

Reporting Summary

Nature Research 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 Research policies, see [Authors & Referees](#) and the [Editorial Policy Checklist](#).

Statistical parameters

When statistical analyses are reported, confirm that the following items are present in the relevant location (e.g. 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
- ☐ ☒ An indication of 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 statistics 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
- ☐ ☒ Clearly defined error bars
State explicitly what error bars represent (e.g. SD, SE, CI)

Our web collection on [statistics for biologists](#) may be useful.

Software and code

Policy information about [availability of computer code](#)

Data collection

Trimmomatic, TAIR10, Bowtie 1.2.2, STAR_2.5.4b

Data analysis

RSEM v1.2.31, Mfuzz package, EBSeq, MACS2, DiffBind package, Integrative Genomics Viewer (IGV)

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/reviewers upon request. We strongly encourage code deposition in a community repository (e.g. GitHub). See the Nature Research [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 list of figures that have associated raw data
- A description of any restrictions on data availability

The ChIP-Seq data used in this study were obtained from the National Center for Biotechnology Information (NCBI) Sequence Read Archive (SRA, <https://www.ncbi.nlm.nih.gov/sra>; accession number SRX746966). The RNA-seq data from this article have been deposited in the Gene Expression Omnibus database (www.ncbi.nlm.nih.gov/geo) and assigned the identifier accession GSE120418.

Field-specific reporting

Please select 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/authors/policies/ReportingSummary-flat.pdf](https://www.nature.com/authors/policies/ReportingSummary-flat.pdf)

Life sciences study design

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

Sample size	We chose the sample size according to previous studies (Chen, et al. Front. Plant Sci. 5:208, 2014)
Data exclusions	No data was excluded from the analysis.
Replication	Each experiment was performed with at least two repeats.
Randomization	We did not apply randomization. Most of the experimental findings were related to comparative analysis between wild-type and transgenic or mutant lines
Blinding	Blinding was not relevant to this study, because there was no individual /subjective bias in experimentation or data analysis.

Reporting for specific materials, systems and methods

Materials & experimental systems

n/a	Involved in the study
☐	☒ Unique biological materials
☐	☒ Antibodies
☒	☐ Eukaryotic cell lines
☒	☐ Palaeontology
☒	☐ Animals and other organisms
☒	☐ Human research participants

Methods

n/a	Involved in the study
☒	☐ ChIP-seq
☒	☐ Flow cytometry
☒	☐ MRI-based neuroimaging

Unique biological materials

Policy information about [availability of materials](#)

Obtaining unique materials All unique materials used are readily available from the authors.

Antibodies

Antibodies used	anti-GFP antibody (for Co-IP, Rohce,11814460001) (dilution volume, 1:1000); anti-trimethyl-H3K36 antibody (for ChIP, Abcam,ab9050) (dilution volume, 1:200); anti-HA antibody (for Co-IP, Rohce,11867431001) (dilution volume, 1:1000); HA isolation kit (for Co-IP, MACS Miltenyi Biotec,130-091-122)
Validation	All antibodies were tested with controls. anti-trimethyl-H3K36 antibody was validated in Arabidopsis thaliana.