

Supplementary figures



Figure S1 The cultivated variety 'Chengsebaoshi' of *H. fulva*. A, leaves of *H. fulva*; B, flower of *H. fulva*

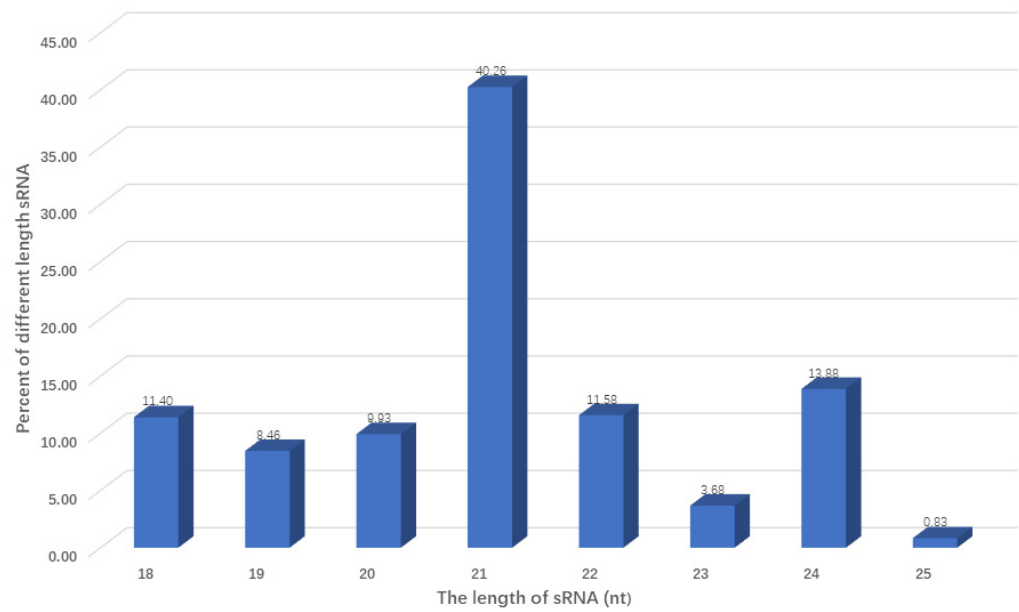


Figure S2 The distribution of different length sRNA in the sequencing libraries of *H. fulva*

