

Figure S1. Temperature and UV differences between the two regions. A, The highest and lowest temperature changes in the two regions during the whole color transition period. B, UV difference between two regions on a sunny day during the color transition period.

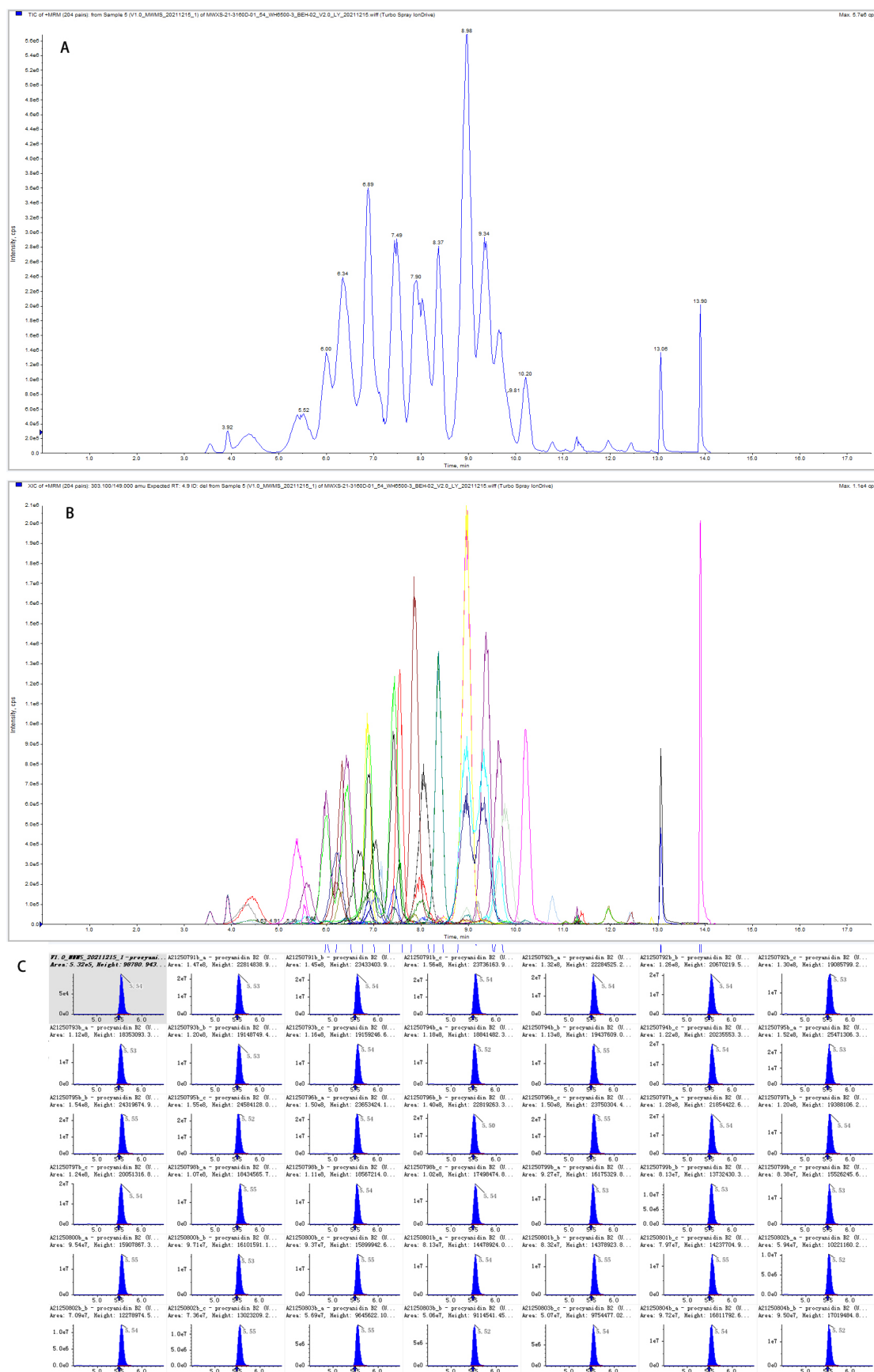


Figure S2. The representative MS chromatograms. A, Total ion current chromatogram. B, Extraction ion current chromatogram. C, Integral correction chart. The quantitative

analysis integral correction results of a randomly selected substance in different samples are displayed. The abscissa is the retention time (Time, min), and the ordinate is the ion current intensity (Intensity, cps).

