

Fig. S1

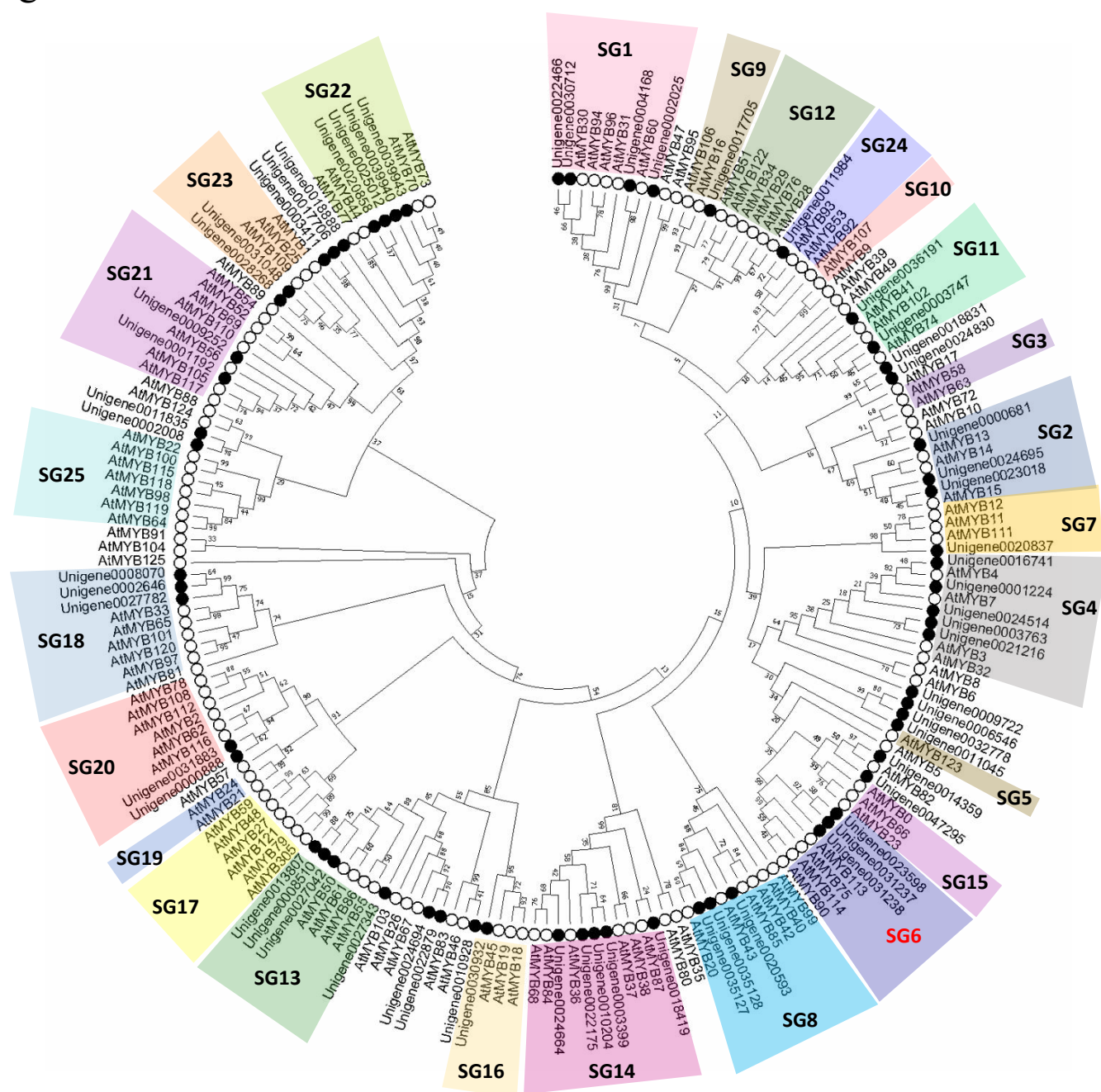


Fig. S1. Phylogenetic analysis of R2R3-MYBs from sweetpotato and Arabidopsis. Only the R2R3 domains were included in the analysis. The black dots show the sweetpotato unigenes and the white dots show the Arabidopsis R2R3-MYB members. The subgroup (SG) classification followed that of Dubos et al. (2010).

