

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

Data analysis

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 RNA-Seq data generated in this study have been deposited in the NCBI Sequence Read Archive database under accession code PRJNA1000775 [<https://www.ncbi.nlm.nih.gov/bioproject/PRJNA1000775/>]. Processed data have been deposited in the NCBI GEO database under the accession number GSE269425 [<https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE269425>]. The protein mass spectrometry of NopL interaction protein raw data used in this study are

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

Use the terms *sex* (biological attribute) and *gender* (shaped by social and cultural circumstances) carefully in order to avoid confusing both terms. Indicate if findings apply to only one sex or gender; describe whether sex and gender were considered in study design; whether sex and/or gender was determined based on self-reporting or assigned and methods used. Provide in the source data disaggregated sex and gender data, where this information has been collected, and if consent has been obtained for sharing of individual-level data; provide overall numbers in this Reporting Summary. Please state if this information has not been collected. Report sex- and gender-based analyses where performed, justify reasons for lack of sex- and gender-based analysis.

Reporting on race, ethnicity, or other socially relevant groupings

Please specify the socially constructed or socially relevant categorization variable(s) used in your manuscript and explain why they were used. Please note that such variables should not be used as proxies for other socially constructed/relevant variables (for example, race or ethnicity should not be used as a proxy for socioeconomic status). Provide clear definitions of the relevant terms used, how they were provided (by the participants/respondents, the researchers, or third parties), and the method(s) used to classify people into the different categories (e.g. self-report, census or administrative data, social media data, etc.) Please provide details about how you controlled for confounding variables in your analyses.

Population characteristics

Describe the covariate-relevant population characteristics of the human research participants (e.g. age, genotypic information, past and current diagnosis and treatment categories). If you filled out the behavioural & social sciences study design questions and have nothing to add here, write "See above."

Recruitment

Describe how participants were recruited. Outline any potential self-selection bias or other biases that may be present and how these are likely to impact results.

Ethics oversight

Identify the organization(s) that approved the study protocol.

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

The sample size and the results of statistical analyses are described in the relevant figure legends or methods section. Sample size was determined based on experimental trials.

Data exclusions

No data were excluded.

Replication

Each experiment was repeated at least three times. Results were reproducible in all repeats with the same trend.

Randomization

Plants of different genotypes were grown side by side to minimize unexpected environmental variations during growth and experimentation. Soybean module samples of similar ages were collected randomly for all experiments.

Blinding

The investigators were not blinded to group allocation during experiment performing and data analysis. The research materials are plants so the blinding design is not applicable in the field (partially because different plant genotypes may grow differently and show different morphology making blinding impossible). Experiments were conducted based on routine practice in the field and all experiments were repeated at least three times with similar trends. Experiments were repeated by different authors, whenever possible.

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

Methods

n/a	Involved in the study
<input type="checkbox"/>	<input checked="" type="checkbox"/> Antibodies
<input checked="" type="checkbox"/>	<input type="checkbox"/> Eukaryotic cell lines
<input checked="" type="checkbox"/>	<input type="checkbox"/> Palaeontology and archaeology
<input checked="" type="checkbox"/>	<input type="checkbox"/> Animals and other organisms
<input checked="" type="checkbox"/>	<input type="checkbox"/> Clinical data
<input checked="" type="checkbox"/>	<input type="checkbox"/> Dual use research of concern
<input type="checkbox"/>	<input checked="" type="checkbox"/> Plants

n/a	Involved in the study
<input checked="" type="checkbox"/>	<input type="checkbox"/> ChIP-seq
<input checked="" type="checkbox"/>	<input type="checkbox"/> Flow cytometry
<input checked="" type="checkbox"/>	<input type="checkbox"/> MRI-based neuroimaging

Antibodies

Antibodies used

Commercial antibodies used:

