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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	No software was used for data collection.

Data analysis	DNA-FISH images were analyzed with Icy - Version 1.9.5.1 (http://icy.bioimageanalysis.org) with a custom made protocol available upon request. HiC data was analyzed with HiC-Pro (version 2.10.0) (doi:10.1186/s13059-015-0831-x). Compartments were called using the HiTC Bioconductor package Release (3.6) (10.1093/bioinformatics/bts521). Cutadapt (http://dx.doi.org/10.14806/ej.17.1.200) was used to trim the fastq reads; pre-processed reads were aligned to the reference genome using bwa (version bwa-0.7.12) (DOI: 10.1093/bioinformatics/btp324) ; SNPsplit_genome_preparation (version SNPsplit_v0.3.0/) (http://www.bioinformatics.babraham.ac.uk/projects/SNPsplit/) was used for the nucleotide substitution in the mm10 genome assembly; PCR duplicates were removed using picard tools (version picard-tools-1.130) (http://broadinstitute.github.io/picard/); hisat2 (version hisat2-2.0.3-beta) (DOI: 10.1038/nmeth.3317) was used to align mRNA reads to a the mm10 transcriptional model and htseq-count (version 0.6.0) (doi: 10.1101/002824) and kallisto (version 0.44.0) (doi: 10.1038/nbt.3519) were used to quantify the counts; the R programming language (versions R-3.1.2, R-3.4.0 and R-3.4.3) (https://www.R-project.org/) was widely used within the study for statistical analysis and data plotting. The R package edgeR (doi: 10.1093/bioinformatics/btp616) was used for RNA expression differential analysis. Pheatmap was used for the generation of heatmaps of relative gene expression (version 1.10.12) (https://cran.r-project.org/web/packages/pheatmap/). Basecalling and filtering were performed using standard software of the Illumina HiSeq 2500 (https://www.illumina.com/systems/sequencing-platforms/hiseq-2500.html).

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

Data produced in this study is available at GSE112551. Publicly available data used for RNAseq and H3K4me3 ChIPseq can be found under the accession numbers GSE45719 and GSE71434; for HiC data at GSE82185 and PRJCA000241.
Figures with associated raw data: figure 1b, figure 1c, figure 1d, figure 1e, figure 1h, figure 1j, figure 2a, figure 2b , figure 2d , figure 2e, figure 2f, figure 2g, figure 3b, figure 3d, figure 3h, figure 4c, figure 4f , figure 4g, figure s1f, figure s1g, figure s1h, figure s2a, figure s2h, figure s2i, figure s3, figure s4a, figure s4b, figure s4f, figure s4g, figure s4i, figure s4j, figure s5c, figure s6h, figure s6g, figure s6i.

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

Life sciences study design

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

Sample size	Three biological replicates were generated for all stages. These biological replicates showed high concordance and increasing sample size beyond three would not result in increased data quality improvement (reduce false positives/negatives).
Data exclusions	Samples with less than 30,000 unique GATCs were excluded from the data.
Replication	Experiments were successfully replicated n=3 or more
Randomization	In each experiment embryos from 4-8 female mice were pooled and randomly allocated to experimental groups.
Blinding	No blinding was done, since no manual assessment of images or experimets was performed

Reporting for specific materials, systems and methods

Materials & experimental systems

n/a	Involved in the study
☐	☒ Unique biological materials
☐	☒ Antibodies
☐	☒ Eukaryotic cell lines
☒	☐ Palaeontology
☐	☒ Animals and other organisms
☒	☐ Human research participants

Methods

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

Unique biological materials

Policy information about availability of materials

Obtaining unique materials	No restricted availability.

Antibodies

Antibodies used	Lamin B1 sc-6216 Santa Cruz (1:100) Lamin A/C 39288 Active Motif (1:200) mAb414 (nuclear pores) ab24609 Abcam (1:1000) HA-tag 11867423001 Roche (1:250) H3K4me3 C15410003 Diagenode (1:250) H3K9me2 07-441 Millipore Upstate (1:250) H3K9me3 17-625 Millipore Upstate (1:250) 488 GAR Life Tech A11034 (1:500) 488 GAM Invitrogen A11001 (1:500) 647 GAR Life Tech A21245 (1:500) 647 GAM Life Tech A21236 (1:500)
Validation	Lamin B1 antibody was validated in KO mESC (DOI: 10.1126/science.1211222). mAb414 antibody was validated in preimplantation embryo (doi:10.1038/nsmb.2839). HA-tag antibody is validated by the manufacturer (https://www.sigmaaldrich.com/catalog/product/roche/roahaha?lang=de&region=DE). H3K4me3 antibody is validated on dot-blot by the manufacturer (https://www.diagenode.com/en/p/h3k4me3-polyclonal-antibody-premium-50-ug-50-ul). Lamin A/C antibody is validated on KO mESC (doi:10.4161/nucl.23384). H3K9me2 antibody was validated by the manufacturer (http://www.merckmillipore.com/HU/hu/product/Anti-dimethyl-Histone-H3-Lys9-Antibody,MM_NF-07-441?ReferrerURL=https%3A%2F%2Fwww.google.hu%2F). H3K9me3 antibody was validated by the manufacturer (http://www.merckmillipore.com/HU/hu/product/ChIPAb+-Trimethyl-Histone-H3-Lys9-ChIP-Validated-Antibody-and-Primer-Set,MM_NF-17-625?ReferrerURL=https%3A%2F%2Fwww.google.hu%2F).

Eukaryotic cell lines

Policy information about cell lines

Cell line source(s)	F1 hybrid 129/Sv:Cast/Eij mouse embryonic stem cells (doi:10.1016/j.cell.2007.12.036)
Authentication	F1 hybrid 129/Sv:Cast/Eij mouse embryonic stem cells were not authenticated
Mycoplasma contamination	The F1 hybrid 129/Sv:Cast/Eij mouse embryonic stem cells has been tested negative for mycoplasma
Commonly misidentified lines (See ICLAC register)	No commonly misidentified cell lines were used

Animals and other organisms

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

Laboratory animals	Preimplantation embryos were collected from 5-8 weeks old F1 (CBAxC57BL/6J) females mated with CAST/EiJ males for hybrid crosses and with F1 males for non-hybrid crosses.
Wild animals	This study did not involve wild animals
Field-collected samples	This study did not involve field-collected samples