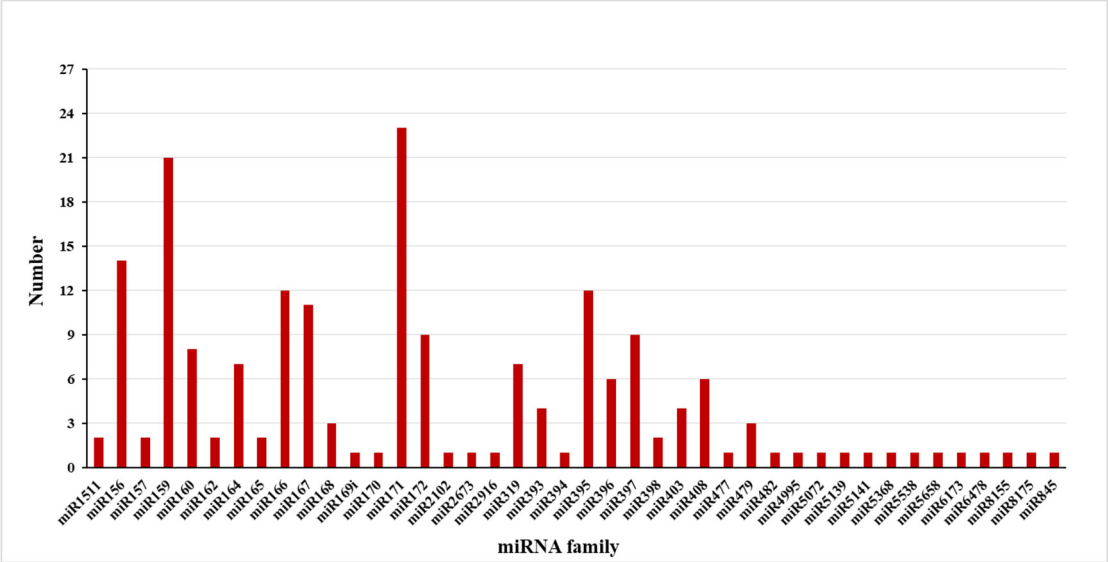


Figure S1. Number of miRNA family members in *T. tuan* seed.

