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	Elemental analyzer (Vario Micro Cube, CN model, Elementar, Hanua, Germany) was used for determine nitrogen content; NovaSeq high-throughput sequencing platform (Guangzhou Gene Denovo Biotechnology Co., Ltd., China) was used for RNA sequencing; Stable Isotope Ratio Mass Spectrometry (Flash EA-DELTA V Advantage, USA) was used for determine the δ15N/14N ‰ of each oocyte; CFX96 real-time system (Bio-Rad, USA) was used for qRT-PCR; Nikon confocal laser scanning microscope (C2-ER, Japan) was used for subcellular localization; Leica stereoscopic microscope (M205 FA, Germany) was used for GUS staining; Delta-T Scan (Delta-T Devices Ltd., UK) and WinRHIZO (Regent Instrument Inc., Ottawa, Canada) was used for root morphological analyses; Dumas analyzer (Beijing Nord DN3000, China) was used for determine nitrogen content in the shoots and roots; Isotope ratio mass spectrometer (Finnigan Delta Plus XP, Thermo Fisher Scientific, USA) with an elemental analyzer (Flash EA 1112, Thermo Fisher Scientific, USA) was used for ^{15}N-Nitrate uptake; Typhoon 9400 imager (GE Healthcare, USA) was used for EMSA; Nikon confocal laser scanning microscope (Nikon, C2-ER) was used for BiFC; Tanon 5200 Chemiluminescence Imaging System (Tanon 5200, China) was used for LCI and WB; GloMax® 20/20 Luminometer (Promega, USA) was used for Dual-LUC.
Data analysis	3VmrMLM method was used to conduct the association analysis; AlphaFold3 was used for protein-DNA interactions; P values and sample sizes (n) are indicated in the individual figures and figure legends. Statistical analyses were performed using SPSS v22 (IBM Corp. Armonk, NY, USA) software (a two-tailed Student's t test was used to assess differences between two groups, while one-way ANOVA with Duncan's new multiple range test was applied to evaluate differences among multiple groups). Data visualization were performed using GraphPad Prism 8.

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 in the paper and its supplementary information files. The raw sequence data reported in this paper have been deposited in the Genome Sequence Archive (Genomics, Proteomics & Bioinformatics 2025) in National Genomics Data Center (Nucleic Acids Res 2025), China National Center for Bioinformation (CNCB) (GSA: CRA037933 with BioProject: PRJCA057114), and are publicly accessible at https://ngdc.cncb.ac.cn/gsa/browse/CRA037933. The variation data reported in this paper have been deposited in the Genome Variation Map (GVM) in CNCB (GVM: GVM001307 with BioProject: PRJCA057114), and are publicly accessible at https://bigd.big.ac.cn/gvm/getProjectDetail?Project=GVM001307. 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	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	No statistical methods were used to predetermine the sample size. The relevant figure legends and supplementary information describe the sample size, which enables researchers to conduct confident statistical analysis. Previous publications considered to determine sample size include: Agronomic traits (Liu et al., Nature 2020, 250: 600-605;)
Data exclusions	No data were exclueded from the analyses
Replication	All experiments were repeated at least three times, and the number of independent experiments or biological replicates is indicated in the figure legends.
Randomization	Measurements and samplings were performed by randomly selecting plants grown under the same conditions. All samples were randomly allocated into experimental groups.
Blinding	The research materials are plants so the blind design is not applicable in the field. For molecular biology experiments, bias could not be introduced since samples were treated identically and collected randomly, Experiments were repeated by different authors. The researchers also evaluated agronomic traits.

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	Mouse monoclonal anti-Flag (Abmart, Cat#M20008) Mouse monoclonal anti-Myc (Abmart, Cat#M20002) Rabbit polyclonal anti-H3 (Beyotime, Cat#AH433) Mouse monoclonal anti-Actin (Beijing Zomanbio, Cat#ZN101A-1)
Validation	For commercial antibodies: Used according to the instructions provided by the company.

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 plant materials, including near-isogenic line, Zhengmai7698, Fielder, transgenic plants (NPF7.6, JAZ1, and EIL3) as well as were generated in this work and kept in our laboratory.
Novel plant genotypes	Different transgenic plants were obtained using Agrobacterium transformation method and two positive lines were selected for the experiments. Gene editing materials were obtained by Agrobacterium transformation using CRISPR/Cas9 vector targeting specific targets. All transgenic lines were at generation T2 or above.
Authentication	Specific primers are designed to identify complementary or overexpressed transgenic materials and the expression levels of the relevant genes are detected using RT-qPCR. Specific primers are designed to PCR amplify specific fragments and then sequenced to identify the gene edited plants. All transgenic plants are planted, managed and post-harvested in a uniform manner to avoid secondary effects.