

Supplementary Figures

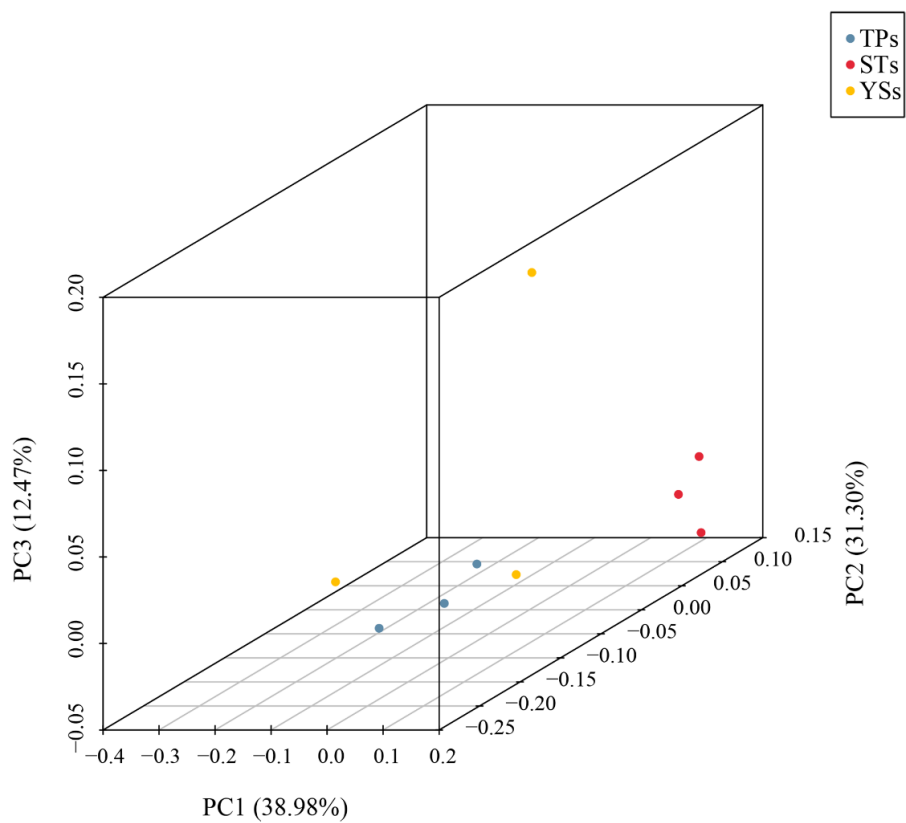


Figure S1 The PCA map among the samples of transcriptome sequencing

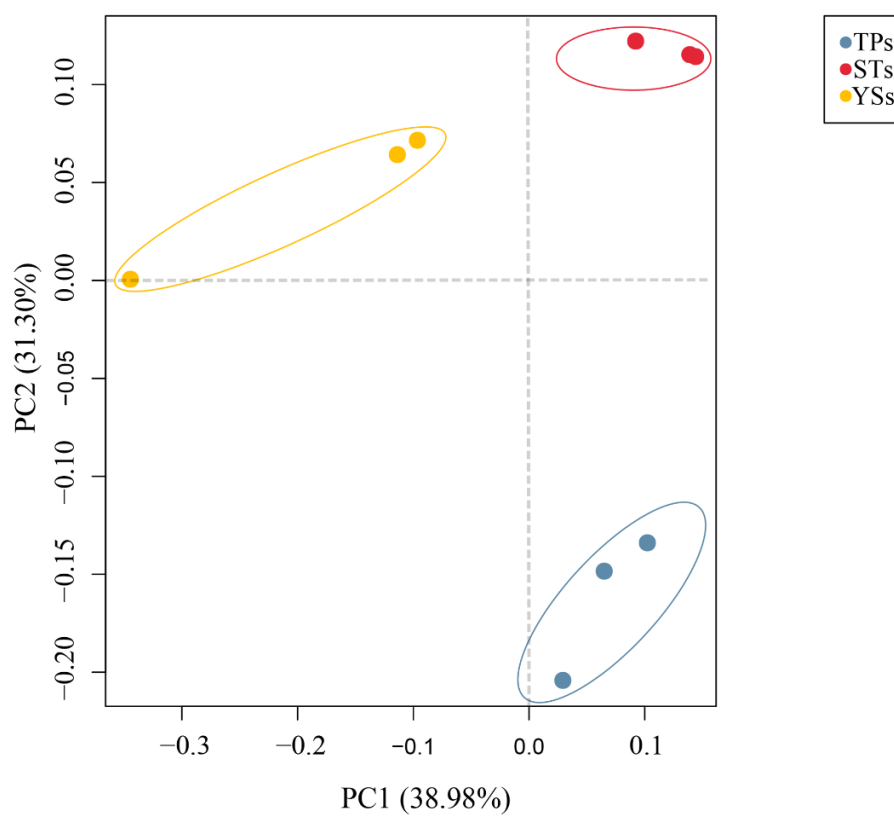


Figure S2 The two-dimensional map of PCA among the transcriptome sequencing samples

