

Supplementary Materials

Table S1 List of the primers used for the qRT-PCR experiment

gene name	Forward primer	Reverse primer
<i>CmUBI</i>	AGCTGAGCAGACTCCCGATG	AGGCGAATCATCAGTACCAAGT
<i>HEMA1</i>	ACTAGAAACCGTTCCTACAATCC	AAGTCCTGTCATCACTTCCGTC
<i>HEMA2</i>	AGGTCACCGAATGGATGTCTAAGG	CCGCCAATCTTCCTATCAAATCC
<i>GSA1</i>	ATGTATGGGTGTAAGGCTAG	AATGTCATTATAGGGTGATGTTAGG
<i>HEMB1</i>	ATTCGGCTGCTCAAAGACAAGTATC	TCACTAGGGCTCACGACATCTGC
<i>HEMC1</i>	ACTCAACCTCTTGCAGATATTGGTG	TTGTCAGGCAGATAAGTTGGGAC
<i>HEMD1</i>	ATCCACTGTTTTGTATCCTGCCTC	GGTAGAAGATTGACCCAAGCACG
<i>HEMF1</i>	CCAGGAGCACCAAGGCAGTG	CTCGCCTCTCATTTTCGGTGC
<i>HEMG1</i>	TGAGAAAGATGGGTATTTGTGGGAG	GGTCAAAGAAAGGTATATCAGAAGG
<i>CHLD1</i>	ATTGTTGAAAGGGAAGGAATCAG	CCTCATTACTCTGTTCTTGAAACTGTG
<i>CHLH1</i>	GACTAACCTTGTCTGGGAGTCTAAGG	CACCCTCATAGCCACTAGACAGC
<i>CHLI1</i>	TTACAGTGGTTGCTGCCGACC	ATGCTTTAACACCCTCTGTGAGTGC
<i>CHLM1</i>	CTTGAACGGGAAATACGATACGG	GATCATAATAGAATGTCTTGGGTGC
<i>CRD1</i>	TTGAGAACTGGTGCCAAGACG	GAAAGCGGTTCTTTGAGTATCATTC
<i>DVR1</i>	AATTTGAGGGTGAGTTGGTTG	CATCGCCAAACATCACATAAG
<i>PORA1</i>	AATGCAAGAGTTCATAGACGATAC	AAGCTTGAATCACTTACTACCTGTG
<i>CHLG1</i>	TGGAACCCTTACACCTGACATAG	TGCCAATGCGTAATATGGTTTAC
<i>CAO1</i>	ATCCCTTCACTACTACCACCTCC	ATCCCAGTATCCTTGAAGACCAG
<i>NYC1</i>	TCAGGGGATCGAGTGGTTATTG	CACAAACATCACATGACGTGCC
<i>NYC2</i>	TGATTTGATTTGGTATAGTTGGGTC	CCTGAAAGTAGGAACTCACGAGC
<i>NYC3</i>	TTTGATTTGGTATAGTTGGGTCG	TAACCACACGATCTCCTGAAAGTAG
<i>CLH1</i>	CTAAAGGGATTAGAGGGGAAATCTAC	TCATCTTTTATTGCCATTAAATGAC
<i>PPH1</i>	ACTTCGCAGCATGTAACCCTAAC	CATCTTCTCCCAAACAATTTCTATG
<i>PAO1</i>	GGGCATCTGCAATGTTCTTACC	CCATACAAAGAGCAAACCTTGAGAC
<i>PAO2</i>	ATGGCACGAACATATGACTTCAAAC	TAAGCCAATTTCTAAACGCCAGTAC
<i>RCCR1</i>	TTGTAGTCTTCCACCTGATGTCC	ACTTGTGATGTTCAAGGCTCCTC
<i>SGR1</i>	GTCGCTTCACGTTCAATTGTCA	GGACCCCAACACTCGACTTT
<i>CmERF</i>	CGTATCTGGCTAGGTTCTTACTCCTC	AGGGCGTCAACTTTAGCTCCAA
<i>CmbHLH</i>	TCGCTGGTCTGCTTATTTTCA	TTAAATTGCTTCCTTCCTACGC
<i>CmCLO16a</i>	CGTGCTCGGTGGTATTGT	CTGGCTTCATCACTTCCTATCT
<i>CmCOL16b</i>	TCGGTTATGATTCCACGATGA	AGGATTGCTATTCCCAGTCCA

