A putative *R3 MYB* repressor is the candidate gene underlying *atroviolacium*, a locus for anthocyanin pigmentation in tomato fruit

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Supplementary data

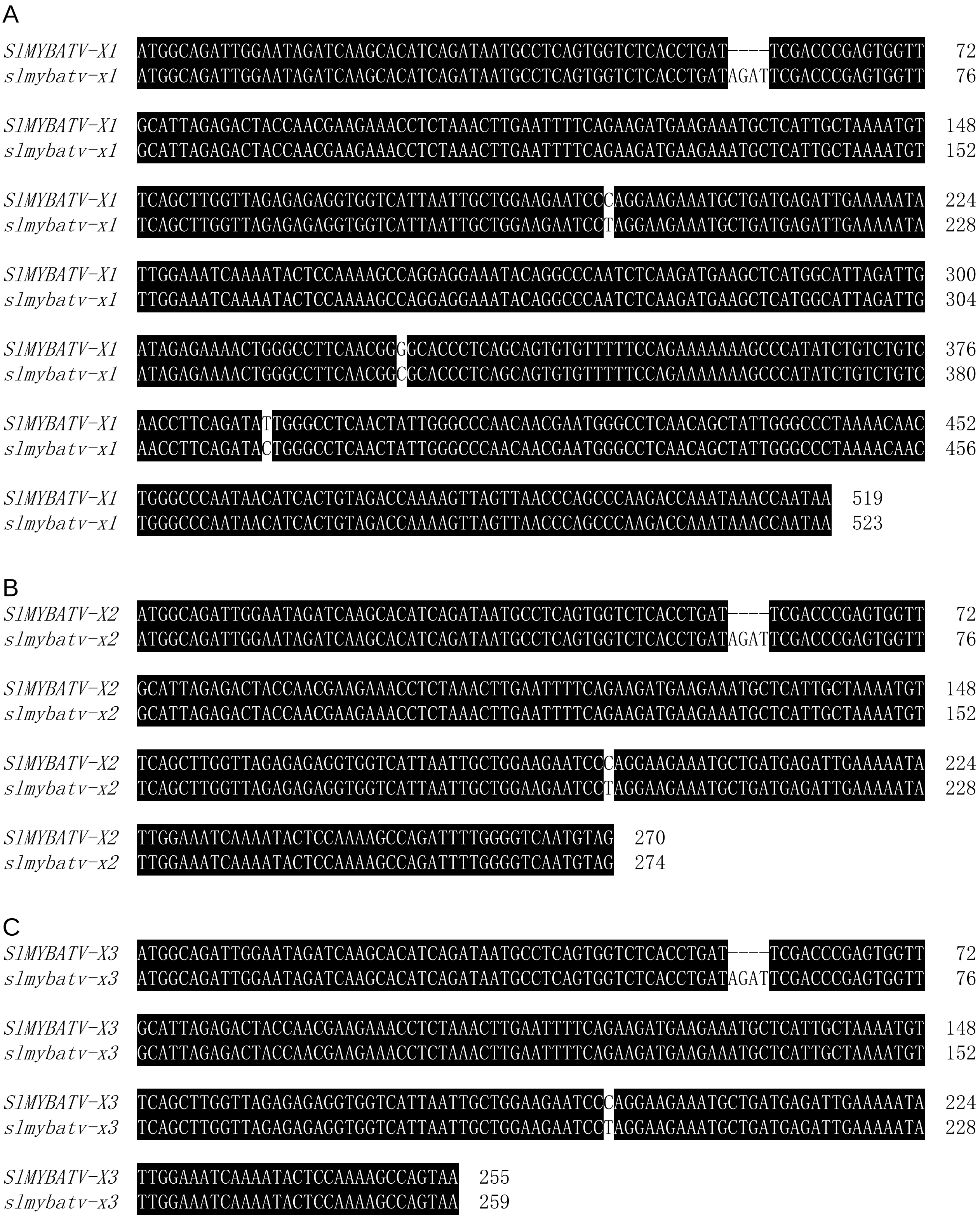

Fig. S1 Sequence polymorphism of the coding DNA sequence of *SlMYBATV*. Entire coding sequences were aligned by using Clustal X ver. 2 (Larkin *et al.*, 2007) with default settings, and the conserved nucleotides were shaded by using GeneDoc (2.6) (Nicholas *et al.*, 1997). *SlMYBATV-X1*, *SlMYBATV-X2*, and *SlMYBATV-X3* were three transcripts of the *SlMYBATV* gene from Heinz1706; *slmybatv-x1*, *slmybatv-x2*, and *slmybatv-x3* were three transcripts of the *SlMYBATV* gene from Indigo Rose.

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Indigo-Rose   TGCCACCGTTTAATTAATTAAGGACATGTCCAATCTAGTTAATGTTGATTAAGAGTGTAAATACGGTTAAAAAGA     75
Heinz1706     TGCCACCGTTTAATTAATTAAGGACATGTCCAATCTAGTTAATGTTGATTAAGAGTGTAAATACGGTTAAAAAGA     75

Indigo-Rose   AAAAGAGATACTAATTATTTTTTGGGGAAAATATTTTGAATCATTAACACTAATAGAGGTAGTTTTAAACTAAAA    150
Heinz1706     AAAAGAGATACTAATTATTTTTTGGGGAAAATATTTTGAATCATTAACACTAATAGAGGTAGTTTTAAACTAAAA    150

Indigo-Rose   TATTAGTAATAGAGATATTTTTGGTATTTTGGTTCAATTTTACGTAGTTTAATTTTTTTTTAATTTCTTTCAGTA    225
Heinz1706     TATTAGTAATAGAGATATTTTTGGTATTTTGGTTCAATTTTACGTAGTTTAATTTTTTTTTAATTTCTTTCAGTA    225

Indigo-Rose   AAATATATAAATACTCCTATAGTTAACACTAGGATCGTATTAATAGTTTAATACCATACATAAATTAATATTAGG    300
Heinz1706     AAATATATAAATACTCCTATAGTTAACACTAGGATCGTATTAATAGTTTAATACCATACATAAATTAATATTAGG    300

Indigo-Rose   AATTTATAGATGTGAATAGCGAATAATAACTCATTATACATAGAGATATAATAATGTAAGACAATTATCTCTTAT    375
Heinz1706     AATTTATAGATGTGAATAGCGAATAATAACTCATTATACATAGAGATATAATAATGTAAGACAATTATCTCTTAT    375

Indigo-Rose   GATACAATTTTTTTTCTTACTAAATTTCACATATAGTAAAAAACAAGACGAAATTTATACCTTTGTAAAATCCAT    450
Heinz1706     GATACAATTTTTTTTCTTACTAAATTTCACATATAGTAAAAAACAAGACGAAATTTATACCTTTGTAAAATCCAT    450

Indigo-Rose   CTTGTCCAATTATGTTGAAGTGTATAGACAATTTTAATGAGGAAGCAAATCAAGAAAAATGAGCTTCCTCTAGTA    525
Heinz1706     CTTGTCCAATTATGTTGAAGTGTATAGACAATTTTAATGAGGAAGCAAATCAAGAAAAATGAGCTTCCTCTAGTA    525

Indigo-Rose   CAGATTTTCAAAGGTTCACAAATGTGATTTAACACTAATAAAGCCAAGATGAATTACCTTAAACAAAGGGCATAT    600
Heinz1706     CAGATTTTCAAAGGTTCACAAATGTGATTTAACACTAATAAAGCCAAGATGAATTACCTTAAACAAAGGGCATAT    600

Indigo-Rose   GTATGTCTGTTAACTAGCAATTCGTCCTTCCGTTTCATATCAGTTTTCATATTTATTTTTTAAAAAATTAATTTA    675
Heinz1706     GTATGTCTGTTAACTAGCAATTCGTCCTTCCGTTTCATATCAGTTTTCATATTTATTTTTTAAAAAATTAATTTA    675

Indigo-Rose   ACTAATTCTTTTCCATAATTTAAAATTCAATTGATACAAAAATTATTATAAATTATAATTTTTTTCTCAAGTCAA    750
Heinz1706     ACTAATTCTTTTCCATAATTTAAAATTCAATTGATACAAAAATTATTATAAATTATAATTTTTTTCTCAAGTCAA    750

Indigo-Rose   CATTAATAACAATATGTTCAGAGGAATCCCGCAAATGAAATATAGAGAAGATAAAGTGTATGTAGTACTTGTCAT    825
Heinz1706     CATTAATAACAATATGTTCAGAGGAATCCCGCAAATGAAATATAGAGAAGATAAAGTGTATGTAGTACTTGTCAT    825

Indigo-Rose   GATTCGTAGAAGTAGATAAATTGTTTCTGAAAAAACATTGCTTCAACATTCAAGAATAAGAAAACATAGCAACTA    900
Heinz1706     GATTCGTAGAAGTAGATAAATTGTTTCTGAAAAAACATTGCTTCAACATTCAAGAATAAGAAAACATAGCAACTA    900

Indigo-Rose   AAAAAGGAAGTAGTGGAAATCCTACAAGAAAGGAACAAAAACAACAAAATAGTGTGATAATTAAAATACAGTAAA    975
Heinz1706     AAAAAGGAAGTAGTGGAAATCCTACAAGAAAGGAACAAAAACAACAAAATAGTGTGATAATTAAAATACAGTAAA    975

Indigo-Rose   CAATTAAAGATAATAGATATGATCCAAAGAAAGAACTATAGTACAATGACAAACACCAATGAGCCCAAACCCTCA   1050
Heinz1706     CAATTAAAGATAATAGATATGATCCAAAGAAAGAACTATAGTACAATGACAAACACCAATGAGCCCAAACCCTCA   1050

Indigo-Rose   AAAATAAGAAAACACTCCACTGTCTATTATAATAGACGTCCTTCACACCTTTATATATAAAATTATCTATCCTCG   1125
Heinz1706     AAAATAAGAAAACACTCCACTGTTTATTATAATAGACGTCCTTCATACCTTTATATATAAAATTATCTATCCTCG   1125

Indigo-Rose   CGGATAACCTGAAGTTTTGCAATATCCAGTCTGATCACTTTTTCTCAATACTTCTTTGCCTACATCTAAATCTTC   1200
Heinz1706     CGGATAACCTGAAGTTTTGCAATATCCAGTCTGATCACTTTTTCTCAATACTTCTTTGCCTACATCTAAATCTTC   1200

Indigo-Rose   TAGTACAATACCATAATCAACTTCTTGCACCTGCTCCCTGGAGCGTCTGTACATCTCTTCTTTACAAAGGTATAA   1275
Heinz1706     TAGTACAATACCATAATCAACTTCTTGCACCTGCTCCCTGGAGCGTCTGTACATCTCTTCTTTACAAAGGTATAA   1275

Indigo-Rose   ATTTGTAAAGGTATAAATTTTCTAAACATCCTCATCGCCTCAACATTCTCATTGACTCAACATGTATATCTGAAC   1350
Heinz1706     ATTTGTAAAGGTATAAATTTTCTAAACATCCTCATCGCCTCAACATTCTCATTGACTCAACATGTATATCTGAAC   1350

Indigo-Rose   ATGAAAGTTCTTGACAAGCTAACATTGCGCTTGATACAACAAAATCTATCTAACTATCACTTAATAAAAAACTTA   1425
Heinz1706     ATGAAAGTTCTTGACAAGCTAACATTGCGCTTGATACAACAAAATCTATCTAACTATCACTTAATAAAAAACTTA   1425

Indigo-Rose   CCTTCAA-GTTTCAATGGTACATTTTATCAAGTAAGACTCCGGATGCAACCTTCCACTTCATTCACGTACAGTCG   1499
Heinz1706     CCTTCAAAGTTTCAATGGTACATTTTATCAAGTAAGACTCCGGATGCAACCTTCCACTTCATTCACGTACAGTCG   1500
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Indigo-Rose  TGCACCAATACGATGTGTGATATCATCGTCAATATCTCCATTTTCCTCGATTGAAAATCCAATTTACTTGAAACT  1574
Heinz1706    TGCACCAATACGATGTGTGATATCATCGTCAATATCTCCATTTTCCTCGATTGAAAATCCAATATACTTGAAACT  1575

Indigo-Rose  ATAATGAAAAAATATTTTGAAATCATGTTTATCAAACATACATAGTTTCACTCTCAAAAAATAAAACATGACATA  1649
Heinz1706    ATAATGAAAAAATATTTTGAAATCATGTTTATCAAACATACATAGTTTCACTCTCAAAAAATAAAACATGACATA  1650

Indigo-Rose  CTAATTTGAAACAAAAGAAGCATTTGCTTAGCACGATTAATAATTAAAATAAAAATACTTCTAGTATTGAGGAGT  1724
Heinz1706    CTAATTTGAAACAAAAGAAGCATTTGCTTAGCACGATTAATAATTAAAATAAAAATACTTCTAGTATTGAGGAGT  1725

Indigo-Rose  AGTAACACTTCGTTGTTTGGTAAAAATGTTGAAAATAATTTCCAACTAACCAATCGATATTTGAGTATCCACTTA  1799
Heinz1706    AGTAACACTTCGTTGTTTGGTAAAAATGTTGAAAATAATTTCCAACTAACCAATCGATATTTGAGTATCCACTTA  1800

Indigo-Rose  CTTCTTTGGCCTACTTATACCTCTCCTCGTACATACCATAACTAACTTCTCGCACCTCTTCACTGGGGCATCTGC  1874
Heinz1706    CTTCTTTGGCCTACTTATACCTCTCCTCGTACATACCATAACTAACTTCTCGCACCTCTTCACTGGGGCATCTGC  1875

Indigo-Rose  GCATATTCTCTTCACATGTTCAAATCATTTTAATCTTAATTCTATCATCTTGTCCACCACGGACTACGGAGCCAC  1949
Heinz1706    GCATATTCTCTTCACATGTTCAAATCATTTTAATCTTAATTCTATCATCTTGTCCACCACGGACTACGGAGCCAC  1950

Indigo-Rose  TCTCATCTTATTTAGAATATTCTCAACATCCTCATTAACTCGACATGCATCTTCTGAACATGGGTAGCCATCACT  2024
Heinz1706    TCTCATCTTATTTAGAATATTCTCAACATCCTCATTAACTCGACATGCATCTTCTGAACATGAGTAGCCATCACT  2025

Indigo-Rose  CCGCCTTATACAACAAAGTTTGTCTAACTACCAACTTATAGAAACTTACCTTGAAATTTCAATGGTACATTTTTG  2099
Heinz1706    CCGCCTTATACAACAAAGTTTGTCTAACTACCAACTTATAGAAACTTACCTTGAAATTTCAATGGTACATTTTTG  2100

Indigo-Rose  TCATACAAGACTCCGGATGCAACCTTTCACTTCATTCACATGCACCAATACGATATATAATATCATCGTCAATAT  2174
Heinz1706    TCATACAAGACTCCGGATGCAACCTTTCACTTCATTCACATGCACCAATACGATATATAATATCATCGTCAATAT  2175

Indigo-Rose  CTCCATTTCCTTCTATTATAAATTCAAGATACTTGAAACTATGATAAAAAAAAATACTTCAAAATCGTATTCACC  2249
Heinz1706    CTCCATTTCCTTCTATTATAAATTCAAGATACTTGAAACTATGATAAAAAAAA-TACTTCAAAATCGTATTCACC  2249

Indigo-Rose  AAAATTTCACAGTTTCACTCTCGAAAAATAAAACATGACACGAAAGAAGAATTTGTATCGTACAATTCATAATTA  2324
Heinz1706    AAAATTTCACAGTTTCACTCTCGAAAAATAAAACATGACACGAAAGAAGAATTTGTATCGTACAATTCATAATTA  2324

Indigo-Rose  AAATAAAAATAGTTCTAATATTGAGGAGTAGTAACACTTCGTTGTTTGGTGAAAATGTTAGGCAAATAATTTCCA  2399
Heinz1706    AAATAAAAATAGTTCTAATATTGAGGAGTAGTAACACTTCGTTGTTTGGTGAAAATGTTAGGCAAATAATTTCCA  2399

Indigo-Rose  ACTAACCAGTCGATATTTGAGTATCCACCTACCTCAATTTATTGGACCACCACACACTTCACTGTCATCTACCAT  2474
Heinz1706    ACTAACCAGTCGATATTTGAGTATCCACCTACCTCAATTTATTGGACCACCACACACTTCACTGTCATCTACCAT  2474

Indigo-Rose  TCTTCATATGTTTGTCTTTTTTTTATTTTATTCACTCAAATCAGAACCACCCCTTCTTTTTAGAATCCTTTTTTT  2549
Heinz1706    TCTTCATATGTTTGTCTTTTTTTTATTTTATTCACTCAAATCAGAACCACCCCTTCTTTTTAGAATCCTTTTTTT  2549

Indigo-Rose  TTTAATCATATAGTAGTAATAAAATTTTCTATGTATATATATAGACCACATTCAAATCTTTGTTCTCCACATATA  2624
Heinz1706    TTTAATCATATAGTAGTAATAAAATTTTCTATGTATATATATAGACCACATTCAAATCTTTGTTCTCCACATATA  2624

