



Extended Data Figure 5 | Highly reproducible induction of *C. campestris* miRNAs in different hosts. **a**, Mean abundance plot from original experiment on *A. thaliana* hosts of *C. campestris* small-RNA loci comparing interface to parasite stem samples. Significantly upregulated loci are highlighted (alternative hypothesis: true difference > 2-fold, $FDR \leq 0.05$ after correction for multiple testing with the Benjamini–Hochberg procedure). Reproduced from Fig. 1a. **b**, **c**, As **a**, except for a new set of *A. thaliana* hosts (**b**) or from an experiment using

N. benthamiana as hosts (**c**). Significantly upregulated loci are highlighted (alternative hypothesis: true difference > 2-fold, $FDR \leq 0.05$ after correction for multiple testing with the Benjamini–Hochberg procedure). **d**, Area-proportional Euler diagram showing overlaps of upregulated *C. campestris* 21–22-nucleotide miRNA loci among the three small-RNA-seq experiments. The locations of the six miRNA loci of special interest are highlighted in green.