

## **Supplementary Materials**

**Figure S1.** The correlation heatmap among biological replicates of RNA-seq from five tissues.

**Figure S2.** Co-expression network of the top 30 genes in the black (a) and red (b) modules with the highest correlation to stem tissue.

**Figure S3.** Expression pattern of genes related to the CAM pathway in five tissues.

**Figure S4.** Length distribution of small RNAs detected in the five tissues of *M. micrantha*.

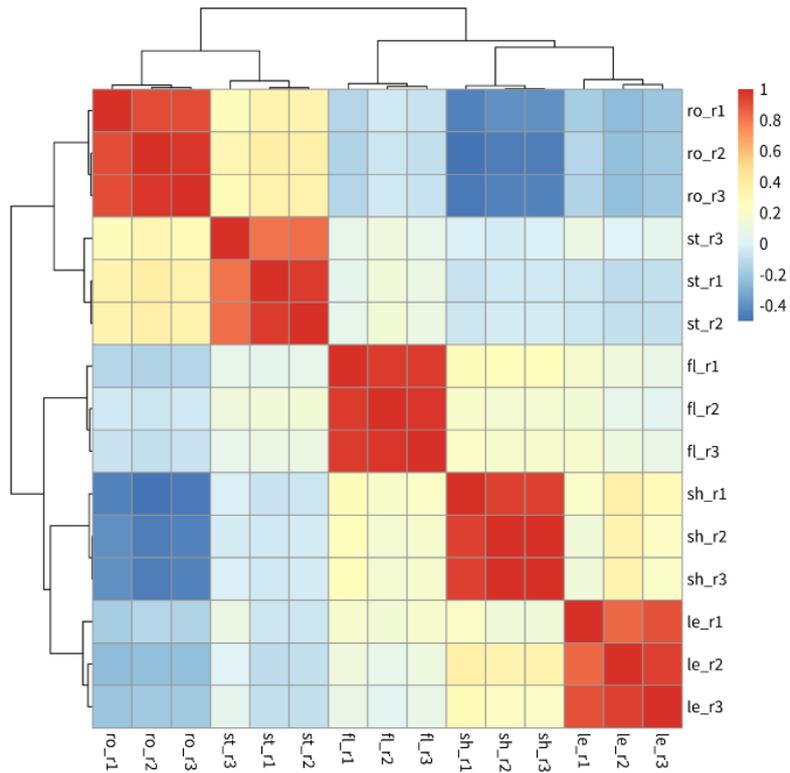
**Figure S5.** Stem-loop structure of predicted novel miRNA precursors.

**Figure S6.** Validation of miRNAs in five tissues.

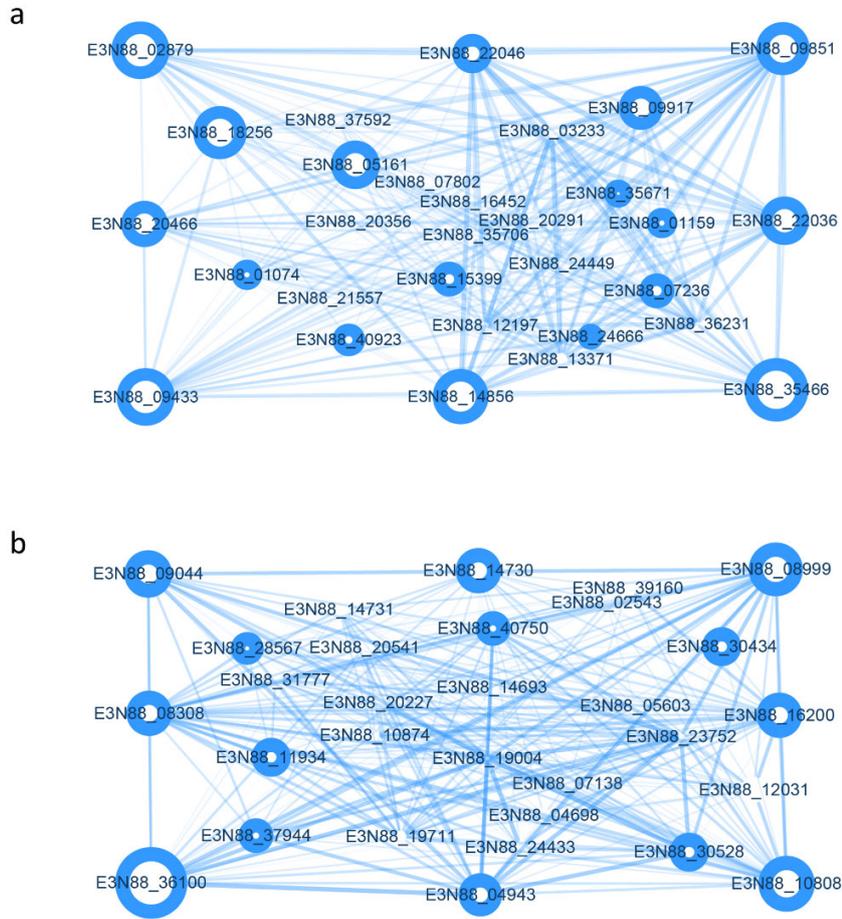
**Figure S7.** GO analysis of putative mmi-miR165/166 target genes.

