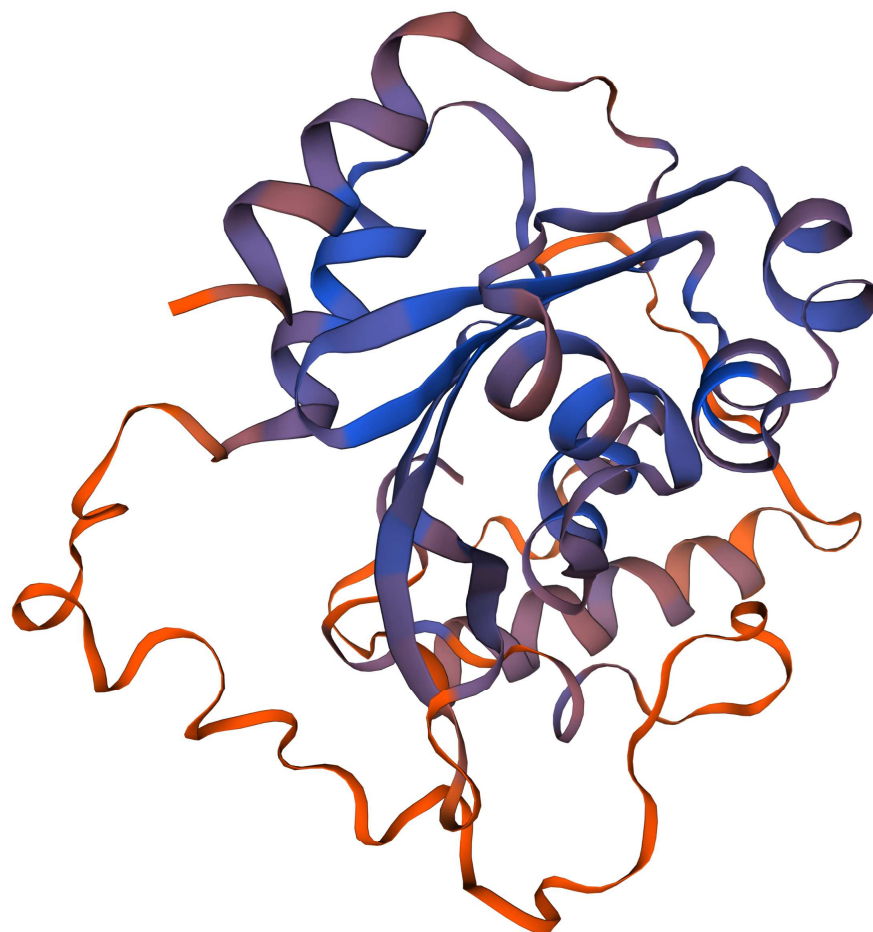
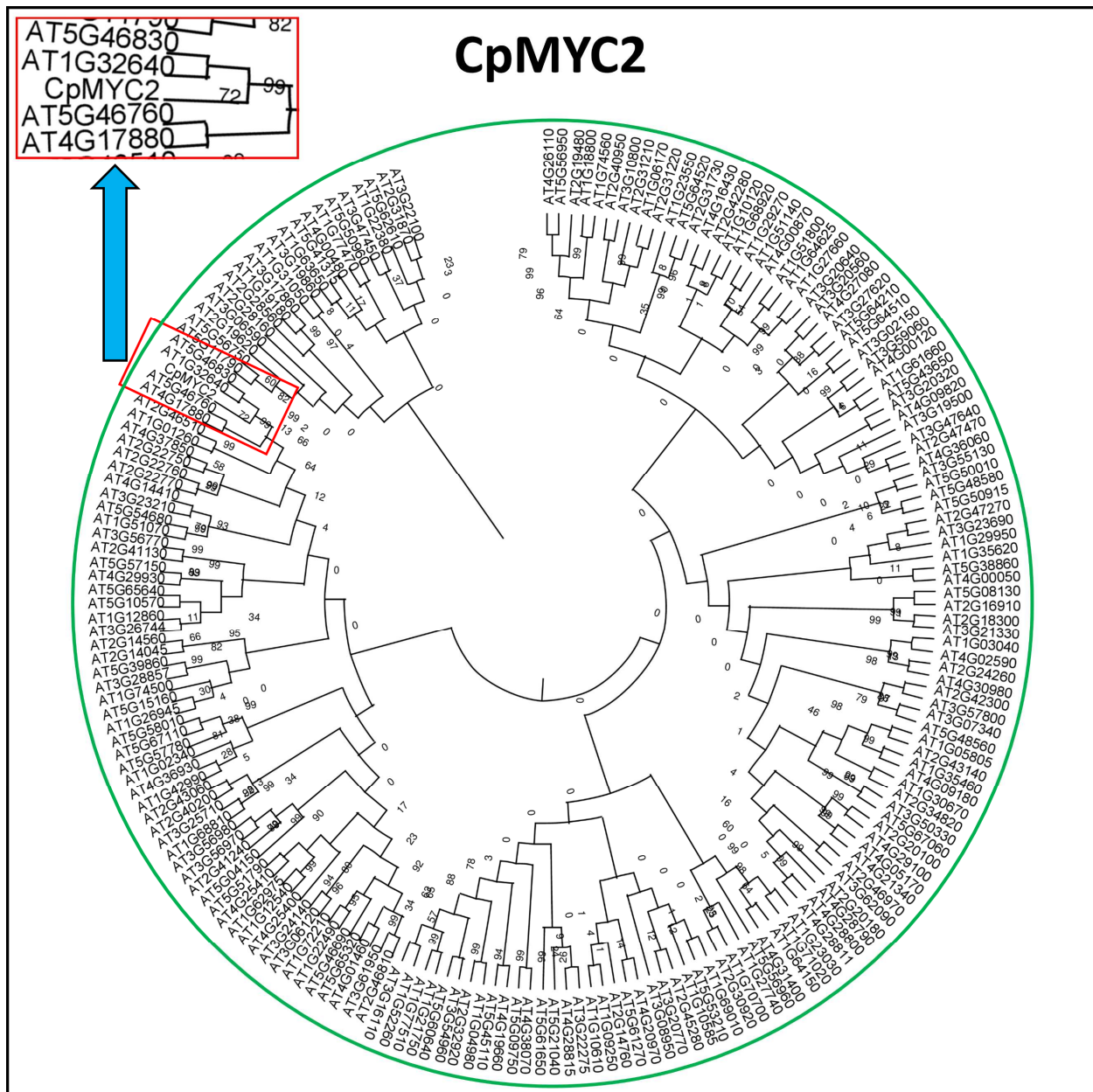


