

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 (<i>n</i>) 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. <i>F</i> , <i>t</i> , <i>r</i>) with confidence intervals, effect sizes, degrees of freedom and <i>P</i> 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 <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	ZEN 2012 imaging software blue edition (Carl Zeiss Microscopy GmbH) was used to collect the micrographs. Image Lab version 3.0 build 11 (Bio-Rad) was used for DNA electrophoresis and immunoblot data collection. Images for EMAS analysis were captured using a charge-coupled device (CCD) camera on Touch Imager (eBlot14). dPCR analysis were performed via QIAcuity software v.2.2.0.26.
Data analysis	GraphPad Prism version 9.5.0 was used for producing bar charts and determining statistical significance by log-rank test. Microsoft Excel version 15.0 was used for calculating the probability value (P-value) by the two-sided Student's t-test and one-way ANOVA with post hoc Tukey analysis. ImageJ Fiji 2.0.3, available at www.imagej.nih.gov/ij/ , is utilized for analyzing and processing photographs. The miRbase at https://www.mirbase.org/ is the miRNA database utilized for predicting targets of miRNA. Coding Potential Calculator 2, available at http://cpc2.cbi.pku.edu.cn/ , is used for analyzing the non-coding potential value for lncRNAs. The potential target genes of miRNA were determined by psRNATarget tool at https://www.zhaolab.org/psRNATarget/ . Blast v2.12 software is used for local blast analysis. WebLogo 3 at https://weblogo.threeplusone.com/ is employed to construct the sequence logo according to the alignment of relevant sequences representing the level of nucleotide conservation in each position.

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](#)

Representative genomes of microbes and plants used for identifying similar DNA sequence were downloaded from the Ensembl database (<http://ensemblgenomes.org/>). The transcriptomic data of *M. oryzae* have been deposited and stored in China National Center for Bioinformation under accession PRJCA023211. All data are available in the main text or the supplementary materials. All data are additionally available from the authors in other formats upon request.

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

N/A

Reporting on race, ethnicity, or other socially relevant groupings

N/A

Population characteristics

N/A

Recruitment

N/A

Ethics oversight

N/A

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](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

When conducting phenotypic analyses, we used the sample size following standard procedures from previous publications (Ryder, L.S., Dagdas, Y.F., Kershaw, M.J. et al. A sensor kinase controls turgor-driven plant infection by the rice blast fungus. *Nature* 2019, 574, 423–427). Sample sizes were as large as practicable for observations of phenotypes such as appressorium function, pathogenecity test or plant disease resistance. The sample size was included in the main text where possible. No statistical methods were used to predetermine sample sizes.

Data exclusions

No data were excluded.

Replication

In a parallel experiment, we set up triple replications for determining the mean value and standard deviation. For all the experiments, at least two consistent results were obtained to verify reproducibility.

Randomization

The experimental groups were allocated based on the genotype as wild-type strain or deletion mutants, wild-type plant line or transgenic plant lines, or based on control and different chemical treatments. Within each experiment group, the samples were randomly selected for statistic analysis.

Blinding

The data collection was not blinded because it was not relevant to most of the experiments carried out. Blinding was not possible as the investigators were conducting the experiments and had to be aware of controls and treated groups.

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	Involvement 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	Involvement in the study
☒	☐ ChIP-seq
☒	☐ Flow cytometry
☒	☐ MRI-based neuroimaging

Antibodies

Antibodies used

GFP antibody (BBI Life Science, D191040); HRP-conjugated mouse secondary antibody (Invitrogen, 31430).

Validation

The primary anti-GFP mouse monoclonal antibody (BBI Life Science, D191040) was validated for use with GFP-transformed plants or pure GFP protein. The GFP antibody and HRP-conjugated mouse secondary antibody were used in immunoblot analysis by diluting 5,000-fold and 10,000-fold, respectively. The results showed that these antibodies allow detection of the specific corresponding protein with expected size.

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

Hazards

The fungal and bacterial strains used in this study can infect crops or animals with compromised immunity. But they are commonly used model microbes for research. Despite they can pose potential threats, they are always handled properly in laboratory conditions according to strict restrictions.

For examples of agents subject to oversight, see the United States Government [Policy for Institutional Oversight of Life Sciences Dual Use Research of Concern](#).

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

Precautions and benefits

Biosecurity precautions This study did not involve biosecurity precautions.

Biosecurity oversight This study did not involve biosecurity oversight.

Benefits	Not applicable.
Communication benefits	Not applicable.

Plants

Seed stocks	Rice and wheat seeds were maintained in Sichuan Agricultural University at Chengdu, China.
Novel plant genotypes	CRISPR (clustered regularly interspaced short palindromic repeats)/Cas9 construction method was used to produce rice lines with corresponding DNA regions disrupted. Two targeting sequences of 23-bp length (including PAM) were chosen inside the regions for deleting a 59-bp fragment. WimiBio Co., Ltd assisted us on rice gene knockout constructions and transformations. Three independent transgenic rice lines were used for analysis.
Authentication	PCR-dependent genotyping was conducted to confirm the authentication of transgenic rice lines.