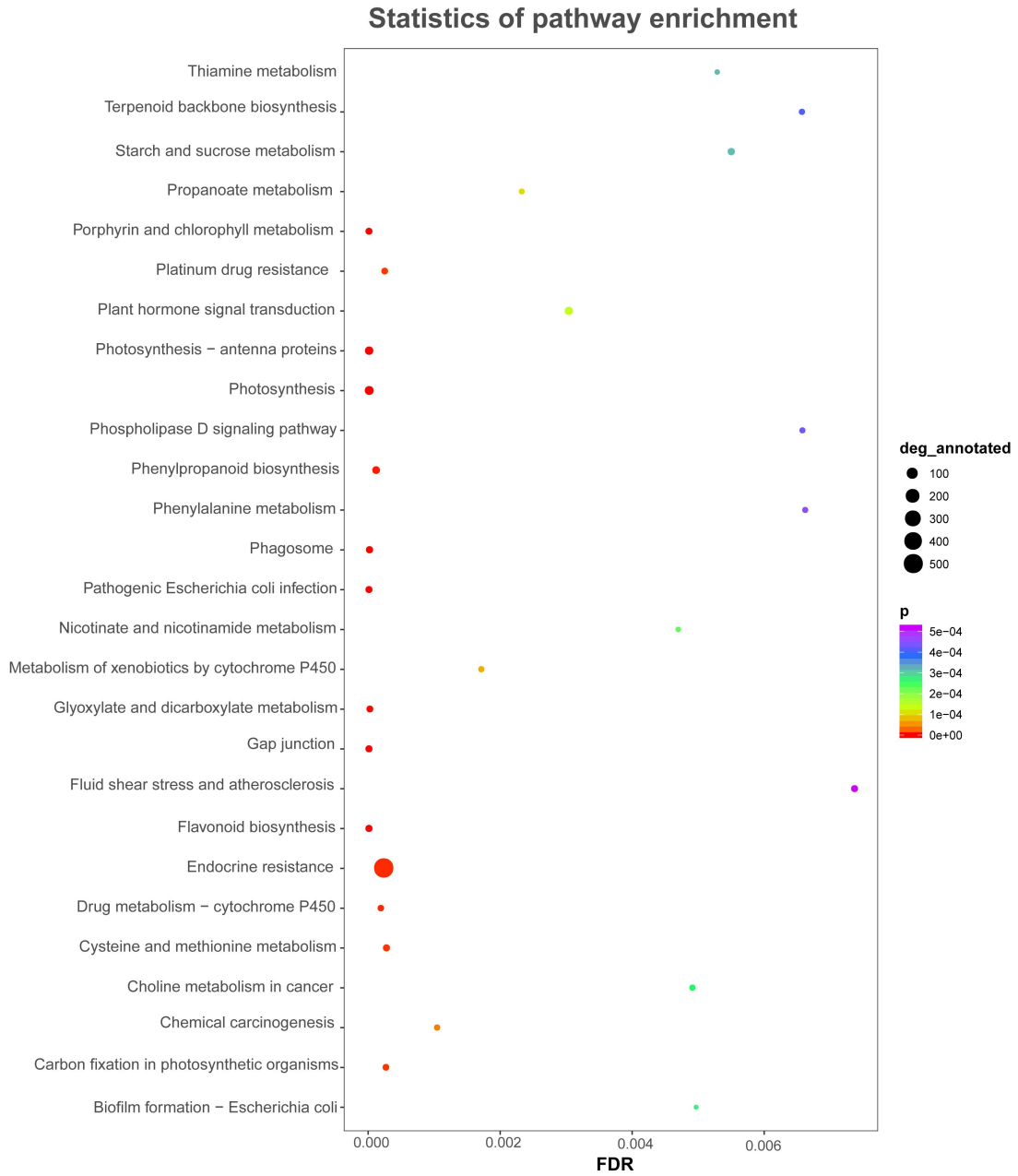
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39

40 **Supplemental Figure S4.** The appearance of *FaRAV1* overexpression fruit (right) 9 d  
41 after injection, compared to the control (left).

