Supplementary Data

FaMYB44.2 negatively regulates sucrose accumulation in strawberry receptacles through interplay with FaMYB10

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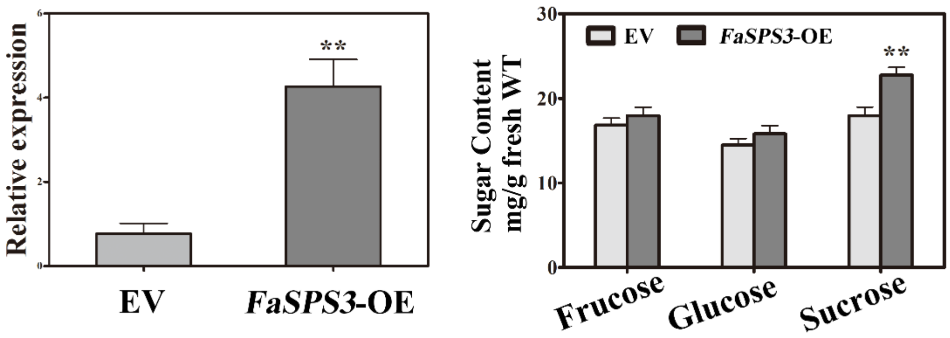
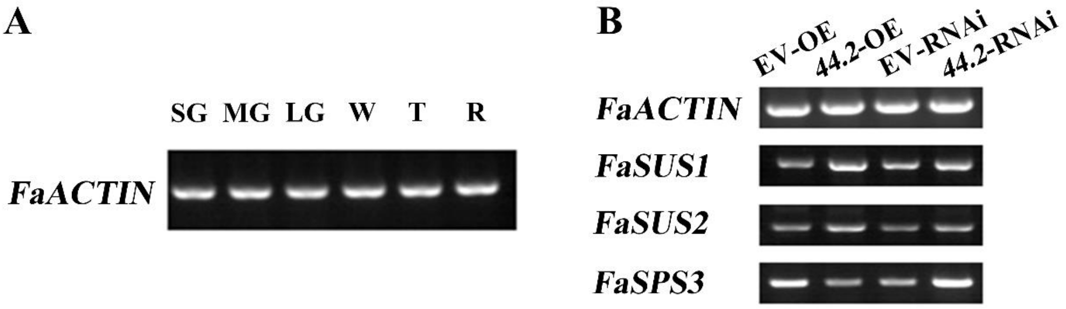
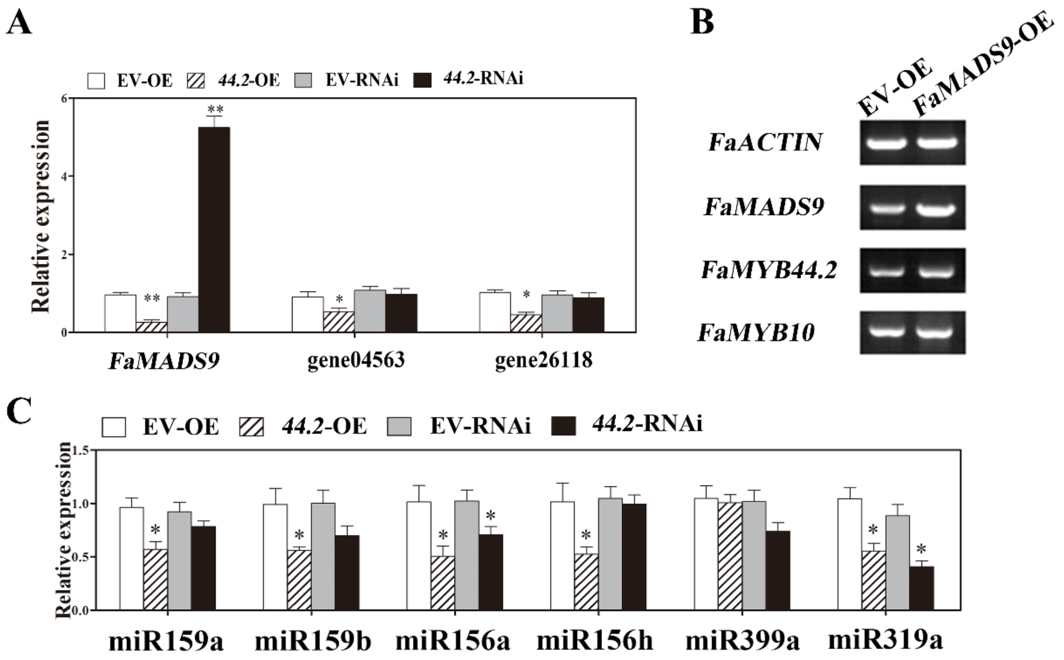
Figures and Tables



