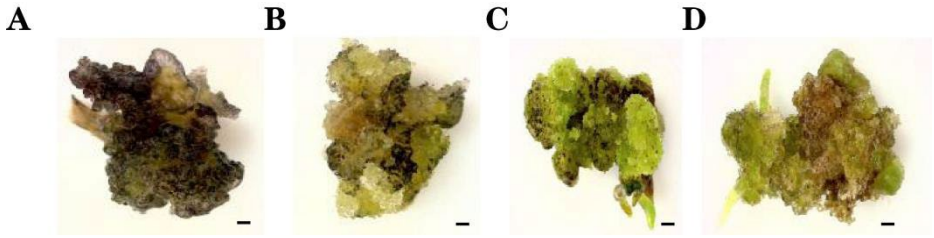
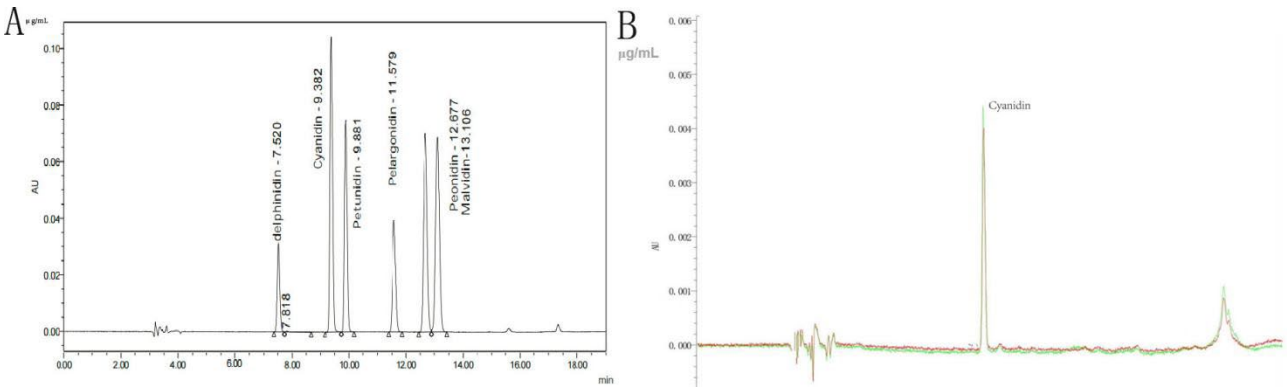


Figure S1. Different concentrations of NAA induced the accumulation of anthocyanins in the callus tissue. (**A**) Induction of callus tissues by 0.2 mg/L NAA. (**B**) Induction of callus tissues by 0.1 mg/L NAA. (**C**) Induction of callus tissues by 0.5 mg/L NAA. (**D**) Induction of callus tissues by 1.0 mg/L NAA. Scale=1cm.



FigureS2. Testing and analysing anthocyanins in lilies. (**A**) The chromatographic peaks of the six anthocyanin standards at 530nm. (**B**) The chromatography peaks of cyanidin in Lilium concolor var. pulchellum.

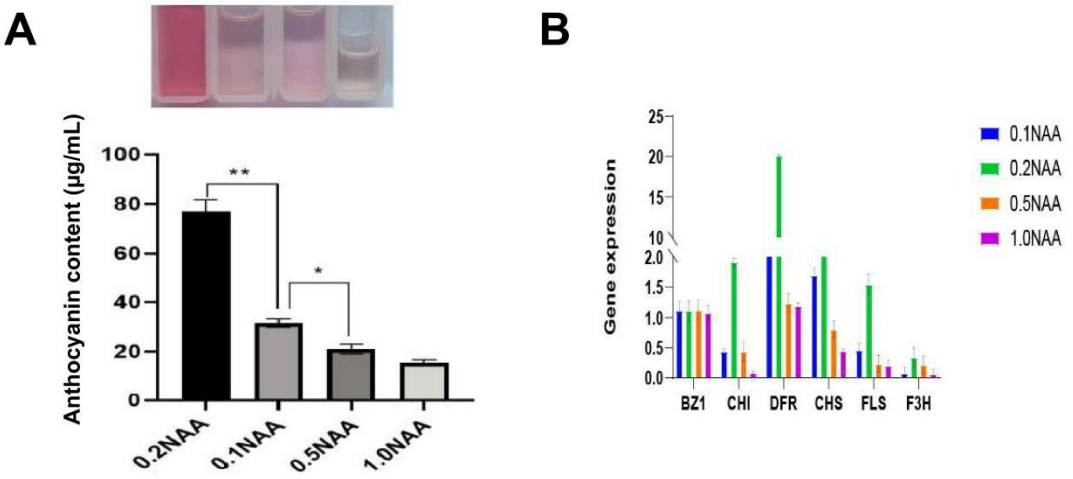


Figure S3. Extraction analysis of anthocyanins and gene expression analysis of the pathways involved in flavonoids metabolism. (**A**) Extraction and analysis of callus tissues in different concentrations of NAA. (**B**) Relative quantitative analysis of the expression of genes involved in the flavonoid metabolic pathway. The one and two asterisk indicates a significant difference between different NAA treatments at $P < 0.05$ and $P < 0.01$ respectively, t-test.