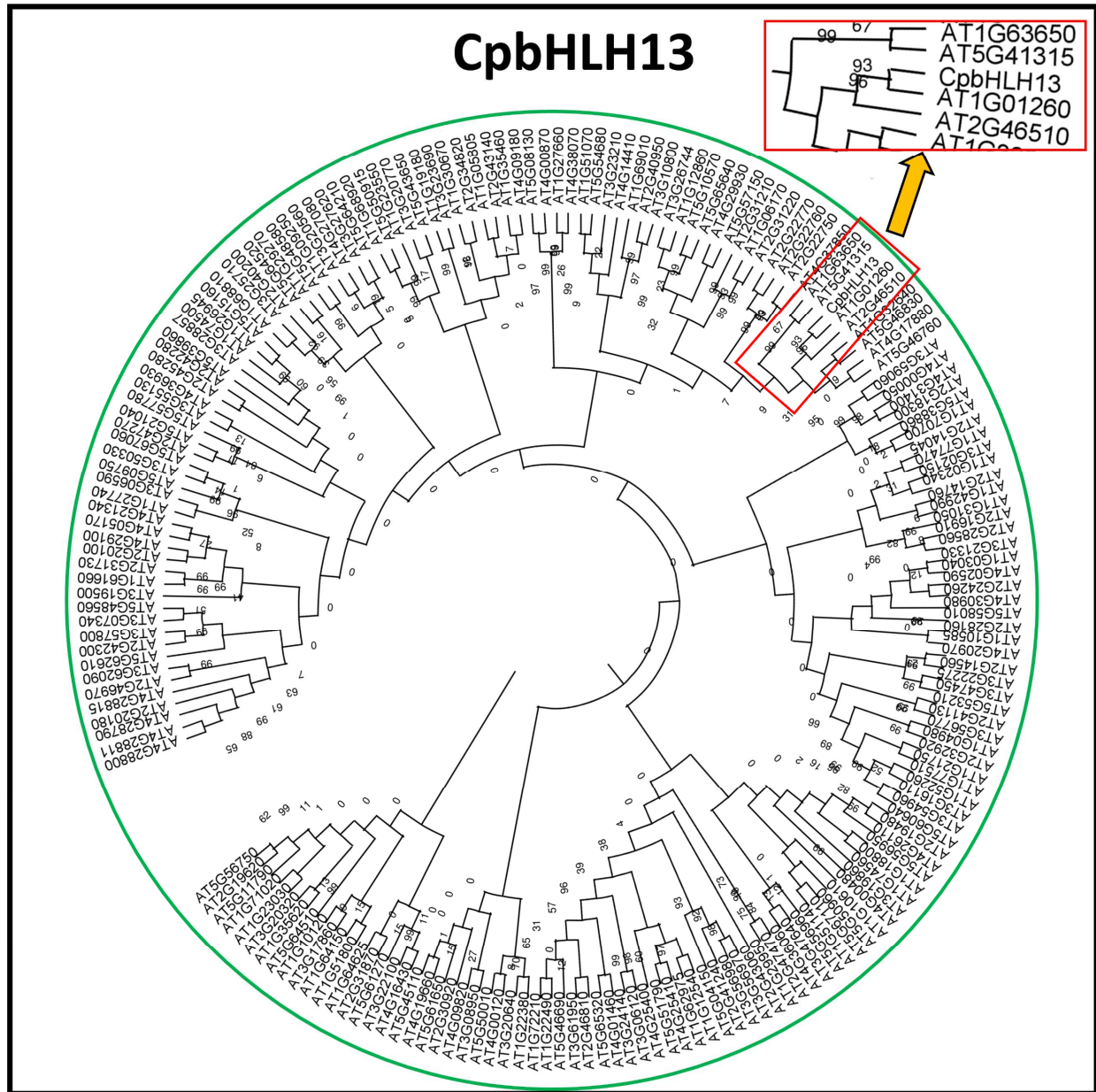
Supplementary Fig 1- Three dimensional structure prediction of the protein encoded by *CpMYC2* Gene.



