

Figure S1. Comparison of petal color between (A) green leaf cotton XinLuZao 74 (X74), (B) *Pink Flower* mutant cultivars (*PF*) and (C) sub-red leaf cotton cultivars (*Rs*) grown in natural light. Scale bar: 1 cm.

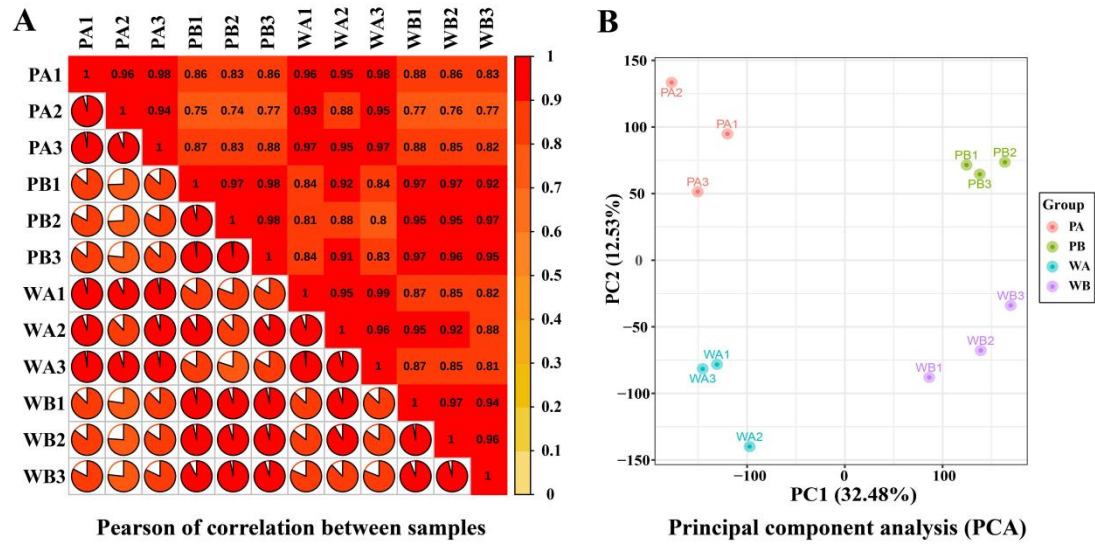


Figure S2. Pearson correlation (**A**) and principal component analysis (**B**) between samples. PA, PB, WA and WB represent the spot region and non-spot region of pink and white petals, respectively. PA1/PA2/PA3, PB1/PB2/PB3, WA1/WA2/WA3, and WB1/WB2/WB3 represents three biological replicates for each sample, respectively.