Fig. S2

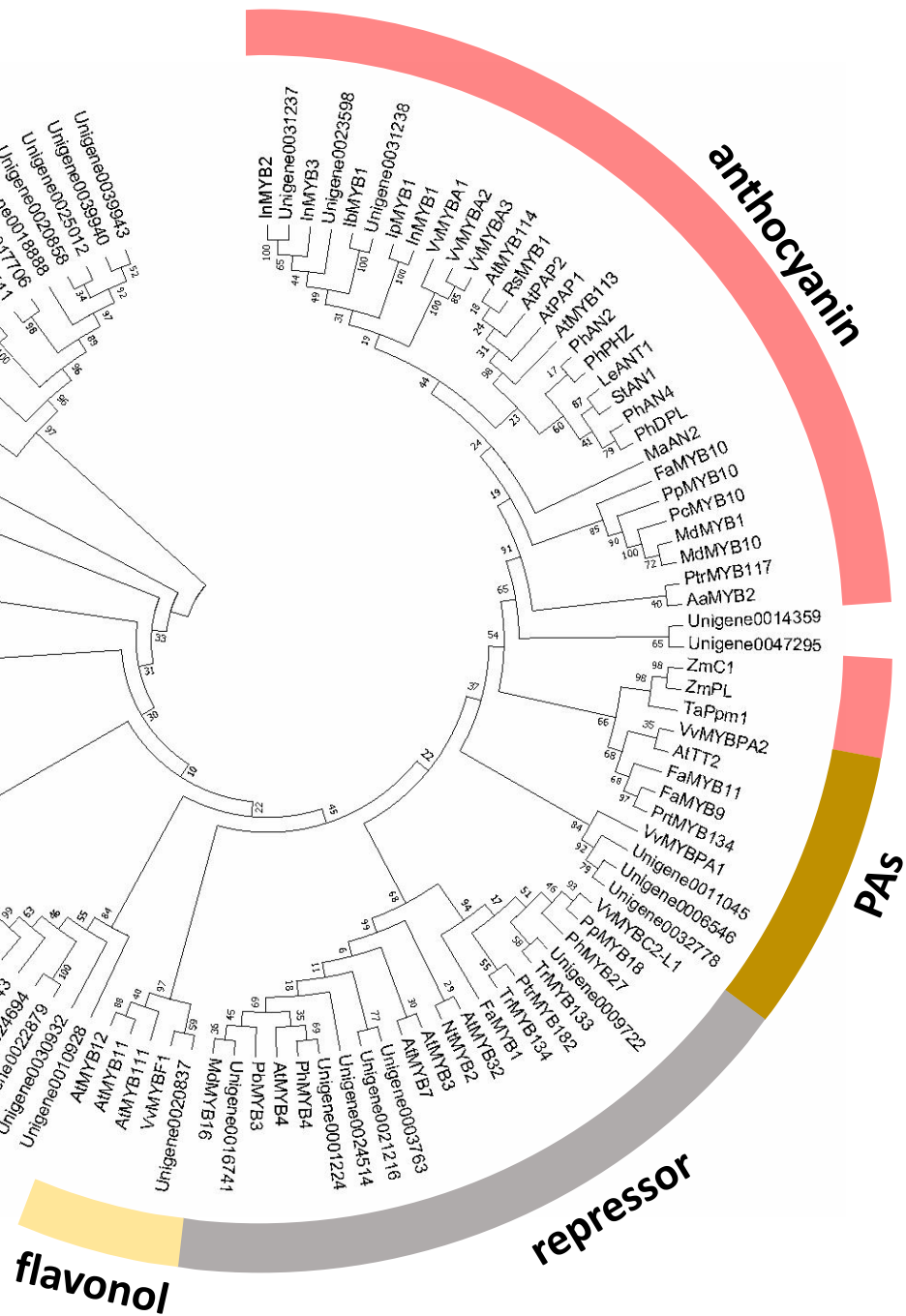


Fig. S2. Phylogenetic analysis of sweetpotato R2R3-MYBs with functional verified flavonoid-related MYBs in other species. Only the R2R3 domains were included in the analysis. The red, brown, and yellow regions represent R2R3-MYB activators of anthocyanins, PAs, and flavonols, respectively, while the gray region represents inhibitory R2R3-MYBs.

