

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	Sequencing data was collected using Illumina platform. Western blot (chemiluminescent) images were collected using a ChemiDoc MP from BioRad. Confocal microscopy images were obtained using Zeiss LSM900 with Airyscan 2. Live-cell super-resolution microscopy images were obtained using Zeiss Elyra 7.
Data analysis	Super-resolution microscopy images were analyzed using qSR software (Andrews et al. 2018). Confocal microscopy images were processed, wherever required, on Zen2 Blue Software (version 3.1 and 3.2) or Zen Black Software (version 2012, Service pack 5) by Zeiss. For the analysis and visualization of genomics and transcriptomics datasets, following tools and softwares were used: snakePipes (v. 2.5.1 for ChIP-Seq), snakePipes (v. 2.1.2 for TT-Seq), featureCounts (v.2.0.0), DESeq2 (v.1.26.0), RStudio (v. 4.1), ggplot2(v.3.3.5), pyGenomeTracks (v.3.7), EnhancedVolcano (v. 1.12.0), deepTools (v. 3.5.6), DiffBind (v. 3.4.11), CutAdapt (v. 3.5), UMI-tools (v. 1.1.2), BWA-MEM2 (v. 2.3.0), samtools (v. 1.22.1), sambamba (v. 0.8.1), bedtools (v. 2.31.1), PolTools tsrFinder (v. 1.0.7), STAR (v. 2.7.4a)

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](#)

All the NGS datasets and differential expression analysis tables generated in this study are available via the Gene Expression Omnibus (GSE271982).

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	N/A
Reporting on race, ethnicity, or other socially relevant groupings	N/A
Population characteristics	N/A
Recruitment	N/A
Ethics oversight	N/A

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	Sample size, number of replicates, number of clones, error bars and statistical tests were chosen based on accepted practices in the field and stated in each figure legend. Generally, experiments were performed independently and reproduced using at least 3 independent replicates. Exceptions to this are indicated in the figure legends and methods section.
Data exclusions	No data were excluded from the analyses performed in this paper.
Replication	All experiments were performed at least two times. All replication efforts yielded successful outcomes, demonstrating consistent results. Details on replication of each individual experiment together with the statistical parameters used are provided in each figure legend and the method section.
Randomization	Samples were allocated into experimental groups randomly.
Blinding	Blinding was not relevant as the analytical techniques employed did not involve subjective evaluations; instead, they generated readily interpretable outputs that were not susceptible to investigator-induced biases.

Behavioural & social sciences study design

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

Study description	Briefly describe the study type including whether data are quantitative, qualitative, or mixed-methods (e.g. qualitative cross-sectional, quantitative experimental, mixed-methods case study).
Research sample	State the research sample (e.g. Harvard university undergraduates, villagers in rural India) and provide relevant demographic

Research sample	<i>information (e.g. age, sex) and indicate whether the sample is representative. Provide a rationale for the study sample chosen. For studies involving existing datasets, please describe the dataset and source.</i>
Sampling strategy	<i>Describe the sampling procedure (e.g. random, snowball, stratified, convenience). Describe the statistical methods that were used to predetermine sample size OR if no sample-size calculation was performed, describe how sample sizes were chosen and provide a rationale for why these sample sizes are sufficient. For qualitative data, please indicate whether data saturation was considered, and what criteria were used to decide that no further sampling was needed.</i>
Data collection	<i>Provide details about the data collection procedure, including the instruments or devices used to record the data (e.g. pen and paper, computer, eye tracker, video or audio equipment) whether anyone was present besides the participant(s) and the researcher, and whether the researcher was blind to experimental condition and/or the study hypothesis during data collection.</i>
Timing	<i>Indicate the start and stop dates of data collection. If there is a gap between collection periods, state the dates for each sample cohort.</i>
Data exclusions	<i>If no data were excluded from the analyses, state so OR if data were excluded, provide the exact number of exclusions and the rationale behind them, indicating whether exclusion criteria were pre-established.</i>
Non-participation	<i>State how many participants dropped out/declined participation and the reason(s) given OR provide response rate OR state that no participants dropped out/declined participation.</i>
Randomization	<i>If participants were not allocated into experimental groups, state so OR describe how participants were allocated to groups, and if allocation was not random, describe how covariates were controlled.</i>