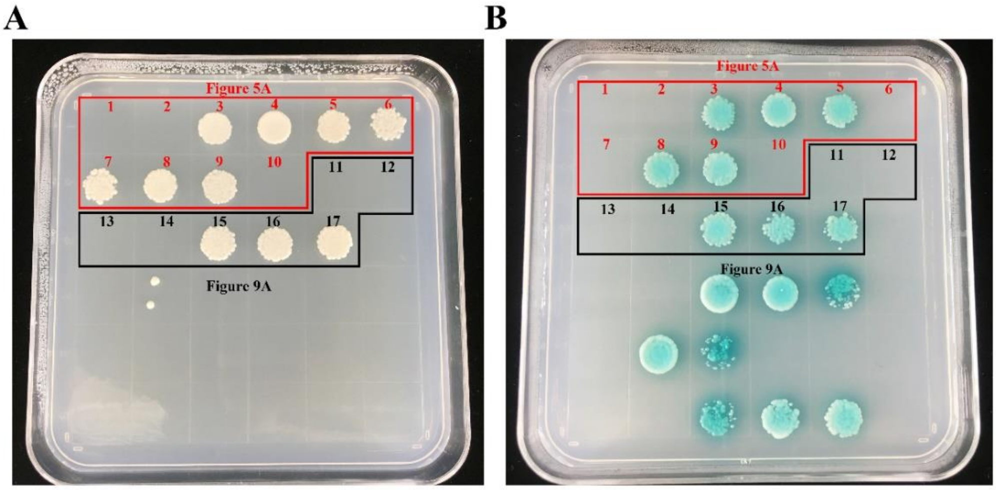
Supplementary Figure S1. The effects of *FaSPS3*-OE on sucrose accumulation in strawberry fruits. *FaSPS3* was overexpressed in white strawberry fruits using pBI121 vector, and the main sugar contents were analyzed by HPLC assay. Values are means ± SD of three biological replicates and normalized using *FaACTIN* as an internal control. The ΔCT of EV sample was chosen as the calibrator. Statistically significant were tested by Student's t test: *P < 0.05 and **P < 0.01. Thirty fruits were pooled as one sample and three biological replicates were performed.



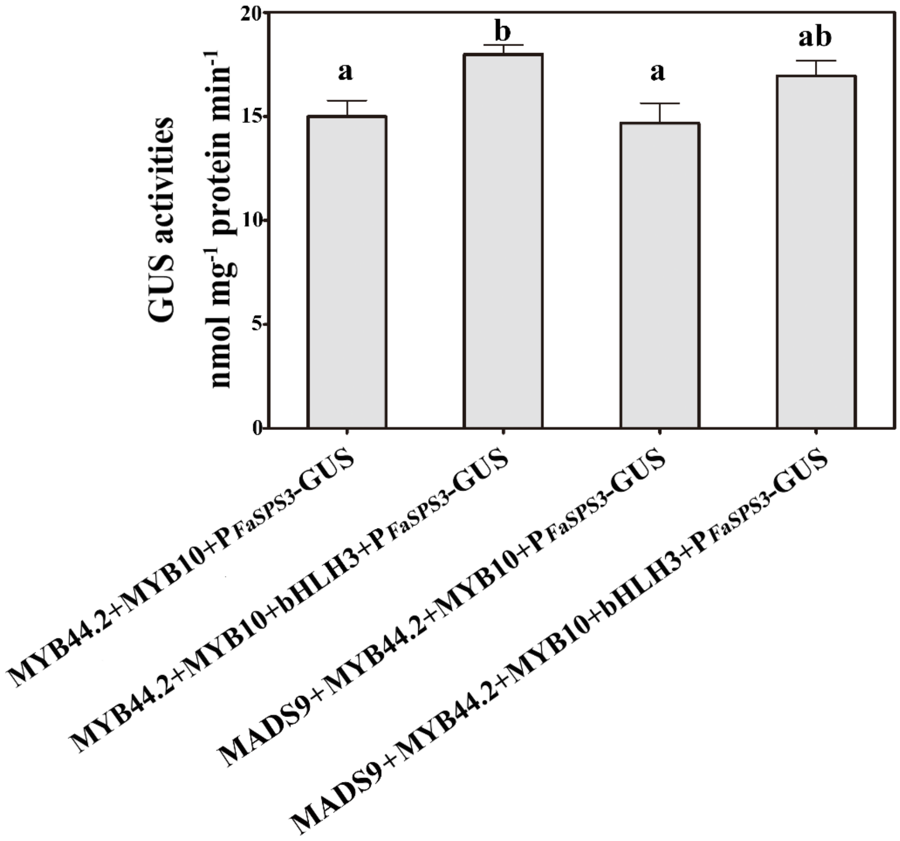
Supplementary Figure S2. Detect the expression levels of *FaACTIN*, *FaSUS* and *FaSPS3* in strawberry fruits. A, The expression pattern of *FaACTIN* during strawberry fruit ripening. SG, small green fruit; MG, middle green fruit; LG, large green fruit; W, white fruit; T, turning fruit and R, red fruit. **B,** The expression levels of *FaSUS1*, *FaSUS2* and *FaSPS3* in *FaMYB44.2*-OE and *FaMYB44.2*-RNAi fruits.