                                                            Start code
                                                                ---
Indigo-Rose  CTCTTCCTTAATTAGTACTCCAATTCATTTAATTAAAGTTTATTTCTCTTGATGGCAGATTGGAATAGATCAAG  2699
Heinz1706    CTCTTCCTTAATTAGTACTCCAATTCATTTAATTAAAGTTTATTTCTCTTGATGGCAGATTGGAATAGATCAAG  2699

Indigo-Rose  CACATCAGATAATGCCTCAGTGGTCTCACCTGGTAATTAACAATTCTTTTTTATTTTTATCGCAAGAGCTTTTAA  2774
Heinz1706    CACATCAGATAATGCCTCAGTGGTCTCACCTGGTAATTAACAATTCTTTTTTATTTT-ATCGCAAGAGCTTTTAA  2773

Indigo-Rose  TTATTCTTTTCGTTCACTTTTATTGATCTATTTTGGACATCTCATGCTCCTTACCAAAATTTTTTTTTGATATAA  2849
Heinz1706    TTATTCTTTTCGTTCACTTTTATTGATCTATTTTGGACATCTCATGCTCCTTACCAAAAATTTCTTTTGATATAA  2848

Indigo-Rose  GGGTCCTACAGTACATATTAATTGATATTTGATATTATGTTTTGAAAGAAGATTTGAGAAATAAATAACTAATGA  2924
Heinz1706    GGGTCCTACAGTACATATTAATTGATATTTGATATTATGTTTTGAAAGAAGATTTGAGAAATAAATAACTAATGA  2923

Indigo-Rose  GCTAAGGGTAAACATGAAATAAAATATTTGTCTTTTTTTCATGTTAAAAAGTAACGAGTAAAAATGAACGGATAC  2999
Heinz1706    GCTAAGGGTAAACATGAAATAAAATATTTGTCTTTTTTTCATGTTAAAAAGTAACGAGTAAAAATGAACGGATAC  2998
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Indigo-Rose  TTTTATATTTGCTTATAAATATATTCCTTAAAGGAATTTGGAGAACATTATGATATGATTATCTGCGTCTAACCA  3074
Heinz1706    TTTTATATTTGCTTATAAATATATTCCTTAAAGGAATTTGGAGAACATTATGATATGATTATCTGCGTCTAACCA  3073

Indigo-Rose  TATACTCTAATAATGCCATAAGTAAACAAATATTTATCCTTTTGGCTACTTCCAAAATACATGTTCATTTATGAA  3149
Heinz1706    TATACTCTAATAATGCCATAAGTAAACAAATATTTATCCTTTTGGCTACTTCCAAAATACATGTTCATTTATGAA  3148

Indigo-Rose  ATCATTTTTTTAATAATAAGTTAGTTAGTCGGAATTTAGACTTTAAAATTTATATATTTTTTTACATCAAGTTA  3224
Heinz1706    ATCATTTTTTTAATAATAAGTTAGTTAGTCGGAATTTAGAATTTAAAATTTATGTATTTTTATACATCAAGTTA  3223

Indigo-Rose  ATATATTATACTACTTATAAGTTCACAATTAAATATTCAATTTTGTTAATAATTTTCTTAATATATTTATAAGTC  3299
Heinz1706    ATATATTACACTACTTATAAGTTCACAATTAAATATTCAATTTTGTTAATAATTTTCTTAATATATTTATAAGTC  3298

                                    4-bp insertion
Indigo-Rose  TAAATAAAAGTTATTGAGTTCACGTGAATTCATTATAGATAGATTCGACCCGAGTGGTTGCATTAGAGACTACCA  3374
Heinz1706    TAAATAAAAGTTATTGAGTTCACGTGAATTCATTATAGA----TTCGACCCGAGTGGTTGCATTAGAGACTACCA  3369

Indigo-Rose  ACGAAGAAACCTCTAAACTTGAATTTTCAGAAGATGAAGAAATGCTCATTGCTAAAATGTTCAGCTTGGTTAGAG  3449
Heinz1706    ACGAAGAAACCTCTAAACTTGAATTTTCAGAAGATGAAGAAATGCTCATTGCTAAAATGTTCAGCTTGGTTAGAG  3444

Indigo-Rose  AGAGGTACGTTTAATATTTTTTTAAAAAAATTCTTGAATTTTGTGTATTAATTATTTAAGGTTTAATATAAAATT  3524
Heinz1706    AGAGGTACGTTTAATATTTTTTTAAAAAAATTCTTGAATTTTGTGTATTAATTATTTAAGGTTTAATATAAAATT  3519

Indigo-Rose  GTCATGGTGTAATTTTAATTAGGTGGTCATTAATTGCTGGAAGAATCCTAGGAAGAAATGCTGATGAGATTGAAA  3599
Heinz1706    GTCATGGTGTAATTTTAATTAGGTGGTCATTAATTGCTGGAAGAATCCCAGGAAGAAATGCTGATGAGATTGAAA  3594

Indigo-Rose  AATATTGGAAATCAAAATACTCCAAAAGCCAGTAAATTTCTTCAAATTACTTTTTCCCTCAGATGAATATTTTTA  3674
Heinz1706    AATATTGGAAATCAAAATACTCCAAAAGCCAGTAAATTTCTTCAAATTACTTTTTCCCTCAGATGAATATTTTTA  3669

Indigo-Rose  TCTATTTTTATTTATCTAATATTAATTCGATGTACTTCATAATATTTTTAAAAATTTCATAGTAAATAACAAAGA  3749
Heinz1706    TCTATTTTTACTTATCTAATATTAATTCGATGTACTTCATAATATTTTTAAAAATTTCATAGTAAATAACAAAGA  3744

Indigo-Rose  TAAATAATAAGTGATAAGCTTATCTCTAGATTTCTAAGTTGGATAAGTAAGAATGTTGTAGAAACTAGAGAGGAA  3824
Heinz1706    TAAATAATAAGTGATAAGCTTATCTCTAGATTTCTAAGTTGGATAAGTAAGAATGTTGTAGAAACTAGATAGGAA  3819

Indigo-Rose  GTAGTTCTTTCGTTCACTTCTATTTATCTAACTTATCTACTGTAGATTATAATTTTTTAAAAAATTACTTTTAAA  3899
Heinz1706    GTAGTTCTTTCGTTCACTTCTATTTATCTAACTTATCTACTGTAGATTATAATTTTTTTTAAAAATACTTTTAAA  3894

Indigo-Rose  ACTTATTTCTCAAATTATTTTTCAAGACTTAGAGATTAAAATCAAATATATATATATTTAACATAGGGTAGAGGA  3974
Heinz1706    ACTTATTTTTCAAATTATTTTTCAAGACTTAGAGATTAAAATCAA---TATATATATTTAACATAGGGTAGAGGA  3966

Indigo-Rose  CAAAAATTACATACTTTTAAGGTAAAATTACTATTTGTTCCTTGTAAATTTATAATTGCAAATATCTCTCAAACT  4049
Heinz1706    CAAAAATCACATACTTTTAAGGTAAAATTACTATTTGTTCCTTGTAAATTTATAATTACAAATATCTCTCAAACT  4041

Indigo-Rose  GATACAATAATACAAACGTTGATACATTAATCTAATTGCGCGGATACATTATTCGTTAGGTAAGATACAATAAAT  4124
Heinz1706    GATACAATAATACAA----------------------GCGCGAATACATTATTCGTTAGGTAAGATACAATAAAT  4094

Indigo-Rose  TTTATATATGATACACTGATCTAATGTATATTTTATACATGATACACTAATCTGATGCGCGGAATACATTAATAT  4199
Heinz1706    TTTATATA-----CACTGATCTAATGTATATTTTATACATGATACACTAATCTGATGCGCAAGATACATTAATAT  4164

Indigo-Rose  GAAGTGTGAAAATGAAAATTTTGGAAATTTATAAAACTAATAGGAAATAATTATAACAAAAATTTAAAAATGAAA  4274
Heinz1706    GAAGCGTGAAAATG-------------------------------------------------------------  4178

Indigo-Rose  TTTTTGTCATATATCCTTTAATATAAGTATTGTAATAAAATACTCATGTGAAACATTATTTTTTAAAAGAATATA  4349
Heinz1706    ---------------------------------------------------------------------------     -

Indigo-Rose  TAAAGTCTAATTAAACAAATAAGAATGAACAAAGAAAGTATATCATCACTTCAACCTAGCTGAATGCAATGACAG  4424
Heinz1706    ---------------------------------------------------------------------------     -

Indigo-Rose  TACAAGCTAAAATATGTTTTTGAACAAGATTTCAATTTTAGGAATTTGAATTTTTCAAAAAATTATATAGTATCG  4499
Heinz1706    ---------------------------------------------------------------------------     -
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Indigo-Rose   TAGATATTAAATATATTATTTATAAAATATTTTCAAAATAAAAATATAAAGTTTACCTAAGTCTAAGATGATTAA   4574
Heinz1706     ---------------------------------------------------------------------------      -

Indigo-Rose   ATTCTGTTAAACTCGTAATCGTAAACAAACTTGAAACTCCGTCCCTTGTGGTTTATGTACTTTCAGAAGTTCGTG   4649
Heinz1706     ------TTAAATTCGTAATCGTAAACAAACTTGAAACTCCGTCCCTTGTGGTTTATGTACTTTCAGAAGTTCGTG   4247

Indigo-Rose   TATCTTGCATGAAATTTAATATTTTTATTATTTGAACAGTATACACAGTGAATATCATGTCATTTCAGGATCTTC   4724
Heinz1706     TATCTTGCATGAAATTTAATATTTTTATTATTTGAACAGTATACACAGTGAATATCATGTCATTTCAGGATCTTC   4322

Indigo-Rose   ACATTTACTTTATTTTTACTTTATCTACTTTTAATTTAACGATCCTTAGAAAAAATGATATAATTATTTTATGAT   4799
Heinz1706     ACATTTACTTTATTTTTACTTTATCTACTTTTAATTTAACGATCCTTAGAAAAAATGATATAATTATTTTATGAT   4397

Indigo-Rose   AATATTTGTATTAATTGATGTTTAATATTATCTTTTGAAAAATAATTTAGAAAATAAGTAATTAATGTTAAGAAA   4874
Heinz1706     AATATTTGTATTAATTGATGTTTAATATTATCTTTTGAAAAATAATTTAGAAAATAAGTAATTAATGTTAAGAAA   4472

Indigo-Rose   AAAATCAAATATTTTTATACGTTAAAAGTGACAAGTAAATGCAAATAAAAAGTATTATTCACTAGATATCAATAA   4949
Heinz1706     AAAATCAAATATTTTTATACGTTAAAAGTGACAAGTAAATGCAAATAAAAAGTATTATTCACTAGATATCAATAA   4547

Indigo-Rose   GCGAGTAAAAATATTCAGTAAGAAGATTCAACATATATTATATATATGAACATAAAAAAAAATTTCAATCCTTTT   5024
Heinz1706     GCGAGTAAAAATATTCAGTAAGAAGATTCAACATATATTATATATATGAACATAAAAAAAAATTTCAATCCTTTT   4622

Indigo-Rose   TGATTCTTTGGTGACTTGAACTTACATCCTTAGTATAATGATTGTTTACCATTTGAGCAACTTCCATGAAAATCT   5099
Heinz1706     TGATTCTTTGGTGACTTAAACTTACATCCTTAGTATATTGATTGTTTACCATTCGAGCAACTTCCATGAAAATCT   4697

Indigo-Rose   TTTCATTATCTGTAACGTTTTTATTAGGAGTTTTTTTAAAAAAAAAAATAATAAAAACAAAAATTTGTACTCTTC   5174
Heinz1706     TTTCATTATCTGTAACGTTTTTATTAGGAGTTTTTTTAAAAAAAATAATAATAAAAACAAAAATTTGTACTCTTC   4772

Indigo-Rose   ATTTAGGGAGGAAATACAGGCCCAATCTCAAGATGAAGCTCATGGCATTAGATTGATAGAGAAAACTGGGCCTTC   5249
Heinz1706     ATTTAGGGAGGAAATACAGGCCCAATCTCAAGATGAAGCTCATGGCATTAGATTGATAGAGAAAACTGGGCCTTC   4847

Indigo-Rose   AACGGCGCACCCTCAGCAGTGTGTTTTTCCAGAAAAAAAGCCCATATCTGTCTGTCAACCTTCAGATACTGGGCC   5324
Heinz1706     AACGGGGCACCCTCAGCAGTGTGTTTTTCCAGAAAAAAAGCCCATATCTGTCTGTCAACCTTCAGATATTGGGCC   4922

Indigo-Rose   TCAACTATTGGGCCCAACAACGAATGGGCCTCAACAGCTATTGGGCCCTAAAACAACTGGGCCCAATAACATCAC   5399
Heinz1706     TCAACTATTGGGCCCAACAACGAATGGGCCTCAACAGCTATTGGGCCCTAAAACAACTGGGCCCAATAACATCAC   4997

Indigo-Rose   TGTAGACCAAAAGTTAGTTAACCCAGCCCAAGACCAAATAAACCAATAACTTATGCCCAGCCCAGCCCAAGATTG   5474
Heinz1706     TGTAGACCAAAAGTTAGTTAACCCAGCCCAAGACCAAATAAACCAATAACCTATGCCCAGCCCAGCCCAAGATTG   5072

Indigo-Rose   GTCAAACATGACACTAGACAAACCTACAATATATTTTCTATTTACATATTTTCGCAAATACCTACTACTCAATTA   5549
Heinz1706     GTCAAACATGACACTAGACAAACCTACAATATATTTTCTATTTACATATTTTCGCAAATACCTACTACTCAATTA   5147

Indigo-Rose   TGCTATGTATAGCTATAGTTTGCATATTTACTAGTTGTAGTTACAGTTTAAGTTATCTCGTTTGTATAATTTACA   5624
Heinz1706     TGCTATGTATAGCTATAGTTTGCATATTTACTAGTTGTAGTTACAGTTTAAGTTATCTCGTTTGTATAATTTCCA   5222

Indigo-Rose   TGTATGTTTAAATAAGTGAGTTATATTTGTATAAACTCAAAATAATGAATTTATACAAACACAAACATTTAAACT   5699
Heinz1706     TATATGTTTAAATAAGTGAGTTATATTTGTATAAACTCAAAATAATGAATTTATACAAACACAAACATTTAAACT   5297

Indigo-Rose   TTAAATAGTTGTACAGATATATTATACAAAAGTTATACAAATTATATTATACAACTTTCGAATTATACACACTCG   5774
Heinz1706     TTAAATAGTTGTACAGATATATTATACAAAAGTTATACAAATTATATTATACAACTTTCCAATTATACACACTCG   5372

Indigo-Rose   ATTTGATTTTCTTGGAAGTGTTTGACGACACAATTGTTTATATAGACCATGATCATGATCATAATATTTGTGTAT   5849
Heinz1706     ATTTGATTTTCTTGGAAGTGTTTGACGACACAATTGTTTATATAGACCATGATCATGATCATAATATTTGTGTAT   5447

Indigo-Rose   TTGATTAAACTTATAATGTTATTAAATTAATTTATACGTACTTTTTAATAAGTTACAGATATCTCATATCCTTTC   5924
Heinz1706     TTGATTAAACTTATAATGTTATTAAATTAATTTATACGTACTTTTTAATAAGTTACAGATATCTCATATCCTTTC   5522

Indigo-Rose   TAATAAAATATCTTATATCCTTTCTAATAACCTCTCCTCGAACAATTGCTTTAAGTTTCAAAAATTGACTATTTC   5999
Heinz1706     TAATAAAATATCTTATATCCTTTCTAATAACCTCTCCTCGAACAATTGCTTTAAGTTTCAAAAATTGACTATTTC   5597

Indigo-Rose   CTATTTCATTTTTTGATAGTTCCCTATTAAGGGAAAATTACGTGGAATGACAAACATTCCTAAGTAATTAGTCAA   6074
Heinz1706     CTATTTCATTTTTTGATAATTCC-TATTAAGGGAAAATTACGTGGAATGACAAACATTCCTAAGTAATTAGTCAA   5671
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Indigo-Rose  TAAGGGTATATTTTAATTTATTTACTCAATAACTATAGTTTCATTTTTTTGCCATAATTAATGGGACCCACCATC  6149
Heinz1706    TAAGGGTATATTTTAATTTATTGACTCAATAACTATAGTTTCATTTTTTTGCCATAATTAATGGGACCCACCATC  5746

Indigo-Rose  TCTTTGTATATCCAACCATGAAACAAAAAGTTATCTTTTTATATATAATTTTATCAAATCAATTTTATCTCTCCT  6224
Heinz1706    TCTTTGTATATCCAACCATGAAACAAAAAGTTATCTTTTTATATATAATTTTATCAAATCAATTTTATCTCTCCT  5821

Indigo-Rose  ACACTCATTCTATATCTTTCTTCTAAAATCACTCCTCCACTCCTATTTTGAATTTTGAATTTTGGAAAATTTCAC  6299
Heinz1706    ACACTCATTCTATATCTTTCTTCTAAAATCACTCCTCCACTCCTATTTTGAATTTTGAATTTTGGAAAATTTCAC  5896

