***eLife’s* transparent reporting form**

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**Sample-size estimation**

* You should state whether an appropriate sample size was computed when the study was being designed
* You should state the statistical method of sample size computation and any required assumptions
* If no explicit power analysis was used, you should describe how you decided what sample (replicate) size (number) to use

Please outline where this information can be found within the submission (e.g., sections or figure legends), or explain why this information doesn’t apply to your submission:

*No explicit power analysis was used. All sequencing experiments comprised three biological replicates per condition. This was based on cost limitations of sequencing and current practices in the field.*

**Replicates**

* You should report how often each experiment was performed
* You should include a definition of biological versus technical replication
* The data obtained should be provided and sufficient information should be provided to indicate the number of independent biological and/or technical replicates
* If you encountered any outliers, you should describe how these were handled
* Criteria for exclusion/inclusion of data should be clearly stated
* High-throughput sequence data should be uploaded before submission, with a private link for reviewers provided (these are available from both GEO and ArrayExpress)

Please outline where this information can be found within the submission (e.g., sections or figure legends), or explain why this information doesn’t apply to your submission:

*All types of sequencing experiments comprised three biological replicates. Biological replicates are pooled samples from different plants grown at either the same or different times. This is described in the methods section. All -seq data have been deposited at NCBI SRA (Bioproject number PRJNA543296). A private reviewer link to the data is listed at the top of Table S1. Data will be publicly released upon publication of our study.*

**Statistical reporting**

* Statistical analysis methods should be described and justified
* Raw data should be presented in figures whenever informative to do so (typically when N per group is less than 10)
* For each experiment, you should identify the statistical tests used, exact values of N, definitions of center, methods of multiple test correction, and dispersion and precision measures (e.g., mean, median, SD, SEM, confidence intervals; and, for the major substantive results, a measure of effect size (e.g., Pearson's r, Cohen's d)
* Report exact p-values wherever possible alongside the summary statistics and 95% confidence intervals. These should be reported for all key questions and not only when the p-value is less than 0.05.

Please outline where this information can be found within the submission (e.g., sections or figure legends), or explain why this information doesn’t apply to your submission:

*Statistical analysis to identify haustorial-induced small RNAs used the R-package DE-Seq2; we used a cutoff of adjusted P <= 0.1 (Benjamini-Hochberg false-discovery rate). Details are described in the methods. The linear modeling in Figure S4b is also described in the methods section (n=between 20 and 28, depending; p-values from R function lm).*

(For large datasets, or papers with a very large number of statistical tests, you may upload a single table file with tests, Ns, etc., with reference to sections in the manuscript.)

**Group allocation**

* Indicate how samples were allocated into experimental groups (in the case of clinical studies, please specify allocation to treatment method); if randomization was used, please also state if restricted randomization was applied
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*This does not apply to our study.*

**Additional data files (“source data”)**

* We encourage you to upload relevant additional data files, such as numerical data that are represented as a graph in a figure, or as a summary table
* Where provided, these should be in the most useful format, and they can be uploaded as “Source data” files linked to a main figure or table
* Include model definition files including the full list of parameters used
* Include code used for data analysis (e.g., R, MatLab)
* Avoid stating that data files are “available upon request”

Please indicate the figures or tables for which source data files have been provided:

*Data file S1 contains most of the primary data used in this study -- it details each haustorium-induced small RNA from each species, along with other relevant data such as superfamily membership. Additionally, the large multi-page supplemental figures S5, S11, and S12 contain full details about each of the targets and superfamilies that we found.*