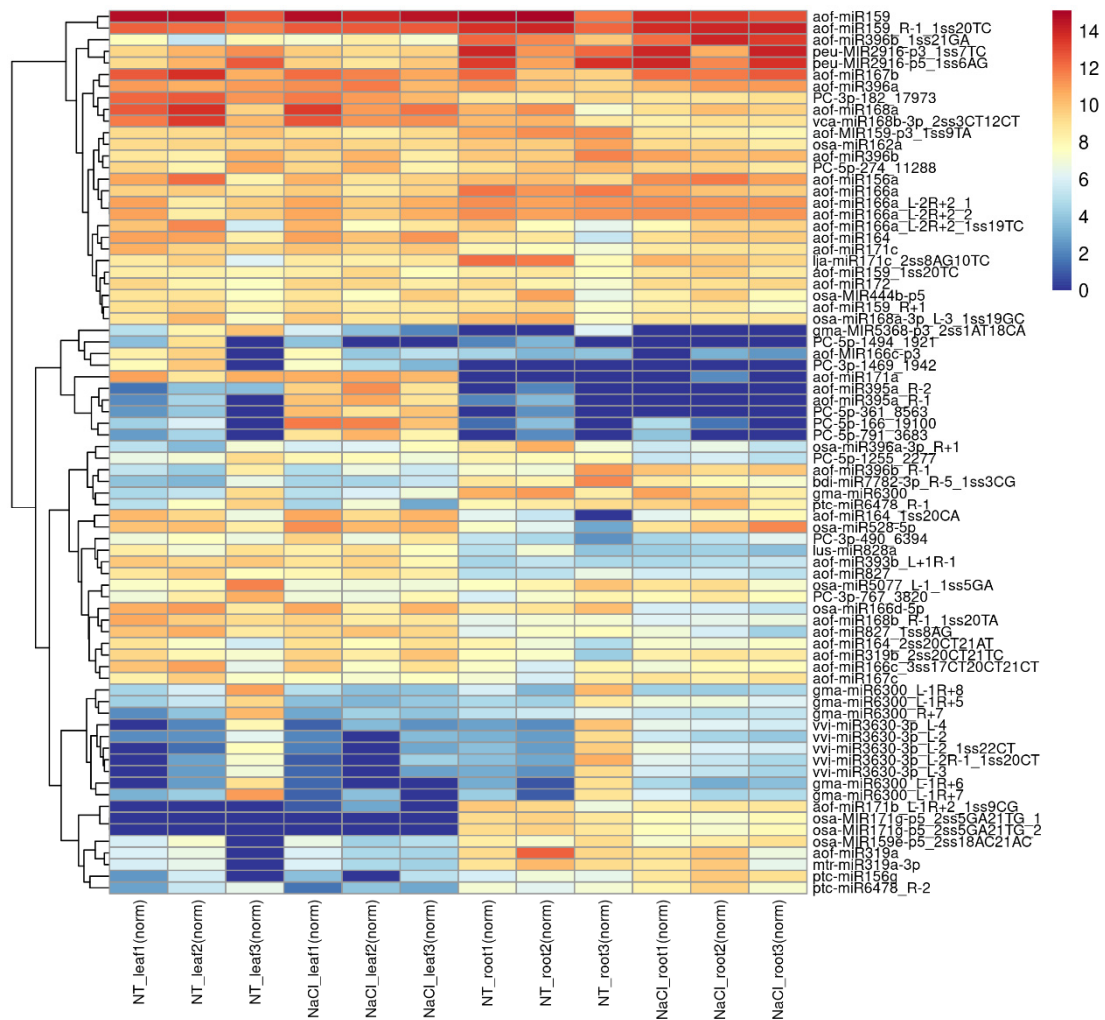
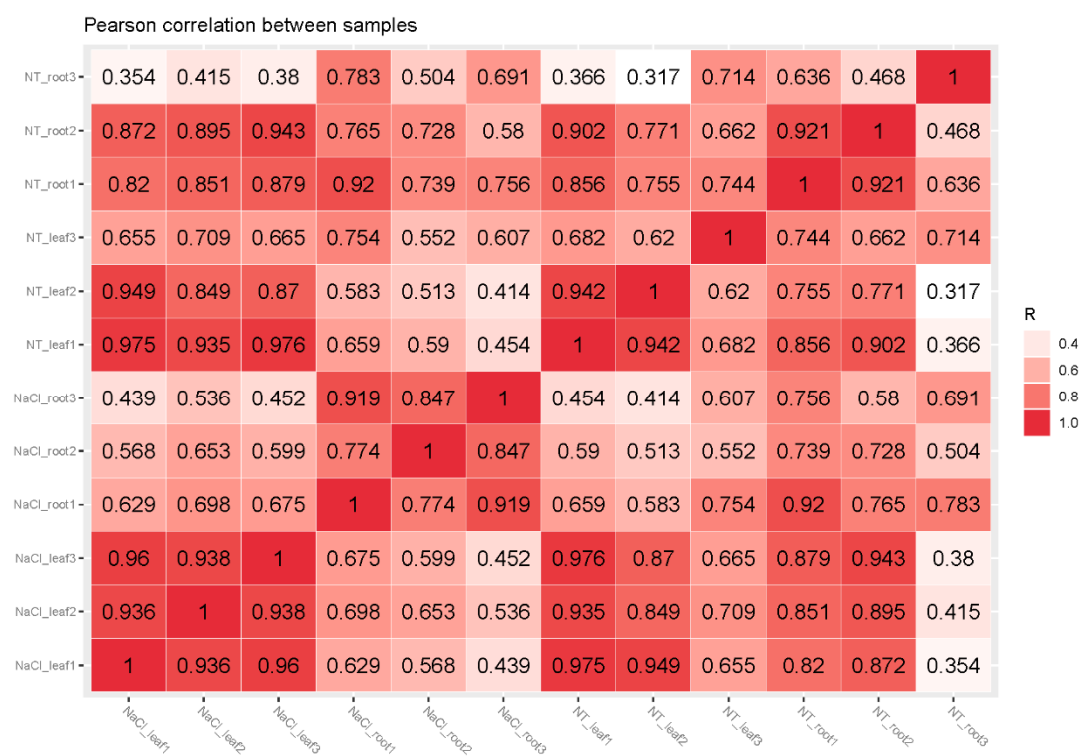
