

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	The fluorescence signal was detected using a confocal microscopy (LSM710, Zeiss). Images from immunoblotting were collected with Molecular Imager® ChemiDoc™M XRS+ (Bio-Rad). The luciferase activity was detected using a low-light cooled charge-coupled device imaging apparatus (NightOWL II LB983 with IndiGO software version 2.0.4.0). The luciferase activity was measured using a GLO-MAX 20/20 luminometer (Promega). Bio-Rad CFX96 with CFX Maestro 1.1 software was used in qRT-PCR analysis. For endogenous phytohormone quantification, JA analysis was performed on a mass spectrometer (UPLC 1290-MS/MS 6495). EASY-nLC 1200 liquid chromatography system and a C18 column coupled with a Thermo Fusion Lumos mass spectrometer were used to conduct IP-LC-MS/MS assays. The MST assays were performed on a Microscale Thermophoresis Monolith NT.115 instrument (NanoTemper Technologies, Munich, Germany). BioTek Cytation5 was used to quantify the H2O2 levels together with the Amplex Red Hydrogen Peroxide/Peroxidase Assay Kit.
Data analysis	Image analysis: ImageJ (version 1.45). Statistical analysis: GraphPad Prism (version 7.0). Phylogenetic tree: MEGA11. Conserved motif analysis: online MEME website (http://meme-suite.org/tools/meme). Raw sequence data quality control: FastQC software (version 0.12.0). The LC-MS/MS results were processed via Proteome Discoverer 2.2 software. MST data analyses were performed using the MO.Affinity analysis 3 software.

Sequence analysis: SnapGene (version 4.1.9).

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](#)

All source data associated with this work are available as part of the manuscript's supplementary information or as detailed below. OsRBRL (LOC_Os03g42760), OsRBRL-like (LOC_Os03g42780), OsNINJA1 (LOC_Os03g11550), OsNINJA2 (LOC_Os07g41160), OsNINJA3 (LOC_Os03g30570), OsNINJA4 (LOC_Os05g48500) are available from the Rice Genome Annotation Project Database (<https://rice.uga.edu/>). RNA-seq raw data have been deposited at the Genome Sequence Archive in National Genomics Data Center, China National Center for Bioinformation / Beijing Institute of Genomics, Chinese Academy of Sciences (GSA accession: CRA020855) that are publicly accessible at <https://ngdc.cncb.ac.cn/gsa>. Uncropped immunoblotting images are provided in Supplementary Fig. 1.

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	NA
Reporting on race, ethnicity, or other socially relevant groupings	NA
Population characteristics	NA
Recruitment	NA
Ethics oversight	NA

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 figures or method section. Sample size was determined based on experimental trials and previous publications on similar experiments (Yang et al., 2020, Cell Host & Microbe, 28, 89-103; Wang et al., 2020, Nature Communications, 11, 5830; Yao et al., 2022, Science Advances, 8, eabm0660; Yao et al., 2019, Molecular Plant, 12, 1114-1122; Wu et al., 2017, Nature Plants, 3, 16203; Wang et al., 2014, Nature Communications, 5, 4768).
Data exclusions	There is a pre-established criteria. For these experiments we always chose the plants in the same growth status to analysis infection rates, genes expressions, hormone contents and so on. Other plants will be excluded.
Replication	All experiments were repeated at least two or three times, and the number of independent experiments or biological replicates is indicated in the figure legends.
Randomization	All samples were arranged randomly into experimental groups. Plants for experiments were grown side by side to minimize unexpected environmental variations during growth.
Blinding	For different rice lines experiments, we firstly numbered these lines by one partner and the following analysis were done by other members to avoid subjective influence. For example, the virus-infection assay, different rice lines were numbered at first, the investigator was blinded to the group allocation during the experiments including the inoculation of viruliferous small brown planthopper, the infection rates statistics, and virus RNAs qRT-PCR analysis.

