

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 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 (n) 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. F , t , r) with confidence intervals, effect sizes, degrees of freedom and P 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 type="checkbox"/> | <input checked="" type="checkbox"/> 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 Data were downloaded from NCBI GEO and ENCODE portal via BioQueue (2.0.0).

Data analysis Data were analyzed using following software tools: BioQueue (2.0.0), fastp (0.20.0), STAR (2.7.1a), samtools (1.11), Picard (2.19.2), Python (2.7.5 & 3.6.9), bedtools (2.29.2), deeptools (multiBamSummary, 3.3.2), numpy (1.19.4), pandas (1.1.4), scipy (1.5.2), statsmodels (0.11.0), pybedtools (0.8.1), pyBigWig (0.3.17), pysam (0.16.0.1), biopython (1.78), MACS2 (2.2.6), HOMER (4.11.1), FivePrime (d39ca4f), GROcapTSSMM (0.1), dREG (1.4.0), dREG.HD (1.0.1), Tfit (20eb2aa), TSScall (709d2f4), groHMM (1.26.0), STAN (2.20.0), bwa (0.7.17-r1188), Django (3.1.3), bedToBigBed (version 407), bigBedToBed (version 407), bigWigToBedGraph (version 399), bedGraphToBigWig (version 399), bigWigMerge (version 399), liftOver (version 399), JASPAR (version 2020).
The source code of PINTS is freely available at <https://github.com/hyulab/PINTS>. Analytic pipelines and scripts used to generate results that are reported in this study can be retrieved from https://github.com/hyulab/PINTS_analysis.

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 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

Processed TRE calls are publicly accessible via our web portal (<https://pints.yulab.org>). Data that support the findings of this study are available within the paper and

its supplementary information files. All sequencing data analyzed in this study were retrieved from public databases (NCBI GEO and ENCODE portal); lists of accessions are available in Supplementary Tables 1 and 4.

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 sizes were determined by data availability. No statistical method was used to predetermine sample size. -- We used all available libraries for each of the assays compared in this study.
Data exclusions	No data was excluded from analysis
Replication	Not applicable -- We performed only computational analysis of published data. All available data were used for analyses. Therefore experimental replication is not applicable. The number of repetitions for each analysis (when random subsampling is performed) is provided in the figure legends in the main manuscript and Supplementary Table 1.
Randomization	Not applicable -- no group-wise experimental testing was performed
Blinding	Not applicable -- no group-wise experimental testing was performed

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 checked="" type="checkbox"/>	<input 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"/> Human research participants
<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 checked="" type="checkbox"/>	<input type="checkbox"/> ChIP-seq
<input checked="" type="checkbox"/>	<input type="checkbox"/> Flow cytometry
<input checked="" type="checkbox"/>	<input type="checkbox"/> MRI-based neuroimaging