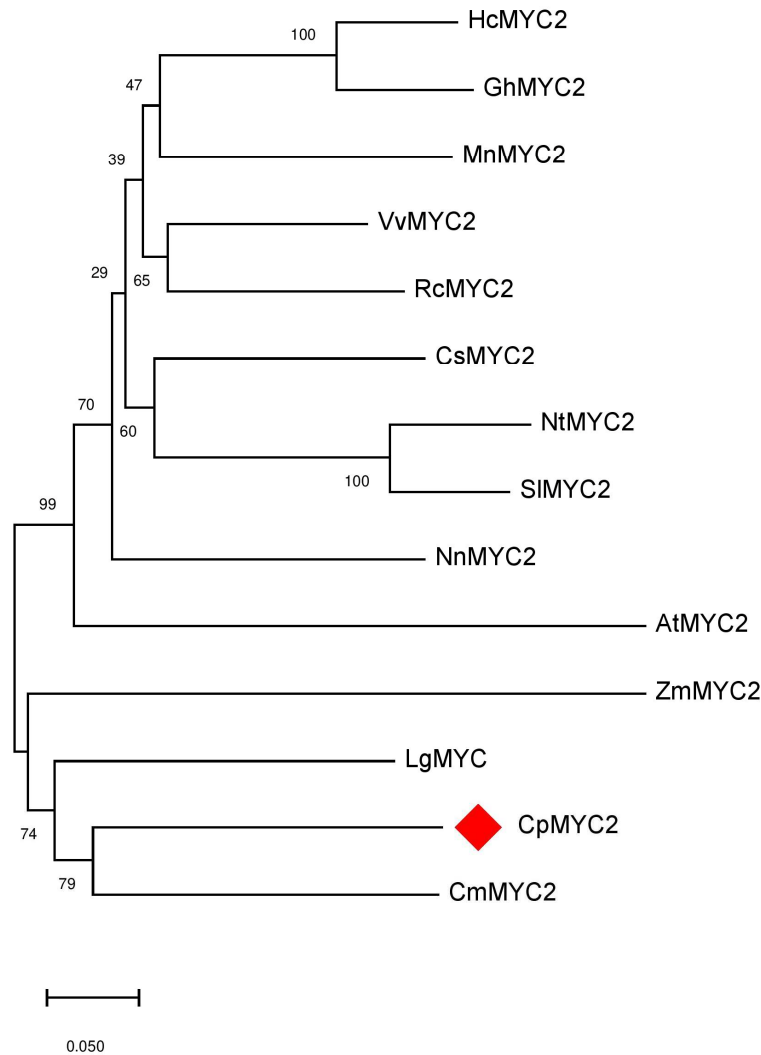
Supplementary Fig 2- Three dimensional structure prediction of the protein encoded by *CpbHLH13* gene.