Fig. S3

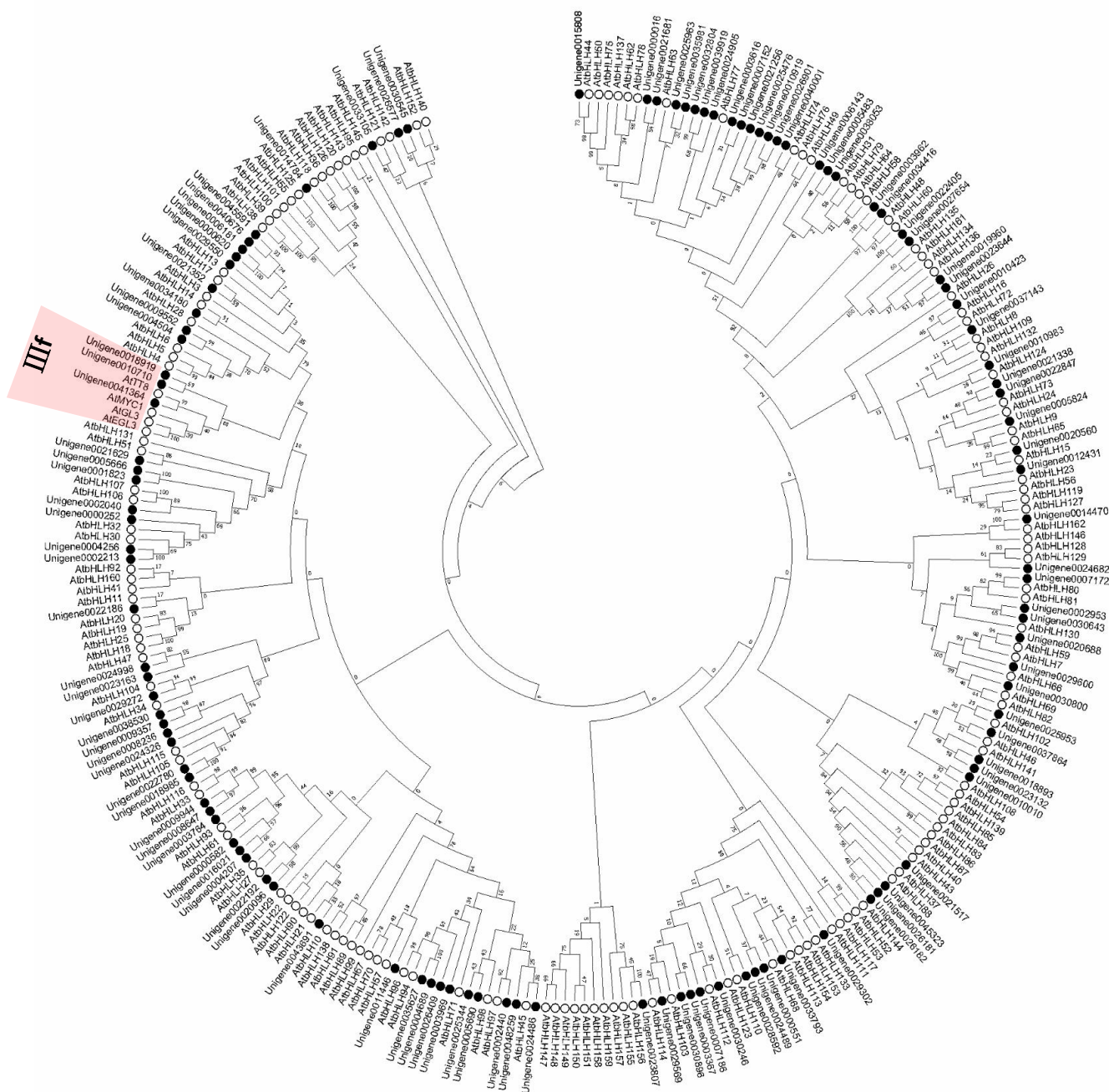
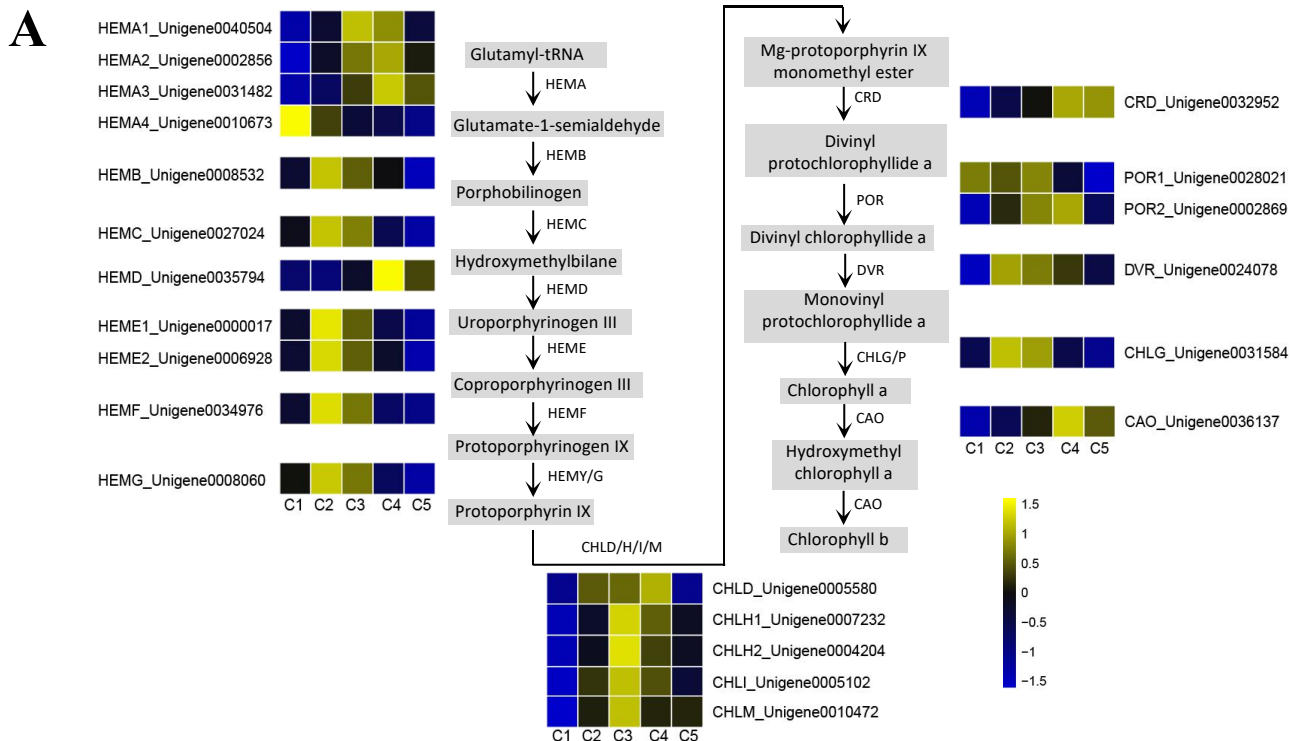


