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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.

   This study uses the fission yeast Schizosaccharomyce pombe as a model. Synchronous cultures of several million cells formed the basis for the Hi-C analyses. When individual cells were analyzed to determine centromere clustering or the chromosome condensation status, we scored at least 100 cells to ensure robust and statistically significant comparisons.

2. Data exclusions

   Describe any data exclusions.

   No data was excluded, the results of all cells was always included in our analyses.

3. Replication

   Describe whether the experimental findings were reliably reproduced.

   We confirmed all results reported in this manuscript in three independently performed repeats of each experiment. In the case of the Hi-C analyses, the major tool in our study, the reproducibility among these three repeats is documented in Supplementary Figure 2c. In the case of the cytological analysis contained in Figure 2f, all three obtained datapoints, their mean and standard deviations are reported.

4. Randomization

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

   n/a

5. Blinding

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

   n/a

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 the software used in our study has been deposited in GitHub and can be freely accessed using the link provided in the Online Methods section.

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 are no restrictions. All data and software is freely available from the indicated repositories (GEO and GitHub). Any other reagents, e.g. yeast strains, are available from the corresponding author.

9. Antibodies

Describe the antibodies used and how they were validated for use in the system under study (i.e. assay and species).	Antibodies were only used for the western blot contained in Supplementary Figure 2c. The details of these antibodies are contained in the Online Methods, including clone and catalogue number. The specificity of the anti-aid antibody is confirmed in our own study by depletion of the signal in response to auxin-induced degradation of the respectively tagged condensin subunits.

10. Eukaryotic cell lines

a. State the source of each eukaryotic cell line used.	The widely used Leupold's 972 isogenic fission yeast strain background was used in all experiments.
b. Describe the method of cell line authentication used.	n/a
c. Report whether the cell lines were tested for mycoplasma contamination.	n/a
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.	n/a

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.

n/a

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.

n/a