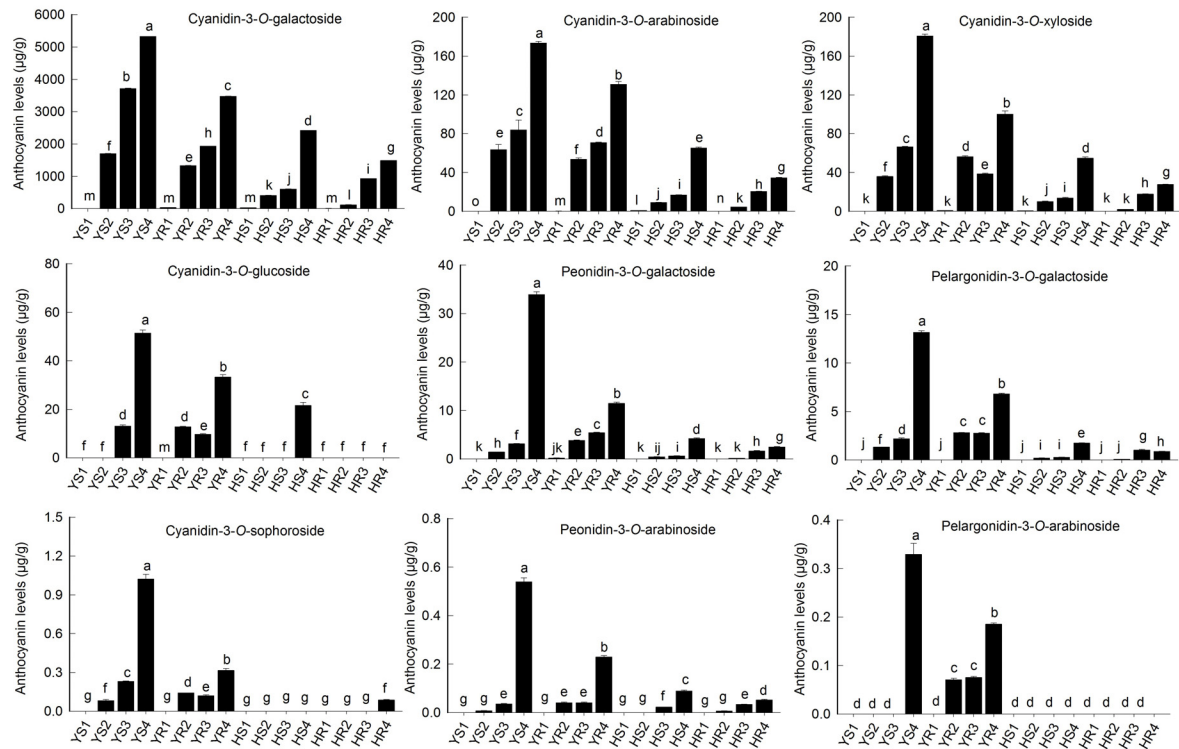


Figure S3. Contents of gradually increasing anthocyanins in each samples. Different lowercase letters on the bar in each graph indicate significant differences at $p < 0.05$ by Duncan's multiple range test. YS, Huashuo in Zhaotong city; YR: Huarui in Zhaotong city; HS, Huashuo in Zhengzhou city; HR, Huarui in Zhengzhou city.