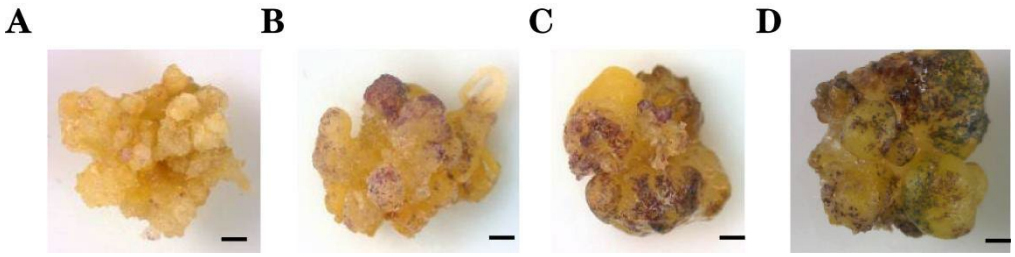


Figure S4. Phenotypic observation of 0.2 mg/L NAA induced healing tissues at different times. (**A**) The phenotype of anthocyanin accumulation in 2d. (**B**) The phenotype of anthocyanin accumulation in 5d. (C) The phenotype of anthocyanin accumulation in 10d. (**D**) The phenotype of anthocyanin accumulation in 15d. Scale=1cm.

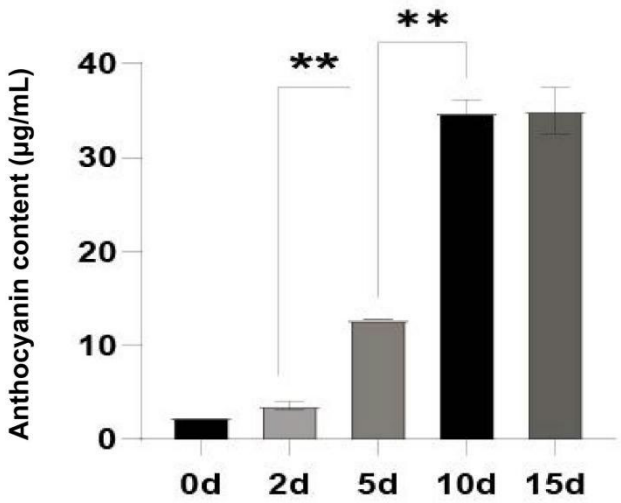


Figure S5. Determination of anthocyanin deposition by 0.2 mg/L NNAA during induction of lily callus tissue in different time by HPLC. The two asterisk indicates a significant difference between different NAA treatments at $P < 0.01$, t-test.

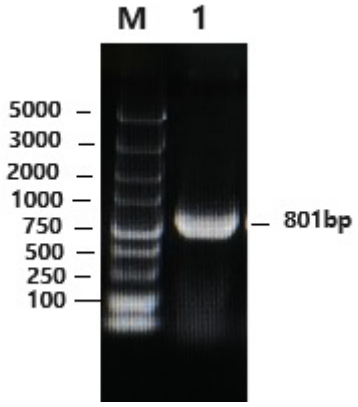


Figure S6. Cloning of *LhMYB1* gene. M refer to DNA 5000 marker; 1 refer to the PCR

fragment of *LhMYB1* gene.

LhMYB1 gene cDNA whole sequence:

