

## 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 [Authors & Referees](#) 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

No software for data collection was used

Data analysis

Published code

Cutadapt (version 1.15): Martin, M. et al. Cutadapt Removes Adapter Sequences From High-Throughput Sequencing Reads. *EMBnet.journal* 17, 10-12 (2011)

Bowtie 2 (version 2.2.9): Langmead, B. & Salzberg, SL. Fast gapped-read alignment with Bowtie 2. *Nat Methods* 9(4):357-9 (2012)

BWA-mem (version 0.7.16): Li, H. et al. Fast and accurate short read alignment with Burrows-Wheeler transform. *Bioinformatics* 25 (14):1754-60 (2009)

SAMtools (version 1.8): Li, H. et al. The Sequence Alignment/Map format and SAMtools. *Bioinformatics* 25(16):2078-9. (2009)

R (version 3.5.0): R Core Team. A language and environment for statistical computing. R Foundation for Statistical Computing. <https://www.R-project.org/> (2018)

R package GenomicFeatures: Lawrence, M. & Huber, W. Software for computing and annotating genomic ranges. *PLoS Comput Biol* 9, e1003118 (2013).

R package DESeq2 (version 1.20.0): Love, M. I., Huber, W. & Anders, S. Moderated estimation of fold change and dispersion for RNA-seq data with DESeq2. *Genome Biol* 15, 550 (2014)

Python (version 3.6): van Rossum, G. & de Boer, J. Interactively Testing Remote Servers Using the Python Programming Language. CWI

Quarterly 4(4):283-303. (1991)

COVERnant (version 0.3.2): <https://github.com/bgbrink/COVERnant>

ImageJ: <https://imagej.nih.gov/ij/index.html>

PEAKS studio X (Bioinformatics Solutions Inc., Canada)

GraphPad Prism version 7.0c (GraphPad Software, USA)

FIPQuant: ElBashir, R., Vanselow, J. T., Kraus, A., Janzen, C. J., Siegel, T. N., & Schlosser, A. Fragment ion patchwork quantification for measuring site-specific acetylation degrees. *Anal Chem*, 87(19), 9939-9945. (2015)

The RNA-seq and ChIP-seq data used in this publication have been deposited in EBI's European Nucleotide Archive and are accessible through ENA Study accession number PRJEB33216. The mass spectrometry proteomics data have been deposited to the ProteomeXchange Consortium via the PRIDE partner repository with the dataset identifier PXD014452. The Workflows and custom-made Unix Shell, Python and R scripts have been deposited at Zenodo [<https://doi.org/10.5281/zenodo.3662776>]. Documentation to reproduce the data analysis is provided.

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/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

All sequencing data and coverage tracks generated for this publication have been deposited in the Gene Expression Omnibus (GEO) and will be accessible through the accession number GSE145812 [<https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE145812>].

Mass spectrometry proteomics data generated for this publication have been deposited in the ProteomeXchange Consortium via the PRIDE 76 partner repository and will be accessible through the accession number PXD014452 [<https://www.ebi.ac.uk/pride/archive/projects/PXD014452>].

The source data underlying Figures 1a–b, 2b, 3a–b, 4, 5a–b, 6a–c, 7a–c, 8a–c, and Supplementary Figures 1a–c, 10a–b, 11, 12, 13, 14a–b and 15a–b are provided as a Source Data file.

## 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 sizes were not statistically predetermined. Whole-histone extraction and TY1-H2A immunoprecipitation experiments were performed in triplicates to rule out experimental and biological biases and to increase the resolution. TY1-H2A.Z-immunoprecipitation experiments were performed in 6 replicates, since the H2A.Z protein sequence harbors a long lysine array, which could lead to technical variations. Only one H2A.Z-immunoprecipitation experiment was performed to compare it with TY1-H2A.Z immunoprecipitation experiments. The H2A.Z immunoprecipitation experiment did not demonstrate a difference. H2A.Z-immunoprecipitation experiments after 48h HAT1 depletion were performed in triplicates to rule out experimental and biological biases and to increase the resolution. H2A.Z-immunoprecipitation experiments after 48h HAT2 depletion were performed in duplicates, since immunoprecipitation of H2A.Z-containing nucleosomes did not recover complete TSS-nucleosomes. RNA-seq experiments were performed in triplicates to rule out experimental biases and to be able to perform differential gene expression analysis. ChIP-seq experiments were performed in duplicates to rule out experimental biases. H2A.Z-ChIP-seq experiments following 0 h and 48 h of HAT1 or HAT2 depletion were performed in quadruplicates, since they are the core experiments. Experiments analyzing chromatin-bound proteins were performed in triplicates to rule out experimental biases.

