

Table 1 Suppl. List of primer sequences of *FanMYBs*.

Gene name	Primer sequence ( 5'-3')
<i>FanMYB13</i>	forward primer: CGATAACGCCATCAAGAACC reverse primer: TTGCGAGGGAGGAACCACG
<i>FanMYB18</i>	forward primer: AGAAGAACAAAGTCACCTACGC reverse primer: CAGATGGTCCTCCTCCGA
<i>FanMYB43</i>	forward primer: AACGGGTTTTGTTTGGATTC reverse primer: GTAGTGGTGGTTGTGGCAGA
<i>FanMYB47</i>	forward primer: CGCAGGTTTGAAGAGATGTG reverse primer: TTGCCAAGAAGATTATGGAGTC
<i>FanMYB60</i>	forward primer: TGTTTGTGTGTTCAAGATGGTC reverse primer: GACTTGTCATTGTTGAGGC
<i>FanMYB62</i>	forward primer: GAGCAGTCCCAACCAACAC reverse primer: GCACCTCAATAACCCTTTCG
<i>Actin-2</i>	forward primer: AGCCGCTCGTGTGATAA reverse primer: CAGGATACCTCTTTGGATTGA

Table 2 Suppl. *FanMYB* genes information from *Fragaria × ananassa* (CDS coding sequence, aa - number of amino acids, pI - theoretical isoelectric point, Mr - relative molecular mass).

Gene name	Gene ID	CDS [bp]	Length [aa]	pI	Mr [kDa]	Paralogous gene in strawberry
<i>FanMYB1</i>	FANhyb_icon00000113_a.1.g00001.1	1101	366	6.33	39.98	
<i>FanMYB2</i>	FANhyb_icon00000211_a.1.g00001.1	1068	355	9.99	41.02	
<i>FanMYB3</i>	FANhyb_icon00003944_a.1.g00001.1	753	250	8.13	27.58	
<i>FanMYB4</i>	FANhyb_icon00010807_a.1.g00001.1	326	108	10.31	12.44	
<i>FanMYB5</i>	FANhyb_rscf00000007.1.g00024.1	1101	366	4.82	40.61	
<i>FanMYB6</i>	FANhyb_rscf00000009.1.g00012.1	1023	340	6.44	38.09	
<i>FanMYB7</i>	FANhyb_rscf00000036.1.g00002.1	843	280	4.71	31.96	
<i>FanMYB8</i>	FANhyb_rscf00000036.1.g00003.1	846	281	4.60	32.13	
<i>FanMYB9</i>	FANhyb_rscf00000056.1.g00007.1	1020	339	6.99	38.12	
<i>FanMYB10</i>	FANhyb_rscf00000058.1.g00005.1	840	279	4.77	31.25	
<i>FanMYB11</i>	FANhyb_rscf00000075.1.g00026.1	576	191	8.30	21.51	
<i>FanMYB12</i>	FANhyb_rscf00000093.1.g00003.1	3192	1063	5.23	119.63	
<i>FanMYB13</i>	FANhyb_rscf00000096.1.g00022.1	966	321	9.73	34.70	
<i>FanMYB14</i>	FANhyb_rscf00000101.1.g00008.1	1071	356	7.91	38.02	<i>FaMYB5</i>
<i>FanMYB15</i>	FANhyb_rscf00000147.1.g00015.1	852	283	6.09	32.01	
<i>FanMYB16</i>	FANhyb_rscf00000155.1.g00005.1	912	303	7.69	32.65	
<i>FanMYB17</i>	FANhyb_rscf00000212.1.g00004.1	1077	358	7.10	39.86	<i>FaMYB30</i>
<i>FanMYB18</i>	FANhyb_rscf00000230.1.g00005.1	1440	479	5.59	52.36	
<i>FanMYB19</i>	FANhyb_rscf00000234.1.g00004.1	672	223	8.47	25.75	
<i>FanMYB20</i>	FANhyb_rscf00000290.1.g00010.1	1443	480	6.04	54.41	
<i>FanMYB21</i>	FANhyb_rscf00000309.1.g00008.1	1329	442	7.46	48.71	
<i>FanMYB22</i>	FANhyb_rscf00000315.1.g00012.1	855	284	9.53	32.29	<i>FvMYB12</i>
<i>FanMYB23</i>	FANhyb_rscf00000337.1.g00009.1	1095	364	6.37	41.70	
<i>FanMYB24</i>	FANhyb_rscf00000430.1.g00002.1	1647	548	5.03	63.28	
<i>FanMYB25</i>	FANhyb_rscf00000496.1.g00002.1	768	255	8.42	29.22	
<i>FanMYB26</i>	FANhyb_rscf00000563.1.g00001.1	834	277	8.88	32.51	
<i>FanMYB27</i>	FANhyb_rscf00000586.1.g00002.1	687	228	9.04	26.05	
<i>FanMYB28</i>	FANhyb_rscf00000649.1.g00006.1	1692	563	4.94	61.17	
<i>FanMYB29</i>	FANhyb_rscf00000669.1.g00004.1	1326	441	7.65	49.15	
<i>FanMYB30</i>	FANhyb_rscf00000692.1.g00004.1	1029	342	9.20	38.10	
<i>FanMYB31</i>	FANhyb_rscf00000733.1.g00002.1	834	277	5.89	30.73	
<i>FanMYB32</i>	FANhyb_rscf00000787.1.g00009.1	873	290	9.38	32.26	
<i>FanMYB33</i>	FANhyb_rscf00000794.1.g00002.1	1260	419	7.61	46.46	
<i>FanMYB34</i>	FANhyb_rscf00000804.1.g00005.1	894	297	9.83	33.23	
<i>FanMYB35</i>	FANhyb_rscf00000839.1.g00002.1	678	225	6.25	25.03	
<i>FanMYB36</i>	FANhyb_rscf00000866.1.g00004.1	969	322	6.56	36.09	
<i>FanMYB37</i>	FANhyb_rscf00000962.1.g00004.1	1119	372	6.09	41.44	

