nature portfolio

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Last updated by author(s): Jun 26, 2026

Reporting Summary

Nature Portfolio wishes to improve the reproducibility of the work that we publish. This form provides structure for consistency and transparency in reporting. For further information on Nature Portfolio policies, see our Editorial Policies and the Editorial Policy Checklist.

Statistics

For all statistical analyses, confirm that the following items are present in the figure legend, table legend, main text, or Methods section.

n/a	Confirmed
☐	☒ The exact sample size (*n*) for each experimental group/condition, given as a discrete number and unit of measurement
☐	☒ A statement on whether measurements were taken from distinct samples or whether the same sample was measured repeatedly
☐	☒ The statistical test(s) used AND whether they are one- or two-sided *Only common tests should be described solely by name; describe more complex techniques in the Methods section.*
☒	☐ A description of all covariates tested
☐	☒ A description of any assumptions or corrections, such as tests of normality and adjustment for multiple comparisons
☐	☒ A full description of the statistical parameters including central tendency (e.g. means) or other basic estimates (e.g. regression coefficient) AND variation (e.g. standard deviation) or associated estimates of uncertainty (e.g. confidence intervals)
☐	☒ For null hypothesis testing, the test statistic (e.g. *F*, *t*, *r*) with confidence intervals, effect sizes, degrees of freedom and *P* value noted *Give P values as exact values whenever suitable.*
☒	☐ For Bayesian analysis, information on the choice of priors and Markov chain Monte Carlo settings
☒	☐ For hierarchical and complex designs, identification of the appropriate level for tests and full reporting of outcomes
☐	☒ Estimates of effect sizes (e.g. Cohen's *d*, Pearson's *r*), indicating how they were calculated

Our web collection on statistics for biologists contains articles on many of the points above.

Software and code

Policy information about availability of computer code

Data collection	No custom code or software was used for data collection. Data were generated using standard experimental procedures, including RNA sequencing, quantitative PCR, survival assays, and feeding experiments, following established protocols.
Data analysis	All analyses were performed in R. Two-group comparisons (e.g., dsRNA-treated vs. control) for RNA editing levels, transcript ratios, gene expression, and fecundity were conducted using Wilcoxon rank-sum tests. Differences in ADAR TPM across hosts were analyzed by one-way ANOVA, with normality and homogeneity of variances assessed using the Shapiro–Wilk and Levene's tests, respectively; post-hoc pairwise comparisons were performed using Tukey's HSD or Games–Howell tests as appropriate. Survival curves were compared using the log-rank test. Host-dependent RNA editing at individual sites was assessed by linear regression (lm(value ~ host)), with statistical significance determined by ANOVA F-tests ($P < 0.05$). A fold-change threshold of ≥2 was applied to define biologically meaningful differences. The distribution of A-to-I RNA editing sites across genomic regions and the proportions of synonymous and nonsynonymous sites within CDS regions were evaluated using Pearson's chi-square tests, with post-hoc pairwise comparisons where appropriate.

For manuscripts utilizing custom algorithms or software that are central to the research but not yet described in published literature, software must be made available to editors and reviewers. We strongly encourage code deposition in a community repository (e.g. GitHub). See the Nature Portfolio guidelines for submitting code & software for further information.

Data

Policy information about availability of data

All manuscripts must include a data availability statement. This statement should provide the following information, where applicable:

- Accession codes, unique identifiers, or web links for publicly available datasets
- A description of any restrictions on data availability
- For clinical datasets or third party data, please ensure that the statement adheres to our policy

The source data underlying all statistical analyses and figures are provided in Supplementary Data 10. The RNA-seq and corresponding DNA-seq data generated in this study have been deposited in the NCBI Sequence Read Archive (SRA) under BioProject accession numbers PRJNA1211840 and PRJNA1344291, respectively.

Research involving human participants, their data, or biological material

Policy information about studies with human participants or human data. See also policy information about sex, gender (identity/presentation), and sexual orientation and race, ethnicity and racism.