Data exclusions

No data were excluded from the analyses.

Replication

All attempts to reproduce the data were successful.

Whole histone extraction experiments were performed in triplicates. TY-H2A-immunoprecipitation experiments were performed in triplicates.

TY-H2A.Z-immunoprecipitation experiments was performed in 6 replicates.  
 Only one H2A.Z-immunoprecipitation experiment was performed demonstrating no difference to TY-H2A.Z-immunoprecipitations.  
 H2A.Z-immunoprecipitation experiments after 48h HAT1 depletion were performed in triplicates.  
 H2A.Z-immunoprecipitation experiments after 48h HAT2 depletion were performed in duplicates.  
 RNA-seq experiments were performed in triplicates.  
 Only one H2A.Z-MNase-ChIP-seq experiment in WT cells was performed reproducing previous findings.  
 H2A.Z-MNase-ChIP-seq experiments in HAT1-depleted cells were performed in replicates (0h: n=4; 24h: n=2; 48h: n=4) with an input control for each experiment.  
 H2A.Z-MNase-ChIP-seq experiments in HAT2-depleted cells were performed in replicates (0h: n=4; 24h: n=2; 48h: n=4; 72h: n=2) with an input control for each experiment, except for replicate 1.  
 H2A.Z-MNase-ChIP-seq experiments in HAT2-depleted cells were performed in replicates (0h: n=4; 24h: n=2; 48h: n=4; 72h: n=2) with an input control for each experiment.  
 TY-H2A-MNase-ChIP-seq experiments were performed in duplicates with an input control for each experiment.  
 RPB9-ChIP-seq experiments in HAT1 and HAT2 depleted cells were performed in duplicates with an input control for each experiment.  
 Experiments analyzing chromatin-bound H2A.Z after HAT2 depletion were performed in triplicates.  
 Experiments analyzing chromatin-bound RPB9 after HAT1 depletion were performed in triplicates.

Randomization Not relevant for this study; Allocation of samples/organisms into experimental groups was not needed, since the experiments were performed at particular conditions.

Blinding Not relevant for this study; Blinding was not needed, since the experiments were performed at particular conditions.

## 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
- Animals and other organisms
- Human research participants
- Clinical data

### Methods

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

## Antibodies

### Antibodies used

Mouse Monoclonal BB2 antibody; purified from hybridoma cells (MAB Monoclonal Antibody Core Facility, Helmholtz Zentrum München Germany)  
 Bastin, P., Bagherzadeh, A., Matthews, K. R. & Gull, K. A novel epitope tag system to study protein targeting and organelle biogenesis in *Trypanosoma brucei*. *Mol. Biochem. Parasitol.* 77, 235-239 (1996).

Polyclonal Rabbit H2A.Z antibody; purified (ordered from Pineda Antikörper-Service, Berlin; available in the Siegel Lab)  
 Wedel, C., Förstner, K. U., Derr, R. & Siegel, T. N. GT-rich promoters can drive RNA pol II transcription and deposition of H2A.Z in African trypanosomes. *EMBO J* 36, 2581-2594 (2017).

Polyclonal Rabbit H3 antibody; serum (provided by Prof. C. J. Janzen; University of Würzburg)  
 Gassen, A., Brechtelfeld, D., Schandry, N., Arteaga-Salas, J. M., Israel, L., Imhof, A. & Janzen, C. J. DOT1A-dependent H3K76 methylation is required for replication regulation in *Trypanosoma brucei*. *Nucleic Acids* 40, 10302-11 (2012).

### Validation

Primary antibodies were validated regarding specificity and checked for cross-reactivity as described in the according publications:

#### BB2 antibody

Bastin, P., Bagherzadeh, A., Matthews, K. R. & Gull, K. A novel epitope tag system to study protein targeting and organelle biogenesis in *Trypanosoma brucei*. *Mol. Biochem. Parasitol.* 77, 235-239 (1996).