**Figure S8.** GO analysis of putative mmi-miR319 target genes.

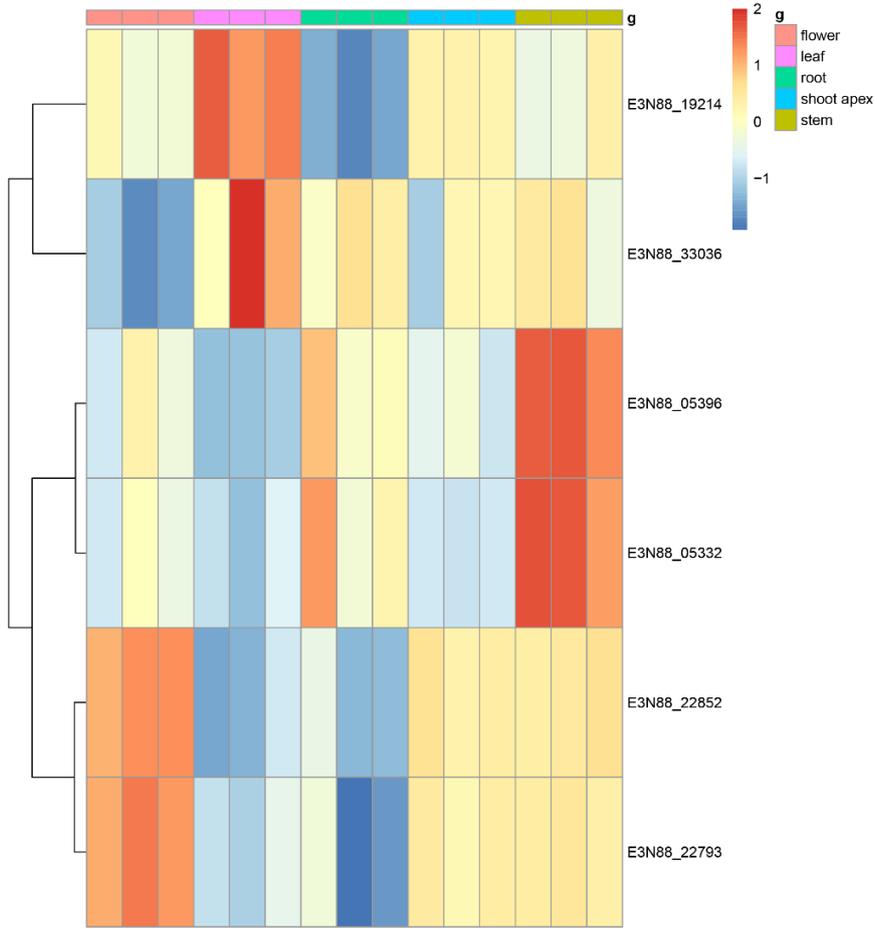
**Figure S9.** GO analysis of putative mmi-miR156 target genes.



