nature portfolio

Corresponding author(s): Takuya Sakamoto, Sachihiro Matsunaga

Last updated by author(s): 2022-6-16

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	We used ImageJ software for the collection of imaging data, comet assay data, and data of root phenotype. NGS datasets were generated on Illumina's sequencers.
Data analysis	We used the Subread package v2.0.0 (http://subread.sourceforge.net) and HiCdat (https://github.com/MWSchmid/HiCdat) for Hi-C data processing. We used the R software (https://www.r-project.org) for the analyses of microarray and Hi-C data. The Bioconductor limma package v2.12.1 (http://www.bioconductor.org) and HiCdatR package (https://github.com/MWSchmid/HiCdat) in R was used for microarray and Hi-C data analyses, respectively. We used ImageJ software (http://rsb.info.nih.gov/ij/) plugins, CometAssay (https://www.med.unc.edu/microscopy/resources/imagej-plugins-and-macros/comet-assay) and MtrackJ (https://imagescience.org/meijering/software/mtrackj/) for the analyses of comet assay and centromere movement, respectively. We used FastQC v0.11.9 (https://www.bioinformatics.babraham.ac.uk/projects/fastqc/), Trimmomatic v0.39 (http://www.usadellab.org/cms/?page=trimmomatic), STAR v2.7.10a (https://github.com/alexdobin/STAR), featureCounts v2.0.0 (http://subread.sourceforge.net), R packages DESeq2 v1.34.0 (https://bioconductor.org/packages/release/bioc/html/DESeq2.html) and EnhancedVolcano v1.13.2 (https://bioconductor.org/packages/release/bioc/html/EnhancedVolcano.html) for the analysis of RNA-seq data. We used bismark v0.23.0 (https://www.bioinformatics.babraham.ac.uk/projects/bismark/), and R packages methylKit v1.22.0 (https://bioconductor.riken.jp/packages/3.9/bioc/vignettes/methylKit/inst/doc/methylKit.html) and circlize v0.4.15 (https://jokergoo.github.io/circlize_book/book/). R scripts for Hi-C, BS-seq analysis (https://doi.org/10.5281/zenodo.6631550) and RNA-seq analysis (https://doi.org/10.5281/zenodo.6637416) are available on Zenodo (https://zenodo.org/record/6631550).

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

The data supporting the findings of this study are available within the paper and its supplementary information files. The microarray data (GEO ID: GSE179466) are available on the GEO website (https://www.ncbi.nlm.nih.gov/geo/). The Hi-C (DRA013016), RNA-seq (DRA014243), BS-seq (DRA014250) data are available on the DDBJ website (https://www.ddbj.nig.ac.jp/index-e.html). We used a modified version of Araport11 downloaded from https://plants.ensembl.org for RNA-seq data analysis and a TAIR10 genome downloaded from https://www.arabidopsis.org/index.jsp for Hi-C and BS-seq data analysis.

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	No sample-size calculation was performed. Samples size was chosen according to convention in the filed of plant cell biology for all experiments.
Data exclusions	No data were excluded.
Replication	All data shown is based on multiple biologically independent replicates. The number of replicates for each experiment was stated in the Figure or Figure legends and Method section of the manuscript. At least each experiment was independently repeated twice with similar results.
Randomization	Plants were grown on at least three plates placed randomly in the growth chamber to eliminate the influence of position during growth. With the exception of a few experiments, all plants grown were used in the experiments to avoid arbitrary sample selection. In DNA damage related experiments involving transplanting of plants, DNA damage treatments were performed on plants showing similar growth selected from large number of prepared plants to more accurately assess the effects of DNA damage.
Blinding	No blinding was applied. This is because the first author was involved in all experimental design and data collection and in most of the data analysis except for the analysis of NGS data. In addition, regarding NGS data analysis, we applied identical settings to all samples, blinding was not essential.

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
☒	☐ Human research participants
☒	☐ Clinical data
☒	☐ Dual use research of concern

Methods

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

Antibodies

Antibodies used	Rabbit polyclonal anti-GFP antibody (ab290, Abcam) Rabbit polyclonal anti-RFP antibody (R10367, Thermo Fisher Scientific) Goat polyclonal anti-rabbit IgG pAb-HRP (458, MBL)

Rabbit polyclonal anti-γH2AX antibody (Hirakawa et al, https://doi.org/10.1111/tpj.13499)
Goat polyclonal anti-rabbit IgG Alexa Fluor 488 (A32731, Thermo Fisher Scientific)

Validation

The antibodies used in this study has been validated previously. Information of these antibodies are available on the web sites.
ab290; Abcam (https://www.abcam.com/gfp-antibody-ab290.html)
R10367; Thermo Fisher Scientific (https://www.thermofisher.com/antibody/product/RFP-Antibody-Polyclonal/R10367)
458; MBL (https://ruo.mbl.co.jp/bio/e/dtl/A/?pcd=458)
γH2AX; Plant Journal (https://doi.org/10.1111/tpj.13499)
A32731; Thermo Fisher Scientific (https://www.thermofisher.com/antibody/product/Goat-anti-Rabbit-IgG-H-L-Highly-Cross-Adsorbed-Secondary-Antibody-Polyclonal/A32731)