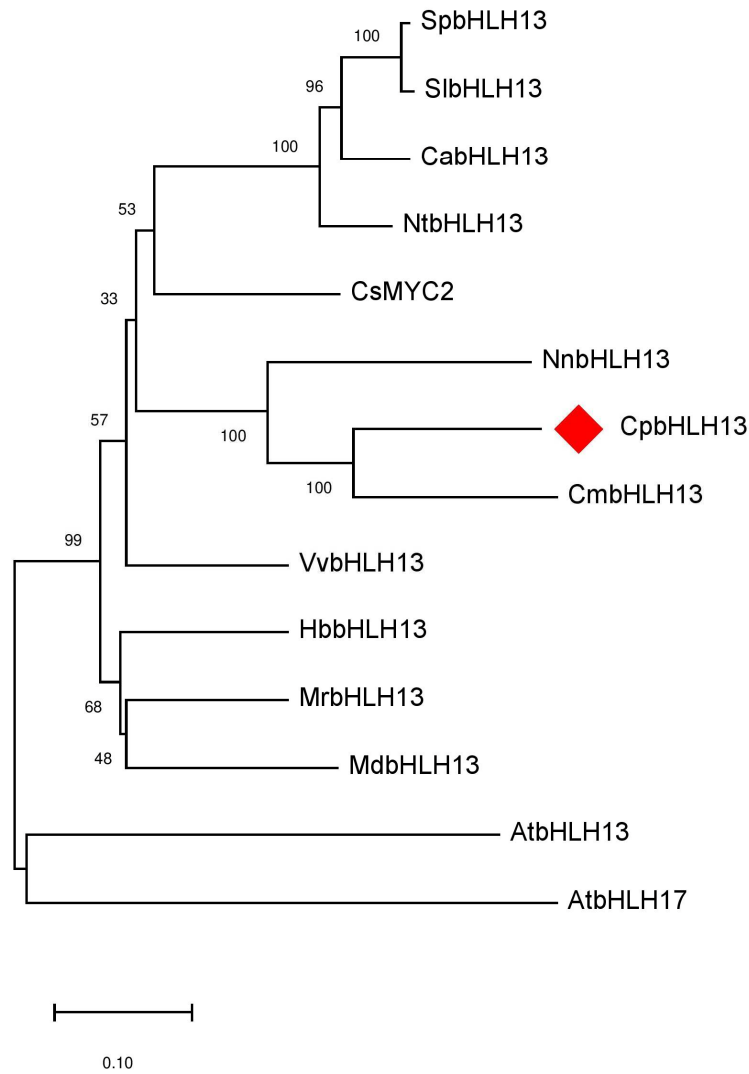
Supplementary Fig 3- Phylogenetic analysis of wintersweet *CpMYC2* with *Arabidopsis* bHLH transcription factor gene family. **The red** box indicates the close homologous bHLH of *Arabidopsis* with *CpMYC2*.