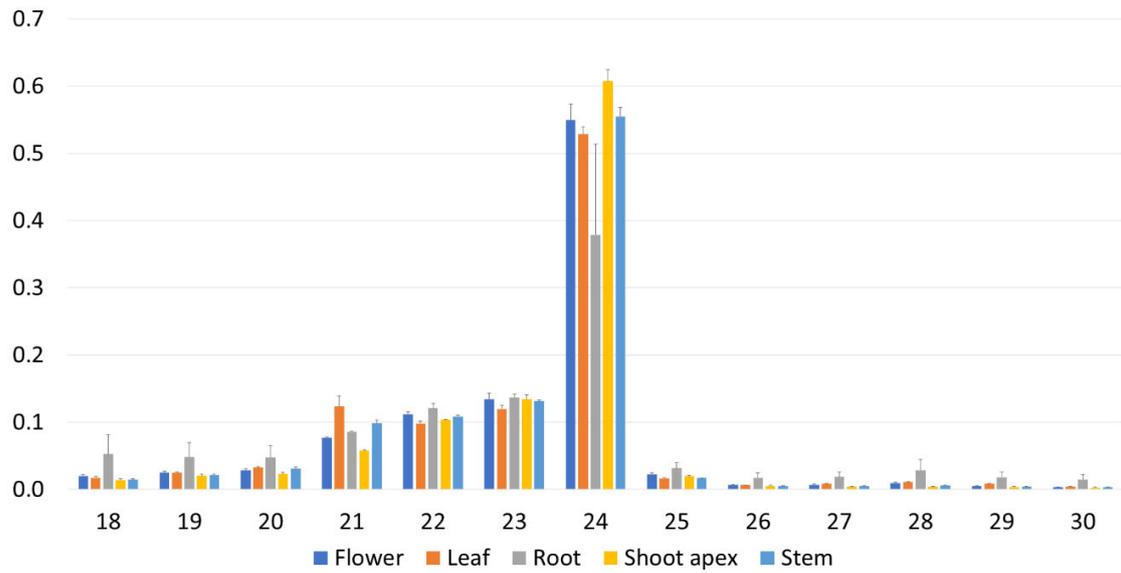
**Figure S1. The correlation heatmap among biological replicates of RNA-seq from five tissues.** fl, flower; le, leaf; ro, root; sh, shoot apex; st, stem. r1, r2, r3 represent three biological replicates.



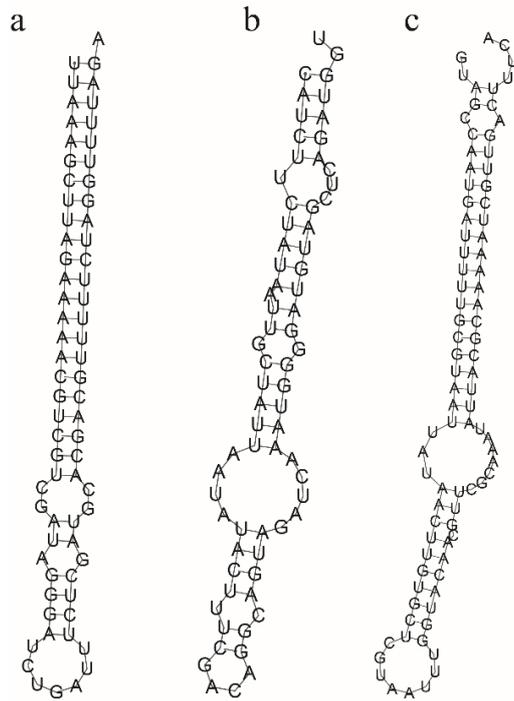
**Figure S2.** Co-expression network of the top 30 genes in the black (a) and red (b) modules with the highest correlation to stem tissue.