Reporting on sex and gender	Our research did not have any reports on sex and gender.
Reporting on race, ethnicity, or other socially relevant groupings	Our research did not have any reports on race, ethnicity, or other socially relevant groupings.
Population characteristics	Our research did not have any reports on population characteristics
Recruitment	Our research did not have any reports on recruitment.
Ethics oversight	We did not conduct any experiments that require ethics oversight.

Note that full information on the approval of the study protocol must also be provided in the manuscript.

Field-specific reporting

Please select the one below that is the best fit for your research. If you are not sure, read the appropriate sections before making your selection.

☒ Life sciences ☐ Behavioural & social sciences ☐ Ecological, evolutionary & environmental sciences

For a reference copy of the document with all sections, see nature.com/documents/nr-reporting-summary-flat.pdf

Life sciences study design

All studies must disclose on these points even when the disclosure is negative.

Sample size	In the bioassay experiments, sample sizes were chosen so to satisfy and exceed thresholds for statistical power.
Data exclusions	There is no data exclusions in the article.
Replication	All attempts at replication were successful. Please refer to figure legend and Methods for number of replicates.
Randomization	There is no application in the article.
Blinding	There is no application in the article

Reporting for specific materials, systems and methods

We require information from authors about some types of materials, experimental systems and methods used in many studies. Here, indicate whether each material, system or method listed is relevant to your study. If you are not sure if a list item applies to your research, read the appropriate section before selecting a response.

Materials & experimental systems

n/a	Involved in the study
☒	☐ Antibodies
☒	☐ Eukaryotic cell lines
☒	☐ Palaeontology and archaeology
☐	☒ Animals and other organisms
☒	☐ Clinical data
☒	☐ Dual use research of concern
☐	☒ Plants

Methods

n/a	Involved in the study
☒	☐ ChIP-seq
☒	☐ Flow cytometry
☒	☐ MRI-based neuroimaging

Animals and other research organisms

Policy information about studies involving animals; ARRIVE guidelines recommended for reporting animal research, and Sex and Gender in Research

Laboratory animals	M. persicae (GPA) Clone Xibei was obtained from a stock culture maintained on cabbage (B. oleracea) in Prof. Tongxian Liu's laboratory at Northwest A&F University (Yangling, Shaanxi).
Wild animals	The study did not involved wild animals.
Reporting on sex	Our research did not have any reports on sex.
Field-collected samples	We did not use field-collected samples in this study.
Ethics oversight	We did not conduct any experiments that require ethics oversight.

Note that full information on the approval of the study protocol must also be provided in the manuscript.

Dual use research of concern

Policy information about dual use research of concern

Hazards

Could the accidental, deliberate or reckless misuse of agents or technologies generated in the work, or the application of information presented in the manuscript, pose a threat to:

No	Yes	
☒	☐	Public health
☒	☐	National security
☒	☐	Crops and/or livestock
☒	☐	Ecosystems
☒	☐	Any other significant area

Experiments of concern

Does the work involve any of these experiments of concern:

No	Yes	
☒	☐	Demonstrate how to render a vaccine ineffective
☒	☐	Confer resistance to therapeutically useful antibiotics or antiviral agents
☒	☐	Enhance the virulence of a pathogen or render a nonpathogen virulent
☒	☐	Increase transmissibility of a pathogen
☒	☐	Alter the host range of a pathogen
☒	☐	Enable evasion of diagnostic/detection modalities
☒	☐	Enable the weaponization of a biological agent or toxin
☒	☐	Any other potentially harmful combination of experiments and agents

Plants

Seed stocks	The four host plant species used in this study included Zea mays B73, Brassica napus Zhongshuang 11, Arabidopsis thaliana, and Triticum aestivum. All plant materials were derived from germplasm resources maintained in our laboratory and were propagated continuously using standard cultivation practices.
Novel plant genotypes	We did not use novel plant genotypes.
Authentication	We did not use any plants that require authentication.