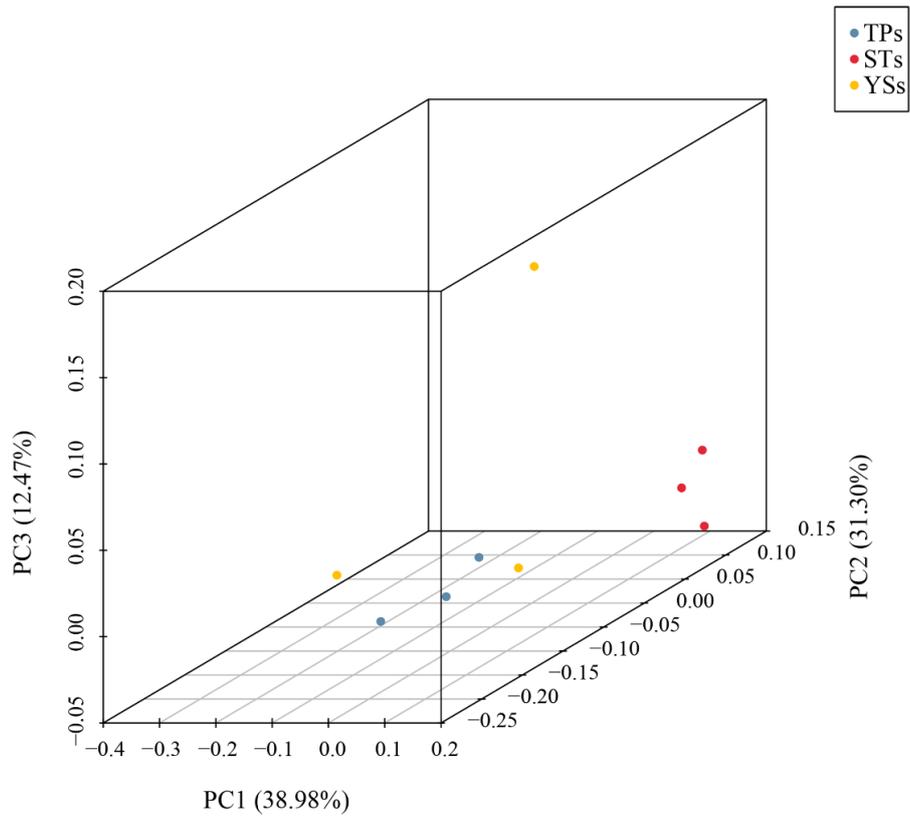
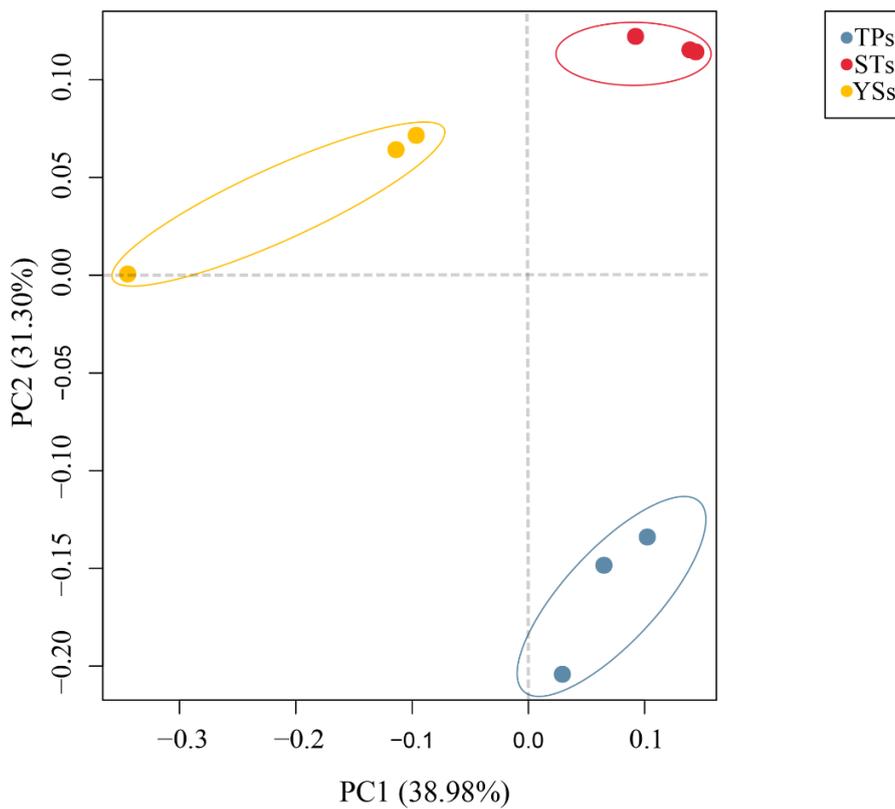