Ecological, evolutionary & environmental sciences study design

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

Study description	<i>Briefly describe the study. For quantitative data include treatment factors and interactions, design structure (e.g. factorial, nested, hierarchical), nature and number of experimental units and replicates.</i>
Research sample	<i>Describe the research sample (e.g. a group of tagged <i>Passer domesticus</i>, all <i>Stenocereus thurberi</i> within Organ Pipe Cactus National Monument), and provide a rationale for the sample choice. When relevant, describe the organism taxa, source, sex, age range and any manipulations. State what population the sample is meant to represent when applicable. For studies involving existing datasets, describe the data and its source.</i>
Sampling strategy	<i>Note the sampling procedure. Describe the statistical methods that were used to predetermine sample size OR if no sample-size calculation was performed, describe how sample sizes were chosen and provide a rationale for why these sample sizes are sufficient.</i>
Data collection	<i>Describe the data collection procedure, including who recorded the data and how.</i>
Timing and spatial scale	<i>Indicate the start and stop dates of data collection, noting the frequency and periodicity of sampling and providing a rationale for these choices. If there is a gap between collection periods, state the dates for each sample cohort. Specify the spatial scale from which the data are taken</i>
Data exclusions	<i>If no data were excluded from the analyses, state so OR if data were excluded, describe the exclusions and the rationale behind them, indicating whether exclusion criteria were pre-established.</i>
Reproducibility	<i>Describe the measures taken to verify the reproducibility of experimental findings. For each experiment, note whether any attempts to repeat the experiment failed OR state that all attempts to repeat the experiment were successful.</i>
Randomization	<i>Describe how samples/organisms/participants were allocated into groups. If allocation was not random, describe how covariates were controlled. If this is not relevant to your study, explain why.</i>
Blinding	<i>Describe the extent of blinding used during data acquisition and analysis. If blinding was not possible, describe why OR explain why blinding was not relevant to your study.</i>

Did the study involve field work? ☐ Yes ☐ No

Field work, collection and transport

Field conditions	<i>Describe the study conditions for field work, providing relevant parameters (e.g. temperature, rainfall).</i>
Location	<i>State the location of the sampling or experiment, providing relevant parameters (e.g. latitude and longitude, elevation, water depth).</i>
Access & import/export	<i>Describe the efforts you have made to access habitats and to collect and import/export your samples in a responsible manner and in compliance with local, national and international laws, noting any permits that were obtained (give the name of the issuing authority, the date of issue, and any identifying information).</i>

Disturbance

Describe any disturbance caused by the study and how it was minimized.

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

MOF (WB 1:1000 dilution), Abcam Cat#ab200660, clone EPR15803, Lot#GR3247613-1
 V5-HRP (WB: 1:1000 dilution), Invitrogen Cat#46-0708, Lot#2735075
 H4K16ac (WB 1:1000 dilution, ChIP: 1.5ul/IP), Millipore Cat#07329, Lot#3429632
 Beta-Actin-HRP (WB 1:5000 dilution), Santa Cruz Cat#sc-47778, Lot#B0221
 H4-HRP (WB, 1:1000 dilution), Abcam Cat#ab197517, Lot#GR3357384-6
 V5 (ChIP: 2.5-3 µL/IP, IF: 1/500), CST Cat#D3H8Q, Lot#7
 FLAG M2 (ChIP:2.5-3 µL/IP, WB: 1/1000), Sigma F1804
 H4K5ac (ChIP: 2 µg/IP, WB: 1/1000), Abcam Ab51997, Lot 1000211-1
 H4K8ac (ChIP: 2 µg/IP, WB: 1/1000), Abcam Ab45166, Lot: GR3273232-6
 H4K12ac (ChIP: 2 µg/IP, WB: 1/1000), Abcam Ab46983, Lot:1026765-3
 H4K16ac (ChIP: 2 µg/IP, WB: 1/1000), Abcam Ab109463, Lot: GR3357884-18
 BRD2 (ChIP: 2.5-3 µL/IP, WB: 1/1000, IF: 1/500), Bethyl A302-583A, Lot #7
 BRD3 (ChIP: 2.5-3 µL/IP, WB: 1/1000, IF: 1/500), Active Motif Cat # 61489
 BRD4 (WB 1:1000 dilution, ChIP: 3ug/IP), Bethyl cat#A301-985A100, Lot# 8
 RNA POL II CTD (ChIP:3ug/IP), MAB Institute, Cat#MCA-MAB10601 clone MAB10601, Lot#21028
 H3K9ac (WB: 1/1000, ChIP: 3µL/IP), CST #C5B11, Lot #13
 H3K27ac (WB: 1/1000, ChIP: 3µL/IP), Active Motif #39133, Lot#31521015
 H3K14ac (WB: 1/1000, ChIP: 3µL/IP), Active Motif #61433, Lot#20319004
 H3-HRP (WB: 1/1000), CST #12648S, Lot #1
 RPB1 NTD (ChIP: 3µL/IP), CST #D8L4Y, Lot #6

