

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	Hitachi FE-SEM Field Emission Scanning Electron Microscope, S-4700 (scanning electron microscopy); ImageJ 1.54d (ligular width, cell length and width, and protein levels); OLYMPUS CX23, and ToupView (histological analysis); Applied Biosystems 7500 (RT-qPCR); ChemiScope6000 (immunoblot image); Tanon-5200 (the split firefly luciferase complementation assays); Thermo Scientific Ultimate 3000 UHPLC coupled with TSQ Quantiva (endogenous brassinosteroid contents); LI-1500 Light Sensor Logger (photosynthetically active radiation); LI-COR 6400XT instrument (photosynthesis of maize plants).
Data analysis	SAS v.9.2 (ANOVA, PROC Mixed); Microsoft Excel 2010 (two-sided Students' test); R v4.0.1 (Correlation analysis); MEGA 6.06 (phylogenetic analysis); BioEdit 7.0.9.1 (Sequence alignment).

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](#)

Provide your data availability statement here.

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](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	No statistical methods were used to predetermine sample size. The sample size and the results of statistical analyses were described in the relevant figures or method section. Required experimental sample sizes were estimated based on past experience performing similar experiments and previously published results (Tian et al, Science 365:658-664).
Data exclusions	No data was excluded from the analyses.
Replication	All molecular experiments in this study were repeated independently at least three times. A split-plot design with three replications was used in all field trials. Plant densities were randomized in the main plots and genotypes were subplots. Related information is indicated in figure legends.
Randomization	Samples of the same genotypes were randomly collected.
Blinding	The research materials are edited plants, which need to be strictly regulated and clearly labeled during the experimental process, so the blinding design is not applicable to this system, field trials were designed with three replicates in four locations over four years under regular and high planting densities.

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-RAVL1 antibody (made by Shanghai Youke Biotechnology Co., Ltd, 1:1500); anti-phyA antibody (made by Beijing Protein Innovation, 1:1000); anti-ACTIN (ABclonal Technology, Cat. NO: AC009, 1:8000); anti-HSP82 (Beijing Protein Innovation, CATALOG # AbM51099-31-PU, 1:6000); anti-His (YEASEN, CAT:30401ES80, 1:6000); anti-GST (ABclonal Technology, Cat. NO: AE001, 1:6000); anti-MYC (MBL, M047-3, 1: 6000); anti-GFP (TransGen, HT801, 1:6000).
Validation	Residues 192–206 of RAVL1 was used to make antibodies by Shanghai Youke Biotechnology Co., Ltd, and WT and RAVL1-KO1 were used to validate anti-RAVL1 antibody. His-phyA1-C protein was used to make antibodies by Beijing Protein Innovation, and WT and phyA-KO1 was used to validate anti-phyA antibody. The antibodies of ACTIN, HSP82, His-tag, GST, MYC and GFP are commercially available from the manufacturer. Anti-ACTIN antibody manufacturer's website: https://abclonal.com.cn/catalog/AC009 Anti-HSP82 antibody manufacturer's website: http://www.proteomics.org.cn/product/202.html Anti-His-tag antibody manufacturer's website: https://www.yeasen.com/products/detail/888 Anti-GST antibody manufacturer's website: https://abclonal.com.cn/catalog/AE001 Anti-MYC antibody manufacturer's website: http://www.mbl-chinawide.cn/search012?keyword=M047-3 Anti-GFP antibody manufacturer's website: https://www.transgen.com/antibody_tag/390.html

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

Seed stocks	lac1 is a naturally occurred mutant initially discovered in a population of maize inbred line W22 genetic background. The knockout lines for lac1, D11 and the phyA1 phyA2 double mutants were generated in the LH244 background. The lac1 overexpression lines were generated in the B104 background.
Novel plant genotypes	The CRISPR-Cas9 technique was used to generate knockout lines for lac1, D11 and phyA. The endogenous sequences targeted for editing, the number of independent transgenic events and the edited sites were indicated in figures or figure legends, and Agrobacterium-mediated transformation using maize immature embryos was performed to generate transgenic plants.
Authentication	Primers used for genotyping lac1 were provided in Supplementary Table 1. The target sequences for lac1, D11 and phyA genes were individually designed and cloned into the pBUE411 vector under the control of the maize Ubiquitin 1 promoter, and then transformed to the maize inbred line LH244 to generate lac1, D11 and phyA knockout lines respectively. The lac1 and D11 double mutants were generated by crossing lac1-KO2 and D11-KO1/D11-KO2. The full-length coding sequence of lac1 was cloned into pCAMBIA3300-GFP and transformed to the maize inbred line B104 to generate lac1-OE1 and lac1-OE2. The CRISPR-Cas9 cassette targeting lac1 was transformed into HI3. The HI3 plants carrying the CRISPR-Cas9 cassette targeting lac1 were crossed with different maize inbred lines to generate gene-edited haploids in these inbred line backgrounds. The gene-edited haploids were then doubled using the mitotic inhibitor colchicine. Sanger sequencing was used to identify knockout lines and overexpressing lines, and primers were provided in Supplementary Table 4.