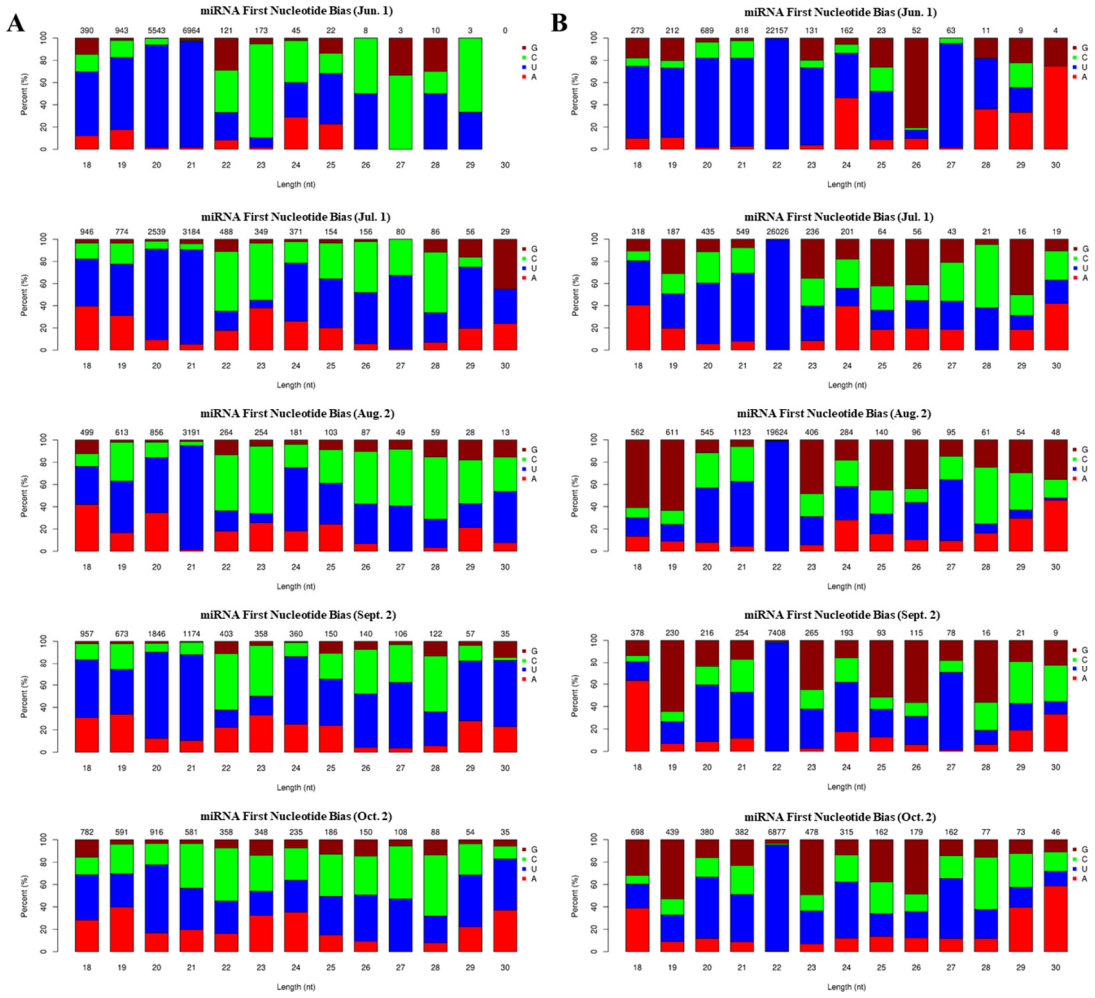


Figure S2. First base composition bias of miRNAs (18-30 nt) in *T. tuan*. (A) Known miRNAs. (B) Novel miRNAs. The abscissa is the length of miRNAs, and the ordinate is the percentage of A/U/C/G in the first base of miRNA at that length (the value above the column chart is the total number of miRNAs at that length).