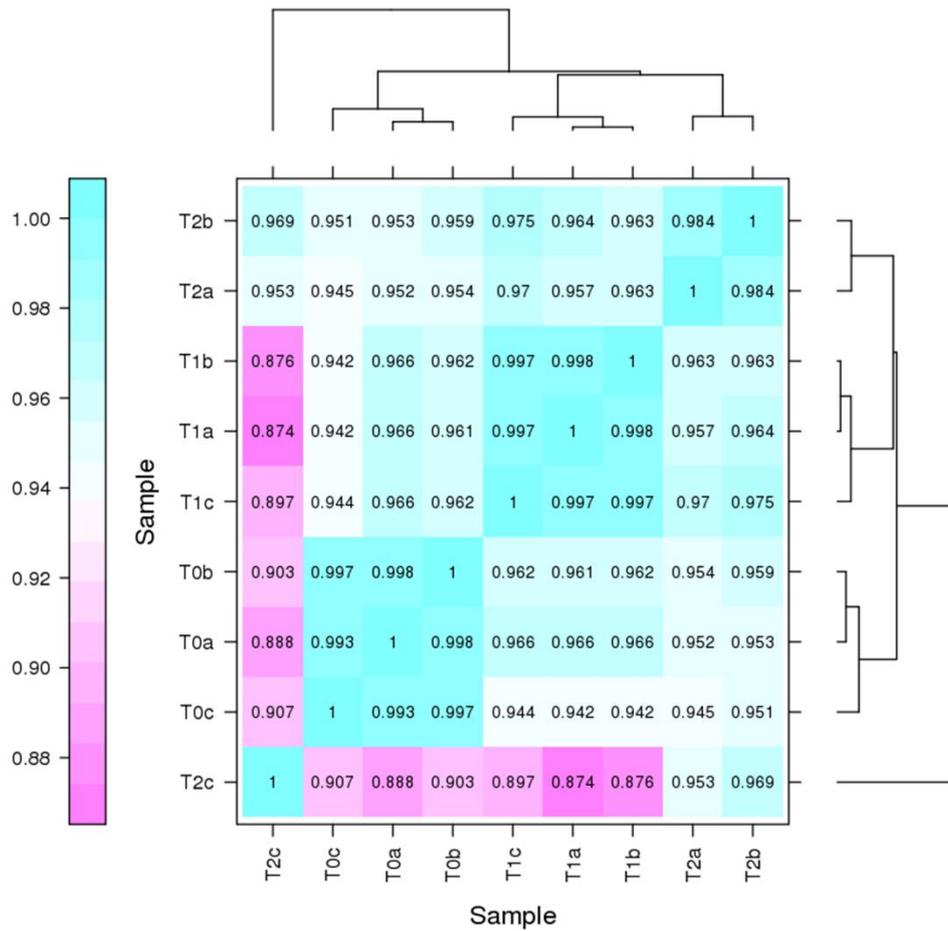
## Supplementary Figures



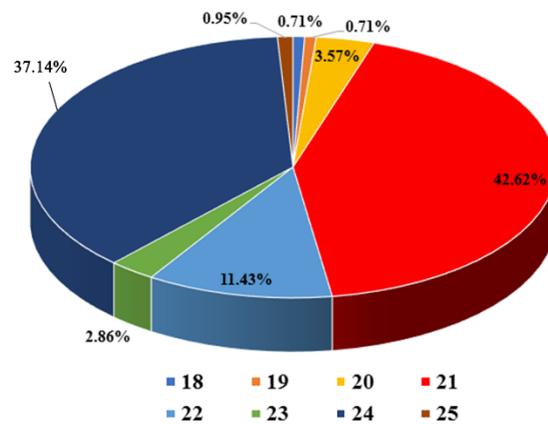
**Figure S1** The PCA map among the samples of transcriptome sequencing