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

Antibodies

Antibodies used

anti-CM-LOX2 (custom-developed by ABclonal® Technology, China, generated in Yang et al., 2020, Cell Host & Microbe, DOI: 10.1016/j.chom.2020.05.001, and was preserved by our laboratory);
 anti-AOS2 (custom-developed by ABclonal® Technology, China, generated in Yang et al., 2020, Cell Host & Microbe, DOI: 10.1016/j.chom.2020.05.001, and was preserved by our laboratory);
 anti-RSV CP (provided by Dr. Jianxiang Wu from Zhejiang University, generated in Fu et al., 2018, Molecular Plant, DOI: 10.1016/j.molp.2017.11.011);
 anti-RDV P2 (custom-developed by ABclonal® Technology, China, generated in Jin et al., 2016, PLoS Pathogens, DOI: 10.1371/journal.ppat.1005847, and was preserved by our laboratory);
 anti-AGO18 (custom-developed by ABclonal® Technology, China, generated in Wu et al., 2015, eLife, DOI: 10.7554/eLife.05733, and was preserved by our laboratory);
 anti-AO (custom-developed by Integrated R&D Services- WuXi AppTec, generated in Wu et al., 2017, Nature Plants, DOI: 10.1038/nplants.6 2016.203, and was preserved by our laboratory);
 anti-RBRL (custom-developed by ABclonal® Technology, China, generated in this study);
 anti-NINJA3 (custom-developed by ABclonal® Technology, China, generated in this study);
 anti-MYC (ABclonal, Wuhan, China, Cat#AE010);
 anti-HA (ABclonal, Wuhan, China, Cat#AE008);
 anti-GFP/YFP (ABclonal, Wuhan, China, Cat#AE012);
 anti-GST (ABclonal, Wuhan, China, Cat#AE001);
 anti-MBP (ABclonal, Wuhan, China, Cat#AE016);
 anti-FLAG (TransGen Biotech, Beijing, China, Cat#HT201);
 anti-S (EarthOx, Cat#E022130);
 anti-OsFBPA (Beijing Protein Innovation, Beijing, China, Cat#AbP80247-A-SE);
 anti-Histone H3 (Abcam, Cat#ab1791);
 anti-cLUC (Sigma-Aldrich, America, Cat#L2164);
 anti-Actin (CWBIO, Beijing, China, Cat#CW0096M);
 anti-PAG1 (generated in Han et al., 2019, New Phytologist, DOI:10.1111/nph.15471, and was preserved by our laboratory).

Validation

Validation statements and experiments can be obtained from the following websites and publications:
 Anti-CM-LOX2 (DOI: 10.1016/j.chom.2020.05.001), species: *Oryza sativa* subsp. japonica, application: immunoblotting;
 anti-AOS2 (DOI: 10.1016/j.chom.2020.05.01), species: *Oryza sativa* subsp. japonica, application: immunoblotting;
 anti-RSV CP (DOI: 10.1016/j.chom.2020.05.001), species: Rice stripe virus, application: immunoblotting and immunoprecipitation;
 anti-RDV P2 (DOI: 10.1093/mp/ssu007), species: Rice dwarf virus, application: immunoblotting;
 anti-AGO18 (DOI: 10.7554/eLife.05733), species: *Oryza sativa* subsp. japonica, application: immunoblotting;
 anti-AO (DOI: 10.1038/nplants.6 2016.203), species: *Oryza sativa* subsp. japonica, application: immunoblotting;
 anti-RBRL (generated in this study), species: *Oryza sativa* subsp. japonica, application: immunoblotting;
 anti-NINJA3 (generated in this study), species: *Oryza sativa* subsp. japonica, application: immunoblotting;
 anti-MYC (<https://abclonal.com.cn/catalog/AE010>), application: immunoblotting;
 anti-HA (<https://abclonal.com.cn/catalog/AE008>), application: immunoblotting;
 anti-GFP/YFP (<https://abclonal.com.cn/catalog/AE012>), application: immunoblotting;
 anti-GST (<https://abclonal.com.cn/catalog/AE001>), application: immunoblotting;
 anti-MBP (<https://abclonal.com.cn/catalog/AE016>), application: immunoblotting;
 anti-FLAG (https://www.transgen.com/antibody_tag/371.html), application: immunoblotting;
 anti-S (EarthOx, Cat#E022130, <https://earthox.net/product-category/life-science-products/antibodies/>), application: immunoblotting;
 anti-OsFBPA (<http://www.proteomics.org.cn/product/818.html>), species: *Oryza sativa* subsp. japonica, application: immunoblotting;
 anti-Histone H3 (<https://www.abcam.cn/products/primary-antibodies/histone-h3-antibody-nuclear-marker-and-chip-grade-ab1791.html>), species: *Oryza sativa* subsp. japonica, application: immunoblotting;
 anti-cLUC (<https://www.sigmaaldrich.cn/CN/zh/product/sigma/I2164>), application: immunoblotting;
 anti-Actin (<https://www.cwbio.com/goods/index/id/10113>), species: *Oryza sativa* subsp. japonica and *Nicotiana benthamiana*, application: immunoblotting;
 anti-PAG1 (DOI:10.1111/nph.15471), species: *Oryza sativa* subsp. japonica and *Arabidopsis thaliana*, application: immunoblotting.

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 wild-type NPB were preserved by our laboratory. The wild-type DJ was provided by Dr. Lizhong Xiong from the National Key Laboratory of Crop Genetic Improvement, Hubei Hongshan Laboratory, Huazhong Agricultural University.
Novel plant genotypes	The overexpression rice lines of OsRBRL, RSV CP, OsNINJA2 and OsNINJA3 were generated through transgenic methods. The knockout rice lines of OsRBRL, OsNINJA1, OsNINJA2 and OsNINJA3 were generated using CRISPR/Cas9.
Authentication	The coi1-13 mutant was identified through qRT-PCR and phenotypic observation, which is consistent with prior reports. The jamyb mutant was identified by sequencing, as previously described. The ninja1 (modd-2) mutant was identified by genotyping using gene-specific and T-DNA-specific primers as described previously. The rice lines overexpressing OsRBRL, RSV CP, and OsNINJA3 were verified by immunoblotting. The genome-edited mutants were confirmed by sequencing and analyzed using SnapGene (https://www.snapgene.com).