

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	For plant phenotype, Y1H and Y2H images : Canon EOS70D camera (Canon, Tokyo, Japan) For gel images : ImageQuant LAS 4000mini system (GE HealthCare, Illinois, USA) For mass spectrometry : Mass Spectrometer LTQ Orbitrap Elite (Thermo, Massachusetts, USA) For confocal microscopy: FV3000 Olympus confocal microscope (Olympus, Tokyo, Japan) For qRT-PCR : LightCycler 480 system (Roche, Basel, Switzerland) For Nuclease activity assay : FlexStation 3 microplate reader (Molecular Devices, California, USA) For Dual-luciferase images : Photek's HRPC55 photon-counting camera system (East Sussex, United Kingdom) For RNA-seq : Illumina HiSeq 1000 (paired-end model) For CLIP-seq : Illumina NovaSeq 6000 (paired-end model) For SEC-HPLC : Agilent 1100 (Agilent, California, USA)
Data analysis	The images from western blot and confocal microscope were cut using Adobe Photoshop 2023 and Adobe Illustrator 2023, some information represented of their intensities or co-localizations were analyzed by Image J software; The qRT-PCR , CLIP-qPCR , dual-luciferase signal, nuclease activity were analyzed by Graphpad Prism 8 software (Student's t test or one-way ANOVA with Tukey's least significant difference tests); The recovery curves in FRAP were performed by Graphpad Prism 8 software; The protein curves in SEC-HPLC analysis were performed by Graphpad Prism 8 software; The height and root length of rice were manually measured by ruler and then analyzed by Graphpad Prism 8 software; The gel images were analyzed by Image J software; The RNA-seq data were analyzed by FastQC (V0.12.0), Trimmomatic (V 0.38), Cutadapt (V1.9.1), Tophat (V1.4.6), Samtools (V1.6), HTSeq

(v0.6.1), DESeq2 software and R package ggplot2;

The CLIP-seq data were analyzed by RSeQC (V2.6), bedtools (V2.25.0), deepTools (V2.4.1), STAR (V2.5.3a), R package exomePeak, Integrative Genomics Viewer (V2.14.1) and KOBAS (<http://bioinfo.org/kobas>);

The mass spectrometry data were analyzed by Proteome Discoverer (V 3.1);

Phylogenetic analyses were performed by MEGA 11 and iTOL (<https://itol.embl.de/>);

The protein structures were analyzed by AlphaFold2 (<https://alphafold.ebi.ac.uk/>) and displayed by Pymol(V1.7.4.5 Edu);

The models were created by Adobe Illustrator 2023 software.

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 and CLIP-seq data supporting the findings of this study have been deposited at Gene Expression Omnibus (GEO) under accession no. GSE283860 (<https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE283860>) and GSE283861 (<https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE283861>)

The mass spectrometry data of co-immunoprecipitation protein in this study have been deposited to the ProteomeXchange Consortium via the PRIDE partner repository with the dataset identifier PXD059146.

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

For inoculation assays, at least 15 transgenic seedlings were used for each line. For TRV-based VIGS assay, each independent experiment contains 10-12 plants.

Data exclusions

No data were excluded.

Replication

Three independent biological replicates for RNA-seq, RT-qPCR, CLIP-RT-qPCR and Dul-luciferase assays. Three independent biological replicates mixed to one sample for CLIP-seq and mass spectrometry. All experiments were repeats in multiple independent biological replicates.

Randomization

The plant materials used in this literature were grown on the same condition in the growth chamber. The sample were collected randomly without any bias.

Blinding

For all experiments involving phenotypes with randomized block design, the distribution of each line was generated randomly before planting.