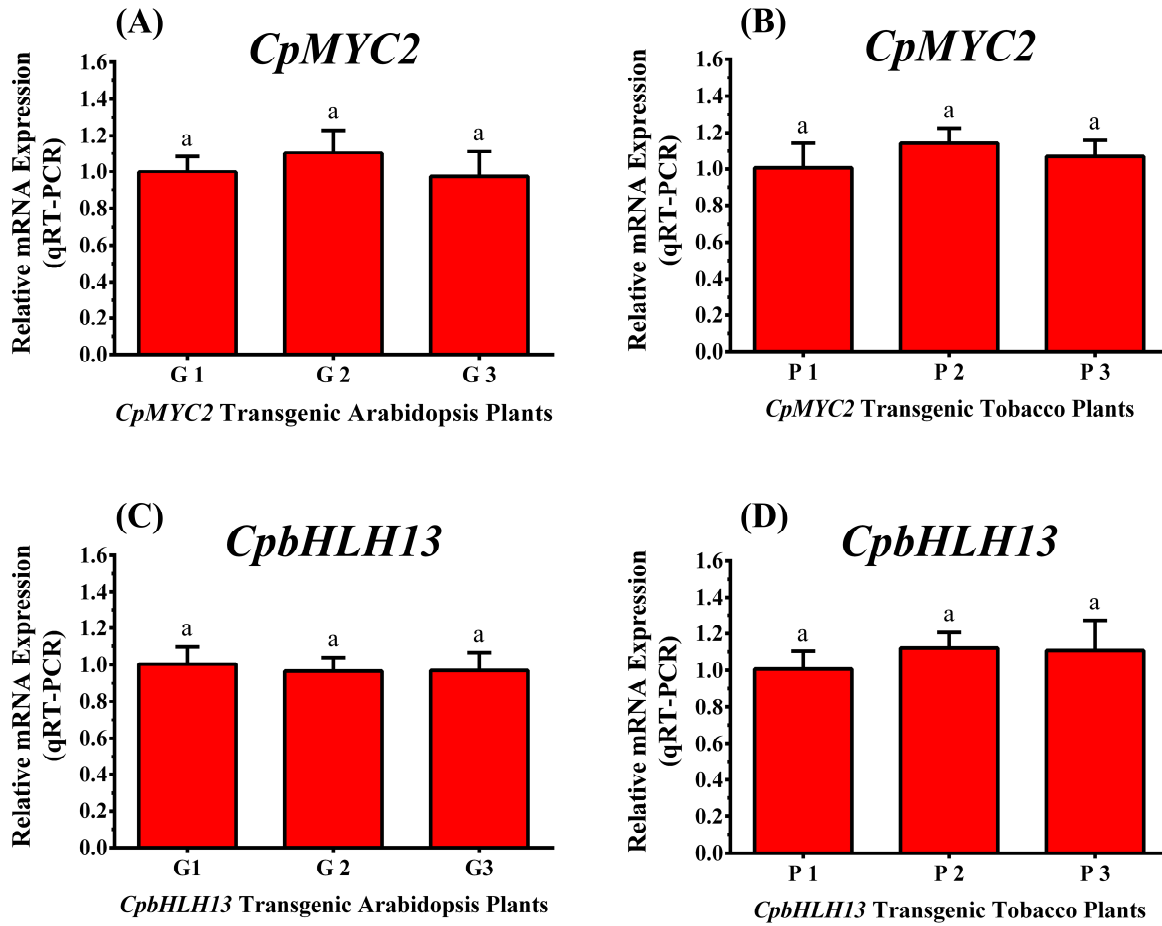
Supplementary Fig 4- Phylogenetic analysis of wintersweet *CpbHLH13* with the *Arabidopsis* *bHLH* transcription factor gene family. The red box indicates the close homologous *bHLH* of *arabidopsis* *Arabidopsis* with *CpbHLH13*.



