

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](#).
Please do not complete any field with "not applicable" or n/a. Refer to the help text for what text to use if an item is not relevant to your study.
For final submission: please carefully check your responses for accuracy; you will not be able to make changes later.

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 P 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	No specific software was used for data collection
Data analysis	Bowtie2 (v2.4.1) was used for NGS read alignment; and Samtools (v1.10) was used for accessing BAM files. Python2 (v2.7.18) was utilized for all other custom analyses. Further details on data analysis and custom scripts can be found in the GitHub repository: https://github.com/spark159/condense-seq .

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](#)

NCBI GEO under accession number GSE252941

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

NA

Reporting on race, ethnicity, or other socially relevant groupings

NA

Population characteristics

NA

Recruitment

NA

Ethics oversight

NA

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

The particular sample size calculation is not relevant for this study.

However, we always numerate data size, for example, nucleosome numbers, in the figure legend for any statistical comparison.

Data exclusions

No data exclusion were conducted in this study

Replication

All biochemical studies were performed in triplicate (n=3) for all experiments. Genomic studies from cell lines were all carried out in duplicate. More specific summary is the following.

Randomization

3 biological replicates (Nucleosome condensation assay), 2 biological replicates (Condense-seq with genomic nucleosomes), 3 biological replicates (Histone Chip-seq), 3 biological replicates (Immunofluorescence), 3 biological replicates (PTM library)

Blinding

The randomization was not required at any other stage of this study.

Blinding was not necessary in this study since it was not a clinical trial involving human patients.

Behavioural & social sciences study design

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

Study description

Research sample

Sampling strategy

Data collection

Timing

Data exclusions

Non-participation

Randomization

Ecological, evolutionary & environmental sciences study design

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

Study description	
Research sample	
Sampling strategy	
Data collection	
Timing and spatial scale	
Data exclusions	
Reproducibility	
Randomization	
Blinding	

Did the study involve field work? ☐ Yes ☐ No

Field work, collection and transport

Field conditions	
Location	
Access & import/export	
Disturbance	

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
☒	☐ Clinical data
☒	☐ Dual use research of concern
☒	☐ Plants

Methods

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

Antibodies

Antibodies used	Western Blot: H3 (polyclonal, abcam, Cat# ab1791), H3K4me3 (C42D8, Cell Signaling Technology, Cat# 9751), H3K9me3 (polyclonal, abcam, Cat# ab8898), H3K9ac (C5B11, Cell Signaling Technology, Cat# 9649), H3K27ac (polyclonal, abcam, ab4729), H2BK120ub (D11, Cell Signaling Technology, Cat# 5546). Chip-seq: H3K27ac (polyclonal, abcam, Cat# ab4729), H3K27me3 (EPR18607, abcam, Cat# ab192985). Immunofluorescence: H3K36me3 (polyclonal, abcam, Cat# ab9050), H3K4me3 (C42D8, Cell Signaling Technology, Cat# 9751), H3K27ac (D5E4, Cell Signaling Technology, Cat# 8173), H3K27me3 (C36B11, Cell Signaling Technology, Cat# 9733), H3K9ac (C5B11, Cell Signaling Technology, Cat# 9649)
Validation	

All validation studies and other referenced research were conducted and can be found through commercial vendors, accessible via catalog numbers on their websites.

Eukaryotic cell lines

Policy information about [cell lines and Sex and Gender in Research](#)

Cell line source(s)	Cell lines used in this study: H1-hESC (WiCell), GM12878 (Coriell Institute), ES-E14TG2a (ATCC)
Authentication	Cell line authentication details can be found on the vendor's website.
Mycoplasma contamination	All cell lines used in this study were routinely tested for mycoplasma contamination and confirmed to be negative throughout the duration of the study.
Commonly misidentified lines (See ICLAC register)	None of the cell lines used in this study are known to be commonly misidentified.

Palaeontology and Archaeology

Specimen provenance	
Specimen deposition	
Dating methods	
☐ Tick this box to confirm that the raw and calibrated dates are available in the paper or in Supplementary Information.	
Ethics oversight	

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

Animals and other research organisms

Policy information about [studies involving animals; ARRIVE guidelines](#) recommended for reporting animal research, and [Sex and Gender in Research](#)

Laboratory animals	C57BL/6 wild-type and ODC (flox/flox) mice with Cre recombinase (purchased from Jackson Laboratories) were used in this study. Mice of all strains were typically 8–12 weeks old. All mice were housed in individually ventilated microisolator cages in a facility maintained at Johns Hopkins University, on a 12 hr light/dark cycle maintained at 40–60% humidity and 72 degree F +/- 2 degrees.
Wild animals	No wild animals were used in the study.
Reporting on sex	In this study, we investigated the effect of polyamine depletion on chromatin organization by comparing wild-type and knockout mice. As gender was not the focus of this study and not a critical factor, mice were randomly assigned to groups regardless of sex.
Field-collected samples	No field collected samples were used in the study.
Ethics oversight	All mice were bred and maintained under specific pathogen free conditions under protocols approved by the Animal Care and Use Committee (IACUC) of the Johns Hopkins University, Baltimore, USA, in accordance with the Guide for the Care and Use of Animals.

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

Clinical data

Policy information about [clinical studies](#)

All manuscripts should comply with the ICMJE [guidelines for publication of clinical research](#) and a completed [CONSORT checklist](#) must be included with all submissions.

Clinical trial registration	
Study protocol	
Data collection	
Outcomes	

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	
Novel plant genotypes	
Authentication	

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 <i>May remain private before publication.</i>	NCBI GEO under accession number GSE252941
Files in database submission	Detail information could be found at GSE252941
Genome browser session (e.g. UCSC)	no longer applicable

Methodology

Replicates	3 biological replicates
Sequencing depth	All raw and processed data deposited at GSE252941
Antibodies	Detail information could be found at method section of main text
Peak calling parameters	Detail information could be found at method section of main text
Data quality	All raw and processed data deposited at GSE252941

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

Instrument

Software

Cell population abundance

Gating strategy

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

Magnetic resonance imaging

Experimental design

Design type

Design specifications

Behavioral performance measures

Imaging type(s)

Field strength

Sequence & imaging parameters

Area of acquisition

Diffusion MRI

☐ Used

☐ Not used

Preprocessing

Preprocessing software

Normalization

Normalization template

Noise and artifact removal

Volume censoring

Statistical modeling & inference

Model type and settings

Effect(s) tested

Specify type of analysis: ☐ Whole brain ☐ ROI-based ☐ Both

Statistic type for inference

(See [Eklund et al. 2016](#))

Correction

Models & analysis

n/a | Involved in the study

☐ ☐ Functional and/or effective connectivity

☐ ☐ Graph analysis

☐ ☐ Multivariate modeling or predictive analysis

Functional and/or effective connectivity

Graph analysis

Multivariate modeling and predictive analysis