#### H2A.Z antibody

Wedel, C., Förstner, K. U., Derr, R. & Siegel, T. N. GT-rich promoters can drive RNA pol II transcription and deposition of H2A.Z in African trypanosomes. *EMBO J* 36, 2581-2594 (2017).

#### H3 antibody

Gassen, A., Brechtelfeld, D., Schandry, N., Arteaga-Salas, J. M., Israel, L., Imhof, A. & Janzen, C. J. DOT1A-dependent H3K76

## Eukaryotic cell lines

Policy information about [cell lines](#)

Cell line source(s)	<i>Trypanosoma brucei brucei</i> Lister 427 was originally obtained from Prof. George Cross (Rockefeller University, NYC, USA). Subsequent genetic modifications were performed by the authors.
Authentication	RNA-seq provided authentication.
Mycoplasma contamination	Mycoplasma contamination check carried out approx. every 3 years - no positive results from those tests to date.
Commonly misidentified lines (See <a href="#">ICLAC</a> register)	<i>T. b. brucei</i> L427 is not a commonly misidentified line.

## ChIP-seq

### Data deposition

- Confirm that both raw and final processed data have been deposited in a public database such as [GEO](#).
- Confirm that you have deposited or provided access to graph files (e.g. BED files) for the called peaks.

#### Data access links

*May remain private before publication.*

Raw ChIP-seq data (.fq) used in this publication have been deposited in the Gene Expression Omnibus (GEO) and will be accessible through the accession number GSE145812 [<https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE145812>].

Partially processed datasets (.bam), workflows and custom-made Unix Shell, Python and R scripts have been deposited on our university folder and can be accessed through Zenodo [<https://doi.org/10.5281/zenodo.3662776>]. Documentation to reproduce the data analysis is provided.

Final processed data (coverage tracks .wig) have been deposited in the Gene Expression Omnibus (GEO) and will be accessible through the accession number GSE145812 [<https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE145812>].

#### Files in database submission

H2A.Z ChIP Raw sequencing files:

NS263\_WT\_ChIP\_H2AZ\_R1.fq.bz2; NS263\_WT\_ChIP\_H2AZ\_R2.fq.bz2  
 NS276\_2T1\_HAT2\_KD\_ChIP\_0h\_1\_R1.fq.gz; NS276\_2T1\_HAT2\_KD\_ChIP\_0h\_1\_R2.fq.gz  
 NS277\_2T1\_HAT2\_KD\_ChIP\_24h\_1\_R1.fq.gz; NS277\_2T1\_HAT2\_KD\_ChIP\_24h\_1\_R2.fq.gz  
 NS278\_2T1\_HAT2\_KD\_ChIP\_48h\_1\_R1.fq.gz; NS278\_2T1\_HAT2\_KD\_ChIP\_48h\_1\_R2.fq.gz  
 NS283\_HAT2\_KD\_2T1\_ChIP\_0h\_2\_R1.fq.gz; NS283\_HAT2\_KD\_2T1\_ChIP\_0h\_2\_R2.fq.gz  
 NS284\_HAT2\_KD\_2T1\_ChIP\_24h\_2\_R1.fq.gz; NS284\_HAT2\_KD\_2T1\_ChIP\_24h\_2\_R2.fq.gz  
 NS285\_HAT2\_KD\_2T1\_ChIP\_48h\_2\_R1.fq.gz; NS285\_HAT2\_KD\_2T1\_ChIP\_48h\_2\_R2.fq.gz  
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 NS546\_HAT2KD\_48h\_H2AZ\_Input\_4\_R1.fq.bz2; NS546\_HAT2KD\_48h\_H2AZ\_Input\_4\_R2.fq.bz2