Indigo-Rose  CATATCCCTGTTGTCTTACTTTCATTAATCCAATTTTTTTTAAAAAAATTTCTTCATCAACACAATTATATATGT  6374
Heinz1706    CATATCCCTGTTGTCTTACTTTCATTAATCCAATTTTTTTTTAAAAAATTTCTTCATCAACACAATTATATATGT  5971

Indigo-Rose  ATTATTTTTCTTAGTTTTTTTCATATTTTTTTTAAAAAAAATTCTTTCTTTCTTTTCAGTTTAAAGTTCTTCAAA  6449
Heinz1706    ATTATTTTTCTTAGTTTTTTTCATATATTTTTTTAAAAAAATTCTTTCTTTCTTTTCAGTTTAAAGTTCTTCAAA  6046

Indigo-Rose  ATGAGAATAAAGAATTCATCTCCATATATGAGTATTAGCATAGGTATGTCATTACATGTCAATATTGTTGATAAT  6524
Heinz1706    ATGAGAATAAAGAATTCATCTCCATATATGAGTATTAGCATAGGTATGTCATTACATGTCAATATTGTTGATAAT  6121

Indigo-Rose  CCACCTTCGTTTTCAATTGAGTTATTTCAGGATTTTGGGGTCAATGTAGGGTATATGACAAAACCTAAAAAAGTT  6599
Heinz1706    CCACCTTCGTTTTCAATTGAGTTATTTCAGGATTTTGGGGTCAATGTAGGGTATATGACAAAACCTAAAAAAGTT  6196

Indigo-Rose  CAAGTTGAACAATATCTTGAATAGAGATTCAAGAAAAAAATGACCCAATTACAATTCAGAAAGTCATCAACAACG  6674
Heinz1706    CAAGTTGAACAATATCTTGAATAGAGATTCAAGAAAAAAATGACCCAATTACAATTCAGAAAGTCATCAACAACG  6271

Indigo-Rose  CGAAATCTAGCGGCATTATAGTTGAAGGTTGAAGCAAGAGAAAAGTCAAACATAAATTCAGACGAGATCGGATCT  6749
Heinz1706    CGAAATCTAGCGGCATTATAGTTGAAGGTTGAAGCAAGAGAAAAGTCAAACATAAATTCAGACGAGATCGGATCT  6346

Indigo-Rose  ATCTCATCAAAACTGGACAGAACTAGACAAATCTGAAGAACATCAGGTTGTGTAATTTATATACAAATTACTAAA  6824
Heinz1706    ATCTCATCAAAACTGGACAGAACTAGACAAATCTGAAGAACATCAGGTTGTGTAATTTATATACAAATTACTAAA  6421

Indigo-Rose  GTTATGTATATAGTGGGTTGTGTATTAAGGTAATATATACAAAGTATTATGAGATAATTGTTATTTGTATACAAA  6899
Heinz1706    GTTATGTATATAGTGGGTTGTGTATTAAGGTAATATATACAAAGTATTATGAGATAATTGTTATTTGTATACAAA  6496

Indigo-Rose  TATTTGTATAAAAGAAATTTGTTAATCATTGTATAATACATATATAAAATTATAGTACATTATACAACTTTGTCG  6974
Heinz1706    TATTTGTATAAAAGAAATTTGTTAATCATTGTATAATACATATATAAAATTATAGTACATTATACAACTTTGTCG  6571

Indigo-Rose  ATATATAAAAAAAATTATGAACATGATAAAATATTGTATATATAAACATTACACACTAAATACACAAACATATTT  7049
Heinz1706    ATATATAAAAAAAATTATGAACATGATAAAATATTGTATATATAAACATTACACACTAAATACACAAACATATTT  6646

Indigo-Rose  CAAGTTTACCATATATACAATTGACAAATGAATATTATACAATCATTTTGATCATTAATTTTTTTAAAAAACAT  7124
Heinz1706    CAAGTTTACCATATATACAATTGACAAACGAATATTATACAATCATTTTGATCATTAATTTTTTTTAAAAACAT  6721

Indigo-Rose  GAAATTACATATGTACATATACAAATATGATTCATATACCAAATTATTGTATATTATACAAATCCATACATATAT  7199
Heinz1706    GAAATTACATATGTACATATACAAATATGATTCATATACCAAATTATTGTATATTATACAAATCCATACATATAT  6796

Indigo-Rose  ACTATAAAAAAATGAACATAATAAAATATTGTATACAAATAAACTACAGAAAATAATTAAGAACAAATACAACAC  7274
Heinz1706    ACTATAAAAAAATGAACATAATAAAATATTGTATACAAATAAACTACAGAAAATAATTAAGAACAAATACAACAC  6871

Indigo-Rose  ACTTTTATTTTAAAAAACAAACATAATTGTCATATATACAATTTTCATATTTATGATGAATAATACATAATAAAT  7349
Heinz1706    ACTTTTATTTTAAAAAACAAACATAATTGTCATATATACAATTTTCATATTTATGATGAATAATACATAATAAAT  6946

Indigo-Rose  TACACATGAAATTGTATAAAAAAATTATTTACAATTTTTCAAATATATACAATATAATCAATGTGTGTGTGTATAT  7424
Heinz1706    TACACATGAAATTGTATAAAAAAATTATTTACAATTTCTCAAATATATACAATATAATCAATGTGTGTGTGTATAT  7021

Indigo-Rose  ATATATATATAAATAAAATCATTAACGTCTAAGTGTTTCATACAACTTATTTTTAAATAAAATTGAGAAAATATT  7499
Heinz1706    ATATATATATAAATAAAATCATTAACGTCTAAGTGTTTCATACAACTTATTTTTAAATAAAATTGAGAAAATATT  7096

Indigo-Rose  TGATTTTGAATGGTTAGCTTAAATAATGGGATTGTGTAAATGTTTGTTACCTTATTTAGCGATATTGTTACCATT  7574
Heinz1706    TGATTTTGAATGGTTAGCTTAAATAATGGGATTGTGTAAATGTTTGTTACCTTATTTAGCGATATTGTTACCATT  7171

Indigo-Rose  CAATGAATAAGTAAAATATTAAATAAATTAAAAATAAAAAAATATTTTTTTACAAATTAAAAGATACATAACAAA  7649
Heinz1706    CAATGAATAAGTAAAATATTAAATAAATTAAAAATAAAAAAATATTTTTTTACAAATTAAAAGATACATAACAAA  7246
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Indigo-Rose    CTAAACTATACCTATAAAATGTAATTATGTAAACTACACCTATATAATATTATTTAATAAATTATGTTTGCTATT   7724
Heinz1706      CTAAACTATACCCATAAAATGTAATTATGTAAACCACACCTATATAATATTATTTAATAAATTATGTTTGCCATT   7321

Indigo-Rose    TATGAAATTTTCCTTATTAATTAATTACACGATTTACAAGCAGTGAGGAACAAAAATTGAGGTGGCAAAACTTAT   7799
Heinz1706      TATGAAATTTTCCTTATTAATTAATTACACGATTTACAAGCAGTGAGGAACAAAAATTGAGGTGGCAAAACTTAT   7396

Indigo-Rose    CCTGATGATGCGGCATGTATAGCTTCATTTTGATGTCACACTAATACTATAGTCTATATATAGTAGCAATACTTG   7874
Heinz1706      CCTGATGATGCGGCATGTATAGCTTCATTTTGATGTCACACTAATACTATAGTCTATATATAGTAGCAATACTTG   7471

Indigo-Rose    ATAGAATCTTCAAATAATCAACCCAACTTAATAAAGTACTAAACAATATTTCGTGTGGATAACTATGAATAGAAT   7949
Heinz1706      ATAGAATCTTCAAATAATCAACCCAACTTAATAACGTACTAAACAATATTTCGTGTGGATAACTATGAATAGAAT   7546

Indigo-Rose    CGGAT   7954
Heinz1706      CGGAT   7551
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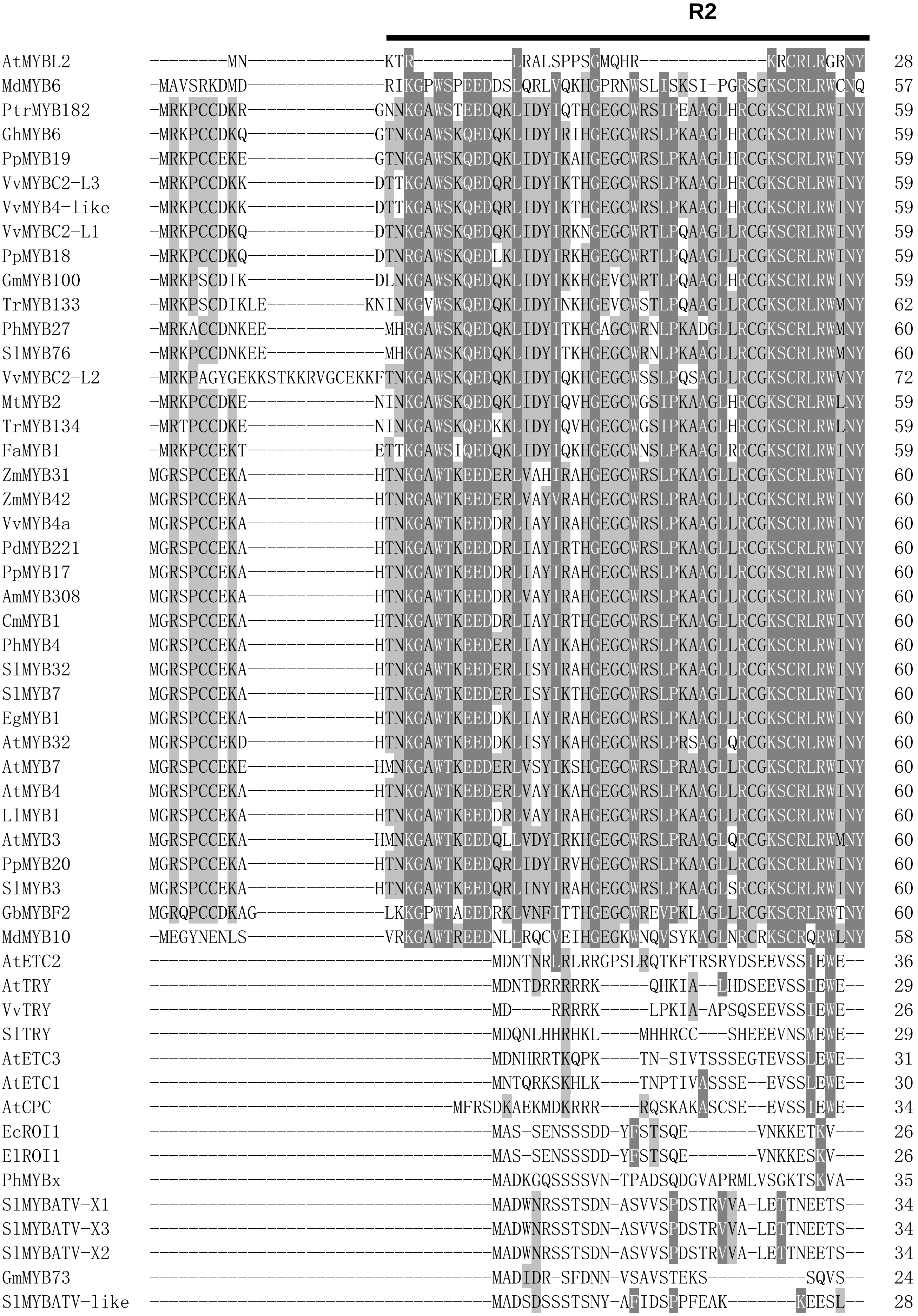
Fig. S2 Sequence polymorphism of the genomic sequence of *SlMYBATV*. Sequences were aligned by using Clustal X ver. 2 (Larkin *et al.*, 2007) with default settings, and conserved nucleotides were shaded by GeneDoc (2.6) (Nicholas *et al.*, 1997).