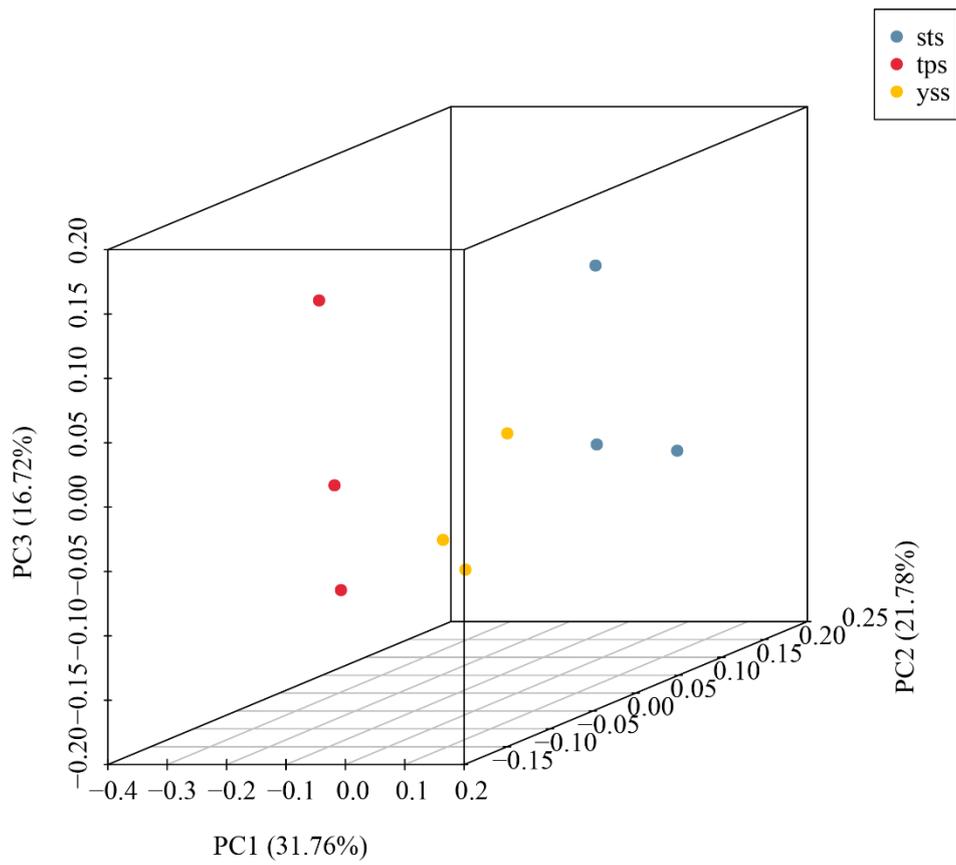
**Figure S2** The two-dimensional map of PCA among the transcriptome sequencing samples



