

>a. *LOC115700576*, genomic DNA

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GCCATAAGAAAAAATAATTTTGGACCCCTTATGTTAGAAAAAATATGTTATTTTCAAAGTCAGTAAATATATAATTTTAAAAAGGGAAA
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ATTACACACGGTACTGTTTTTTTATAAACTTCTTTTTTACTGTTACACGCATATATTTCTTTTTTACTGTATAATCTACATATTGCATACTGA
ATTAGTATAAAGTTTTTCCCTTTTATGTTTTTGTCACTTCAAGATATGTTTTTTTATTATTTTTTAAAAAATAATAAAGTTGATGGAA
AAATCGATTGTCACGTACGTACATATATATATATATATATTTTTTTTTTAAAAAATAAATATGAAAGTTTATTGTATTAAATAG
TAAAAAAGTTTTGATGTGATGGTGTGTCATTTGTGAATTTTTTTTTTTTTTAAAAAATAAATAAATAATCATGAAGAGCTTAATATA
CATCTTCTAGTTTCTACACATTATCTTTTTCTTTTTAAGTATAATAGCTTTTATTACTTATTTTCATTGTATTGAGCTCTCTCTACTATTAC
CTTCTTCTTCAATTATTTCTTTTTTTTTTCTCAAATCTATAATATTACCAAATAAAGTATCTCTCTCTTTTGTAGTATGTAATAAAT
AAAAACAGCATGTGAAGGAGGAAGAAGAAGAAATGAGAAAGATGAGAGTGTGGTTCTGTGTGTGAGAGAGATGGAGAGCTTGCTCT
GTGATGAACCTCTTGTAGAAATCTTTCAGAACTCC

>c. *LOC115701144*, PREDICTED: Cannabis sativa truncated transcription factor CAULIFLOWER A, mRNA

TATTTGCTTCTGTCTCTGTCTTTTTTGGAAAAATAAATATCTATGCTAATGTTATGGTATACGGTAGGTAAGAGAGGATTAGAAAACTTTAA
CCTAAAGGCCGATAAGAAAAAGGCATAAGGCTTATACAAGAACTATATTTATATATATATATAGTAGTTTAGCATATGAAGATTACTATATA
CATTTAAATTCATAATTTGGCTATATAGAAATATATATTTTATATTTGAATATGGTAGGGGAAAGGTGGAAGTGAAGAGGATTGAAAACAAGA
TAAATCGACAAGTGACCTTTGCTAAAAGAAGGAATGTTTGCAGGAAGGCTTATGAGCTCTCCGTTTATGTGATGCTGAGGTTGCTCTAA
TAATCTTTTCTGCTCGAGGCAAACTCTTTGAGTTTTCGACGGCCCTAGCATCACCAAGACACTTGAGAGGTATGAAAGATGCTGCTATGCAG
AACAGGAAAGCAAACTACTATCAGGAAAGGACATAGAGTGGTCAATTATCATACATACAGAGTACCTATCAAGAGTATCTAAAGCTGAAAGAA
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TGGAAGAAAAACAATTTAAAAAATAAGTTGGAGGAAATTTGTGGATTGTTGGTAAACAAGGTGATGATCATGGGCAGCACAATGTTGCA
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GTACTGCTAATCAAGAATGATGAGTGGTCTGGAGAAAATGTGGGTGCAGCCCTTCAATGAAAAATTTGATGGCTTTCAATTCAGTAGACC
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TCGTAAAAGAGAGCACAGCTATCTTTAGCTACTCATTGGGAATTACATATATGTTAAAAGATTAAATATTATTATACAATATATATACATTATT
ATGTTATC

>f. *LOC115701144*

MGRGKVELKRIENKINRQVTFAKRRNGLLKKAYELSVLCDAEVALIIFSARGKLFECGSPSITKTLERYERCCYAEQESKLLSGKDIEWLSYIQST
YQEYLKLKEKVEHLRRTQRNILEGDEHLGLNEIQLEQKLDMSLKKIRSTKNEHMIDEFSLHRGQEMLMEENNKNKLEEICGLFGKQGGD
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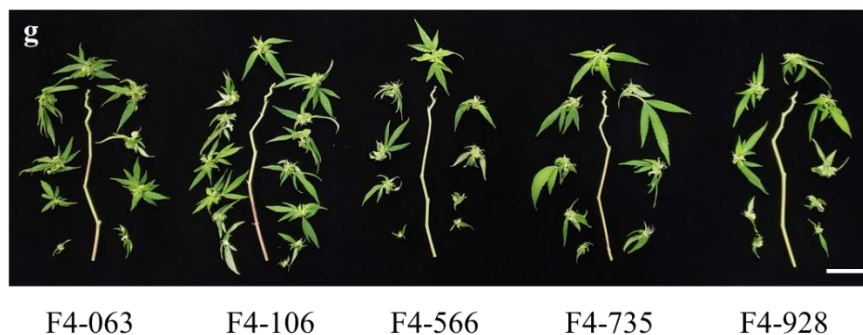


Figure S1. Additional sequence variation in the targeted region from 33,283,738 bp to 33,422,574 bp on chromosome 8 for cloning of *QId.ibfc-8L*. a. *LOC115700576* gDNA sequence. The *LOC115700576* sequence is located between 33413255 bp and 33421815 bp in the NCBI Cannabis Sativa.cs10 reference genome. The start codon, the stop codon, and splicing sites of the intron are highlighted in yellow and with red letters. The highlighted sequences at the 5' end and 3' end served as primers to amplify *LOC115700576* in DMG12 and YMG26. The sequence differences in the promoter region are highlighted in red and square brackets. b.

