

## 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

All sequencing libraries were prepared in house and raw reads were generated on Illumina high-throughput sequencing platform with manufacturer's instruction. No software was used for data collection.

Data analysis

Software used include: BWA (0.7.13), Tophat2 (2.1.0), Trimmomatic (0.36), MACS2 (2.1.0), deepTools (2.5.3), BatMeth2, ChromHMM v1.12, BEDTools (2.25.0), Cufflinks (2.2.1), SAMTools (1.3.1), as well as R version 3.2.1 (2015-06-18) and Python to run many of the mentioned programs. Detailed parameters of each of the programs are mentioned in relevant sections in Methods.

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

All of raw data has been uploaded to the NCBI GEO under accession numbers GSE142570 (<https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE142570>)

## 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	The effective sample size is the the number of loci studied, which are described through the manuscript.
Data exclusions	No exclusion of data was made.
Replication	All experimental data was reliably reproduced in two independent experiments as indicated in the figure legends.
Randomization	The plants were grown in the same conditions (see Methods) and randomly allocated into experimental groups.
Blinding	No blinding was used since measurements were not vulnerable to observer bias. Whenever separate groups were compared, the same analysis pipelines were performed in parallel.

## Reporting for specific materials, systems and methods

### Materials & experimental systems

n/a	Involved in the study
<input checked="" type="checkbox"/>	<input type="checkbox"/> Unique biological materials
<input type="checkbox"/>	<input checked="" type="checkbox"/> Antibodies
<input checked="" type="checkbox"/>	<input type="checkbox"/> Eukaryotic cell lines
<input checked="" type="checkbox"/>	<input type="checkbox"/> Palaeontology
<input checked="" type="checkbox"/>	<input type="checkbox"/> Animals and other organisms
<input checked="" type="checkbox"/>	<input type="checkbox"/> Human research participants

### Methods

n/a	Involved in the study
<input type="checkbox"/>	<input checked="" type="checkbox"/> ChIP-seq
<input checked="" type="checkbox"/>	<input type="checkbox"/> Flow cytometry
<input checked="" type="checkbox"/>	<input type="checkbox"/> MRI-based neuroimaging

## Antibodies

Antibodies used	H3K4me1 polyclonal antibody (Abclonal, A2355), H3K4me3 polyclonal antibody (Abclonal, A2357), H3K9me2 monoclonal antibody (Abcam, ab1220), H3K27me3 polyclonal antibody (Abclonal, A2363), H3K27ac polyclonal antibody (Abclonal, A7253), and RNAPII monoclonal antibody (BioLegend, 920102)
Validation	The antibodies have been validated both by the companies and by ourselves. The companies have used dot plot, western blot, immunofluorescence, ChIP-qPCR or ChIP-seq experiments. Please refer to the information below: H3K4me1 antibody: <a href="https://www.abclonal.com.cn/catalog/A2355">https://www.abclonal.com.cn/catalog/A2355</a> ; H3K4me3 antibody: <a href="https://www.abclonal.com.cn/catalog/A2357">https://www.abclonal.com.cn/catalog/A2357</a> ; H3K9me2 antibody: <a href="https://www.abcam.cn/histone-h3-di-methyl-k9-antibody-mabcam-1220-chip-grade-ab1220.html">https://www.abcam.cn/histone-h3-di-methyl-k9-antibody-mabcam-1220-chip-grade-ab1220.html</a> ; H3K27me3 antibody: <a href="https://www.abclonal.com.cn/catalog/A2363">https://www.abclonal.com.cn/catalog/A2363</a> ; H3K27ac antibody: <a href="https://www.abclonal.com.cn/catalog/A7253">https://www.abclonal.com.cn/catalog/A7253</a> ; These commercial antibodies are well used and reported in many previous publications of our and other labs. We have carefully checked the specificity reports of the antibodies from the companies, and have validated the specificity of the antibodies in house. According to the human ENCODE guidelines, we carried out the primary characterization (western blot) and the secondary characterization

## 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.*

The raw sequence data are available at NCBI GEO under accession numbers GSE142570 (<https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE142570>)

### Files in database submission

510 data files including 352 ChIP-Seq datasets , 58 RNA-Seq data,58 FAIRE-Seq data, 38 Bisulfite-Seq data and 4 ChIP-reChIP data (summarized in Extended Data Table 2) .