#### H2A.Z ChIP processed files:

NS263\_WT\_ChIP\_H2AZ\_to\_HGAP3\_Tb427v9\_bwt2.sorted.bam  
 NS276\_2T1\_HAT2\_KD\_ChIP\_0h\_1\_to\_HGAP3\_Tb427v9\_bwt2.sorted.bam  
 NS277\_2T1\_HAT2\_KD\_ChIP\_24h\_1\_to\_HGAP3\_Tb427v9\_bwt2.sorted.bam  
 NS278\_2T1\_HAT2\_KD\_ChIP\_48h\_1\_to\_HGAP3\_Tb427v9\_bwt2.sorted.bam  
 NS283\_HAT2\_KD\_2T1\_ChIP\_0h\_2\_to\_HGAP3\_Tb427v9\_bwt2.sorted.bam  
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 NS531\_HAT1KD\_0h\_H2AZ\_ChIP\_3\_to\_HGAP3\_Tb427v9\_bwt2.sorted.bam  
 NS532\_HAT1KD\_0h\_H2AZ\_ChIP\_4\_to\_HGAP3\_Tb427v9\_bwt2.sorted.bam  
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 NS534\_HAT1KD\_48h\_H2AZ\_ChIP\_4\_to\_HGAP3\_Tb427v9\_bwt2.sorted.bam  
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 NS537\_HAT1KD\_48h\_H2AZ\_Input\_3\_to\_HGAP3\_Tb427v9\_bwt2.sorted.bam  
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 NS540\_HAT2KD\_0h\_H2AZ\_ChIP\_4\_to\_HGAP3\_Tb427v9\_bwt2.sorted.bam  
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 NS545\_HAT2KD\_48h\_H2AZ\_Input\_3\_to\_HGAP3\_Tb427v9\_bwt2.sorted.bam  
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#### H2A.Z ChIP coverage:

CpB\_ws5001\_ss1001\_ratio\_NS565\_SM\_TyH2A\_Input\_1\_to\_HGAP3\_Tb427v9\_bwt2.sorted\_vs\_NS263\_WT\_ChIP\_H2AZ\_to\_HGAP3\_Tb427v9\_bwt2.sorted.wig;  
 CpB\_ws5001\_ss1001\_numerator\_NS263\_WT\_ChIP\_H2AZ\_to\_HGAP3\_Tb427v9\_bwt2.sorted.wig  
 CpB\_ws5001\_ss1001\_numerator\_NS285\_HAT2\_KD\_2T1\_ChIP\_48h\_2\_to\_HGAP3\_Tb427v9\_bwt2.sorted.wig  
 CpB\_ws5001\_ss1001\_numerator\_NS486\_2T1\_HAT1\_KD\_48h\_ChIP\_1\_to\_HGAP3\_Tb427v9\_bwt2.sorted.wig  
 CpB\_ws5001\_ss1001\_ratio\_NS565\_SM\_TyH2A\_Input\_1\_to\_HGAP3\_Tb427v9\_bwt2.sorted\_vs\_NS563\_SM\_TyH2A\_ChIP\_1\_to\_HGAP3\_Tb427v9\_bwt2.sorted.wig  
 CpB\_ws5001\_ss1001\_ratio\_NS565\_SM\_TyH2A\_Input\_1\_to\_HGAP3\_Tb427v9\_bwt2.sorted\_vs\_NS263\_WT\_ChIP\_H2AZ\_to\_HGAP3\_Tb427v9\_bwt2.sorted.wig;  
 CpB\_ws5001\_ss1001\_ratio\_NS565\_SM\_TyH2A\_Input\_1\_to\_HGAP3\_Tb427v9\_bwt2.sorted\_vs\_NS563\_SM\_TyH2A\_ChIP\_1\_to\_HGAP3\_Tb427v9\_bwt2.sorted.wig  
 CpB\_ws1\_ss1\_numerator\_NS263\_WT\_ChIP\_H2AZ\_to\_HGAP3\_Tb427v9\_bwt2.sorted.wig  
 CpB\_ws1\_ss1\_numerator\_NS276\_2T1\_HAT2\_KD\_ChIP\_0h\_1\_to\_HGAP3\_Tb427v9\_bwt2.sorted.wig