LOC115700576 mRNA sequence. No difference was found in the coding region between the DMG12 and YMG26 allele. c. *LOC115700576* is annotated as a transcriptional regulator of MEF2-like/Type II subfamily of MADS box family. d. *LOC115701144* gDNA sequence. The *LOC115701144* sequence is located between 33,319,405 bp and 33,379,536 bp in the NCBI Cannabis Sativa.cs10 reference genome. The start codon, the stop codon, and splicing sites of the intron are highlighted in yellow and with red letters. The highlighted sequences at the 5' end and 3' end served as primers to amplify *LOC115701144* in DMG12 and YMG26. Two SNPs that did not result in amino acid substitution are highlighted in red and square brackets. No difference was found in the promoter region between the DMG12 and YMG26 allele. e. *LOC115701144* mRNA sequence. No difference was found in the coding region between the DMG12 and YMG26 allele. f. *LOC115701144* is annotated as a transcription factor CAULIFLOWER A F-box protein. However, the deduced protein from the coding region does not match with any F-box protein or any other known proteins. The deduced protein from the coding region of *LOC115701144* is a hypothetical protein (GenBank accession no. XP_030484710.1) in Cannabis. g. Image of dissected branches for the five critical recombinants (F4-063, F4-106, F4-566, F4-735 and F4-928). The scale bars represent 1 cm.

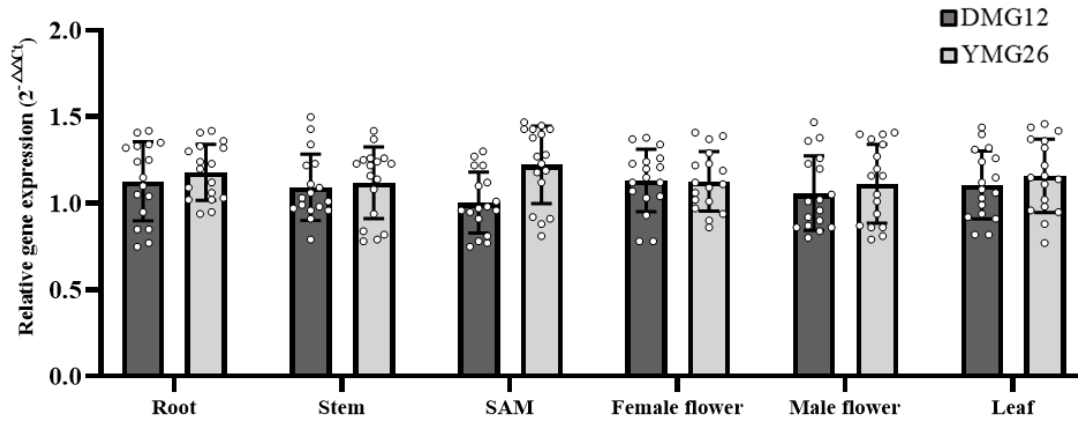
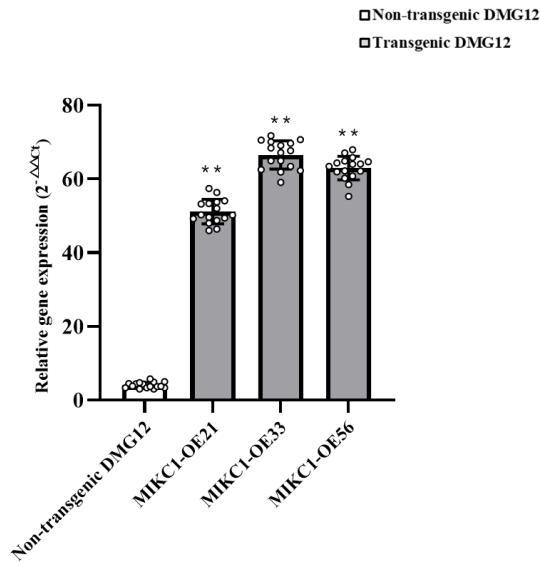


Figure S2. Transcript levels of *LOC115701144* in different tissues in DMG12 and YMG26. The RNA samples were collected one week after anthesis from different plant tissues, including root, stem, shoot apical meristem (SAM), female flower, male flower, and leaf. Transcript levels of *LOC115701144* were analyzed using qRT-PCR and calculated using the $2^{-\Delta\Delta CT}$ method, where CT is the threshold cycle. The mean transcript level between the two alleles using a two-tailed unpaired Student's t test; the bars indicate the standard error.

a.



b.