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MdMYB6         -MAVSRKDMD--------------RIKGPWSPEEDDSLQRLVQKHGPRNWSLISKSI-PGRSGKSCRLRWCNQ   57
PtrMYB182      -MRKPCCDKR-------------GNNKGAWSTEEDQKLIDYIQTHGEGCWRSIPEAAGLHRCGKSCRLRWINY   59
GhMYB6         -MRKPCCDKQ-------------GTNKGAWSKQEDQKLIDYIRIHGEGCWRSLPKAAGLHRCGKSCRLRWINY   59
PpMYB19        -MRKPCCEKE-------------GTNKGAWSKQEDQKLIDYIKAHGEGCWRSLPKAAGLHRCGKSCRLRWINY   59
VvMYBC2-L3     -MRKPCCDKK-------------DTTKGAWSKQEDQRLIDYIKTHGEGCWRSLPKAAGLHRCGKSCRLRWINY   59
VvMYB4-like    -MRKPCCDKK-------------DTTKGAWSKQEDQRLIDYIKTHGEGCWRSLPKAAGLHRCGKSCRLRWINY   59
VvMYBC2-L1     -MRKPCCDKQ-------------DTNKGAWSKQEDQKLIDYIRKNGEGCWRTLPQAAGLLRCGKSCRLRWINY   59
PpMYB18        -MRKPCCDKQ-------------DTNRGAWSKQEDLKLIDYIRKHGEGCWRTLPQAAGLLRCGKSCRLRWINY   59
GmMYB100       -MRKPSCDIK-------------DLNKGAWSKQEDQKLIDYIKKHGEVCWRTLPQAAGLHRCGKSCRLRWINY   59
TrMYB133       -MRKPSCDIKLE----------KNINKGVWSKQEDQKLIDYINKHGEVCWSTLPQAAGLLRCGKSCRLRWMNY   62
PhMYB27        -MRKACCDNKEE------------MHRGAWSKQEDQKLIDYITKHGAGCWRNLPKADGLLRCGKSCRLRWMNY   60
SlMYB76        -MRKPCCDNKEE------------MHKGAWSKQEDQKLIDYITKHGEGCWRNLPKAAGLLRCGKSCRLRWMNY   60
VvMYBC2-L2     -MRKPAGYGEKKSTKKRVGCEKKFTNKGAWSKQEDQKLIDYIQKHGEGCWSSLPQSAGLLRCGKSCRLRWVNY   72
MtMYB2         -MRKPCCDKE-------------NINKGAWSKQEDQKLIDYIQVHGEGCWGSIPKAAGLHRCGKSCRLRWLNY   59
TrMYB134       -MRTPCCDKE-------------NINKGAWSKQEDKKLIDYIQVHGEGCWGSIPKAAGLHRCGKSCRLRWLNY   59
FaMYB1         -MRKPCCEKT-------------ETTKGAWSIQEDQKLIDYIQKHGEGCWNSLPKAAGLRRCGKSCRLRWINY   59
ZmMYB31        MGRSPCCEKA-------------HTNKGAWTKEEDERLVAHIRAHGEGCWRSLPKAAGLLRCGKSCRLRWINY   60
ZmMYB42        MGRSPCCEKA-------------HTNRGAWTKEEDERLVAYVRAHGEGCWRSLPRAAGLLRCGKSCRLRWINY   60
VvMYB4a        MGRSPCCEKA-------------HTNKGAWTKEEDDRLIAYIRAHGEGCWRSLPKAAGLLRCGKSCRLRWINY   60
PdMYB221       MGRSPCCEKA-------------HTNKGAWTKEEDDRLIAYIRTHGEGCWRSLPKAAGLLRCGKSCRLRWINY   60
PpMYB17        MGRSPCCEKA-------------HTNKGAWTKEEDDRLIAYIRAHGEGCWRSLPKAAGLLRCGKSCRLRWINY   60
AmMYB308       MGRSPCCEKA-------------HTNKGAWTKEEDDRLVAYIRAHGEGCWRSLPKAAGLLRCGKSCRLRWINY   60
CmMYB1         MGRSPCCEKA-------------HTNKGAWTKEEDDRLIAYIRTHGEGCWRSLPKAAGLLRCGKSCRLRWINY   60
PhMYB4         MGRSPCCEKA-------------HTNKGAWTKEEDERLIAYIKAHGEGCWRSLPKAAGLLRCGKSCRLRWINY   60
SlMYB32        MGRSPCCEKA-------------HTNKGAWTKEEDERLISYIRAHGEGCWRSLPKAAGLLRCGKSCRLRWINY   60
SlMYB7         MGRSPCCEKA-------------HTNKGAWTKEEDERLISYIKTHGEGCWRSLPKAAGLLRCGKSCRLRWINY   60
EgMYB1         MGRSPCCEKA-------------HTNKGAWTKEEDDKLIAYIRAHGEGCWRSLPKAAGLLRCGKSCRLRWINY   60
AtMYB32        MGRSPCCEKD-------------HTNKGAWTKEEDDKLISYIKAHGEGCWRSLPRSAGLQRCGKSCRLRWINY   60
AtMYB7         MGRSPCCEKE-------------HMNKGAWTKEEDERLVSYIKSHGEGCWRSLPRAAGLLRCGKSCRLRWINY   60
AtMYB4         MGRSPCCEKA-------------HTNKGAWTKEEDERLVAYIKAHGEGCWRSLPKAAGLLRCGKSCRLRWINY   60
LlMYB1         MGRSPCCEKA-------------HTNKGAWTKEEDDRLVAYIRAHGEGCWRSLPKAAGLLRCGKSCRLRWINY   60
AtMYB3         MGRSPCCEKA-------------HMNKGAWTKEEDQLLVDYIRKHGEGCWRSLPRAAGLQRCGKSCRLRWMNY   60
PpMYB20        MGRSPCCEKA-------------HTNKGAWTKEEDQRLIDYIRVHGEGCWRSLPKAAGLLRCGKSCRLRWINY   60
SlMYB3         MGRSPCCEKA-------------HTNKGAWTKEEDQRLINYIRAHGEGCWRSLPKAAGLSRCGKSCRLRWINY   60
GbMYBF2        MGRQPCCDKAG-------------LKKGPWTAEEDRKLVNFITTHGEGCWREVPKLAGLLRCGKSCRLRWTNY   60
MdMYB10        -MEGYNENLS--------------VRKGAWTREEDNLLRQCVEIHGEKWNQVSYKAGLNRCRKSCRQRWLNY   58
AtETC2         -----------------------------------MDNTNRLRLRRGPSLRQTKFTRSRYDSEEVSSIEWE--   36
AtTRY          -----------------------------------MDNTDRRRRRK-----QHKIA--LHDSEEVSSIEWE--   29
VvTRY          -----------------------------------MD----RRRRK-----LPKIA-APSQSEEVSSIEWE--   26
SlTRY          -----------------------------------MDQNLHHRHKL----MHHRCC---SHEEEVNSMEWE--   29
AtETC3         -----------------------------------MDNHRRTKQPK----TN-SIVTSSSEGTEVSSLEWE--   31
AtETC1         -----------------------------------MNTQRKSKHLK----TNPTIVASSSE--EVSSLEWE--   30
AtCPC          -------------------------------MFRSDKAEKMDKRRR----RQSKAKASCSE--EVSSIEWE--   34
EcROI1         -----------------------------------MAS-SENSSSDD-YFSTSQE-------VNKKETKV---   26
ElROI1         -----------------------------------MAS-SENSSSDD-YFSTSQE-------VNKKESKV---   26
PhMYBx         -----------------------------------MADKGQSSSSVN-TPADSQDGVAPRMLVSGKTSKVA--   35
SlMYBATV-X1    -----------------------------------MADWNRSSTSDN-ASVVSPDSTRVVA-LETTNEETS--   34
SlMYBATV-X3    -----------------------------------MADWNRSSTSDN-ASVVSPDSTRVVA-LETTNEETS--   34
SlMYBATV-X2    -----------------------------------MADWNRSSTSDN-ASVVSPDSTRVVA-LETTNEETS--   34
GmMYB73        -----------------------------------MADIDR-SFDNN-VSAVSTEKS----------SQVS--   24
SlMYBATV-like  -----------------------------------MADSDSSSTSNY-AFIDSPPFEAK-------KEESL--   28
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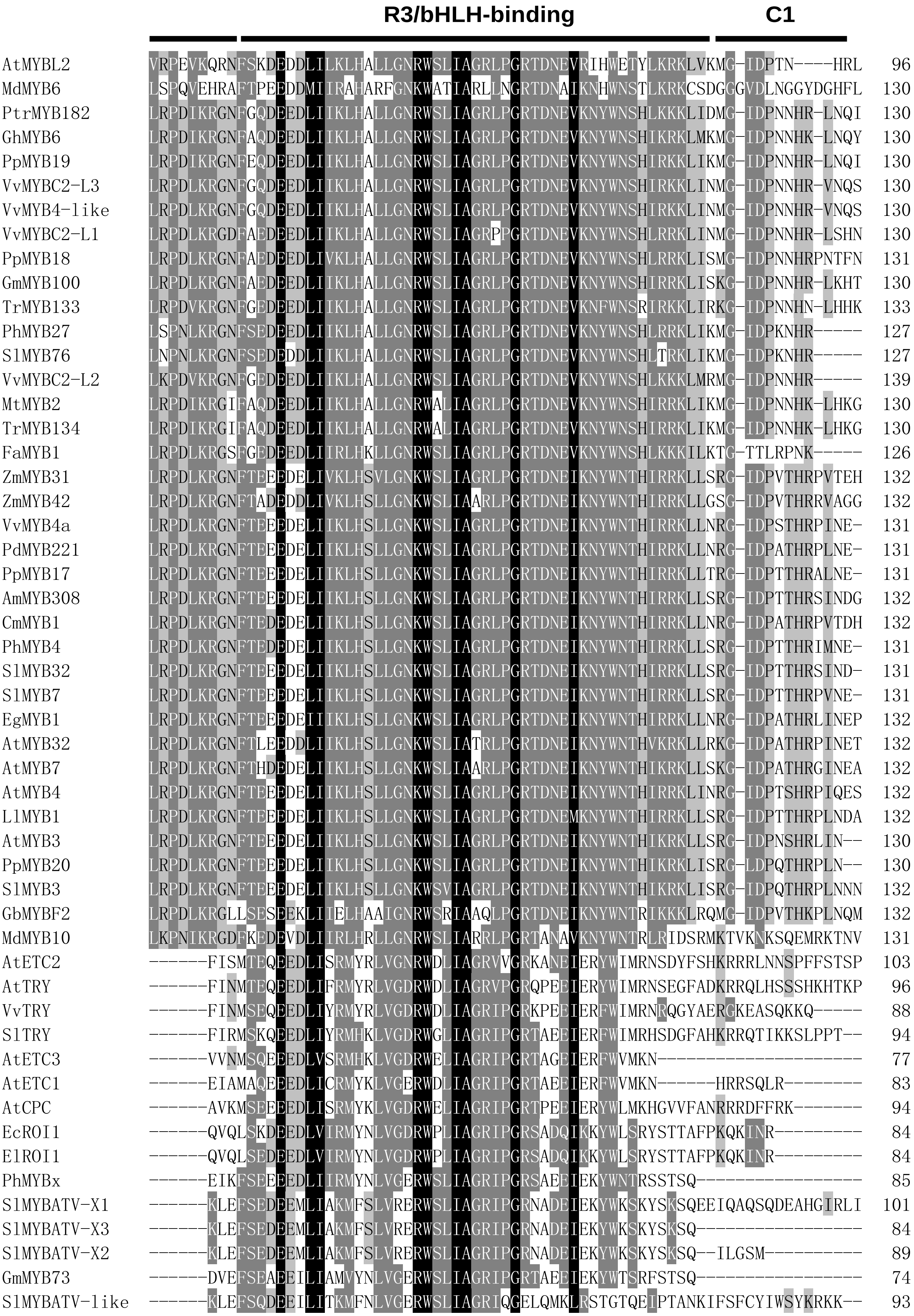

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PtrMYB182       LRPDIKRGNFGQDEEDLIIKLHALLGNRWSLIAGRLPGRTDNEVKNYWNSHLKKKLIDMG-IDPNNHR-LNQI  130
GhMYB6          LRPDIKRGNFAQDEEDLIIKLHALLGNRWSLIAGRLPGRTDNEVKNYWNSHIKRKLMKMG-IDPNNHK-LNQY  130
PpMYB19         LRPDIKRGNFEQDEEDLIIKLHALLGNRWSLIAGRLPGRTDNEVKNYWNSHIRKKLIKMG-IDPNNHR-LNQI  130
VvMYBC2-L3      LRPDLKRGNFGQDEEDLIIKLHALLGNRWSLIAGRLPGRTDNEVKNYWNSHIRKKLINMG-IDPNNHR-VNQS  130
VvMYB4-like     LRPDLKRGNFGQDEEDLIIKLHALLGNRWSLIAGRLPGRTDNEVKNYWNSHIRKKLINMG-IDPNNHR-VNQS  130
VvMYBC2-L1      LRPDLKRGDFAEDEEDLIIKLHALLGNRWSLIAGRPPGRTDNEVKNYWNSHLRRKLINMG-IDPNNHR-LSHN  130
PpMYB18         LRPDLKRGNFAEDEEDLIVKLHALLGNRWSLIAGRLPGRTDNEVKNYWNSHLRRKLISMG-IDPNNHRPNTFN  131
GmMYB100        LRPDLKRGNFAEDEEDLIIKLHALLGNRWSLIAGRLPGRTDNEVKNYWNSHIRRKLISKG-IDPNNHR-LKHT  130
TrMYB133        LRPDVKRGNFGEDEEDLIIKLHALLGNRWSLIAGRLPGRTDNEVKNFWNSRIRKKLIRKG-IDPNNHN-LHHK  133
PhMYB27         LSPNLKRGNFSEDEEDLIIKLHALLGNRWSLIAGRLPGRTDNEVKNYWNSHLRRKLIKMG-IDPKNHR-----  127
SlMYB76         LNPNLKRGNFSEDEDDLIIKLHALLGNRWSLIAGRLPGRTDNEVKNYWNSHLTRKLIKMG-IDPKNHR-----  127
VvMYBC2-L2      LKPDVKRGNFGEDEEDLIIKLHALLGNRWSLIAGRLPGRTDNEVKNYWNSHLKKKLMRMG-IDPNNHR-----  139
MtMYB2          LRPDIKRGIFAQDEEDLIIKLHALLGNRWALIAGRLPGRTDNEVKNYWNSHIRRKLIKMG-IDPNNHK-LHKG  130
TrMYB134        LRPDIKRGIFAQDEEDLIIKLHALLGNRWALIAGRLPGRTDNEVKNYWNSHIRRKLIKMG-IDPNNHK-LHKG  130
FaMYB1          LRPDLKRGSFGEDEEDLIIRLHKLLGNRWSLIAGRLPGRTDNEVKNYWNSHLKKKILKTG-TTLRPNK-----  126
ZmMYB31         LRPDLKRGNFTEEEDELIVKLHSVLGNKWSLIAGRLPGRTDNEIKNYWNTHIRRKLLSRG-IDPVTHRPVTEH  132
ZmMYB42         LRPDLKRGNFTADEDDLIVKLHSLLGNKWSLIAARLPGRTDNEIKNYWNTHIRRKLLGSG-IDPVTHRRVAGG  132
VvMYB4a         LRPDLKRGNFTEEEDELIIKLHSLLGNKWSLIAGRLPGRTDNEIKNYWNTHIRRKLLNRG-IDPSTHRPINE-  131
PdMYB221        LRPDLKRGNFTEEEDELIIKLHSLLGNKWSLIAGRLPGRTDNEIKNYWNTHIRRKLLNRG-IDPATHRPLNE-  131
PpMYB17         LRPDLKRGNFTEEEDELIIKLHSLLGNKWSLIAGRLPGRTDNEIKNYWNTHIRRKLLTRG-IDPTTHRALNE-  131
AmMYB308        LRPDLKRGNFTEEEDELIIKLHSLLGNKWSLIAGRLPGRTDNEIKNYWNTHIRRKLLSRG-IDPTTHRSINDG  132
CmMYB1          LRPDLKRGNFTEDEDELIIKLHSLLGNKWSLIAGRLPGRTDNEIKNYWNTHIRRKLLNRG-IDPATHRPVTDH  132
PhMYB4          LRPDLKRGNFTEDEDELIIKLHSLLGNKWSLIAGRLPGRTDNEIKNYWNTHIRRKLLSRG-IDPTTHRIMNE-  131
SlMYB32         LRPDLKRGNFTEEEDELIIKLHSLLGNKWSLIAGRLPGRTDNEIKNYWNTHIRRKLLSRG-IDPTTHRSIND-  131
SlMYB7          LRPDLKRGNFTEEEDELIIKLHSLLGNKWSLIAGRLPGRTDNEIKNYWNTHIRRKLLSRG-IDPTTHRPVNE-  131
EgMYB1          LRPDLKRGNFTEEEDEIIIKLHSLLGNKWSLIAGRLPGRTDNEIKNYWNTHIRRKLLNRG-IDPATHRLINEP  132
AtMYB32         LRPDLKRGNFTLEEDDLIIKLHSLLGNKWSLIATRLPGRTDNEIKNYWNTHVKRKLLRKG-IDPATHRPINET  132
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AtMYB4          LRPDLKRGNFTEEEDELIIKLHSLLGNKWSLIAGRLPGRTDNEIKNYWNTHIRRKLINRG-IDPTSHRPIQES  132
LlMYB1          LRPDLKRGNFTEEEDELIIKLHSLLGNKWSLIAGRLPGRTDNEMKNYWNTHIRRKLLSRG-IDPTTHRPLNDA  132
AtMYB3          LRPDLKRGNFTEEEDELIIKLHSLLGNKWSLIAGRLPGRTDNEIKNYWNTHIKRKLLSRG-IDPNSHRLIN--  130
PpMYB20         LRPDLKRGNFTEEEDELIIKLHSLLGNKWSLIAGRLPGRTDNEIKNYWNTHIKRKLISRG-LDPQTHRPLN--  130
SlMYB3          LRPDLKRGNFTEEEDELIIKLHSLLGNKWSVIAGRLPGRTDNEIKNYWNTHIKRKLISRG-IDPQTHRPLNNN  132
GbMYBF2         LRPDLKRGLLSESEEKLIIELHAAIGNRWSRIAAQLPGRTDNEIKNYWNTRIKKKLRQMG-IDPVTHKPLNQM  132
MdMYB10         LKPNIKRGDFKEDEVDLIIRLHRLLGNRWSLIARRLPGRTANAVKNYWNTRLRIDSRMKTVKNKSQEMRKTNV  131
AtETC2          ------FISMTEQEEDLISRMYRLVGNRWDLIAGRVVGRKANEIERYWIMRNSDYFSHKRRRLNNSPFFSTSP  103
AtTRY           ------FINMTEQEEDLIFRMYRLVGDRWDLIAGRVPGRQPEEIERYWIMRNSEGFADKRRQLHSSSHKHTKP   96
VvTRY           ------FINMSEQEEDLIYRMYRLVGDRWDLIAGRIPGRKPEEIERFWIMRNRQGYAERGKEASQKKQ-----   88
SlTRY           ------FIRMSKQEEDLIYRMHKLVGDRWGLIAGRIPGRTAEEIERFWIMRHSDGFAHKRRQTIKKSLPPT--   94
AtETC3          ------VVNMSQEEEDLVSRMHKLVGDRWELIAGRIPGRTAGEIERFWVMKN---------------------   77
AtETC1          ------EIAMAQEEEDLICRMYKLVGERWDLIAGRIPGRTAEEIERFWVMKN------HRRSQLR--------   83
AtCPC           ------AVKMSEEEEDLISRMYKLVGDRWELIAGRIPGRTPEEIERYWLMKHGVVFANRRRDFFRK-------   94
EcROI1          ------QVQLSKDEEDLVIRMYNLVGDRWPLIAGRIPGRSADQIKKYWLSRYSTTAFPKQKINR---------   84
ElROI1          ------QVQLSEDEEDLVIRMYNLVGDRWPLIAGRIPGRSADQIKKYWLSRYSTTAFPKQKINR---------   84
PhMYBx          ------EIKFSEEEEDLIIRMYNLVGERWSLIAGRIPGRSAEEIEKYWNTRSSTSQ-----------------   85
SlMYBATV-X1     ------KLEFSEDEEMLIAKMFSLVRERWSLIAGRIPGRNADEIEKYWKSKYSKSQEEIQAQSQDEAHGIRLI  101
SlMYBATV-X3     ------KLEFSEDEEMLIAKMFSLVRERWSLIAGRIPGRNADEIEKYWKSKYSKSQ-----------------   84
SlMYBATV-X2     ------KLEFSEDEEMLIAKMFSLVRERWSLIAGRIPGRNADEIEKYWKSKYSKSQ--ILGSM----------   89
GmMYB73         ------DVEFSEAEEILIAMVYNLVGERWSLIAGRIPGRTAEEIEKYWTSRFSTSQ-----------------   74
SlMYBATV-like   ------KLEFSQDEEILITKMFNLVGERWSLIAGRIQGELQMKLRSTGTQEIPTANKIFSFCYIWSYKRKK--   93
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MdMYB6         RDHEQPPLKRSVSAGSGVPVSTGLYMSPGSPSGSDASDSSAQVMSLSDCHVYRPL------------------  185
PtrMYB182      LPRLQAEP-AAPVIATST----------------TTGSKNNVAASKPKNLSD---------------------  165
GhMYB6         P--HHVGP-LSPITTNSM----------------DVACKLRVFSTE---------------------------  157
PpMYB19        IPRPNPQNDCVSAAATSS----------------GSMSNISACTKAPIKSSR---------------------  166
VvMYBC2-L3     F----AAPLNRCASAATM----------------SSGSMTGACDNKSLKPS----------------------  161
VvMYB4-like    F----AAPLNRCASAATM----------------SSGSMTGACDNKSLKPS----------------------  161
VvMYBC2-L1     FPRPRDPCTAATAT--------------------SSGLNNHAS-PPVKS-VG---------------------  160
PpMYB18        LPRPHHKNSQAISSTAKL----------------SAGLKTPTNDQPARS-GG---------------------  166
GmMYB100       IPSS--LQNSLMSDDSSK----------------AFSMKDTNKNETSKLPRV---------------------  164
TrMYB133       IPP---LQNQIMSN-SLK----------------YFGLKEISKNETTKT-HL---------------------  164
PhMYB27        -----------ISHYLH------------------RKRLEYWSENSS---RG---------------------  147
SlMYB76        -----------LSHYLH------------------IKRLELLQENNT---RL---------------------  147
VvMYBC2-L2     -----------LGERASG----------------TSKSFESRDQTSNPLISA---------------------  164
MtMYB2         FPT---------VGTSS------------------CVESMNKENNKLS-IKS---------------------  154
TrMYB134       FPSP---HHVFAAGTSSS----------------SCDKERNINNLTLIKSKS---------------------  163
FaMYB1         -----------------------------------PHENNHAPNNKLVKLFN---------------------  143
ZmMYB31        HASNITISFETEVAAAARDD--------------KKGAVFRLEEEEERNKAT---------------------  170
ZmMYB42        AATTISFQPSPNTAVAAAAE--------------TAAQAPIKAEETAAVKAP---------------------  170
VvMYB4a        PSPDV--TTISFA-----------------------AAVKEE-EKINISSTG---------------------  157
PdMYB221       PAQEAS-TTISFSTTTSVKEE-------------SLSSVKEESNKEKIISAA---------------------  169
PpMYB17        AAQDSATTTISFAAS---------------------ANIKEEDQKSSIIN-----------------------  160
AmMYB308       TASQDQVTTISFSNANSKE---------------EDTKHKVAVDIMIKEE-----------------------  167
CmMYB1         PTTTTTTTTTVATTVNNNHNVTSPPPDIISFATTKTTDHVVKNEDMEQETK----------------------  183
PhMYB4         PSTQ-KVTTISFAAGNEDIK---------------DQKISIKAEFEQIK------------------------  164
SlMYB32        PTTIPKVTTITFAAAHENIKDIDQ----------QDEMINIKAEFVETSKES---------------------  173
SlMYB7         PGTTQKVTTISFAGGDHKTKDIEED---------HNKMINVKAESGLSQ------------------------  171
EgMYB1         AQDHHDEPTISFAANSKE-----------------IKEMKNNAELNFMCN-----------------------  165
AtMYB32        KTSQDSSDSSKTEDPLVK----ILSFG---PQLEKIANFG--DERIQKRV-----------------------  173
AtMYB7         KIS----DLKKTKDQIVK----DVSFV---TKFEETDKSG--DQKQNKYIRN---------------------  171
AtMYB4         SASQ---DSKPTQLEPVTSNTINISFTS-APKVETFHESISFPGKSEKISML---------------------  180
LlMYB1         SQNQSHASSASAAKQHDS------------------EILITDTDANSKRP-----------------------  164
AtMYB3         --ESVVSPSSLQNDVVETIH-------------LDFSGPVKPEPVREEIG---------MVNNCES-------  172
PpMYB20        --DTTTAAAAAA-ATTPASR-------------LDFRNISPPSAVVDKTTNKNSILHHKTINKTSSNNNNHNS  187
SlMYB3         ATNSHTTTNITTAVTTKNIN-------------LDFTNVDQKQPNIMIATSS-------SYDETKCN------  179
GbMYBF2        QMDYMIRPHAPMNAEENNKFEP------------PLEPENVAEASSPENIRG---------------------  172
MdMYB10        IRPQPQKFNRSSYYLSSKEP-----------ILDHIQSAEDLSTPPQTSSSTK--------------------  173
AtETC2         LNLQENLKL----------------------------------------------------------------  112
AtTRY          HRPRFSIYPS---------------------------------------------------------------  106
VvTRY          -------------------------------------------------------------------------    -
SlTRY          -------------------------------------------------------------------------    -
AtETC3         -------------------------------------------------------------------------    -
AtETC1         -------------------------------------------------------------------------    -
AtCPC          -------------------------------------------------------------------------    -
EcROI1         -------------------------------------------------------------------------    -
ElROI1         -------------------------------------------------------------------------    -
PhMYBx         -------------------------------------------------------------------------    -
SlMYBATV-X1    EKTGPSTGHPQQCVFPEKKPISVCQPSDIGPQLLGPTTNGPQQLLGPKTTGPNNITVDQKLVNPAQDQINQ--  172
SlMYBATV-X3    -------------------------------------------------------------------------    -
SlMYBATV-X2    -------------------------------------------------------------------------    -
GmMYB73        -------------------------------------------------------------------------    -
SlMYBATV-like  -------------------------------------------------------------------------    -
```

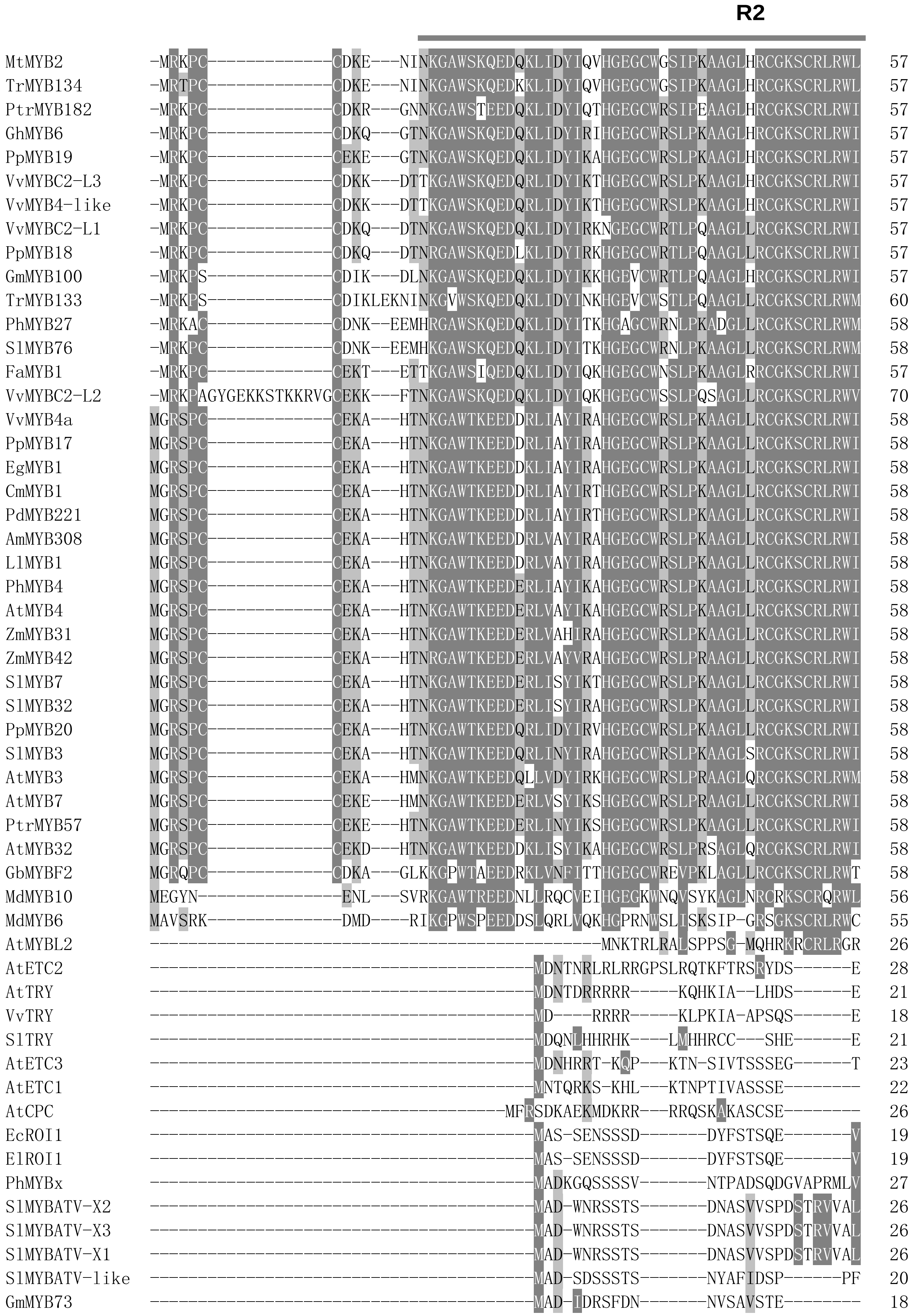
C2/EAR