<i>FanMYB38</i>	FANhyb_rscf00000991.1.g00009.1	813	270	8.28	30.19	
<i>FanMYB39</i>	FANhyb_rscf00001061.1.g00003.1	930	309	8.58	34.94	
<i>FanMYB40</i>	FANhyb_rscf00001096.1.g00005.1	690	229	5.05	26.64	
<i>FanMYB41</i>	FANhyb_rscf00001164.1.g00006.1	816	271	9.60	31.33	
<i>FanMYB42</i>	FANhyb_rscf00001287.1.g00002.1	1137	378	4.79	42.18	<i>FaMYB63</i>
<i>FanMYB43</i>	FANhyb_rscf00001324.1.g00001.1	801	266	9.01	29.41	
<i>FanMYB44</i>	FANhyb_rscf00001535.1.g00003.1	810	269	7.80	30.48	
<i>FanMYB45</i>	FANhyb_rscf00001620.1.g00003.1	981	326	4.83	36.81	
<i>FanMYB46</i>	FANhyb_rscf00002068.1.g00002.1	879	292	6.10	31.67	
<i>FanMYB47</i>	FANhyb_rscf00002302.1.g00001.1	828	275	7.73	30.46	<i>FaMYB9</i>
<i>FanMYB48</i>	FANhyb_rscf00002387.1.g00001.1	1248	415	7.33	45.73	
<i>FanMYB49</i>	FANhyb_rscf00002470.1.g00001.1	999	333	6.03	38.00	
<i>FanMYB50</i>	FANhyb_rscf00002586.1.g00001.1	954	317	7.47	35.27	
<i>FanMYB51</i>	FANhyb_rscf00002824.1.g00001.1	1095	364	6.60	41.25	
<i>FanMYB52</i>	FANhyb_rscf00003136.1.g00001.1	942	313	6.70	35.49	<i>MYB65</i>
<i>FanMYB53</i>	FANhyb_rscf00003340.1.g00001.1	1569	522	7.02	58.68	
<i>FanMYB54</i>	FANhyb_rscf00003425.1.g00001.1	915	304	7.50	34.64	
<i>FanMYB55</i>	FANhyb_rscf00003591.1.g00001.1	1008	335	4.84	37.30	
<i>FanMYB56</i>	FANhyb_rscf00003768.1.g00001.1	1092	363	7.82	40.63	
<i>FanMYB57</i>	FANhyb_rscf00004083.1.g00001.1	765	254	6.51	28.87	
<i>FanMYB58</i>	FANhyb_rscf00004186.1.g00001.1	1152	383	6.40	42.53	<i>MYB21</i>
<i>FanMYB59</i>	FANhyb_rscf00004369.1.g00001.1	825	274	4.69	30.57	
<i>FanMYB60</i>	FANhyb_rscf00004588.1.g00001.1	780	259	5.42	29.61	
<i>FanMYB61</i>	FANhyb_rscf00004636.1.g00001.1	1089	362	9.92	40.63	
<i>FanMYB62</i>	FANhyb_rscf00005380.1.g00001.1	1026	341	7.57	37.95	
<i>FanMYB63</i>	FANhyb_rscf00005479.1.g00001.1	894	297	6.24	33.18	
<i>FanMYB64</i>	FANhyb_rscf00005798.1.g00001.1	1107	368	5.80	41.32	
<i>FanMYB65</i>	FANhyb_rscf00005962.1.g00001.1	693	230	5.01	26.04	
<i>FanMYB66</i>	FANhyb_rscf00006802.1.g00001.1	813	270	4.95	31.01	

