

Reporting Summary

Nature Research 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 Research 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
<i>Only common tests should be described solely by name; describe more complex techniques in the Methods section.</i> |
| ☒ | ☐ 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
<i>Give P values as exact values whenever suitable.</i> |
| ☒ | ☐ 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

Phosphorimaging: Typhoon FLA 7000 (GE Healthcare)
RT-qPCRs: AriaMx Real-time PCR System (Agilent)
Initial structural models for the dsRNAs: NAB (Nucleic Acid Builder)
MD simulations: Amber 14 package
Structural parameters for the dsRNAs: Curves+

Data analysis

Secondary structures of miRNA precursors: Mfold web server (<http://unafold.rna.albany.edu/?q=mfold/RNA-Folding-Form>)
small RNA blot quantifications: GelQuant.NET software (biochemlabsolutions.com)
Phosphorimage and in vitro RNA structure quantification: FIJI software
Base pair conformational clustering: Amber 14 (ccptraj module)
Structural parameters for the dsRNAs: Curves+
RNA parameters plots: matplotlib library of Python
RT-qPCR and plant phenotype data were analyzed with InfoStat software (www.infostat.com.ar)

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 Research [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 list of figures that have associated raw data
- A description of any restrictions on data availability

Data used in this work are available in the main text, the Supplementary Information file, Supplementary Data files and Source Data.

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](https://www.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	RNA analysis (small RNA blot and RT-qPCRs) were performed with samples composed of pools, each pool representing at least 10 independent primary transgenic plants. For small RNA blots two or three independent samples were analyzed. For RT-qPCR three biological replicates were analyzed (Except Fig4j and Suppl. Fig. 7i) and two technical replicates were performed. In vitro RNA structures of pri-miRNAs were evaluated twice for each variant.
Data exclusions	No data exclusions were made
Replication	Several independent biological samples were analyzed in each case (details stated in the main text, figure captions, supplementary information and source data).
Randomization	Plants were grown in the same conditions. Plants from different genotypes were placed randomly in the growth rooms and rotated.
Blinding	Blinding design was not applied in this work. Experimental material were plants.

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
☒	☐ Human research participants
☒	☐ Clinical data
☒	☐ Dual use research of concern

Methods

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