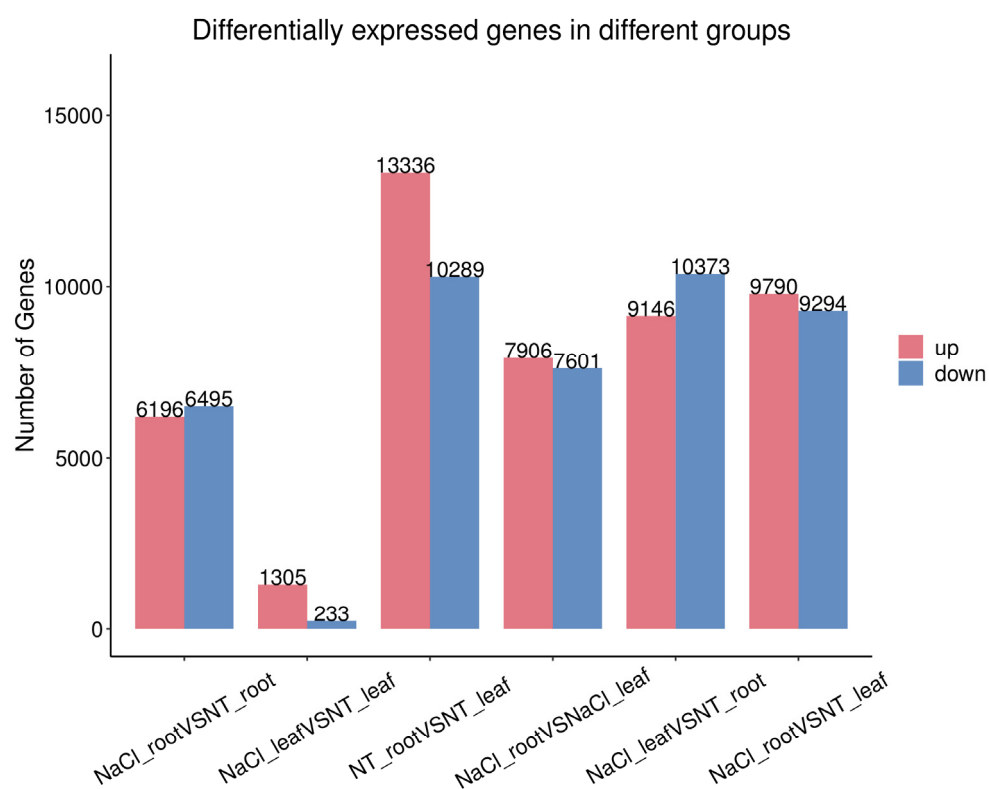


