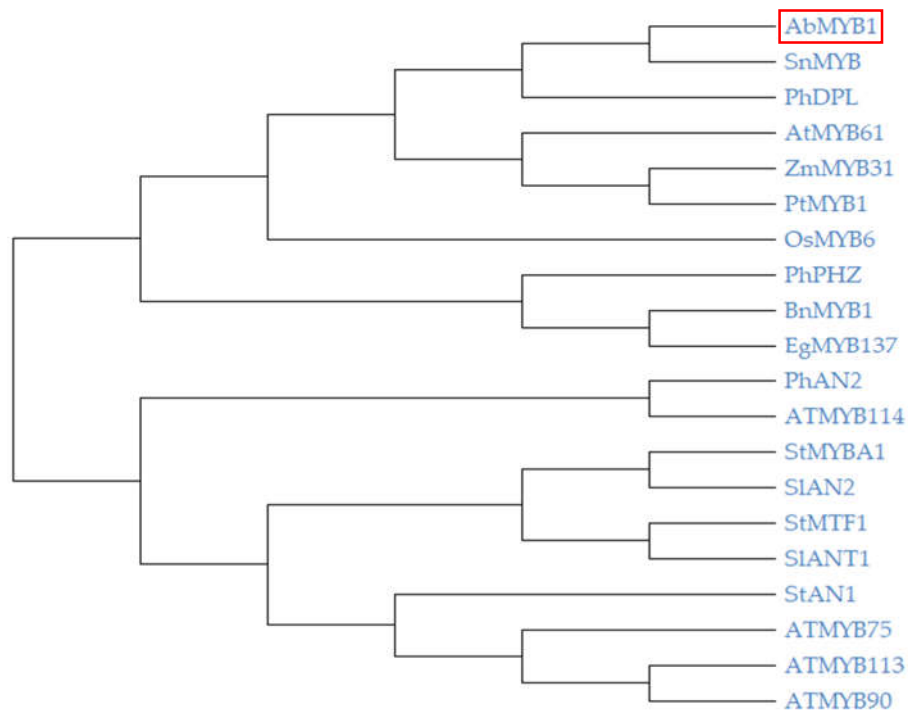


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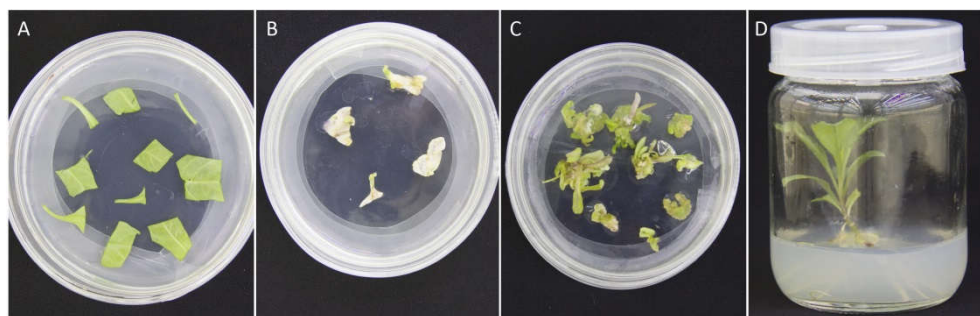
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    M N S T S S T K S S E V R K G A W T E E E D L L L R K C I D
186  AAGTACGGTGAAGGAAAGTGGCATCAAATTCCTAGAGCTGGTCTAAATAGATGCAGAAAGAGCTGCAGACTGAGGTGGTTGAATTAT
    K Y G E G K W H Q I P I R A G L N R C R K S C R L R W L N Y
276  CTAAGGCCACATATTAAGAGAGGTGACTTCGCTTCGGATGAAATAGATCTCATCTTCAGGCTTCATAAGCTCTTAGGCAACAGATGGTCA
    L R P H I K R G D F A S D E I D L I F R L H K L L G N R W S
366  CTTATTGCTGGTAGACTTCGGGAAGAACAGCAAACGATGTGAAAAATTACTGGAACACACCTACATAGAAAGTTAATTTCCTCCTCAG
    L I A G R L P G R T A N D V K N Y W N T H L H R K L I S P Q
456  AGACAGGAGAGAAAGTACAATAATGCCCTCAAGATCACTGAAAACACCATAATAAGACCTTGGCCTCGGACCTTCTCAAGTGCAACGAAA
    R Q E R K Y N N A L K I T E N T I I R P W P R T F S S A T K
546  CCTTGGTGCAACAACAAAAGTATCACAAATACAATAGACAAAGACATCGCAACAACGAAACAGTACTAAATATTTGTGAGAAGCCA
    P W C N N K S I T N T I D K D K H R N N E T V L N I C E K P
636  ACAGGCGAAACAACGAGGTCGTCGATGGACGAGGGAGTTCAATGGTGGACAAGTTTACTGGAAAAATTGCAATGAATTTGAGGAAGCAGTT
    T G E T T R S S M D E G V Q W W T S L L E N C N E F E E A V
726  GGGAGATTTGATGAAGAAAATAAGTTACCAAGTTTGTGTCATGACGAAAACTCACCGCCAATGCAAGAAGGACAAAGTGATGGCTGGAAT
    G R F D E E N K L P S L L H D E N S P P M Q E G Q S D G W N
816  GACTTTTCTGCTGATATTGACCTATGGGATCTACTTAATTAAtttagtttcatcaatcaccattaacacatagataattaatggtattg
    D F S A D I D L W D L L N *
906  tgtacttgtaatagggatacattctattctatgccgtttgaactttgtatcccaagtacaagtagggatctattactattttcattctag
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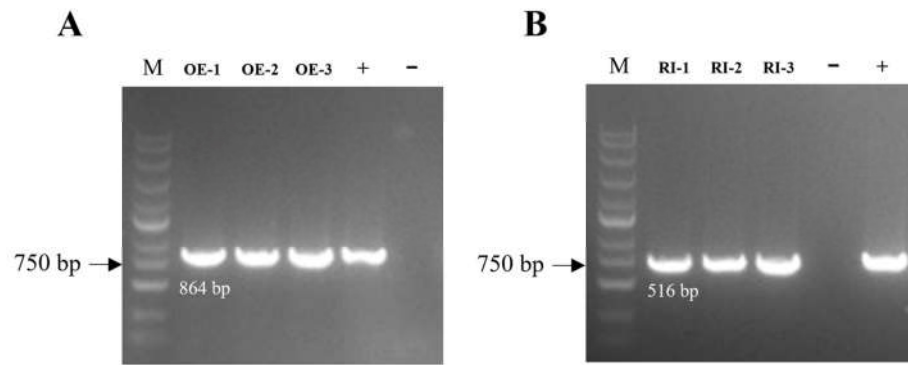
**Figure S1.** The cDNA sequence and derived amino acids sequence of *AbMYB1*.



