

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
<input type="checkbox"/>	<input checked="" type="checkbox"/> The exact sample size (<i>n</i>) for each experimental group/condition, given as a discrete number and unit of measurement
<input type="checkbox"/>	<input checked="" type="checkbox"/> A statement on whether measurements were taken from distinct samples or whether the same sample was measured repeatedly
<input type="checkbox"/>	<input checked="" type="checkbox"/> 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>
<input checked="" type="checkbox"/>	<input type="checkbox"/> A description of all covariates tested
<input type="checkbox"/>	<input checked="" type="checkbox"/> A description of any assumptions or corrections, such as tests of normality and adjustment for multiple comparisons
<input type="checkbox"/>	<input checked="" type="checkbox"/> 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)
<input type="checkbox"/>	<input checked="" type="checkbox"/> 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>
<input checked="" type="checkbox"/>	<input type="checkbox"/> For Bayesian analysis, information on the choice of priors and Markov chain Monte Carlo settings
<input checked="" type="checkbox"/>	<input type="checkbox"/> For hierarchical and complex designs, identification of the appropriate level for tests and full reporting of outcomes
<input checked="" type="checkbox"/>	<input type="checkbox"/> 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 software was used for data collection
Data analysis	Cutadapt (v2.5), Tophat2 (v2.1.1), DESeq2 (v1.24.0), Bowtie2 (v2.3.3.1), SICER (v1.1), BEDTools (v2.29.0), htseq (v0.7.0), SAMtools (v1.8), in-house python script for normalization of read coverage at genome features, in-house python script for GO Term enrichment testing with FDR correction, XGBoost (v1.4.1.1), DescTools (v0.99.43)

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 raw and processed sequencing data generated in this study have been submitted to the NCBI Gene Expression Omnibus (GEO; <https://www.ncbi.nlm.nih.gov/geo/>) under accession number GSE196887.

Human research participants

Policy information about [studies involving human research participants and Sex and Gender in Research](#).

Reporting on sex and gender

Population characteristics

Recruitment

Ethics oversight

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

Life sciences study design

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

Sample size

Data exclusions

Replication

Randomization

Blinding

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
<input type="checkbox"/>	<input checked="" type="checkbox"/> Antibodies
<input checked="" type="checkbox"/>	<input type="checkbox"/> Eukaryotic cell lines
<input checked="" type="checkbox"/>	<input type="checkbox"/> Palaeontology and archaeology
<input checked="" type="checkbox"/>	<input type="checkbox"/> Animals and other organisms
<input checked="" type="checkbox"/>	<input type="checkbox"/> Clinical data
<input checked="" type="checkbox"/>	<input type="checkbox"/> Dual use research of concern

Methods

n/a	Involved in the study
<input type="checkbox"/>	<input checked="" type="checkbox"/> ChIP-seq
<input checked="" type="checkbox"/>	<input type="checkbox"/> Flow cytometry
<input checked="" type="checkbox"/>	<input type="checkbox"/> MRI-based neuroimaging

Antibodies

Antibodies used

Validation

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.

To review GEO accession GSE196887:

Go to <https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE196887>

Enter token cribcyamdpabbil into the box

Files in database submission

C01_1.fq.gz C01_2.fq.gz
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 GSE196887_root_SICER_df.tar.gz
 GSE196887_shoot_SICER_df.tar.gz
 GSE196887_shoot_SICER_df_K9.tar.gz

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

Provide a link to an anonymized genome browser session for "Initial submission" and "Revised version" documents only, to enable peer review. Write "no longer applicable" for "Final submission" documents.

Methodology

Replicates

Three independent biological replicates for each tissue and condition

Sequencing depth

All sequencing was paired end 2x150bp reads.

