Supporting information for
The control of red color by a family of MYB transcription factors in octoploid strawberry (*Fragaria × ananassa*) fruits

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Figures: S1-S7

Tables: S1-S7
Figure S1 Fruit developmental stages of white and red octoploid strawberry

(a) Based on the seed (lower row) and fruit colors (upper row) of the white octoploid strawberry, six visual developmental stages were defined as: small green fruit stage (G1), large green fruit stage (G2), white fruit stage (W), turning fruit stage (T), ripe fruit stage (R), and over-ripe fruit stage (OR) at 13, 17, 24, 30, 46, and 50 d after anthesis. (b) Based on the seed (lower row) and fruit colors (upper row) of red octoploid strawberry, six visual developmental stages were defined at 7, 12, 17, 19, 26, and 30 d after anthesis. Scale bars in (a, b), Fruit, 1 cm, Seed, 5mm.
Figure S2 Chromatographs of anthocyanins, flavonols, and proanthocyanins. Chromatographic peaks were identified as shown in Table 1.
**Figure S3** Transcript levels of structural genes and regulatory genes not included in Figure 3 in the white and red strawberry varieties. Asterisks (*) represent that the values of the corresponding transcript levels (n=3, ±SE) are significantly different at $p < 0.05$ as determined using independent t-test.
**Figure S4** Transcript levels of regulatory genes in the white and red strawberry varieties. RT-PCR products were examined for *FaMYB1*, *FaMYB10*, *FaMYB9*, and *FaMYB11* transcripts on 1% (w/v) agarose gels, stained with EtBr. *Actin* was used as loading control. At the top, the corresponding developmental stages are shown as G1, G2, W, T, R, and OR with the fruit images of corresponding stages at the left, white strawberry variety and at the right, red strawberry variety.
**Figure S5** The constructs and results from yeast two-hybrid assay of FaMYB10-1 or FaMYB10-2 with two regulators (FaWD40 and PavbHLH) for the formation of MBW ternary complex. (a) Schematics of FaMYB10-1, FaMYB10-2, FaWD40, and PavbHLH constructs used in yeast two-hybrid assays. (b) The results of interaction of FaMYB10-2, the different regions of FaMYB10-1 protein (the full-length coding region, the R2R3 MYB domain-containing N-terminal region, the C-terminal region) with FaWD40, PavbHLH.
Figure S6 Genomic sequence analysis for *FaMYB1* alleles in red and white strawberry varieties. (a) The agarose gel of *FaMYB1* alleles. (b) Schematic graph for gene structure of *FaMYB1* alleles. Open and filled black circles represent start codon and stop codon; light gray and dark gray boxes represented R2 and R3 domains in the schematic graph.
Figure S7 PCA analysis of key flavonoid components against flavonoid biosynthetic structural genes and transcription-related genes. Two PCA components ‘anthocyanidin index’ and ‘proanthocyanin index’ explained 80.32% of the variance in fruit coloration of red and white strawberry varieties.
| Flavonoid Components | W-T (µg/g) | R-T (µg/g) | W-R (µg/g) | R-R (µg/g) | W-T/R-T (%) | W-R/R-R (%) |
|----------------------|------------|------------|------------|------------|--------------|--------------|
| PA                   | 1584.76    | 2123.50    | 922.83     | 1716.64    | 74.63%       | 53.76%       |
| AC                   | 189.93     | 447.65     | 188.47     | 126418.85  | 42.43%       | 0.15%        |
| FL                   | 25.47      | 260.28     | 13.50      | 52.29      | 9.79%        | 25.82%       |
| PP                   | 1623.32    | 983.71     | 166.94     | 209.51     | 165.02%      | 79.68%       |

Note: PA: proanthocyanins, AC: anthocyanins, FL: flavonols, PP: the precursors of proanthocyanidins, catechin, and epi-catechin, W-T: White strawberry turning fruit stage, R-T: Red strawberry turning fruit stage, W-R: White strawberry ripe fruit stage, R-R: Red strawberry ripe stage.
Table S2 The expression of structural genes, *FaANS*, *FaUFGT*, and *FaDFR* in flavonoid biosynthesis in red and white strawberry varieties.

