

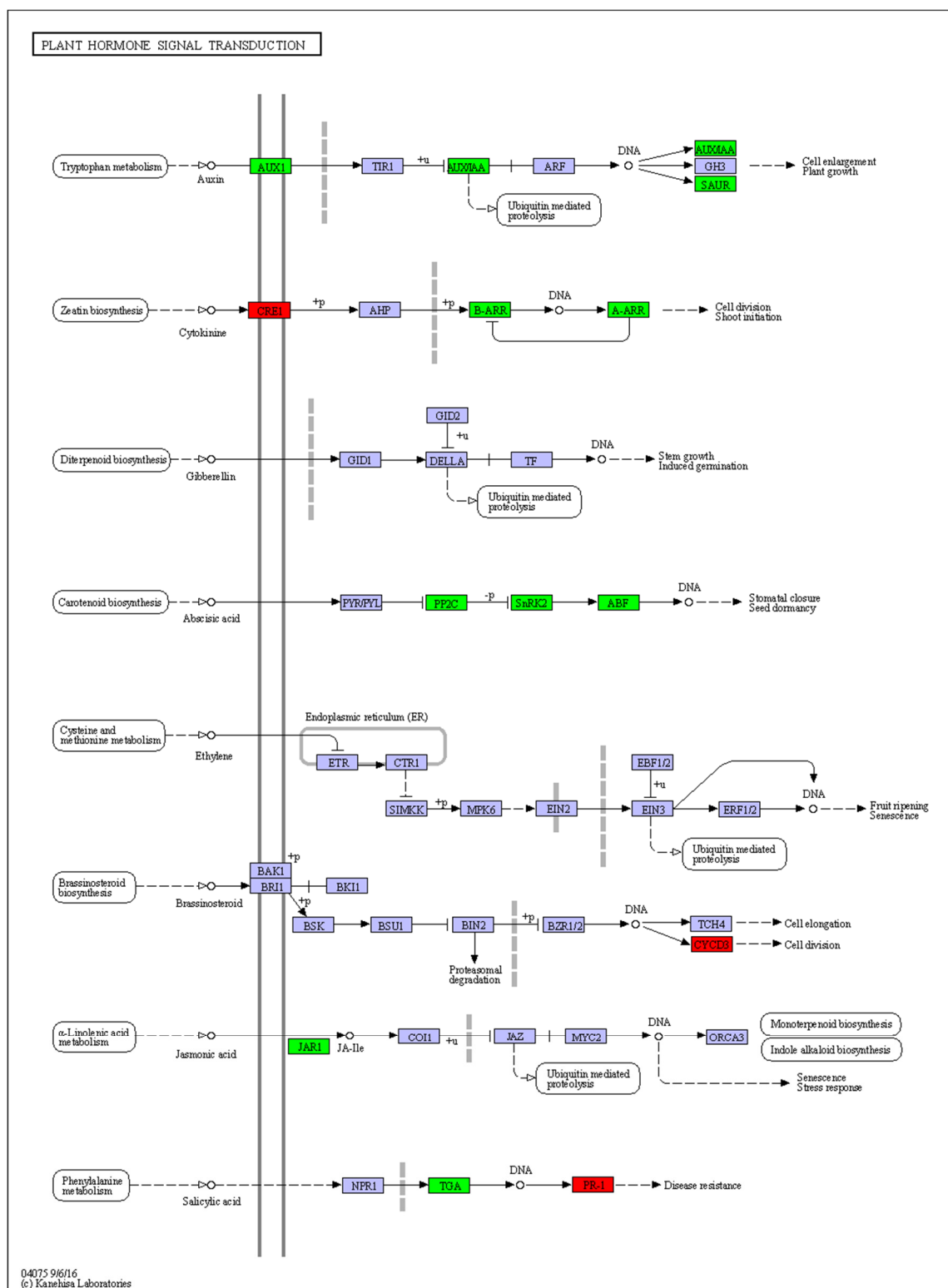


Figure S1. Plant hormone signal transduction.