anti-GFP (Catalog number: M20004, Abmart, used at 1:2000);
 Rabbit IgG (Catalog number: NIO1, Sigma-Aldrich, used at 1: 500 for IP);
 anti-GFP (Catalog number: 598, MBL, used at 1: 500 for IP);
 anti-Myc (Catalog number: M20002, Abmart, used at 1:2500);
 anti-FLAG (Catalog number: MA1-91878, Invitrogen, used at 1:10000);
 anti-GST (Catalog number: MA4-004, Invitrogen, used at 1:2500);
 anti-His (Catalog number: M30111, Abmart, used at 1:2500);
 Cy3-conjugated goat anti-Rabbit IgG (Catalog number: A22220, Abbkine, used at 1:500);
 FITC-conjugated goat anti-Rabbit IgG (Catalog number: A22120, Abbkine, used at 1:500);
 10 nm diameter gold particles-conjugated anti-Rabbit IgG (Catalog number: G7402, Sigma-Aldrich, used at 1:20);
 anti-Actin (Catalog number: M20009, Abmart, used at 1:5000);
 anti-Histone H3.1 (Catalog number: P30266, Abmart, used at 1:5000);
 anti-ATPB (Catalog number: M40013, Abmart, used at 1:1000);
 Goat Anti-Mouse IgG HRP (Catalog number: M21001, Abmart, used at 1:5000);
 Goat Anti-Rabbit IgG-HRP (Catalog number: M21002, Abmart, used at 1:5000).
 Non-commercial antibodies used:
 anti-NopL (Preparation of polyclonal antibodies by Abmart, used at 1:5 for Electron microscopy, 1:1000 for WB, 1:150 for IHC and IF)
 anti-GmREM1a (Preparation of polyclonal antibodies by Abmart, used at 1:5 for Electron microscopy, 1:2500 for WB, 1: 150 for IHC and IF).

Validation

All antibodies used in this study are commercially available and validated according to the manufacturers specifications.

anti-GFP (Abmart), <http://www.ab-mart.com.cn/page.aspx?node=%2059%20&id=%20971>;
 Rabbit IgG, <https://www.sigmaaldrich.cn/CN/zh/product/mm/ni01>;
 anti-GFP (MBL), <https://www.mbl-chinawide.cn/search012?keyword=598>;
 anti-Myc, <http://www.ab-mart.com.cn/page.aspx?node=%2059%20&id=%20962>;
 anti-FLAG, <https://www.thermofisher.cn/cn/zh/antibody/product/DYKDDDDK-Tag-Antibody-clone-FG4R-Monoclonal/MA1-91878>;
 anti-GST, <https://www.thermofisher.cn/cn/zh/antibody/product/GST-Tag-Antibody-clone-8-326-Monoclonal/MA4-004>;
 anti-His, <http://www.ab-mart.com.cn/page.aspx?node=%2059%20&id=%20974>;
 Cy3-conjugated goat anti-Rabbit IgG, https://www.abbkine.cn/?s_type=productsearch&s=A22220;
 FITC-conjugated goat anti-Rabbit IgG, https://www.abbkine.cn/?s_type=productsearch&s=A22120;
 10 nm diameter gold particles-conjugated anti-Rabbit IgG, <https://www.sigmaaldrich.cn/CN/zh/product/sigma/g7402>;
 anti-Actin, <http://www.ab-mart.com.cn/page.aspx?node=%2059%20&id=%20985>;
 anti-Histone H3.1, <http://www.ab-mart.com.cn/page.aspx?node=%2059%20&id=%20996>;
 anti-ATPB, <http://www.ab-mart.com.cn/page.aspx?node=%2077%20&id=%201034>;
 Goat Anti-Mouse IgG HRP, <http://www.ab-mart.com.cn/page.aspx?node=%2062%20&id=%20960>;
 Goat Anti-Rabbit IgG-HRP, <http://www.ab-mart.com.cn/page.aspx?node=%2062%20&id=%20980>.

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 |
|-------------------------------------|---|
| <input checked="" type="checkbox"/> | <input type="checkbox"/> Public health |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> National security |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> Crops and/or livestock |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> Ecosystems |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> Any other significant area |

Experiments of concern

Does the work involve any of these experiments of concern:

- | No | Yes |
|-------------------------------------|--|
| <input checked="" type="checkbox"/> | <input type="checkbox"/> Demonstrate how to render a vaccine ineffective |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> Confer resistance to therapeutically useful antibiotics or antiviral agents |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> Enhance the virulence of a pathogen or render a nonpathogen virulent |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> Increase transmissibility of a pathogen |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> Alter the host range of a pathogen |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> Enable evasion of diagnostic/detection modalities |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> Enable the weaponization of a biological agent or toxin |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> Any other potentially harmful combination of experiments and agents |

Plants

Seed stocks

All soybean materials are stored in the College of Agriculture, Northeast Agricultural University, and the variety name is the corresponding storage catalog number

Novel plant genotypes

For Gmrem1a, gene editing of GmREM1a was performed using the method of Agrobacterium tumefaciens infecting soybean cotyledons. The Cas9 and sgRNA (CCTACTACTACTACTAGGACGGATTC)+sgRNA Scaffold are controlled by the pM4 promoter. A total of 6 independent transgenic lines were obtained, among which the three transgenic lines with the most significant phenotypic differences were used for phenotype analysis in this work. All genetically modified strains are T4 generation.

Authentication

Identification of off target effects of homologous genes of target genes using PCR and sequencing