

Figure S1. Diagram of the anthocyanin pathway in apple (*MYB10*, *bHLH*, and *WD* are transcription factor; *PAL*, phenylalanine ammonia lyase; *CHS*, chalcone synthase; *CHI*, chalcone isomerase; *F3H*, flavone 3-hydroxylase; *F3'H*, flavonoid 3'-hydroxylase; *DFR*, dihydroflavonol reductase; *LDOX*, Leucoanthocyanidin dioxygenase; *UFGT*, UDP-glucose: flavonoid 3-O-glucosyl transferase; *GST*, glutathione S-transferase).

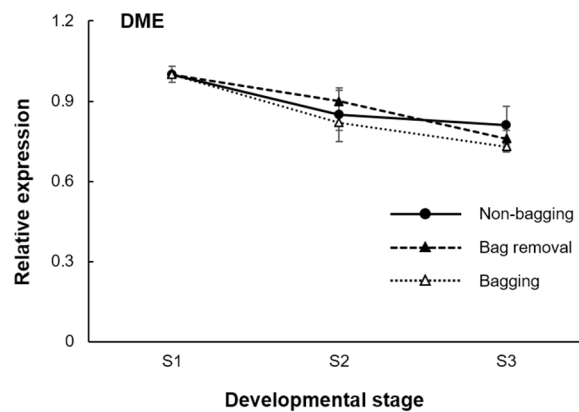


Figure S2. Quantitative real-time PCR analysis of demethylation-related gene, DEMETER (*DME*), in 'Fuji' apples cultivated under different bagging treatments: no bagging (control; labeled as "non-bagging"), bagging followed by bag removal (labeled as "bag removal"), and bagging with no bag removal (labeled as "bagging"). Apples were harvested at three time points: before paper-bagging (S1, DAFB 97) and then 1 and 4 weeks after bag removal (S2, DAFB 169 and S3, DAFB 191). The x-axis and y-axis indicate the time of harvesting and relative expression, respectively. The expression level at S1 was set as 1. Bars represent the standard error of triplicate samples. * and ** indicate significance levels of $p < 0.05$ and $p < 0.01$, respectively. DAFB, days after full bloom.

Table S1. Primers for quantitative real-time PCR and methylation analyses used in this study.

| Gene name | Forward | Reverse |
|-------------------------------|------------------------------|-----------------------------|
| Related to anthocyanin | | |
| Actin | CTGAACCCAAAGGCTAATCG | ACTGGCGTAGAGGGAAAGAA |
| MYB10 | AGGCAGTGC GTTGAGATTC | CAGCTCTTCCTGCACCTGT |
| bHLH | AGAGGAGGAAGTTACCGGCT | CATGGCTCTGACCTGCATCT |
| WD | GCCATTTTCATGGTCTCCAG | TCCAGGTCTCACCACATCC |
| PAL | AGGAACACCGTAAAGAACA | ACATACTCCCTATCGACAAC |
| CHS | AAGGACTCAAAACGACCGGG | TAAACCCACGCTGTGAAGCA |
| CHI | GTCAAGGAATTACCGACATTGA | CACAACTTCAGGGTCCAAGTAA |
| F3H | CTGGGGTATTTTCCAGATTGTT | TGGCAAAGCAAAGA ACTCTCTA |
| F3'H | CAACAAGAGCTGGACCAAGTAG | TTACTGCTTGGAGGTAGGTCAA |
| DFR | GAGCAAGCTGCATGGAAAT | CATGAGAAATGGCCCAATC |
| LDOX | GTTCCAAATTCCATCGTCAT | TCACCTTTTCCTTGTTACC |
| UFGT | TGCAGACCAGAGGCTTAATG | CCTCCCTGGTAAAACTCCA |
| GST | GGAAGGCCACA ACTTCAACG | TGGCTCAGATCAGCCAGAGT |
| Related to methylation | | |
| Actin | CTGAACCCAAAGGCTAATCG | ACTGGCGTAGAGGGAAAGAA |
| MET | CGGAATAAGGGTGCTGAC | AGATACTCCTGGGAACGA |
| CMT | GTGCACTGTACACACCTCGT | ACTGCGTCGTAAACAGCGTA |
| DRM | GAGCAAACCAACCAGAG | ATCAAATCCGCCAAACT |
| DME | AGAATCCTGGGCTTGCTT | TCTCCATGCCTACGCTTT |
| McrBC-PCR | | |
| M1 (-440 to +1) | GGTATCTTATGGTGGTCAAAGATG | CTTATCTGCTAGCAGCTAAGCTTA |
| M2 (-856 to -383) | CTGAGATTGACTCTTGTGAAAGCT | GTGAATGCAGAATCGTGTAAGTAGT |
| M3 (-1246 to -780) | TTAACGGAATCCAACGAAGACAAG | GCTACACCTAACACATTGCTCAAT |
| M4 (-1657 to -1184) | TGAGATAGGTCCGGTTCTATTTCT | ATCCCTTTCCCTTATTTGTTCCGT |
| M5 (-2044 to -1590) | CAATTGCAGTGCTCAGAAATCGTT | CCGGACCCGTTTATAAATAGAACA |
| M6 (-2255 to -1872) | CCATTTCCACCGTTCATTTCTAAG | AACAGCAAACACCCAAAATCCCTT |
| M7 (-2585 to -2117) | CACTAGCTTCGGATTCCTTAGGA | CGGTTTAGTTTCTGGGAATTCACA |
| Bisulfite sequencing | | |
| M7B | YGGATTTTTTAGGAATTTTGAAGTTAAG | AACAACAAACACCCAAAATCCCTTTAA |