Table 3 Suppl. The identity of orthologous proteins.

Protein 1	Protein 2	Identity [%]	Group
FanMYB13	MdMYB6	43.87	G1
FanMYB46	MdMYB6	63.49	G1
FanMYB62	AtMYB60	39	G2
FanMYB42	FaMYB63	95.24	G3
FanMYB36	SmMYB52	44.72	G4
FanMYB18	SmMYB97	24.95	G5
FanMYB47	FaMYB9	95.67	G6
FanMYB22	FtMYB13	51.82	G7
FanMYB6	GmMYB12B2	36.18	G8
FanMYB19	SmMYB36	34.53	G9
FanMYB27	SmMYB36	35.96	G9
FanMYB4	GbMYBF2	26.01	G10
FanMYB10	GbMYBF2	35.26	G10
FanMYB25	PhMYB27	43.75	G11
FanMYB25	VvMYBC2-L1	56.08	G11
FanMYB25	PpMYB18	63.53	G11
FanMYB39	FtMYB15	43.04	G12
FanMYB43	MdMYB16	77.07	G12
FanMYB43	CsMYB4a	71.8	G12
FanMYB43	VvMYB4a	69.4	G12

Table 4 Suppl. List of key genes from the phenylpropanoid pathway in *Fragaria × ananassa*.