Supplementary Figure S3. The expression levels of *miRNA* and *MADS* in transgenic *FaMYB44.2* and *FaMADS9* fruits. A, The expression levels of *FaMADS9* and its homologues in *FaMYB44.2*-OE and *FaMYB44.2*-RNAi fruits (Feng, 2015). **B**, *FaMADS9* was overexpressed in white strawberry fruits using pSPYCE vector, and the expression of *FaMADS9*, *FaMYB44.2* and *FaMYB10* was analyzed with RT-PCR. **C**, The expression levels of *miRNA 159*, *miRNA156*, *miRNA399* and *miRNA319* (Liu and Carroll, 2010; Csukasi *et al*., 2012; Ren and Tang, 2012; Yang *et al*., 2013; Qian *et al*., 2017) in *FaMYB44.2*-OE and *FaMYB44.2*-RNAi fruits. The primers for RT-PCR were listed in Table S7.



Supplementary Figure S4. Identify the interaction proteins of FaMYB44.2 and FaMYB10 by yeast two-hybrid assay. A, –Leu/–Trp/–His (SD-3) of Fig. 5A. 1, pGAD+pGBK; 2, pGAD+BD-FaMYB44.2; 3, AD-FaMYB44.1+BD-FaMYB44.2; 4, AD-FaMYB44.2+BD-FaMYB44.2; 5, AD-FaMYB44.3+BD-FaMYB44.2; 6, AD-FabHLH3+BD-FaMYB44.2; 7, AD-FabHLH33+BD-FaMYB44.2; 8, AD-FaTTG1+BD-FaMYB44.2; 9, AD-FaMYB1+BD-FaMYB44.2; 10, AD-FaMYB10+BD-FaMYB44.2. –Leu/–Trp/–His (SD-3) of Fig. 9A. 11, pGAD+pGBK; 12, pGAD+BD-FabHLH3; 13, pGAD+BD-FabHLH33; 14, pGAD+BD-FaTTG1; 15, AD-FaMYB10+BD-FabHLH3; 16, AD-FaMYB10+BD-FabHLH33; 17, AD-FaMYB10+BD-FaTTG1. **B,** –Leu/–Trp/–His/–adenine (SD-4) of Fig. 5A and Fig. 9A. The panel was in the same order as shown in Fig. S4A.



Supplementary Figure S5. Detecting the effects of FaMDS9 on FaMYB44.2/FaMYB10-mediated P*$_{FaSPS3}$* activity.

Table S1. The full-length protein sequences for MYB44 and MYB1 genes. Please see the details in the attached Excel file.

Table S2. Primers used for vector construction. The restriction enzyme sites in the primer sequences are underlined.

Primer name	**Enzyme sites**	**Forward primer (5’-3’)**	**Reverse primer (5’-3’)**
***FaMYB44.2*-OE**	Gateway adapters	AAAAAGCAGGCTATGGCTTCTTCTTCAACCAAGA	AGAAAGCTGGGTCTACTCCACCTTGCTAATCCCAA
***FaMYB44.2*-RNAi-P**	AscI/SwaI	GGCGCGCCATCACCCCTCTTCTCTCTCAGAACAA	ATTTAAATTACGCCGGGCAGACTAGAATCGCTC
***FaMYB44.2*-RNAi-N**	PacI/AvrII	TTAATTAATCACCCCTCTTCTCTCTCAGAACAAG	CCTAGGGTACGCCGGGCAGACTAGAATCGC
***FaSPS3*-OE**	BamHI/SacI	GGATCCATGCCGGAGGGTACCAGAAC	GAGCTCCTAGTTCTTGACAACCTCTAATTTCTC
pGEX-4T-1-MYB44.2	EcoRI/XhoI	GAATTCATGGCTTCTTCTTCAACCAAGAAAGC	CTCGAGCTACTCCACCTTGCTAATCCCAATC