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W081\_young\_leaf\_H3K9me2\_rep1  
W081\_young\_leaf\_H3K9me2\_rep2  
W081\_young\_leaf\_RNAPII\_rep1  
W081\_young\_leaf\_RNAPII\_rep2  
W306\_young\_leaf\_H3K4me3\_rep1  
W306\_young\_leaf\_H3K4me3\_rep2  
W306\_young\_leaf\_H3K27ac\_rep1  
W306\_young\_leaf\_H3K27ac\_rep2  
W306\_young\_leaf\_H3K27me3\_rep1  
W306\_young\_leaf\_H3K27me3\_rep2  
W306\_young\_leaf\_H3K4me1\_rep1  
W306\_young\_leaf\_H3K4me1\_rep2  
W306\_young\_leaf\_H3K9me2\_rep1  
W306\_young\_leaf\_H3K9me2\_rep2  
W306\_young\_leaf\_RNAPII\_rep1  
W306\_young\_leaf\_RNAPII\_rep2  
MH63\_young\_leaf\_RNA\_rep1  
MH63\_young\_leaf\_RNA\_rep2  
MH63\_panicle\_RNA\_rep1  
MH63\_panicle\_RNA\_rep2  
MH63\_root\_RNA\_rep1  
MH63\_root\_RNA\_rep2  
MH63\_mature\_leaf\_RNA\_rep1

MH63\_mature\_leaf\_RNA\_rep2  
ZS\_young\_leaf\_RNA\_rep1  
ZS\_young\_leaf\_RNA\_rep2  
ZS\_panicle\_RNA\_rep1  
ZS\_panicle\_RNA\_rep2  
ZS\_root\_RNA\_rep1  
ZS\_root\_RNA\_rep2  
ZS97\_mature\_leaf\_RNA\_rep1  
ZS97\_mature\_leaf\_RNA\_rep2  
Nip\_young\_leaf\_RNA\_rep1  
Nip\_young\_leaf\_RNA\_rep2  
Nip\_panicle\_RNA\_rep1  
Nip\_panicle\_RNA\_rep2  
Nip\_root\_RNA\_rep1  
Nip\_root\_RNA\_rep2  
Nip\_mature\_leaf\_RNA\_rep1  
Nip\_mature\_leaf\_RNA\_rep2  
W105\_young\_leaf\_RNA\_rep1  
W105\_young\_leaf\_RNA\_rep2  
W286\_young\_leaf\_RNA\_rep1  
W286\_young\_leaf\_RNA\_rep2  
C019\_young\_leaf\_RNA\_rep1  
C019\_young\_leaf\_RNA\_rep2  
C135\_young\_leaf\_RNA\_rep1  
C135\_young\_leaf\_RNA\_rep2  
C139\_young\_leaf\_RNA\_rep1  
C139\_young\_leaf\_RNA\_rep2  
C151\_young\_leaf\_RNA\_rep1  
C151\_young\_leaf\_RNA\_rep2  
C148\_young\_leaf\_RNA\_rep1  
C148\_young\_leaf\_RNA\_rep2  
W161\_young\_leaf\_RNA\_rep1  
W161\_young\_leaf\_RNA\_rep2  
W169\_young\_leaf\_RNA\_rep1  
W169\_young\_leaf\_RNA\_rep2  
C051\_young\_leaf\_RNA\_rep1  
C051\_young\_leaf\_RNA\_rep2  
W125\_young\_leaf\_RNA\_rep1  
W125\_young\_leaf\_RNA\_rep2  
W128\_young\_leaf\_RNA\_rep1  
W128\_young\_leaf\_RNA\_rep2  
W261\_young\_leaf\_RNA\_rep1  
W261\_young\_leaf\_RNA\_rep2  
W294\_young\_leaf\_RNA\_rep1  
W294\_young\_leaf\_RNA\_rep2  
W257\_young\_leaf\_RNA\_rep1  
W257\_young\_leaf\_RNA\_rep2  
W081\_young\_leaf\_RNA\_rep1  
W081\_young\_leaf\_RNA\_rep2  
W306\_young\_leaf\_RNA\_rep1  
W306\_young\_leaf\_RNA\_rep2  
MH63\_young\_leaf\_FAIRE\_rep1  
MH63\_young\_leaf\_FAIRE\_rep2  
MH63\_panicle\_FAIRE\_rep1  
MH63\_panicle\_FAIRE\_rep2  
MH63\_root\_FAIRE\_rep1  
MH63\_root\_FAIRE\_rep2  
MH63\_mature\_leaf\_FAIRE\_rep1  
MH63\_mature\_leaf\_FAIRE\_rep2  
ZS97\_young\_leaf\_FAIRE\_rep1  
ZS97\_young\_leaf\_FAIRE\_rep2  
ZS97\_panicle\_FAIRE\_rep1  
ZS97\_panicle\_FAIRE\_rep2  
ZS97\_root\_FAIRE\_rep1  
ZS97\_root\_FAIRE\_rep2  
ZS97\_mature\_leaf\_FAIRE\_rep1  
ZS97\_mature\_leaf\_FAIRE\_rep2  
Nip\_young\_leaf\_FAIRE\_rep1  
Nip\_young\_leaf\_FAIRE\_rep2  
Nip\_panicle\_FAIRE\_rep1  
Nip\_panicle\_FAIRE\_rep2  
Nip\_root\_FAIRE\_1  
Nip\_root\_FAIRE\_2  
Nip\_mature\_leaf\_FAIRE\_1  
Nip\_mature\_leaf\_FAIRE\_2



