

## 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 [Authors & Referees](#) 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                                                                                                                                                                                                                                                                                      |
| <input checked="" type="checkbox"/> | <input checked="" type="checkbox"/> The exact sample size ( <i>n</i> ) for each experimental group/condition, given as a discrete number and unit of measurement                                                                                                                               |
| <input checked="" type="checkbox"/> | <input checked="" type="checkbox"/> A statement on whether measurements were taken from distinct samples or whether the same sample was measured repeatedly                                                                                                                                    |
| <input checked="" type="checkbox"/> | <input checked="" type="checkbox"/> The statistical test(s) used AND whether they are one- or two-sided<br><i>Only common tests should be described solely by name; describe more complex techniques in the Methods section.</i>                                                               |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> A description of all covariates tested                                                                                                                                                                                                                                |
| <input checked="" type="checkbox"/> | <input checked="" type="checkbox"/> A description of any assumptions or corrections, such as tests of normality and adjustment for multiple comparisons                                                                                                                                        |
| <input checked="" type="checkbox"/> | <input checked="" type="checkbox"/> 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) |
| <input checked="" type="checkbox"/> | <input checked="" type="checkbox"/> For null hypothesis testing, the test statistic (e.g. <i>F</i> , <i>t</i> , <i>r</i> ) with confidence intervals, effect sizes, degrees of freedom and <i>P</i> value noted<br><i>Give P values as exact values whenever suitable.</i>                     |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> For Bayesian analysis, information on the choice of priors and Markov chain Monte Carlo settings                                                                                                                                                                      |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> For hierarchical and complex designs, identification of the appropriate level for tests and full reporting of outcomes                                                                                                                                                |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> Estimates of effect sizes (e.g. Cohen's <i>d</i> , Pearson's <i>r</i> ), 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 software were used for data collection                                                                                                                                                                                                                                                                              |
| Data analysis   | Adobe Photoshop CS6, Adobe Illustrator CS6, SPSS statistics 17.0, GraphPad Prism 8.0.1, MEGA 7.0.26 were used to analyse the data. NGS QC Toolkit_v2.3.3, hisat2-v.2.1.0, cufflinks-2.2.1, htseq-count-0.7.2, DESeq functions estimateSizeFactors and nbinomTest library were used to process the RNA sequencing data. |

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/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

All data generated or analyzed during this study are included in this published article and its Supplementary Information. Sequencing data for gene-expression analysis (RNA-seq) reported in this study have been deposited in the publicly available National Center for Biotechnology Information (NCBI) under the BioProject PRJNA599246, accession no. SAMN13741852-SAMN13741857. RNA-seq data of the 24 h and 120 h post *S. meliloti* spot inoculation were obtained from Schiessl et al, 201930 (Data S1) (<https://doi.org/10.1016/j.cub.2019.09.005>). The *M. truncatula* Tnt1 transposon insertion lines used in this study were obtained from the Noble Foundation Tnt1 database (<http://medicago-mutant.noble.org/mutant/database.php>). The blot source data are in Supplementary information. Source data are provided with this paper.

## 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     | The parametric test is used for statistical analyses because the data indicate that the population is normally distributed and the population variance is equal. In general, the sample size is guaranteed with $n \geq 6$ in those tests. For these reasons, we determined the sample size of key data as $n \geq 10$ in our analysis. |
| Data exclusions | No data were excluded from the analyses.                                                                                                                                                                                                                                                                                                |
| Replication     | All attempts at replication were successful.                                                                                                                                                                                                                                                                                            |
| Randomization   | All samples were allocated randomly into experimental groups.                                                                                                                                                                                                                                                                           |
| Blinding        | All experiments were blinded during data acquisition and analyses.                                                                                                                                                                                                                                                                      |

## 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                                |
|-------------------------------------|------------------------------------------------------|
| <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               |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> Animals and other organisms |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> Human research participants |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> Clinical data               |

### Methods

| 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 | we use Cy3-conjugated Goat Anti-Mouse IgG (115-165-003, Jackson ImmunoResearch, 1:500) to perform immunolocalization, use anti- $\beta$ glucuronidase (GUS) antibody (ab50148, Abcam, 1:2000 dilution) to test MtSHR1-GUS protein in vivo, use anti-FLAG (30503ES20, YEASEN, 1:4000) and anti-HA (66006-2-Ig, Proteintech, 1:4000) antibody to perform Co-IP assay.                                                                                                                                                                                                                                                                                           |
| Validation      | Anti-gus antibody was used according to Cai Q et al. Jasmonic acid regulates spikelet development in rice. Nat Commun 5:3476 (2014). WB . manufacturer's website: <a href="https://www.abcam.cn/beta-glucuronidase-gus-antibody-aminoterminal-end-ab50148.html">https://www.abcam.cn/beta-glucuronidase-gus-antibody-aminoterminal-end-ab50148.html</a><br>Anti-HA antibody manufacturer's website: <a href="http://www.ptgcn.com/results?q=HA+antibody#Ab">http://www.ptgcn.com/results?q=HA+antibody#Ab</a><br>Anti-Flag antibody manufacturer's website: <a href="https://www.yeasen.com/products/detail/87">https://www.yeasen.com/products/detail/87</a> |