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	The data collection in this study was preformed using open source software.
Data analysis	All software used in the present study are publicly available from the Internet and software versions are described in detail in the Methods sections. The software include HISAT2 (version 2.2.1), SAMtools (version 1.9), StringTie (version 2.1.4), DESeq2 (version 1.38.3), DIAMOND (version 0.9.27), WGCNA tools (version 1.71), TrimGalore (version 0.6.6), Bowtie2 (Version 2.4.4), MACS2 (version 2.2.7.1), Irreproducible Discovery Rate (version 2.0.3), ChIPseeker (version 1.34.1), deepTools (version 3.5.0), HINT (version 1.0.0), HiCRes (version 1.0.0), 3Dchromatin_ReplicateQC pipeline (version 1.0.1), cworld (version 1.0.1), CALDER (version 0.7), HiTAD (version 1.0.0), cooltools (version 0.5.1), Fit-Hi-C (version 2.0.8), Mustache (version 1.0.1), Chromosight (version 1.6.3), Peakachu (version 1.2.0), BLASTX (version 2.9.0), GENOVA (version 0.94).

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 raw sequencing data generated in this paper have been deposited into the National Center for Biotechnology Information database, a public database (BioProject ID: PRJNA1041939). The raw data is available for sharing for scientific research.

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

Life sciences study design

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

Sample size	We collected 12 tissue samples of Gossypium hirsutum J668, including the radicle, root, stem, leaf, hypocotyl, cotyledon, ovule, anther, petal, stigma, and developmental fibers at 10 days post-anthesis (DPA) and 20 DPA for Hi-C, ChIP-Seq (H3K4me3 and H3K27ac), ATAC-Seq, and RNA-Seq experiments.
Data exclusions	No data were excluded from analyses.
Replication	The Hi-C, ChIP-Seq and ATAC-Seq experiments were conducted with two biological replicates of two independent experiments. The RNA-Seq experiment was conducted with three biological replicates of three independent experiments.
Randomization	All samples were randomly sampled from at least 20 plants and mixed together.
Blinding	The investigators were blind in sample collection and data processing involving of group 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: Antibodies for chromatin modifications (H3K4me3, H3K27ac) were used in this study.

Validation: The antibodies were bought from commercial companies including Abcam (ab8580, ab4729).

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 seeds are conserved in the seed storage vault at Huazhong Agricultural University, and are cultivated at the same institution.

Novel plant genotypes: NA

Authentication: NA

ChIP-seq

Data deposition

☒ Confirm that both raw and final processed data have been deposited in a public database such as GEO.

☒ Confirm that you have deposited or provided access to graph files (e.g. BED files) for the called peaks.

Data access links
May remain private before publication.

All raw ChIP-seq data generated in this study have been deposited in the BioProject database (http://www.ncbi.nlm.nih.gov/bioproject) under accession number PRJNA1041939.

Files in database submission

J668_anther_H3K4me3_rep1
J668_anther_H3K4me3_rep2
J668_cotyledon_H3K4me3_rep1
J668_cotyledon_H3K4me3_rep2
J668_hypocotyl_H3K4me3_rep1
J668_hypocotyl_H3K4me3_rep2
J668_leaf_H3K4me3_rep1
J668_leaf_H3K4me3_rep2
J668_ovule_H3K4me3_rep1
J668_ovule_H3K4me3_rep2
J668_petal_H3K4me3_rep1
J668_petal_H3K4me3_rep2
J668_radicle_H3K4me3_rep1
J668_radicle_H3K4me3_rep2
J668_stem_H3K4me3_rep1
J668_stem_H3K4me3_rep2
J668_stigma_H3K4me3_rep1
J668_stigma_H3K4me3_rep2
J668_cotyledon_H3K27ac_rep1
J668_cotyledon_H3K27ac_rep2
J668_hypocotyl_H3K27ac_rep1
J668_hypocotyl_H3K27ac_rep2
J668_ovule_H3K27ac_rep1
J668_ovule_H3K27ac_rep2
J668_radicle_H3K27ac_rep1
J668_radicle_H3K27ac_rep2
J668_root_H3K27ac_rep1
J668_root_H3K27ac_rep2
J668_stem_H3K27ac_rep1
J668_stem_H3K27ac_rep2
J668_stigma_H3K27ac_rep1
J668_stigma_H3K27ac_rep2

Genome browser session
(e.g. UCSC)

Not applicable.

Methodology

Replicates: Each sample within the ChIP-seq dataset (H3K4me3 and H3K27ac) is represented by two replicates.

Sequencing depth: Sequencing depth is detailed in Supplementary Table 6.

Antibodies: In this study, two antibodies were used, including H3K27ac (Abcam, ab4729) and H3K4me3 (Abcam; ab8580). Both antibodies are from Abcam company. The sample undergoes incubation with 5μl of the antibody, at a concentration of 1μg/μl.

Peak calling parameters: macs2 callpeak -t H3K27ac.bwt.sorted.rmdup.bam -c Input.bwt.sorted.rmdup.bam -f BAM -g 2.3e9 -n H3K27ac -B -q 0.01 --outdir

Peak calling parameters	peaks macs2 callpeak -t H3K4me3.bwt.sorted.rmdup.bam -c Input.bwt.sorted.rmdup.bam -f BAM -g 2.3e9 -n H3K4me3 -B -q 0.01 --outdir peaks
Data quality	We used the FRiP value to evaluate the signal-to-noise ratio of datasets and applied an IDR <0.05 threshold to filter out repeated peaks of two replicated datasets. The detail information can be found in Supplementary Table 6.
Software	Mapping was performed using bowtie2 (v2.2.4), the read normalization (per million reads) and peak calling were performed using MACS2 (v2.2.7.1).