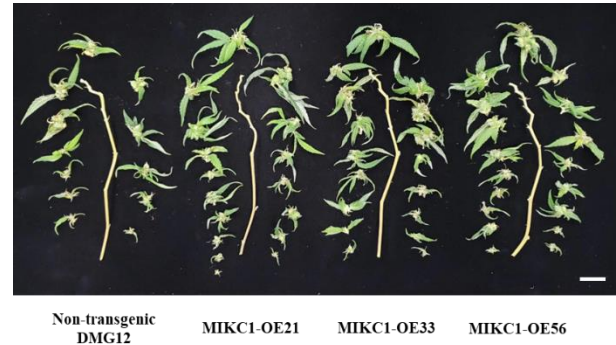
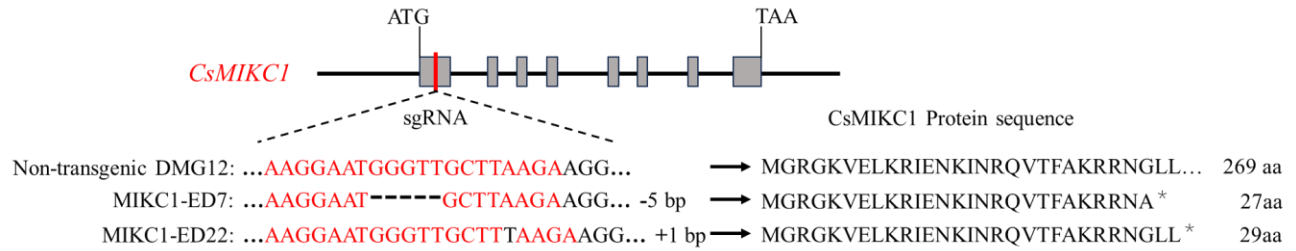
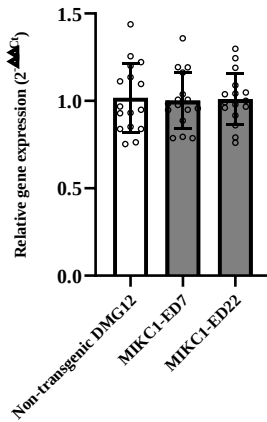


Figure S3. a. Transcript levels of *CsMIKC1* in non-transgenic DMG12 plants, MIKC1-OE21, MIKC1-OE33 and MIKC1-OE56 transgenic plants. The RNA samples were collected from seedling leaves. Specific primers MIKC1-rt-F1 and MIKC1-rt-R1 were used to amplify overexpressed *CsMIKC1* in the host plant DMG12. The transcript levels in the leaves were calculated using the $2^{-\Delta\Delta CT}$ method, where CT is the threshold cycle. The mean transcript level was analyzed ($n = 16$), and the ANOVA with a Tukey's HSD test shows no significance in *CsMIKC1* transcript level between different transgenic plants. b. Image of dissected branches of non-transgenic DMG12 plants, MIKC1-OE21, MIKC1-OE33 and MIKC1-OE56 transgenic plants. The scale bar represents 1 cm.

a.



b.



c.

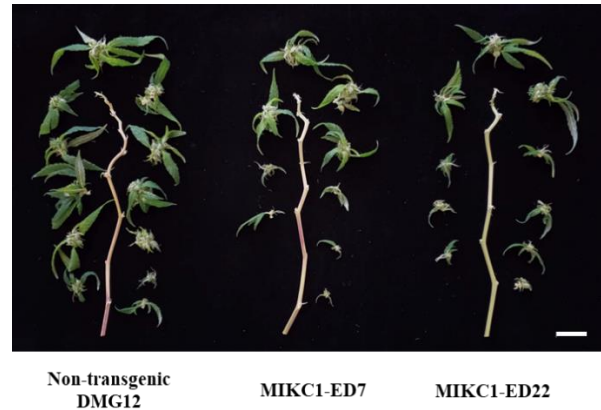


Figure S4. a. CRISPR/Cas9-mediated mutations in *CsMIK1*. The position and sequence of the gRNA used to edit *CsMIK1* are indicated. Edited sequences (highlighted in red) include a 5-bp deletion in the MIKC1-ED7 plant and a 1-bp insertion in the MIKC1-ED22 plant. Protein sequence alignment indicates a predicted loss of 242 a.a. starting at position 27 in the MIKC1-ED7 plant, and a loss of 240 a.a. starting at position 29 in the MIKC1-ED22 plant. The symbols ‘-’ show the nucleotide deletion. The symbols ‘*’ represents early termination of translation. b. Transcript levels of *CsMIK1* in non-transgenic DMG12 plants, MIKC1-ED7 and MIKC1-ED22 transgenic plants. The RNA samples were collected from seedling leaves. Specific primers MIKC1-rt-F1 and MIKC1-rt-R1 were used to amplify expressed *CsMIK1* in the host plant DMG12. The transcript levels in the leaves were calculated using the $2^{-\Delta\Delta CT}$ method, where CT is the threshold cycle. The mean transcript level was analyzed (n = 16), and the ANOVA with a Tukey’s HSD test shows no significance in *CsMIK1* transcript level between non-transgenic and transgenic plants. c. Image of dissected branches of non-transgenic DMG12, MIKC1-ED7 and MIKC1-ED22 mutants. The scale bar represents 1 cm.

