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Reporting Summary

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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 computer code were used to collect the data.
Data analysis	ChIP-seq reads were aligned to the mouse genome build mm9 using the bwa (v0.7.12) mem command. Signal tracks for each sample were generated using the MACS2 (v2.0.10.20131216) pile up function and were normalized to 1 million reads for visualization. The RNA-seq reads were mapped to the mm9 reference genome using Tophat (v1.3.3). Expression levels for all Refseq genes were quantified to FPKM using Cufflinks (v1.2.0), and FPKM values of replicates were averaged. All the BS-seq reads were first processed using TrimGalore (v0.3.3) to trim adaptor and low-quality reads. Adaptor-trimmed reads were then mapped to a combined genome with mm9 and 48052 lambda sequence using bsmap (v2.89). The methylation level of each CpG site was estimated using mcall (v1.3.0).The ChIP-seq peaks were called by MACS14 (v1.4.2)(Zhang et al., 2008) with the parameters --nomodel --nolambda --shiftsize=73 over input files. Functional annotation was performed using the Database for Annotation, Visualization and Integrated Discovery (DAVID) Bioinformatics Resource. To assess the expression level of repeats elements, all the RNA-seq files were re-mapped to the mm9 genome using the STAR aligner software allowing up to 3 mismatches and filtering out reads mapping to more than 500 positions in the genome(Dobin et al., 2013). Mapped files were then processed using the makeTagDirectory script of HOMER with -keepOne option. To perform differential gene expression analysis, we first calculated the reads count of each RNA-seq sample using HTSeq (v0.6.0). Then the results were fed into edgeR to perform differential analysis. Bedtools (v2.20.1) were used to calculate the Jaccard index in the analysis. We retrieved the genome wide motif sites based on the results of BINOCh (v1.0.0). All custom codes were generated using Python or R, and can be available upon request.

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 the ChIP-seq, RNA-seq and WGBS data generated in this study have been deposited in the Gene Expression Omnibus under the accession number GSE97778. H3K4me3 and H3K27me3 data were from GSE73952. Allelic H3K4me3, H3K27me3 and ATAC-seq data were downloaded from GSE66390, GSE71434 and GSE76687.

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

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	500 cells or 5 × 10*6 sperms per reaction for ChIP-seq, 100 cells per eaction for WGBS and 200 cells per reaction for total RNA-sequencing. This is the minimum number of cells for the corresponding experiments to get high quality sequencing data under current conditions in our lab. As the sequencing depth of samples in this study is less than 50x, thus the cell number is sufficient for detecting the majority of the modification signal. No statistical method were used to predetermine the sample size.
Data exclusions	No data were excluded from the analyses.
Replication	ChIP-seq and RNA-seq were performed 2-4 times for each stage with the number of replications shown in Supplementary Table 1. WGBS was performed once for each stage, the number of replicates is sufficient to determine the corresponding modification level. All attempts at replication were successful.
Randomization	All oocytes or embryos were collected from the oviducts of female mice and separated to single cells . Single cells were randomly allocated for ChIP-seq, RNA-seq and WGBS.
Blinding	During the siRNA injection , investigators injected the siRNA to the embryos without knowing the types of the siRNA.

Materials & experimental systems

Policy information about availability of materials

n/a	Involved in the study
☒	☐ Unique materials
☐	☒ Antibodies
☐	☒ Eukaryotic cell lines
☐	☒ Research animals
☒	☐ Human research participants

Antibodies

Antibodies used	Histone H3K4me3 antibody (Cell signaling Technology, #9727) ,1ug per ChIP reaction Histone H3K27me3 antibody (Diagenode, pAb-069-050) ,1ug per ChIP reaction Histone H3K9me3 antibody (Active Motif, 39161),1ug per ChIP reaction
Validation	Histone H3K4me3 antibody (Cell signaling Technology, #9727) This antibody can be used for ChIP, immunoprecipitation, Western Blotting and Immunofluorescence in human ,mouse, rat and monkey cells according to the manufacture's description. There are validation data for ChIP with Hela cells on the manufactures's website. In our experiment, we validated this antibody by performing ChIP-seq with Mouse R1 ES cells. The sequencing result is consistent with data in ENCODE database.

Histone H3K27me3 antibody (Diagenode, pAb-069-050) This antibody can be used for ChIP, ELISA, Dot Bloting ,Western Blotting and Immunofluorescence in human ,mouse and rat cells according to the manufacture's description. There are validation data for ChIP with Hela cells and HelaS3 cells on the manufactures's website. In our experiment, we validated this antibody by performing ChIP-seq with Mouse R1 ES cells. The sequencing result is consistent with data in ENCODE database.

Histone H3K9me3 antibody (Active Motif, 39161)This antibody can be used for ChIP, Dot Bloting ,Western Blotting and Immunofluorescence with wide range reactivity according to the manufacture's description. There are validation data for ChIP with D425 human Medulloblastoma cells on the manufactures's website. In our experiment, we validated this antibody by performing ChIP-seq with Mouse R1 ES cells. The sequencing result is consistent with data in ENCODE database.

Eukaryotic cell lines

Policy information about cell lines

Cell line source(s)	The R1 ESCs were purchased from the American Type Culture Collection (ATCC) . The RO-7 TSCs were derived in our lab and published before.
Authentication	For TS cell line, we performed immunofluorescent staining of Cdx2 and found the TS cell line is positive for Cdx2. We also perform RT-PCR of marker genes in TS cells, such as Esrrb, Sox2 and Eomes, and these genes are positively expresssed in our TS cell line. The R1 ES cell line was purchased and used in several paper published by our lab, no further authentication were performed for this cell line.
Mycoplasma contamination	All cell lines tested negetive for mycoplasma contamination.
Commonly misidentified lines (See ICLAC register)	No commonly misidentified cell lines were used.