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-His(ABclonal, cat#AE003, 1:5000 dilution)
 Anti-GFP(ABclonal, cat#AE078, 1:5000 dilution)
 Anti-mCherry(ABclonal, cat#AE127, 1:5000 dilution)
 Anti-DDDDK tag(ABclonal, cat#AE005, 1:5000 dilution)
 Anti-Actin(ABclonal, cat#AC0009, 1:5000 dilution)
 Anti-GST (Beyotime, cat#AF0174, 1:5000 dilution)
 Anti-MBP (Beyotime, cat#AF2912, 1:5000 dilution)
 Anti-HA (Beyotime, cat#AF2858, 1:5000 dilution)
 HRP-labeled Streptavidin(Beyotime, cat#A0303, 1:5000 dilution)
 Goat Anti-Rabbit IgG (whole molecule)–HRP(Sigma, cat#A6154, 1:5000 dilution)
 Goat Anti-Mouse IgG (whole molecule)–HRP(Sigma, cat#A5278, 1:5000 dilution)
 Rabbit IgG control(Beyotime, cat#A7016)

Validation

OsTSN1, SRBSDV P6, SRBSDV P10 , RBSDV P10 and RSV P10 antibodies were made from our lab.
 All other antibody used in this literature as cited on the manufacturer's websites as well as by the data sheets they provide.
 Anti-His(ABclonal, cat#AE003, 1:5000 dilution):<https://abclonal.com.cn/catalog/AE003>
 Anti-GFP(ABclonal, cat#AE078, 1:5000 dilution):<https://abclonal.com.cn/catalog/AE078>
 Anti-mCherry(ABclonal, cat#AE127, 1:5000 dilution):<https://abclonal.com.cn/catalog/AE127>
 Anti-DDDDK tag(ABclonal, cat#AE005, 1:5000 dilution):<https://abclonal.com.cn/catalog/AE005>
 Anti-Actin(ABclonal, cat#AC0009, 1:5000 dilution):<https://abclonal.com.cn/catalog/AC009>
 Anti-GST (Beyotime, cat#AF0174, 1:5000 dilution):<https://www.beyotime.com/product/AF0174.htm>
 Anti-MBP (Beyotime, cat#AF2912, 1:5000 dilution):<https://www.beyotime.com/product/AF2912.htm>
 Anti-HA (Beyotime, cat#AF2858, 1:5000 dilution):<https://www.beyotime.com/product/AF2858.htm>
 HRP-labeled Streptavidin(Beyotime, cat#A0303, 1:5000 dilution):<https://www.beyotime.com/product/A0303.htm>
 Goat Anti-Rabbit IgG (whole molecule)–HRP(Sigma, cat#A6154, 1:5000 dilution):<https://www.sigmaaldrich.cn/CN/zh/product/sigma/a6154>
 Goat Anti-Mouse IgG (whole molecule)–HRP(Sigma, cat#A5278, 1:5000 dilution):<https://www.sigmaaldrich.cn/CN/zh/product/sigma/a5278>
 Rabbit IgG control(Beyotime, cat#A7016):<https://www.beyotime.com/product/A7016.htm>

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 knockout mutant rice lines in this literature were purchased from the Biogle Genome Editing Center (http://biogle.cn/) (Jiangsu, China);
Novel plant genotypes	The OsTSN1 overexpression (OsTSN1-OE) and SRBSDV P6 expression (P6-OE) transgenic rice were saved in our lab. The OsTSN1 overexpression (OsTSN1-OE) and SRBSDV P6 expression (P6-OE) transgenic Nipponbare (NPB) rice lines were generated by Agrobacterium mediated transformation protocols. The ostsn1 knockout mutant rice lines in NBP background and osnac90, osnac75, osnac15, ostga6, oslhy, osjaz6, osjaz12, osjaz15, and osatg8c knockout mutant rice lines in Zhong hua 11 (ZH11) background produced using the CRISPR/Cas9 methods from Biogle
Authentication	Genome Editing Center, the edit-types of knockout mutant rice plants were performed in Fig S14. The OsTSN1 overexpression (OsTSN1-OE) and SRBSDV P6 expression (P6-OE) transgenic Nipponbare (NPB) rice lines were detected by Western blot or qRT-PCR; The editing-sites of ostsn1, osnac90, osnac75, osnac15, ostga6, oslhy, osjaz6, osjaz12, osjaz15, and osatg8c knockout mutant rice were detected by PCR and Sanger Sequencing.