Relative gene expression ($2^{-\Delta\Delta C_t}$)

Legend: DMG12 YMG26

Tissue	DMG12 (Mean)	YMG26 (Mean)
Root	~1.0	~1.0
Stem	~1.4	~1.5
SAM	~1.4	~1.3
Female flower	~1.5	~1.4
Male flower	~1.35	~1.35
Leaf	~1.45	~1.45

>a. *LOC115722185*, PREDICTED: Cannabis sativa protein BASIC PENTACYSTEINE2, genomic DNA

[illegible]

b.

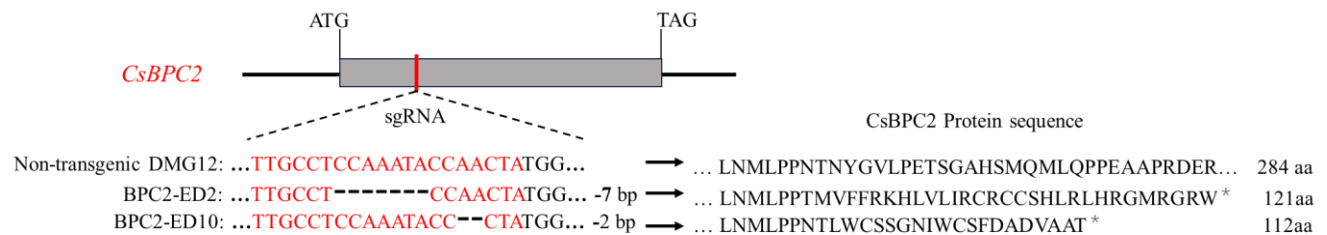


Figure S6. CRISPR/Cas9-mediated mutations in *CsBPC2*. a. *LOC115722185* gDNA sequence. The *LOC115722185* sequence is located between 56503735 bp and 56505825 bp in the NCBI Cannabis Sativa.cs10 reference genome. The start codon, the stop codon, and splicing sites of the intron are highlighted in yellow and with red letters. b. The position and sequence of the gRNA used to edit *CsBPC2* are indicated. Edited sequences (highlighted in red) include a 7-bp deletion in the BPC2-ED2 plant and a 2-bp deletion in the BPC2-ED10 plant.

Protein sequence alignment indicates a predicted loss of 163 a.a. starting at position 121 in the BPC2-ED2 plant, and a loss of 172 a.a. starting at position 112 in the BPC2-ED10 plant. The symbols ‘-’ show the nucleotide deletion. The symbols ‘*’ represents early termination of translation.

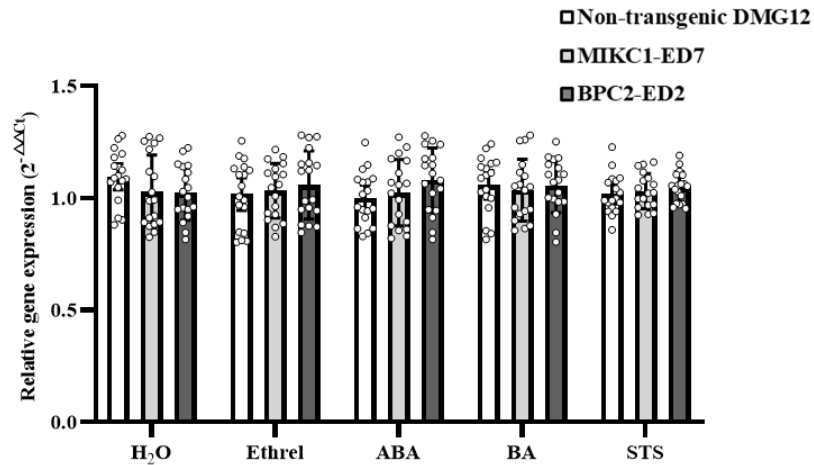


Figure S7. Relative expression levels of *CsBPC2* in non-transgenic DMG12, MIK1-ED7 and BPC2-ED2 treated with H₂O, Ethrel (synthetic ethylene), abscisic acid (ABA), Benzyladenine (BA, a kind of synthetic cytokinin) and silver thiosulfate (STS, a ethylene inhibitor). Gene expressions were quantified by qRT-PCR with eighteen replications and calculated using the $2^{-\Delta\Delta CT}$ method, where CT was the threshold cycle. Data are presented as mean ratio $\pm$ SEM.