Number	Gene ID	Gene name	Annotation
1. Phenylalanine (PAL)			
1	FANhyb_rscf00000079.1.g00001.1	<i>FanPAL1</i>	phenylalanine ammonia-lyase 1 (AtPAL1)
2	FANhyb_rscf00000868.1.g00006.1	<i>FanPAL4</i>	phenylalanine ammonia-lyase 4 (AtPAL4)
2. Cinnamic acid - C4H			
1	FANhyb_rscf00000062.1.g00009.1	<i>FanCAD1</i>	probable cinnamyl alcohol dehydrogenase 1 (AtCAD1)
2	FANhyb_rscf00000027.1.g00015.1	<i>FanCAD9-1</i>	probable cinnamyl alcohol dehydrogenase 9 (AtCAD9)
3	FANhyb_icon00003379_a.1.g00001.1	<i>FanC4H1</i>	trans-cinnamate 4-monooxygenase (AtC4H)
4	FANhyb_rscf00003780.1.g00001.1	<i>FanCAD8</i>	probable cinnamyl alcohol dehydrogenase 8 (AtCAD8)
5	FANhyb_icon00014010_a.1.g00001.1	<i>FanCAD9-2</i>	probable cinnamyl alcohol dehydrogenase 9 (AtCAD9)
6	FANhyb_rscf00001371.1.g00003.1	<i>FanCAD4-1</i>	probable cinnamyl alcohol dehydrogenase 4 (AtCAD 4)
7	FANhyb_rscf00001371.1.g00002.1	<i>FanCAD4-2</i>	probable cinnamyl alcohol dehydrogenase 4 (AtCAD 4)
8	FANhyb_rscf00000282.1.g00007.1	<i>FanC4H2</i>	trans-cinnamate 4-monooxygenase (AtC4H)
3. Coumaroyl-CoA			
1	FANhyb_rscf00001339.1.g00001.1	<i>Fan4CL2</i>	4-coumarate-CoA ligase 2 (At4CL 2)
2	FANhyb_rscf00000016.1.g00006.1	<i>Fan4CL9</i>	4-coumarate-CoA ligase-like 9 (At4CL9)
3	FANhyb_rscf00001265.1.g00004.1	<i>Fan4CL1</i>	4-coumarate-CoA ligase-like 1 (At4CL1)
4	FANhyb_rscf00001388.1.g00002.1	<i>Fan4CL7</i>	4-coumarate-CoA ligase-like 7 (At4CL7)
5	FANhyb_rscf00000061.1.g00019.1	<i>Fan4CL3</i>	4-coumarate-CoA ligase 3 (At4CL 3)
6	FANhyb_rscf00000195.1.g00007.1	<i>Fan4CL6</i>	4-coumarate-CoA ligase-like 6 (At4CL6)
7	FANhyb_rscf00000067.1.g00020.1	<i>FanCCoAOMT1</i>	probable caffeoyl-CoA O-methyltransferase At4g26220 (CCoAOMT)
8	FANhyb_rscf00000067.1.g00019.1	<i>FanCCoAOMT2</i>	probable caffeoyl-CoA O-methyltransferase At4g26220 (CCoAOMT)
9	FANhyb_rscf00000067.1.g00018.1	<i>FanCCoAOMT3</i>	probable caffeoyl-CoA O-methyltransferase At4g26220 (CCoAOMT)
10	FANhyb_rscf00000219.1.g00012.1	<i>TEFanCAOMT</i>	caffeic acid 3-O-methyltransferase (CAOMT)
4. Chalcone			
1	FANhyb_rscf00000241.1.g00008.1	<i>FanCH11</i>	chalcone-flavonone isomerase
2	FANhyb_rscf00001140.1.g00004.1	<i>FanCH12</i>	chalcone-flavonone isomerase
5. Flavanone			
1	FANhyb_rscf00000717.1.g00004.1	<i>FanFLS1</i>	flavonol synthase/flavanone 3-hydroxylase (FLS)
2	FANhyb_rscf00000717.1.g00005.1	<i>FanFLS2</i>	flavonol synthase/flavanone 3-hydroxylase (FLS)
6. Dihydroflavonol (DFR)/Cinnamoyl-CoA reductase (CCR)			
1	FANhyb_rscf00000134.1.g00014.1	<i>FanDFR1</i>	bifunctional dihydroflavonol 4-reductase/flavanone 4-reductase (DFR) (probable)
2	FANhyb_rscf00000488.1.g00008.1	<i>FanCCR2-1</i>	cinnamoyl-CoA reductase 2 (CCR2)
3	FANhyb_rscf00000488.1.g00005.1	<i>FanCCR2-2</i>	cinnamoyl-CoA reductase 2 (CCR2)
4	FANhyb_rscf00000482.1.g00004.1	<i>FanDFR2</i>	bifunctional dihydroflavonol 4-reductase/flavanone 4-reductase (DFR) (putative)