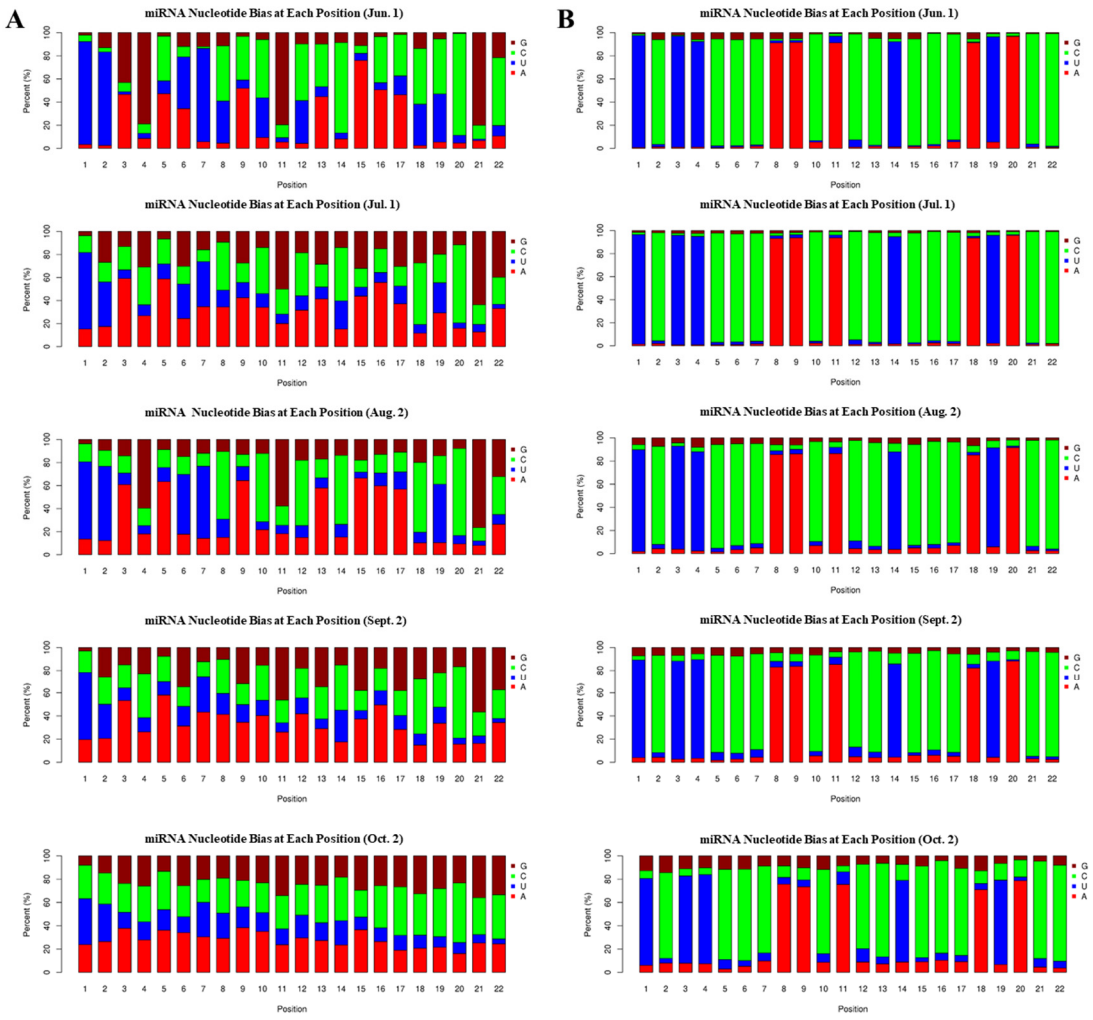


Figure S3. Nucleotide bias at each position of miRNAs in *T. tuan*. (A) Known miRNAs. (B) Novel miRNAs. The abscissa is the base position of miRNA, and the ordinate is the percentage of base A/U/C/G in miRNA at that position.

