nature portfolio

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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	Public RNA-seq data was collected from TCGA (The Cancer Genome Atlas); imaging data was captured by stimulated emission depletion (STED) microscope (Leica, TCS SP8 STED 3X), spinning disk confocal system (Nikon, live SR CSU W), confocal microscope (Carl ZEISS, LSM880), custom-built microscope (Olympus, IX83); FACS data was collected by summit 6.0
Data analysis	R (version 3.6.0), MATLAB (R2020b), Hisat2 (version 2.0.5), bowtie2 (version 2.3.5), Enrichr (https://maayanlab.cloud/Enrichr/), Picard (version 2.9.1), HiC-Pro (version 2.7.9), Perl script matrix2insulation.pl (Crane et al., 2015), SAMtools (version 1.9), MACS2 (version 2.2.5), bedtools (version 2.29.2), Imaris (version 9.7), FIJI (Fiji Is Just ImageJ), Oligominer (https://github.com/brianbeliveau/Oligominer), FlowJo R packages: GenomicFeatures(version 1.30.3), Rsamtools (version 1.30.0), GenomicAlignments(version 1.14.2), DESeq2(version 1.28.0), HiTC(version 1.34.0).

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

To review GEO accession GSE183186 (https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE183186)
Enter token cjmromamlrefver into the box

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	Sample size was not determined by calculations. The sample size (n) of each experiment is provided in the figure/table legends in the main manuscript and supplementary information files.
Data exclusions	No data was excluded from the analysis.
Replication	All experiments were performed a minimum of two times. Next-generation sequencing datasets were generated and analyzed in biological triplicates(RNA-seq). Imaging datasets were generated and analyzed in multiple biological replicates. No replicates were excluded from analyses presented.
Randomization	Samples were not randomized and were grouped according to whether Rad21 was up-regulated.
Blinding	The investigators were not blinded during data collection as the biological groups were well defined and handled in parallel.

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
☒	☐ Human research participants
☒	☐ Clinical data
☒	☐ Dual use research of concern

Methods

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

Antibodies

Antibodies used

Commercial primary antibodies:
Rabbit polyclonal to Histone H2B, abcam (ab1790)
Rabbit polyclonal to Histone H3, abcam (ab1791)
Mouse monoclonal to Histone H3, Ruiying Biological (RLM3038)
Rabbit polyclonal to Histone H3 (tri methyl K4), abcam (ab8580)
Mouse monoclonal to Histone H3 (tri methyl K27), abcam (ab6002)
Rabbit monoclonal to CTCF, abcam (ab128873)
Rabbit polyclonal to RAD21 Antibody, Thermo Scientific (PA5-54128)
Rabbit monoclonal to SMC1A, abcam (ab133643)

Rabbit polyclonal to SMC3, abcam (ab9263)
Goat polyclonal to SA1, abcam (ab4455)
Rabbit polyclonal to NIPBL, abcam (ab220952)
Rabbit monoclonal to Scc4, abcam (ab183033)
Rabbit monoclonal to β-actin, ABclonal (AC026)
Commercial secondary antibodies:
Donkey anti-Rabbit IgG (H+L) Secondary Antibody, Alexa Fluor 488, Thermo Scientific (A-21206)
Donkey anti-Mouse IgG (H+L) Highly Cross-Adsorbed Secondary Antibody, Alexa Fluor 488, Thermo Scientific (A-21202)
Donkey anti-Rabbit IgG (H+L) Highly Cross-Adsorbed Secondary Antibody, Alexa Fluor 594, Thermo Scientific (A-21207)
Donkey anti-Mouse IgG (H+L) ReadyProbes™ Secondary Antibody, Alexa Fluor 594, Thermo Scientific (R37115)

Validation

The antibodies have been used in previous studies:
Rabbit polyclonal to Histone H2B, abcam (ab1790), Norin U et al. Endophilin A2 deficiency protects rodents from autoimmune arthritis by modulating T cell activation. Nat Commun 12:610 (2021).
Rabbit polyclonal to Histone H3, abcam (ab1791), Yuan L et al. The transcriptional repressors VAL1 and VAL2 recruit PRC2 for genome-wide Polycomb silencing in Arabidopsis. Nucleic Acids Res 49:98-113 (2021).
Rabbit polyclonal to Histone H3 (tri methyl K4), abcam (ab8580), Aslam MA et al. Histone methyltransferase DOT1L controls state-specific identity during B cell differentiation. EMBO Rep 22:e51184 (2021).
Mouse monoclonal to Histone H3 (tri methyl K27), abcam (ab6002), Cao Z et al. KDM6B is an androgen regulated gene and plays oncogenic roles by demethylating H3K27me3 at cyclin D1 promoter in prostate cancer. Cell Death Dis 12:2 (2021).
Rabbit monoclonal to CTCF, abcam (ab128873), Li Y et al. The structural basis for cohesin-CTCF-anchored loops. Nature 578:472-476 (2020).
Rabbit monoclonal to SMC1A, abcam (ab133643), Shah VJ & Maddika S CRL7SMU1 E3 ligase complex-driven H2B ubiquitylation functions in sister chromatid cohesion by regulating SMC1 expression. J Cell Sci 131:N/A (2018).
Rabbit polyclonal to SMC3, abcam (ab9263), Olan I et al. Transcription-dependent cohesin repositioning rewires chromatin loops in cellular senescence. Nat Commun 11:6049 (2020).
Goat polyclonal to SA1, abcam (ab4455), Leman AR et al. Human Timeless and Tipin stabilize replication forks and facilitate sister-chromatid cohesion. J Cell Sci 123:660-70 (2010). WB, IP ; Human.
Rabbit monoclonal to Scc4, abcam (ab183033), Parenti I et al. MAU2 and NIPBL Variants Impair the Heterodimerization of the Cohesin Loader Subunits and Cause Cornelia de Lange Syndrome. Cell Rep 31:107647 (2020).
Rabbit monoclonal to β-actin, ABclonal (AC026), Yan, L., Chen, J., Zhu, X., Sun, J., Wu, X., Shen, W., Zhang, W., Tao, Q., and Meng, A. (2018). Maternal Huluwa dictates the embryonic body axis through beta-catenin in vertebrates. Science 362.

Eukaryotic cell lines

Policy information about cell lines

Cell line source(s)	The human HeLa-S3 immortalized cell line was kindly provided by Dr.Wei Guo (UPenn). The human SK-BR-3 cell line (Catalog No. 30-2007), the human MCF10A cell line (Catalog No. CC-3150), the human HCC1395 cell line (Catalog No. CRL-2324) were bought from supplier.
Authentication	Cell lines were not authenticated.
Mycoplasma contamination	Cell lines were not tested for mycoplasma contamination.
Commonly misidentified lines (See ICLAC register)	No commonly misidentified cell lines were used.

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	GFP-positive HeLa-S3 cells transfected with the indicated plasmids for more than 36 h were collected using FACS.
Instrument	FACS sorting was performed on Astrios EQ (BeckMan Coulter).
Software	summit6.0, FlowJo
Cell population abundance	All flow cytometry analyses were performed on 200,000 cells.

Gating strategy	Cells were first gated on a plot of FSC-A vs SSC-A and then on a plot of FSC-H vs FSC-W to discriminate single cells. GFP positive cells were sorted by gating against untreated control cells.

☒ Tick this box to confirm that a figure exemplifying the gating strategy is provided in the Supplementary Information.