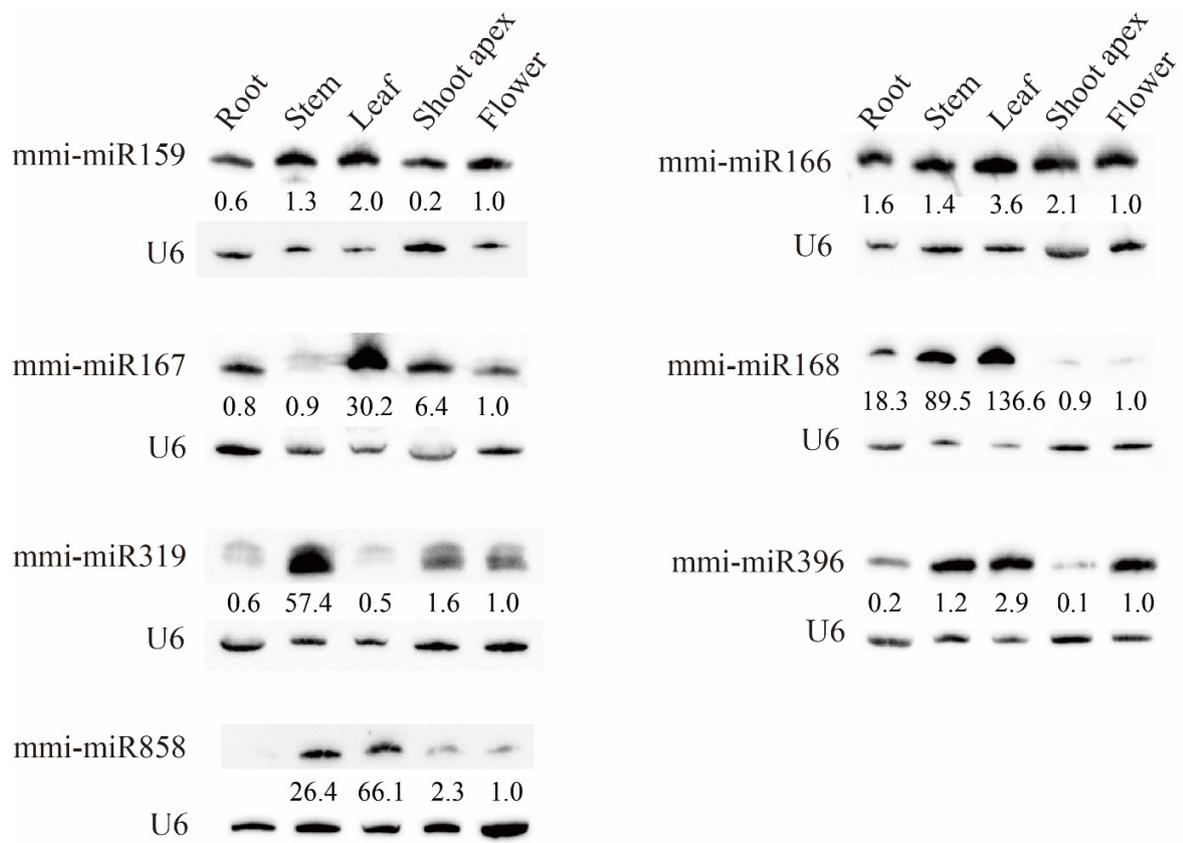
**Figure S3. Expression pattern of genes related to the CAM pathway in five tissues.**



**Figure S4. Length distribution of small RNAs detected in the five tissues of *M. micrantha*.** X-axis represents the length (nt), Y-axis represents the relative percentage of sRNAs in each tissue, which is calculated based on the three biological replicates. Error bar represents standard deviation.



**Figure S5. Stem-loop structure of predicted novel miRNA precursors. (a)** Structure of mmi-cand117 precursor. **(b)** Structure of mmi-cand38 precursor. **(c)** Structure of mmi-cand26b precursor.