W105\_young\_leaf\_FAIRE\_rep1  
 W105\_young\_leaf\_FAIRE\_rep2  
 W286\_young\_leaf\_FAIRE\_rep1  
 W286\_young\_leaf\_FAIRE\_rep2  
 C019\_young\_leaf\_FAIRE\_rep1  
 C019\_young\_leaf\_FAIRE\_rep2  
 C135\_young\_leaf\_FAIRE\_rep1  
 C135\_young\_leaf\_FAIRE\_rep2  
 C139\_young\_leaf\_FAIRE\_rep1  
 C139\_young\_leaf\_FAIRE\_rep2  
 C151\_young\_leaf\_FAIRE\_rep1  
 C151\_young\_leaf\_FAIRE\_rep2  
 C148\_young\_leaf\_FAIRE\_rep1  
 C148\_young\_leaf\_FAIRE\_rep2  
 W161\_young\_leaf\_FAIRE\_rep1  
 W161\_young\_leaf\_FAIRE\_rep2  
 W169\_young\_leaf\_FAIRE\_rep1  
 W169\_young\_leaf\_FAIRE\_rep2  
 C051\_young\_leaf\_FAIRE\_rep1  
 C051\_young\_leaf\_FAIRE\_rep2  
 W125\_young\_leaf\_FAIRE\_rep1  
 W125\_young\_leaf\_FAIRE\_rep2  
 W128\_young\_leaf\_FAIRE\_rep1  
 W128\_young\_leaf\_FAIRE\_rep2  
 W261\_young\_leaf\_FAIRE\_rep1  
 W261\_young\_leaf\_FAIRE\_rep2  
 W294\_young\_leaf\_FAIRE\_rep1  
 W294\_young\_leaf\_FAIRE\_rep2  
 W257\_young\_leaf\_FAIRE\_rep1  
 W257\_young\_leaf\_FAIRE\_rep2  
 W081\_young\_leaf\_FAIRE\_rep1  
 W081\_young\_leaf\_FAIRE\_rep2  
 W306\_young\_leaf\_FAIRE\_rep1  
 W306\_young\_leaf\_FAIRE\_rep2  
 MH63\_young\_leaf\_DNAmeth\_1  
 MH63\_young\_leaf\_DNAmeth\_P1 additional  
 MH63\_panicle\_DNAmeth\_1  
 MH63\_panicle\_DNAmeth\_P1 additional  
 MH63\_root\_DNAmethy\_1  
 MH63\_root\_DNAmethy\_P1 additional  
 MH63\_matrue\_leaf\_DNAmeth\_1  
 MH63\_matrue\_leaf\_DNAmeth\_P1 additional  
 ZS97\_young\_leaf\_DNAmeth\_1  
 ZS97\_young\_leaf\_DNAmeth\_P1 additional  
 ZS97\_panicle\_DNAmeth\_1  
 ZS97\_panicle\_DNAmeth\_P1 additional  
 ZS97\_panicle\_DNAmeth\_P2 additional  
 ZS97\_panicle\_DNAmeth\_P3 additional  
 ZS97\_root\_DNAmeth\_1  
 ZS97\_root\_DNAmeth\_P1 additional  
 Nip\_young\_leaf\_DNAmeth\_1  
 Nip\_panicle\_DNAmeth\_1  
 Nip\_root\_DNAmeth  
 Nip\_mature\_leaf\_DNAmeth  
 ZS97\_mature\_leaf\_DNAmeth  
 W105\_young\_leaf\_DNAmeth  
 W286\_young\_leaf\_DNAmeth  
 C019\_young\_leaf\_DNAmeth  
 C135\_young\_leaf\_DNAmeth  
 C139\_young\_leaf\_DNAmeth  
 C151\_young\_leaf\_DNAmeth  
 C148\_young\_leaf\_DNAmeth  
 W161\_young\_leaf\_DNAmeth  
 W169\_young\_leaf\_DNAmeth  
 C051\_young\_leaf\_DNAmeth  
 W125\_young\_leaf\_DNAmeth  
 W128\_young\_leaf\_DNAmeth  
 W261\_young\_leaf\_DNAmeth  
 W294\_young\_leaf\_DNAmeth  
 W257\_young\_leaf\_DNAmeth  
 W081\_young\_leaf\_DNAmeth  
 W306\_young\_leaf\_DNAmeth  
 MH63\_young\_leaf\_H3K4me3\_H3K27ac  
 MH63\_young\_leaf\_H3K27ac\_H3K4me3  
 MH63\_young\_leaf\_H3K9me2\_H3K4me1