Y2H-AD-FaMYB44.1	EcoRI/BamHI	GAATTCATGGCTATGAATCGGAAGGA	GGATCCTCACTCAATTCTGCTGATC
Y2H-AD-FaMYB44.2	NdeI/EcoRI	CATATGATGGCTTCTTCTTCAACCAG	GAATTCCTACTCCACCTTGCTAATCC
Y2H-BD-FaMYB44.2	NdeI/EcoRI	CATATGATGGCTTCTTCTTCAACCAG	GAATTCCTACTCCACCTTGCTAATCC
Y2H-AD-FaMYB44.3	NdeI/EcoRI	CATATGATGGATTGCGAATCGGTTCAGCAGA	GAATTCTTACGAGAGCTTGGGTATACCAAGG
Y2H-AD-FabHLH3	EcoRI/BamHI	GAATTCATGGGTGAGAAGCTTTGGGTGAAT	GGATCCTTACACGGATGATTTTGAAAGAGC
Y2H-BD-FabHLH3	EcoRI/BamHI	GAATTCATGGGTGAGAAGCTTTGGGTGAAT	GGATCCTTACACGGATGATTTTGAAAGAGC
Y2H-AD-FabHLH33	NdeI/EcoRI	CATATGATGCGGATAATTGAAAACCCATGCT	GAATTCTTAACACTTACCAGCAATTTTCCAA
Y2H-BD-FabHLH33	NdeI/EcoRI	CATATGATGCGGATAATTGAAAACCCATGCT	GAATTCTTAACACTTACCAGCAATTTTCCAA
Y2H-AD-FaTTG1	NdeI/XmaI	CATATGATGGAGAATTCGACCCTCGAATCCCACC	CCCGGGTCAAACCTTCAAGAGCTGCATCTTGTT
Y2H-BD-FaTTG1	NdeI/XmaI	CATATGATGGAGAATTCGACCCTCGAATCCCACC	CCCGGGTCAAACCTTCAAGAGCTGCATCTTGTT
Y2H-AD-FaMYB1	NdeI/XmaI	CATATGATGAGGAAGCCCTGCTGCGAGA	CCCGGGTTAAGCAACTTGAGGATCAGCCA
Y2H-AD-FaMYB10	EcoRI/BamHI	GAATTCATGGAGGGTTATTTCGGTGTG	GGATCCTCATACGTAGGAGATGTTGACTAGAT
PMDC83-FaMYB44.2	SpeI/AscI	ACTAGTATGGCTTCTTCTTCAACCAAGAAAGC	GGCGCGCCTCTCCACCTTGCTAATCCCAATC
SPYCE- FaMYB44.1	SpeI/XhoI	ACTAGTATGGCTATGAATCGGAAGGAAAT	CTCGAGCTCAATTCTGCTGATCCCAATTC
SPYNE- FaMYB44.2	SpeI/SalI	ACTAGTATGGCTTCTTCTTCAACCAAGAA	GTCGACCTCCACCTTGCTAATCCCAATCC
SPYCE- FaMYB44.2	SpeI/SalI	ACTAGTATGGCTTCTTCTTCAACCAAGAA	GTCGACCTCCACCTTGCTAATCCCAATCC
SPYCE- FaMYB44.3	SpeI/XhoI	ACTAGTATGGATTGCGAATCGGTTCAGCAGA	CTCGAGCGAGAGCTTGGGTATACCAAGGTGC
SPYNE-FaMYB10	BamHI/SmaI	GGATCCATGGAGGGTTATTTCGGTGTGAGA	CCCGGGGGAGATGTTGACTAGATC
SPYCE-FaMYB10	BamHI/SmaI	GGATCCATGGAGGGTTATTTCGGTGTGAGA	CCCGGGGGAGATGTTGACTAGATC
SPYCE- FaMYB1	BamHI/SmaI	GGATCCATGAGGAAGCCCTGCTGCGAGA	CCCGGGAGCAACTTGAGGATCAGCCATTC
SPYCE-FabHLH3	SpeI/XhoI	ACTAGTATGGGTGAGAAGCTTTGGGTGAAT	CTCGAGCACGGATGATTTTGAAAGAGCAGC
SPYCE-FabHLH33	BamHI/SmaI	GGATCCATGCGGATAATTGAAAACCCATGCT	CCCGGGACACTTACCAGCAATTTTCCAAAGC

SPYCE-FaTTG1	BamHI/SmaI	GGATCCATGGAGAATTCGACCCTCGAATCC	CCCGGGAACCTTCAAGAGCTGCATCTTGTT
SPYCE-FaMADS9	BamHI/SmaI	GGATCCATGGGGAGGGGAAGAGTGGAGC	CCCGGGGAGCATCCAACCAGGAATGAAA
nLUC-FaMYB44.2	SacI/SalI	GAGCTCATGGCTTCTTCTTCAACCAAGA	GTCGACCTCCACCTTGCTAATCCCAATCC
cLUC-FaMYB44.2	SalI/PstI	GTCGACATGGCTTCTTCTTCAACCAAGAAAG	CTGCAGCTACTCCACCTTGCTAATCCCAATC
cLUC-FabHLH3	KpnI/BamHI	GGTACCATGGGTGAGAAGCTTTGGGTGAAT	GGATCCTTACACGGATGATTTTGAAAGAGC
cLUC-FaTTG1	KpnI/BamHI	GGTACCATGGAGAATTCGACCCTCGAATC	GGATCCTCAAACCTTCAAGAGCTGCATC

Table S3 Primers used for gene expression analysis by qRT-PCR.

Gene	Full Name	Gene ID	Forward primer (5'-3')	Reverse primer (5'-3')	Note (related ripening parameter)
FaMYB44.1	MYB domain protein 44.1	gene24027	ATCCTCCAACTTCGCTGTCC	GCCTGGTTCTGAGTCGACTC	——
FaMYB44.2	MYB domain protein 44.2	gene00185	CTCATTCGCAAGCAGCCTTC	GCTGAGTGATGTCGGTGGAT	Sugar and acid accumulation
FaMYB44.3	MYB domain protein 44.3	gene26289	GCGCATTCGAAATACGGCAA	CATGGACGAGTACTTCCGCT	——
FaSUS1	Sucrose synthase 1	gene12940	CCCTGATTCTGACCTTTACTGG	GATGATGAAGTCGGTGTGGTT	Sugar metabolism
FaSUS2	Sucrose synthase 2	gene11077	TTGCTGAGGATGTTGCAGGT	AACAACGAGGCGACGAGATT	Sugar metabolism
FaSPS1	Sucrose-phosphate synthase 1	gene11606	GAGCCTTGAATGTCCCAATGT	ATCTCCTGTCTGGTGCTGGTT	Sugar metabolism
FaSPS2	Sucrose-phosphate synthase 2	gene22863	ACTGTGCAAAGTTGGCGTCTT	GATCATCGCAATCCACGGCTA	Sugar metabolism
FaSPS3	Sucrose-phosphate synthase 3	gene31122	CGTAGATTGGAGTTATGGAGAGC	CGAATGATGTAAGAACCACTGC	Sugar metabolism
FaSUT1	Sucrose transport protein 1	gene26850	GAGTGTTTGTGTTTGGGTTTTG	CGATGGTCCTTTCCAGTGA	Sucrose transporter
FaNI	Neutral invertase	gene05019	CGACCTCGGTGGATAGTCAG	CCACATCACCATTCCCCGTC	Sugar metabolism
FaHXK1	Hexokinase 1	gene11313	AGCATTGGATGGTGGCTTGT	TATGTGCTCGGCGACATCAT	Sugar metabolism and signaling

