Supplemental Materials

Figures

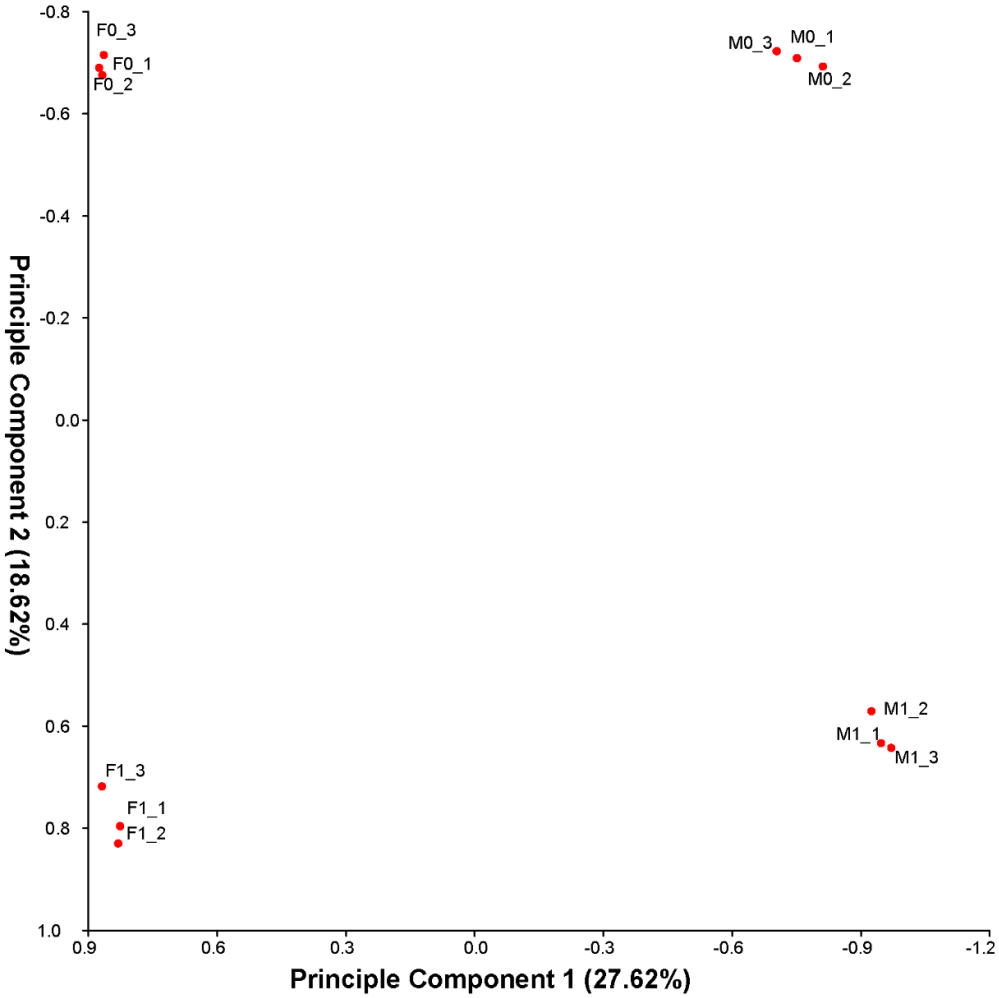

Figure S1. Principal component analysis (PCA) of red bayberry floral buds.

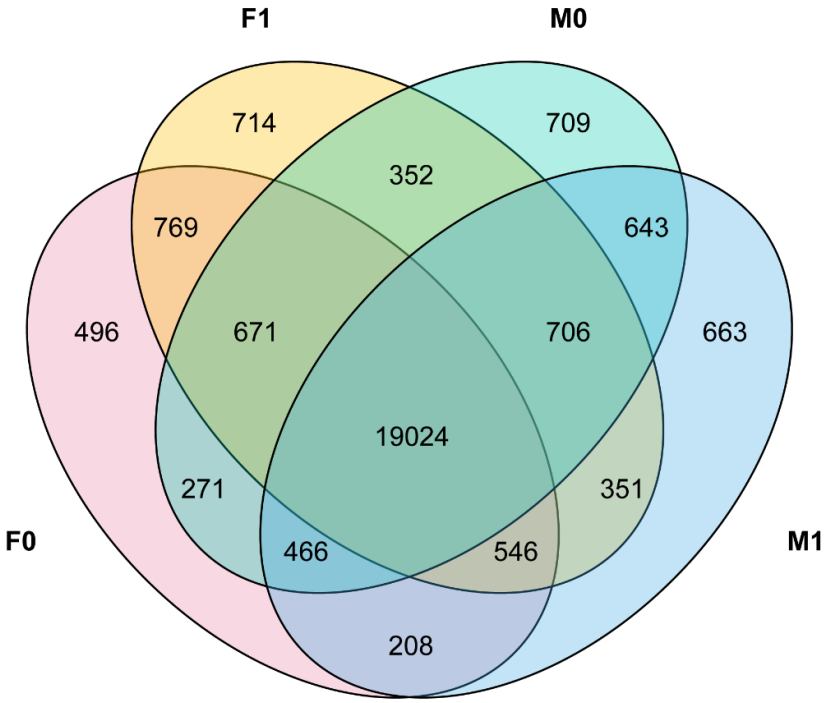

Figure S2. Venn diagram of the 8,889 DEGs in the pair-wise F1 vs F0, M1 vs. M0, M0 vs. F0, and M1 vs. F1.