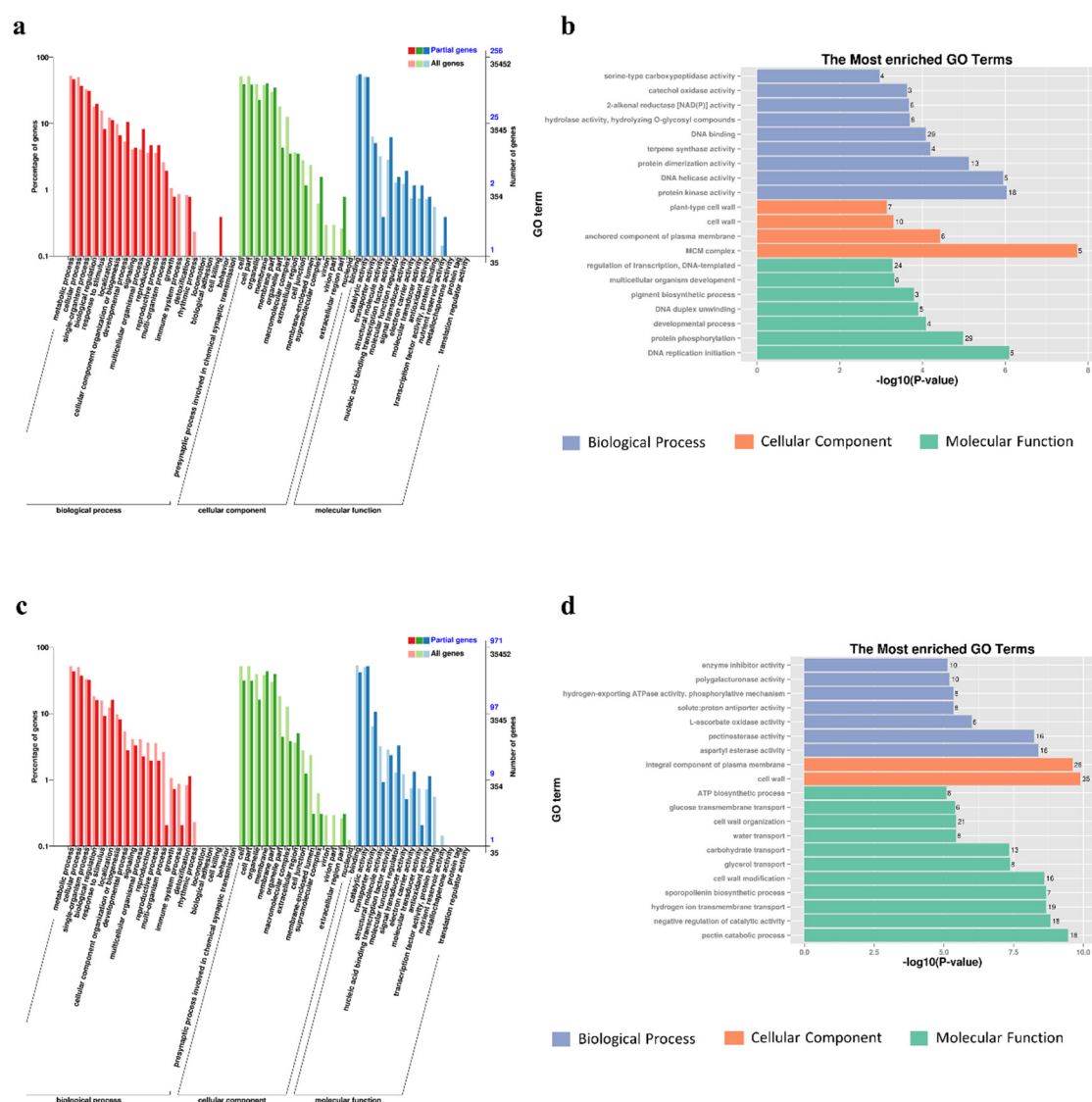


Figure S2. Annotation analysis of GO functions of male and female flowers' DEGs, respectively. (a) The GO functional classification of all down-regulated (highly expression level in female flower buds) DEGs. (b) The most enriched GO terms of all down-regulated (highly expression level in female flower buds) DEGs. (c) The GO functional classification of all up-regulated (highly expression level in male flower buds) DEGs. (d) The most enriched GO terms of all up-regulated (highly expression level in male flower buds) DEGs.