>CsCOL2 (*LOC115714019*), mRNA

ATGGAAAAAATATGTGAATTTTGC TCAGAATTTAGGCCAGTGATTACTGCAAGGCAGATGCAGCACACCTCTGCCTCTGTTGCGACGCGAA
AGTTCATTCCGCGAATGCCCTTTCGAGTAGGCATTCGAGGATGATACTTTGCGATTCTTGCAGATTTAGGCCATCTAGAGTTCAAGTGGTTAGAT
CAGCAAAATGTTTGTGTTGTGGGATCTGTGATGGCGCCGCGCTCCACGAGGCCTCGGGAGGGCTTCAAAGCGAGCCATCGGAAGCTTCATG
GATCCCCCTTCGTAAGGATTTTGCAGCCTTGTGGGTTTAAATTAAGTGATAATGATGATGATGATAAACAAGTTTGTGGCCTCTTCT
TCACATTCTCTGGTGTATACCAATGTGGTCAATCAACAAGTTAAGATAAAAGATGAAAGCAGAGAAGCAGTAGTAGTTTATTATGCAACAA
ATTATGGACTTAAAAAGGCTTCAACTCACTCAAGTGAGTAAACCTTCACCAACAACAACAATACTAATACTAATGGCCAAGAACAAGCAA
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CAGAGTAATCAGTTATGGACTCAAAATATGGAAGACCTTGGAGATGTGTGAAGAACCTTGTGGAAGGATGATTTAATATCCAGATGCGGATT
TGACATTTCGAAACTTTGAAGAACATATTGTACAAAGATCCAAACAGATGCTTTATTGCTGTATGATAAAGATGACTCATACTCTTCTATGGAAAA
GGGTTTGTCTCTTGATAAAATTCATAATCCTCACTCAAGAATCATGGAGGATGCTTCAGTGGATTCTCTCAATTTTGTGACAACAATTCTAATCTAG
CAAGCATGAACATATAGCCTTGTCCAGTTCAACCATCTTATTCAAACATGTCTCTTTCAGTTTCAAATTTAGTGTCGATAGTGACGGTGGTGG
TAACAACCGTGGTGAATCATTTGGACAGCGGCCTTTCCCCGTACTTTGGAGGAGCGCGAGTCTTCTATGAATTTCTCTGATTTCGATTTCGAAGC
TAGAGAAAATGCCAAGTTGAGGTACAAAGAGAAGAAGAACTCGAATGCATGATGACATGATAACCAATTCGATACCCATCTAGGAAGTAA
ATGACAGATGTGAGGAAAAAGAGTAAAGGGCGTTTTGTGAAGAGAGAAGGCTATAATTCCGATAGCGCGACGCTGCACGAAGCTAC**TAA**

>CsCOL3 (*LOC115697429*), mRNA
GTGAATAGTCCCAGATCTCGAACGGGTAACAGTGTGCCCTGTGATTTCTGTAGTGAACAGGTTGCTGTTCTCTTCTGTAGAGCTGACTCT
GCTAAGCTATGTTTGTCTGCGACCAACACGTTCACTCAGCCAACCTTCTTTACGTAAGCATCTCCGATCTCAGATCTGTGACAATTGTGGCT
CCGAACCGTCTCCGTCCGTTGCTCTACCGAGAATCTTGTCCTTTGCCATGACTGTGATTGGGACGCTACCGAACTTGTTCTGTCTCCCGG
CACACGAACGGAATTCGTCGATGGATTCTCCGGTTGCCATCAGCTCTCGAGCTCGCTCGGTTTGGGGTTTTCATCTTGGGAAAAAGAAAT
CGGGTCGGCCCGATTCCACAGGTTACAGAAATACGAGTTGGGTATGGCTATGCCTGAGGTGAGGACACATCTTGGTCTGGAGTGAATTTTCAG
GACCTTATTGTTCCGACCGGGAACCGCTTGTGGAGAAAGGGAAGAAGAAACAGAGGGGAATGGGTGGTGTAGCTGCTCGGGAAGAAGAAG
CAGGTGATGTATAAGCAGTTGGTGAGATTGCTTAAGAGGGATTGTGGTGGCCCTGAAAATGACGAATTTGGCGATGATGGTTGCGGAGGAGA
CAACGGTTGTAGTGGTGGTGGTGGTGTGAGAGCTTAATGCCGAGAATTCAAATCGGAGTAGTTGGCAACGGAATGCTGAAGCAGCACTC
AGTTTGGGTGATGGCTGTGATGCTGTTGATGATGTTGCTTTGCAGCTCAGCCATCTTCACTCAATTCACGTCTCTACTAATGATGCCAATGC
ACTGTGAATTGAAGAAATGATGGCATTGACGATGGTGATTGGCAATGTGGGATACCAACCCCAATGGTCCAACCACTCAGATATGGGATT
TCCATTACGGGAGGTGTAGGGTTAATGAAGAACCAAGTAAGTAACAGGGGCTAATGATGGAGGGTTATGATGAATGAAGACTTTTGTGATCTT
TGAATTGCCCTGTTGCACCATGATGACATGACTATCAATAATAGTAGCCAAGGAGGACGAACCTCGGAGAGCAACAATCTACCTATTGGAAG