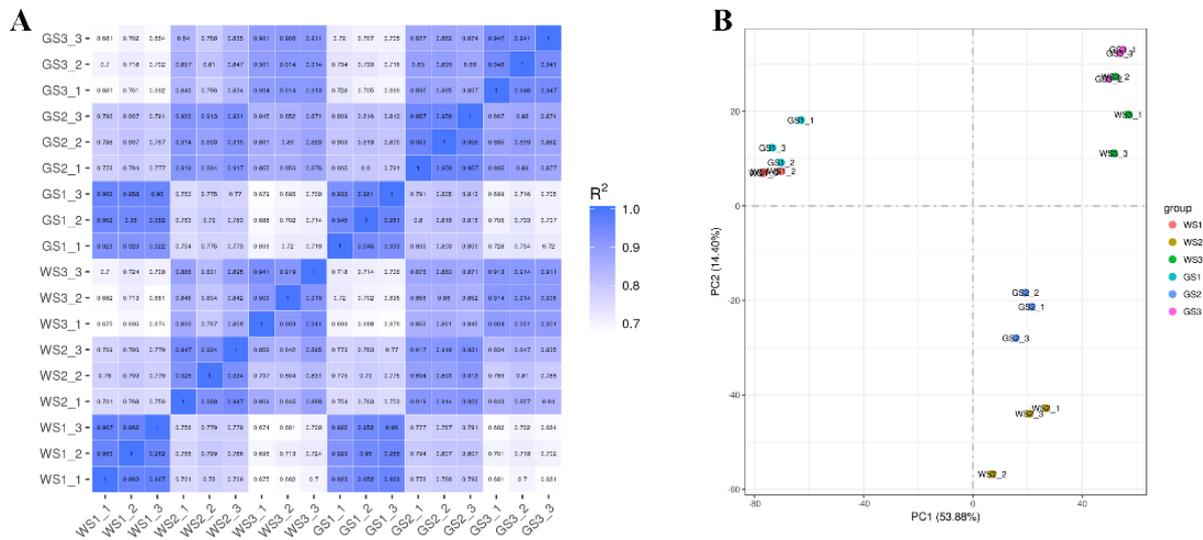


Figure S1 Pearson's correlation and Principal component analysis of gene expressions in each sample of green pools and white pools. **(A)** Pearson's correlation between each sample. **(B)** Principal component analysis of gene expressions in ray florets from green pools and white pools at three stages.

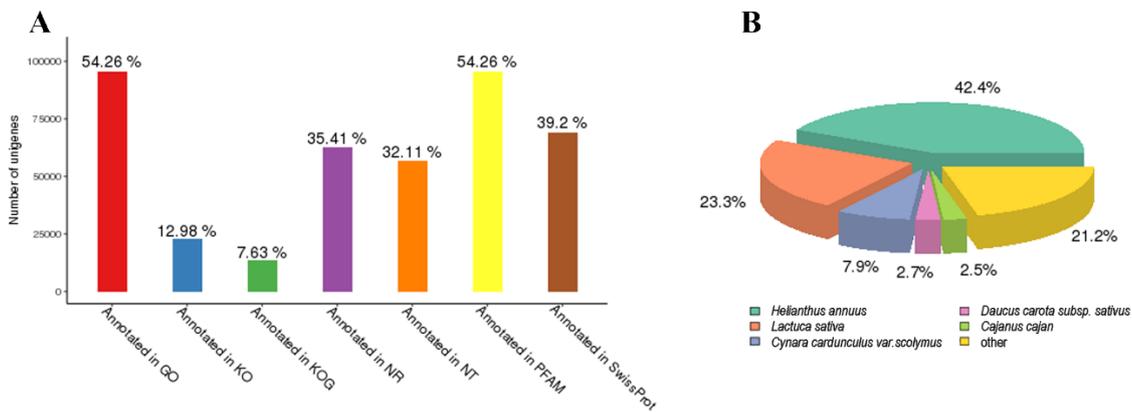


Figure S2 Functional annotations of the transcriptome data. **(A)** Functional annotations of the transcriptome data in seven databases. **(B)** Species distribution of the BLASTX result against the Nr database.