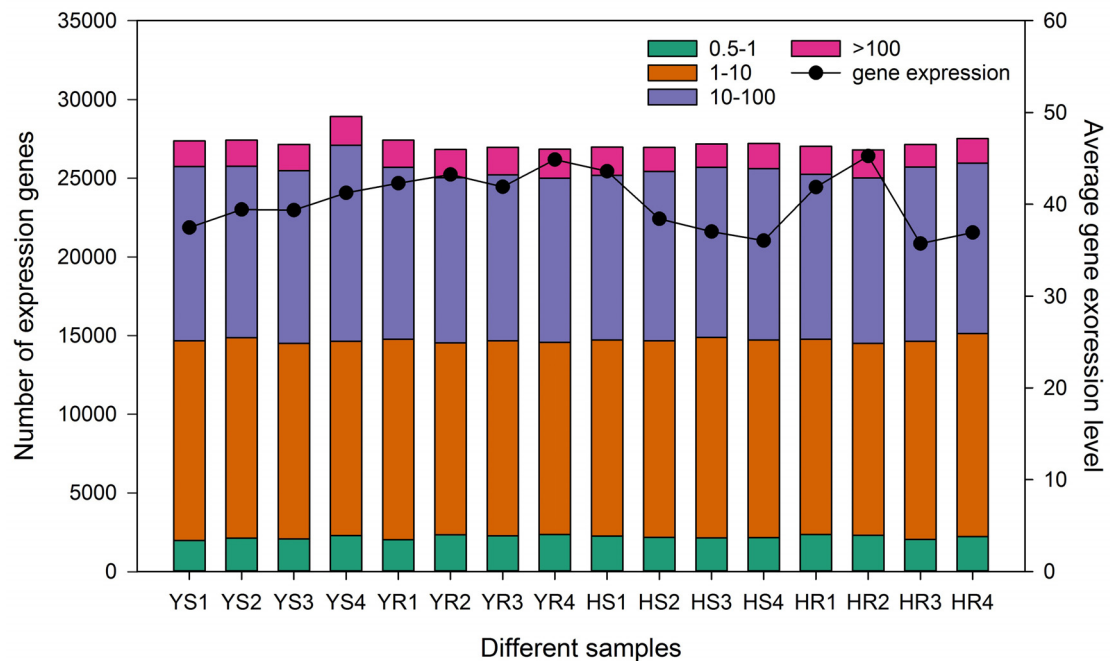


Figure S4. Gene length distribution and average expression level of each sample. YS, Huashuo in Zhaotong city; YR: Huarui in Zhaotong city; HS, Huashuo in Zhengzhou city; HR, Huarui in Zhengzhou city.