Fig. S3. Phylogenetic analysis of sweetpotato bHLHs with the Arabidopsis bHLH family. The whole protein sequences were included in the analysis. The red shade shows the SGIIf subfamily involved in flavonoid regulation, the black dots show the sweetpotato unigenes, and the white dots show the Arabidopsis bHLH members.

Fig. S4



B

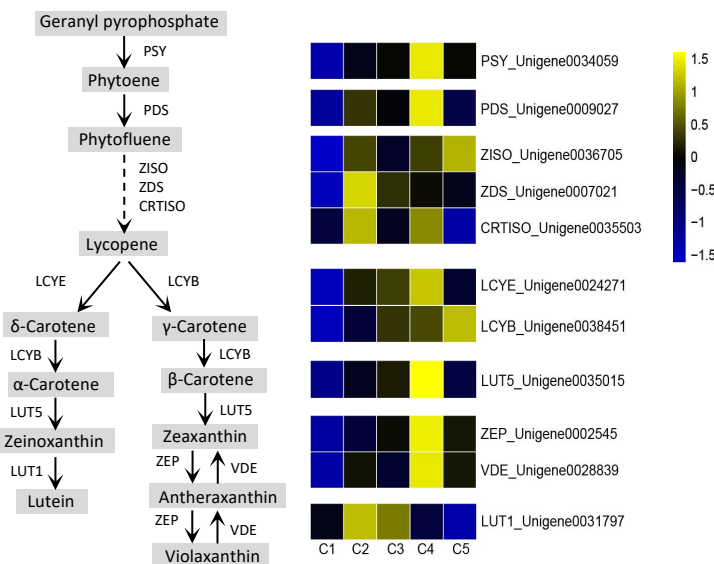


Fig. S4. The gene expressions for chlorophyll metabolism and carotenoid biosynthesis based on RPKMs. (A) Analysis for chlorophyll metabolism. (B) Analysis for carotenoid biosynthesis. HEMA, glutamyl-tRNA reductase; HEMB, porphobilinogen synthase; HEMC, hydroxymethylbilane synthase; HEMD, uroporphyrinogen-III synthase; HEME, uroporphyrinogen decarboxylase; HEMF, coproporphyrinogen III oxidase; HEMY, protoporphyrinogen/coproporphyrinogen III oxidase; HEMG, menaquinone-dependent protoporphyrinogen oxidase; CHLD, magnesium chelatase subunit D; CHLH, magnesium chelatase subunit H; CHLI, magnesium chelatase subunit I; CHLM, magnesium-protoporphyrin *O*-methyltransferase; CRD, magnesium-protoporphyrin IX monomethyl ester cyclase; POR, protochlorophyllide reductase; DVR, divinyl chlorophyllide a 8-vinyl-reductase; CHIG, chlorophyll/bacteriochlorophyll a synthase; CAO, chlorophyllide a oxygenase; PSY, phytoene synthase; PDS, phytoene desaturase; ZISO, zeta-carotene isomerase; ZDS, zeta-carotene desaturase; CRTISO, polycopene isomerase; LCYE, lycopene ϵ -cyclase; LCYB, lycopene β -cyclase; ZEP, zeaxanthin epoxidase; VDE, violaxanthin de-epoxidase. Heatmaps were constructed based on the values of $\log_2$ RPKM.