5	FANhyb_rscf00000482.1.g00003.1	<i>FanDFR3</i>	bifunctional dihydroflavonol 4-reductase/flavanone 4-reductase (DFR) (similar to)
6	FANhyb_icon00005529_a.1.g00001.1	<i>FanDFR4</i>	dihydroflavonol-4-reductase (DFR) (probable)
7	FANhyb_rscf00000259.1.g00003.1	<i>FanDFR5</i>	dihydroflavonol-4-reductase (DFR) (probable)
8	FANhyb_rscf00000259.1.g00002.1	<i>FanDFR6</i>	dihydroflavonol-4-reductase (DFR) (probable)
9	FANhyb_rscf00000571.1.g00005.1	<i>FanCCR2-3</i>	cinnamoyl-CoA reductase 2 (CCR2)
10	FANhyb_rscf00004680.1.g00001.1	<i>FanCCR1</i>	cinnamoyl-CoA reductase 1
7. Leucoanthocyanidin (LDOX/ANS)			
1	FANhyb_rscf00001197.1.g00003.1	<i>FanLDOX</i>	leucoanthocyanidin dioxygenase (LDOX) (probable)

---

Table 5 Suppl. List of miRNAs from the *Fragaria × ananassa*.

miRNA	Validated sequences (5'-3')	Gene family
miR473.1	ACUCUCCCUCAAGGGCUUCU	MIR473
miR447b	ACUCUCCCUCAAGGGCUUCUAG	MIR447
miR172	AGAAUCUUGAUGAUGCUGCAU	MIR172
miR393.1	AUCCAAAGGGAUCGCAUUGAU	MIR393
miR395n	UGAAGUGUUUGGGGGAACUC	MIR395
miR2673b.1	CCUCCUCCUCUUCUUCUCCUC	MIR2673
miR396d	UUCCACAGGCUUUCUUGAAC	MIR396
miR159	UUUGGAUUGAAGGGAGCUCU	MIR159
miR169.1	GAGCCAGGAAUGACUUGCCGG	MIR369
miR2111.1	UAAUCUGCAUCCUGAGGUUUA	MIR2111
miR414.1	UCAUCCUCAUCAUCUUCU	MIR414
miR165b	UCGGACCAGGCUUCAUCCCC	MIR165
miR1030g.1	UCUGCAUUUGCACCUGCACUU	MIR1030
miR5015b.1	GAUGUUGUUGUUGGUGUUGUU	MIR5015
miR399e.1	UGCCAAAGGAGAUUUGCCCAA	MIR399
miR319c	UUGGACUGAAGGGAGCUCCU	MIR319
miR858	UUUCGUUGUCUGUUCGACCU	MIR858
miR3979	UCUCUCUCUCUCUUGAAUAG	MIR3979

Table 6 Suppl. The predicted targets of miRNAs in *F. × ananassa*.