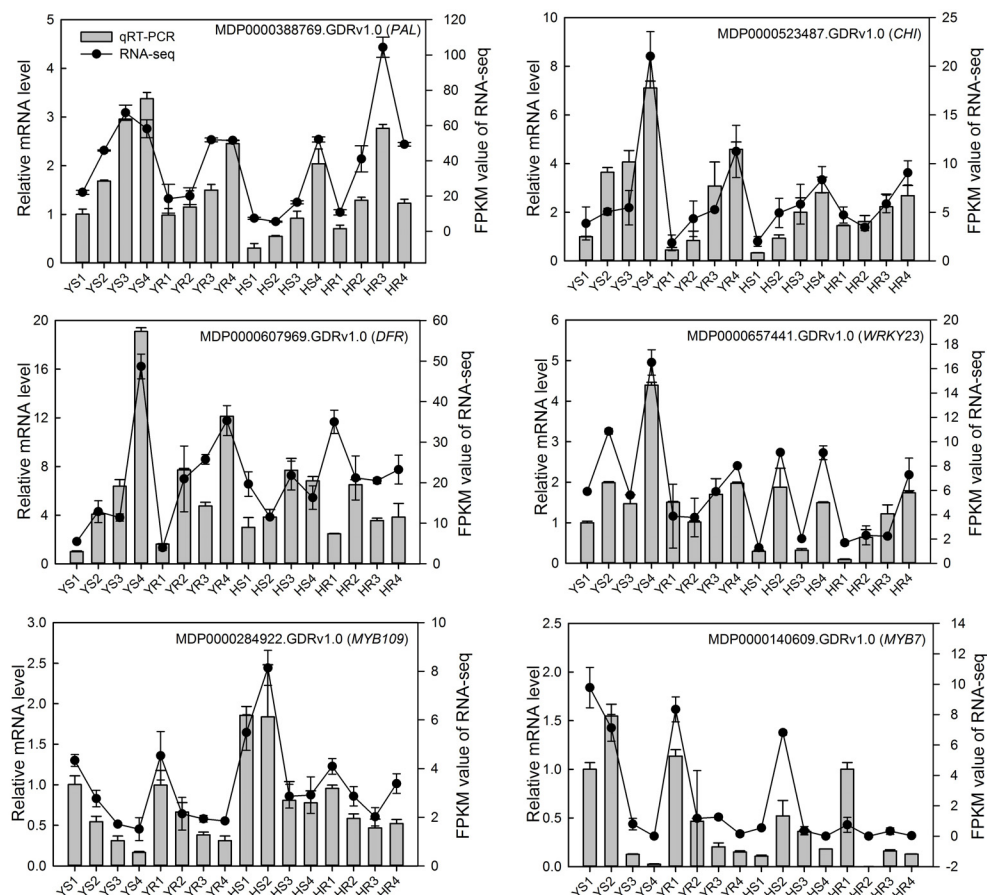


Figure S5. qRT-PCR validation of gene expression level in the transcriptome. YS, Huashuo in

Zhaotong city; YR: Huarui in Zhaotong city; HS, Huashuo in Zhengzhou city; HR, Huarui in Zhengzhou city. YS1, YS2, YS3, and YS4 represent the four color transition periods of YS, and the same rationale was applied to the other samples.

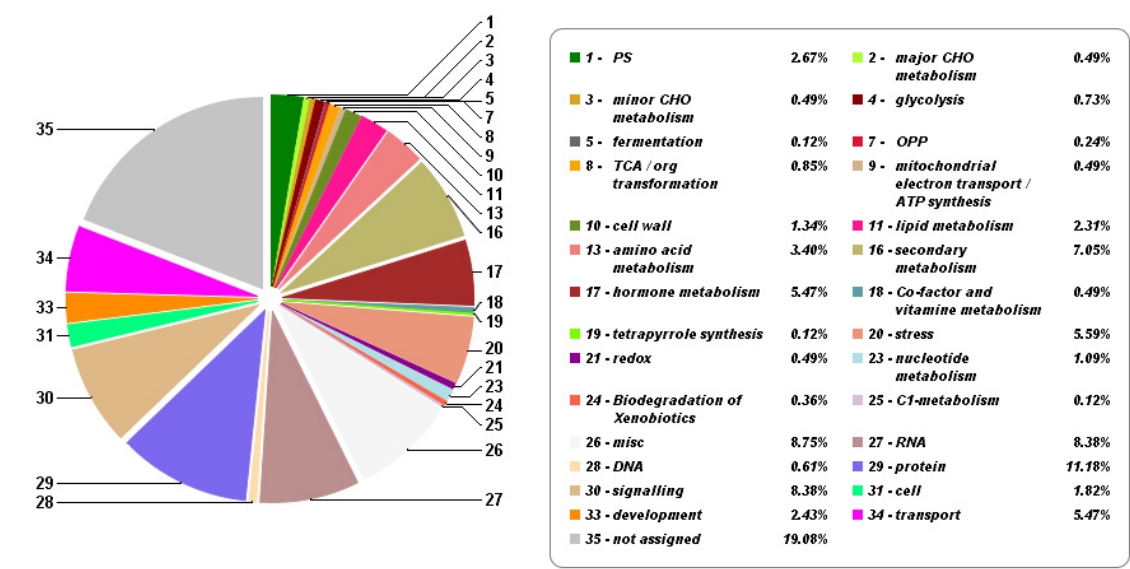


Figure S6. Functional annotation of genes with correlation values of ≥ 0.7 or ≤ -0.7 . The left side shows the screened genes divided into different categories; the right side introduces the name of each part and their proportions in detail.