CpB\_ws1\_ss1\_numerator\_NS277\_2T1\_HAT2\_KD\_Chip\_24h\_1\_to\_HGAP3\_Tb427v9\_bwt2.sorted.wig  
CpB\_ws1\_ss1\_numerator\_NS278\_2T1\_HAT2\_KD\_Chip\_48h\_1\_to\_HGAP3\_Tb427v9\_bwt2.sorted.wig  
CpB\_ws1\_ss1\_numerator\_NS283\_HAT2\_KD\_2T1\_Chip\_0h\_2\_to\_HGAP3\_Tb427v9\_bwt2.sorted.wig  
CpB\_ws1\_ss1\_numerator\_NS284\_HAT2\_KD\_2T1\_Chip\_24h\_2\_to\_HGAP3\_Tb427v9\_bwt2.sorted.wig  
CpB\_ws1\_ss1\_numerator\_NS285\_HAT2\_KD\_2T1\_Chip\_48h\_2\_to\_HGAP3\_Tb427v9\_bwt2.sorted.wig  
CpB\_ws1\_ss1\_numerator\_NS286\_HAT2\_KD\_2T1\_Chip\_72h\_1\_to\_HGAP3\_Tb427v9\_bwt2.sorted.wig  
CpB\_ws1\_ss1\_numerator\_NS287\_HAT2\_KD\_2T1\_Chip\_72h\_2\_to\_HGAP3\_Tb427v9\_bwt2.sorted.wig  
CpB\_ws1\_ss1\_denominator\_NS291\_HAT2\_KD\_2T1\_Input\_0h\_2\_to\_HGAP3\_Tb427v9\_bwt2.sorted.wig  
CpB\_ws1\_ss1\_denominator\_NS292\_HAT2\_KD\_2T1\_Input\_24h\_2\_to\_HGAP3\_Tb427v9\_bwt2.sorted.wig  
CpB\_ws1\_ss1\_denominator\_NS293\_HAT2\_KD\_2T1\_Input\_48h\_2\_to\_HGAP3\_Tb427v9\_bwt2.sorted.wig  
CpB\_ws1\_ss1\_denominator\_NS294\_HAT2\_KD\_2T1\_Input\_72h\_1\_to\_HGAP3\_Tb427v9\_bwt2.sorted.wig  
CpB\_ws1\_ss1\_denominator\_NS295\_HAT2\_KD\_2T1\_Input\_72h\_2\_to\_HGAP3\_Tb427v9\_bwt2.sorted.wig  
CpB\_ws1\_ss1\_denominator\_NS476\_2T1\_HAT1\_KD\_24h\_Input\_1\_to\_HGAP3\_Tb427v9\_bwt2.sorted.wig  
CpB\_ws1\_ss1\_denominator\_NS477\_2T1\_HAT1\_KD\_48h\_Input\_1\_to\_HGAP3\_Tb427v9\_bwt2.sorted.wig  
CpB\_ws1\_ss1\_numerator\_NS484\_2T1\_HAT1\_KD\_0h\_Chip\_1\_to\_HGAP3\_Tb427v9\_bwt2.sorted.wig  
CpB\_ws1\_ss1\_numerator\_NS485\_2T1\_HAT1\_KD\_24h\_Chip\_1\_to\_HGAP3\_Tb427v9\_bwt2.sorted.wig  
CpB\_ws1\_ss1\_numerator\_NS486\_2T1\_HAT1\_KD\_48h\_Chip\_1\_to\_HGAP3\_Tb427v9\_bwt2.sorted.wig  
CpB\_ws1\_ss1\_denominator\_NS487\_2T1\_HAT1\_KD\_0h\_Input\_1\_to\_HGAP3\_Tb427v9\_bwt2.sorted.wig  
CpB\_ws1\_ss1\_numerator\_NS491\_2T1\_HAT1\_KD\_0h\_Chip\_2\_to\_HGAP3\_Tb427v9\_bwt2.sorted.wig  
CpB\_ws1\_ss1\_numerator\_NS492\_2T1\_HAT1\_KD\_24h\_Chip\_2\_to\_HGAP3\_Tb427v9\_bwt2.sorted.wig  