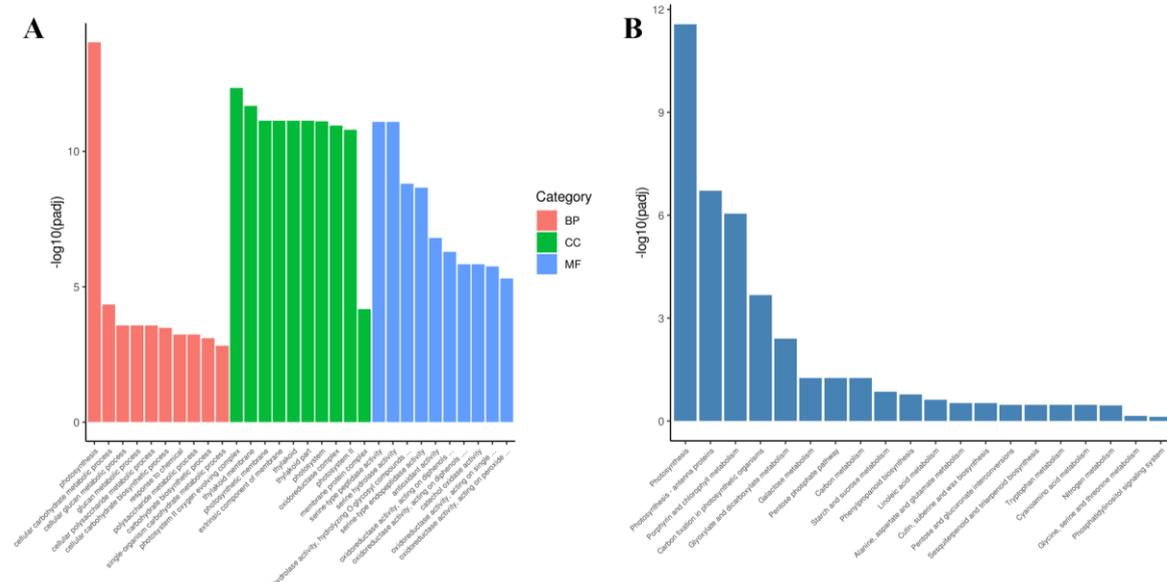


Figure S3 Functional classification of DEGs among different samples. **(A)** GO functional classification of DEGs. **(B)** KEGG functional classification of DEGs.

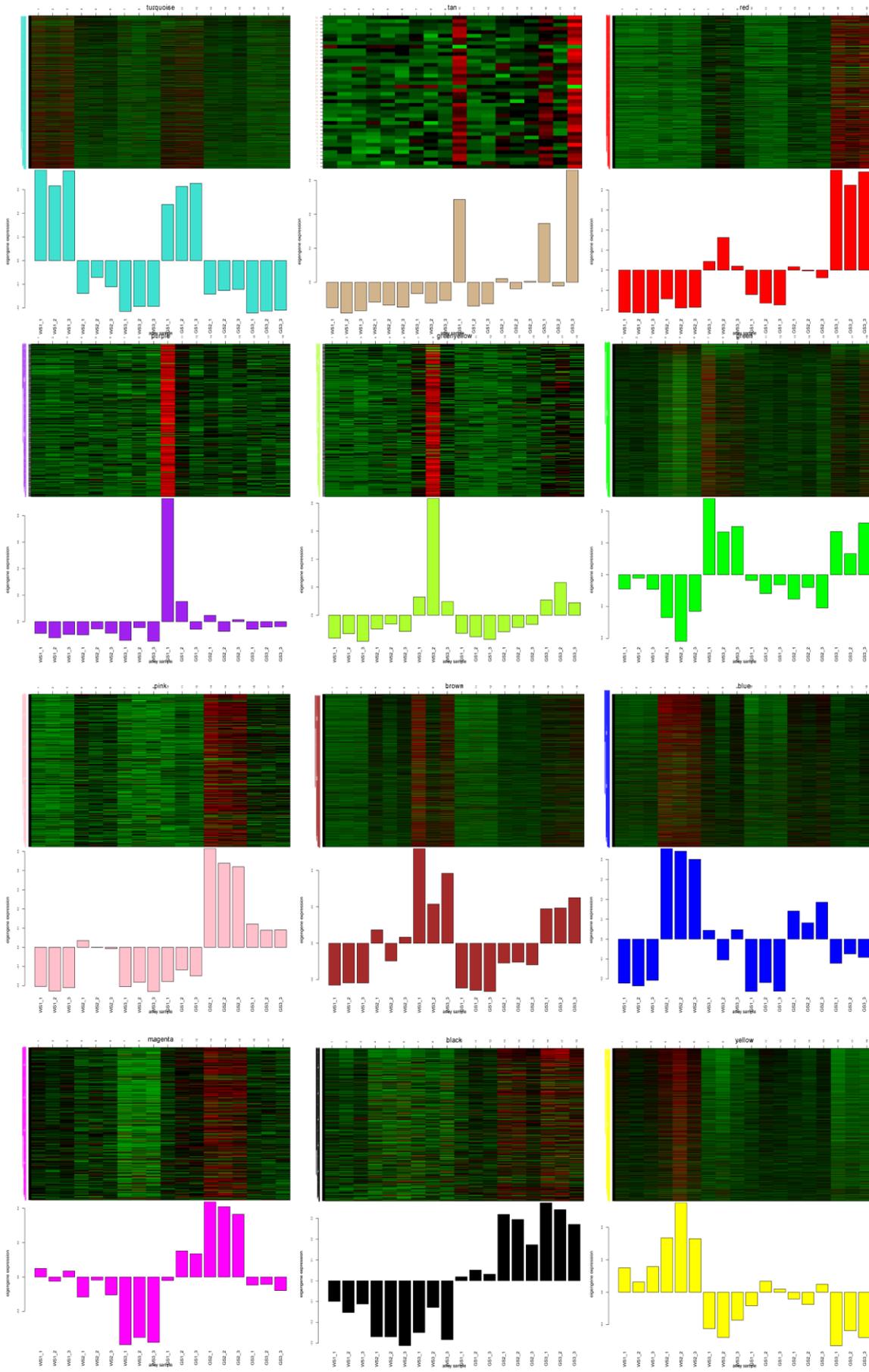


Figure S4 Expression pattern of eigengenes in 12 modules.