miRNA_Acc.	Target_Acc.	Expectation	UPE\$	miRNA_start	miRNA_end	Target_start	Target_end	miRNA_aligned_fragment	Alignment	Target_aligned_fragment	Inhibition
miR858	FanMYB27	1	16.279	1	20	345	364	UUUCGUUGUCUGUUCGACCU	.....	GGGUCGAACAGACAAUGAGA	Cleavage
miR858	FanMYB19	1	14.615	1	20	297	316	UUUCGUUGUCUGUUCGACCU	.....	UGGUCGGACAGACAACGAGA	Cleavage
miR319c	FanMYB28	1.5	25.377	1	20	959	978	UUGGACUGAAGGGAGCUCCU	.....	UGGAGCUGCCUUCACUCCAA	Cleavage
miR858	FanMYB63	1.5	14.195	1	20	291	310	UUUCGUUGUCUGUUCGACCU	:: .....	AGGACGAACAGACAAUGAAA	Cleavage
miR858	FanMYB57	1.5	10.795	1	20	291	310	UUUCGUUGUCUGUUCGACCU	:: .....	AGGGCGAACAGACAAUGAAA	Cleavage
miR858	FanMYB59	1.5	15.681	1	20	291	310	UUUCGUUGUCUGUUCGACCU	.....	GGGUCGCACAGACAAUGAAA	Cleavage
miR858	FanMYB47	1.5	22.346	1	20	285	304	UUUCGUUGUCUGUUCGACCU	:: .....	GGGGCGAACAGACAAUGAAA	Cleavage
miR159	FanMYB45	2	23.082	1	20	101	120	UUUGGAUUGAAGGGAGCUCU	.....	GGAGCUCCAUUCGAUCCAAA	Cleavage
miR858	FanMYB42	2	10.338	1	20	300	319	UUUCGUUGUCUGUUCGACCU	:: .....	UGGAAGAACAGACAACGAAA	Cleavage
miR159	FanMYB28	2.5	25.641	1	20	960	979	UUUGGAUUGAAGGGAGCUCU	.....	GGAGCUCCUUCACUCCAAU	Cleavage
miR858	FanMYB14	2.5	25.981	1	20	369	388	UUUCGUUGUCUGUUCGACCU	:: .....	GGGGCGAACGGACAAUGAGA	Cleavage
miR858	FanMYB53	2.5	14.356	1	20	360	379	UUUCGUUGUCUGUUCGACCU	:: .....	UGGACGAACAGAUAAUGAGA	Cleavage
miR159	FanMYB53	3	8.147	1	20	927	946	UUUGGAUUGAAGGGAGCUCU	: .....	ACAGCUCCUUAAGCCAAG	Cleavage
miR5015b.1	FanMYB55	3	11.942	1	21	850	870	GAUGUUGUUGUUGGUGUUGUU	.....	AGU AACACUAACAAUAUCAUC	Cleavage
miR5015b.1	FanMYB41	3	20.383	1	21	437	457	GAUGUUGUUGUUGGUGUUGUU	.....	AGCAACAGCAGCAACAACAGC	Cleavage
miR858	FanMYB55	3	16.776	1	20	342	361	UUUCGUUGUCUGUUCGACCU	:: .....	AGGGCGAACUGAU AACGAAA	Translation
miR858	FanMYB22	3	19.384	1	20	291	310	UUUCGUUGUCUGUUCGACCU	.....	GGGUCGGACCGAU AACGAGA	Translation
miR858	FanMYB64	3	18.951	1	20	264	283	UUUCGUUGUCUGUUCGACCU	:: .....	AGGAAGAACAGACAAUGAGA	Cleavage
miR858	FanMYB8	3	15.281	1	20	291	310	UUUCGUUGUCUGUUCGACCU	:: .....	GGGUAGGACAGAUAAUGAGA	Cleavage
miR858	FanMYB15	3	10.297	1	20	312	331	UUUCGUUGUCUGUUCGACCU	:: .....	AGGAAGAACAGACAAUGAGA	Cleavage
miR858	FanMYB25	3	19.328	1	20	288	307	UUUCGUUGUCUGUUCGACCU	:: .....	GGGACGUACAGACAAUGAAG	Cleavage
miR858	FanMYB43	3	18.684	1	20	291	310	UUUCGUUGUCUGUUCGACCU	:: .....	GGGAAGAACAGACAAUGAGA	Cleavage
miR858	FanMYB49	3	16.566	1	20	291	310	UUUCGUUGUCUGUUCGACCU	:: .....	UGGAAGAACAGACAAUGAGA	Cleavage
miR858	FanMYB4	3	11.104	1	20	291	310	UUUCGUUGUCUGUUCGACCU	:: .....	UGGAAGAACAGACAAUGAGA	Cleavage
miR858	FanMYB21	3	9.563	1	20	309	328	UUUCGUUGUCUGUUCGACCU	:: .....	UGGGAGAACAGACAAUGAGA	Cleavage
miR319c	FanMYB45	3.5	23.035	1	20	100	119	UUGGACUGAAGGGAGCUCCU	.....	UGGAGCUCCAUUCGAUCCAA	Translation
miR396d	FanMYB51	3.5	17.758	1	20	788	807	UUCCACAGGCUUCUUGAAC	: .....	CUACAAGAAAUCCUGUGGAC	Translation
miR5015b.1	FanMYB35	3.5	25.605	1	21	304	324	GAUGUUGUUGUUGGUGUUGUU	.....	AAUAAUACCAUAACAACGCC	Cleavage