FaHXK2	Hexokinase 2	gene08515	GCTGTCACCGAGCTTCTAGG	CAGCCCCTATACCAGACCCA	Sugar metabolism and signaling
FaTPS7	Trehalose phosphate synthase 7	gene29717	CTGCTGTGAGGGATGGGATG	CTTGGGCCCACTGGATTCTG	Sugar metabolism and signaling
FaFRK4	Fructokinase 4	gene21673	GCCTTGCTCTCCTATGACCC	TGACCTTGATCACGTCTGCC	Sugar metabolism and signaling
FaCS1	Citrate synthase 1	gene00583	ATCCTGATGCCAATCCTGCC	TGGTGCCTTCCCAAGAATCC	Citric acid accumulation
FaCS2	Citrate synthase 2	gene05118	CATCCCACTGCCGATGTCTT	GACTCTGATGGTTGGCTGCT	Citric acid accumulation
FaVHA-A	V-type proton ATPase catalytic subunit A	gene05361	AGAGCGAGTTTGGCTACGTC	CATTTCCGACACGAACCAGC	Acid metabolism
FaMDH1	Malate dehydrogenase 1	gene05605	GGTGTTCAAGAAAGCCGGGA	CCCAGAACCTCTGCCACAAA	Malic acid metabolism
FaMDH2	Malate dehydrogenase 2	gene11464	TGTGACCACATCCGGGATTG	AGCTGGTACACCGTATGAGC	Malic acid metabolism
FaGAD	Glutamate decarboxylase	gene09305	GCCTACACTATGCCAGCCAA	GAGTCTCTCTGCCAAGCTCC	Acid metabolism
FaNADP-ME	NADP-dependent malic enzyme	gene11286	TGGTGACCTTGGTTGTCAGG	GGCAAACATGTTGAGGGACG	Malic acid metabolism
FaAco	Aconitate hydratase	gene23775	CCTTACACGCTTCGCTCTCA	ATGACTTTCCGGAGCCATGG	Acid metabolism
FaVHP	Vacuolar membrane proton pump	gene30771	GTGGGAAGTGCTGCTCTGAA	AGCATAGTCAGGCTTGGCAG	Acid metabolism
FaAMY3	Alpha-amylase 3	gene04016	TAGCTGCGACGTTTGAGTCC	CCCGTGATCCAACCTCACAT	Starch metabolism
FaBAM1	Beta-amylase 1	gene28316	GGGACATGGTCATTCCCTGG	GTGCTACCCCATTCTGGCTT	Starch metabolism
FaFUM1	Fumarate hydratase 1	gene11092	GGACGTACTCACACGCAAGA	TGCACAAGACTCGCTCGATT	Starch metabolism
FaADSS	Adenylosuccinate synthase	gene03239	GGTGTTGTGGTGCATCTTCC	GGTGAGCACGATCAGAGACC	Starch metabolism
FaQR	Quinone oxidoreductase	gene28406	CACTGACTCTCCCCTACCTACA	ATACACTTCATCCCCCACCTTA	Aroma production
FaEXP1	Expansin 1	gene18424	AGGACGGAGTTGGATTGC	TGAGCGTGAGCGTGAAG	Softness