CpB\_ws1\_ss1\_numerator\_NS493\_2T1\_HAT1\_KD\_48h\_Chip\_2\_to\_HGAP3\_Tb427v9\_bwt2.sorted.wig  
CpB\_ws1\_ss1\_denominator\_NS494\_2T1\_HAT1\_KD\_0h\_Input\_2\_to\_HGAP3\_Tb427v9\_bwt2.sorted.wig  
CpB\_ws1\_ss1\_denominator\_NS495\_2T1\_HAT1\_KD\_24h\_Input\_2\_to\_HGAP3\_Tb427v9\_bwt2.sorted.wig  
CpB\_ws1\_ss1\_denominator\_NS496\_2T1\_HAT1\_KD\_48h\_Input\_2\_to\_HGAP3\_Tb427v9\_bwt2.sorted.wig  
CpB\_ws1\_ss1\_numerator\_NS531\_HAT1KD\_0h\_H2AZ\_Chip\_3\_to\_HGAP3\_Tb427v9\_bwt2.sorted.wig  
CpB\_ws1\_ss1\_numerator\_NS532\_HAT1KD\_0h\_H2AZ\_Chip\_4\_to\_HGAP3\_Tb427v9\_bwt2.sorted.wig  
CpB\_ws1\_ss1\_numerator\_NS533\_HAT1KD\_48h\_H2AZ\_Chip\_3\_to\_HGAP3\_Tb427v9\_bwt2.sorted.wig  
CpB\_ws1\_ss1\_numerator\_NS534\_HAT1KD\_48h\_H2AZ\_Chip\_4\_to\_HGAP3\_Tb427v9\_bwt2.sorted.wig  
CpB\_ws1\_ss1\_denominator\_NS535\_HAT1KD\_0h\_H2AZ\_Input\_3\_to\_HGAP3\_Tb427v9\_bwt2.sorted.wig  
CpB\_ws1\_ss1\_denominator\_NS536\_HAT1KD\_0h\_H2AZ\_Input\_4\_to\_HGAP3\_Tb427v9\_bwt2.sorted.wig  
CpB\_ws1\_ss1\_denominator\_NS537\_HAT1KD\_48h\_H2AZ\_Input\_3\_to\_HGAP3\_Tb427v9\_bwt2.sorted.wig  
CpB\_ws1\_ss1\_denominator\_NS538\_HAT1KD\_48h\_H2AZ\_Input\_4\_to\_HGAP3\_Tb427v9\_bwt2.sorted.wig  
CpB\_ws1\_ss1\_numerator\_NS539\_HAT2KD\_0h\_H2AZ\_Chip\_3\_to\_HGAP3\_Tb427v9\_bwt2.sorted.wig  
CpB\_ws1\_ss1\_numerator\_NS540\_HAT2KD\_0h\_H2AZ\_Chip\_4\_to\_HGAP3\_Tb427v9\_bwt2.sorted.wig  
CpB\_ws1\_ss1\_numerator\_NS541\_HAT2KD\_48h\_H2AZ\_Chip\_3\_to\_HGAP3\_Tb427v9\_bwt2.sorted.wig  
CpB\_ws1\_ss1\_numerator\_NS542\_HAT2KD\_48h\_H2AZ\_Chip\_4\_to\_HGAP3\_Tb427v9\_bwt2.sorted.wig  
CpB\_ws1\_ss1\_denominator\_NS543\_HAT2KD\_0h\_H2AZ\_Input\_3\_to\_HGAP3\_Tb427v9\_bwt2.sorted.wig  
CpB\_ws1\_ss1\_denominator\_NS544\_HAT2KD\_0h\_H2AZ\_Input\_4\_to\_HGAP3\_Tb427v9\_bwt2.sorted.wig  
CpB\_ws1\_ss1\_denominator\_NS545\_HAT2KD\_48h\_H2AZ\_Input\_3\_to\_HGAP3\_Tb427v9\_bwt2.sorted.wig  
CpB\_ws1\_ss1\_denominator\_NS546\_HAT2KD\_48h\_H2AZ\_Input\_4\_to\_HGAP3\_Tb427v9\_bwt2.sorted.wig