**Figure S6.** Validation of miRNAs in five tissues. U6 served as a loading control.

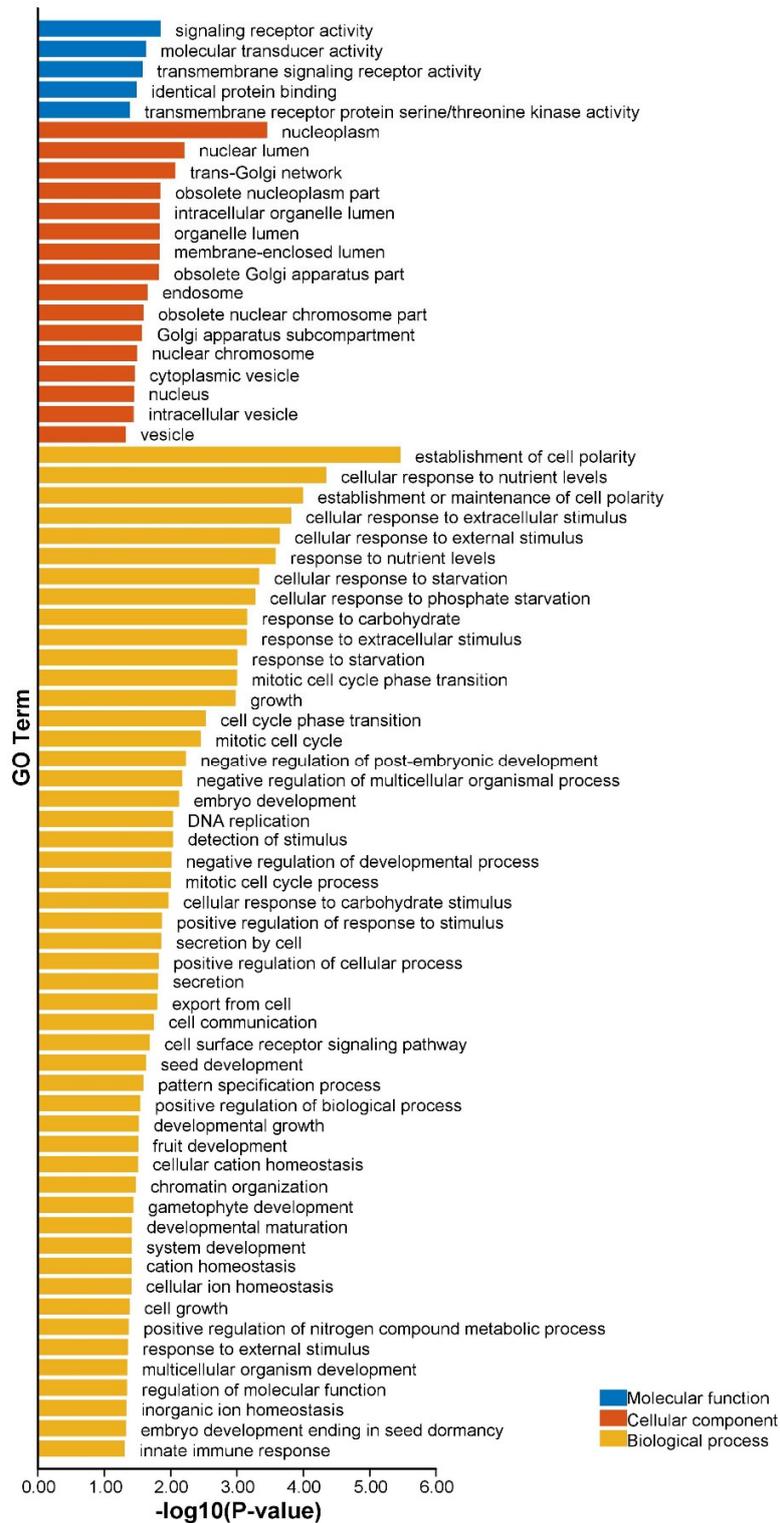


Figure S7. GO analysis of putative mmi-miR165/166 target genes.