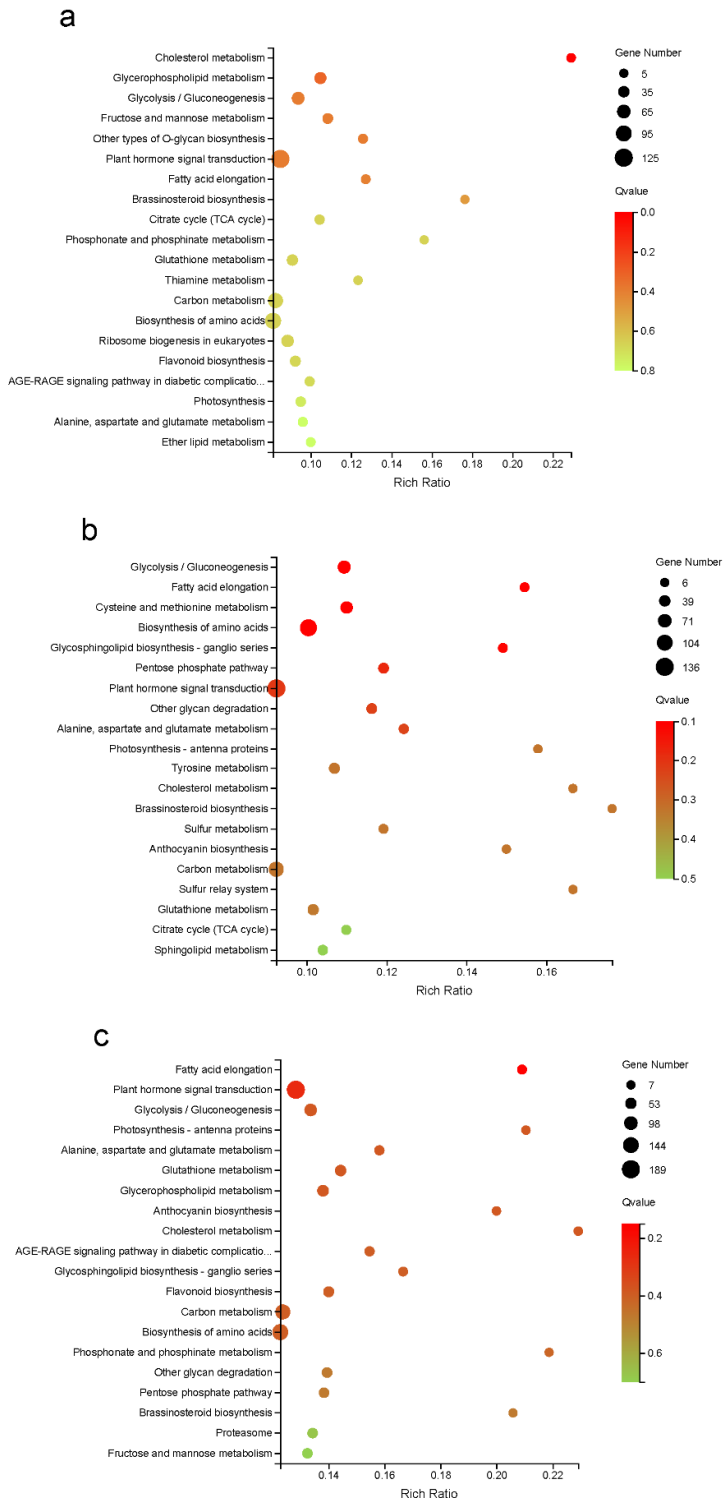

Figure S3. KEGG pathway enrichment analysis of the DEGs in M0 vs. F0 (a), M1 vs. F1 (b), and all the 7,029 DEGs in the pair-wise M0 vs. F0, and M1 vs. F1 comparisons (c).