[sample]	[read pairs]	[unique concordant mapped pairs]
root-N INPUT-1	40,726,832	25,333,516
root-N INPUT-2	41,037,402	27,033,950
root-N INPUT-3	42,349,215	28,428,197
root+N INPUT-1	37,296,583	23,511,742
root+N INPUT-2	35,295,544	23,137,625
root+N INPUT-3	41,331,059	24,474,435
root-N K4me3-1	39,616,752	27,146,428
root-N K4me3-2	42,386,071	23,208,593
root-N K4me3-3	75,551,287	49,063,176
root+N K4me3-1	40,452,819	25,050,308
root+N K4me3-2	41,220,018	27,428,541
root+N K4me3-3	37,414,862	25,075,897
root-N K27ac-1	34,247,685	22,256,577
root-N K27ac-2	38,358,237	25,372,040
root-N K27ac-3	53,234,968	33,384,273
root+N K27ac-1	48,002,019	31,798,795
root+N K27ac-2	35,588,599	24,599,762
root+N K27ac-3	40,699,443	27,696,892
root-N K27me3-1	47,549,878	12,817,481
root-N K27me3-2	49,594,143	15,145,137
root-N K27me3-3	47,527,634	19,124,659
root+N K27me3-1	52,204,065	22,538,199
root+N K27me3-2	45,073,349	22,671,531
root+N K27me3-3	39,290,524	18,441,465
root-N K36me3-1	62,529,938	35,654,487
root-N K36me3-2	42,286,549	25,304,285
root-N K36me3-3	44,887,547	28,783,022
root+N K36me3-1	40,942,690	26,107,570
root+N K36me3-2	33,849,097	19,781,733
root+N K36me3-3	34,916,204	20,643,360
shoot-N INPUT-1	33,157,169	26,116,487
shoot-N INPUT-2	36,945,356	29,326,412
shoot-N INPUT-3	35,368,097	27,807,229
shoot+N INPUT-1	41,707,315	32,815,588
shoot+N INPUT-2	37,977,234	28,558,250
shoot+N INPUT-3	46,559,502	36,338,505
shoot-N K4me3-1	32,758,192	25,085,664
shoot-N K4me3-2	48,199,669	35,164,153
shoot-N K4me3-3	36,810,825	28,630,260

	shoot+N K4me3-1 35,542,805 26,876,197 shoot+N K4me3-2 36,227,384 27,937,978 shoot+N K4me3-3 37,165,829 28,100,955 shoot-N K27ac-1 43,830,887 30,575,311 shoot-N K27ac-2 36,267,217 24,384,385 shoot-N K27ac-3 40,275,418 27,922,767 shoot+N K27ac-1 34,547,391 24,820,416 shoot+N K27ac-2 41,152,573 30,439,443 shoot+N K27ac-3 46,700,030 32,854,377 shoot-N K27me3-1 33,559,976 26,337,264 shoot-N K27me3-2 37,680,987 27,970,871 shoot-N K27me3-3 35,754,049 27,844,668 shoot+N K27me3-1 36,333,975 28,025,110 shoot+N K27me3-2 40,372,440 30,752,874 shoot+N K27me3-3 40,761,982 31,262,594 shoot-N K36me3-1 35,126,029 27,529,200 shoot-N K36me3-2 41,961,379 33,559,414 shoot-N K36me3-3 32,710,937 25,848,260 shoot+N K36me3-1 38,524,595 30,278,024 shoot+N K36me3-2 39,474,776 31,772,212 shoot+N K36me3-3 46,539,714 36,651,443 shoot-N INPUT-4 31,963,532 11,000,998 shoot-N INPUT-5 33,905,357 14,248,223 shoot-N INPUT-6 33,420,422 19,302,850 shoot+N INPUT-4 32,941,875 17,277,013 shoot+N INPUT-5 29,734,019 12,335,668 shoot+N INPUT-6 28,786,293 10,998,991 shoot-N K9me2-4 34,257,248 21,131,927 shoot-N K9me2-5 41,508,405 15,363,862 shoot-N K9me2-6 34,613,805 16,837,490 shoot+N K9me2-4 36,453,698 20,047,934 shoot+N K9me2-5 29,506,286 14,285,624 shoot+N K9me2-6 33,353,501 16,099,272
Antibodies	H3K4me3 (Millipore Sigma 07473), H3K27ac (Millipore Sigma 07360), H3K27me3 (Millipore Sigma 07449), H3K36me3 (Abcam ab9050), H3K9me2 (Abcam ab1220)
Peak calling parameters	bowtie2 --threads 20 -x \$(Sl_genome_4.00) -1 \$(READ1.fq) -2 \$(READ2.fq) -S \$(OUTPUT.sam) sh SICER/SICER-df.sh \$[+N_ChIP_sample.bed] \$[+N_input_sample.bed] \$[-N_ChIP_sample.bed] \$[-N_input_sample.bed] 200 200 0.01 0.05 except for H3K27me3, where the parameters were 200 600 0.01 0.05
Data quality	Data quality was assured by only using consensus peaks present in the majority (2/3) of replicates and SICER performance was visually checked for accuracy in IGV.
Software	Cutadapt (v2.5), Bowtie2 (v2.3.3.1), SICER (v1.1), BEDTools (v2.29.0), SAMtools (v1.8), in-house python script for normalization of read coverage at genome features, in-house python script for GO Term enrichment testing with FDR correction, XGBoost (v1.4.1.1), DescTools (v0.99.43)