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	Western blots: Bio-Rad ChemiDocTM Touch Imaging System Confocal microscopy: NiKon A1 i90, LSCM Gene expression (RT-qPCR): Bio-Rad CFX96 real-time PCR system, CFX Manager (Bio-RAD 3.1) Dul-Luciferase reporter: Bio-Rad ChemiDocTM Touch Imaging System Dul-Luciferase reporter assay: GLOMAXTM96 Photographing of plant: Nikon DIGITAL CAMERA D750
Data analysis	Confocal microscopy: NIS_Viewer_4.20_b972 Gene expression (RT-qPCR): MS Office10 Excel Protein quantification: Image Lab (6.0) and ImageJ software Dul-Luciferase reporter: Adobe Photoshop CC Luciferase reporter assay: MS Office10 Excel and GraphPad 8.0 Statistics: SPSS Statistics 21.0

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 data are available in the main text and supplementary information.

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

Life sciences study design

All studies must disclose on these points even when the disclosure is negative.

Sample size	Sample sizes were determined based on the generation of convincing and compelling results. At least three biological replicates were performed in all experiments. The number of replicates is indicated in the figure legend and/or in the method section.
Data exclusions	No data were excluded.
Replication	All experiments were repeated at least two or three times and were validated.
Randomization	All plants used in this study were randomly grown in the field or greenhouse, and both the experimental and control groups were treated under the same conditions.
Blinding	Because blind design of plant material is not applicable, the researchers first numbered the genotype, and later performed agronomic trait statistics and plaque measurements according to the number.

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-GST (Thermo Fisher Scientific, Cat#MA4-004,)
Anti-MBP (NEW ENGLAND BioLabs, Cat#E8032S, 1:10,000)
Anti-6xHis (Sangon Biotech, Cat#D191001-0200, 1:1,000)
Anti-HA (Thermo Fisher Scientific, Cat#MA1-12429,)
Anti-Ub (Cell Signaling, Cat#58395S, 1:1,000)
Anti-IPA1 (From the Institute of Genetics and Developmental Biology, Chinese Academy of Sciences)
Anti-HSP90 (Thermo Fisher Scientific, Cat#PA5-29042, 1:10,000)
Anti-Actin (Sangon Biotech, Cat#D191048, 1:10,000)
Anti-GFP (Sangon Biotech, Cat#D191040, 1:10,000)
Anti-MYC (Sangon Biotech, Cat#D199941, 1:1,000)
Anti-K6-linkage Specific Polyubiquitin Rabbit pAb (ABclonal, Cat#A18106, 1:5000)
Anti-K11-linkage Specific Polyubiquitin Polyclonal Antibody (Bio-Swamp, Cat#PAB46885, 1:5000)
Anti-K27-linkage Specific Polyubiquitin Rabbit pAb (ABclonal, Cat# A18202, 1:5000)
Anti-K29-linkage Specific Polyubiquitin Rabbit pAb (ABclonal, Cat#A18198, 1:5000)
Anti-K33-linkage Specific Polyubiquitin Rabbit pAb (ABclonal, Cat#A18199, 1:5000)
Anti-K48-linkage Specific Polyubiquitin Rabbit mAb (ABclonal, Cat#A3606, 1:5000)
Anti-K63-linkage Specific Polyubiquitin Rabbit pAb (ABclonal, Cat# A18164, 1:5000)

Validation

Validation statements and experiments can be obtained from the following websites and publications:
Anti-GST (https://www.thermofisher.cn/cn/zh/antibody/product/GST-Tag-Antibody-clone-8-326-Monoclonal/MA4-004)
Anti-MBP (https://www.neb.cn/products/e8032-anti-mbp-monoclonal-antibody#%E4%BA%A7%E5%93%81%E4%BF%A1%E6%81%AF)
Anti-6xHis (https://www.sangon.com/productDetail?productInfo.code=D191001)
Anti-HA (https://www.thermofisher.cn/cn/zh/antibody/product/HA-Tag-Antibody-clone-12CA5-Monoclonal/MA1-12429)
Anti-Ub (https://www.cellsignal.cn/products/primary-antibodies/ubiquitin-p37-antibody/58395?site-search-type=Products&N=4294956287&Ntt=58395s&fromPage=plp&_requestid=1958265)
Anti-IPA1 (DOI: 10.1038/ng.591)
Anti-HSP90 (https://www.thermofisher.cn/cn/zh/antibody/product/HSP90-alpha-Antibody-Polyclonal/PA5-29042)
Anti-Actin (https://www.sangon.com/productDetail?productInfo.code=D191048)
Anti-GFP (https://www.sangon.com/productDetail?productInfo.code=D191040)
Anti-MYC (https://www.sangon.com/productDetail?productInfo.code=D199941)
Anti-K6-linkage Specific Polyubiquitin Rabbit pAb (https://abclonal.com.cn/catalog/A18106)
Anti-K11-linkage Specific Polyubiquitin Polyclonal Antibody (http://enadmin.bio-swamp.com/productSearch?keyword=PAB46885&ms=1705721475988)
Anti-K27-linkage Specific Polyubiquitin Rabbit pAb (https://abclonal.com.cn/catalog/A18202)
Anti-K29-linkage Specific Polyubiquitin Rabbit pAb (https://abclonal.com.cn/catalog/A18198)
Anti-K33-linkage Specific Polyubiquitin Rabbit pAb (https://abclonal.com.cn/catalog/A18199)
Anti-K48-linkage Specific Polyubiquitin Rabbit mAb (https://abclonal.com.cn/catalog/A3606)
Anti-K63-linkage Specific Polyubiquitin Rabbit pAb (https://abclonal.com.cn/catalog/A18164)

Plants

Seed stocks

ALL seeds which used in this study was stored in our lab.

Novel plant genotypes

We used Cas9-SG1 (4356 TGCTGTATCTTCTGCACCTG 4375) and Cas9-SG2 (4380 AGCTCATCCATGCCCATATG 4399) to target the genome sequence of IPI7(LOC_Os05g06270), generating IPI7 knockout plants (ipi7-ko) by the CRISPR/Cas9 technology. Then, we over-expressed IPA1(S163D) in an IPI7 knockout genetic background and obtained SD-OE/ipi7-ko plants.

Authentication

To examine the CRISPR/Cas9-created lines, genomic DNA was extracted from transgenic plants for PCR sequencing.