The Measurement of Structural Genes’ Transcript Levels

| Developmental stage | *FaANS* | *FaUFGT* | *FaDFR* |
|---------------------|---------|----------|---------|
|                     | G1      | G2       | W       | T       | R       | OR      | G1      | G2       | W       | T       | R       | OR      | G1      | G2       | W       | T       | R       | OR      |
| Standardized Transcript Level in White Strawberry Variety | 1.02 ± 0.07 ± 0.05 ± 0.03 ± 0.10 ± 1.00 ± 0.07 ± 0.12 ± 0.14 ± 0.05 ± 6.94×10⁻¹zl | 0.03 ± 0.01 ± 0.01 ± 0.01 ± 0.00 ± 0.00 ± 1.02 ± 1.19 ± 8.59 ± 7.50 ± 5.22 ± 4.70 ± | |
| Standardized Transcript Level in Red Strawberry Variety | 0.47 ± 0.01 ± 7.94×10⁻¹zl ± 0.23 ± 0.81 ± 0.83 ± 0.40 ± 0.13 ± 2.48 ± 6.29 ± 23.16 ± 38.69 ± 0.23 ± 5.16 ± 8.65 ± 9.98 ± 7.88 ± 10.32 ± | 0.06 ± 0.00 ± 0.00 ± 0.07 ± 0.14 ± 0.19 ± 0.05 ± 0.01 ± 0.38 ± 0.97 ± 1.18 ± 2.97 ± 0.02 ± 0.58 ± 0.65 ± 1.67 ± 0.54 ± 1.20 ± | |
| Transcript Ratio between Red and White Strawberry Variety | 0.46 ± 0.15 ± 0.17 ± 6.63 ± 25.23 ± 7.90 ± 0.40 ± 1.87 ± 21.40 ± 44.13 ± 449.61 ± 5572.49 ± 0.23 ± 4.33 ± 1.01 ± 1.33 ± 1.51 ± 2.20 ± | |

Note: *FaANS*: anthocyanidin synthase; *FaUFGT*: flavonol-O-glucosyltransferases; *FaDFR*: dihydroflavonol-4-reductase.
### Table S3 The expression of structural genes, *FaLAR*, *FaANR*, and *FaFLS* in flavonoid biosynthesis in red and white strawberry varieties.

The Measurement of Structural Genes’ Transcript Levels

| Developmental Stage | FaANR | FaLAR | FaFLS |
|---------------------|-------|-------|-------|
|                     | G1    | G2    | W     | T     | R     | OR    | G1    | G2    | W     | T     | R     | OR    | G1    | G2    | W     | T     | R     | OR    |
| Standardized Transcript Level in White Strawberry Variety | 1.00 ± 0.01 | 0.09 ± 0.01 | 0.05 ± 0.00 | 0.03 ± 1.38×10⁻³ | 1.32×10⁻³ | 1.00 ± 0.06 | 0.08 ± 0.01 | 0.11 ± 0.02 | 0.04 ± 6.40×10⁻³ | 0.00 ± 5.02×10⁻³ | 1.04 ± 0.20 | 1.09 ± 0.20 | 2.83 ± 0.57 | 1.60 ± 0.24 | 0.40 ± 0.07 | 0.07 ± 0.01 |
| Standardized Transcript Level in Red Strawberry Variety | 0.17 ± 0.01 | 4.52±10⁻³ | 3.22±10⁻³ | 0.08 ± 0.36 | 0.10 | 0.36 ± 0.01 | 0.09 | 0.06 ± 0.04 | 0.06 ± 0.02 | 0.02 ± 0.02 | 0.71 ± 0.09 | 0.83 | 5.16 ± 0.74 | 0.10 ± 0.02 | 0.24 ± 0.04 | 0.08 ± 0.02 |
| Transcript Ratio between Red and White Strawberry Variety | 0.16 | 0.05 | 0.07 | 2.32 | 259.43 | 274.45 | 0.21 | 0.75 | 0.39 | 1.41 | 2.47 | 3.41 | 0.69 | 4.73 | 0.26 | 0.06 | 0.60 | 1.22 |

Note: *FaANR*: anthocyanidin reductase; *FaLAR*: leucoanthocyanidin reductase; *FaFLS*: flavonol synthase.
Table S4 The expression of regulatory genes, FaMYB1, FaMYB10, and FaWD40 of flavonoid biosynthesis in red and white strawberry varieties.