GGGTCATCGTCTAGTACTTCAGCTTTGGGTAAGCACAAAAACGAAGAGTGTAGTGCCTCGAGAGAGGTGTATTTTCATGGAACAACCTTTTCT
TGTGAGAAATGACACTATGAAAAAGGTGCAACATCAAAGGAAGAGTTGGAGGTTTTGGCTCACAAACAGAGGCAATGCTATGCAACGTTAC
AAGGAAAAAGAAAAACAGAAGATATGACAAACACATAAGGTATGAGTCGAGAAAAAGCAAGAGCTGATACTAGGAAGCGTGTAAGGGT
CGGTTCTGTAAGGCTGCTGAAGCAGCTCCAGACGGC**TAA**

>*CsSOC1 (LOC115706939)*, mRNA

ATGGTGAGAGGGAAGACTCAAATGAGGCGCATAGAGAATGCCACAAGCCGTCAAGTGACGTTTTCTAAAAGGAGAAATGGGCTTCTGAAGA
AGGCCTTTGAGCTCTCAGTTCTTTGTGATGCTGAGGTGGCTCTTATAATCTTCTCCCAAGAGGAAAACTCAATGAATTTGCTAGTTCAGCAT
GCAAGCTACGATAGAACGTTATAGGAAGCACACTAAGGACAATCAAACCTCACAAAAATCTGTTGAACAAACCATGCAGTTGCAGCAATTGA
AACAGAAGCAACTGCCATGATGAAGAAGATAGAGCTTCTGAAATCTCCAAACGGAAATTTTTGGGAGAAGGTCTGGGTTTCATGCTCCCTT
GAAGAACTACAACAAGTAGAACAACAGTTGGAGAAGAGTGTAACAAAAATTCGAGCAAGAAAGAATCAAGTTTTCAAAGACCAGATTGAG
ATACTTAAGGAAAAGGAAAAAGCCCTAACATCTGAAAATGCAAGGCTTTCTGAGAAGTATGGTATTAAACCAATGGTTCAAGCATCAAATAAT
AATAATAATAATAATAACAATAATAATAATAAACCATAAGCAGATAGAGGACTTGAACAACACAGAAAGTAATCCCAGTTCAGATGTGG
AGACTGAACATATTCATTGGGCTACCAGAAACAAGATTAAAGCGTCTACTTCCAAAGAAA**TGA**

>*CsFLK1 (LOC115716317)*, RNA

ATGGCTGAACCAGGTGAACCTCCGTTAAACCCCTTGGGTACCCTCGTTGCGCCTGTTTATGGATCCGAGACCGGTCAATCAGCTGCCGGAAA
GCGCCGCGGGAGGAATATTCTCCGGGTGTGATGTCACCGGTGGGCGATGGAGATGAGTCGGCATCCAAGCGCGGGTCAAGGGCCAGGAC
GTGCTGTTTCAAGATCGTTGTTCCGTCGAGGCAGATTGGCAAGGTCATTGGTAAAGAGGGTTGAGAATACAGAAGATTCCGGGAGGAGAGCA
AAGCCACTATCAAAATCGCCGACGCTGTAGCGCGACATGAAGAAAGAGTGTTATTGTAAATTCAAAGGATAGTGACAACCTCGGTTTCAGAT
GCTGAGAATGCTCTACAGCAAATTGCGAGTTTGATTCTGAAGGAGGATGATAGCACTCCAGAGGCATCCAAAGTTGGGGCTGGACATGTGGC
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TACAGTCCGACCGATCCCACTTACATGGACCCATCATCAGCTGATTATGTAACCTTCGAGATGGTAATATCAGAAACCTGGTTGGTGGTTTG
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ACAAATTCAGTTTGGTGGGAGCACCAACAGGTTGCACTGGCCAAGCAGAGAGTTGACGAATACATATATTCTCAGTTGATCCAACACAGCTG
GCGTCAACAAGCAAGCAACAATACTGAGACAATGAAGGGTGACCCAAGAACTTGGACCATGAATTCAGTTGTATACCTTCATGATAAATAT
CCTTGATTTTCAAGTCTTGCAATGCAAGTTGTGCGCGATGCGGTTTCCGCTCTACCT**TGA**