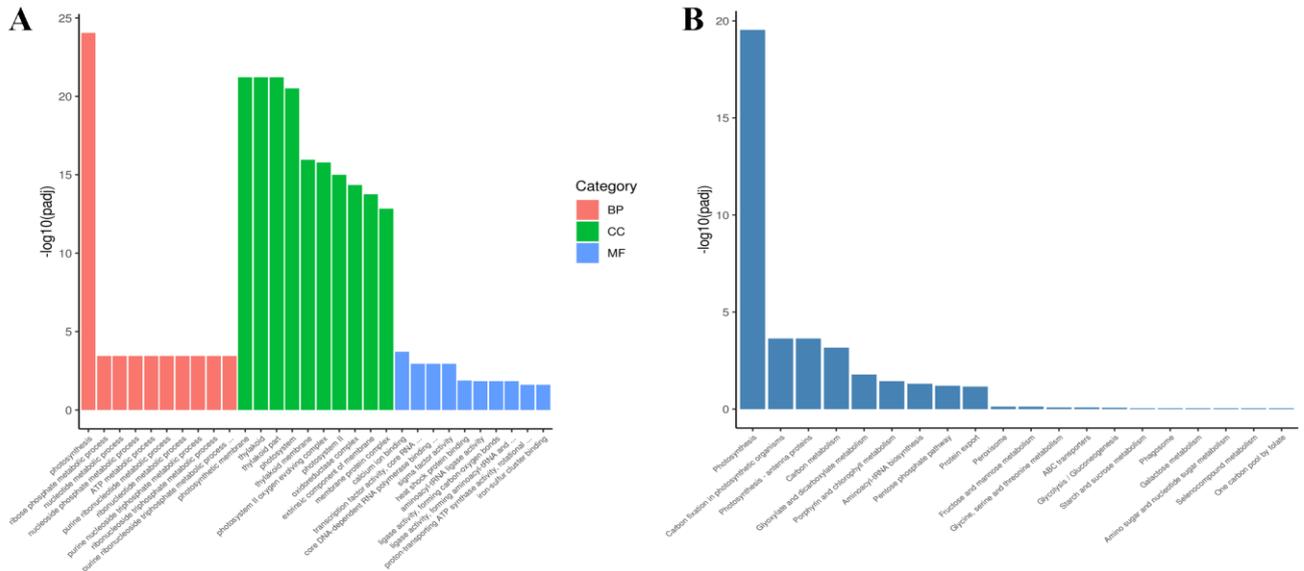


Figure S5 Functional classification of genes in black module. **(A)** GO functional classification of genes in black module. **(B)** KEGG functional classification of genes in black module

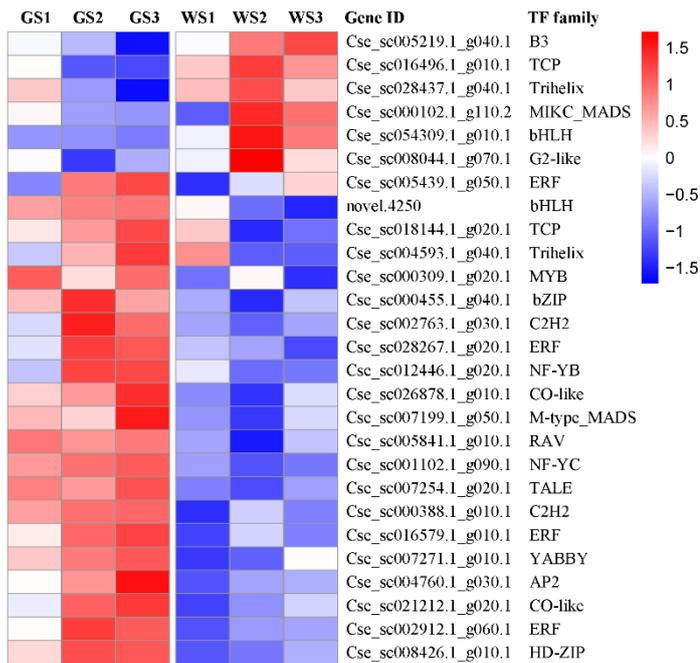


Figure S6 Heatmap of transcription factors in black module.