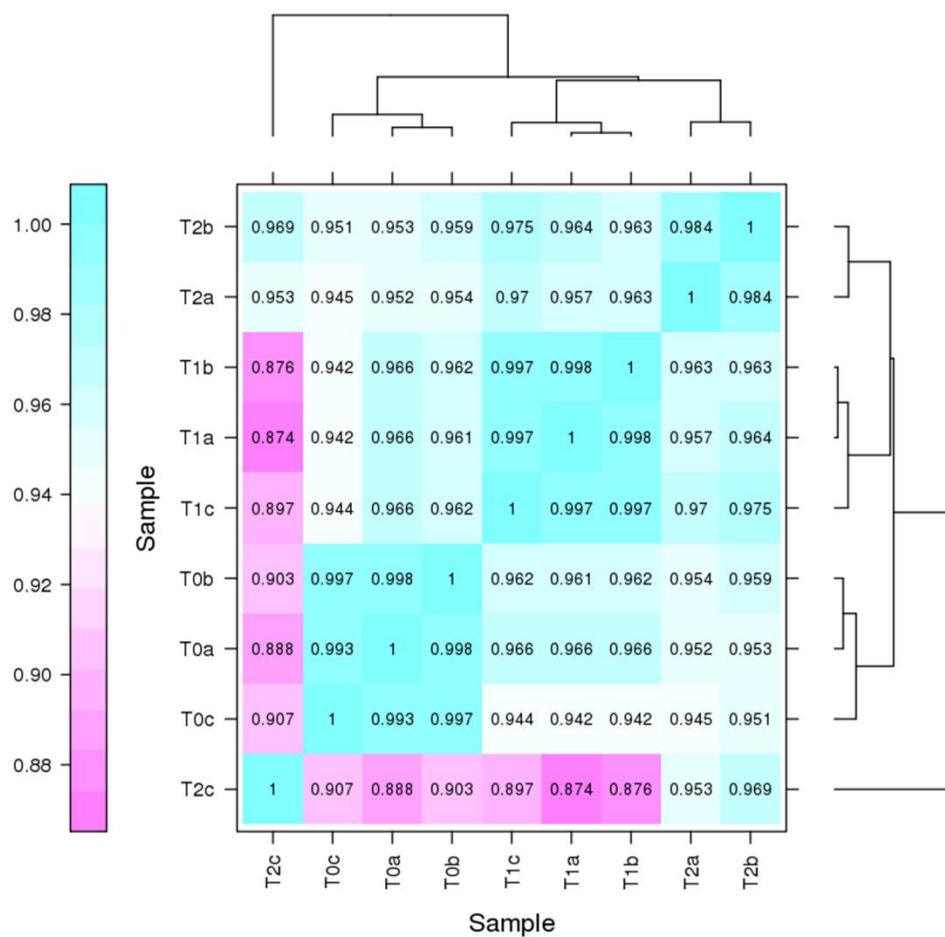


Figure S3 PCC analysis of the transcriptome sequencing samples

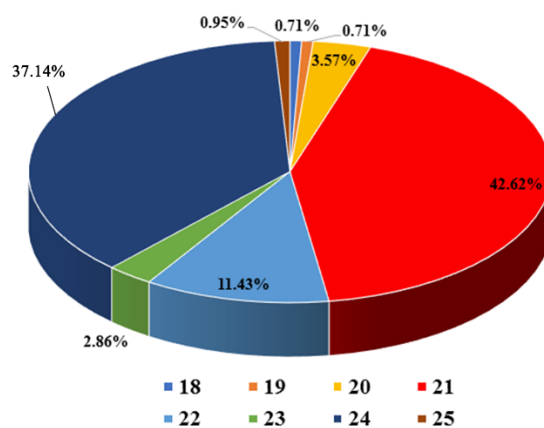


Figure S4 Distribution map of the identified miRNAs with different lengths