>*CsMBP21 (LOC115709018)*, mRNA

ATGGGAAGAGGGAGAGTAGAGTTGAAGAGAATAGAGAAACAAATTAACAGGCAGGTCACATTTGCCAAGAGAAGAAATGGGCTTCTCAAG
AAAGCTTATGAGCTCTCTGTCTCTGTGAGGCTGAGGTTGCCGTTATTATTTTCTCAACCGTGGGAAGCTTTATGAGTTCTGTAGCGGCTCCA
GTAGCATGGTGAAAACGGTAGAAAAGTACAAGAAGTATAGTTATGGAGGACTGGACGCTACTCAACCTTTAATTGACTCTCATGAGAACAGC
TATCAGGAATATTTGAAGCTAAAAGCAAGAGTAGAGGTTCTACAGAAATCTCAGAGAAACCTTCTTGGGGAAGATCTCGGACCGTTGAATAC
AAAGGAGCTCGAGCAGCTAGAGAATCAGCTGGAGATATCTTTGAGGCATATTAGGTCAACAAAGACCCAGTGCCTGCTTGATCAGCTTAATG
ATCTTCAACACAGGGAACAATCTTACTTGAAGCTAACAAAACGTTGAGAAGGAAGTTGGAAGAAAACAGTACTCAAAATCCACTTCGACT
TGGATGGGAAGCTGCAGCGGAGGAACACAATAACAATGCCTACACCCACCTTCTCTCTCAACAGATCAAGGCTTCTATCAGCCTCTCGGAA
ACAATTGTACCTTGCAAACTGGATACAGCAATTCGATGGGCCCACTGAAATGAATGGTGAGCCCCGCCCCAACTTTGAACGGGTACATG
CATGGATGGATGCTT**TGA**

>*CsAGL19 (LOC115716986)*, mRNA

ATGGTTAGGGGAAAAACTCAGATGAAGCGAATAGAAAATGCAGCAAGCAGGCAAGTGACCTTTTGAAGCGTAGAAAATGGTCTTTTGAAGA
AGGCGTTTGAGTTATCAGTTCTCTGTGATGCTGAAGTTGCACCTATAATTTTCTCTCCAAGAGGAAAGCTCTATGAATTCGCAAGTTCTAGATG
CTTCAGCATAAAACAAGACCATGAGCGGTATACTCAAAGGAGAACCAAGGATGGTGGCAGCTGCCTCACCTCTAATAAAAACTATTTCTGAAG
ATGATCATCATGATCTACAGGCTGCTGTAAGTAAGGAAGATTCTTTAGCATGGCAAGAAAATGATCATCTTGAAGTTTCTAAAATGAAGCT
TTTGGGGGATGGATTGGAGTCATGTTCTTCCAAAGAGCTACATCAATAGAGAATCAGTTGGAGAGAAGCTTAGCTAAAATCAGGGCAAGAA
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GTGTGGGATGTTACAAAAAGTTAGTTTCAAGGAAGTGAAGAGAAGGAAGATCAGGTGTTGGTGGTAGTAAATAATAATAACAATGCTCATGATC
ATCATCGTCATAACATGGACGTGGAGACGGAGTTGTTTCATAGGCCTACCTGAAAGAAGAAAA**TAG**

Figure S8. cDNA sequences of the 6 homologous genes which were commonly demonstrated to promote flowering and inflorescence development in dicot plant species. The start and stop codons are highlighted in yellow and with red letters.

>a. *LOC115707890*, genomic DNA

ATAAGTTACACAGTAAAGTGAGGCCCAATTTTAGTGAGCAGAAAGCAGAAACCCAATACCCAAATAAAACCCCTCAGACAACAAAACAACGCA
CAGTGAGTTACTGGCT**ATG**AAACTCGCGGACTCAAATCGTTCCGAGAACGCCACGATGAGTCCATCTGGGCGGCCACGTGGGTTCCGGCA
ACGGAGACCCGATCCGCTTCTCTGACCGGTTCCCTCGACGAGACCGTCAAGCTATGGAAGCCAGATGACCTAATCTCCAGCGAACCA
TACCGGCCACTGTCTCGGAGTGGTCTCCGTCGCCGCTCACCCCTCCGGCCACTTTGCGCGATCCGCCCTCCCTCGACAGCTTCGTTAGGGTTT
CGATGTGACACTAATAACACCTTAGCTAATCTTGAAGCTCCTCCTCCGAAGTCTGGCAATGCAATTTGATCCCAGG**GT**ATACTAACACTCA
AATTACTTTTCTTTTATTATTATTATATATTTTGTGTTGACAAAAATATGTAAAGAGTAGAAGAAAATAACTTTCTTTAGGAACTCAGTGT
TTGTGAAAAATAACGTGGACATATTTATTAGCAAAAATAACCACTTTGGTGGCACAAGAGGAGTCACTCAAAAATTAATTTGGCAAAATTTATT
GACCTTAAGTGAACATTCCGTGATTCAATGGGGTTATTTTACAAATTTTAATGCTGCCTTAAATTAATAATACTATAGACCTTAAATTTAC
ACCATGTGTAATTAATATGTTTATTTGTAAATTTATGCTGTTAGTTTACCAATTTTTCACATATATATGATGAACATAATAGTATTGGGGTT