Research animals

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

Animals/animal-derived materials	B6D2F1 or C57BL/6 female mice (8–10 weeks old) and B6D2Fi or DBA2 male mice (10-16 week old) were used in our study.

Method-specific reporting

n/a	Involved in the study
☐	☒ ChIP-seq
☒	☐ Flow cytometry
☒	☐ Magnetic resonance imaging

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.*	https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE97778
Files in database submission	MIIOocyte.H3K9me3.1.1.fq.gz MIIOocyte.H3K9me3.1.2.fq.gz MIIOocyte.H3K9me3.2.1.fq.gz MIIOocyte.H3K9me3.2.2.fq.gz sperm.input.1.fq.gz sperm.input.2.fq.gz sperm.H3K9me3.1.1.fq.gz sperm.H3K9me3.1.2.fq.gz sperm.H3K9me3.2.1.fq.gz sperm.H3K9me3.2.2.fq.gz zygote.input.1.fq.gz zygote.input.2.fq.gz zygote.H3K4me3.1.1.fq.gz zygote.H3K4me3.1.2.fq.gz zygote.H3K4me3.2.1.fq.gz zygote.H3K4me3.2.2.fq.gz zygote.H3K27me3.1.1.fq.gz zygote.H3K27me3.1.2.fq.gz zygote.H3K27me3.2.1.fq.gz zygote.H3K27me3.2.2.fq.gz

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E85Epi.K27me3.2.bw
E85Epi.K27me3.3.bw
E85Epi.K9me3.1.bw
E85Epi.K9me3.2.bw
ctrl.H3K9me3.1.bw
ctrl.H3K9me3.2.bw
siChaf1a.H3K9me3.1.bw
siChaf1a.H3K9me3.2.bw
siSumo2.H3K9me3.1.bw
siSumo2.H3K9me3.2.bw
siSetdb1.H3K9me3.1.bw
siSetdb1.H3K9me3.2.bw
siUbe2i.H3K9me3.1.bw
siUbe2i.H3K9me3.2.bw
siZfp809.H3K9me3.1.bw
siZfp809.H3K9me3.2.bw
siTrim28.H3K9me3.1.bw
siTrim28.H3K9me3.2.bw
siTrim28.H3K9me3.3.bw
zygote.C57BL-DBA.H3K9me3.1.bw
zygote.C57BL-DBA.H3K9me3.2.bw
early2cell.C57BL-DBA.H3K9me3.1.bw
early2cell.C57BL-DBA.H3K9me3.2.bw
late2cell.C57BL-DBA.H3K9me3.1.bw
late2cell.C57BL-DBA.H3K9me3.2.bw
late2cell.C57BL-DBA.H3K9me3.3.bw
ICM.C57BL-DBA.H3K9me3.1.bw
ICM.C57BL-DBA.H3K9me3.2.bw

Genome browser session (e.g. UCSC)	Not available.

Methodology

Replicates	ChIP-seq were performed 2-4 times for each stage with the number of replications shown in Supplementary Table 1. Replicates were highly agreed and the pearson's correlation coefficient on merged peaks for replicates are greater than 0.8.
Sequencing depth	PCR were performed with KAPA HiFi HotStart enzyme and amplify following the manufactures ,the cycle number for PCR amplification is 12-14. The total number of reads for each experiments is between 15M~50M, and the samples were sequenced using Illumina HiSeq 2000 with 150bp read length and paired-end sequenced. Detailed mapping summary could be referenced in Supplementary Table S1.
Antibodies	Histone H3K4me3 antibody (Cell signaling Technology, #9727) This antibody can be used for ChIP, immunoprecipitation, Western Blotting and Immunofluorescence in human ,mouse, rat and monkey cells according to the manufacture's description. There are validation data for ChIP with Hela cells on the manufactures's website. In our experiment, we validated this antibody by performing ChIP-seq with Mouse R1 ES cells. The sequencing result is consistent with data in ENCODE database. We use 1ug antibody for each ChIP reaction. Histone H3K27me3 antibody (Diagenode, pAb-069-050) This antibody can be used for ChIP, ELISA, Dot Bloting ,Western Blotting and Immunofluorescence in human ,mouse and rat cells according to the manufacture's description. There are validation data for ChIP with Hela cells and HelaS3 cells on the manufactures's website. In our experiment, we validated this antibody by performing ChIP-seq with Mouse R1 ES cells. The sequencing result is consistent with data in ENCODE database. We use 1ug antibody for each ChIP reaction. Histone H3K9me3 antibody (Active Motif, 39161)This antibody can be used for ChIP, Dot Bloting ,Western Blotting and Immunofluorescence with wide range reactivity according to the manufacture's description. There are validation data for ChIP with D425 human Medulloblastoma cells on the manufactures's website. In our experiment, we validated this antibody by performing ChIP-seq with Mouse R1 ES cells. The sequencing result is consistent with data in ENCODE database. We use 1ug antibody for each ChIP reaction.
Peak calling parameters	All ChIP and control files were mapped to mouse genome mm9 using bwa(v0.7.12) mem command with the paremeter bwa mem -t 10 mm9.fa sample.fq > sample.sam, the mapped sam files for replicates were merged and then normalized to 80M reads for comparison between stages. ChIP-seq peaks were generated using MACS14 (v1.4.2) with the parameters --nomodel --nolambda --shiftsize=73 over input files.
Data quality	All ChIP-seq peaks were filtered using 5% FDR and greater than 5-fold over input files. The number of ChIP-seq peaks are between 50K-200K after filter.
Software	DAVID Bioinformatics Resource was used to perform functional analysis. Custom analysis codes were generated using python and R, and can be available upon request.