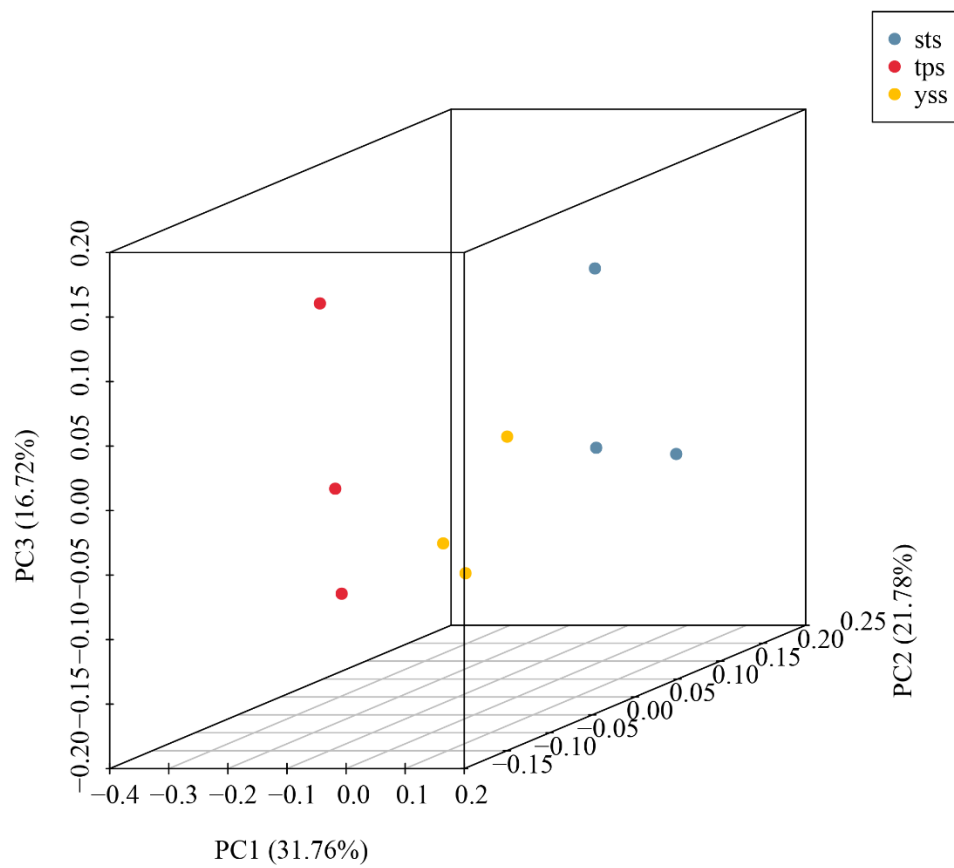


Figure S5 The PCA map among the samples of miRNA sequencing

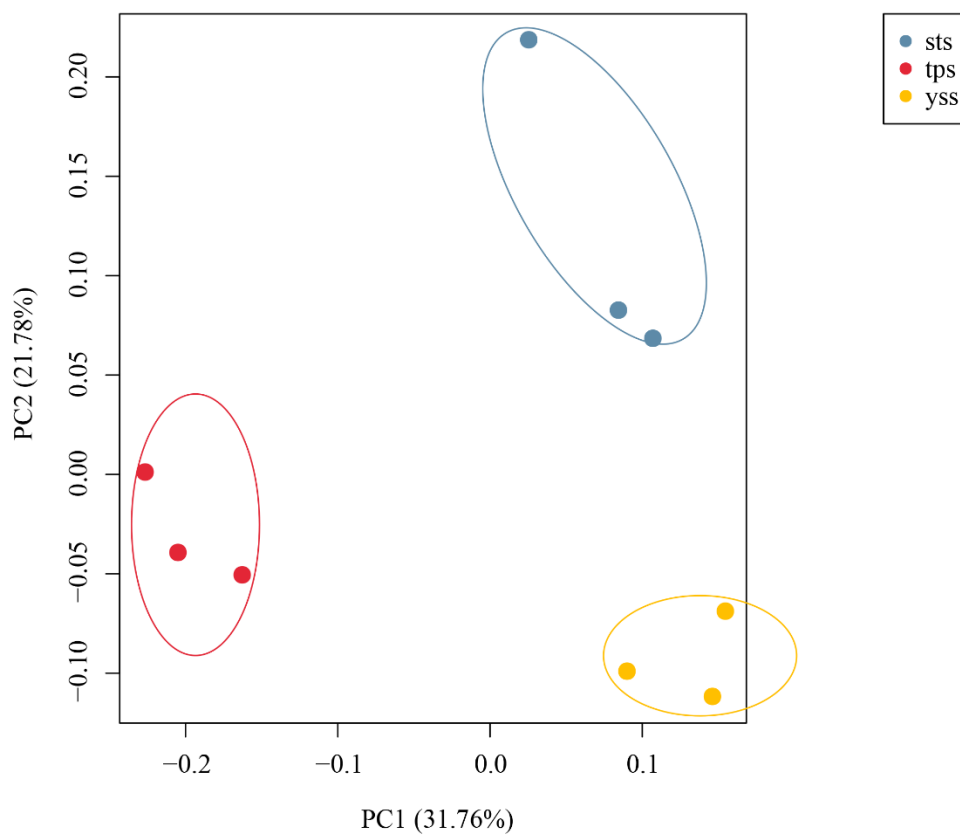


Figure S6 The two-dimensional map of PCA