

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 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: Illumina HiSeq 1500 with software provided by the manufacturer

Data analysis: Data analysis was conducted using the following software: Bowtie v0.12.8, Bowtie2 v2.2.9, Homer v4.1, MEME Suite v5.2, 2.16.0, ChimeraX v0.92, R Base v4.0.2, and R Studio v1.1.463 including the following Bioconductor/R-packages: DNashapeR v1.10.0 and v1.14.0, Biostrings v2.52.0, GenomicAlignments v1.18.1, Gally v2.0.0, ggplot2 v3.3.2 and nucleR v2.16.0 as well as Python v3.8.3 with the following packages: numpy v1.19.2, Biopython v1.78.

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 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

Data that support the findings of this study have been deposited in the NCBI Gene Expression Omnibus with the accession number GSE145093 (<https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE145093>) and GSE140614 (<https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE140614>). The DNA sequence of the yeast genome (SacCer3) was retrieved from the Saccharomyces Genome Database (SGD, <https://www.yeastgenome.org>).

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](https://www.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 equals replicate number stated for each experiment in main or supplementary figures and always in sample description linked to GEO deposition. No sample size was pre-calculated due to exploratory nature of the research. Sample sizes were sufficient to reproduce observations.
Data exclusions	No data were excluded.
Replication	In vitro reconstitutions were replicated with independent SGD chromatin preparations as detailed in statement of replicates (stated for each experiment in main or supplementary figures and always in sample description linked to GEO deposition). Apart from technical failures, all attempts at replication were successful.
Randomization	Randomization was not done as experimenter needed to know experimental conditions for conducting the biochemical experiments as well as data analysis.
Blinding	Blinding was not done as experimenter needed to know experimental conditions for conducting the biochemical experiments as well as data analysis.

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
<input type="checkbox"/>	<input checked="" type="checkbox"/> Antibodies
<input type="checkbox"/>	<input checked="" type="checkbox"/> Eukaryotic cell lines
<input checked="" type="checkbox"/>	<input type="checkbox"/> Palaeontology and archaeology
<input type="checkbox"/>	<input checked="" type="checkbox"/> Animals and other organisms
<input checked="" type="checkbox"/>	<input type="checkbox"/> Human research participants
<input checked="" type="checkbox"/>	<input type="checkbox"/> Clinical data
<input checked="" type="checkbox"/>	<input type="checkbox"/> Dual use research of concern

Methods

n/a	Involved in the study
<input checked="" type="checkbox"/>	<input type="checkbox"/> ChIP-seq
<input checked="" type="checkbox"/>	<input type="checkbox"/> Flow cytometry
<input checked="" type="checkbox"/>	<input type="checkbox"/> MRI-based neuroimaging

Antibodies

Antibodies used	ANTI-FLAG® M2-Affinity Gel (product number A2220, Sigma Aldrich) was used for affinity purification of 2xFLAG-tagged INO80 complex
Validation	ANTI-FLAG® M2-Affinity Gel (product number A2220, Sigma Aldrich) enabled successful affinity purification of 2xFLAG-tagged INO80 complex and required therefore no additional validation.

Eukaryotic cell lines

Policy information about [cell lines](#)

Cell line source(s)	For generation of genomic plasmid libraries, the <i>S. pombe</i> strain Hu0303 (Ekwall group) and <i>E. coli</i> strain (ATCC 11303 strain, 14380, Affymetrix) were used. INO80 wild-type and mutant complexes were expressed in <i>Trichoplusia ni</i> insect cells (Invitrogen B85502) <i>Spodoptera frugiperda</i> sf21 insect cells (Invitrogen 11497013) were used for virus production. Reb1 was purified from <i>E. coli</i> BL21 (DE3) cd+ cells.
Authentication	Insect cell lines were purchased from Invitrogen (SF21: Invitrogen 11497013 Hi5: Invitrogen B85502) and used for Baculovirus mediated protein expression without further authentication.

Mycoplasma contamination

Commonly misidentified lines
(See [ICLAC](#) register)

Animals and other organisms

Policy information about [studies involving animals](#); [ARRIVE guidelines](#) recommended for reporting animal research

Laboratory animals

Wild animals

Field-collected samples

Ethics oversight

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