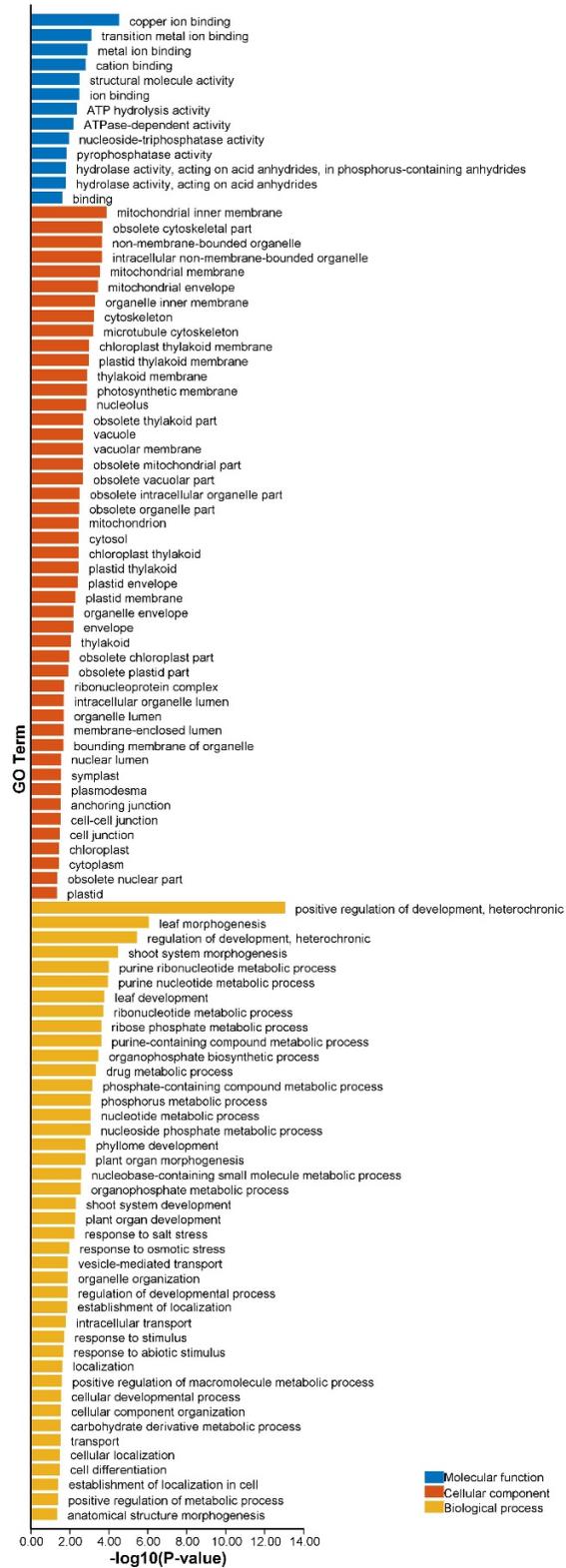


Figure S8. GO analysis of putative mmi-miR319 target genes.

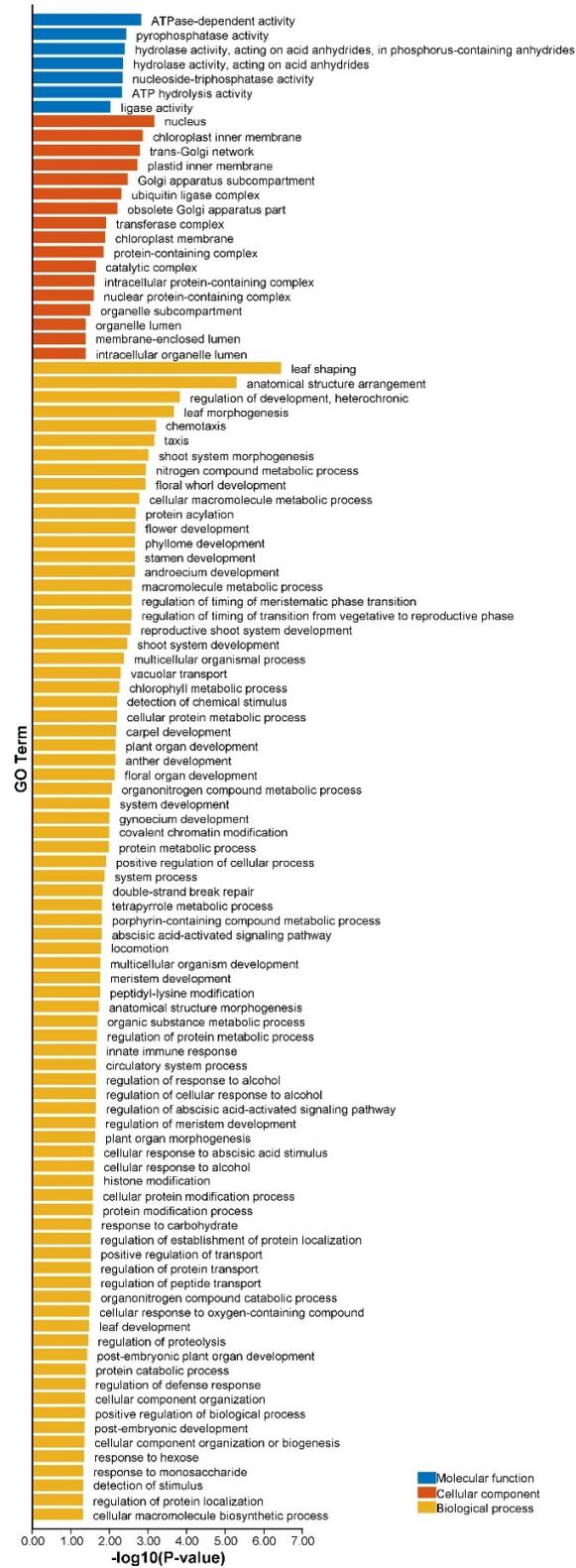


Figure S9. GO analysis of putative mmi-miR156 target genes.