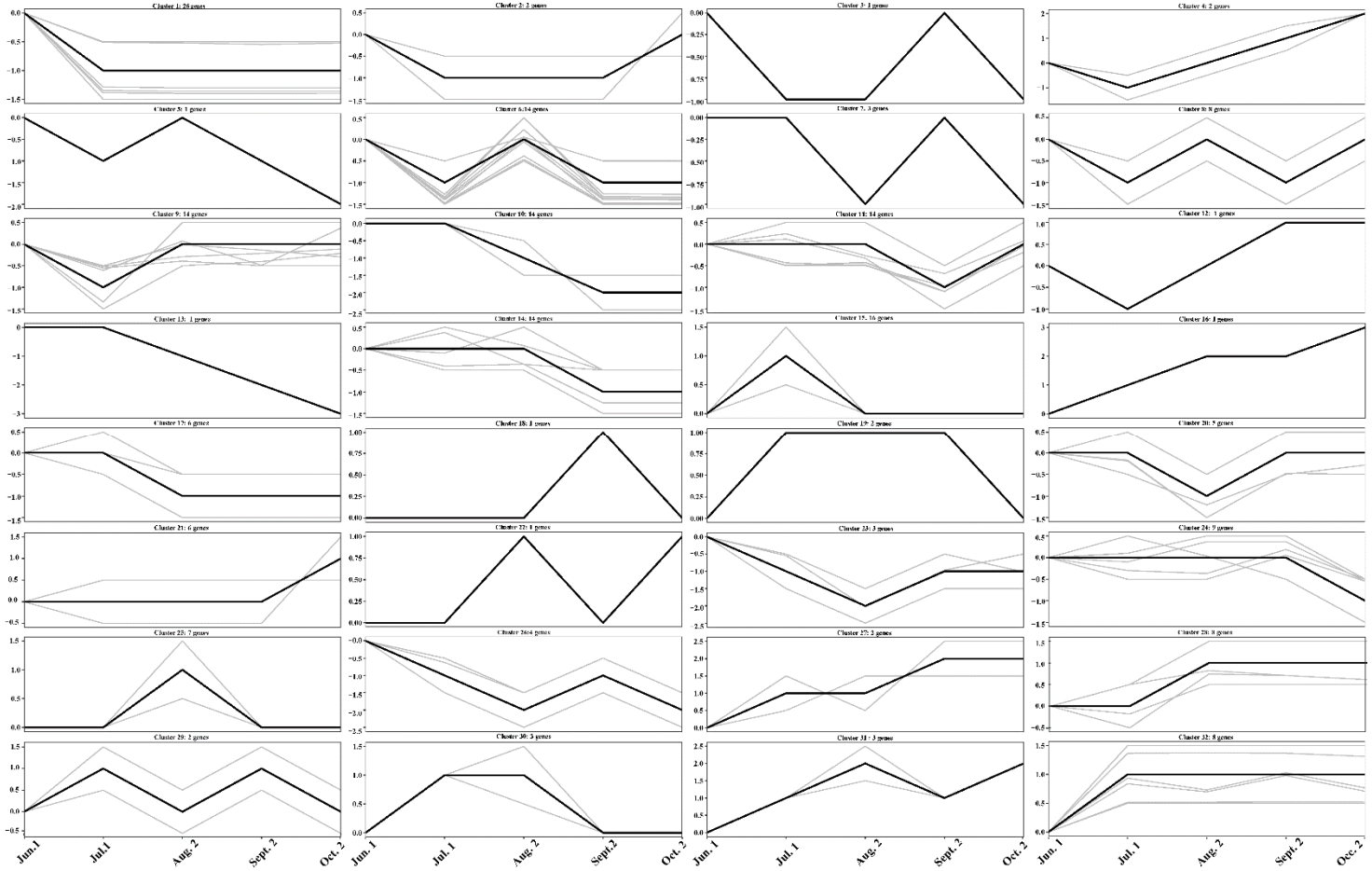


Figure S4. Several distinct expression patterns of known miRNAs and novel miRNAs in *T. tuan* seed.

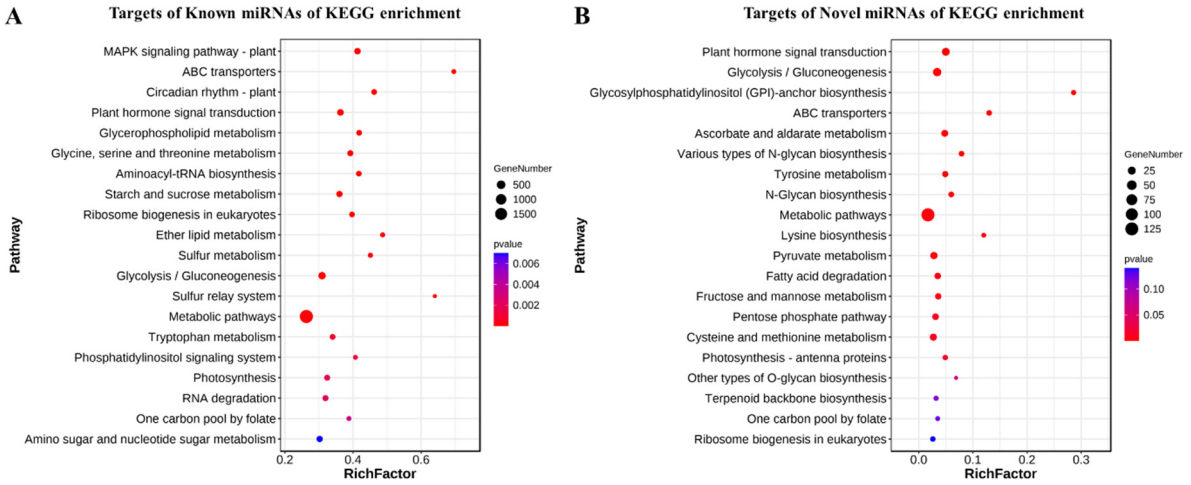


Figure S5. Kyoto Encyclopedia of Genes and Genomes (KEGG) pathway enrichment analysis of known miRNAs and novel miRNAs targets. (A) Targets of known miRNAs of KEGG pathway enrichment. (B) Targets of novel miRNAs of KEGG pathway enrichment. Rich Factor refers to the ratio of the gene number and the number of genes annotated in this pathway and large Rich Factor indicates high degree of enrichment. The area of each colored circle is proportional to the number of genes involved in each pathway, the color indicated the pvalue, and the x-axis is the Rich Factor. Only the top 20 overrepresented KEGG pathways are shown.