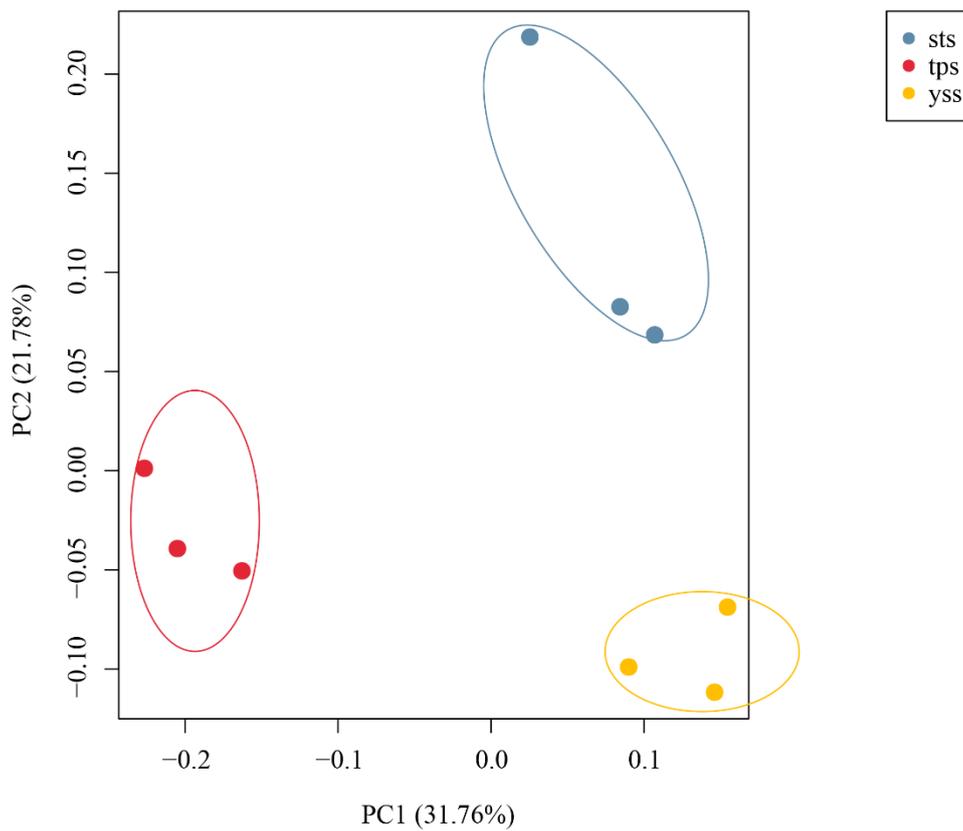
**Figure S3** PCC analysis of the transcriptome sequencing samples



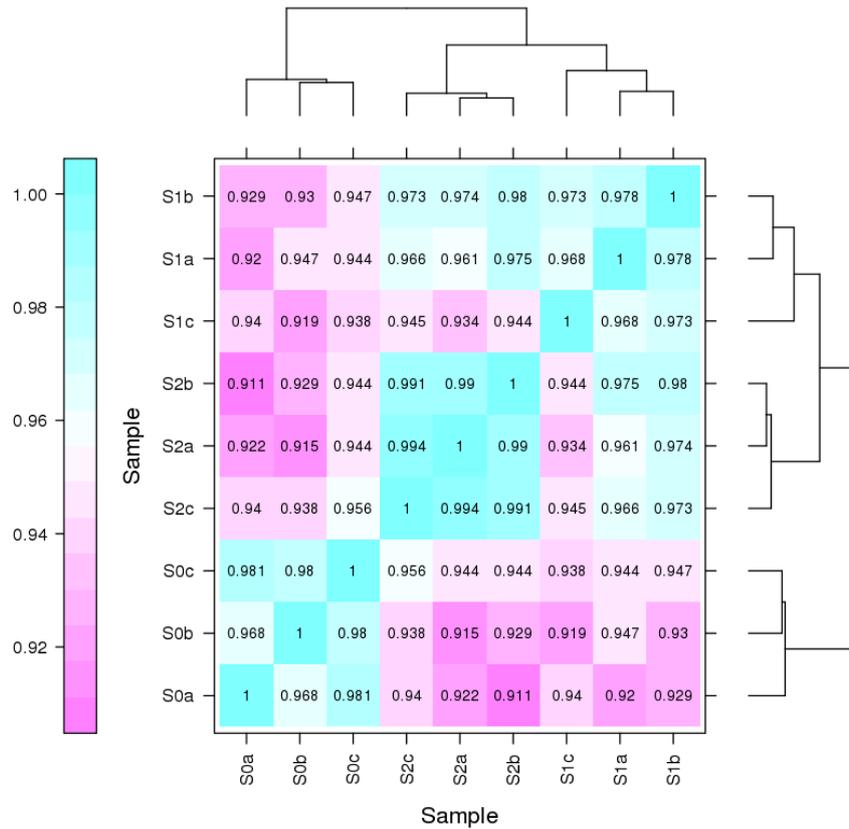
**Figure S4** Distribution map of the identified miRNAs with different lengths