Fig. S5

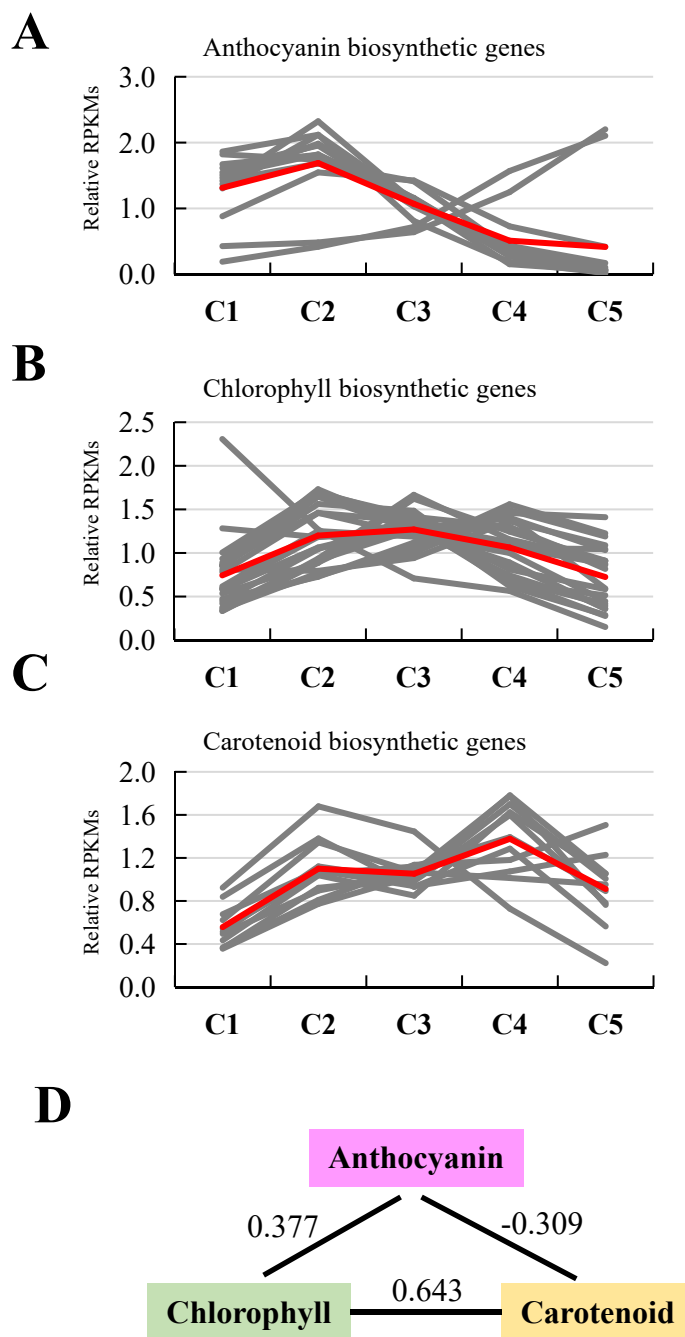
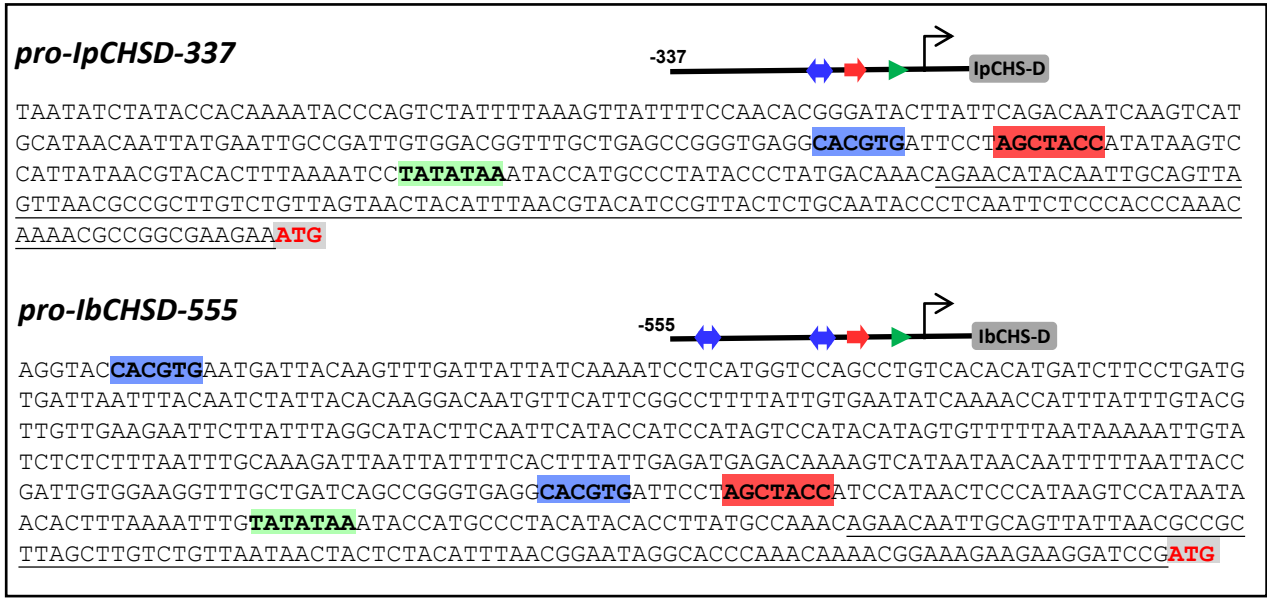