MH63\_young\_leaf\_H3K4me1\_H3K9me2

Genome browser session  
(e.g. [UCSC](#))

Please use the following link: <http://218.199.68.190:8008/basic/main/MH63/> with username: "rice\_encode" and password: "rice\_encode" to visualize peak files.

## Methodology

Replicates

Two biological replicates for each histone mark (H3K4me3, H3K4me1,H3K27ac,H3K27me3,H3K9me2), RNA-Seq and FAIRE-Seq in examined tissues of 3 varieties and another 17 varieties in young leaf.

Sequencing depth

About 13 million pair-end (2x150bp) raw reads on average for each experiment.

Antibodies

H3K4me1 polyclonal antibody (ABclonal, A2355), H3K4me3 polyclonal antibody (ABclonal, A2357), H3K9me2 monoclonal antibody (Abcam, ab1220), H3K27me3 polyclonal antibody (ABclonal, A2363), H3K27ac polyclonal antibody (ABclonal, A7253), and RNAPII monoclonal antibody (BioLegend, 920102)

Peak calling parameters

For narrow peak calling: macs2 callpeak function with "callpeak -t <input file> -c <control file> -f BAM -n <output peak file > -B -g 3.6e+8".For broad peak calling: broad-peak mode was used in MACS2 with FDR < 0.1, see Methods section in the manuscript for the details

Data quality

We used FRiP (fraction of reads in peaks), NSC (normalized strand coefficient) and RSC ( relative strand correlation) to evaluate our data quality following Human ENCODE project guidelines. We also visualized peak signals on genome browser for each dataset. The number of narrow peak (FDR < 0.05, default parameter) is from 12,000 to 28,000; the number of broad peak (FDR < 0.1, default parameter) is from 11,000 to 17,000.

Software

BWA (0.7.13), Tophat2 (2.1.0), Trimmomatic (0.36),MACS2 (2.1.0), deepTools (2.5.3), BatMeth2, ChromHMM v1.12, BEDTools (2.25.0), Cufflinks (2.2.1), SAMTools (1.3.1),