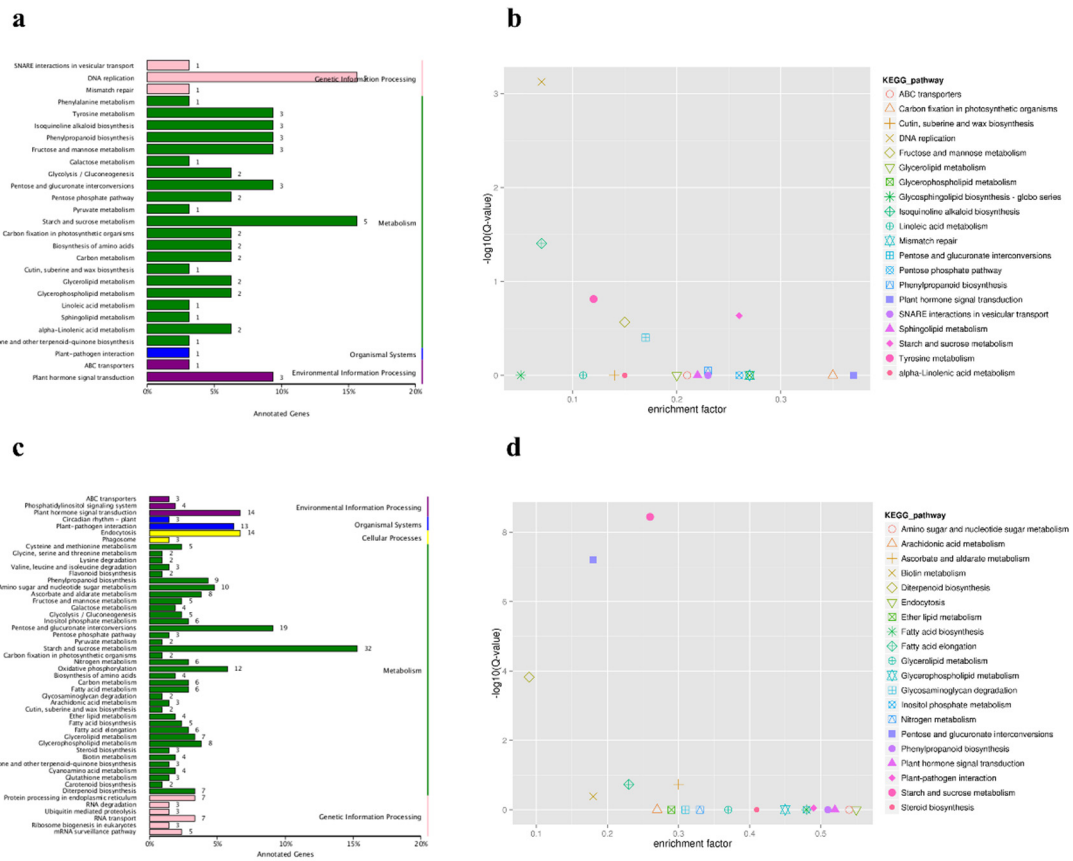


Figure S3. Annotation analysis of KEGG pathway of male and female flowers' DEGs, respectively. (a) Statistic analysis of all down-regulated (highly expression level in female flower buds) DEGs in KEGG pathways, DEGs were grouped into five major pathway categories as mentioned in the right panel. (b) Scatter plot of KEGG pathway enrichment for down-regulated (highly expression level in female flower buds) DEGs. Each small shape in the figure represents a KEGG path, and the path names are shown in the legend on the right. The horizontal coordinate is the enrichment factor, the smaller the enrichment factor, the more significant the enrichment level of DEGs in the pathway. The ordinate is $-\log_{10}(Q\text{-value})$, the larger the ordinate, the more reliable the enrichment of DEGs in the pathway. (c) Statistic analysis of all up-regulated (highly expression level in male flower buds) DEGs in KEGG pathways. (d) Scatter plot of KEGG pathway enrichment for up-regulated (highly expression level in male flower buds) DEGs.