The Measurement of Regulatory Genes’ Transcript Level

| Developmental Stage | FaMYB1 | FaMYB10 | FaWD40 |
|---------------------|--------|---------|--------|
|                      | G1     | G2      | W      | T      | R      | OR     | G1     | G2      | W      | T      | R      | OR     |
| Standardized Transcript Level in White Strawberry Variety | 1.00 ± 0.06 | 0.78 ± 0.09 | 0.69 ± 0.10 | 0.25 ± 0.01 | 3.27 ± 0.18 | 1.53 ± 0.13 | 1.01 ± 0.11 | 4.33 ± 0.85 | 178.42 ± 33.92 | 120.57 ± 18.38 | 18245.68 ± 3809.03 | 7059.18 ± 1502.47 | 1.01 ± 0.11 | 2.93 ± 0.86 | 3.64 ± 0.78 | 1.56 ± 0.31 | 1.37 ± 0.31 | 1.31 ± 0.32 |
| Standardized Transcript Level in Red Strawberry Variety | 3.60 ± 0.52 | 3.28 ± 0.41 | 0.90 ± 0.06 | 1.62 ± 0.15 | 5.39 ± 0.55 | 7.71 ± 0.99 | 24.65 ± 9.77 | 62.78 ± 27.56 | 697.32 ± 21.21 | 5408.22 ± 487.18 | 22578.06 ± 1291.22 | 22472.76 ± 2072.94 | 2.74 ± 0.40 | 4.73 ± 0.79 | 1.49 ± 0.11 | 1.35 ± 0.08 | 1.33 ± 0.47 | 1.27 ± 0.23 |
| Transcript Ratio between Red and White Strawberry Variety | 3.58 ± 4.22 | 1.32 ± 6.57 | 1.64 ± 5.03 | 24.59 ± 14.50 | 3.91 ± 44.86 | 1.24 ± 3.19 | 2.70 ± 1.61 | 0.41 ± 0.86 | 0.98 ± 0.97 |
**Table S5** The expression of regulatory genes, *FaMYB9*, and *FaMYB11* of flavonoid biosynthesis in red and white strawberry varieties.