among the miRNA sequencing samples

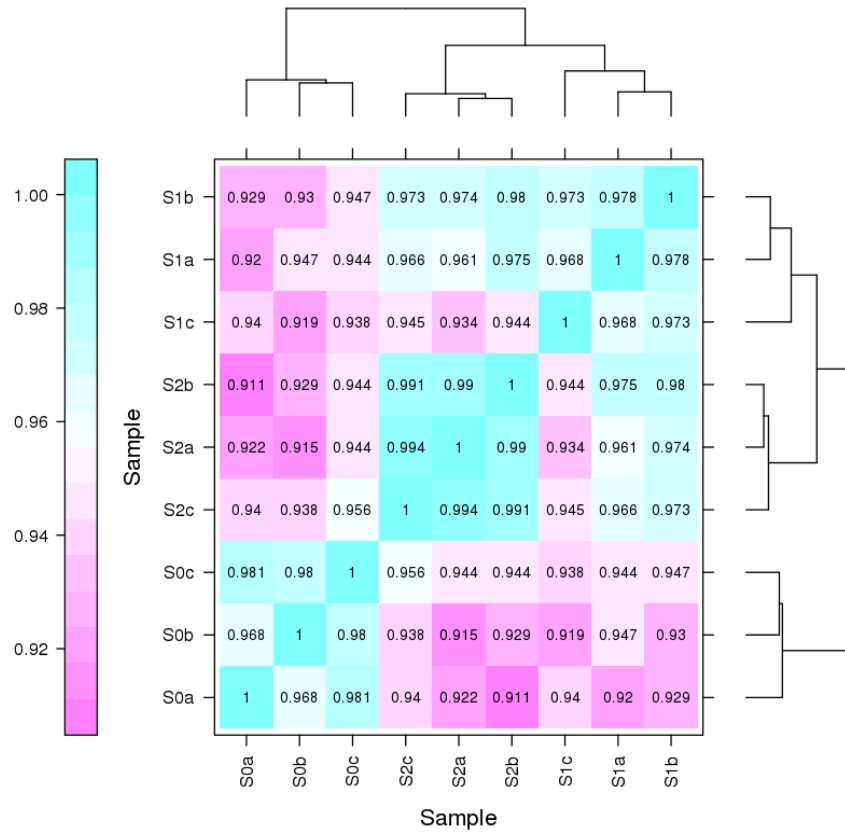


Figure S7 PCC analysis of the small RNA sequencing samples

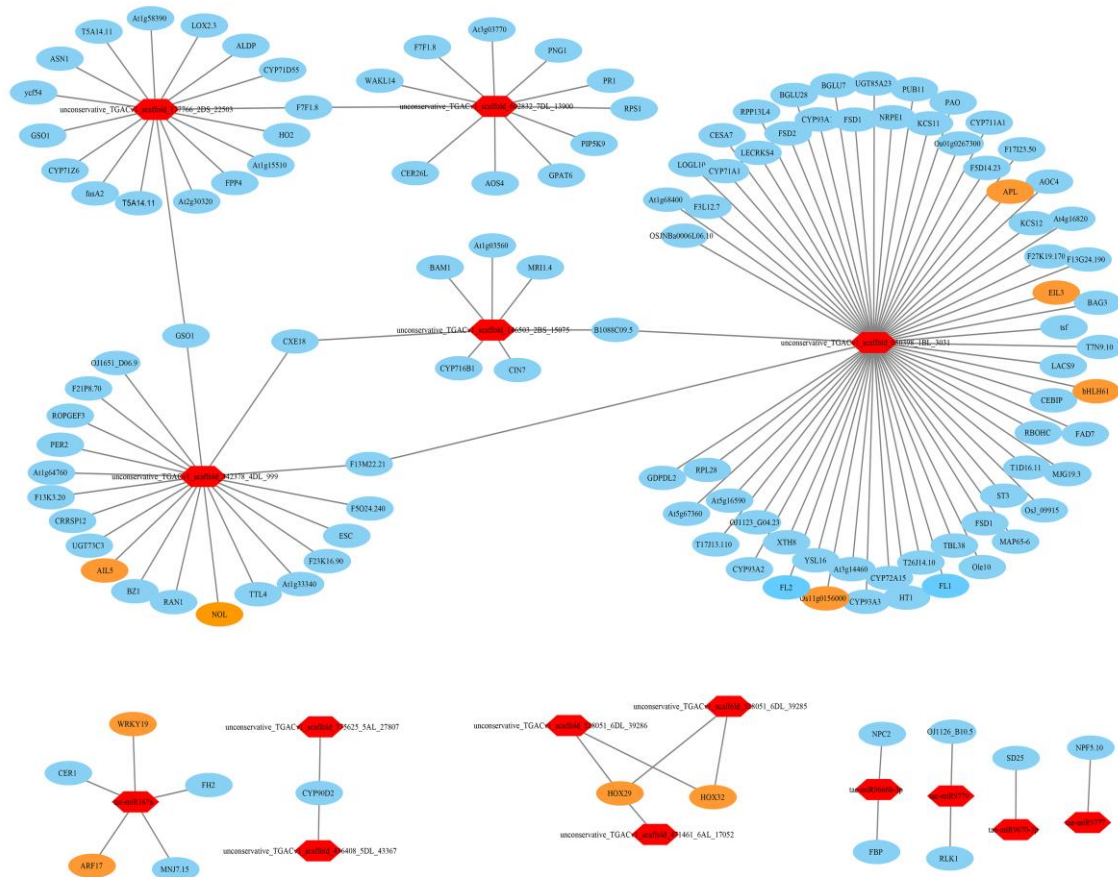


Figure S8 A part of the 372 negative miRNA-mRNA interaction pairs (regulation network) in TPs. Red hexagons represented the highly expressed miRNAs in TPs. Ovals represented the target genes of miRNAs. Yellow ovals represented TFs.

