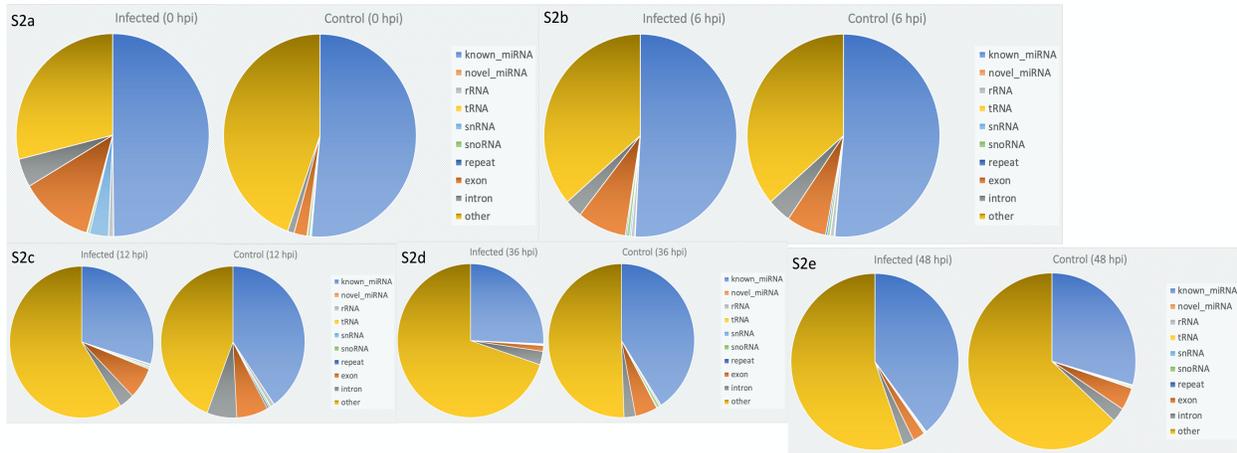
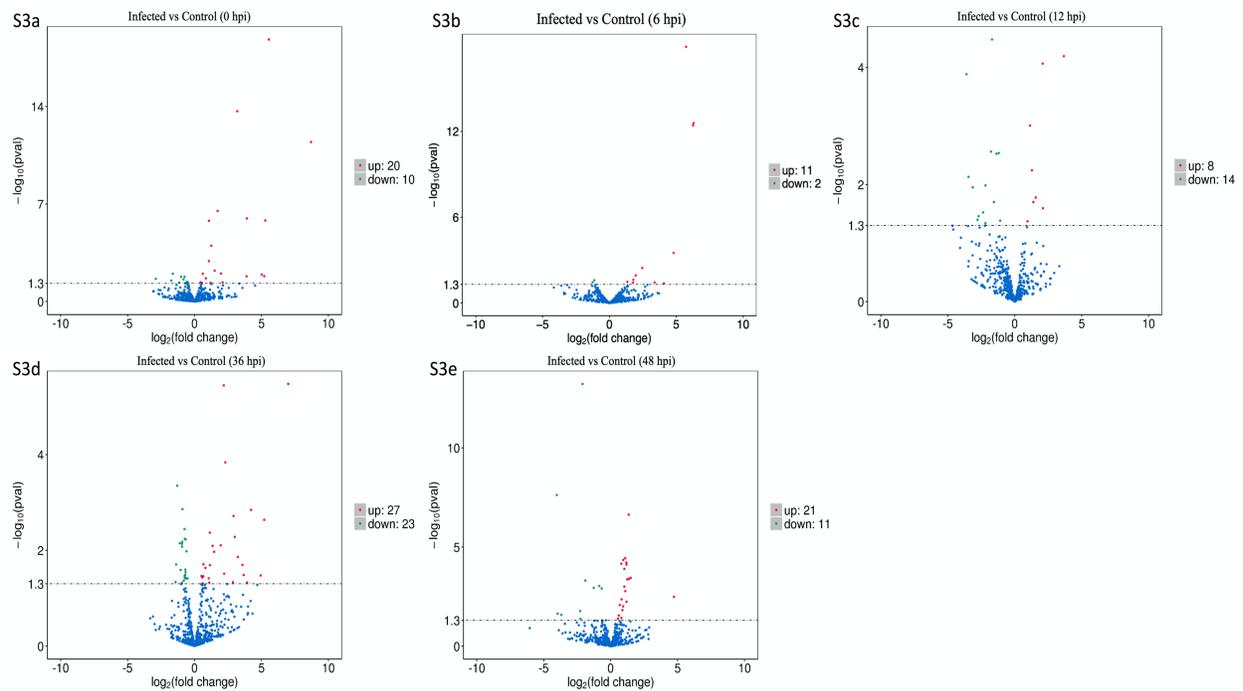


Supplementary Fig. S1a-S1e. The length distribution statistics of total sRNA segments obtained at (0 hpi, 6 hpi, 12 hpi, 36 hpi, 48 hpi). The length of reads is proportional to the reads of that length, 23nt is the main observed length.



Supplementary Fig. S2a-S2e. The pie charts showed total reads of distribution statistics of small RNA and their categories at (0 hpi, 6 hpi, 12 hpi, 36 hpi, 48 hpi). Known miRNAs, novel miRNAs, rRNA, tRNA, snRNA, snoRNA, repeats, exons, introns and other.



Supplementary Fig. S3a-S3e. Volcano chart represents the expression change of miRNA between virus treated and normal non treated cells (0 hpi, 6 hpi, 12 hpi, 36 hpi, 48 hpi). The x-axis shows the \log_2 fold change and y-axis shows the $-\log_{10}(\text{q-value})$. The horizontal dotted lines in the figure correspond to $q\text{-value (default) or adjusted P-value (FDR)} = 0.05$ significant difference threshold. The significant difference threshold of \log_2 fold change >1 , and significant difference threshold of adjusted P-value (FDR) $=0.05$. The up-regulated miRNAs are represented by red dots, down-regulated miRNAs are represented by green dots, and blue dots are miRNAs with no significant changes.