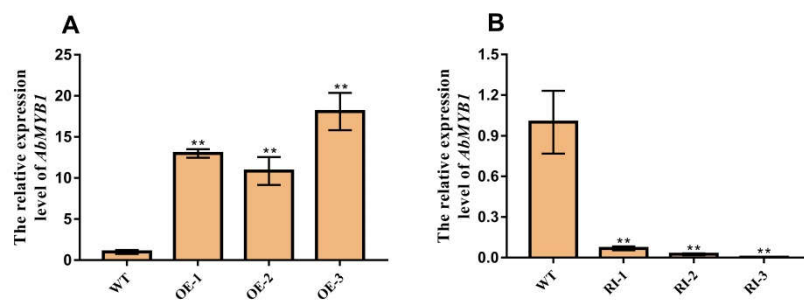
**Figure S2. The Phylogenetic Relationships of AbMYB1 with Other R2R3-MYBs.** *Solanum nigrum* (Sn), *Petunia hybrid* (Ph), *Zea mays* (Zm), *Pinus taeda* (Pt), *Oryza sativa* (Os), *Boehmeria nivea* (Bn), *Eucalyptus gunnii* (Eg), *Solanum tuberosum* (St), *Solanum lycopersicum* (Sl), *Arabidopsis thaliana* (At). SnMYB (AVT28142.1), PhDPL (ADQ00394.1), ZmMYB31 (NP\_001105949.2), PtMYB1 (AAQ62541.1), AtMYB61 (AT1G09540), OsMYB6 (QBM91277.1), BnMYB1 (AXF84304.1), PhPHZ (ADW94951.1), EgMYB137 (APX44023.1), PhAN2 (AUH28246.1), StMYBA1 (ALA13582.1), SIAN2 (NP\_001265992.1), StMTF1 (EU310399), SIANT1 (NP\_001234417.1), StAN1 (AAX53093.1), ATMYB75 (AT1G56650.1), ATMYB114 (AT1G66380.1), ATMYB113 (AT1G66370.1), ATMYB90 (AT1G66390.1).



