nature research

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Life Sciences Reporting Summary

Nature Research wishes to improve the reproducibility of the work we publish. This form is published with all life science papers and is intended to promote consistency and transparency in reporting. All life sciences submissions use this form; while some list items might not apply to an individual manuscript, all fields must be completed for clarity.

For further information on the points included in this form, see Reporting Life Sciences Research. For further information on Nature Research policies, including our data availability policy, see Authors & Referees and the Editorial Policy Checklist.

Experimental design

1. Sample size

   Describe how sample size was determined.

   No statistical methods were used to predetermine sample size

2. Data exclusions

   Describe any data exclusions.

   No data was excluded. All Hi-C libraries generated are included in the analyses.

3. Replication

   Describe whether the experimental findings were reliably reproduced.

   All the Hi-C libraries were replicted other than smc2td (MDsmc2, Supp. Fig 5a). This date was biologically replicated using the smc2K38I allele (which also generates loss of condensin function). Two Hi-C libraries of smc2K38I were generated and results shown.

4. Randomization

   Describe how samples/organisms/participants were allocated into experimental groups.

   Samples were not randomized

5. Blinding

   Describe whether the investigators were blinded to group allocation during data collection and/or analysis.

   Investigators were not blinded

   Note: all studies involving animals and/or human research participants must disclose whether blinding and randomization were used.

6. Statistical parameters

   For all figures and tables that use statistical methods, confirm that the following items are present in relevant figure legends (or the Methods section if additional space is needed).

n/a	Confirmed	
☐	☒	The exact sample size (*n*) for each experimental group/condition, given as a discrete number and unit of measurement (animals, litters, cultures, etc.)
☐	☒	A description of how samples were collected, noting whether measurements were taken from distinct samples or whether the same sample was measured repeatedly.
☐	☒	A statement indicating how many times each experiment was replicated
☒	☐	The statistical test(s) used and whether they are one- or two-sided (note: only common tests should be described solely by name; more complex techniques should be described in the Methods section)
☐	☒	A description of any assumptions or corrections, such as an adjustment for multiple comparisons
☒	☐	The test results (e.g. *p* values) given as exact values whenever possible and with confidence intervals noted
☒	☐	A summary of the descriptive statistics, including central tendency (e.g. median, mean) and variation (e.g. standard deviation, interquartile range)
☒	☐	Clearly defined error bars

See the web collection on statistics for biologists for further resources and guidance.

Software

Policy information about availability of computer code

7. Software

Describe the software used to analyze the data in this study.	All code is publicly available at https://bitbucket.org/mirnylab/openmm-polymer and https://bitbucket.org/mirnylab/hiclib

For all studies, we encourage code deposition in a community repository (e.g. GitHub). Authors must make computer code available to editors and reviewers upon request. The *Nature Methods* guidance for providing algorithms and software for publication may be useful for any submission.

Materials and reagents

Policy information about availability of materials

8. Materials availability

Indicate whether there are restrictions on availability of unique materials or if these materials are only available for distribution by a for-profit company.	There is no restriction on materials

9. Antibodies

Describe the antibodies used and how they were validated for use in the system under study (i.e. assay and species).	Smc4 phospoS4 antibody was a kind gift from Damien D'Amours - characterized in Robellet et al Genes and Dev, 2015, 29 (4) 426-439 . Anti-HA antibody (12Ca5 mouse monoclonal $IgG_{2\beta}K$. Roche, Fisher scientific 10026563). Anti-V5 antibody (mouse monoclonal MCA1360, abD Serotec)

10. Eukaryotic cell lines

a. State the source of each eukaryotic cell line used.	No eukaryotic cell lines were used
b. Describe the method of cell line authentication used.	No eukaryotic cell lines were used
c. Report whether the cell lines were tested for mycoplasma contamination.	No eukaryotic cell lines were used
d. If any of the cell lines used in the paper are listed in the database of commonly misidentified cell lines maintained by ICLAC, provide a scientific rationale for their use.	No eukaryotic cell lines were used

Animals and human research participants

Policy information about studies involving animals; when reporting animal research, follow the ARRIVE guidelines

11. Description of research animals

Provide details on animals and/or animal-derived materials used in the study.	No animals were used in the study

Policy information about studies involving human research participants

12. Description of human research participants

Describe the covariate-relevant population characteristics of the human research participants.	The study did not involve human research participants.

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Flow Cytometry Reporting Summary

Form fields will expand as needed. Please do not leave fields blank.

Data presentation

For all flow cytometry data, confirm that:

☒ 1. The axis labels state the marker and fluorochrome used (e.g. CD4-FITC).

☒ 2. 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).

☒ 3. All plots are contour plots with outliers or pseudocolor plots.

☒ 4. A numerical value for number of cells or percentage (with statistics) is provided.

Methodological details

5. Describe the sample preparation.	Sequential 70% EtOH fixation, RNAase treatment, pepsin digest followed by propidium iodide staining for DNA content
6. Identify the instrument used for data collection.	Becton Dickinson FACScaliber
7. Describe the software used to collect and analyze the flow cytometry data.	CELLQUEST version 3.3
8. Describe the abundance of the relevant cell populations within post-sort fractions.	We acquired 30000 cells
9. Describe the gating strategy used.	For the DNA content experiment of yeast cells a gating strategy is not applicable. The assay sets up conditions to assay cell with 1C and 2C content of propidium iodide cells in the exponential population (as shown in the figure) and then uses this as the comparison for all subsequent test samples acquired under identical conditions. The point of the assay is to show how propidium content increases as cells go through S phase before decreasing as cell divide resulting in cells with half the content. I have ticked the box to confirm that a gating strategy is not required in this case. In this assay Data presentation points 3 and 4 are also not applicable - the histograms show the population of PI stained events and how the distribution of that population varies over the time course of one cell cycle

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