RNAPII ChIP raw sequencing files:

NS470\_BF\_2T1\_TyRPB9\_Chip\_1\_R1.fq.gz; NS470\_BF\_2T1\_TyRPB9\_Chip\_1\_R2.fq.gz  
NS471\_BF\_2T1\_TyRPB9\_Input\_1\_R1.fq.gz; NS471\_BF\_2T1\_TyRPB9\_Input\_1\_R2.fq.gz  
NS474\_BF\_2T1\_TyRPB9\_Chip\_2\_R1.fq.gz; NS474\_BF\_2T1\_TyRPB9\_Chip\_2\_R2.fq.gz  
NS475\_BF\_2T1\_TyRPB9\_Input\_2\_R1.fq.gz; NS475\_BF\_2T1\_TyRPB9\_Input\_2\_R2.fq.gz  
NS512\_HAT1\_KD\_TyRPB9\_0h\_Input\_1\_R1.fq.bz2; NS512\_HAT1\_KD\_TyRPB9\_0h\_Input\_1\_R2.fq.bz2  
NS513\_HAT1\_KD\_TyRPB9\_24h\_Input\_1\_R1.fq.bz2; NS513\_HAT1\_KD\_TyRPB9\_24h\_Input\_1\_R2.fq.bz2  
NS514\_HAT1\_KD\_TyRPB9\_48h\_Input\_1\_R1.fq.bz2; NS514\_HAT1\_KD\_TyRPB9\_48h\_Input\_1\_R2.fq.bz2  
NS515\_HAT2\_KD\_TyRPB9\_0h\_Input\_1\_R1.fq.bz2; NS515\_HAT2\_KD\_TyRPB9\_0h\_Input\_1\_R2.fq.bz2  
NS516\_HAT2\_KD\_TyRPB9\_24h\_Input\_1\_R1.fq.bz2; NS516\_HAT2\_KD\_TyRPB9\_24h\_Input\_1\_R2.fq.bz2  
NS517\_HAT2\_KD\_TyRPB9\_48h\_Input\_1\_R1.fq.bz2; NS517\_HAT2\_KD\_TyRPB9\_48h\_Input\_1\_R2.fq.bz2  
NS518\_HAT1\_KD\_TyRPB9\_0h\_Chip\_1\_R1.fq.bz2; NS518\_HAT1\_KD\_TyRPB9\_0h\_Chip\_1\_R2.fq.bz2  
NS519\_HAT1\_KD\_TyRPB9\_24h\_Chip\_1\_R1.fq.bz2; NS519\_HAT1\_KD\_TyRPB9\_24h\_Chip\_1\_R2.fq.bz2  
NS520\_HAT1\_KD\_TyRPB9\_48h\_Chip\_1\_R1.fq.bz2; NS520\_HAT1\_KD\_TyRPB9\_48h\_Chip\_1\_R2.fq.bz2  
NS521\_HAT2\_KD\_TyRPB9\_0h\_Chip\_1\_R1.fq.bz2; NS521\_HAT2\_KD\_TyRPB9\_0h\_Chip\_1\_R2.fq.bz2  
NS522\_HAT2\_KD\_TyRPB9\_24h\_Chip\_1\_R1.fq.bz2; NS522\_HAT2\_KD\_TyRPB9\_24h\_Chip\_1\_R2.fq.bz2  
NS523\_HAT2\_KD\_TyRPB9\_48h\_Chip\_1\_R1.fq.bz2; NS523\_HAT2\_KD\_TyRPB9\_48h\_Chip\_1\_R2.fq.bz2  
NS567\_2T1\_TyRPB9\_HAT1KD\_0h\_Chip\_2\_R1.fq.bz2; NS567\_2T1\_TyRPB9\_HAT1KD\_0h\_Chip\_2\_R2.fq.bz2  
NS568\_2T1\_TyRPB9\_HAT1KD\_24h\_Chip\_2\_R1.fq.bz2; NS568\_2T1\_TyRPB9\_HAT1KD\_24h\_Chip\_2\_R2.fq.bz2  
NS569\_2T1\_TyRPB9\_HAT1KD\_48h\_Chip\_2\_R1.fq.bz2; NS569\_2T1\_TyRPB9\_HAT1KD\_48h\_Chip\_2\_R2.fq.bz2  
NS570\_2T1\_TyRPB9\_HAT1KD\_0h\_Input\_2\_R1.fq.bz2; NS570\_2T1\_TyRPB9\_HAT1KD\_0h\_Input\_2\_R2.fq.bz2  
NS571\_2T1\_TyRPB9\_HAT1KD\_24h\_Input\_2\_R1.fq.bz2; NS571\_2T1\_TyRPB9\_HAT1KD\_24h\_Input\_2\_R2.fq.bz2  
NS572\_2T1\_TyRPB9\_HAT1KD\_48h\_Input\_2\_R1.fq.bz2; NS572\_2T1\_TyRPB9\_HAT1KD\_48h\_Input\_2\_R2.fq.bz2  
NS573\_2T1\_TyRPB9\_HAT2KD\_0h\_Chip\_2\_R1.fq.bz2; NS573\_2T1\_TyRPB9\_HAT2KD\_0h\_Chip\_2\_R2.fq.bz2  
NS574\_2T1\_TyRPB9\_HAT2KD\_24h\_Chip\_2\_R1.fq.bz2; NS574\_2T1\_TyRPB9\_HAT2KD\_24h\_Chip\_2\_R2.fq.bz2  
NS575\_2T1\_TyRPB9\_HAT2KD\_48h\_Chip\_2\_R1.fq.bz2; NS575\_2T1\_TyRPB9\_HAT2KD\_48h\_Chip\_2\_R2.fq.bz2  
NS578\_2T1\_TyRPB9\_HAT2KD\_0h\_Input\_2\_R1.fq.bz2; NS578\_2T1\_TyRPB9\_HAT2KD\_0h\_Input\_2\_R2.fq.bz2