| Developmental Stage | *FaMYB9* | *FaMYB11* |
|---------------------|----------|-----------|
| Standardized Transcript Level in White Strawberry Variety | G1 | G2 | W | T | R | OR |
|                     | 1.00 ± 0.08 | 0.46 ± 0.07 | 0.51 ± 0.07 | 0.27 ± 0.04 | 0.07 ± 0.01 | 0.01 ± 0.00 |
|                     | 1.03 ± 0.04 | 0.41 ± 0.01 | 0.94 ± 0.02 | 0.56 ± 0.01 | 0.08 ± 0.01 | 0.01 ± 0.00 |
| Standardized Transcript Level in Red Strawberry Variety | G1 | G2 | W | T | R | OR |
|                     | 1.02 ± 0.11 | 0.21 ± 0.03 | 0.02 ± 0.00 | 0.01 ± 0.00 | 0.03 ± 0.00 | 7.37×10^-3± 0.00 |
|                     | 3.11 ± 0.48 | 0.36 ± 0.07 | 0.06 ± 0.02 | 0.01 ± 0.00 | 0.05 ± 0.00 | 0.01± 0.00 |
| Transcript Ratio between Red and White Strawberry Variety | G1 | G2 | W | T | R | OR |
|                     | 1.01 ± 0.01 | 0.45 ± 0.04 | 0.04 ± 0.00 | 0.05 ± 0.00 | 0.40 ± 0.00 | 0.53 ± 0.00 |
|                     | 3.01 ± 0.30 | 0.88 ± 0.06 | 0.02 ± 0.00 | 0.06 ± 0.00 | 0.60 ± 0.00 | 1.39 ± 0.00 |
| Gene     | Accession | PrimerSequence (5’→3’) |
|----------|-----------|------------------------|
|          |           | F:ATGGAGGGTTTCGCTGAGAAAGGT GCATGGACTAAAGAGGAGATGACTTCTG R: TCATACGTAGAGATTGTA | Myb domain protein 10 | Regulating anthocyanin biosynthesis | Cloning | Our results |
| FaMYB10  | MG456859  | F:ATGAGGAAGCCCTGCTGCGA R: TTAAGCAACTTGAGGATCAG | Myb domain protein 1 | Regulating anthocyanin biosynthesis | Cloning | Our results |
| Actin    | AB116565  | F:GGGTCTGCTGAGATGAT R:CATCCCAGTTCGCTCAATA | Actin | Actin | qRT-PCR | Our results |
| FaMYB1   | AF401220  | F:CCTGCTGCGAGAAGACGGAGAC R:CTTCTACACACGGACGCAACCTCT | Myb domain protein 1 | Regulating anthocyanin biosynthesis | qRT-PCR | Aharoni et al., 2001 |
| FaMYB10  | EU155162  | F: TCAATCAGCTTAAACAGA R: TTAAGACCCACTGGTTTACCT | Myb domain protein 10 | Regulating anthocyanin biosynthesis | qRT-PCR | Lin-Wang et al., 2010 |
| FaMYB9   | JQ989281  | F:CGGATCCTCAAGGAACGAG R:CTTATTGCTGGGTGGTTTACTT | Myb domain protein 9 | Modifying PA content | qRT-PCR | Schaart et al., 2013 |
| FaMYB11  | JQ989282  | F:GATGGTCTTATAGCGGGTGAG R:TGGTGGTTTTGTGGTGATAAT | Myb domain protein 11 | Modifying PA content | qRT-PCR | Schaart et al., 2013 |
| FabHLH3-delta | JQ989285 | F:ACCAGTAGTAGACAGCCTGGTTAT R:CCATCTGCCCATATTAACTCGTTTG | Basic helix-loop- helix protein | Regulating anthocyanin biosynthesis | qRT-PCR | Schaart et al., 2013 |
| FaWD40   | JQ989287  | F:GACTTGAGGATCGTACAGGGAGGATGTTT R:TCATCCCACTGGAGCAATAT | W(Trp)D(Asp)-r epitope protein | Regulating anthocyanin biosynthesis | qRT-PCR | Schaart et al., 2013 |
| Gene  | Accession | F Primer | R Primer | Product | Method        | Reference                  |
|-------|-----------|----------|----------|---------|---------------|---------------------------|
| FaPAL | HM641823  | F: TGCTTTGGGTCTGGTATGG | R: ACCTTCTTCGCTTCTTTCAC | Phenylalanine ammonia-lyase | Structural genes in flavonoid biosynthesis | Pombo et al., 2011 |
| FaC4H | DQ898278  | F: TTGCAGAGTTTTGAGTATAATT | R: TCCTCATAGTTGAGCTGTGTGTC | Cinnamate 4-hydroxylase | Structural genes in flavonoid biosynthesis | Saud, et al., 2009 |
| Fa4CL | XM_004309901 | F: AAACGCGACGGTTACGG | R: CAGTCCGTCAAGCAGTCACC | 4-coumarate--C oA ligase | Structural genes in flavonoid biosynthesis | Saud, et al., 2009 |
| FaCHS | AY997297 | F: CACTCCTCAAAGATTCTCTG | R: TGCTCGTGGCTTCTAATCTTCT | Chalcone synthase | Structural genes in flavonoid biosynthesis | Kadomura-Ishi kawa, et al., 2015 |
| FaCHI | AB201755 | F: TTTCTCTCCCTCGTCAAGCC | R: ACTCAACCGACTTGCTCAACTCCT | Chalcone isomerase | Structural genes in flavonoid biosynthesis | Kadomura-Ishi kawa, et al., 2015 |
| FaF3H | AY691918 | F: AGGGTGCTTCATCTGTCC | R: TCAGCTCGTCACTGTACTGTTG | Flavanone 3-hydroxylase | Structural genes in flavonoid biosynthesis | Almeida et al., 2007 |
| FaF3’H | AB665441 | F: AAATCAACGGGTACTACAGGC | R: CCAGCACCACAGGATGTAC | Flavonoid 3’-hydroxylase | Structural genes in flavonoid biosynthesis | Kadomura-Ishi kawa, et al., 2015 |
| FaFLS | DQ087252 | F: GCATGATCAAAATCGTGAA | R: ATCCACCACCCTTCTTCC | Flavonol synthase | Structural genes in flavonoid biosynthesis | Almeida et al., 2007 |