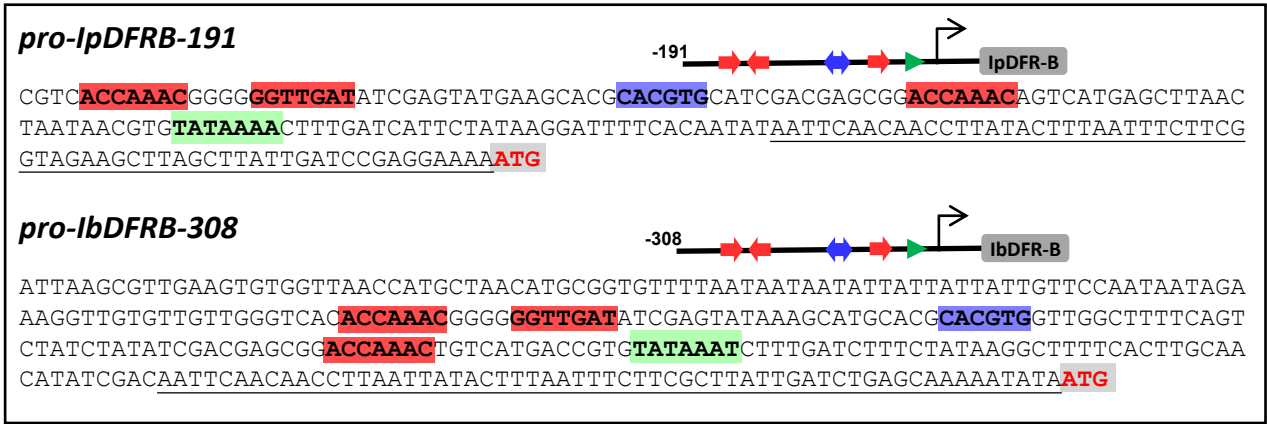
Fig. S5. Relative expression trends of the structural genes for the three pigment biosynthetic pathways. (A-C) The relative RPKMs for anthocyanin, chlorophyll, and carotenoid biosynthetic genes. Relative RPKMs for each gene were calculated from RPKM/mean RPKM of the five stages. Each of the grey lines represent the expression trend of one structural gene. The red lines indicate the average trends of the pathway genes combined. (D) The Pearson's coefficients among the three pathways calculated from the average trends shown in red of (A-C).