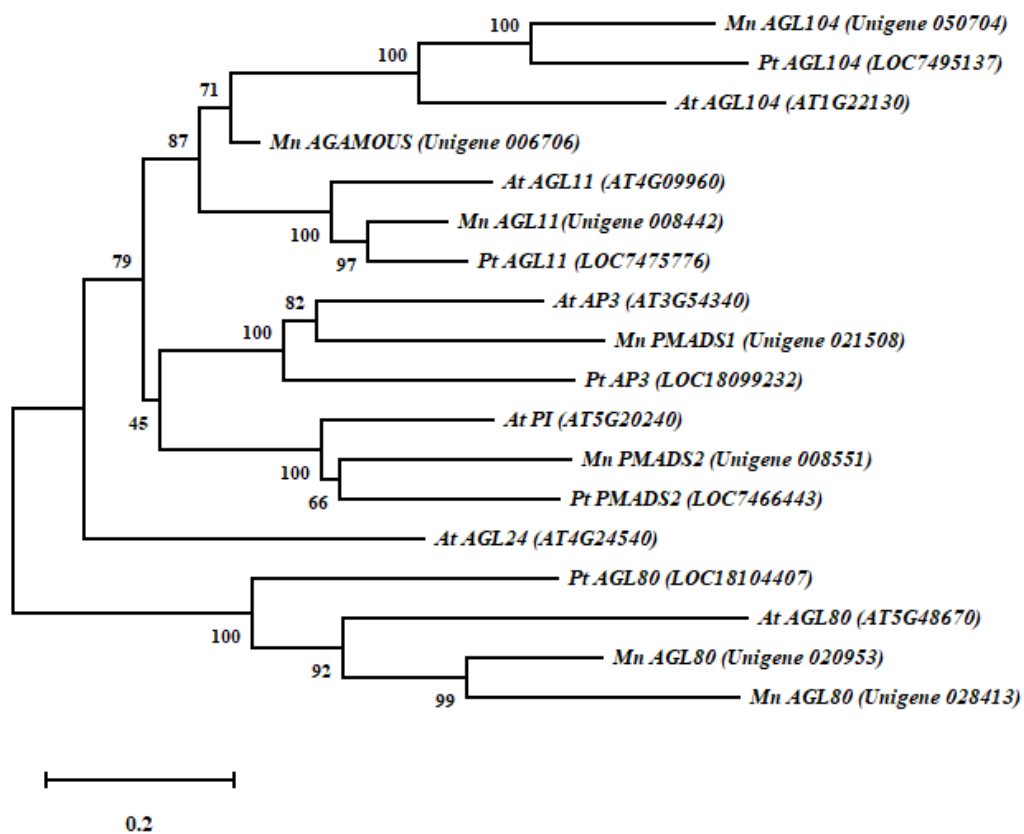


Figure S4. Phylogenetic analysis of MADS-box genes by Neighbor-Joining in *Morus alba* L.

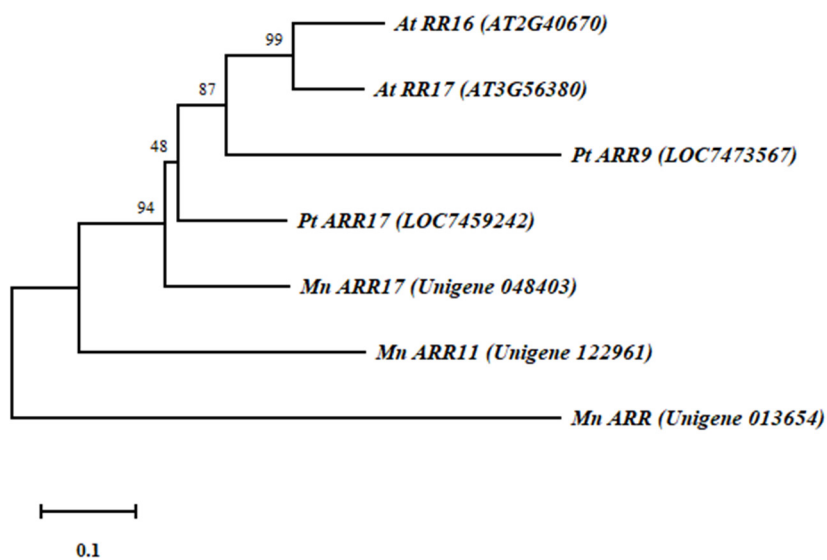


Figure S5. Phylogenetic analysis of ARR genes by Neighbor-Joining in *Morus alba* L.