| FaGT3 | AY663786 | F: CTGCTGAGTGCGAAGGAAAT | R: AGGAAGTTATGACGAGACC | UDP-glucose glucosyltransferase | Structural genes in flavonoid biosynthesis | Lunkenbein et al. 2006 |
| Gene     | Accession | Forward Primer                  | Reverse Primer                  | Function                                      | Expression Assay | Reference                  |
|----------|-----------|---------------------------------|---------------------------------|-----------------------------------------------|-----------------|---------------------------|
| FaDFR    | AF029685  | F: AAGACAGTTCCGGAGGTTGGT        | R: AGAGTTGGGATAATGTAATG         | Dihydroflavonol 1 4-reductase                  | qRT-PCR         | Moyano et al., 1998      |
| FaANS    | AY695817  | F: GAAAGTGCAGTACCAATACATCGT     | R: ACGTTCTCTTGTTGAGCCGACC       | Anthocyanidin synthase                        | qRT-PCR         | Almeida et al., 2007     |
| FaUFGT   | AY575056  | F: TAGCCCTTTCCTTCCTCCTCA        | R: GAAACGCAGTACGACGCTGTG        | UDP glucose:flavonoidid-3-O-glucosyl transferase | qRT-PCR         | Griesser et al., 2008    |
| FaANR    | JX271492  | F: ATGGCAATAGCTATCGGTTCC        | R: ATGGTCTCTCGGCCTGATGG         | Anthocyanidin reductase                       | qRT-PCR         | Schaar et al., 2013      |
| FaLAR    | DQ087253  | F: GTGAGGGGTGGCAGGTTGAGA        | R: TCGACGAAATGGGTATTAACC        | Leucoanthocyanidin reductase                  | qRT-PCR         | Schaar et al., 2013      |
| FaMYB10-2-AD-NdeI | MG456860 | F: GAAATTCATATGGAGGGTTATTCGCTG | R: GAAATTCATATGGAGGGTTATTCGCTG | Myb domain protein 10                        | Yeast two-hybrid | Our results               |
| FaMYB10-2-AD-Xhol |       |                                |                                 | Myb domain protein 10                        | Yeast two-hybrid | Our results               |
| FaMYB10-1-AD-NdeI | MG456859 | F: GAAATTCATATGGAGGGTTATTCGCTG | R: GAAATTCATATGGAGGGTTATTCGCTG | Myb domain protein 10                        | Yeast two-hybrid | Our results               |
| FaMYB10-1-AD-Xhol |       |                                |                                 | Myb domain protein 10                        | Yeast two-hybrid | Our results               |
| FaMYB10-1-N-AD-Xhol |       |                                |                                 | Myb domain protein 10                        | Yeast two-hybrid | Our results               |
| FaMYB10-1-C-AD-Nd |       |                                |                                 | Myb domain protein 10                        | Yeast two-hybrid | Our results               |
| Construct                  | Accession | Forward Primer | Reverse Primer | Protein Type                  | Function                        | Method            | Notes                  |
|---------------------------|-----------|----------------|----------------|-------------------------------|---------------------------------|-------------------|------------------------|
| FaWD40-AD & BK-Ndel       | JQ989287  | F: GAAATTTCATATGATGGAGAATTCGACCCCTCGA | R: GAAATTTGGAATCCCTCAACCTTCAAGAGCTGCATC | WD-repeat protein              | Regulating anthocyanin biosynthesis | Yeast two-hybrid | Our results            |
| FaWD40-AD & BK-BamHI      |           |                |                |                               |                                 |                   |                        |
| PavbHLH-AD & BK-EcoRI     | KP126521  | F: GAAATTGAAATTCATGGCTGCACCGCAAGCAGCA | R: GAAATTCTCGAGTCAGATTGGGGAATTTTGATTGA | Basic helix-loop-helix protein | Regulating anthocyanin biosynthesis | Yeast two-hybrid | Our results            |
| PavbHLH-AD & BK-PstI      |           |                |                |                               |                                 |                   |                        |
| FaMYB10-HT-AgeI           | MG456859  | F: GCGACCCGTTATGGAGGTTTCGGTGTGAGA | R: GCCCTCGAGTCATACGGAGAGATGGACTAGTA | Myb domain protein 10          | Regulating anthocyanin biosynthesis | Transient expression | Our results            |
| FaMYB10-HT-XhoI           |           |                |                |                               |                                 |                   |                        |