Fig. S6

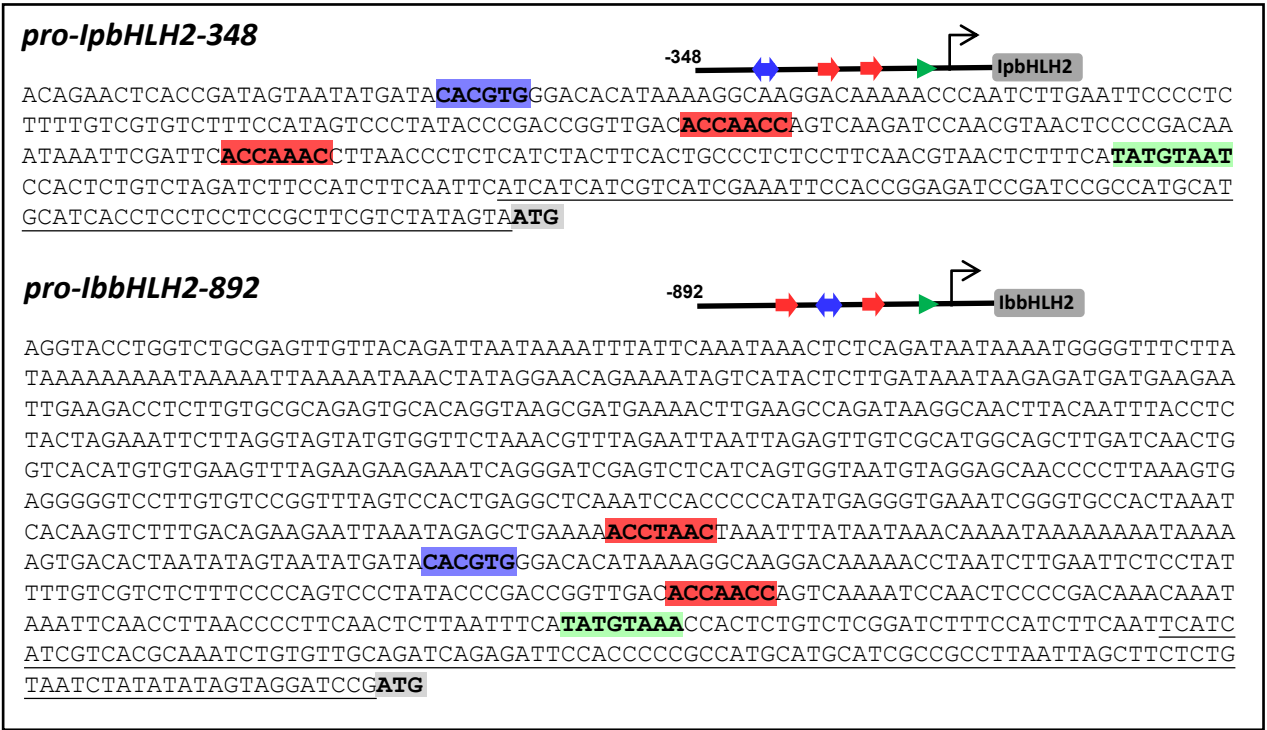
A



B



C



D

AGGTACCAATTACAGGCTGTAGCAAACCTCTCTATTTCTATTAATTTGTGGTTTCATGGCAAACCGCACTATATTCAAT
ATATGAACCACACTTCTTTTAAATTTCAATTTTCAATTTACATGAGAAATTGGAATAATGGATTATACCATAAATTATT
GGGAAATTGGGAAATGACTAATGAGGTAATTGGGAAATCAGAAATGTAATTAGAAAATTAGGTAAGAAAAGGATTATTGT
AGCTTTTCTCAAAAAAAAAAAAAAGGATTATTGTAGCGTGGGAAATTTGGCAGATGAGAGTAAATAACCAAAGTAACAGT
GGAAGT**CACGTG**CCGCCC**AGCTgCC**TGTCCTTTGGATTTACGGG**TATAAAT**ACCACTTAGCTTCTGCACATTCTACGCAC
TCTGAGTCTCTCTGATCTTCAAACAATTAAGTAATTACATTATATTTTGTCTCTGGTCGGCCCCGTGGCATCATATTCT
ACCTGCTAGAAAAATGGTGAGCGTCGAGGAGGTACGGAAGGCGCAACGTGCCCAGGGTCCGGCCACCATCATGGCTATAGG
AACCTCCACTCCCCCTAATTGCGTTGATCAAAGCACCTATCCAGATTATTTTTTTCGTATCACC AATAGCGACCACATGG
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TTCTTCTCTTTTATTAGAACATGTCACTTAAATTTCTTGTTAATTATGAATGTGTATATAGATGTATATGATTCTCTTTT
CTAGTCAATTAGGATAACGATACAATCTAAAGAAACAAGTTATGTACAGCAATCCCACTATAAGATATTTGGTTTACTTGTAT
AACTATAAGGTTACAAATTTAGTCCCAATGGGAACGTGCCTATTGTGACCTTGCATGTGGTCTTTGCTGCTAGGATCA
TAGAGTAGGGTTTATTCTGTGCATACTCTTGAGTAGTAGTAATGGCTGATGTTTATAGTTTTATACCAATTGGGTAATG
TTTACTATATACATGCAGGTGAAAAATCA**ATG**

E

[illegible]

F

AGGTACCAACATCGGTCCCAAT'CCAAAGCTCATCGTATTATATACATAGCGCCTCGCTGTCCCAAGTTTATCAGTACGT
 AAGCTACACTGAGTTGATCATTTATACTTTATAACAAAACATAAATGGTGCTTATTTGCCAAGGACCTTGTGATCCAGTG
 ACATCAAACCCTTCCCTTTATATGGGAGGTGTCTACTCACTATGCACAAAAATCCCTCTCATTTTGAGAGGTTATTCTC
 A**CACGTA**GGTGTCTATTGTGACAAATTTTCATTTTTCATCTGTGTGATCAATTGAGTTATGCATGTAAGTATTGGGTGCA
 ACTCTTACACTACGACTGCTAGAGTTTGATTATGTATCATTACTATAATTAACCTACTTAAAAATCAACTG**AGCTgCC**T
 GTGCGATAATAATTGCTCGTGCAATTATAGTTGAGGTAGTACCATAGAAAGAAAAATTGTATTGATTATGAATTTTATAA
 AAGTGGGTGGTGTGAGTAAGGCATGCATTGCATACATACTAGAGCATGCAGGGCCAAACCACCGGTCAACTCTCTCATG
 GTCCTCCTTTTATTACATAAAACACTATAAAGGTAA**ACCACCC**CCACACCACACCT**ACCACCC**ACCGCCTCCGTCTT
 CACGCAACTA**TATATAA**TTACGCTCTCATCATATATTTTCTATATATATACAACATAGCCAAGGAGTGTACTTTTCTTC
 CCGGATCCACACCCCTAATTCACTTCTTGTCTCTCCGACAACAAACGACTGTCGACT**ATG**

(D-F) The sequences of cloned proximal promoters of *IbCHS-E*, *IbMYB27* and *IbMYB4c*.

Proximal promoter architectures of the promoters were shown. MREs and BREs are indicated with red and blue arrows, respectively. The TATA boxes are indicated with green triangles. The sites are marked for putative MREs (in red and bold), BREs (in blue and bold) along with the expected TATA boxes (in green and bold). Mutated MREs are indicated by the crosses. The 5'utr region was underlined with the starting codon ATG emphasized at the end.