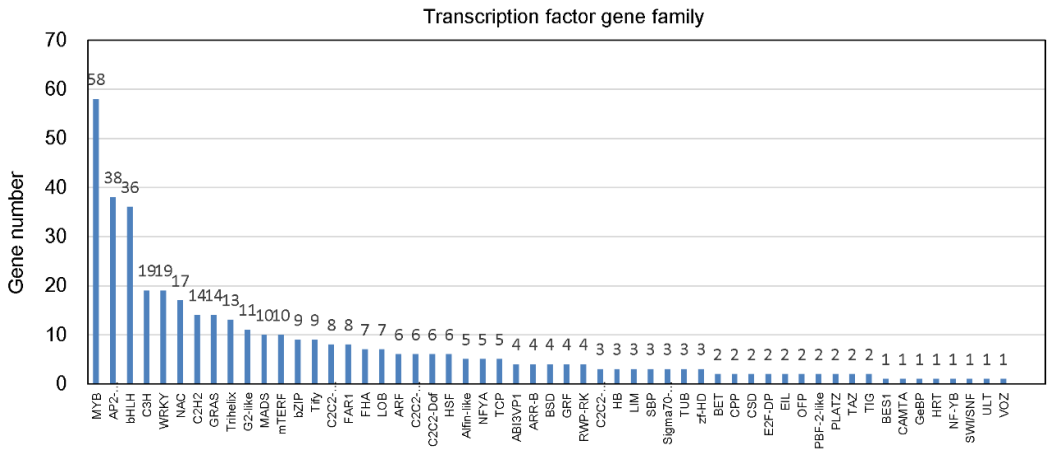

Figure S4. Distribution of the 547 415 transcription factors genes in 8889 7029 DEGs.

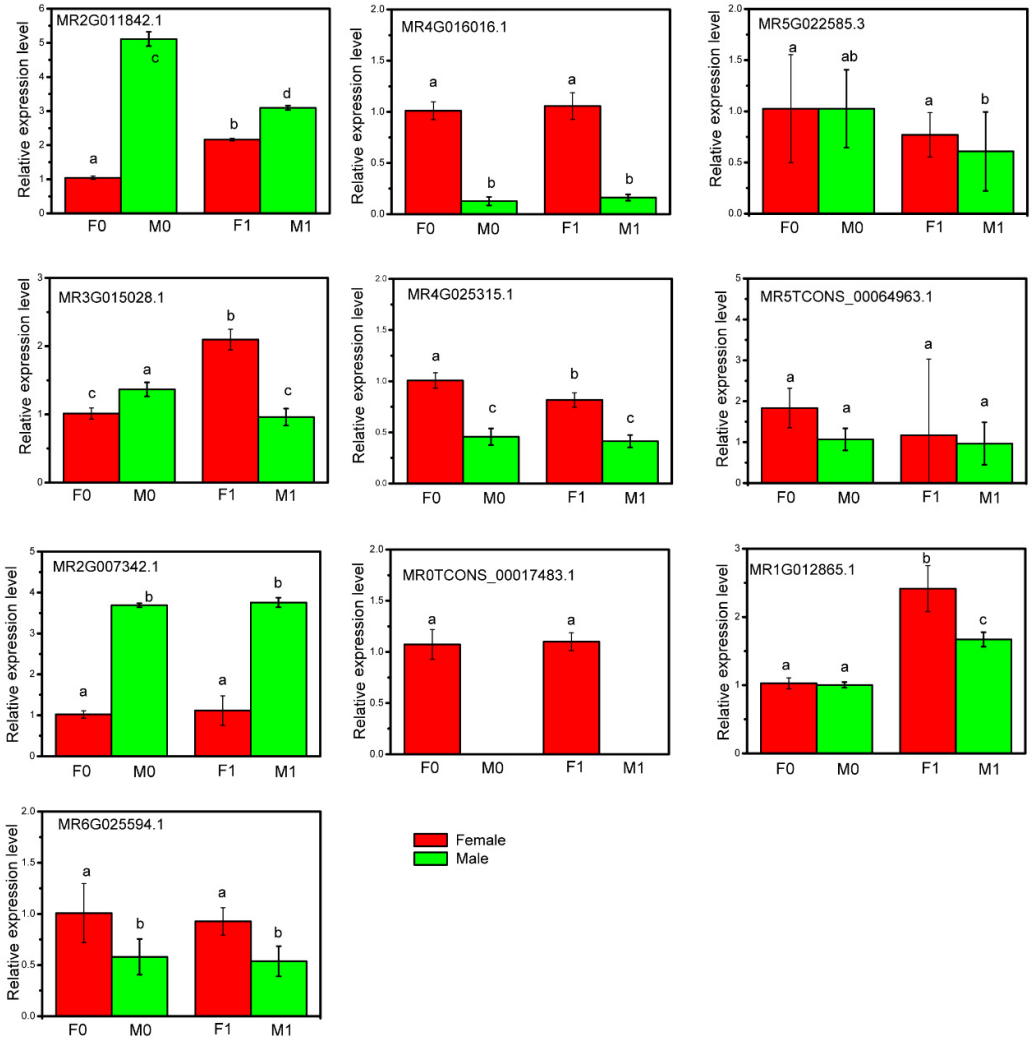

Figure S5. **Validation of the expression patterns of ten DEGs by qRT-PCR.** Capital letters above the black bars represent significant differences between the samples, Values are mean ± SE (n = 3).