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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 <u>Authors & Referees</u> and the <u>Editorial Policy Checklist</u>.

Statistics	
For all statistical analys	es, confirm that the following items are present in the figure legend, table legend, main text, or Methods section.
n/a Confirmed	
☐ ☐ The exact sam	pple size (n) for each experimental group/condition, given as a discrete number and unit of measurement
A statement of	on whether measurements were taken from distinct samples or whether the same sample was measured repeatedly
The statistical Only common to	test(s) used AND whether they are one- or two-sided ests 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
I X I I I	ion of the statistical parameters including central tendency (e.g. means) or other basic estimates (e.g. regression coefficient) (e.g. standard deviation) or associated estimates of uncertainty (e.g. confidence intervals)
For null hypot	thesis testing, the test statistic (e.g. F , t , r) with confidence intervals, effect sizes, degrees of freedom and P value noted sexact values whenever suitable.
For Bayesian a	analysis, information on the choice of priors and Markov chain Monte Carlo settings
For hierarchic	al and complex designs, identification of the appropriate level for tests and full reporting of outcomes
Estimates of e	effect sizes (e.g. Cohen's d , Pearson's r), indicating how they were calculated
•	Our web collection on <u>statistics for biologists</u> contains articles on many of the points above.
Software and c	code
Policy information abou	ut <u>availability of computer code</u>
Data collection	Next-generation sequencing (Illumina).
Data analysis	Capture-C data were analyzed using scripts available at https://github.com/Hughes-Genome-Group/CCseqBasicS. Tri-C data were analyzed using scripts available at https://github.com/Hughes-Genome-Group/CCseqBasicS and https://github.com/oudelaar/TriC.
	om algorithms or software that are central to the research but not yet described in published literature, software must be made available to editors/reviewers. deposition in a community repository (e.g. GitHub). See the Nature Research guidelines for submitting code & software for further information.
Data	
- Accession codes, un - A list of figures that	ut <u>availability of data</u> include a <u>data availability statement</u> . This statement should provide the following information, where applicable: ique identifiers, or web links for publicly available datasets have associated raw data restrictions on data availability
All sequencing data are s	ubmitted to the NCBI Gene Expression Omnibus (GEO; http://www.ncbi.nlm.nih.gov/geo/) under accession number GSE130308.
Field-speci	fic reporting
Please select the one b	elow that is the best fit for your research. If you are not sure, read the appropriate sections before making your selection.
M Life sciences	Rehavioural & social sciences

Life sciences study design

Materials & experimental systems

n/a | Involved in the study

All studies must disclose on these points even when the disclosure is negative.		
Sample size	All Capture-C and Tri-C experiments were performed in biological triplicates to ensure robustness.	
Data exclusions	No data exclusions.	
Replication	Experiments were performed in biological triplicates and the observed biological effects of interest were very robust between replicates.	
Randomization	We studied primary cells derived from 3 wild type mice and 3 mice with mutations in CTCF-binding sites.	
Blinding	Blinding is not relevant to the structure of our study; all data were analyzed in an unbiased way using the exact same procedure.	

Reporting for specific materials, systems and methods

Methods

n/a Involved in the study

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.

Antibodies	ChIP-seq
Eukaryotic cell lines	Flow cytometry
Palaeontology	MRI-based neuroimaging
Animals and other orga	anisms
Human research partic	cipants
Clinical data	
'	
Animals and other	organisms
Policy information about stud	lies involving animals; ARRIVE guidelines recommended for reporting animal research
Laboratory animals	Mus musculus, C57BL/6, female, 3-9 months old.
Wild animals	Our study did not involve wild animals.
Field-collected samples	Our study did not involve samples collected from the field.
Ethics oversight	Experimental procedures were in accordance with the European Union Directive 2010/63/EU and/or the UK Animals (Scientific Procedures) Act (1986) and protocols were approved through the Oxford University Local Ethical Review process.

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