>transcript_HQ_LH_transcript43717/f5p0/1056

ATGGGAAGGCCACCTTGCTGTGACAAGCTGGGAGTGAAGAAAGGCCCTTGGACT
CCAGAGGAGGACATCACTCTGGTGTCCTACATCCAGGAACATGGCCCTGGGAATT
GGAGGGCAGTTCCTACAATTACAGGGCTGATGAGGTGCAGCAAGAGCTGCAGGC
TTAGATGGACCAACTACCTCCGTCCAGGGATCAAGAGAGGCGATTTCACAGATCA
GGAGGAGAAGCTAATAATCCATCTCCAAGCTCTTCTTGGCAATAGATGGGCAGCT
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ACCCATCTCAAGAAGAAGCTGAAGAGGACCCAGACAGGTGTTACCATCGATGAC
ACTCCGACGAGCAGGAGCCAGCAGCCCTCTAAAGGGCAGTGGGAGAGGAGGCT
CCAGACAGACATCAACACAGCAAAGAGGGCCCTCTACGAAGCCATCGCTATTGA
TATCCCCAATTCTCCACCTAGCATGTTGCCCTATCCTCCACTGCCACCACCATCGA
CCACCTATGCGTCGAGCACTGAGAACATAGCTCGACTGCTTGAAGGGTGGATGGG
AGGATCGGGGAAACCGGATGGAGCCTCCACTTCTTCAAGTGAGGCTCGAACGGA
GCCGGAGCCGGAGCCGGAGCCGTCGGAGACAAGCATGTTACAGGAGGGGCCCG
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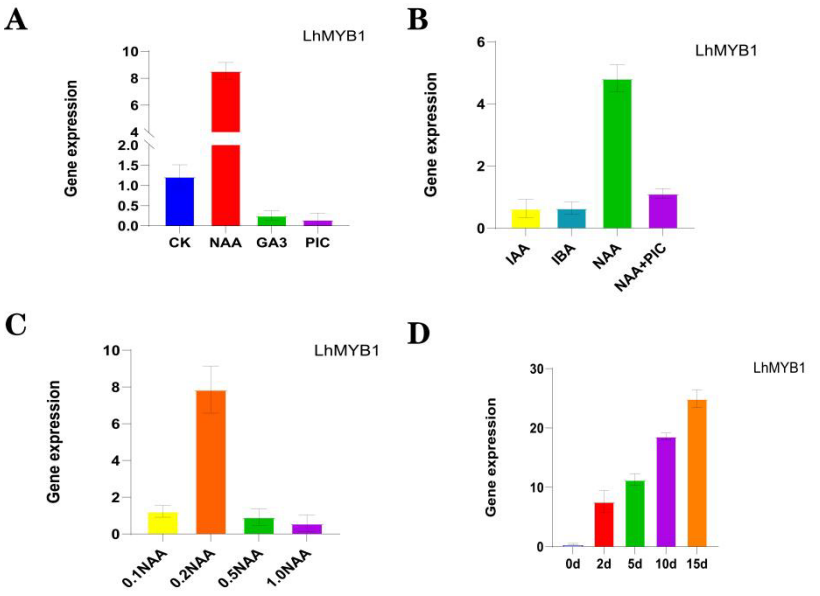

Figure S7. Analysing the relative quantitative expression of *LhMYB1* under varying conditions. (**A**) Relative quantitative expression analysis of LhMYB1 gene under different PGRs, including CK, NAA, GA3 and picloram. (**B**) Relative quantitative expression analysis of LhMYB1 gene under different PGRs, including IAA, IBA, NAA and NAA+picloram. (**C**) Relative quantitative expression analysis of LhMYB1 gene under different NAA concentrations, including 0.1 mg/L, 0.2 mg/L, 0.5 mg/L and 1.0 mg/L NAA. (**D**) Relative quantitative expression analysis of LhMYB1 gene under different days, including 0, 2, 5, 10, and 15 d.

Table S1. List of gene-specific primers used for gene cloning.

	Gene and primer name	Forward primer (5' to 3')	Reverse primer (5' to 3')	Source
Gene cloning for pGXT-LhMYB1	*LhMYB1* (MYBF/MYBR)	ATGGGAAGGCCACCTTGCTGTGAC	TTAGAACAACTCATCCCCAGTATC	This study
Gene cloning for pCAMBIA1302-LhMYB1	*LhMYB1*(MYB1F/MYB1F)	GGCATGGTAGATCTGACTAGTTTTCACA GATCAGGAGGAGA	AAGTTCTTCTCCTTTACTAGTGTGGAGGATAGGG CAACA	This study
Gene cloning for TRV2-LhMYB1	*LhMYB1* (MYB2F/MYB2R)	TGAGTAAGGTTACCGGAATTCATGGGCA GCTATAGCATCCT	GGGACATGCCCGGGCCTCGAGTCAATAGCGATG GCTTCGTA	This study
RT-PCR for CP	*CP* (CPF/CPR)	CTAACAGTGCTCTTGGTGTGATT	CAACTCCATGTTCTCTAACGAAGT	This study
RT-PCR for MP	*MP* (MPF/MPR)	CGCAGTACAAGGTTGAATACAGT	CTCAATCGTCTTCATCTCCACTT	This study
qRT-PCR for LhMYB1	*LhMYB1*(RtMYBF/RtMYBR)	CATTGCTGGAGTGGTTGT	ATCCCCAGTATCAAGTTTC	This study
qRT-PCR for BZ1	*BZ1(BZF/BZR)*	CGAGAAGCAGATTGGGTTGTT	TCAGTGTTGAGGTGGGCAGA	This study
qRT-PCR for CHS	*CHS(CHSF/CHSR)*	CGAGTGCCTGCGTGTTGT	CCATCTTCGCTGATGTCTTTC	This study
qRT-PCR for CHI	*CHI(CHIF/CHIR)*	CTCCTACTCCTTCTCATCACC	GGAGGAAGATGAAGATGGTAG	This study
qRT-PCR for F3′H	*F3′H(F3F/F3R)*	AGAAATGGCTCCGGTTGC	CCGAATCGGTCCATCCTC	This study
qRT-PCR for DFR	*DFR(DFF/DFR)*	*GCAAGAAGGTGATGGCTCAG*	*TGGTTGATCTCGCCTTTCCT*	This study
qRT-PCR for FLS	*FLS(FLF/FLR)*	AGTGCAAGCCCTAGOCACC	ATGCTCGGAGCGGATGAA	This study
EF-1a as an internal reference gene	*EF-1a(EFF/EFR)*	GCATCACACCTTCTACAACG	GAAGAGCATAACCCTCATAGA	This study