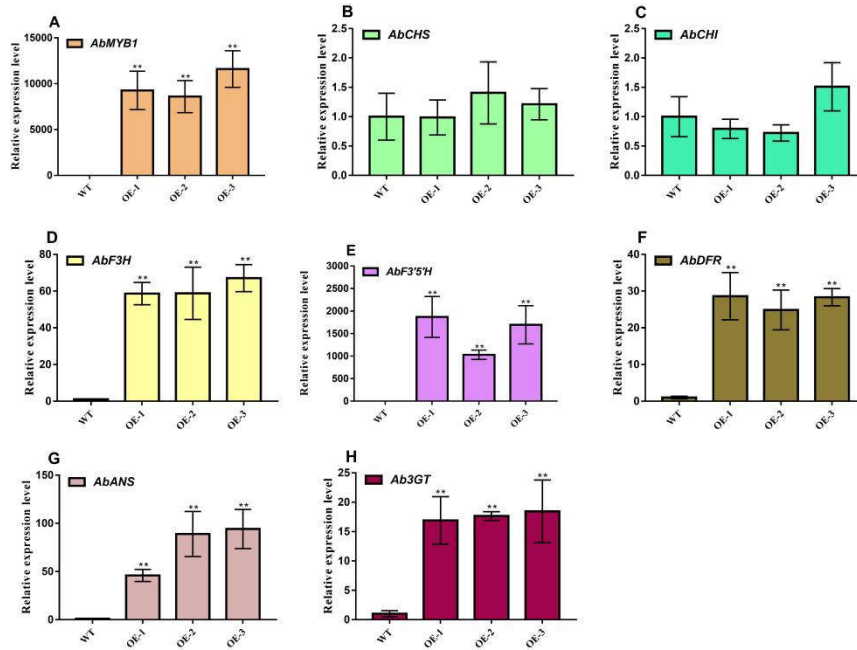
**Figure S3. The process of agrobacterium-mediated genetic transformation.** (A), Leaf discs co-cultured with agrobacterium; (B) Resistant callus; (C) Resistant buds on rooting medium; (D) Regenerated plants.



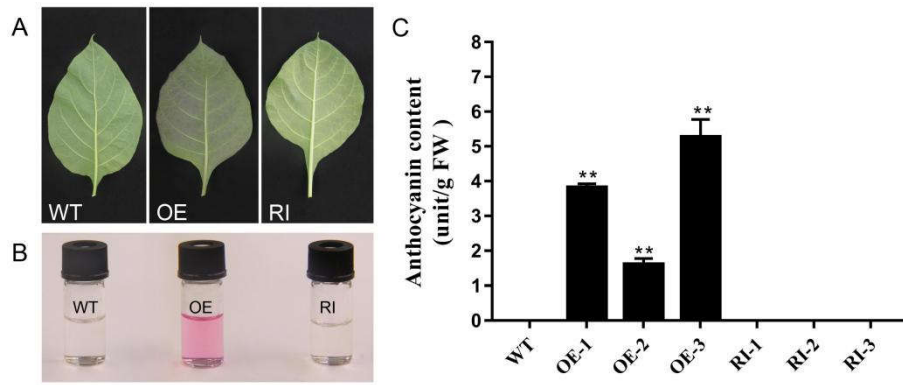
**Figure S4. Detection of transgenic plants by PCR.** (A) Target gene detection in *AbMYB1*-overexpression plants. (B) Target gene detection in *AbMYB1*-RNAi plants. M, Marker (15000 bp-100 bp); +, Positive control (recombinant plasmid containing the target gene); -: Negative control (wild type *A. belladonna*); OE-1, OE-2 and OE-3: the *AbMYB1*-overexpression transgenic plant lines; RI-1, RI-2 and RI-3: the *AbMYB1*-RNAi transgenic plant lines.



**Figure S5. The *AbMYB1* expression levels in the flowers of transgenic lines.** (A) Relative expression of *AbMYB1* in *AbMYB1*-overexpression plants. (B) Relative expression of *AbMYB1* in *AbMYB1*-RNAi lines. WT, wild type *A. belladonna*; OE-1, OE-2 and OE-3: the *AbMYB1*-overexpression transgenic plant lines; RI-1, RI-2 and RI-3: the *AbMYB1*-RNAi transgenic plant lines; \*\* means significant difference in T test ( $P < 0.01$ ).



**Figure S6. The relative expression of genes related to anthocyanin biosynthesis in *A. belladonna* leaves.** A, the expression level of *AbMYB1* in different lines; B, the expression level of *AbCHS* in different lines; C, the expression level of *AbCHI* in different lines; D, the expression level of *AbF3H* in different lines; E, the expression level of *AbF3'5'H* in different lines; F, the expression level of *AbDFR* in different lines; G, the expression level of *AbANS* in different lines; H, the expression level of *Ab3GT* in different lines; WT, the wild type plants; OE-1, OE-2 and OE-3: the *AbMYB1*-overexpression transgenic plant lines; \*\* means significant difference in T test ( $P < 0.01$ ).



