

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	Hiseq2500 (Illumina) and Novaseq 6000 (Illumina) were used for transcriptome analysis, M165 (Leica), FLUOVIEW 451 FV1000 (Olympus), and LSM780 microscope (Carl Zeiss), a confocal laser scanning microscope system CSUWI-IX83 (CSU-WI, Yokogawa Electric, Tokyo, Japan, with an inverted microscope IX83, Olympus, Tokyo, Japan) equipped with an sCMOS camera Zyla 4.2 PLUS (Oxford Instruments, United Kingdom) were used for fluorescence microscopy imaging.
Data analysis	For data analysis following programs were used. For RNA-seq analysis : SRA Toolkit v2.10.0, Fastp v0.20.1, HISAT2 v2.2.0, SAMtools v1.10, StringTie v2.1.3, edgeR v3.24.3, R v4.2.2, R package "genefilter", "gplots", and "prcomp" For phylogenetic and motif analyses : MAFFT version 7, trimAI, IQ-TREE version 1.6.12, FigTree version 1.4.4, Pfam v36.0, SALADA (Interactive analysis, https://salad.dna.affrc.go.jp/CGViewer/en/cgv_upload.html) For Image analysis : Fiji (ImageJ v2) v1

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 manuscript or Supplementary Materials. All sequence reads were deposited in Sequence Read Archive (SRA) database under the project accession number PRJNA993618 and the DNA Data Bank of Japan (DDBJ) under accession numbers DRA016656 and DRA016671. Sequence and motif data in the manuscript or Supplementary Materials can be found in the databases, as follows: MarpolBase MpTak v.6.1 (<https://marchantia.info>), Pfam in InterPro (<https://www.ebi.ac.uk/interpro/>).

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 sample size calculation was performed. We determined sufficient sample sizes considering the time and cost of experiments and the variations of datasets. The validity of the sample size was confirmed by referring to previous studies in the fields of plant molecular biology and plant developmental biology. In the published RNA-seq data, we selected those with at least three biological replicates, but the data of antheridium has two biological replicates.
Data exclusions	No data were excluded from the analysis.
Replication	All experiments and phenotypic analysis were repeated at least three times independently. All attempts at replication were successful. The number of biological replicates of each experiment is shown in the Figure legends of the manuscript.
Randomization	No method of randomization was used. In all comparative experiments and analyses, plants grown under identical conditions were grouped into mutants and wild type.
Blinding	The investigator was not blinded to group allocation during data collection and/or analysis, because the phenotypes were clearly distinguishable. Although the first author performed the almost experiments also analyzed the data, the key phenotypes were obvious confirmed by at least two independent investigators.

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	Involvement 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	Involvement in the study
☒	☐ ChIP-seq
☒	☐ Flow cytometry
☒	☐ MRI-based neuroimaging

Antibodies

Antibodies used	anti-acetylated tubulin 6-11B-1 cat.# T6793-.2ML (Sigma) , Alexa Fluor 488 goat anti-mouse IgG cat.# A11001 (Thermo Fisher Scientific)
Validation	anti-acetylated tubulin 6-11B-1 cat.# A11001 (Sigma) : Evaluated by Western Blotting in HeLa cell lysate (https://www.sigmaaldrich.com/IP/en/product/mm/mabt868)

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