Note: F, forward; R, reverse. Underlines represent the digestion sites of enzymes.
Table S7 Information about the MYB protein sequences used for the construction of the neighbor joining tree.

| Gene     | Accession     | Protein               | Function                                         | Identity          | Reference(s)                          |
|----------|---------------|-----------------------|--------------------------------------------------|-------------------|---------------------------------------|
| AtMYB3   | NP_564176.2   | Myb domain protein 3  | Repressors of phenylpropanoid pathway            | 51% ident with FaMYB1 | Lin-Wang et al., 2010                |
| AtMYB4   | AAC83582.1    | Myb domain protein 4  | Repressors of phenylpropanoid pathway            | 50% ident with FaMYB1 | Aharoni et al., 2001                 |
| AtMYB6   | NP_192684.1   | myb domain protein 6  | Repressors of phenylpropanoid pathway            | 53% ident with FaMYB1 | Lin-Wang et al., 2010                |
| AtMYB24  | NP_198851.1   | myb domain protein 24 | Anther development                               | 100% ident with AtMYB24 | Yang et al., 2007                    |
| AtMYB75  | AAG42001.1    | Myb domain protein 75 | Regulating anthocyanin biosynthesis              | 41% ident with FaMYB10 | Gonzalez et al., 2008                |
| AtMYB90  | NP_176813.1   | Myb domain protein 90 | Regulating anthocyanin biosynthesis              | 42% ident with FaMYB10 | Gonzalez et al., 2008                |
| FaMYB1   | AAK84064.1    | Myb domain protein 1  | Regulating anthocyanin biosynthesis by           | 100% ident with FaMYB1 | Aharoni et al., 2001                 |
|          |               |                       | interacting with other anthocyanin regulators    |                   |                                       |
| FcMYB1   | ADK56163.1    | Myb domain protein 1  | Regulating branching-point of the                | 100% ident with FaMYB1 | Salvatierra et al., 2013             |
|          |               |                       | anthocyanin/PA biosynthesis                     |                   |                                       |
| FaMYB1-1 | MG456857      | Myb domain protein 1  | Regulating anthocyanin biosynthesis              | 100% ident with FaMYB1 | Our results                           |
| FaMYB1-2 | MG456858      | Myb domain protein 1  | Regulating anthocyanin biosynthesis              | 100% ident with FaMYB1 | Our results                           |
| FaMYB9   | AFL02460.1    | Myb domain protein 9  | Modifying PA content                             | 100% ident with FaMYB9 | Schaat et al., 2013                 |
| FaMYB10  | ABX79947.1    | Myb domain protein 10 | Regulating anthocyanin biosynthesis              | 100% ident with FaMYB10 | Lin-Wang et al., 2010                |
| FaMYB10-1| ABX79948.1    | Myb domain protein 10 | Regulating anthocyanin biosynthesis              | 93% ident with FaMYB10 | Lin-Wang et al., 2010                |
| FaMYB10-2| MG456859      | Myb domain protein 10 | Regulating anthocyanin biosynthesis              | 98% ident with FaMYB10 | Our results                           |
| FaMYB11  | AFL02461.1    | Myb domain protein 1  | Regulating anthocyanin biosynthesis              | 100% ident with FaMYB11 | Schaat et al., 2013                 |
| FvMYB305-like | XP_011468270.1 | Myb domain protein 305 | Probably anth development                        | 61% ident with AtMYB24 | NCBI database                       |