FaEXP3	Expansin 3	gene04435	TCACTGCCACTAACTTCTGC	TTATGCCTCCTGCTCTCCT	Softness
FaXYL1	Xylosidase 1	gene05164	ATGGAAAGCCTACTTGTGCTG	CTGGTGTAATGTTGTTGGTCGT	Softness
FaCHS	Chalcone synthase	gene26825	GCCTTTGTTTGGCTGGCT	CCCAGGAACATCTTTGAGGA	Anthocyanin accumulation
FaCHI	Chalcone--flavonone isomerase	gene23367	AGCGAAAGCCATTGAAAAGT	CATTTGGTGATTGTGTGAAGAG	Anthocyanin accumulation
FaPAL	Phenylalanine ammonia-lyase	gene23261	CTTCTGTGGTGCTGTTTGATG	AGGGTGGTGCTTCAGTTTATGT	Flavonoid metabolism
FaMADS9	MADS-box transcription factor 9	gene04229	ACGCTGAGGTTGCTCTCATC	AGGACTCTAGCTGACGCTCA	Ripening-related transcription factor
FaSHP	SHATTERPROOF-like	gene24494	TGATCCTGAGAGCTCTTCCCA	GCGCTTGCAGAATGTGACTT	Ripening-related transcription factor
	MADS-box transcription factor	gene04563	GAGAAGGAACGGGTTGCTGA	ACTCATAGAGCTTGCCACGG	
	MADS-box transcription factor	gene26118	GTGCTCCACTTCATCTGGCA	TGCTGAAAGAAACCTTGCGAC	
FaMYB1	MYB domain protein 1	gene09407	TAGCTGGAAGACTGCCTGGA	GGACGAAGAGTAGTGCCTGT	Anthocyanin accumulation
FaMYB10	MYB domain protein 10	gene31413	CAACAGCACCACCACAGACT	GCTTGCCGATTGTACCGTAT	Anthocyanin accumulation
FaEOBII	Emission of benzenoid II	gene28435	GCAGATCAGGCAAGCACAAG	GAGGCTGAACCAGAGTTGCT	Aroma production
FaGAMYB	Transcription factor GAMYB	gene00431	ATCCAATGTGAAACCTGAACCA	CCAGCCAATCTGAACCAAGTAA	Anthocyanin accumulation
FabHLH3	Basic helix-loop-helix 3	gene08231	CAGGAGTTGTGGAGCTTGGT	GCCTGGACAGAGCTAGGAAC	Ripening-related transcription factor
FabHLH33	Basic helix-loop-helix 33	gene19321	TGACAAGGCATCGATCCTCG	GTGCTTCCACAGTGTCCATG	Ripening-related transcription factor
FaTTG1	Transparent testa glabra 1	gene12450	GGACTTGAGGTACATGGCGA	ATTCACACTCCCTCTGTGCC	Ripening-related transcription factor
FaCOI1	Coronatine-insensitive protein 1	gene20913	GAGGAGATTGCGGAGTCGTT	CGGAGCACTTGTCCAGCTTA	JA receptor
FaJAZ1	Jasmonate-zim-domain protein 1	gene12541	AACCTCGTCGACATGCAGTT	ATTTGAAGCCTCTGGGAGCC	JA signaling

FaJAZ2	Jasmonate-zim-domain protein 2	gene00583	AGACATGCAACCTCCTCAGC	GATCTCCTTGGCCTTCTCCG	JA signaling
FaJAZ8	Jasmonate-zim-domain protein 8	gene30624	ATTTGGAGCTCCGCCTTAAT	GAAGATCGTCAATGGCTGCT	JA signaling
FaMYC2	Transcription factor MYC2	gene10501	CTCTCCGAGCTGTTGTTCCA	TCTGACTCCGTCGTTTGCAG	JA signaling
FaOPR3	Oxophytodienoate reductase 3	gene12480	GGAGCCGTTATTTTCTGTCAGC	TCAAAACCTGCTCGAATGGC	JA biosynthesis
FaARF6A	Auxin response factor 6A	gene22728	TGAAGTGCAACAAATGGGAA	CGGCTTACGTAGTCGTCACA	Auxin signaling
FaARF6B	Auxin response factor 6B	gene30394	TGGCTTGCAGACAGACATGT	GCAGAAGGGACGTAGGTAGC	Auxin signaling
FaPIN8	Auxin efflux carrier component 8	gene16792	ACCCTCCCACTCTTCACCTT	GCACAACCACGATGATGAGC	Auxin transporter
FaMRLK47	FERONIA/FER-like receptor kinase 47	gene13568	GCTTAGGTCTTGGTATGATGA	TAGTTGAGGTTGATGTTGTTATTC	Ripening-related protein kinase
FaPYL1	Pyrabactin resistance like 1	gene10508	GCTTCGTAATGAGCGTGGGA	CTCTCCTCGTCCAGCAAGTC	ABA receptor
FaPYL8	Pyrabactin resistance like 8	gene13100	GGAGGAGGTGCGAGTGAGTA	TGAACAGGCGCTTTGATGTG	ABA receptor
FaPYL9	Pyrabactin resistance like 9	gene19210	ACTGGAGCTTCTGGATGACG	ACCTCAGGATGGACGGTGAT	ABA receptor
FaSnRK2.6	SNF1-related protein kinase2.6	gene31902	GCTACACTCGCAACCAAAATC	ACCCCACAAGACCAGACATC	Ripening-related protein kinase
FaNCED1	9-cis-epoxycarotenoid dioxygenase 1	gene31335	ACTGCTTCTGCTTCCATCTCT	AGACACTCGTCGCATTCATT	ABA biosynthesis
FaNCED2	9-cis-epoxycarotenoid dioxygenase 2	gene30616	GACACCTTTTGCTTCCACTTG	GGATTTCGGACAACACACTCT	ABA biosynthesis

FaNCED3	9-cis-epoxycarotenoid dioxygenase 3	gene24386	CAAACCCTATCACCCTTCTCAC	TGGGCAACTTCTGCTTCTTT	ABA biosynthesis
FaACTIN	Actin protein	gene22626	GCCAACCGTGAGAAGATG	TCCAGAGTCAAGAACAATACCAG	——

Table S4. Primers used to construct the vectors for the GUS activity assay. The enzyme sites in the primer sequences are underlined.