Fig. S7

A

ZmCHS_CAA42763 TAGCCATACCCACGCGACCCAACTAACTACTAAAGCACCCGTTGGCGGCCCTTGCGCCGTCCAACCTACCTAACCCGACCGCGCGGTATATAAGCACCGCACC
AmCHS_CAA27338 TGCTAATAACACGTATCTCAGCTACCATACTTGGTACCATCATTTATAAAATTCATTGATA
PsCHS_BAA22043 TTTAGTAAACACGTGATGTTTCAGCTACCTTCCAATATCCTTACTATATAAACCATCTCATC
PhCHS_CAA32737 GTTGCTAAACACGTGAACACTAGCTACCGAGTTATGAAATTTCTTATAAAATACCAAACTCAT
VvCHS_CAA32731 GTTATAGCTACACGTGATTACTATCTACCATTTCTCTTTAGGGTTCTCGTATAAAATCTCTACAATC
IpCHS_CAN75038 ATTGGTCGAGGACGTGACTCCAGCTACCCGAGTTAGCTCTGCGGTAATAAAACCAACCTCTCT
LpCHSD_AF358654 CCGGGTGAGGACGTGATTCTTAGCTACCATATAAGTCCATTATAACGTACACTTTAAAAATCTTATATAAATACCATGCCC
IbCHSD_BAA87336 CCGGGTGAGGACGTGATTCTTAGCTACCATATAAGTCCATTATAACGTACACTTTAAAAATCTTATATAAATACCATGCCC
IbCHSE_M1231499 CCGGGTGAGGACGTGATTCTTAGCTACCATATAAGTCCATTATAACGTACACTTTAAAAATCTTATATAAATACCATGCCC
IbCHSE_M1231500 CAGTGGAAATCACGTGCGGCCAGCTgCCTGTCTTGGATTACGGGTATAAATACCACTTAGCTCTCTGCAC
TsCHS5_AAA73939 TGTGTTGAAGCACGTGAAGTTCACTACCTCCAAATATTCACTACCTCTACCTTCAATATATATAAACCATCTCACC
TsCHS6_AAA67701 TTCAATCAACACGTGATCCACAACCTACCATCAATATCCACCATCTCCCTTTCCAAATCTTCCATCTTTTCATTCAATATATAAACCATCTCACC
RiCHS_ACF72868 AATTGGCAAGCACGTGATCCCCAGCTACCCACCCCTCCCTTCTCAACCTTTGTTTCATCAAAATATAAATAACAACC
DcCHS_BAA03784 GGGGGTGGTACGTGCTGCTTCTAGCTACCTACTTATTTATCTATCGCTTATAAATACATTTCGGTA
PsCHS_BAA01512 TTTTGTGAAGCACGTGAAGTAAATGTTCACTACCTACCTCTAATATCCACTCTTCCTTTTCAATAAAATCTTCCCTCT
AtCHS_BAB11121 AACCACTAGACAGTAGATCTTCATCTGCGCGTCACTCTAACCTACCACTCTCATCTCTTTTCCCGTGTGAGTTTGTATATATAAGCTCTCACTC
AcCHS_CAI30817 AACCACTAGCCAGTAGTGTCTCATCGCCGTCATCTAACCTACCACTCTCATCTCTTTTCCCGTGTGAGTTTGTATATATAAAGCTCTCACTCT

GmCHS7_AAA33950 ATGGTGATGACAGGTGATCTCACTACCTACCTCCATCTCTCCCTACAATATATAAGATGCTATC
GmCHS8_AA067373 TTGGTGATGACAGGTGATGATACTACCTACCTCTCAACCTCAATACAATAAATGCGCATCTCTCAA
GmCHS9_ABQ63059 AGGAACGATGCACGCGCTCACTTAACGGGGAACCTACCTACCTCTTTCAGTTATGTATATATATCCAACTTC
GmCHS6_AAA33951 AAAGCGCAGCCACGAGTCATAGGAAGCATGCATGATCTACGTACCTTAGCTAACCTACCACTTTACCTATGTATATATATCCAACTTT
GmCHS1_AAQ62590 AAAGCGCAGCCACGAGTCAGAGGAAGCATGCATGATCTACGTACCTTAGCTAACCTACCACTTTACCTATGTATATATATCCAACTTT

B

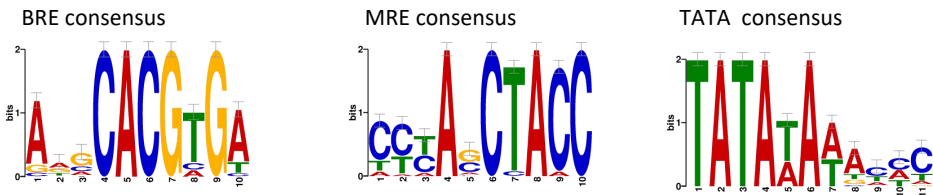


Fig. S7. Conservation of the *cis* elements for the MBW complex on *CHS* promoters from multiple species.

(A) The *CHS* proximal promoter fragments from various species with MREs (in red and bold), BREs (in blue and bold), and TATA boxes (in green and bold) marked. The promoters for *IbCHS-D* and *IbCHS-E* were in red and bold. Zm for *Zea mays* (maize), Am for *Antirrhinum majus* (snapdragon), Ps for *Pisum sativum*, Ph for *Petunia hybrida*, Vv for *Vitis vinifera* (grape), Ip for *Ipomoea purpurea*, In for *Ipomoea nil*, Ib for *Ipomoea batatas*, Ts for *Trifolium subterraneum*, Ri for *Rubus idaeus*, Dc for *Daucus carota*, At for *Arabidopsis thaliana*, Ac for *Arabidopsis croatica*, Gm for *Glycine max*.

(B) The consensus sequences of BREs, MREs, and TATA boxes for the above *CHS* promoters concluded by MEME (<http://meme.nbcr.net/meme/>).