

Reporting Summary

Nature Portfolio wishes to improve the reproducibility of the work that we publish. This form provides structure 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

Provide a description of all commercial, open source and custom code used to collect the data in this study, specifying the version used OR state that no software was used.

Data analysis

QGRS Mapper(<https://bioinformatics.ramapo.edu/QGRS/index.php>)
MEME version 5.4.1 (<https://meme-suite.org/meme/>)
MEGA11 (<https://www.megasoftware.net/>)
RNAfold web server (<http://rna.tbi.univie.ac.at/cgi-bin/RNAWebSuite/RNAfold.cgi>)
UGENE v49.1 (<https://ugene.net/>)
GraphPad Prism 9.0 (<https://www.graphpad.com/>)

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](#)

miRbase (<https://www.mirbase.org/>)
 miRex2.0 (<http://www.combio.pl/mirex2/>)
 PLncDB (<https://www.tobaccodb.org/plncdb/>)
 tRex (<http://combio.pl/trex>)
 TAIR10 (<https://www.arabidopsis.org/>)

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](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	For qRT-PCR and FRET analysis, more than 3 samples were used. For phenotype analysis, more than 15 samples were used.
Data exclusions	No data were excluded.
Replication	All experiments were performed at least 3 times.
Randomization	Samples were randomly collected.
Blinding	The investigators were blinded to group allocation during data collection and analysis.

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

Horseradish peroxidase(HRP)-conjugated high affinity anti-HA (Invitrogen)
 Horseradish peroxidase(HRP)-conjugated high affinity anti-FLAG (Cell Signaling Technology)
 Horseradish peroxidase(HRP)-conjugated high affinity anti-GFP (Invitrogen)
 NWSHPQFEK Tag Monoclonal Antibody (GenScript)
 m-IgG1 BP-HRP: sc-525408 (Santa Cruz)

Validation

1. Horseradish peroxidase(HRP)-conjugated high affinity anti-HA (Invitrogen)
 HA Tag Monoclonal Antibody (2-2.2.14), HRP, Cat No. 26183-HRP, Invitrogen
<https://www.thermofisher.com/antibody/product/HA-Tag-Antibody-clone-2-2-2-14-Monoclonal/26183-HRP>

2. Horseradish peroxidase(HRP)-conjugated high affinity anti-FLAG (Cell Signaling Technology)
 DYKDDDDK Tag (D6W5B) Rabbit mAb (HRP Conjugate), Cat No. 86861, Cell signaling Technology
<https://www.cellsignal.com/products/antibody-conjugates/dykdddk-tag-d6w5b-rabbit-mab-binds-to-same-epitope-as-sigma-aldrich-anti-flag-m2-antibody-hrp-conjugate/86861>

3. Horseradish peroxidase(HRP)-conjugated high affinity anti-GFP (Santa Cruz Biotechnology)
 GFP Polyclonal Antibody, HRP, Cat No. A10260, Invitrogen
<https://www.thermofisher.com/antibody/product/GFP-Antibody-Polyclonal/A10260>

4. NWSHPQFEK Tag Monoclonal Antibody (GenScript)
 NWSHPQFEK Tag Monoclonal Antibody (5A9F9), THE™, Cat No. A01732-100, GenScript
<https://www.thermofisher.com/antibody/product/NWSHPQFEK-Tag-Antibody-clone-5A9F9-Monoclonal/A01732-100>

5. m-IgG1 BP-HRP: sc-525408 (Santa Cruz)
 m-IgG1 BP-HRP: sc-525408, HRP conjugate, Cat No. SC-525408, Santa Cruz
https://www.scbt.com/ko/p/m-igg1-bp-hrp?srltid=AfmBOorwK7P0fykIl6mwbGo50Z6s7vunhqN9STz6_BI312PWrGqay74Y

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	<p>jul2 (TAIR [https://arabidopsis.org/index.jsp], GK-268A03-015068)</p> <p>jul1 jul2 [Park et al., PNAS, 2025]</p>
Novel plant genotypes	<p>The jul1 line was generated by backcrossing the jul1 jul2 line with Col-0.</p> <p>Two independent jul1 proJUL1:JUL1-HA, jul1 jul2 proRPS5A:STTM165/166, jul1 jul2 proFIL:JUL1-StrepII, jul1 jul2 proAPL:JUL1-StrepII, jul1 jul2 proBOP1:JUL1-StrepII, proMIR165a:MIR165a_WT, proMIR165a:MIR165a_mut#3, jul1 jul2 proMIR165a:MIR165a_WT, and jul1 jul2 proMIR165a:MIR165a_mut#3 were used respectively.</p>
Authentication	<p>One proMIR165a:GUS-GFP, proJUL1:3xGFP, jul1 jul2 proJUL1:JUL1-GFP, proSMXL5:YFP-ER, jul1 LhGR-JUL1, and LhGR-ami-JUL1 were used respectively.</p> <p><i>Describe any authentication procedures for each seed stock used or novel genotype generated. Describe any experiments used to assess the effect of a mutation and, where applicable, how potential secondary effects (e.g. second site T-DNA insertions, mosaicism, off-target gene editing) were examined.</i></p>