```
AtMYBL2         -------------ESCGVTILPIPSTNCSEDSTSTG------RSHLPDLNIGL-IPAVTS-------------  168
MdMYB6          -------------ARTGGVLPPAETTSSSNNNSSNS------EKNDPPTSLSLSLPGVDSEEVS---------  230
PtrMYB182       ----------------GDSDRVSDTATCLEDDYESLVTQQAATSGSSSINIDLNIAAPASPGHR---------  213
GhMYB6          -----------------NDDGVSDAASYLEDETP--------PTGVSNLDLDLTIAFPSSP-IK---------  195
PpMYB19         ----------------EIDQRASQATSVLEDETS--------GSSSRDLNLDLTIAFPNPPLLV---------  206
VvMYBC2-L3      ----------------ADNDPLSDSASGLEDEIS----------ASLDLNLDLTIAIPASS-LT---------  198
VvMYB4-like     ----------------ADNDPLSDSASGLEDEIS----------ASLDLNLDLTIAIPASS-LT---------  198
VvMYBC2-L1      ----------------DN-DQTSDAGSCLDDN----------RRALPDLNLDVAITIPQPS--V---------  195
PpMYB18         ----------------NNCDQVSDGTSCLEDESC--------GHQLPDLNLDLTMTAPLSNSEP---------  206
GmMYB100        ----------------YNHVEVSDAASGEAES----------PCALPDLNLDLSITNPSAS-QS---------  201
TrMYB133        ----------------DNYDKVSNATSGNKDE----------SYALLDLNLELSL------------------  193
PhMYB27         ----------------TDHEVVSDAGSSCAKHQ---------PSSLPDLNS-----PPSIH------------  178
SlMYB76         ----------------ENVGVISDATSSYANKDQQI------TSSLLDLNL-----IP---------------  178
VvMYBC2-L2      ----------------ADNNAVLDSTCGSASKT---------TSSLPDLNLNLNVGAPSVD------------  200
MtMYB2          ----------------CDAP-INNDVSFTKKDTT------SIINSSSSLNLDLTIALPSPNR-----------  193
TrMYB134        ----------------CEEEYINSSVSFTKKETS------IINNSSSSLNLELTIALPSPN------------  202
FaMYB1          ----------------KMDDEVVDEVSSADSAAG---------CLVPELNLDLTLSIKTST------------  179
ZmMYB31         ----------------MVVGRDRQSQSQSHSHPAGEWGQGKRPLKCPDLNLDLCISPPCQEE----EEMEEAA  223
ZmMYB42         --------------------------------------------RCPDLNLDLCISPPCQHEDDGEEEEEELD  199
VvMYB4a         ----------------GFGCKTEKNPVTEKC---------------PDLNLELRISPPY--Q-------PQAE  190
PdMYB221        ----------------AFICKEEKTPVQERC---------------PDLNLELRISLPCQNQ-------PDRH  204
PpMYB17         ----------------GLLGKDSKKPVQERC---------------PDLNLELQISPPCQ-P-------QQPS  194
AmMYB308        ---------------------NSP--VQERC---------------PDLNLDLKISPPCQQQ------INYHQ  196
CmMYB1          ------------------LNITSPDQKQERC---------------PDLNLELRIGPPQHHSSNMIPSISYMQ  223
PhMYB4          -----------------DDEIISK-PIKEQC---------------PDLNLELKISPPYQQH-------SDRA  197
SlMYB32         ----------------DNNEIIQE-KSSSCL---------------PDLNLELRISPPHHQQ-------LDHH  207
SlMYB7          ----------------LEDEIISSSPFREQC---------------PDLNLELRISPPSLQN-------YQHS  206
EgMYB1          ----------------LEESADVASSARERC---------------PDLNLELGISPPSHQL-------HQPE  200
AtMYB32         ----------------------EYSVVEERC---------------LDLNLELRISPPWQDKL----------  199
AtMYB7          ----------------GLVCKEERVVVEEKIG--------------PDLNLELRISPPWQNQ-----------  203
AtMYB4          ----------------TFKEEKDECPVQEKF---------------PDLNLELRISLPDDVDR----------  212
LlMYB1          -------------------------GVFEVC---------------PDLNLELTISLPHHHQ-----------  186
AtMYB3          ------------------SGTTSEKDYGNEED--------------WVLNLELSVGPS-YRYES-----TRKV  207
PpMYB20         NIVLFKPKMEEDNIEEASSGTTTEEDQQQQQQQQQQKLQDHYMYKCSDLNLDLSIGLEPFQSEP-----TRAS  255
SlMYB3          ------------------SGTTEETKPLEIIIPKIP--------SQVMINLELSIGLPLHTDHI-----SSPE  221
GbMYBF2         ----------------PDEEMGMNMPACSSLESLEIDLPLRMEDSMPLLNLCLPISVISLPGRTEEVDSDDSN  229
MdMYB10         ----------------NGNDWWETLLEGEDTFER---------AAYPSIELEEELFTSFWFDDR---------  212
AtETC2          -------------------------------------------------------------------------    -
AtTRY           -------------------------------------------------------------------------    -
VvTRY           -------------------------------------------------------------------------    -
SlTRY           -------------------------------------------------------------------------    -
AtETC3          -------------------------------------------------------------------------    -
AtETC1          -------------------------------------------------------------------------    -
AtCPC           -------------------------------------------------------------------------    -
EcROI1          -------------------------------------------------------------------------    -
ElROI1          -------------------------------------------------------------------------    -
PhMYBx          -------------------------------------------------------------------------    -
SlMYBATV-X1     -------------------------------------------------------------------------    -
SlMYBATV-X3     -------------------------------------------------------------------------    -
SlMYBATV-X2     -------------------------------------------------------------------------    -
GmMYB73         -------------------------------------------------------------------------    -
SlMYBATV-like   -------------------------------------------------------------------------    -
```

```
AtMYBL2         ------------------LPALCLQDSSESSTNGSTGQETLLLFR----------------------------  195
MdMYB6          ------------------NQVAPVTESTQAPAPAPVSTTSVAVQNIPVELLAVMQGMIRKEVRNYMAGLEQSG  285
PtrMYB182       -------------------TTFGNNQQNCKWGKTSQVERDPSSL-----------------------------  238
GhMYB6          -------------------NIIEESQQKTASIVTNDEE-EQYTV-----------------------------  219
PpMYB19         -------------------GEEMQKNIKGSFTMAREIETNLQHS-----------------------------  231
VvMYBC2-L3      -------------------DVIDKKRQDTKSIFSREVEGDAN-------------------------------  221
VvMYB4-like     -------------------DVIDKKRQDTKSIFSREVEGDAN-------------------------------  221
VvMYBC2-L1      -------------------DTTEEAKKHNEPKVSRELEPGPS-------------------------------  218
PpMYB18         -------------------ENLKEEQNLMSLKCHRNLPRPPI-------------------------------  229
GmMYB100        -------------------ISGNNVKPFHESNSSRKVQFDSP-------------------------------  224
TrMYB133        -------------------------------------------------------------------------    -
PhMYB27         -----------------------SSCAQP--------------------------------------------  184
SlMYB76         -------------------------------------------------------------------------    -
VvMYBC2-L2      -----------------------EQMQLTGANSHKELEPAPF-------------------------------  219
MtMYB2          -----------------------IVIPNCESPKTRDMDIDLNC------------------------------  213
TrMYB134        ---------------------------DCESPKIRDIDIDLNC------------------------------  218
FaMYB1          ------------------------------GMADPQVA-----------------------------------  187
ZmMYB31         MRVRPAVKREA---------GLCFGCSLGLPR-TADCKCSS------------------------SSFLGLR-  261
ZmMYB42         LIKPAVVKREALQAGHGHGHGLCLGCGLGGQKGAAGCSCSNG-----------------------HHFLGLR-  248
VvMYB4a         TPLKTGGRSSS--------TTLCFACSLGIPN-SEECSCS------------IGTSSGS--SSSGYDFLGL--  238
PdMYB221        QAFKTGG---S--------TSLCFACSLGLQN-SKDCSCSVIVG-------TIGSSSSAG-SKTGYDFLGM--  255
PpMYB17         EPLKSGG------------RGVCFSCSLGLQD-AKNCSCG--ID-------TIGSSTTSGTTNVGYDFLGL--  243
AmMYB308        ENLKTGGRNGS--------STLCFVCRLGIQN-SKDCSCSDG--------------VGN--------------  232
CmMYB1          QPLMTGG-------------TICFACSLGVQD-NKECRCSTNGT------------SGNNNSNVGFDFFKI--  268
PhMYB4          LQQSTTGSGGA--------STICFTCSLGLKN-NKGCSCSRNR---------------SMN-VAGYDFLGLK-  244
SlMYB32         RHHQRS-------------SSLCFTCSLGIQN-SKDCSCGSESNGN-----GWSNNMVSMNIMAGYDFLGLK-  260
SlMYB7          -------------------PSRCFACSLGIQN-SKDCNCSKNN-------------------IASYNFLGLK-  239
EgMYB1          PLLRFTGR--K--------SDLCXECNLGLKN-SQNCRCSVG--------------VIESETSVGYDFLGL--  246
AtMYB32         HDERNLRFGRV--------KYRCSACRFGFGN-GKECSCNNVKCQTEDSSSSSYSSTDISSS-IGYDFLGLNN  262
AtMYB7          ---------RE--------ISTCTASRFYMEN-DMECSSETVKCQTENSSSISYSSIDISSSNVGYDFLGLK-  257
AtMYB4          LQGHG---KST--------TPRCFKCSLGMIN-GMECRCGRMRCDVVGGSS---KGSDMSNG---FDFLGLAK  267
LlMYB1          -------------------HQQPDQISLKSIN-SESSTAGDG-----------------------FDFLESK-  215
AtMYB3          SVVDSAESTRR-------WGSELFG----AHESDAVCLCCRIG------------------------LFRNES  245
PpMYB20         SGNSAESRLQQ-------NNYQVFGTVHKAGVTQAVCLCCQVG------------------------FQSSDA  297
SlMYB3          STASYNFLTTV-------APPPTAAVPAAEMMAKTVCLCWQIG------------------------YHGGGG  263
GbMYBF2         IVDQVN-------------NPLSDSHKNNANNNMTTSCCSFNNGGN---IHSRSSDIKAETPSLWGDQMGVLG  286
MdMYB10         ---------------------LSPRSCANFPEGQSRSEFSFS-------------------------------  233
AtETC2          -------------------------------------------------------------------------    -
AtTRY           -------------------------------------------------------------------------    -
VvTRY           -------------------------------------------------------------------------    -
SlTRY           -------------------------------------------------------------------------    -
AtETC3          -------------------------------------------------------------------------    -
AtETC1          -------------------------------------------------------------------------    -
AtCPC           -------------------------------------------------------------------------    -
EcROI1          -------------------------------------------------------------------------    -
ElROI1          -------------------------------------------------------------------------    -
PhMYBx          -------------------------------------------------------------------------    -
SlMYBATV-X1     -------------------------------------------------------------------------    -
SlMYBATV-X3     -------------------------------------------------------------------------    -
SlMYBATV-X2     -------------------------------------------------------------------------    -
GmMYB73         -------------------------------------------------------------------------    -
SlMYBATV-like   -------------------------------------------------------------------------    -
```