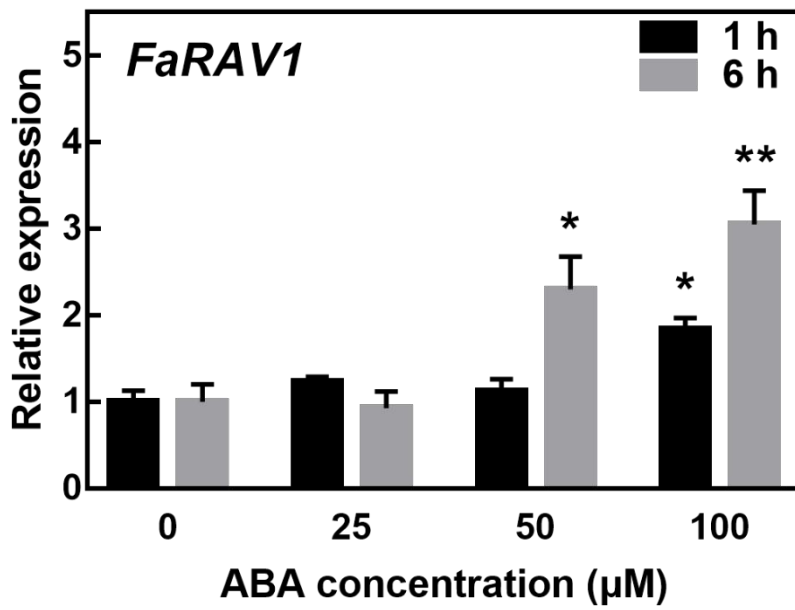
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43

44 **Figure S5.** PEGG analysis of DEGs between *FaRAVI* OE fruit and control fruit.

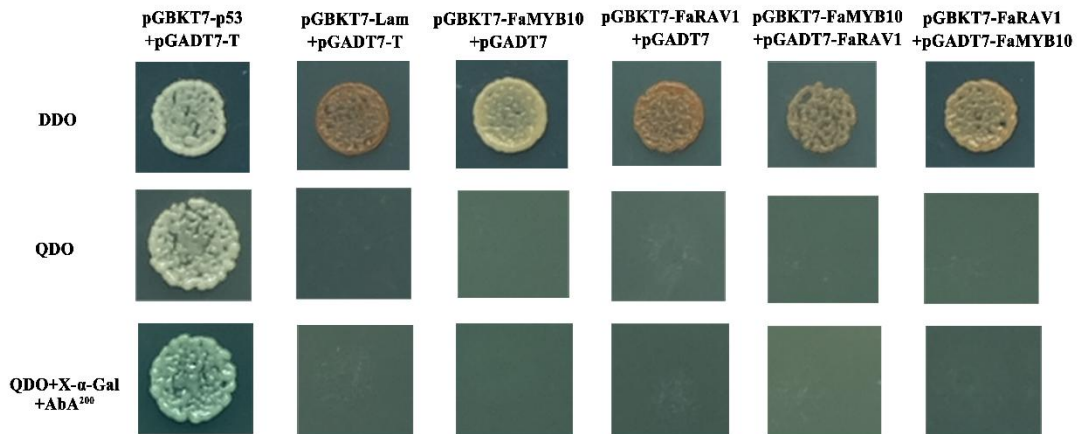
45



46

47 **Supplemental Figure S6.** RT-qPCR analysis of *FaRAV1* expression in response to  
 48 ABA treatment in strawberry fruit. Detached fruit slices at the green stage were  
 49 treated with different concentrations of ABA for 1 or 6 h and then *FaRAV1* expression  
 50 was tested. Error bars are the SE of three biological replicates. Asterisks denote  
 51 significant differences using Student's t test, \* $P < 0.05$ , \*\* $P < 0.01$ .