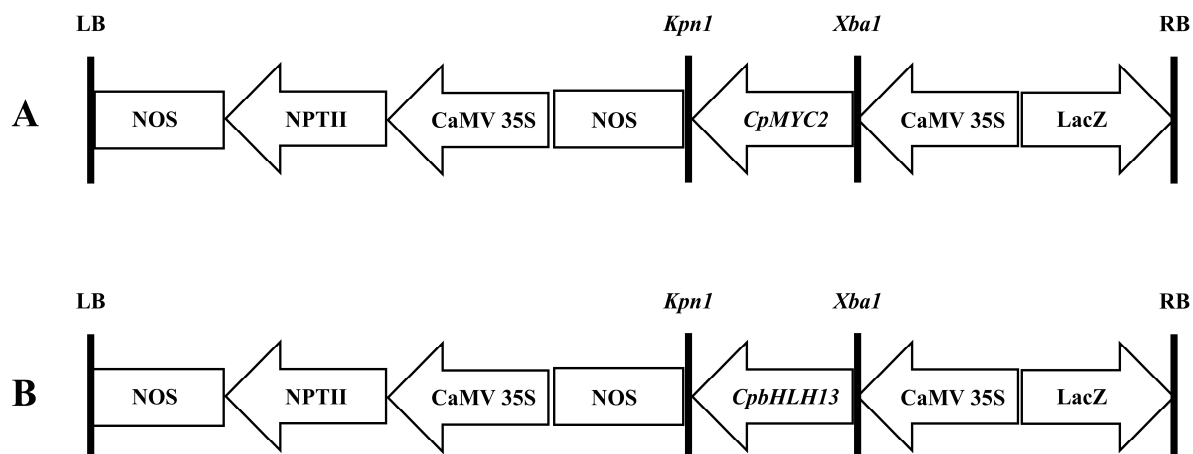
Supplementary Fig 5- Phylogenetic analysis of *Chimonanthus praecox* *CpMYC2* with different plant species. The phylogenetic tree was ~~mad-constructed~~ based on the amino acid sequences of *CpMYC2* and the MYC2 transcription factors from the plants, such as *Hibiscus cannabinus* HcMYC2 (AYU74917.1), *Gossypium hirsutum* GhMYC2 (NP_001314093.1), *Morus notabilis* MnMYC2 (XP_010104300.1), *Vitis vinifera* VvMYC2 (XP_002280253.2), *Ricinus communis* RcMYC2 (XP_002519814.1), *Camellia sinensis* CsMYC2 (XP_028062859.1), *Nicotiana tabacum* NtMYC2 (XP_016500373.1), *Solanum lycopersicum* SIMYC2 (NP_001311412.1), *Nelumbo nucifera* NnMYC2 (XP_010275210.1), *Arabidopsis thaliana* AtMYC2 (At1g32640), *Zea mays* ZmMYC2 (PWZ55921.1), *Lindera glauca* LgMYC (ALE71301.1) and *Cinnamomum micranthum* CmMYC2 (RWR86802.1). The sequences were aligned using the CLUSTALW program and the phylogenetic tree was generated with the neighbor binding method with 1000 repetitions of the start test, p-distance using the MEGA X software.