Figure S3 The heatmap analysis of transcription level of identified candidate miRNAs in leaf and root of *H. fulva* high throughput sequencing



**Figure S4** The Pearson correlation analysis based on the normalized expression levels between the samples of leaf and root with and without NaCl treatment in *H. fulva*



**Figure S5** The bar plot showing the up- and down-differentially expressed genes in leaf and root under NaCl stress in *H. fulva*

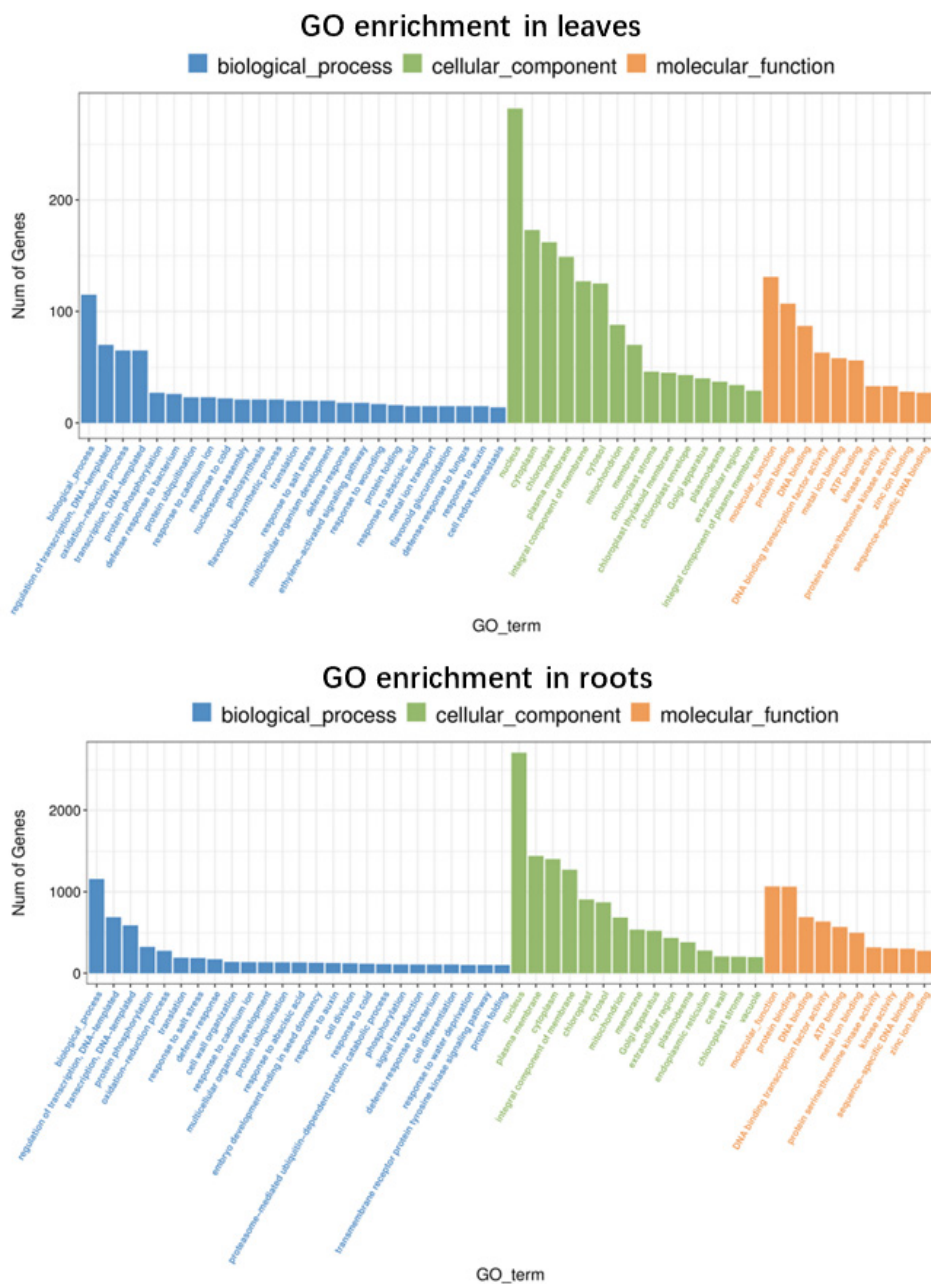


Figure S6 GO enrichment analysis of NaCl-stress responsive genes in leaf and root of *H. fulva*