52

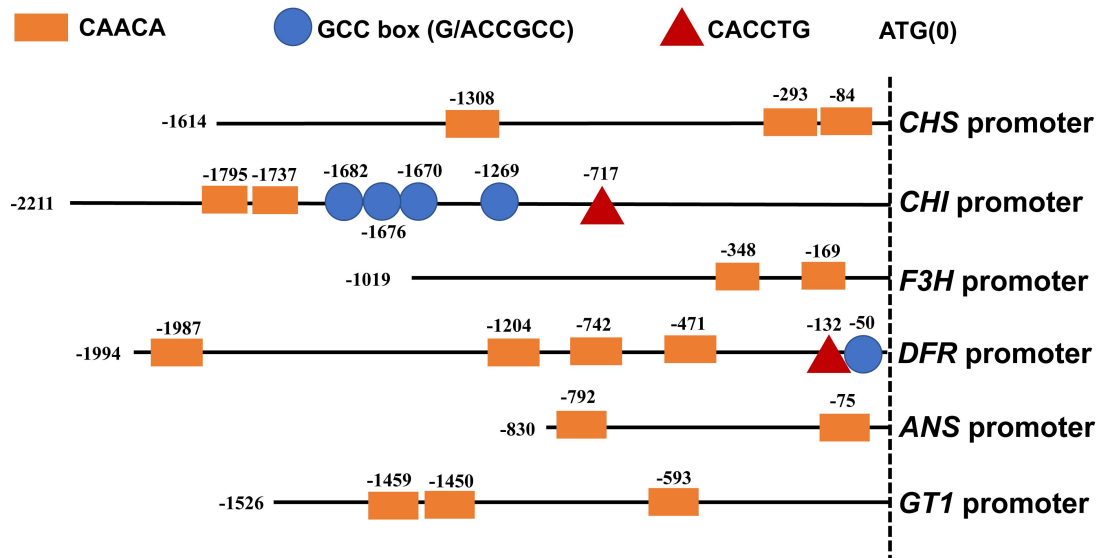


54

55 **Supplemental Figure S7.** Yeast two-hybrid analysis of the interactions between  
 56 FaRAV1 and FaMYB10. FaRAV1 and FaMYB10 were separately fused into  
 57 pGADT7 and pGBKT7 vectors. pGBKT7-p53 and pGBKT7-T were used as positive  
 58 control, while pGBKT7-Lam and pGBKT7-T were used as negative control.  
 59 Protein-protein interactions were detected on SD medium lacking Leu, Trp, His and  
 60 Ade, with AbA<sup>200</sup> and X- $\alpha$ -Gal.