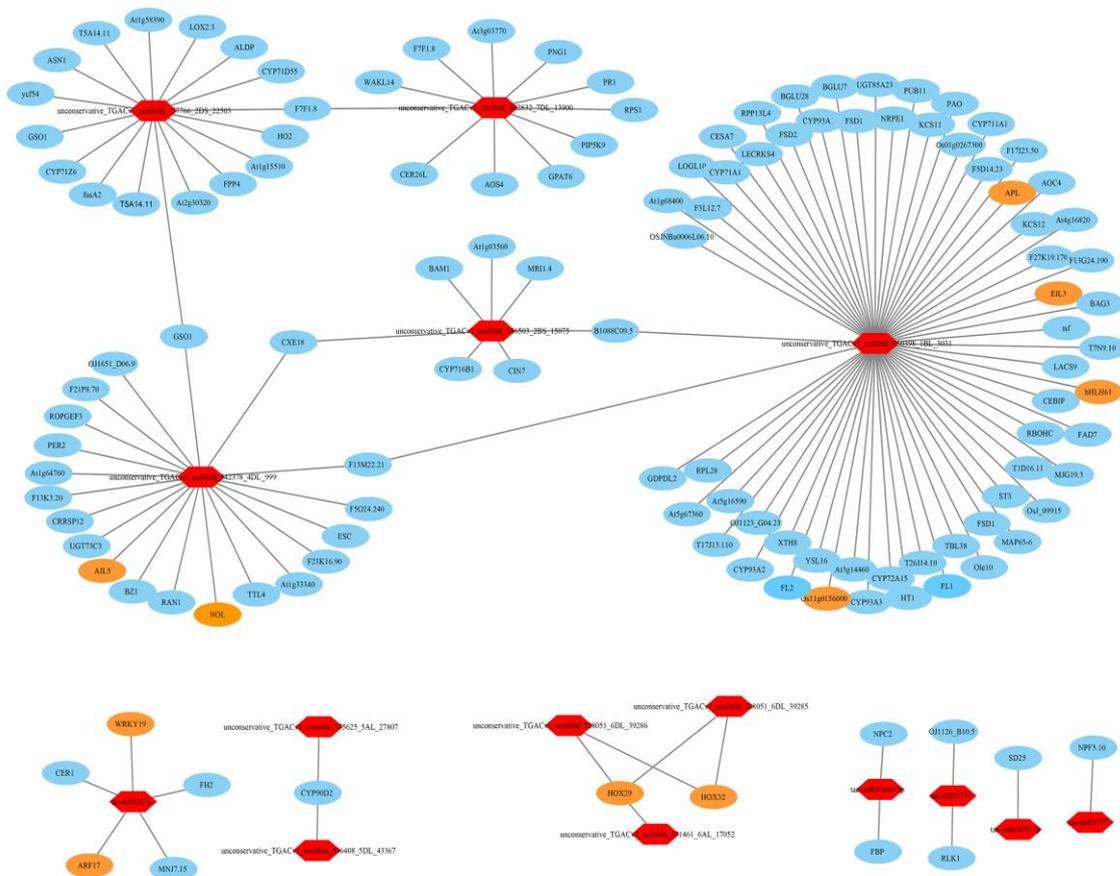
**Figure S5** The PCA map among the samples of miRNA sequencing



**Figure S6** The two-dimensional map of PCA among the miRNA sequencing samples



**Figure S7** PCC analysis of the small RNA sequencing samples



**Figure S8** A part of the 372 negative miRNA-mRNA interaction pairs (regulation network) in TPs. Red hexagons represented the highly expressed miRNAs in TPs. Ovals represented the target genes of miRNAs. Yellow ovals represented TFs.

