nature portfolio

Corresponding author(s): Edith Heard and Haruhiko Koseki

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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	RNA FISH and IF/RNA FISH: Apoptome (Zeiss) and Deltavision (GE healthcare). Allele-specific RNA-seq: HiSeq 2500 (Illumina) and NovaSeq 6000 (Illumina).
Data analysis	RNA FISH and IF/RNA FISH analyses: Adobe Photoshop (v10.0.1). Allele specific RNA-seq analyses: cutadapt (v2.1), FLASH2 (v2.2.00), and seqtk (v1.3) for read cleaning; fermi (v1.1), bwa (v0.7.10), and samtools (v0.1.19) for de novo assembly-based variant calling; bwa (v0.7.10), samtools (v0.1.19), bedtools (v2.28.0), cufflinks (v2.2.1), and UCSC genome browser utilities (v379) for mapping and counting of RNA-seq reads. Statistical analyses: Python SciPy Library (v1.4.1). Figure assembly: Adobe Illustrator (v16.0.0).

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 allele-specific RNA-seq dataset is publicly available through Sequence Read Archive (SRA). The accession number is GSE168140.

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	More than three biological replicates were analyzed in all experiments using mouse embryos, except for the control embryo analyzed in Figure 2a, where only one embryo was analyzed. This is because the control embryo was known to have stable low values for the analysis, which was published previously (Corbel et al. 2013, Reference 28 in the manuscript). More than two biological replicates and more than 20 cells were counted in all experiments using tissue-derived cells. These sample sizes were enough for calculating a significance of each experiment.
Data exclusions	In RNA FISH and immuno-RNA FISH experiments, embryos with normal morphology were analyzed and the other embryos showing abnormal morphology were excluded from further analysis. Examples are presented in Figure 1c.
Replication	All experiments analyzing mouse embryos were performed using at least three biological replicates, except for the control embryo analyzed in Figure 2.
Randomization	The mice used in this study were randomly chosen from several independent mouse colonies for all experiments.
Blinding	Two investigators independently analyzed the state of gene expression, i.e. monoallelic expression or biallelic expression, in RNA FISH images used in Figures 2, 3b and 5c. Two investigators also independently analyzed the State of Histone mark accumulation (H2AK119ub1 and H3K27me3) on the Xi, two positive, either strong i.e., a compact and dense staining or weak i.e., a loose and relaxed staining and one negative in Extended Data Fig. 1b-d, 2c and 4b-d. If there was a disagreement between two investigators, the third investigator analyzed the same image to have a conclusion.

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	Primary antibodies H3K27me3 (#7B11, a gift from R Margueron, mouse mAb, also available from Active Motif #39535), 1:200 H3K27me3 (#MABI0323, Takara, mouse mAb), 1:200 H2AK119ub1 (#8240S, Cell Signaling, rabbit mAb), 1:50 Secondary antibodies Goat anti-mouse IgG Alexa568 (#A11031, Thermo Fisher Scientific), 1:500 Goat anti-mouse IgG Alexa488 (#A11029, Thermo Fisher Scientific), 1:800 Goat anti-rabbit IgG Alexa 488 (#A11034, Thermo Fisher Scientific), 1:800 Goat anti-rabbit IgG Alexa647 (#A21044, Thermo Fisher Scientific), 1:800
Validation	All primary antibodies were validated by the producer or manufacturer. Information for antibody validation is provided on the manufacturer's website. Consistently, these primary antibodies failed to detect the epitope in cells lacking responsible enzymes for each Histone modification.

Animals and other organisms

Policy information about studies involving animals; ARRIVE guidelines recommended for reporting animal research

Laboratory animals	For both C57BL/6 and B6-ChrXT^MSM mouse strains, 8 to 16 week-old female mice and 10 to 24 week-old male mice were used in all experiments. The mice were bred in 12h light/12h dark condition, 21 to 25 degrees temperature and 40 to 60% humidity.
Wild animals	Wild animals were not used in this study.
Field-collected samples	Field-collected samples were not used in this study.
Ethics oversight	All animal breeding and experiments were performed according to the in-house guidelines for care and use of laboratory animals in RIKEN, Japan and Curie Institute, France.

Note that full information on the approval of the study protocol must also be provided in the manuscript.