Validation

MOF (Abcam Cat#A300-992A), was validated in a published study through WBs of the respective knockout system in brain tissue (Sheikh BN et al, Nat Cell Biol, 2020).
 BRD4 (Bethyl Cat#A301-985A100) was validated in a previous study through dBet treatment followed by WB in mouse ESCs through WB (Gaub et al, Nat Comms 2020).
 RNA POLII (MAB Institute, Cat#MCA-MAB10601) was validated by the manufacturer (https://www.mblintl.com/assets/MAB10601_ver1.1.pdf).
 H4K16Ac (Millipore Cat#07329) was validated in a previous study using human dermal fibroblasts by IF, WB and ChIP-qPCR (Basilicata MF. et al., Nat Gen, 2018).
 β-Actin-HRP (Santa Cruz Cat#sc-47778) was validated in a previous study through WB of subcellular fractions of Hela cells (Chatterjee et al, Cell, 2016).
 H4-HRP (WB, 1:1000 dilution), Abcam Cat#ab197517 was validated by the manufacturer by using recombinant H4 (https://www.abcam.com/hrp-histone-h4-antibody-mabcam-31830-ab197517.html).
 BRD2 (Bethyl A302-583A) has been validated in this study using the degenon mESCs.
 BRD3 (Active Motif Cat#61489) has been validated in this study using dBET6 treatment.
 V5-HRP (Invitrogen Cat#46-0708) has been validated in this study using degenon mESCs.
 H4-ac antibodies have been validated in Radzisheuskaya et al. (2021) using a histone peptide array and ChIP-Seq experiments.
 Anti-FLAG M2 antibody (Sigma, F1804) has been validated previously (Keller Valsecchi & Basilicata et al., 2021).
 V5 (CST Cat#D3H8Q) has been validated in this study by IF and ChIP-seq experiments using degenon mESCs.
 H3K9ac (CST # C5B11) has been validated by the manufacturer: https://www.cellsignal.com/about-us/our-approach-process/validation-histone-modification?srsltid=AfmBOopNfNfe2_YuzPPgnK_hqPd5yrnF3i-sGDtDmspY5Nk1_7QXQmbU
 H3K27ac (Active Motif #39133) has been validated by the manufacturer: https://www.activemotif.com/documents/tds/39133.pdf
 H3K14ac (Active Motif #61433) has been validated in a previous publication: Pena-Hernandez et al. (2021)

Eukaryotic cell lines

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

Cell line source(s)	WT26 male mouse embryonic stem cell line was a kind gift of Thomas Jenuwein. The rest of the cell lines reported in this study are generated by genome editing of this cell line using CRISPR-Cas9 and TALEN. NIH-3T3 was a kind gift of Rolf Kemler and Hepa 1-6 cells were obtained from BIOS Toolbox.
Authentication	WT26 male mouse ESCs have been extensively characterized in previous studies (Lehnertz et al. 2003, Chelmicki et al. 2014). The genome-edited cell lines reported in this study have been confirmed by western blot and genomic DNA PCR to ensure their genotypes.
Mycoplasma contamination	The cell lines have been tested regularly for mycoplasma contamination and all of them were negative.
Commonly misidentified lines (See ICLAC register)	N/A

