**Supplementary Images**

**Figure S1.** Different precursor miRNAs detected in all treatments (numbers in brackets are the numbers of precursor miRNAs with at least one sequence ≥10 after normalisation)

**Figure S2.** Relative expression evaluated by qRT-PCR. To validate the results of deep sequencing, we used qPCR to analyse the expression of five novel miRNAs.

**Supplementary Tables**

**Table S1.** Details of the primers used in this study.

**Table S2.** The proportions of specific and common small RNAs in the libraries.

**Table S3.** All detected reads mapped to known miRNAs in our study. (All reads with a normalised count of less than 10 TPM in all libraries were excluded.)

**Table S4.** Comparison of the most abundant read for each precursor with mature miRNAs deposited in miRBase

**Table S5.** Novel miRNAs identified in this study.

**Table S6.** Various responses to stress of two driven main sequences from the same miRNA.

**Table S7.** Differentially expressed known and novel miRNAs and their predicted target genes.