Primer name	**Enzyme sites**	**Forward primer (5'-3')**	**Reverse primer (5'-3')**
PBI121-FaMYB10	XbaI/SacI	TCTAGAATGGAGGGTTATTTCGGTGTG	GAGCTCGGATCCTCATACGTAGGAGATGTTGACTAGAT
1304- P$_{FaSPS3}$	NcoI/BglII	CCATGGTTAGCGTCTACTCTCCACAGTTTCCTGCC	AGATCTCGTCGGAGCTCGAATTCAGACCAAATC
1304-FaMYB44.2	EcoRI/XhoI	GAATTCATGGCTTCTTCTTCAACCAAGAAAGC	CTCGAGCTACTCCACCTTGCTAATCCCAATCC
1304-FabHLH3-S	PstI/BamHI	CTGCAGATGGGTGAGAAGCTTTGGGTGAATGA	GGATCCTTACACGGATGATTTTGAAAGAGCAG
1304-FabHLH3-D	PstI/SalI	CTGCAGATGGGTGAGAAGCTTTGGGTGAATGA	GTCGACTTACACGGATGATTTTGAAAGAGCAG
1304-FaTTG1-S	HindIII/XbaI	AAGCTTATGGAGAATTCGACCCTCGAATCC	TCTAGATCAAACCTTCAAGAGCTGCATC
1304-FaTTG1-D	BamHI/KpnI	GGATCCATGGAGAATTCGACCCTCGAATCC	GGTACCTCAAACCTTCAAGAGCTGCATC

Table S5. Probes used for the EMSA. The sequences of cis-elements are underlined.

Primer name	**Forward primer (5'-3')**	**Reverse primer (5'-3')**
P$_{FaSPS3}$-MBS	ATTGCATTTTAGTTTTCAACTGTTTTACGTGTTTAGTCAG	CTGACTAAACACGTAAAACAGTTGAAAACTAAAATGCAAT
P$_{FaSPS3}$-CGTCA-motif	ATCAATTTTCTTTGGAATGACGAGTGTATGGTAAACTAAA	TTTAGTTTACCATACACTCGTCATTCCAAAGAAAATTGAT
P$_{FaSPS3}$-TGA-element	TTAAAACTAGGGTGGAAACGACAGAGATAAGGCGTTTACG	CGTAAACGCCTTATCTCTGTCGTTTCCACCCTAGTTTTAA
P$_{FaCS}$-MBS	TGTGGTGAACATAACTGCTTTCTTAATTGATTACTTTAAA	TTTAAAGTAATCAATTAAGAAAGCAGTTATGTTCACCACA
P$_{FaSUS1}$-HSE+TC-rich	GTGGGTAAGAGAAAATTCATAGTCTTCTGGGAAGAAAATATAGTATATAT	ATATATACTATATTTTCTTCCCAGAAGACTATGAATTTTCTCTTACCCAC
P$_{FaSUS1}$-TC-rich	CCAAGTCTTTGCATTTACTCCATTTCTGTTTCGCGCTTCT	AGAAGCGCGAAACAGAAATGGAGTAAATGCAAAGACTTGG

P$_{FaSUS1}$-TATCCAT	TATACAGAAAAGGAGAGTATCCATGGATGGACATGCAAGA	TCTTGCATGTCCATCCATGGATACTCTCCTTTTCTGTATA
P$_{FaHXK2}$-G-box	AATAAAAACCAACGTGTTGATCTCATACTTCATTTTCGTAGATCTCCACGTAATAACTG	CAGTTATTACGTGGAGATCTACGAAAATGAAGTATGAGATCAACACGTTGGTTTTTATT
P$_{FaHXK2}$-ABRE	TTCGTAGATCTCCACGTAATAACTGTAACC	GGTTACAGTTATTACGTGGAGATCTACGAA
P$_{FaHXK2}$-MBS	TCCACGTAATAACTGTAACCGTACGTCAACCAACTCAGCA	TGCTGAGTTGGTTGACGTACGGTTACAGTTATTACGTGGA
P$_{FaHXK2}$-CGTCA-motif	TAGTAGCTGCGCTTCCGTCATGCTCCATGGACCAATGACGATCGTAAACT	AGTTTACGATCGTCATTGGTCCATGGAGCATGACGGAAGCGCAGCTACTA
P$_{FaHXK2}$-TATCCAT	TCACTATGTCAAATGAAACTATCCATGGGCGGCAACTCGA	TCGAGTTGCCGCCCATGGATAGTTTCATTTGACATAGTGA
P$_{FaMDH1}$-MBS	TTCTTGCTTTCTGAAACTGATAACTGATTCAAATTGTGAT	ATCACAATTTGAATCAGTTATCAGTTTCAGAAAGCAAGAA
P$_{FaMDH1}$-TATCCAT	TTTATGTCTGATAACGTGGTTTATCCATGACATTGTATTT	AAATACAATGTCATGGATAAACCACGTTATCAGACATAAA

Table S6. Sequences and primers used for microRNA expression analysis by qRT-PCR.