```
                  TLLLFR
AtMYBL2        ------------------------------------------------------------     -
MdMYB6         VCFQQAAAGNEGFWNVGVKRIGFSRIE---------------------------------   312
PtrMYB182      ---PTLLLFR--------------------------------------------------   245
GhMYB6         ---PTLLLFR--------------------------------------------------   226
PpMYB19        ---PTLALFR--------------------------------------------------   238
VvMYBC2-L3     ---PTLILFR--------------------------------------------------   228
VvMYB4-like    ---PTLILFR--------------------------------------------------   228
VvMYBC2-L1     ---STLLLFG--------------------------------------------------   225
PpMYB18        ---SFLS-----------------------------------------------------   233
GmMYB100       ---STLLLFQ--------------------------------------------------   231
TrMYB133       ------------------------------------------------------------     -
PhMYB27        ------------------------------------------------------------     -
SlMYB76        ------------------------------------------------------------     -
VvMYBC2-L2     ---TTLLLFG--------------------------------------------------   226
MtMYB2         ------------------------------------------------------------     -
TrMYB134       ------------------------------------------------------------     -
FaMYB1         ------------------------------------------------------------     -
ZmMYB31        ---TAMLDFRSLEMK---------------------------------------------   273
ZmMYB42        ---TSVLDFRGLEMK---------------------------------------------   260
VvMYB4a        --TSGVLDYRGLEMK---------------------------------------------   251
PdMYB221       --KSGVLDYRGLEMK---------------------------------------------   268
PpMYB17        --KSGVLDYRSLEMK---------------------------------------------   256
AmMYB308       ------------------------------------------------------------     -
CmMYB1         --KNGALDYRSLEMK---------------------------------------------   281
PhMYB4         --TNG-LDYRTLETRTK-------------------------------------------   258
SlMYB32        --TNGLLDYRTLETK---------------------------------------------   273
SlMYB7         --SNGVLDYRTLETK---------------------------------------------   252
EgMYB1         --KASVLDYRS-------------------------------------------------   255
AtMYB32        ---TRVLDFSTLEMK---------------------------------------------   274
AtMYB7         ---TRILDFRSLEMK---------------------------------------------   269
AtMYB4         KETTSLLGFRSLEMK---------------------------------------------   282
LlMYB1         ---SSVLDCRSSVTQIDWRALTE-------------------------------------   235
AtMYB3         --CRNCRVSD--VRTH--------------------------------------------   257
PpMYB20        --CRNCQCTNGFYRFHRPLNS---------------------------------------   316
SlMYB3         QWCGKCKNTNGFYRYC--------------------------------------------   279
GbMYBF2        DPISDYLQWNDLELWSAGLDAASGWIQQLPECNWSEMQGDIEISSNCPELQRLASILDEM   346
MdMYB10        ---TDLWNHSKEE-----------------------------------------------   243
AtETC2         ------------------------------------------------------------     -
AtTRY          ------------------------------------------------------------     -
VvTRY          ------------------------------------------------------------     -
SlTRY          ------------------------------------------------------------     -
AtETC3         ------------------------------------------------------------     -
AtETC1         ------------------------------------------------------------     -
AtCPC          ------------------------------------------------------------     -
EcROI1         ------------------------------------------------------------     -
ElROI1         ------------------------------------------------------------     -
PhMYBx         ------------------------------------------------------------     -
SlMYBATV-X1    ------------------------------------------------------------     -
SlMYBATV-X3    ------------------------------------------------------------     -
SlMYBATV-X2    ------------------------------------------------------------     -
GmMYB73        ------------------------------------------------------------     -
SlMYBATV-like  ------------------------------------------------------------     -
```

Fig. S3 Multiple sequence alignment of MYB flavonoid repressor based on its full-length proteins. Entire protein sequences were aligned by using Clustal X ver. 2 (Larkin *et al.*, 2007) with default settings, and the conserved amino acids were shaded by using GeneDoc (2.6) (Nicholas *et al.*, 1997). The R2, R3/bHLH-binding, C1, C2/EAR, and TLLLFR domains (or motifs) are marked above the alignment.



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MtMYB2          -MRKPC-------------CDKE---NINKGAWSKQEDQKLIDYIQVHGEGCWGSIPKAAGLHRCGKSCRLRWL   57
TrMYB134        -MRTPC-------------CDKE---NINKGAWSKQEDKKLIDYIQVHGEGCWGSIPKAAGLHRCGKSCRLRWL   57
PtrMYB182       -MRKPC-------------CDKR---GNNKGAWSTEEDQKLIDYIQTHGEGCWRSIPEAAGLHRCGKSCRLRWI   57
GhMYB6          -MRKPC-------------CDKQ---GTNKGAWSKQEDQKLIDYIRIHGEGCWRSLPKAAGLHRCGKSCRLRWI   57
PpMYB19         -MRKPC-------------CEKE---GTNKGAWSKQEDQKLIDYIKAHGEGCWRSLPKAAGLHRCGKSCRLRWI   57
VvMYBC2-L3      -MRKPC-------------CDKK---DTTKGAWSKQEDQRLIDYIKTHGEGCWRSLPKAAGLHRCGKSCRLRWI   57
VvMYB4-like     -MRKPC-------------CDKK---DTTKGAWSKQEDQRLIDYIKTHGEGCWRSLPKAAGLHRCGKSCRLRWI   57
VvMYBC2-L1      -MRKPC-------------CDKQ---DTNKGAWSKQEDQKLIDYIRKNGEGCWRTLPQAAGLLRCGKSCRLRWI   57
PpMYB18         -MRKPC-------------CDKQ---DTNRGAWSKQEDLKLIDYIRKHGEGCWRTLPQAAGLLRCGKSCRLRWI   57
GmMYB100        -MRKPS-------------CDIK---DLNKGAWSKQEDQKLIDYIKKHGEVCWRTLPQAAGLHRCGKSCRLRWI   57
TrMYB133        -MRKPS-------------CDIKLEKNINKGVWSKQEDQKLIDYINKHGEVCWSTLPQAAGLLRCGKSCRLRWM   60
PhMYB27         -MRKAC-------------CDNK--EEMHRGAWSKQEDQKLIDYITKHGAGCWRNLPKADGLLRCGKSCRLRWM   58
SlMYB76         -MRKPC-------------CDNK--EEMHKGAWSKQEDQKLIDYITKHGEGCWRNLPKAAGLLRCGKSCRLRWM   58
FaMYB1          -MRKPC-------------CEKT---ETTKGAWSIQEDQKLIDYIQKHGEGCWNSLPKAAGLRRCGKSCRLRWI   57
VvMYBC2-L2      -MRKPAGYGEKKSTKKRVGCEKK---FTNKGAWSKQEDQKLIDYIQKHGEGCWSSLPQSAGLLRCGKSCRLRWV   70
VvMYB4a         MGRSPC-------------CEKA---HTNKGAWTKEEDDRLIAYIRAHGEGCWRSLPKAAGLLRCGKSCRLRWI   58
PpMYB17         MGRSPC-------------CEKA---HTNKGAWTKEEDDRLIAYIRAHGEGCWRSLPKAAGLLRCGKSCRLRWI   58
EgMYB1          MGRSPC-------------CEKA---HTNKGAWTKEEDDKLIAYIRAHGEGCWRSLPKAAGLLRCGKSCRLRWI   58
CmMYB1          MGRSPC-------------CEKA---HTNKGAWTKEEDDRLIAYIRTHGEGCWRSLPKAAGLLRCGKSCRLRWI   58
PdMYB221        MGRSPC-------------CEKA---HTNKGAWTKEEDDRLIAYIRTHGEGCWRSLPKAAGLLRCGKSCRLRWI   58
AmMYB308        MGRSPC-------------CEKA---HTNKGAWTKEEDDRLVAYIRAHGEGCWRSLPKAAGLLRCGKSCRLRWI   58
LlMYB1          MGRSPC-------------CEKA---HTNKGAWTKEEDDRLVAYIRAHGEGCWRSLPKAAGLLRCGKSCRLRWI   58
PhMYB4          MGRSPC-------------CEKA---HTNKGAWTKEEDERLIAYIKAHGEGCWRSLPKAAGLLRCGKSCRLRWI   58
AtMYB4          MGRSPC-------------CEKA---HTNKGAWTKEEDERLVAYIKAHGEGCWRSLPKAAGLLRCGKSCRLRWI   58
ZmMYB31         MGRSPC-------------CEKA---HTNKGAWTKEEDERLVAHIRAHGEGCWRSLPKAAGLLRCGKSCRLRWI   58
ZmMYB42         MGRSPC-------------CEKA---HTNRGAWTKEEDERLVAYVRAHGEGCWRSLPRAAGLLRCGKSCRLRWI   58
SlMYB7          MGRSPC-------------CEKA---HTNKGAWTKEEDERLISYIKTHGEGCWRSLPKAAGLLRCGKSCRLRWI   58
SlMYB32         MGRSPC-------------CEKA---HTNKGAWTKEEDERLISYIRAHGEGCWRSLPKAAGLLRCGKSCRLRWI   58
PpMYB20         MGRSPC-------------CEKA---HTNKGAWTKEEDQRLIDYIRVHGEGCWRSLPKAAGLLRCGKSCRLRWI   58
SlMYB3          MGRSPC-------------CEKA---HTNKGAWTKEEDQRLINYIRAHGEGCWRSLPKAAGLSRCGKSCRLRWI   58
AtMYB3          MGRSPC-------------CEKA---HMNKGAWTKEEDQLLVDYIRKHGEGCWRSLPRAAGLQRCGKSCRLRWM   58
AtMYB7          MGRSPC-------------CEKE---HMNKGAWTKEEDERLVSYIKSHGEGCWRSLPRAAGLLRCGKSCRLRWI   58
PtrMYB57        MGRSPC-------------CEKE---HTNKGAWTKEEDERLINYIKSHGEGCWRSLPKAAGLLRCGKSCRLRWI   58
AtMYB32         MGRSPC-------------CEKD---HTNKGAWTKEEDDKLISYIKAHGEGCWRSLPRSAGLQRCGKSCRLRWI   58
GbMYBF2         MGRQPC-------------CDKA---GLKKGPWTAEEDRKLVNFITTHGEGCWREVPKLAGLLRCGKSCRLRWT   58
MdMYB10         MEGYN---------------ENL---SVRKGAWTREEDNLLRQCVEIHGEGKWNQVSYKAGLNRCRKSCRQRWL   56
MdMYB6          MAVSRK--------------DMD----RIKGPWSPEEDDSLQRLVQKHGPRNWSLISKSIP-GRSGKSCRLRWC   55
AtMYBL2         -----------------------------------------------MNKTRLRALSPPSG-MQHRKRCRLRGR   26
AtETC2          ----------------------------------------MDNTNRLRLRRGPSLRQTKFTRSRYDS------E   28
AtTRY           ----------------------------------------MDNTDRRRRR-----KQHKIA--LHDS------E   21
VvTRY           ----------------------------------------MD----RRRR-----KLPKIA-APSQS------E   18
SlTRY           ----------------------------------------MDQNLHHRHK----LMHHRCC---SHE------E   21
AtETC3          ----------------------------------------MDNHRRT-KQP---KTN-SIVTSSSEG------T   23
AtETC1          ----------------------------------------MNTQRKS-KHL---KTNPTIVASSSE--------   22
AtCPC           -------------------------------------MFRSDKAEKMDKRR---RRQSKAKASCSE--------   26