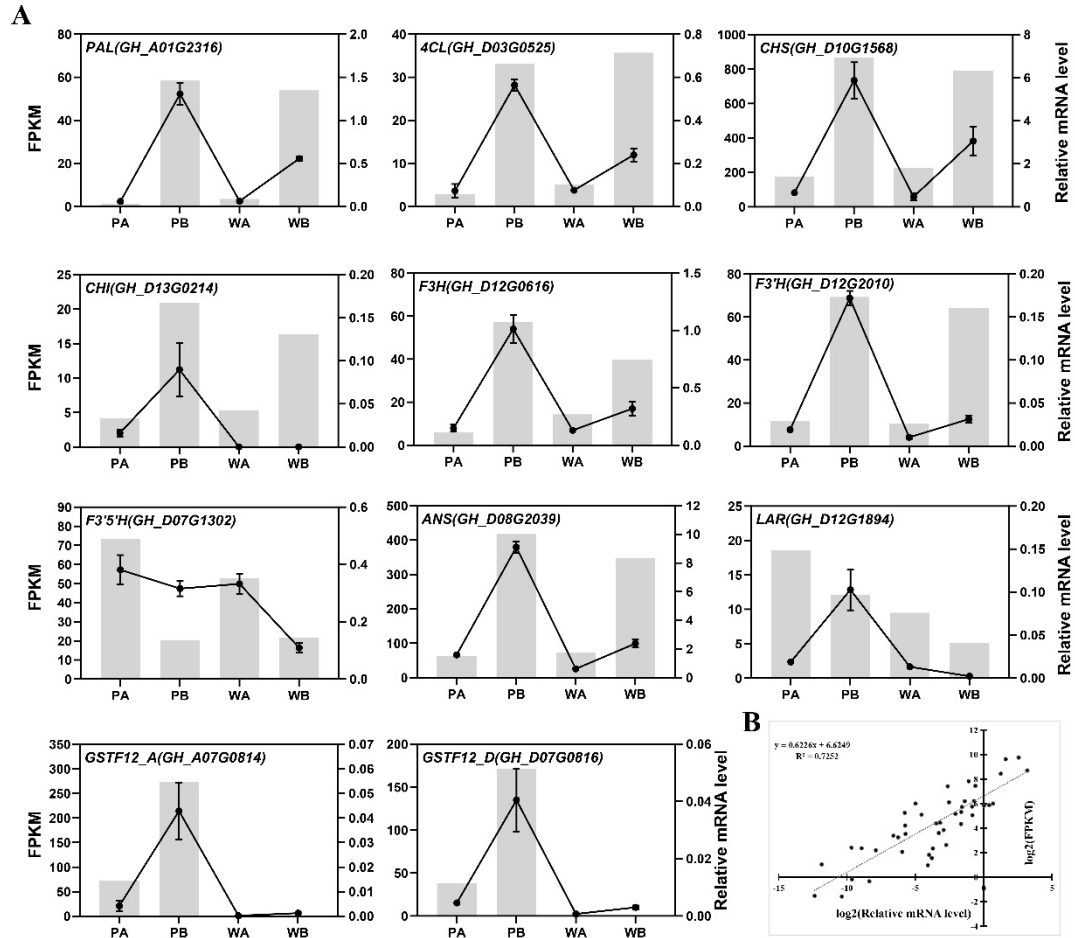


Figure S3. Expression analysis of 11 DEGs related to anthocyanin biosynthesis in different samples. **(A)** Transcript levels and qRT-PCR results of 11 selected genes from RNA-sequencing. The left y-axis shows the corresponding RNA-Seq expression data (FPKM) and the right y-axis indicates the relative gene expression levels analyzed by qRT-PCR. Each value in the histogram represents the mean \pm standard error. **(B)** The scatter plot of 11 selected genes based on the log2 of the gene expression ratios from qRT-PCR and RNA-seq results indicates the correlation between them. PA, PB, WA and WB represent the spot region and non-spot region of pink and white petals, respectively.

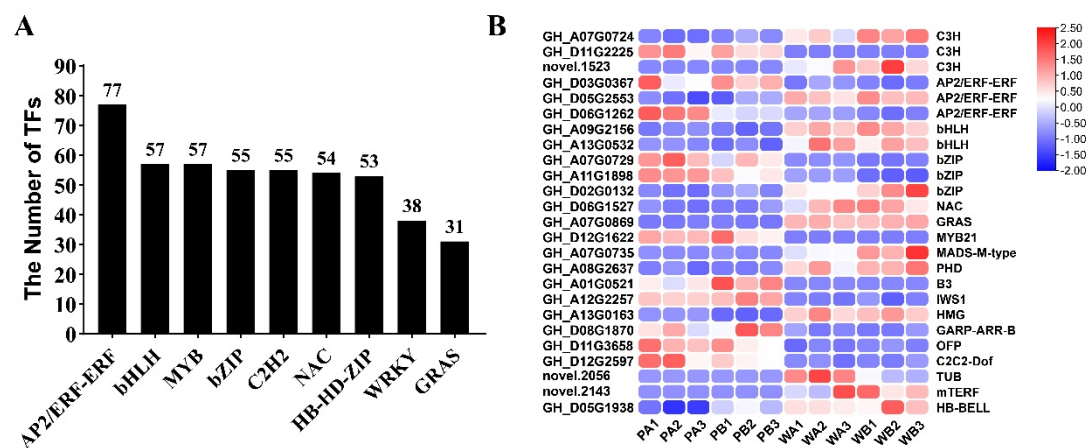


Figure S4. Analysis of transcription factors in DEGs. **(A)** The top 9 transcription factors in DEGs. **(B)** The heatmap analysis of 25 transcription factors highly correlated ($|PCC| \geq 0.9$) with Cyanidin-3-O-glucoside. PCC: Pearson's Correlation Coefficient.