Palaeontology and Archaeology

Specimen provenance	<i>Provide provenance information for specimens and describe permits that were obtained for the work (including the name of the issuing authority, the date of issue, and any identifying information). Permits should encompass collection and, where applicable, export.</i>
Specimen deposition	<i>Indicate where the specimens have been deposited to permit free access by other researchers.</i>
Dating methods	<i>If new dates are provided, describe how they were obtained (e.g. collection, storage, sample pretreatment and measurement), where they were obtained (i.e. lab name), the calibration program and the protocol for quality assurance OR state that no new dates are provided.</i>
☐ Tick this box to confirm that the raw and calibrated dates are available in the paper or in Supplementary Information.	
Ethics oversight	<i>Identify the organization(s) that approved or provided guidance on the study protocol, OR state that no ethical approval or guidance was required and explain why not.</i>

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	<i>For laboratory animals, report species, strain and age OR state that the study did not involve laboratory animals.</i>
Wild animals	<i>Provide details on animals observed in or captured in the field; report species and age where possible. Describe how animals were caught and transported and what happened to captive animals after the study (if killed, explain why and describe method; if released, say where and when) OR state that the study did not involve wild animals.</i>
Reporting on sex	<i>Indicate if findings apply to only one sex; describe whether sex was considered in study design, methods used for assigning sex. Provide data disaggregated for sex where this information has been collected in the source data as appropriate; provide overall numbers in this Reporting Summary. Please state if this information has not been collected. Report sex-based analyses where performed, justify reasons for lack of sex-based analysis.</i>
Field-collected samples	<i>For laboratory work with field-collected samples, describe all relevant parameters such as housing, maintenance, temperature, photoperiod and end-of-experiment protocol OR state that the study did not involve samples collected from the field.</i>
Ethics oversight	<i>Identify the organization(s) that approved or provided guidance on the study protocol, OR state that no ethical approval or guidance was required and explain why not.</i>

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	<i>Provide the trial registration number from ClinicalTrials.gov or an equivalent agency.</i>
Study protocol	<i>Note where the full trial protocol can be accessed OR if not available, explain why.</i>

Data collection

Describe the settings and locales of data collection, noting the time periods of recruitment and data collection.

Outcomes

Describe how you pre-defined primary and secondary outcome measures and how you assessed these measures.

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

N/A

Novel plant genotypes

N/A

Authentication

N/A

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.

The raw sequencing datasets and associated processed files have been submitted to the Gene Expression Omnibus (GEO: GSE271982) repository.