| MdMYB1   | ABK58136.1    | Myb domain protein 1  | Regulating anthocyanin biosynthesis              | 46% ident with FaMYB10 | Takos et al., 2006                  |
| MdMYB1-like | XP_008374828.1 | Myb domain protein 6  | Probably regulating anthocyanin biosynthesis     | 61% ident with FaMYB1 | Gao et al., 2011                     |
| MdMYB9   | NP_001280749.1| Myb domain protein 9  | Regulating anthocyanin and PA biosynthesis      | 66% ident with FaMYB9 | An et al., 2015                      |
| MdMYB10  | ACQ45201.1    | Myb domain protein 10 | Regulating anthocyanin biosynthesis              | 46% ident with FaMYB10 | Espley et al., 2007                 |
| Protein  | Accession   | Description                          | Identity with FaMYB  | Reference     |
|----------|-------------|--------------------------------------|-----------------------|---------------|
| MdMYB11  | NP_001280958.1 | Myb domain protein 11                | Regulating anthocyanin and PA biosynthesis | 62% | An et al., 2015 |
| MdMYB16  | ADL36756.1   | Myb domain protein 16                | Inhibiting anthocyanin synthesis | 52% | Xu et al., 2017 |
| MdMYB17  | ADL36757.1   | Myb domain protein 17                | Inhibiting anthocyanin synthesis | 56% | Lin-Wang et al., 2011 |
| MdMYB21  | NP_001280981.1 | Myb domain protein 21               | Probably anther development | 43% | NCBI database   |
| MdMYB111 | ADL36754.1   | Myb domain protein 111               | Inhibiting anthocyanin synthesis | 60% | Lin-Wang et al., 2011 |
| MdMYB305-like | XP_008341440.1 | Myb domain protein 305          | Probably anther development | 66% | NCBI database   |
| MsMYB10  | ABX71485.1   | Myb domain protein 10               | Regulating anthocyanin biosynthesis | 46% | Wang et al., 2010 |
| ParMYB10 | ABX71490.1   | Myb domain protein 10               | Regulating anthocyanin biosynthesis | 51% | Lin-Wang et al., 2010 |
| PavMYB10.1 | ALM31951.1 | Myb domain protein 10              | Regulating anthocyanin biosynthesis | 55% | Jin et al., 2016 |
| PavMYB11 | ALH21142.1   | Myb domain protein 10               | Probably regulating PA biosynthesis | 61% | NCBI database   |
| PavMYB111 | ALH21138.1  | Myb domain protein 111              | Probably regulating anthocyanin biosynthesis | 61% | NCBI database   |
| PavMYBR  | ADY15315.1   | Myb domain protein R                | Regulating flavonoid biosynthesis | 51% | NCBI database   |
| PcfMYB10 | ABX71495.1   | Myb domain protein 10               | Regulating anthocyanin biosynthesis | 52% | Lin-Wang et al., 2010 |
| PdmMYB10 | ABX71492.1   | Myb domain protein 10               | Regulating anthocyanin biosynthesis | 50% | Lin-Wang et al., 2010 |
| PpyMYB10 | ABX71488.1   | Myb domain protein 10               | Regulating anthocyanin biosynthesis | 47% | Lin-Wang et al., 2010 |
| VvMYBA1  | BA96751.1    | Myb domain protein A1               | Regulating anthocyanin biosynthesis | 44% | Yakushiji et al., 2006 |
| VvMYB6   | XP_002273328.1 | Myb domain protein 6             | Transcription repressor | 61% | NCBI database   |
| VvMYB24  | NP_001268062.1 | Myb domain protein 24           | Probably regulating anther development | 65% | NCBI database   |
| VvMYB308 | XP_010648383.1 | Myb domain protein 308         | Probably regulating PA biosynthesis | 57% | NCBI database   |
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