nature portfolio

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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	Bio-Rad ChemiDocTM XRS+(western blotting); Bio-Rad CFX Manger v3.1(qPCR data); Zeiss LSM710 (subcellular location).
Data analysis	Microsoft Excel 2010, GraphPad Prism 6 and Spss v17.0 (one-way ANOVA, Duncan's multiple range testwere used for statistical analysis. Quantitative analysis of immunoblots and fluorescence intensity is performed using Quantity Tools of Image Lab software (Bio-Rad). MEGA7 is used for constructing phylogenetic tree of OsGLS1s.

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

Data supporting the findings of this work are available within the paper and its supplementary information files. A reporting summary for this article is available as a supplementary information file. The datasets and genetic materials generated and analyzed during the current study are available from the corresponding author

upon request. Sequence of genes used in this study can be found in the MSU database (http://rice.plantbiology.msu.edu/) under the following accession numbers: OsGLS1 (LOC_Os04g01160), OsPIN2 (LOC_Os06g44970) OsAUX1 (LOC_Os05g37470) OsPIN1a (LOC_Os11g04190) and OsPIN1b (LOC_Os02g50960). Sequence for constructing the phylogenetic tree of GLS1s can be found in The Phytozome v13 database (https://phytozome-next.jgi.doe.gov/). The source data are provided with this paper.

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	No human participants involved.
Reporting on race, ethnicity, or other socially relevant groupings	No human participants involved.
Population characteristics	No human participants involved.
Recruitment	No human participants involved.
Ethics oversight	No human participants involved.

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	Samples sizes for each experiment is indicated in legends. Each experiment contains at least three biological replicates.
Data exclusions	No data is excluded from the analyses.
Replication	All experiments in this study are repeated independently at least three times. For RT-qPCR at least three biologically independent samples are used each time. For subcellular location, field and physiological and biochemical experiments, the results representative of three independent experiments. The number of biological replicates in each experiment is indicated in the legends.
Randomization	For field experiments, the mutant and wild type plants were grown in a completely-randomized block design with three replicates.
Blinding	The investigators were blinded to group allocation during data collection.

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

OsPIN1a,OsPIN1b and OsPIN2 were customized by ABclonal Technology Co.,Ltd.; anti-GFP, Sigma-Aldrich, G1544; anti-FLAG, Sigma-Aldrich, F1804; Anti-His, Abclonal, AE003; anti-actin, Sigma-Aldrich, A3853; anti-ubiquitin, Santa Cruz Biotechnology, sc-8017; anti-GST, TransGen Biotechnology, HT601; anti-MBP, Sigma-Aldrich, A4213; rabbit anti-mouse IgG secondary antibody conjugated to peroxidase, Sigma-Aldrich, A9044; Alexa Fluor 555, Invitrogen, A-21428;

Validation

The antibodies of OsPIN1a,OsPIN1b and OsPIN2 have been reported in previous paper; Other antibodies can be found at their respective company websites.

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 seeds were stored in the State Key Laboratory of Plant Environmental Resilience, College of Life Sciences, Zhejiang University.

Novel plant genotypes

The gls1 and pin2 single mutants were generated by ethyl methanesulfonate and CRISPR/Cas9-mediated gene editing; gls1 pin2 double mutants were generated by hybridization; Agrobacterium-based transformation was used to generate the transgenic lines and two independent lines were analyzed.

Authentication

PCR and Sanger sequencing were used to verify the genome editing generated at the designated genomic targets. RT-qPCR and western blotting were used to verify the expression of the transgenes.