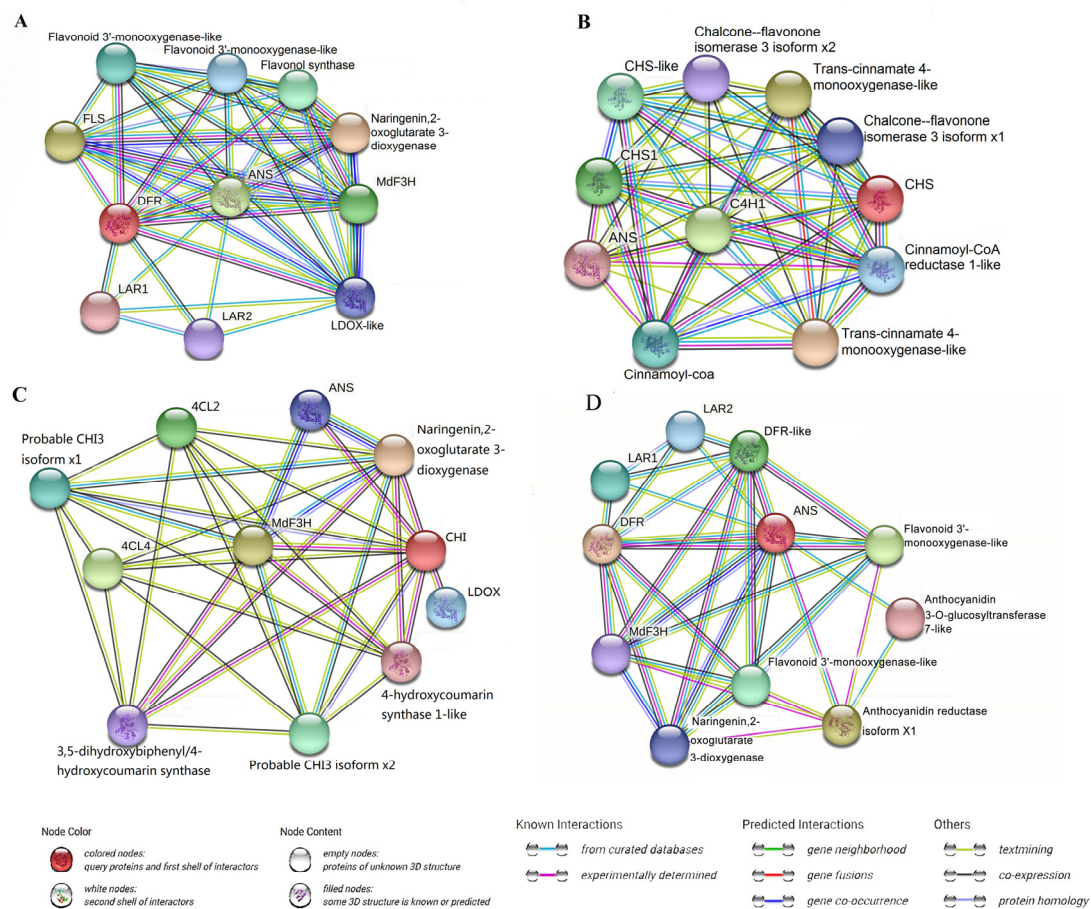


Figure S7. Interaction network analysis for MdDFR, MdCHS, MdCHI and MdANS. Colored nodes represent different proteins, and the red one was the target protein I typed in. Node content, empty nodes represent proteins with known or predicted 3D structure, filled nodes represent proteins of 3D structure is known or predicted. Lines of different colors in the middle of nodes represent different relationships of proteins.