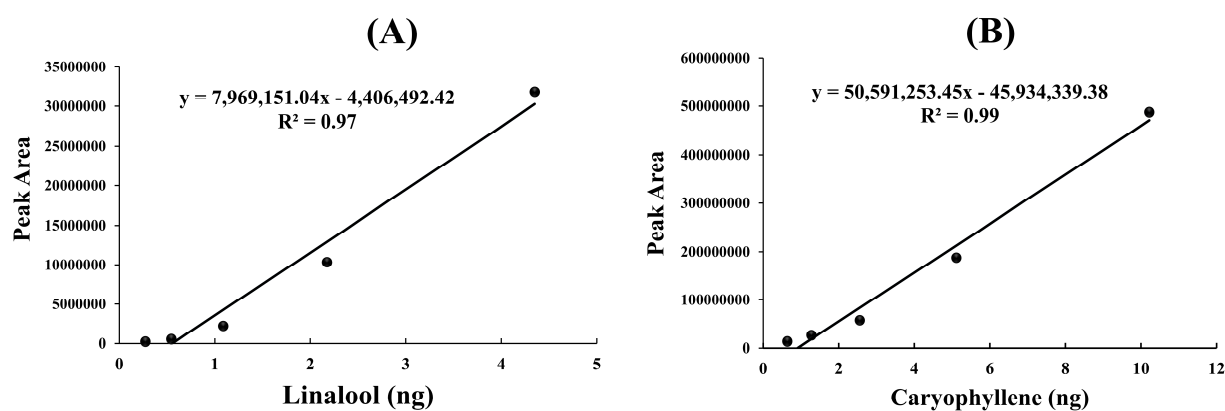
Supplementary Fig 6- Phylogenetic analysis of *Chimonanthus praecox* *CpbHLH13* with different plant species. The phylogenetic tree was constructed based on the amino acid sequences of *CpbHLH13* and the *bHLH* transcription factors from the plants, such as *Solanum pennellii* SpbHLH13 (XP_015063116.1), *Solanum lycopersicum* SlbHLH13 (XP_004229991.1), *Capsicum annuum* CabHLH13 (KAF3659155.1), *Nicotiana tabacum* NtbHLH13 (XP_016459177.1), *Camellia sinensis* CsbHLH13 (ANB66342.1), *Nelumbo nucifera* NnbHLH13 (XP_010242396.1), *Cinnamomum micranthum* CmbHLH13 (RWR96436.1), *Vitis vinifera* VvbHLH13 (RVW95465.1), *Hevea brasiliensis* HbbHLH13 (XP_021664882.1), *Morella rubra* MrHLH13 (KAB1219634.1), *Malus domestica* MdbHLH13 (XP_028955372.1), *Arabidopsis thaliana* AtbHLH13 (AT1G01260) and *Arabidopsis thaliana* AtbHLH17 (At2g46510). The sequences were aligned using the ClustalW program and the phylogenetic tree was generated with the neighbor binding method with 1000 repetitions of the start test, p-distance using the MEGA X software.



Supplementary Fig 7- Expression of *CpMYC2* genes in transgenic (A) Arabidopsis and (B) Tobacco and expression of *CpbHLH13* genes in (C) Arabidopsis and (D) Tobacco by qRT-PCR. P_(1-3) represents the number of the transgenic tobacco plant and G_(1-3) indicates the group number of *Arabidopsis-arabidopsis* plants. The ~~Different~~ different letters on the bars show significance between the treatments by using least significant ~~least~~ difference (LSD) at $p < 0.05$.



Supplementary Fig 8- Partial diagram of the pCAMBIA 2300S transformation vector with (A) *CpMYC2* ~~&-and~~ (B) *CpbHLH13* genes under the control of CaMV 35S promoter, followed by NOS terminator. The ~~Neomycin-neomycin~~ *Phosphotransferase-phosphotransferase Gene-gene* (NPT II) is driven by CaMV 35S promoter as a selectable.



Supplementary Fig 9- ~~The Standard-standard~~ curve of (A) linalool and (B) Caryophyllene. The curve was generated by three repeats. X stands for the content of Linalool (ng) and Y for the peak area.

Supplementary Sequence S1. Nucleotide sequence of *CpMYC2* candidate gene.

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GAGAAAATTGGCAACAGATAG

Supplementary Sequence S2. Nucleotide sequence of *CpbHLH13* candidate gene.

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