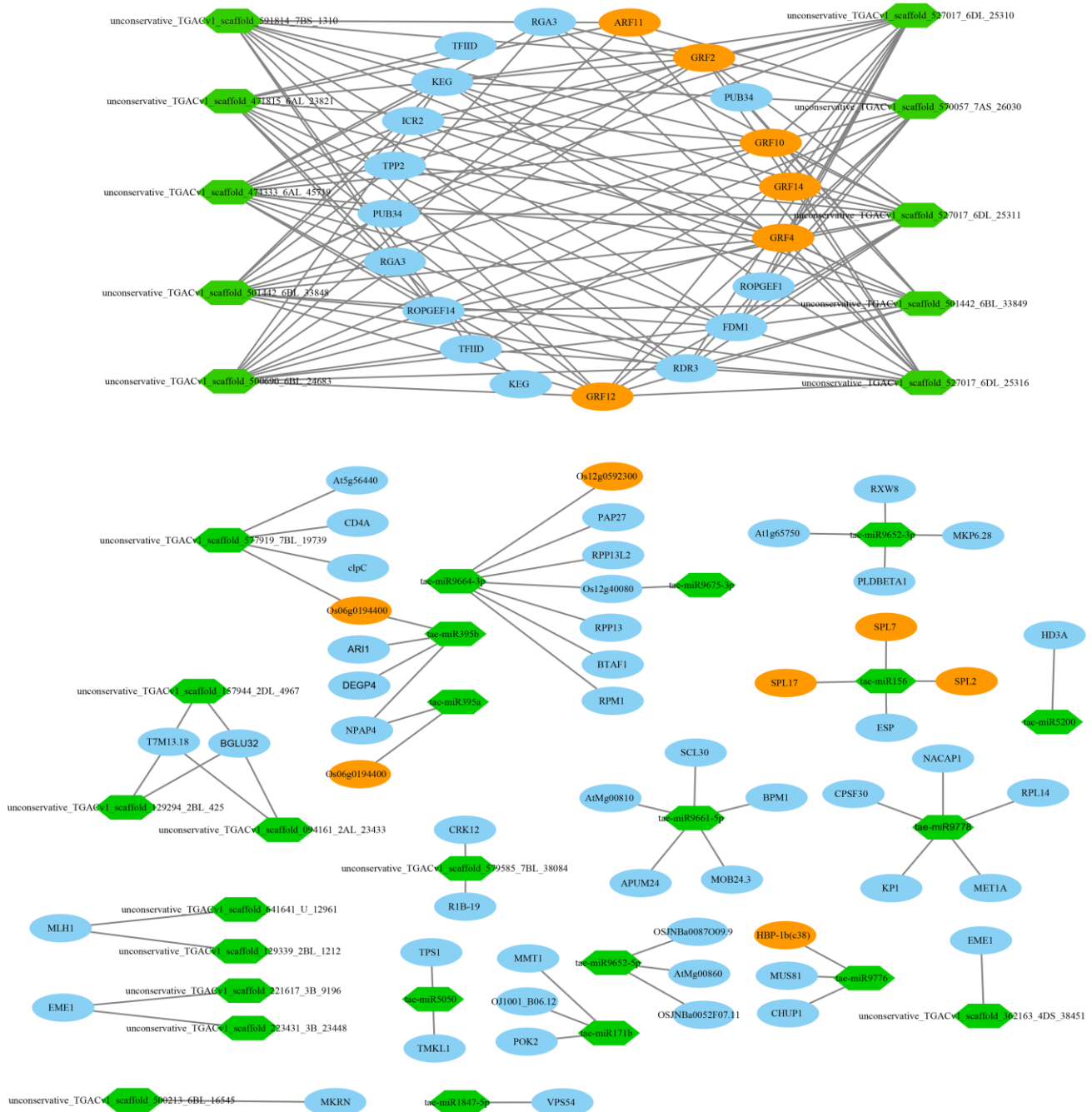


Figure S9 A part of the 279 negative miRNA-mRNA interaction pairs (regulation network) in YSs. Green hexagons represented the highly expressed miRNAs in YSs. Ovals represented the target genes of miRNAs. Yellow ovals represented TFs.