miRNA family	**miRNA name**	**Forward primer (5'-3')**	**Sequence**
miR159	**fve-miR159a**	ATTGGATTGAAGGGAGCTCTC	AUUGGAUUGAAGGGAGCUCUC
miR159b	**fve-miR159b**	CGTTGGATTGAAGGGAGCTCTA	UUUGGAUUGAAGGGAGCUCUA
miR828	**fve-miR828**	GCCTCTTGCTTAAATGAGTATTCCA	UCUUGCUUAAAUGAGUAUUCCA
miR156	**fve-miR156a**	GCTTGACAGAAGAGAGTGAGCAC	UUGACAGAAGAGAGUGAGCAC
miR156	**fve-miR156h**	GCCTGACAGAAGAGAGTGAGCTC	UGACAGAAGAGAGUGAGCUC
miR399	**fve-miR399a**	TGCCAAAGGAGAGTTGCCCT	UGCCAAAGGAGAGUUGCCCUG
miR319	**fve-miR319a**	CTTGGACTGAAGGGTGCTCCTT	CUUGGACUGAAGGGUGCUCCUU
U6		GGGGACATCCGATAAAATT	

Table S7. Primers used for gene expression analysis by RT-PCR.

Gene	**Full Name**	**Gene ID**	**Forward primer (5'-3')**	**Reverse primer (5'-3')**
FaSUS1	Sucrose synthase 1	gene12940	TCCGATATTCTTCGTGTTCCC	TGATGTTCTTTACACGGTCCA
FaSUS2	Sucrose synthase 2	gene11077	GAATGATCCATCAAAGCCC	AGACATACTTCCAGAAACCGTA
FaSPS3	Sucrose-phosphate synthase 3	gene31122	CCGCATGGTGGTAATTCCTC	CCCTTTGTCTTTGCTGCGAGA
FaMYB44.2	MYB domain protein 44.2	gene00185	TCAAGCGCAAATTCTCGTCCATGTCC	GAACTGCTTATCAATCCCCACCTCACT

FaMADS9	MADS-box transcription factor 9	gene04229	ATGGGGAGGGGAAGAGTGGAGC	GAGCATCCAACCAGGAATGAAA
FaMYB10	MYB domain protein 10	gene31413	ATGGAGGGTTATTTCGGTGTG	TCATACGTAGGAGATGTTGACTAGAT
FaACTIN	Actin protein	gene22626	TGGGTTTGCTGGAGATGAT	CAGTTAGGAGAACTGGGTGC

Table S8. *FaSUS, FaSPS and FabHLH33* expression at different developmental and ripening stages according to RNA-sequence data. The RNA-seq was performed with diploid strawberry (*Fragaria* × *ananassa* 'Benihoppe'). RPKM (Reads Per Kilobase Million) value was used to present the gene expression levels, while the changed fold of genes was calculated using the log2 ratio of RPKM value between two different samples. Gene ID of FaSUSs and FaSPSs were obtained using the protein sequences of AtSUS and AtSPS as queries BLAST against the strawberry genome database.

Gene Description		**Expression Level (RPKM)**			**Fold Change (Log$_2$*)**	
Gene Name	**Gene ID**	**Green fruit**	**White fruit**	**Red fruit**	**White/Green***	**Red/White***
Sucrose synthase 1	gene12940	213.37	146.73	48.83	-0.54	-1.58
Sucrose synthase 2	gene11077	37.68	44.91	74.31	0.25	0.72
Sucrose synthase 3	gene07050	1.75	0.76	0.05	-1.19	-3.89
Sucrose synthase 4	gene11429	5.89	6.14	3.73	0.06	-0.71
Sucrose synthase 5	gene31666	6.64	5.36	0.87	-0.30	-2.62
Sucrose-phosphate synthase 1	gene11606	0.65	0.56	4.68	-0.22	3.06
Sucrose-phosphate synthase 2	gene22863	7.89	14.38	15.23	0.86	0.08
Sucrose-phosphate synthase 3	gene31122	52.34	91.67	156.54	0.81	0.77
Sucrose-phosphate synthase 4	gene06523	1.62	1.43	0.40	-0.17	-1.83
Sucrose-phosphate synthase 5	gene31164	19.03	11.61	9.41	-0.71	-0.30
Sucrose-phosphate synthase 6	gene04429	11.54	12.67	7.65	0.13	-0.72
Sucrose-phosphate synthase 7	gene03841	0.13	0.04	0.17	-1.69	2.04
Sucrose-phosphate synthase 8	gene04408	9.34	10.96	14.37	0.23	0.39

FabHLH33	gene19321	0.10	0.18	0.88	0.75	0.07

Table S9. Quantitative analysis of *FaMYB10* and *FaMYB44.2* expression levels by qRT-PCR. The $2^{-\Delta\Delta CT}$ method was used to calculate transcript levels (Schmittgen and Livak, 2008). Transcript values were normalized using *FaACTIN* as an internal control. The ΔCT of small green fruit was chosen as the calibrator (Livak & Schmittgen, 2001). The ratio of gene expression levels in different fruit stages between FaMYB10 and FaMYB44.2 was calculated by transcript values. Three biological replicates were repeated.

Fruit Stage	**Ratio of gene expression levels**
Green fruit	*FaMYB10*: *FaMYB44.2* = 0.16
White fruit	*FaMYB10*: *FaMYB44.2* =4.67
Turning fruit	*FaMYB10*: *FaMYB44.2* = 6.28
Red fruit	*FaMYB10*: *FaMYB44.2* = 13.22