GTGTGAAGTGTGAACAATTAGGTAAAGATTGATTGAGGAATGGGGTTTGAAAGTTCATAATTAACCCATTCTTGATATGGTATGAATATATGTTT
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CTGAGCTTTGGATTGTCTAGAAAACCTTGTTACTCAAACAAAACAGTTATCAGTTTAAAAAATTCATGGAACAATATCTATTTTACCAGGGCACCA
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TTCTCCCACCGAACCGAGGCTGCTGTTTTTCAGCCTCAGATGATGCCATGTACACATGTACGATGCTGAGGGTAAGACTCTTGTGGGGCCAT
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GGGACATCGGCATGAGGGTGTCTGTCCAGACAATGAGCAACCACGCCGACCAAGTTTGGGGAGTGGCCTTTGGACCAGCCGAGGGGCTG
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GTGATAGTTTAGAGTCATTGCAAAATTCTTGTGGTTTTAAATTTATCGAAAAATTGATTTTCATACATTGTAAATTATATAAAGCACTTCTAATAT
TTAATTTAAAATTGCCTAAAAAGAGGATCTTACTCCCATTTGTGAAATTTGCCTGTATTATGCTACTAGCCGAATTGTTGGCTTATTGCATTCAT
CAATATCATCAATGTTCCATGAAA

>b. *LOC115707890*, PREDICTED: Cannabis sativa VERNALIZATION INDEPENDENCE 3, mRNA

ATGAAACTCGCGGACTCAAATCGTTCGAGAACGCCACGATGAGTCCATCTGGGCGGCCACGTGGGTTCCGGCAACGGAGACCCGATCCG
CCTTGCTTCTGACCGGTTCCCTCGACGAGACCGTCAAGCTATGGAAGCCAGATGACCTAATCTCCAGCGAACCAATACCGGCCACTGTCTC
GGAGTGGTCTCCGTCGCGGCTCACCCCTCCGGCCACTTTGCCGATCCGCTCCCTCGACAGCTTCGTTAGGGTTTTTCGATGTCGACACTAAT
AACACCTTAGCTAATCTTGAAGCTCCTCCTCCGAAGTCTGGCAAATGCAATTTGATCCAGGGGCACCATCCTAGCAGTTGCAGGCGGGG
CAGCGCATCAGTGAAGCTTTGGGACACAGCCACATGGAATTTGGTTGCCACTTTATCGATTCTCCTGGCCTGAAGCAGCAAAACCATCTGAGA
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CTGTTTTACGCCTCAGATGATGCCATGTACACATGTACGATGCTGAGGGTAAGACTCTTGTGGGGCCATGTCGGGGCACTCTAGCTGGGTG
CTGAGTGTGGATGTTAGCCAGATGGGACAGCTATTGCAACAGGTTCAAGTGACAGAACAGTGCAGCTATGGGACATCGGCATGAGGGCTG
CTGTCCAGACAATGAGCAACCACGCCGACCAAGTTTGGGGAGTGGCCTTTGGACCAGCCGAGGGCCTGGTTCGGCTTGCTAGTGATCAGA
TGATAAGAGTATATCCCTATATGACTTCTCCATGAGAAAAGTCTCTCCTTGCAAATGAGGACTAAGAAGATT

>c. *LOC115707890*

MKAGKSNAHDSWAATWVATRSATGSDTVKWKDDRTNTGHCGVVSVAHSGHAASASDSVRVDVDTNNTANASVWMDRGTAVAGGGSASVK
WDTATWNVATSRAAKSKNSSKKVSVAVSDGRRACGMDGTSVDVGRSKHHGMVRSAYSTRSASDDAHVHMYDAGKTVGAMSGHSSWVSV
DVSDGTAATGSSDRTVRWDMRAAVTMSNHADVWGVAGAGGGRASVSDDKSSYDS

d.

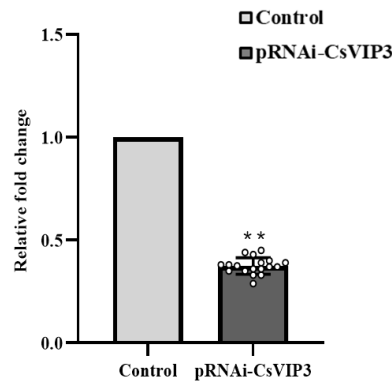


Figure S9. Effect of pRNAi-CsVIP3 vector on *CsVIP3* relative expression change. a. *LOC115707890* gDNA sequence. The *LOC115707890* sequence is located between 50441750 bp and 50443740 bp in the NCBI Cannabis Sativa.cs10 reference genome. The start codon, the stop codon, and splicing sites of the intron are highlighted in yellow and with red letters. b. *LOC115707890* mRNA sequence. c. *LOC115707890* is annotated as a WD repeat-containing protein VERNALIZATION INDEPENDENCE 3 (VIP3). d. Relative fold change was investigated three days post agroinfiltration. Leaf material infiltrated with disarmed *Agrobacterium* were set as control. Significance is determined by paired t-test, ($p < 0.01$) is denoted by **. Error bars represented SE.