Files in database submission

MOF Degron mESCs: Control_Input_for_V5-ChIP_Rep1

MOF Degron mESCs: Control_Input_for_V5-ChIP_Rep2

MOF Degron mESCs: Auxin_Input_for_V5-ChIP_Rep1

MOF Degron mESCs: Auxin_Input_for_V5-ChIP_Rep2

MOF Degron mESCs: Control_IP_for_V5-ChIP_Rep1
 MOF Degron mESCs: Control_IP_for_V5-ChIP_Rep2
 MOF Degron mESCs: Auxin_IP_for_V5-ChIP_Rep1
 MOF Degron mESCs: Auxin_IP_for_V5-ChIP_Rep2
 MOF Degron mESCs: Control_Input_for_H4ac-ChIP_Rep1
 MOF Degron mESCs: Control_Input_for_H4ac-ChIP_Rep2
 MOF Degron mESCs: Control_Input_for_H4ac-ChIP_Rep3
 MOF Degron mESCs: Auxin_Input_for_H4ac-ChIP_Rep1
 MOF Degron mESCs: Auxin_Input_for_H4ac-ChIP_Rep2
 MOF Degron mESCs: Auxin_Input_for_H4ac-ChIP_Rep3
 MOF Degron mESCs: Control_IP_for_H4K5ac-ChIP_Rep1
 MOF Degron mESCs: Control_IP_for_H4K5ac-ChIP_Rep2
 MOF Degron mESCs: Control_IP_for_H4K5ac-ChIP_Rep3
 MOF Degron mESCs: Auxin_IP_for_H4K5ac-ChIP_Rep1
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 MOF Degron mESCs: Control_IP_for_H4K8ac-ChIP_Rep2
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 MOF Degron mESCs: Control_IP_for_H4K16ac-ChIP_Rep2
 MOF Degron mESCs: Control_IP_for_H4K16ac-ChIP_Rep3
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 MOF Degron mESCs: Auxin_Input_for_BRD-ChIP_Rep2
 MOF Degron mESCs: Auxin_Input_for_BRD-ChIP_Rep3
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 MOF Degron mESCs: Control_IP_for_BRD2-ChIP_Rep3
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 MOF Degron mESCs: Auxin_IP_for_BRD2-ChIP_Rep3
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 MOF Degron mESCs: Control_IP_for_BRD4-ChIP_Rep3
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 MOF Degron mESCs: Auxin_IP_for_BRD4-ChIP_Rep2
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 MOF Degron mESCs: Control_IP_for_TAF1-ChIP_Rep3
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 MOF Degron mESCs: Auxin_IP_for_TAF1-ChIP_Rep2
 MOF Degron mESCs: Auxin_IP_for_TAF1-ChIP_Rep3
 MOF Degron mESCs: Control_Input_for_BRD3-ChIP_Rep1
 MOF Degron mESCs: Control_Input_for_BRD3-ChIP_Rep2
 MOF Degron mESCs: Control_Input_for_BRD3-ChIP_Rep3
 MOF Degron mESCs: Auxin_Input_for_BRD3-ChIP_Rep1
 MOF Degron mESCs: Auxin_Input_for_BRD3-ChIP_Rep2
 MOF Degron mESCs: Auxin_Input_for_BRD3-ChIP_Rep3
 MOF Degron mESCs: Control_IP_for_BRD3-ChIP_Rep1
 MOF Degron mESCs: Control_IP_for_BRD3-ChIP_Rep2
 MOF Degron mESCs: Control_IP_for_BRD3-ChIP_Rep3
 MOF Degron mESCs: Auxin_IP_for_BRD3-ChIP_Rep1
 MOF Degron mESCs: Auxin_IP_for_BRD3-ChIP_Rep2
 MOF Degron mESCs: Auxin_IP_for_BRD3-ChIP_Rep3

Genome browser session
(e.g. [UCSC](#))

N/A

Methodology

Replicates	ChIP profiles of at least two independent replicates were generated per antibody per sample.
Sequencing depth	For ChIP-Seq samples, there is a sequencing depth of 30 Mio reads. For nascent RNA samples, there is at least a sequencing depth of 60 Mio reads. For total RNA samples, there is a sequencing depth of at least 30 Mio reads.
Antibodies	V5 (ChIP: 2.5-3 µL/IP, IF: 1/500), CST Cat#D3H8Q, Lot#7 FLAG M2 (ChIP: 2.5-3 µL/IP), Sigma F1804 H4K5ac (ChIP: 2 µg/IP), Abcam Ab51997, Lot 1000211-1 H4K8ac (ChIP: 2 µg/IP), Abcam Ab45166, Lot: GR3273232-6 H4K12ac (ChIP: 2 µg/IP), Abcam Ab46983, Lot:1026765-3 H4K16ac (ChIP: 2 µg/IP), Abcam Ab109463, Lot: GR3357884-18 BRD2 (ChIP: 2.5-3 µL/IP, WB: 1/1000), Bethyl A302-583A, Lot #7 BRD3 (ChIP: 2.5-3 µL/IP, WB: 1/1000), Active Motif Cat # 61489 BRD4 (WB 1:1000 dilution, ChIP: 3µg/IP), Bethyl cat#A301-985A100, Lot# 8 RNA POL II CTD (ChIP:3µg/IP), MAB Institute, Cat#MCA-MAB10601 clone MAB10601, Lot#21028 H3K9ac (WB: 1/1000, ChIP: 3µL/IP), CST #C5B11, Lot #13 H3K27ac (WB: 1/1000, ChIP: 3µL/IP), Active Motif #39133, Lot#31521015 H3K14ac (WB: 1/1000, ChIP: 3µL/IP), Active Motif #61433, Lot#20319004 RBP1 NTD (ChIP: 3µL/IP), CST #D8L4Y, Lot #6
Peak calling parameters	For peak calling on individual replicates, MACS2 was used with standard parameters to check for sample quality. To identify consistent peaks across replicates, PePr pipeline was used with its standard parameters.
Data quality	MultiQC from Snakepipes has been used to integrate all the quality control information, including FASTQC, mapping quality and GC content etc. Before and after deep-sequencing, fragment sizes have been checked and paired-end sequencing of sufficient depth has been achieved for all the samples.
Software	snakePipes (v. 2.5.1), deepTools (v. 3.5.3), PePr, DiffBind (v. 3.4.11).