EcROI1          ----------------------------------------MAS-SENSSSD-------DYFSTSQE-------V   19
ElROI1          ----------------------------------------MAS-SENSSSD-------DYFSTSQE-------V   19
PhMYBx          ----------------------------------------MADKGQSSSSV-------NTPADSQDGVAPRMLV   27
SlMYBATV-X2     ----------------------------------------MAD-WNRSSTS-------DNASVVSPDSTRVVAL   26
SlMYBATV-X3     ----------------------------------------MAD-WNRSSTS-------DNASVVSPDSTRVVAL   26
SlMYBATV-X1     ----------------------------------------MAD-WNRSSTS-------DNASVVSPDSTRVVAL   26
SlMYBATV-like   ----------------------------------------MAD-SDSSSTS-------NYAFIDSP------PF   20
GmMYB73         ----------------------------------------MAD-IDRSFDN-------NVSAVSTE--------   18
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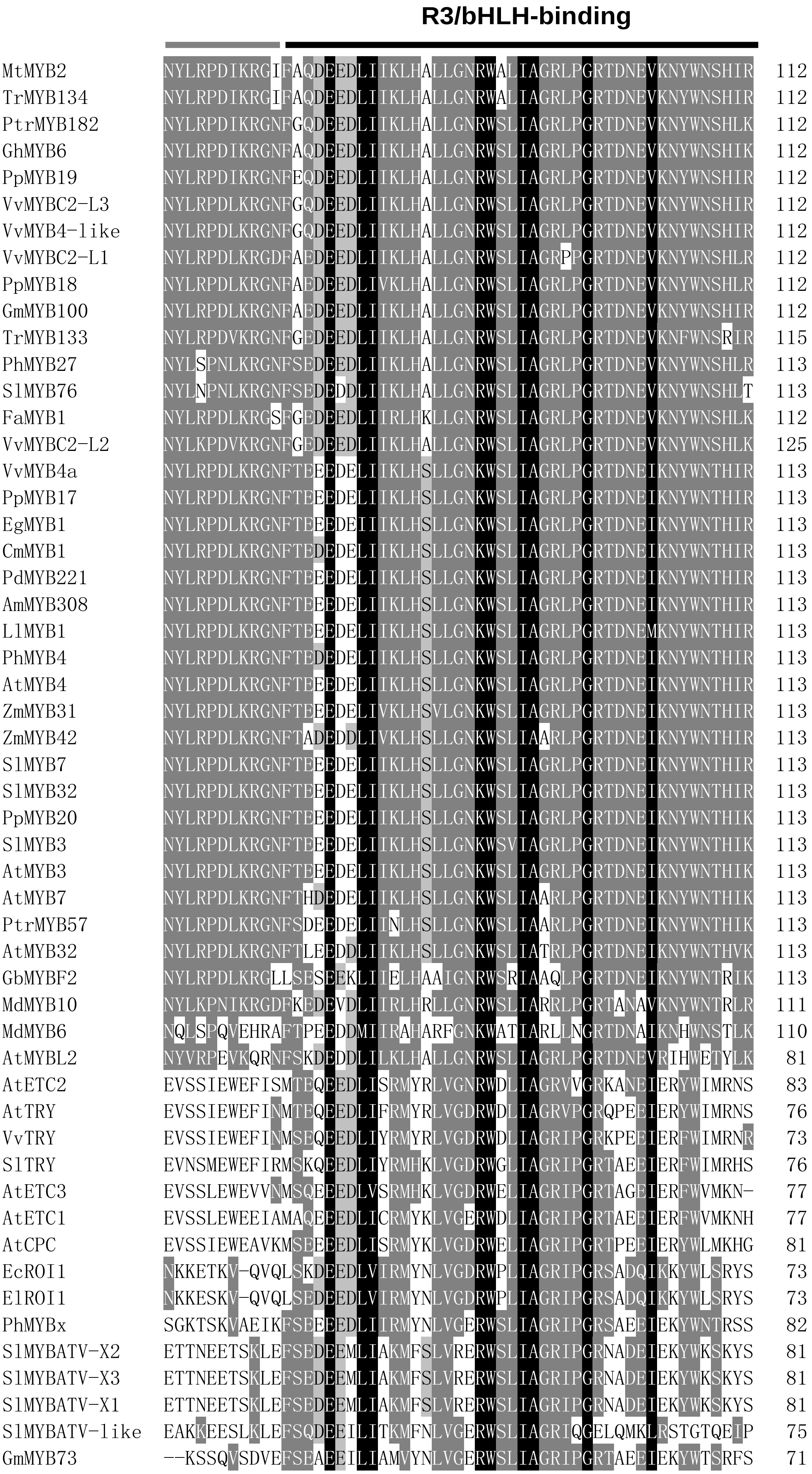

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MtMYB2         NYLRPDIKRGIFAQDEEDLIIKLHALLGNRWALIAGRLPGRTDNEVKNYWNSHIR  112
TrMYB134       NYLRPDIKRGIFAQDEEDLIIKLHALLGNRWALIAGRLPGRTDNEVKNYWNSHIR  112
PtrMYB182      NYLRPDIKRGNFGQDEEDLIIKLHALLGNRWSLIAGRLPGRTDNEVKNYWNSHLK  112
GhMYB6         NYLRPDIKRGNFAQDEEDLIIKLHALLGNRWSLIAGRLPGRTDNEVKNYWNSHIK  112
PpMYB19        NYLRPDIKRGNFEQDEEDLIIKLHALLGNRWSLIAGRLPGRTDNEVKNYWNSHIR  112
VvMYBC2-L3     NYLRPDLKRGNFGQDEEDLIIKLHALLGNRWSLIAGRLPGRTDNEVKNYWNSHIR  112
VvMYB4-like    NYLRPDLKRGNFGQDEEDLIIKLHALLGNRWSLIAGRLPGRTDNEVKNYWNSHIR  112
VvMYBC2-L1     NYLRPDLKRGDFAEDEEDLIIKLHALLGNRWSLIAGRPPGRTDNEVKNYWNSHLR  112
PpMYB18        NYLRPDLKRGNFAEDEEDLIVKLHALLGNRWSLIAGRLPGRTDNEVKNYWNSHLR  112
GmMYB100       NYLRPDLKRGNFAEDEEDLIIKLHALLGNRWSLIAGRLPGRTDNEVKNYWNSHIR  112
TrMYB133       NYLRPDVKRGNFGEDEEDLIIKLHALLGNRWSLIAGRLPGRTDNEVKNFWNSRIR  115
PhMYB27        NYLSPNLKRGNFSEDEEDLIIKLHALLGNRWSLIAGRLPGRTDNEVKNYWNSHLR  113
SlMYB76        NYLNPNLKRGNFSEDEDDLIIKLHALLGNRWSLIAGRLPGRTDNEVKNYWNSHLT  113
FaMYB1         NYLRPDLKRGSFGEDEEDLIIRLHKLLGNRWSLIAGRLPGRTDNEVKNYWNSHLK  112
VvMYBC2-L2     NYLKPDVKRGNFGEDEEDLIIKLHALLGNRWSLIAGRLPGRTDNEVKNYWNSHLK  125
VvMYB4a        NYLRPDLKRGNFTEEEDELIIKLHSLLGNKWSLIAGRLPGRTDNEIKNYWNTHIR  113
PpMYB17        NYLRPDLKRGNFTEEEDELIIKLHSLLGNKWSLIAGRLPGRTDNEIKNYWNTHIR  113
EgMYB1         NYLRPDLKRGNFTEEEDEIIIKLHSLLGNKWSLIAGRLPGRTDNEIKNYWNTHIR  113
CmMYB1         NYLRPDLKRGNFTEDEDELIIKLHSLLGNKWSLIAGRLPGRTDNEIKNYWNTHIR  113
PdMYB221       NYLRPDLKRGNFTEEEDELIIKLHSLLGNKWSLIAGRLPGRTDNEIKNYWNTHIR  113
AmMYB308       NYLRPDLKRGNFTEEEDELIIKLHSLLGNKWSLIAGRLPGRTDNEIKNYWNTHIR  113
LlMYB1         NYLRPDLKRGNFTEEEDELIIKLHSLLGNKWSLIAGRLPGRTDNEMKNYWNTHIR  113
PhMYB4         NYLRPDLKRGNFTEDEDELIIKLHSLLGNKWSLIAGRLPGRTDNEIKNYWNTHIR  113
AtMYB4         NYLRPDLKRGNFTEEEDELIIKLHSLLGNKWSLIAGRLPGRTDNEIKNYWNTHIR  113
ZmMYB31        NYLRPDLKRGNFTEEEDELIVKLHSVLGNKWSLIAGRLPGRTDNEIKNYWNTHIR  113
ZmMYB42        NYLRPDLKRGNFTADEDDLIVKLHSLLGNKWSLIAARLPGRTDNEIKNYWNTHIR  113
SlMYB7         NYLRPDLKRGNFTEEEDELIIKLHSLLGNKWSLIAGRLPGRTDNEIKNYWNTHIR  113
SlMYB32        NYLRPDLKRGNFTEEEDELIIKLHSLLGNKWSLIAGRLPGRTDNEIKNYWNTHIR  113
PpMYB20        NYLRPDLKRGNFTEEEDELIIKLHSLLGNKWSLIAGRLPGRTDNEIKNYWNTHIK  113
SlMYB3         NYLRPDLKRGNFTEEEDELIIKLHSLLGNKWSVIAGRLPGRTDNEIKNYWNTHIK  113
AtMYB3         NYLRPDLKRGNFTEEEDELIIKLHSLLGNKWSLIAGRLPGRTDNEIKNYWNTHIK  113
AtMYB7         NYLRPDLKRGNFTHDEDELIIKLHSLLGNKWSLIAARLPGRTDNEIKNYWNTHIK  113
PtrMYB57       NYLRPDLKRGNFSDEEDELIINLHSLLGNKWSLIAARLPGRTDNEIKNYWNTHIK  113
AtMYB32        NYLRPDLKRGNFTLEEDDLIIKLHSLLGNKWSLIATRLPGRTDNEIKNYWNTHVK  113
GbMYBF2        NYLRPDLKRGLLSESEEKLIIELHAAIGNRWSRIAAQLPGRTDNEIKNYWNTRIK  113
MdMYB10        NYLKPNIKRGDFKEDEVDLIIRLHRLLGNRWSLIARRLPGRTANAVKNYWNTRLR  111
MdMYB6         NQLSPQVEHRAFTPEEDDMIIRAHARFGNKWATIARLLNGRTDNAIKNHWNSTLK  110
AtMYBL2        NYVRPEVKQRNFSKDEDDLILKLHALLGNRWSLIAGRLPGRTDNEVRIHWETYLK   81
AtETC2         EVSSIEWEFISMTEQEEDLISRMYRLVGNRWDLIAGRVVGRKANEIERYWIMRNS   83
AtTRY          EVSSIEWEFINMTEQEEDLIFRMYRLVGDRWDLIAGRVPGRQPEEIERYWIMRNS   76
VvTRY          EVSSIEWEFINMSEQEEDLIYRMYRLVGDRWDLIAGRIPGRKPEEIERFWIMRNR   73
SlTRY          EVNSMEWEFIRMSKQEEDLIYRMHKLVGDRWGLIAGRIPGRTAEEIERFWIMRHS   76
AtETC3         EVSSLEWEVVNMSQEEEDLVSRMHKLVGDRWELIAGRIPGRTAGEIERFWVMKN-   77
AtETC1         EVSSLEWEEIAMAQEEEDLICRMYKLVGERWDLIAGRIPGRTAEEIERFWVMKNH   77
AtCPC          EVSSIEWEAVKMSEEEEDLISRMYKLVGDRWELIAGRIPGRTPEEIERYWLMKHG   81
EcROI1         NKKETKV-QVQLSKDEEDLVIRMYNLVGDRWPLIAGRIPGRSADQIKKYWLSRYS   73
ElROI1         NKKESKV-QVQLSEDEEDLVIRMYNLVGDRWPLIAGRIPGRSADQIKKYWLSRYS   73
PhMYBx         SGKTSKVAEIKFSEEEEDLIIRMYNLVGERWSLIAGRIPGRSAEEIEKYWNTRSS   82
SlMYBATV-X2    ETTNEETSKLEFSEDEEMLIAKMFSLVRERWSLIAGRIPGRNADEIEKYWKSKYS   81
SlMYBATV-X3    ETTNEETSKLEFSEDEEMLIAKMFSLVRERWSLIAGRIPGRNADEIEKYWKSKYS   81
SlMYBATV-X1    ETTNEETSKLEFSEDEEMLIAKMFSLVRERWSLIAGRIPGRNADEIEKYWKSKYS   81
SlMYBATV-like  EAKKEESLKLEFSQDEEILITKMFNLVGERWSLIAGRIQGELQMKLRSTGTQEIP   75
GmMYB73        --KSSQVSDVEFSEAEEILIAMVYNLVGERWSLIAGRIPGRTAEEIEKYWTSRFS   71
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Fig. S4 Multiple sequence alignment of MYB flavonoid repressor based on the R3 and R2R3 domains. The N-terminal protein sequences comparing the R2R3 domain or only the R3 domain for small MYB proteins were aligned by using Clustal X ver. 2 (Larkin *et al.*, 2007) with default settings, and the conserved amino acids were shaded by using GeneDoc (2.6) (Nicholas *et al.*, 1997). The R2 and R3/bHLH-binding domains are marked above the alignment.

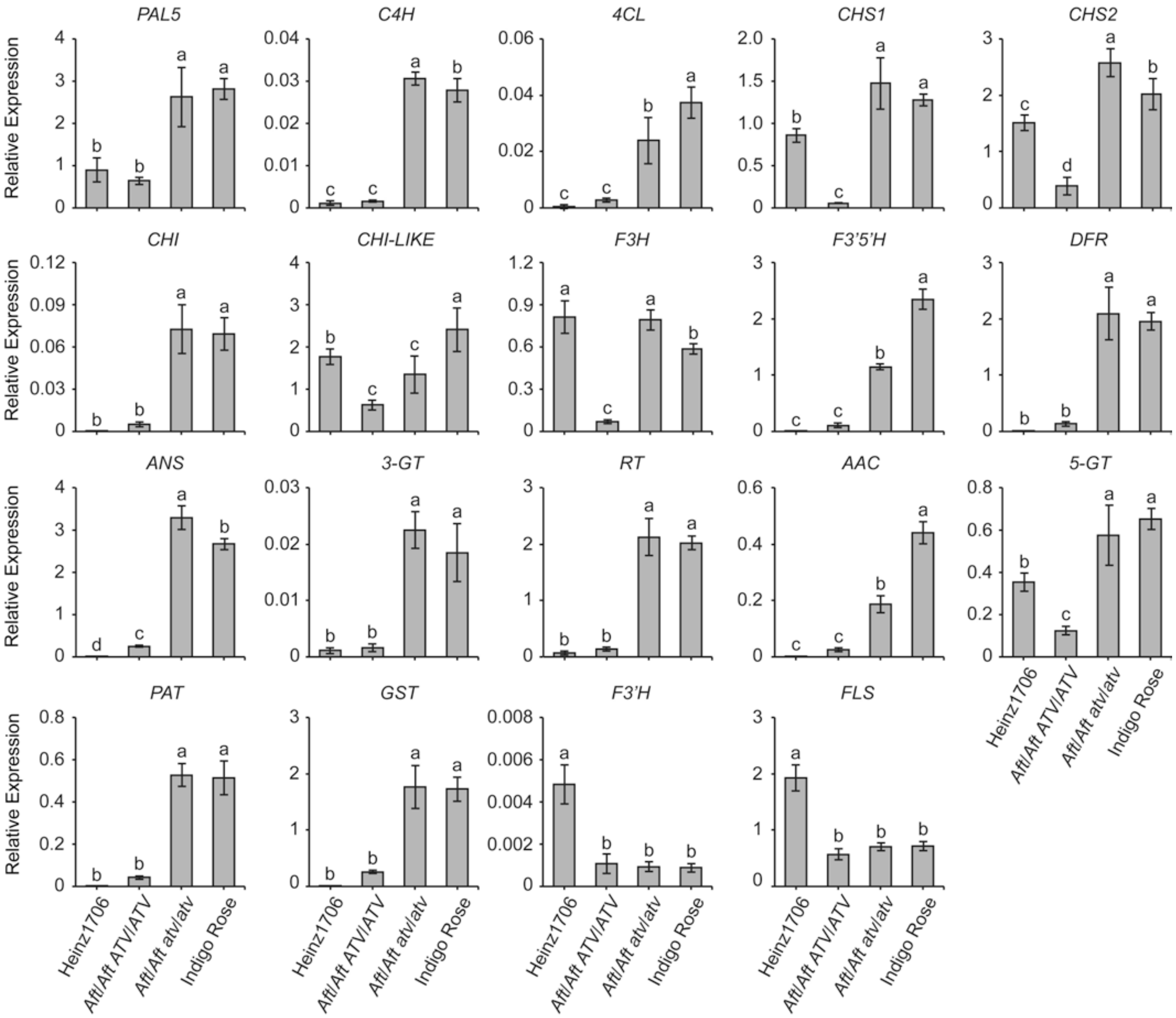

Fig. S5 Transcriptional analysis of the structural genes of the anthocyanin biosynthetic pathway in the peel of tomato fruit at the fully ripened stage. Transcriptional profiling of these genes was determined by qRT-PCR in the fruit peel of *Aft*/*Aft ATV*/*ATV* (abbreviated as *Aft*/*Aft*) and *Aft*/*Aft atv*/*atv* in a F5 population, and the two parent lines Heinz1706 (genotype, *AFT*/*AFT ATV*/*ATV*) and Indigo Rose (*Aft*/*Aft atv*/*atv*). A tomato *ACTIN* (*Solyc03g078400*) gene was used as the reference: relative expression levels are shown. Different letters indicate statistically significant differences among groups (Tukey's honestly significant difference test, *P*<0.01). PAL, phenyl alanine ammonia-lyase; C4H, cinnamate-4-hydroxylase; 4CL, 4-coumaroyl:CoA-ligase; CHS, chalcone synthase; CHI, chalcone isomerase; CHI-LIKE, chalcone isomerase-like; F3H, flavanone 3-hydroxylase; F3´5´H, flavonoid 3´5´-hydroxylase; DFR, dihydroflavonol 4-reductase; ANS, leucoanthocyanidin dioxygenase; 3-GT, 3-O-glucosyltransferase; RT, rhamnosyl transferase; AAC, anthocyanin acyltransferase; 5-GT, 5-O-glucosyltransferase; PAT, putative anthocyanin transporter; GST, glutathione S-transferase; F3´H, flavonoid 3´-hydroxilase; FLS, flavonol synthase.

Table S1. General information on the DNA markers used in this study

Marker name	Genome position	Forward primer	Reverse primer	Marker type	Restriction enzyme	Heinz1706 allele (bp)	Indigo Rose allele (bp)
ATV-In	SL2.50ch07: 61,003,572	GAGGTTTCTTCGTTGGTAGTC	CTAAATAAAAGTTATTGAGTTCACG	InDel		85	89
HP1865	SL2.50ch07: 25,351,236	TTATGCCAAAGCTTCAACGG	ACGAGTTTATTTTAAGTTTCCTTG	InDel		158	176
HP1877	SL2.50ch07: 59,804,770	CACGGGAATAAGAAATTGGCG	TGGTTGACTCTTGAAGTTTCAGT	InDel		148	171
HP1885	SL2.50ch07: 62,676,901	AGGTACTTGTGACCAAACCC	TTCAGCATGAACTGACTGGG	InDel		136	157
HP1891	SL2.50ch07: 64,799,803	AGCTTTGCTAAGACATACTAAGAC	ACTGTTTTCGATAGATCCTCGG	InDel		151	137
HP1915	SL2.50ch07: 60,726,148	CTTAAGAAGGAAGTATGAAGAGAG	CCATCAATCATAGTTTCACCG	InDel		97	108
HP1917	SL2.50ch07: 60,982,128	TCACAAGTAAAGGAGCATCC	CTCTTCTTATAGTCACGTAAGTTAG	InDel		138	117
HP1919	SL2.50ch07: 61,321,298	CTCTCAACGATTCTATCTTCAC	CCCAATTTGATATCTGAACC	InDel		119	132
HP1949	SL2.50ch10: 65,012,425	TGTGGCACCTCCACCGTAAC	CCGCATGACCTATAAGCGAC	InDel		124	154
HP1953	SL2.50ch10: 65,134,020	TTCTTAGTAACCGCGATGCTC	GACTTTGCTCCAGATGAAGTG	InDel		768	376
HP2675	SL2.50ch07: 60,920,438	CTGTTGATGGTAAACACTTTTCTC	CAAAAGTTTCATAAAAGCAGACC	InDel		148	160
HP2677	SL2.50ch07: 61,044,268	GTGTTACCAAAAAAAGGAAAGTG	GATCATTGCTTCTAGAAATAGGC	InDel		131	143
HP3195	SL2.50ch10: 65,177,657	GAGTAAACATATAAGCATTCCTTTG	CAATCACTAAGTAGTTGTTGCTCA	InDel		89	69
HP3217	SL2.50ch07: 61,013,666	ACATTGGTGGCATTGAATATGAG	ACAAGTATCACCCTATCCGTCTC	InDel		200	236
JP13	SL2.50ch07: 60,995,265	CTGGTATAATCTCCCTTTAGCG	AAGGTCTAAGAAAAGCTGACAAC	CAPS	MseI	176	128
JP17	SL2.50ch07: 61,004,897	GTTGTATAAGGCGGAGTGATGGCGAC	GCATCTGCGCATATTCTCTTC	dCAPS	HinfI	148	172

Table S2. Primers used for sequencing and cDNA cloning

Primer Name	**Forward primer (5'->3')**	**Reverse primer (5'->3')**	**Notes**
ATVg-1	CCGAAGTTAACAAATACACGAAC	CGAGATCGGATCTATCTCATCA	Sequencing *SlMYBATV* gene
ATVg-2	ATATCGACAAAGTTGTATAATGTACTAT	CAACTTTCCAATTATACACACTCG	Sequencing *SlMYBATV* gene
ATVg-3	AGCAATTGTTCGAGGAGAGG	CTTTCAGAAGTTCGTGTATCTTGC	Sequencing *SlMYBATV* gene
ATVg-4	GTAAATGTGAAGATCCTGAAATGAC	ATGATATGATTATCTGCGTCTAACC	Sequencing *SlMYBATV* gene
ATVg-5	GAACATGTATTTTGGAAGTAGCC	CTTCTCGCACCTCTTCACTG	Sequencing *SlMYBATV* gene
ATVg-6	GCATGTCGAGTTAATGAGGATG	AAGGAAGTAGTGGAAATCCTACAAG	Sequencing *SlMYBATV* gene
ATVg-7	GGGTTTGGGCTCATTGGTGT	AGGATCAGAAATTAGTTGCCAC	Sequencing *SlMYBATV* gene
