



Extended Data Figure 6 | *C. campestris* miRNAs cause slicing and phased siRNA production from *N. benthamiana* mRNAs. Small-RNA-seq coverage across the indicated *N. benthamiana* transcripts are shown in blue for host stem, interface, and parasite stem samples. For display, the two biological replicates of each type were merged. Red marks and vertical lines show position of complementary sites to *C. campestris* miRNAs, with the alignments shown above. Fraction indicates numbers of

5'-RLM-RACE clones with 5'-ends at the indicated positions; the locations in red are the predicted sites for miRNA-directed slicing remnants. Bar charts show the length and polarity distribution of transcript-mapped siRNAs. Radar charts show the fractions of siRNAs in each of the 21 possible phasing registers; the registers highlighted in magenta are those predicted by the miRNA target sites.