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	<i>Describe the sample preparation, detailing the biological source of the cells and any tissue processing steps used.</i>
Instrument	<i>Identify the instrument used for data collection, specifying make and model number.</i>
Software	<i>Describe the software used to collect and analyze the flow cytometry data. For custom code that has been deposited into a community repository, provide accession details.</i>
Cell population abundance	<i>Describe the abundance of the relevant cell populations within post-sort fractions, providing details on the purity of the samples and how it was determined.</i>
Gating strategy	<i>Describe the gating strategy used for all relevant experiments, specifying the preliminary FSC/SSC gates of the starting cell population, indicating where boundaries between "positive" and "negative" staining cell populations are defined.</i>

☐ 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	<i>Indicate task or resting state; event-related or block design.</i>
Design specifications	<i>Specify the number of blocks, trials or experimental units per session and/or subject, and specify the length of each trial or block (if trials are blocked) and interval between trials.</i>
Behavioral performance measures	<i>State number and/or type of variables recorded (e.g. correct button press, response time) and what statistics were used</i>

Behavioral performance measures *to establish that the subjects were performing the task as expected (e.g. mean, range, and/or standard deviation across subjects).*

Acquisition

Imaging type(s) *Specify: functional, structural, diffusion, perfusion.*

Field strength *Specify in Tesla*

Sequence & imaging parameters *Specify the pulse sequence type (gradient echo, spin echo, etc.), imaging type (EPI, spiral, etc.), field of view, matrix size, slice thickness, orientation and TE/TR/flip angle.*

Area of acquisition *State whether a whole brain scan was used OR define the area of acquisition, describing how the region was determined.*

Diffusion MRI ☐ Used ☐ Not used

Preprocessing

Preprocessing software *Provide detail on software version and revision number and on specific parameters (model/functions, brain extraction, segmentation, smoothing kernel size, etc.).*

Normalization *If data were normalized/standardized, describe the approach(es): specify linear or non-linear and define image types used for transformation OR indicate that data were not normalized and explain rationale for lack of normalization.*

Normalization template *Describe the template used for normalization/transformation, specifying subject space or group standardized space (e.g. original Talairach, MNI305, ICBM152) OR indicate that the data were not normalized.*

Noise and artifact removal *Describe your procedure(s) for artifact and structured noise removal, specifying motion parameters, tissue signals and physiological signals (heart rate, respiration).*

Volume censoring *Define your software and/or method and criteria for volume censoring, and state the extent of such censoring.*

Statistical modeling & inference

Model type and settings *Specify type (mass univariate, multivariate, RSA, predictive, etc.) and describe essential details of the model at the first and second levels (e.g. fixed, random or mixed effects; drift or auto-correlation).*

Effect(s) tested *Define precise effect in terms of the task or stimulus conditions instead of psychological concepts and indicate whether ANOVA or factorial designs were used.*

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

Statistic type for inference *Specify voxel-wise or cluster-wise and report all relevant parameters for cluster-wise methods.*

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

Correction *Describe the type of correction and how it is obtained for multiple comparisons (e.g. FWE, FDR, permutation or Monte Carlo).*

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 *Report the measures of dependence used and the model details (e.g. Pearson correlation, partial correlation, mutual information).*

Graph analysis *Report the dependent variable and connectivity measure, specifying weighted graph or binarized graph, subject- or group-level, and the global and/or node summaries used (e.g. clustering coefficient, efficiency, etc.).*

Multivariate modeling and predictive analysis *Specify independent variables, features extraction and dimension reduction, model, training and evaluation metrics.*