3RACE-RT	AAGCAGTGGTATCAACGCAGAGTACTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTVN		3'-RACE CDS Primer, Clontech
SlAN2	GAATACTCCTATGTGTGCATCG	CCAACTAAGGATATGTCATAGTAATAAG	Clonging *SlAN2* cDNA
SlAN2-like	TGCAGTATTTGTGACTTAACATATC	GGTATTGTAGTACTACTTGTACTAGCA	Clonging *SlAN2-like* cDNA
SlMYB76	CTTCTTCACATAGTCACCATCC	AAGCAGTGGTATCAACGCAGAGT (3RACE-NUP, Clontech)	Clonging *SlMYBATV*-like cDNA
SlMYBATV	GACCACATTCAAATCTTTGTTC	AAGCAGTGGTATCAACGCAGAGT (3RACE-NUP, Clontech)	Clonging *SlMYBATV*-like cDNA
SlMYBATV-like	TGCCAAGTTATTTCCATCTC	AAGCAGTGGTATCAACGCAGAGT (3RACE-NUP, Clontech)	Clonging *SlMYBATV*-like cDNA
SlTRY	CAGAAGCTGTCCCTCCTAATC	GCAACTCTCTGCTAGTCCTCT	Clonging *SlTRY* cDNA

Table S3. Information regarding the known MYB repressors for the phenylpropanoid and flavonoid pathway

Name	Full Name	Type	GenBank Accession Number	Reference
AmMYB308	*Antirrhinum majus* MYB308	R2R3 MYB	P81393	Jackson *et al.*, 1991
AtCPC	*Arabidopsis thaliana* CAPRICE	R3 MYB	BAA21917	Wada *et al.*, 1997
AtETC1	*Arabidopsis thaliana* Enhancer of TRY and CPC 1	R3 MYB	NP_171645	Kirik *et al.*, 2004a
AtETC2	*Arabidopsis thaliana* Enhancer of TRY and CPC 2	R3 MYB	NP_850145	Kirik *et al.*, 2004b
AtETC3	*Arabidopsis thaliana* Enhancer of TRY and CPC 2	R3 MYB	NP_192015	Simon *et al.*, 2007
AtMYB3	*Arabidopsis thaliana* MYB3	R2R3 MYB	Q9S9K9	Kranz *et al.*, 1998
AtMYB4	*Arabidopsis thaliana* MYB4	R2R3 MYB	Q9SZP1	Kranz *et al.*, 1998
AtMYB7	*Arabidopsis thaliana* MYB7	R2R3 MYB	NP_179263	Fornale *et al.*, 2014
AtMYB32	*Arabidopsis thaliana* MYB32	R2R3 MYB	O49608	Preston *et al.*, 2004
AtMYBL2	*Arabidopsis thaliana* MYB-Like 2	R3 MYB	AEE35154	Dubos *et al.*, 2008; Matsui *et al.*, 2008
AtTRY	*Arabidopsis thaliana* TRIPTYCHON	R3 MYB	Q8GV05	Schnittger *et al.*, 1999
CmMYB1	*Chrysanthemum x morifolium* MYB1	R2R3 MYB	AEO27497.1	Zhu *et al.*, 2013
EcROI1	*Erythranthe cardinalis* rose intensity 1	R3 MYB	AGC66792.1	Yuan *et al.*, 2013
EgMYB1	*Eucalyptus gunnii* MYB1	R2R3 MYB	CAE09058.1	Legay *et al.*, 2010
ElROI1	*Erythranthe lewisii* rose intensity 1	R3 MYB	AGC66791.1	Yuan *et al.*, 2013
FaMYB1	*Fragaria x ananassa* MYB1	R2R3 MYB	AAK84064	Aharoni *et al.*, 2001
GbMYBF2	*Ginkgo biloba* MYBF2	R2R3 MYB	AFD36431	Xu *et al.*, 2014
GhMYB6	*Gossypium hirsutum* MYB6	R2R3 MYB	AAN28286	Cedroni *et al.*, 2003
GmMYB73	*Glycine max* MYB73	R3 MYB	ABH02868	Liu *et al.*, 2014
GmMYB100	*Glycine max* MYB100	R2R3 MYB	Glyma07g33960.1	Yan *et al.*, 2015
LlMYB1	*Leucaena leucocephala* MYB1	R2R3 MYB	ADY38393	Omer *et al.*, 2013
MdMYB6	*Malus domestica* MYB6	R2R3 MYB	AAZ20429	Gao *et al.*, 2011
MdMYB10	*Malus domestica* MYB10	R2R3 MYB	ACQ45201	Lin-Wang *et al.*, 2011
MtMYB2	*Medicago truncatula* MYB2	R2R3 MYB	AES99346	Jun *et al.*, 2015
PdMYB221	*Populus trichocarpa* MYB221	R2R3 MYB	ACN97176	Tang *et al.*, 2015
PhMYB4	*Petunia* x *hybrid* MYB4	R2R3 MYB	ADX33331	Colquhoun *et al.*, 2011
PhMYB27	*Petunia* x *hybrid* MYB27	R2R3 MYB	AHX24372	Albert *et al.*, 2011

PhMYBx	*Petunia* x *hybrid* MYBx	R3 MYB	AHX24371	Kroon, 2004
PpMYB17	*Prunus persica* MYB17	R2R3 MYB	ALO81020	Zhou *et al.*, 2016
PpMYB18	*Prunus persica* MYB18	R2R3 MYB	ALO81021	Zhou *et al.*, 2016
PpMYB19	*Prunus persica* MYB19	R2R3 MYB	ALO81022	Zhou *et al.*, 2016
PpMYB20	*Prunus persica* MYB20	R2R3 MYB	ALO81023	Zhou *et al.*, 2016
PtrMYB57	*Populus trichocarpa* MYB57	R2R3 MYB	XP_002325733	Wan *et al.*, 2017
PtrMYB182	*Populus tremula* x *Populus tremuloides* MYB182	R2R3 MYB	AJI76863	Yoshida *et al.*, 2015
Tr-MYB133	*Trifolium repens* MYB133	R2R3 MYB	AMB27081	Albert, 2015
Tr-MYB134	*Trifolium repens* MYB134	R2R3 MYB	AMB27082	Albert, 2015
VvMYBC2-L1	*Vitis vinifera* MYBC2-Like 1	R2R3 MYB	ABW34393	Huang *et al.*, 2014
VvMYBC2-L2	*Vitis vinifera* MYBC2-Like 2	R2R3 MYB	ACX50288	Cavallini *et al.*, 2015
VvMYBC2-L3	*Vitis vinifera* MYBC2-Like 3	R2R3 MYB	AIP98385	Cavallini *et al.*, 2015
VvMYB4a	*Vitis vinifera* MYB4a	R2R3 MYB	ABL61515	Jun *et al.*, 2015
VvMYB4-like	*Vitis vinifera* MYB4-like	R2R3 MYB	XP_002273328.1	Perez-Diaz *et al.*, 2016
VvTRY	*Vitis vinifera* TRIPTYCHON	R3 MYB	ABW34395	Jun *et al.*, 2015
ZmMYB31	*Zea mays* MYB31	R2R3 MYB	NP_001105949	Fornale *et al.*, 2010
ZmMYB42	*Zea mays* MYB42	R2R3 MYB	NP_001106009	Sonbol *et al.*, 2009

Table S4. Primers for quantitative RT-PCR

Gene name	**Gene ID**	**Forward primer**	**Reverse primer**	**Reference**
3GT	*Solyc10g083440*	CGATCGAACGACGAAACACTG	GCAGCATAGATGGCATTGGC	Developed in this study
4CL	*Solyc06g068650*	TTCACCTCAGGGATATCATGCTCATC	CATGTGAACAAGGTGAAGGATTATGC	Developed in this study
5GT	*Solyc09g092500*	GTGGCATTTCCTCATTGGAC	TCATCACTCTCAACCACACCA	Qiu *et al.*, 2016
AAC	*Solyc12g088170*	CTTGCTGGAAGGTTGTCTGAAGATG	CAAGGTCACTATCTTTGTATGCTTTGTC	Developed in this study
ANS	*Solyc08g080040*	GAACTAGCACTTGGCGTCGAA	TTGCAAGCCAGGCACCATA	Qiu *et al.*, 2016
C4H	*Solyc05g047530*	AAGAAGGAAACTAATGGCTGAAA	GCTGCAACATTGATATTCTCCA	Developed in this study
CHI	*Solyc05g010320*	CGGCGCAGGGAATAGAGGTTT	CCGTCAAGGGCAAGATCATAGTCAC	Developed in this study
CHI-LIKE	*Solyc05g052240*	TTGATGGGCCATGGAATAACAGATA	GTCAACTGGAGCATTCACAATAGCCT	Developed in this study
CHS1	*Solyc09g091510*	TGGTCACCGTGGAGGAGTATC	GATCGTAGCTGGACCCTCTGC	Povero *et al.*, 2011
CHS2	*Solyc05g053550*	GGCGACTCCTTCGAACTGTGTTG	ATCCAAAGAAGGAGCCATGTATTCAC	Developed in this study
DFR	*Solyc02g085020*	AGTCCAAGGATCCAGAGAACGAAGTA	TGGACATCAAGAGTTCCAGCAGAT	Developed in this study
F3'5'H	*Solyc11g066580*	GGTACATGTGGGATGGTTGTTGC	ACTTCCAACGTGGTCCATAGGG	Developed in this study
F3'H	*Solyc03g115220*	ACCACCATTAACTTGAACTCCTCC	GCCATGTCCGACAGGAAGAAG	Developed in this study
F3H	*Solyc02g083860*	GTGAAAAGTTGATGGATTTGGC	GTAATGGTTCCTGGATCGGTGTGT	Qiu *et al.*, 2016
FLS	*Solyc11g013110*	CATACAGGGAAGCAAATGAGGAA	AGTATGAGCCACAACTCCAAGAGC	Developed in this study
GST	*Solyc02g081340*	TGCTTTTACAGCCATTTGGACAGG	CCGGTTAGTTTCTTTCCCTTGTCTTC	Developed in this study
PAL	*Solyc03g071870*	GGTGGTGCTCTTCAAAAGGAAC	GGAATGCTTCATGAGCGTCAAGTT	Developed in this study
PAL5	*Solyc09g007900*	GGAATTGCAGGGTTGCCACTTT	AAGGCCGCGTTGCCTAAAGAAG	Povero *et al.*, 2011
PAT	*Solyc03g025190*	CGGTGTTTCAGTCCCTCCTA	TTGCATCTCCTTGCTGTTTG	Povero *et al.*, 2011
RT	*Solyc09g059170*	CTGGCAATGCAAACAGAGTGA	TCGACTTGCGGAAGAGTGAGA	Qiu *et al.*, 2016
SlACTIN	*Solyc03g078400*	GGGATGGAGAAGTTTGGTGGTGG	CTTCGACCAAGGGATGGTGTAGC	Qiu *et al.*, 2016
SlAN1	*Solyc09g065100*	CTAAGAGTGCCCGCATACAGAC	ATCCGAAGTGGAGTGCTCAGATA	Qiu *et al.*, 2016
SlAN2	*Solyc10g086250*	CCAGCTCTAGCAGGAACAAGATG	AACTCTTAGGCAATAGGTGGTCACT	Developed in this study
SlAN2-like	*Solyc10g086290*	CAAGCTTCTAGGCAATAGATGGTCACT	TTGGTCGTGGTCGTAGTATAGTGC	Developed in this study
SlAN11	*Solyc03g097340*	CCGTCTCTGGGATGTTACTGATACT	CTTCTCGGCTCCACTTCATTCC	Developed in this study
SlANT1	*Solyc10g086260*	AAGCTCTTAGGCAACAGATGGTCAC	TGAGAAATACTTGCGTCGTTGAGG	Developed in this study
SlANT1-like	*Solyc10g086270*	AGGTGACTTCGCTTCGGATGA	CGTTTACTCTTAAACTTTTCACGTGG	Developed in this study
SlJAF13	*Solyc08g081140*	TCAGGGGATCACTACCGAAC	TCCCATCAAGGTTGGAAGAC	Kiferle *et al.*,2015
SlMYB3	*Solyc06g065100*	AGCTGCAGGATTGTCAAGATGTG	GAGCACGTATATAATTGATGAGGCG	Developed in this study
SlMYB7	*Solyc01g111500*	CCTCCTTGGTAACAAATGGTCACT	TTGGATCAATGCCCCGACTC	Developed in this study

SlMYB12	*Solyc01g079620*	ATGCCGGATTATTGAGATGCG	GCTATCAACTTTTCGACTTAGATGAGAG	Developed in this study
SlMYB32	*Solyc10g055410*	ACAAGTGGTCGCTTATAGCAGGAA	TCATGAGCAGCAGCAAAAGTAATC	Developed in this study
SlMYB76	*Solyc05g008250*	CTGCTGGCCTGCTTCGTTGT	CCGTTCGTCCTGGCAATCTTC	Developed in this study
SlMYBATV-like	*Solyc12g005800*	CCTTCATAGACTCCCCTCCATTTG	GACCACCTCTCACCAACCAAGTT	Developed in this study
SlMYBATV-X1	*Solyc07g052490*	TCAGCTTGGTTAGAGAGAGGTG	AAAACACACTGCTGAGGGTGC	Developed in this study
SlMYBATV-X2	*Solyc07g052490*	TCAGCTTGGTTAGAGAGAGGTG	CGCTAGATTTCGCGTTGTTGA	Developed in this study
SlMYBATV-X3	*Solyc07g052490*	TCAGCTTGGTTAGAGAGAGGTG	CATCTGAGGGAAAAAGTAATTTGAAG	Developed in this study
SlTRY	*Solyc01g095640*	GCAGCCATGAAGAAGAGGTTAATAGTAT	TATAAGCCCCCACCTGTCTCCA	Developed in this study

Table S5. Preliminary mapping of the *atv* locus

HP1865[a]	**HP1877**	**HP1885**	**HP1891**	**Plant number**[b]	**Fruit color**[c]
3	3	3	3	7	Fully purple
1	2	3	3	1	Fully purple
1	3	3	3	1	Fully purple
2	2	3	3	2	Fully purple
2	3	2	2	4	Fully purple
2	3	3	2	1	Fully purple
2	3	3	3	3	Fully purple
3	3	2	2	2	Fully purple
3	3	3	2	3	Fully purple
1	1	1	1	12	Purple spots
2	2	2	2	25	Purple spots
1	1	1	2	3	Purple spots
1	1	1	3	1	Purple spots
1	1	2	2	6	Purple spots
1	1	2	3	1	Purple spots
1	2	1	1	1	Purple spots
1	2	2	2	2	Purple spots
1	2	2	3	1	Purple spots
1	2	3	3	4	Purple spots
2	1	1	1	7	Purple spots
2	1	2	2	1	Purple spots
2	2	1	1	9	Purple spots
2	2	2	1	3	Purple spots
2	2	2	3	3	Purple spots
2	2	3	2	1	Purple spots
2	2	3	3	3	Purple spots
3	1	1	1	3	Purple spots
3	2	1	1	1	Purple spots
3	2	2	1	1	Purple spots
3	2	2	2	4	Purple spots
3	2	2	3	1	Purple spots
3	3	2	2	4	Purple spots

a Marker score on parent plant: 1, homozygous Heinz1706; 2, heterozygous; 3, homozygous Indigo Rose.

b The number of plants with same phenotype and genotype.

c Purple spots or Fully purple was exhibited on the fruit peel which was exposed to high light.

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