61

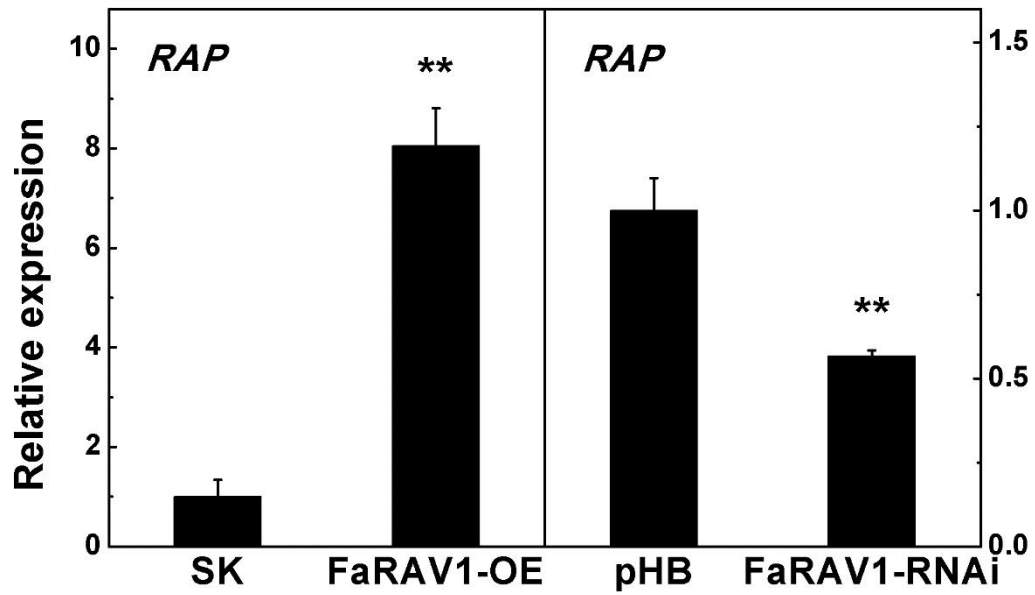




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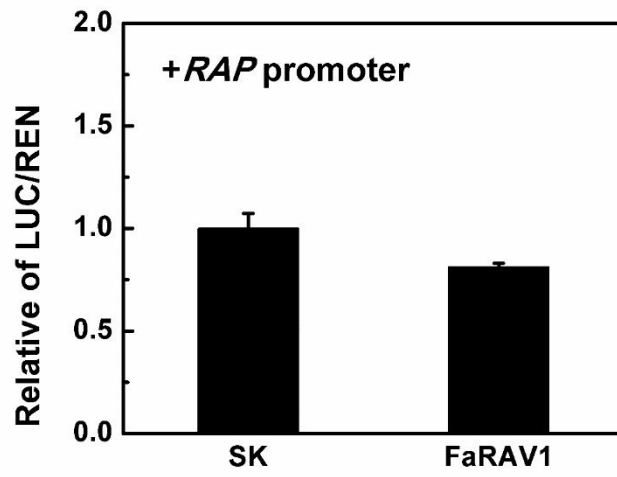
63 **Supplemental Figure S8.** *Cis* regulatory elements in promoters of anthocyanin  
 64 biosynthetic genes. Putative AP2/ERF binding sites: CAACA motif, GCC box  
 65 (A/GCCGCC), CACCTG motif are indicated in the promoter regions of genes  
 66 encoding the anthocyanidin synthase.

67



69

70 **Supplemental Figure S9.** Relative expression of *RAP* in *FaRAV1* OE and RNAi fruit  
71 compared with the control fruit. Asterisks denote significant differences using  
72 Student's t test, \*\* $P < 0.01$ .



73

74 **Supplemental Figure S10.** Regulatory effect of FaRAV1 on the promoter of *RAP*.

75

76 **Supplemental Table S1. Primers used for reverse transcription quantitative PCR.**

<b>Gene</b>	<b>Forward (5'-3')</b>	<b>Reverse (5'-3')</b>
<i>FaRIB413</i>	ACCGTTGATTGCACAATTGGTCATCG	TACTGCGGGTCGGCAATCGGACG
<i>FaRAV1</i>	AGAGCGCATTCCAAAGTCAG	CACAATCCCCTGTTCTTCA
<i>FaMYB10</i>	AGACGGCTTCATACGCAAAGA	ATGAAGGTTCTGGTTCGAGG
<i>CHS</i>	GGCTCACCGTCGAGACCG	GGAGAAGATCACTCGAATCA
<i>CHI</i>	GCCGGAAATGGGAAAGTG	GCTCAGTTTCATGCCTTGAC
<i>F3H</i>	CCCTAAGGTGGCCTACAACCAAT	CTTCTTGCAAATCTCAGCGC
<i>DFR</i>	CACGATTCACGACATTGCGAAATT	GAACTCAAACCCCATCTCTTTCAGCTT
<i>ANS</i>	GAAGTGCGTACCCAATCCATCGT	ACCTTCTCCTTGTTGACGAGCCC
<i>GT1</i>	CCTGGCGCATGGTTCAGT	CGAGTTCCAACCGCAATGT
<i>RAP</i>	GCTACTACTGCTCGATCACC	TGAAGAGACTCGCAAAAGACA
<i>FaRAV1-RNAi</i>	TGGGAGCGGAGATTACATTC	TGGTGAAATACGAAAGGCTGT