**Figure S7. The anthocyanin accumulation in the leaves of transgenic *A. belladonna* plants.** (A) the anthocyanin accumulation in the leaves of transgenic plant lines and wild type plant lines; (B) total anthocyanin extracted from the leaves of transgenic plant lines and wild type plant lines; (C) total anthocyanin content in the leaves of transgenic plant lines and wild type plant lines. WT, the leaves of wild type plants; OE-1, OE-2 and OE-3: the leaves of *AbMYB1*-overexpression plants; RI-1, RI-2 and RI-3: the leaves of *AbMYB1*-RNAi plants; \*\* means significant difference in T test ( $P < 0.01$ ).

**Table S1.** Primers used in PCR experiments.

Primers	Sequences (5'-3')	Application
F-cAbMYB1	CGGCCGGGGGACTTTACCTCACGT	Full length cDNA cloning of <i>AbMYB1</i>
R-cAbMYB1	GATGTAAAATTTTTTCCACGGTAT	Full length cDNA cloning of <i>AbMYB1</i>
qF-AbMYB1	CGCGGATCCATGAATTCTACTAGTAGTACT	Analysis of tissue expression profile
qR-AbMYB1	CGCGAGCTCTTAATTAAGTAGATCCCATA	Analysis of tissue expression profile
qF-AbPGK	TCGCTCTTGGAGAAGGTTGAC	Analysis of tissue expression profile
qR-AbPGK	CTTGTCGGCAATCACTACATCAG	Analysis of tissue expression profile
qF-CHS	TCGGGCTACAAGGCAAGTC	Gene expression analysis in different stages
qR-CHS	AAAAGCACACCCCAATCAAGG	Gene expression analysis in different stages
qF-CHI	AGTTGTCAATGCTCCAGTTG	Gene expression analysis in different stages
qR-CHI	GCTCTTCTTCTTCATGTTTATCG	Gene expression analysis in different stages
qF-F3H	CCTTCAACACTAACGGCTCTG	Gene expression analysis in different stages
qR-F3H	ACCTCTTCTTCCACTCTCAATATC	Gene expression analysis in different stages
qF-F3'H	ATTCACCAACCTTAGCCAAAC	Gene expression analysis in different stages
qR-F3'H	CTTAGCATCTCCCTCACAAAC	Gene expression analysis in different stages
qF-F3'5'H	CTTCTCCAATCGTCCACCTAATG	Gene expression analysis in different stages
qR-F3'5'H	CGAATGTTTGCCCAATCTTCTAAG	Gene expression analysis in different stages
qF-ANS	GGAAGAAGGAAGACTGGAGAAG	Gene expression analysis in different stages
qR-ANS	CATATTGTGGAGGATGAATGTCAG	Gene expression analysis in different stages
qF-DFR	ACTGTTGATGCTCCGATGG	Gene expression analysis in different stages
qR-DFR	ATGCTTCACCTTCTTCTTGTTT	Gene expression analysis in different stages
qF-3GT	TCCTTCTTCAACACATCACAATCC	Gene expression analysis in different stages
qR-3GT	AGTTTCCTCCTCTGCCTCTTTC	Gene expression analysis in different stages
F-AbMYB1	CGCGGATCCATGAATTCTACTAGTAGTACT	Overexpression plasmid construction
R-AbMYB1	CGCGAGCTCTTAATTAAGTAGATCCCATA	Overexpression plasmid construction
F-iAbMYB1	CGCGGTACCAAGCTTCTCATCTTCAGGCTT CATAA	RNAi plasmid construction
R-iAbMYB1	CGCCTCGAGTCTAGATTCTTCATCAAATCT CCCAACT	RNAi plasmid construction
F-35S	GACGCACAATCCCACTATCC	Identify positive transgenic plants
R-iAbMYB1	CGCCTCGAGTCTAGATTCTTCATCAAATCT CCCAACT	Identify positive transgenic plants
R-AbMYB1	5'- CGCGAGCTCTTAATTAAGTAGATCCCATA	Identify positive transgenic plants



**Table S2.** The genes involved in anthocyanin biosynthesis in *A. belladonna*.

<b>gene name</b>	<b>gene number</b>
<i>AbCHS</i>	aba_locus_13102_iso_4_len_1413_ver_
<i>AbCHI</i>	aba_locus_14819_iso_3_len_853_ver_2
<i>AbF3H</i>	aba_locus_4270_iso_5_len_1419_ver_2
<i>AbF3'H</i>	aba_locus_10531_iso_1_len_1673_ver_2
<i>AbF3'5'H</i>	aba_locus_368_iso_2_len_1707_ver_2
<i>AbDFR</i>	aba_locus_7485_iso_2_len_1452_ver_2
<i>AbANS</i>	aba_locus_408_iso_2_len_1550_ver_2
<i>Ab3GT</i>	aba_locus_729_iso_1_len_1448_ver_2