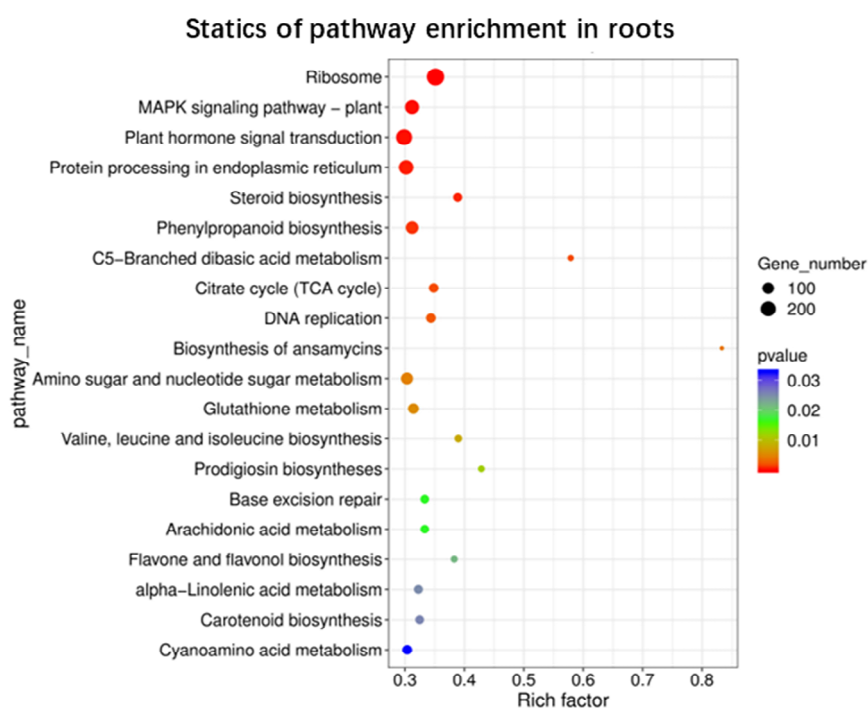
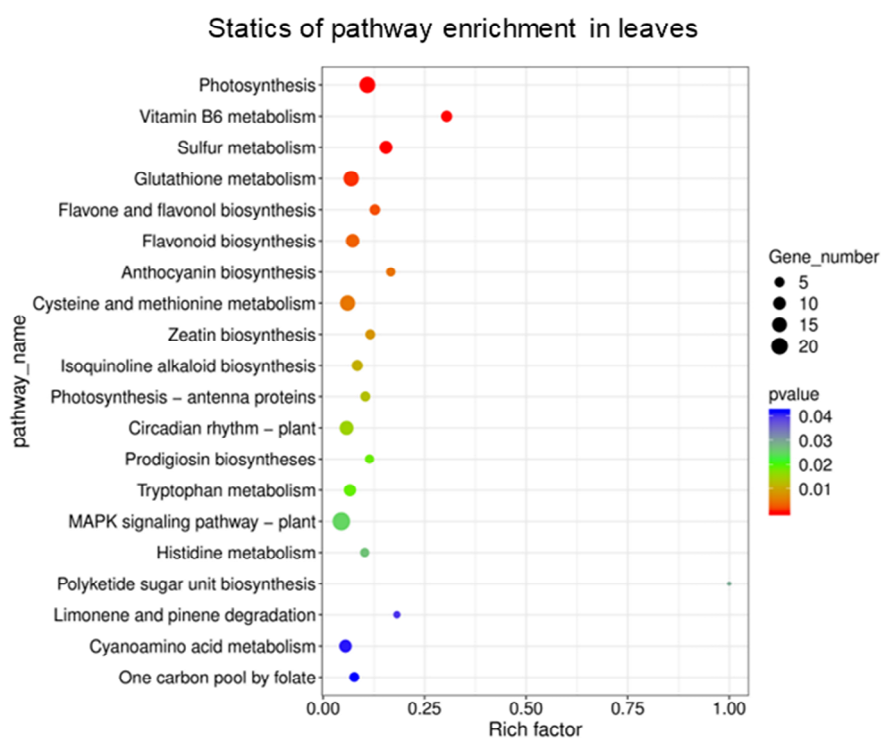


Figure S7 KEGG pathway analysis for the DE-mRNAs in leaf and root of *H. fulva*

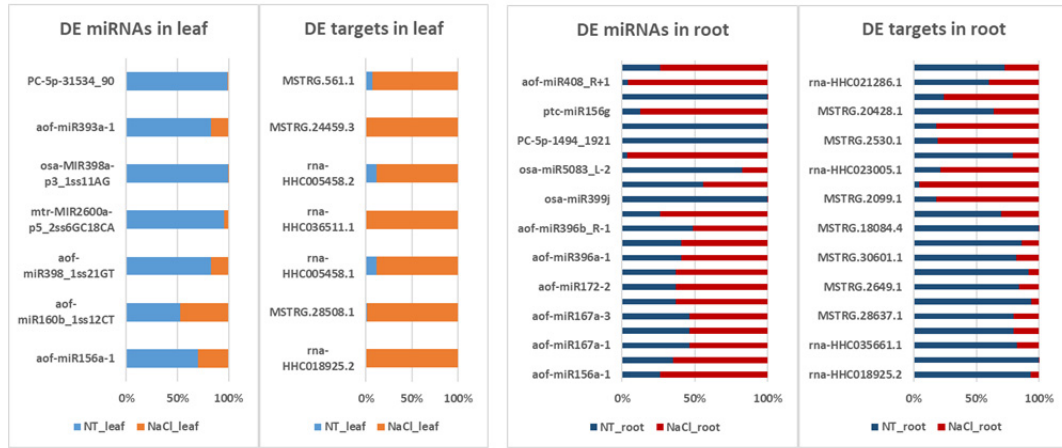


Figure S8 The opposite expression patterns of miRNA::targets pairs in leaf and root of *H. fulva*