

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 <i>P</i> 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	The HiSeq 4000 system (Illumina) was used for RNA-seq. The HiSeq X ten platform (Illumina) was used for the whole-genome bisulfite sequencing, CUT&RUN and snRNA-seq analysis.
Data analysis	SNP calling: Cutadapt version 1.17 and Trimmomatic version 0.36, Bowtie2 version 2.3.4.1, Genome Analysis Toolkit (GATK) version 3.8. RNA-seq analysis: Cutadapt version 1.17 and Trimmomatic version 0.36, prinseq-lite.pl version 0.20.4, HISAT version 2.1.0, Samtools version 1.9, SNPsplit version 0.3.2, FeatureCounts version 1.4.6, edgeR version 3.31.4. Whole-genome bisulfite sequencing: Cutadapt version 1.17 and Trimmomatic version 0.36, Bismark version 0.22.3, Picard version 2.18.3, Samtools version 1.9, DeepTools 2.0, SNPsplit version 0.3.2. CUT&RUN analysis: Cutadapt version 1.17 and Trimmomatic version 0.36, Bowtie2 version 2.3.4.1, Picard version 2.18.3, Samtools version 1.9, DeepTools 2.0, SNPsplit version 0.3.2. Gene ontology analysis was used by clusterProfiler version 3.16. Motif analysis: MEME Suite version 5.4.1. snRNA-seq: Cell Ranger version 7.1.0, Cell Bender version 0.3.0, DoubletFinder version 2.0.3, Seurat version 5.0.1, GATK version 4.3.0, edgeR version 3.31.4. All data were visualized by ggplot2 version 3.4.0 and the ComplexHeatmap version 2.13.4. Venn diagrams were generated by Multiple List Comparator (https://molbiotools.com). All statistical analyses were performed in R version 4.2.1 under Rstudio version 2022.12.0+353. The identification of imprinted genes and snRNA-seq analysis using custom R scripts that deposited on GitHub (https://github.com/ktonosaki/Nat.Plants_rice_imprinting.git).

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](#)

Published sequence data used in this study were listed in Supplementary Data 1. All sequence data generated in this work have been deposited in DDBJ Sequence Read Archive (accession numbers DRA015294, DRA015356, DRA018338 and DRA018337). PANTHER database (<https://www.pantherdb.org/>) were used in this study. The genes can be found in GenBank or Rice Genome Annotation Project database (http://rice.plantbiology.msu.edu/analyses_search_locus.shtml) under the following accession numbers: OsMADS77, LOC_Os09g02780; OsEMF2a, LOC_Os04g08034; Waxy, LOC_Os06g04200; GE1, LOC_Os07g41240; Oryza;CycB1;1, LOC_Os01g59120; OslAA29, LOC_Os11g11430; OsNF-YB1, LOC_Os02g49410; OsYUCCA12, LOC_Os02g17230.

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	Sample size were determined based on previous publications on similar experiments to ensure confident statical analysis (Moreno-Romero et al. 2016, Yuan et al. 2017, Rodrigues et al. 2021, Han et al. 2023).
Data exclusions	No data were excluded from this analysis.
Replication	All experiments in this work were independently replicated at least two times.
Randomization	Plants were arranged randomly in the growing field, and plants used for the experiments (crosses) were randomly chosen among the available individuals.
Blinding	Most of the analyses done in this study were performed using bioinformatics (sequencing data). Since the same bioinformatics pipeline with the same settings was applied for every sample, blinding was not necessary and therefore not applied.

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

Methods

- | 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 |

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

Antibodies

Antibodies used

H3K27me3 rabbit polyclonal antibody (Millipore 07-449) was used for CUT&RUN analysis.

Validation

anti-H3K27me3 antibody was commercially available and the data sheet were provided by companies.
https://www.merckmillipore.com/JP/en/product/Anti-trimethyl-Histone-H3-Lys27-Antibody,MM_NF-07-449

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	A three rice varieties, Nipponbare, Kasalath and 93-11 were used in this study. H2B-GFP reporter line was provided from Tokyo Metropolitan University.
Novel plant genotypes	n/a
Authentication	H2B-GFP reporter line was authenticated by PCR and observation of GFP signals.

Flow Cytometry

Plots

Confirm that:

- ☒ The axis labels state the marker and fluorochrome used (e.g. CD4-FITC).
- ☒ The axis scales are clearly visible. Include numbers along axes only for bottom left plot of group (a 'group' is an analysis of identical markers).
- ☒ All plots are contour plots with outliers or pseudocolor plots.
- ☒ A numerical value for number of cells or percentage (with statistics) is provided.

Methodology

Sample preparation	The endosperm tissue was manually dissected and strained by a 100-µm cell strainer. After gentle shaking, the slurry was filtered through a 70-µm and then a 40-µm mini cell strainer. Endosperm nuclei were stained using Hoechst 33342.
Instrument	SH800S sorter (Sony)
Software	Cell Sorter software version 2.1
Cell population abundance	Approximately 15,000 nuclei
Gating strategy	Back scatter , fluorescence of GFP, the fluorescence of Hoechst 33342 and the fluorescence of PE.

- ☒ Tick this box to confirm that a figure exemplifying the gating strategy is provided in the Supplementary Information.