78 **Supplemental Table S2. Primers used for vector construction.**

Primer name	Sequence (5'-3')
<b>LUC:</b>	
FaMYB10pro-LUC-FP-BamHI	CAGCCCGGGGATCCAAAAAATGGTACAATTAAG
FaMYB10pro-LUC-RP-NcoI	TGGCGTCTCCATGGGAAAATTAAGCAGATTTC
CHSpro-LUC-FP-BamHI	CAGCCCGGGGATCCGAAAATTAATAATGGTGGGGG
CHSpro-LUC-RP-NcoI	TGGCGTCTCCATGGTTGATTCTCAGAGAAGTG
CHIpro-LUC-FP-BamHI	CAGCCCGGGGATCCCATTTCCCGGAGAGATG
CHIpro-LUC-RP-NcoI	TGGCGTCTCCATGGTTGATTTCTTGGTTTTG
F3Hpro-LUC-FP-BamHI	CAGCCCGGGGATCCGCAATGATTGCCTATAATTA
F3Hpro-LUC-RP-NcoI	TGGCGTCTCCATGGTCTGATATATGCTCTCTAGC
DFRpro-LUC-FP-BamHI	CAGCCCGGGGATCCCTTGCCCCAACAAAGGAATT
DFRpro-LUC-RP-NcoI	TGGCGTCTCCATGGGCCCTAGCTAGTTAGTGCCGT
ANSpro-LUC-FP-BamHI	CAGCCCGGGGATCCAACTCCGATCCCGAACAAAGT
ANSpro-LUC-RP-NcoI	TGGCGTCTCCATGGTGTGCGTTCTAGCTATAGCT
GT1pro-LUC-FP-BamHI	CAGCCCGGGGATCCACATTCTTGTACTGAACTT
GT1pro-LUC-RP-NcoI	TGGCGTCTCCATGGTTCTAGCTAGTCAAGCTACT
RAPpro-LUC-FP-BamHI	CAGCCCGGGGATCCAGGAGACTTCGTCGTCGGA
RAPpro-LUC-RP-NcoI	TGGCGTCTCCATGGTATAGCCACCTGAAAACCTC
<b>pAbAi:</b>	
FaMYB10pro-pAbAi-FP-SacI	AAGCTTGAATTCGAGCTCAAAAAAATGGTACAATTAAG
FaMYB10pro-pAbAi-RP-XhoI	AGCACATGCCTCGAGGAAAATTAAGCAGATTTC
CHSpro-pAbAi-FP-SacI	AAGCTTGAATTCGAGCTCGAAAATTAATAATGGTGGGGG
CHSpro-pAbAi-RP-XhoI	AGCACATGCCTCGAGTTTGTATTCTCAGAGAAGTG
CHIpro-pAbAi-FP-SacI	AAGCTTGAATTCGAGCTCCATTTCCCGGAGAGATG
CHIpro-pAbAi-RP-XhoI	AGCACATGCCTCGAGTTGATTTCTTGGTTTTG
F3Hpro-pAbAi-FP-SacI	AAGCTTGAATTCGAGCTCGCAATGATTGCCTATAATTA
F3Hpro-pAbAi-RP-XhoI	AGCACATGCCTCGAGTCTGATATATGCTCTCTAGC
DFRpro-pAbAi-FP-SacI	AAGCTTGAATTCGAGCTCTTGCCCCAACAAAGGAATT

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DFR <sub>pro</sub> -pAbAi-RP-XhoI	AGCACATGCCTCGAGGCCTAGCTAGTTAGTGCCGT
ANS <sub>pro</sub> -pAbAi-FP-SacI	AAGCTTGAATTCGAGCTCAACTCCGATCCCGAACAAAGT
ANS <sub>pro</sub> -pAbAi-RP-XhoI	AGCACATGCCTCGAGTGTCGCTTCTAGCTATAGCT
GT1 <sub>pro</sub> -pAbAi-FP-SacI	AAGCTTGAATTCGAGCTCCACATTCTGTACTGAACTT
GT1 <sub>pro</sub> -pAbAi-RP-XhoI	AGCACATGCCTCGAGTTCTAGCTAGTCAAGCTACT

**GFP:**

FaRAV1-GFP-FP-KpnI	GACGAGCTCGGTACCATGTCGATAGATCTCAGTTC
FaRAV1-GFP-RP-SalI	GCTCACCATGTCGACACCACTAATCTGAACACCAA

**pGADT7:**

FaRAV1-AD-FP-EcoRI	GAGGCCAGTGAATTCATGTCGATAGATCTCAGTT
FaRAV1-AD-RP-BamHI	GAGCTCGATGGATCCCTTAACCACTAATCTGAACAC
FaMYB10-AD-FP-EcoRI	GAGGCCAGTGAATTCATGGAGGGTTATTTCCGGT
FaMYB10-AD-RP-BamHI	GAGCTCGATGGATCCCTCATACGTAGGAGATGTTGA

