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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 Authors & Referees and the Editorial Policy Checklist.

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	SRA-Toolkit version 2.8.1
Data analysis	TECtool depends on the python packages HTSeq version 0.9.1, Bedtools version 2.26.0, Pybedtools version 0.7.10, pyfasta version 0.5.2, numpy version 1.13, scipy version 0.19 and scikit-learn version 0.19.0, pandas version 0.2 and progress version 1.3. Additional software was used for data analysis. These are the following: cutadapt version 1.13, STAR version v2.5.3a, samtools version 1.3, cufflinks version 2.2.1, salmon version 0.9.1, StringTie version 1.3.3, blast version 2.6.0. For analysis or plotting the following packages were additionally used. Python packages: Biopython version 1.70, matplotlib version 2.1.0, seaborn version 0.8.1, R packages: optparse version 1.6.0, rtracklayer version 1.38.3, biomaRt version 2.34.2, Gviz version 1.22.3, GenomicFeatures version 1.30.3, ggplot2 version 2.2.1, vioplot version 0.2.

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

Accession numbers of all data analysed in this study are listed in this published article (and its supplementary information files).

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   ☐ Ecological, evolutionary & environmental 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	Our computational method was tested on previously published data sets. We have performed quality checks and considered available samples/replicates in our analysis. Sample sizes are reported where statistical tests were performed.
Data exclusions	All accession numbers of data included/excluded in this study are specified in the supplementary materials.
Replication	Not applicable. Our study involved the development of a computational method which we applied to publicly available data sets.
Randomization	Not applicable. Our study involved the development of a computational method which we applied to publicly available data sets.
Blinding	Not applicable. Our study involved the development of a computational method which we applied to publicly available data sets.

Reporting for specific materials, systems and methods

Materials & experimental systems

n/a	Involved in the study
☒	☐ Unique biological materials
☒	☐ Antibodies
☒	☐ Eukaryotic cell lines
☒	☐ Palaeontology
☒	☐ Animals and other organisms
☒	☐ Human research participants

Methods

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