**pGBKT7:**

FaRAV1-BD-FP-EcoRI	ATGGAGGCCGAATTCATGTCGATAGATCTCAGTT
FaRAV1-BD-RP-BamHI	CAGGTCGACGGATCCCTTAACCACTAATCTGAACAC
FaMYB10-BD-FP-EcoRI	ATGGAGGCCGAATTCATGGAGGGTTATTTCCGGT
FaMYB10-BD-RP-BamHI	CAGGTCGACGGATCCCTCATACGTAGGAGATGTTGA

**SK:**

FaRAV1-SK-FP-BamHI	TAGAAGTAGTGGATCCATGTCGATAGATCTCAGTT
FaRAV1-SK-RP-EcoRI	GCTTGATATCGAATTCCTTAACCACTAATCTGAACAC

**PET:**

FaRAV1-PET-FP-BamHI	GCTGATATCGGATCCATGTCGATAGATCTCAG
FaRAV1-PET-RP-NotI	TTGTCGACGGCGGCCGACCACTAATCTGAACAC

**RNAi:**

FaRAV1-FP1-pSK	GCTCTCGAGTCTAGAATGTCGATAGATCTCAGTTC
FaRAV1-RP1-pSK	CACAAGCTTGACACATTCATACACAATCC
FaRAV1-FP2-pSK	GGTGGATCCATGTCGATAGATCTCAGTTC
FaRAV1-RP2-pSK	CACGAATTCGACACATTCATACACAATCC

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**EMSA:**

Probe-FP-biotin	AGGGTGGGGACTCGACAGCAACAAGCTAACTTCCACATGCAATGGATCGAAAT
Probe-RP-biotin	ATTTCGATCCATTGCATGTGGAAGTTAGCTTGTTGCTGTCGAGTCCCCACCCT
Probe-FP	AGGGTGGGGACTCGACAGCAACAAGCTAACTTCCACATGCAATGGATCGAAAT
Probe-RP	ATTTCGATCCATTGCATGTGGAAGTTAGCTTGTTGCTGTCGAGTCCCCACCCT
Mutant-Probe-FP-biotin	AGGGTGGGGACTCGACAGTTTTTAGCTAACTTCCACATGCAATGGATCGAAAT
Mutant-Probe-RP-biotin	ATTTCGATCCATTGCATGTGGAAGTTAGCTAAAAACTGTCGAGTCCCCACCCT

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79 Note: Added restriction enzyme sites are underlined.

80

81 **Supplemental Table S3.** Motifs in the *FaRAVI* promoter identified in silico by  
 82 PlantCARE.

Elements	Sequences	Sites (+) = current strand; (-) = opposite strand	Putative functions
ABRE	ACGTG	1412 (-), 1243 (-)	<i>Cis</i> -acting element involved in the abscisic acid responsiveness
AE-box	AGAAACAA	1504 (+)	Part of a module for light response
ARE	AAACCA	1470 (+)	<i>Cis</i> -acting regulatory element essential for the anaerobic induction
AT-rich element	ATAGAAATCAA	589 (+)	Binding site of AT-rich DNA binding protein (ATBP-1)
AuxRR-core	GGTCCAT	425 (+)	<i>Cis</i> -acting regulatory element involved in auxin responsiveness
Box 4	ATTAAT	1216 (-)	Part of a conserved DNA module involved in light responsiveness
CAAT-box	CAAAT, CCAAT	949 (-), 1743 (+), 247 (+), 504 (+)	Common <i>cis</i> -acting element in promoter and enhancer regions
CAT-box	GCCACT	368 (-)	<i>Cis</i> -acting regulatory element related to meristem expression
CGTCA-motif	CGTCA	1007 (+)	<i>Cis</i> -acting regulatory element involved in the MeJA-responsiveness
G-box	CACGTC	1243 (+), 1412 (+)	<i>Cis</i> -acting regulatory element involved in light responsiveness
I-box	AAGATAAGGCT	1098 (-)	Part of a light responsive element
MRE	AACCTAA	1482 (-)	MYB binding site involved in light responsiveness
P-box	CCTTTTG	782 (+), 1519 (+)	Gibberellin-responsive element
TGACG-motif	TGACG	1007 (-)	<i>Cis</i> -acting regulatory element involved in the MeJA-responsiveness