NS579\_2T1\_TyRPB9\_HAT2KD\_24h\_Input\_2\_R1.fq.bz2; NS579\_2T1\_TyRPB9\_HAT2KD\_24h\_Input\_2\_R2.fq.bz2  
 NS580\_2T1\_TyRPB9\_HAT2KD\_48h\_Input\_2\_R1.fq.bz2; NS580\_2T1\_TyRPB9\_HAT2KD\_48h\_Input\_2\_R2.fq.bz2

RNA Pol II ChIP processed files:

NS470\_BF\_2T1\_TyRPB9\_ChIP\_1\_to\_HGAP3\_Tb427v9\_bwt2.sorted.bam  
 NS471\_BF\_2T1\_TyRPB9\_Input\_1\_to\_HGAP3\_Tb427v9\_bwt2.sorted.bam  
 NS474\_BF\_2T1\_TyRPB9\_ChIP\_2\_to\_HGAP3\_Tb427v9\_bwt2.sorted.bam  
 NS475\_BF\_2T1\_TyRPB9\_Input\_2\_to\_HGAP3\_Tb427v9\_bwt2.sorted.bam  
 NS512\_HAT1\_KD\_TyRPB9\_0h\_Input\_1\_to\_HGAP3\_Tb427v9\_bwt2.sorted.bam  
 NS513\_HAT1\_KD\_TyRPB9\_24h\_Input\_1\_to\_HGAP3\_Tb427v9\_bwt2.sorted.bam  
 NS514\_HAT1\_KD\_TyRPB9\_48h\_Input\_1\_to\_HGAP3\_Tb427v9\_bwt2.sorted.bam  
 NS515\_HAT2\_KD\_TyRPB9\_0h\_Input\_1\_to\_HGAP3\_Tb427v9\_bwt2.sorted.bam  
 NS516\_HAT2\_KD\_TyRPB9\_24h\_Input\_1\_to\_HGAP3\_Tb427v9\_bwt2.sorted.bam  
 NS517\_HAT2\_KD\_TyRPB9\_48h\_Input\_1\_to\_HGAP3\_Tb427v9\_bwt2.sorted.bam  
 NS518\_HAT1\_KD\_TyRPB9\_0h\_ChIP\_1\_to\_HGAP3\_Tb427v9\_bwt2.sorted.bam  
 NS519\_HAT1\_KD\_TyRPB9\_24h\_ChIP\_1\_to\_HGAP3\_Tb427v9\_bwt2.sorted.bam  
 NS520\_HAT1\_KD\_TyRPB9\_48h\_ChIP\_1\_to\_HGAP3\_Tb427v9\_bwt2.sorted.bam  
 NS521\_HAT2\_KD\_TyRPB9\_0h\_ChIP\_1\_to\_HGAP3\_Tb427v9\_bwt2.sorted.bam  
 NS522\_HAT2\_KD\_TyRPB9\_24h\_ChIP\_1\_to\_HGAP3\_Tb427v9\_bwt2.sorted.bam  
 NS523\_HAT2\_KD\_TyRPB9\_48h\_ChIP\_1\_to\_HGAP3\_Tb427v9\_bwt2.sorted.bam  
 NS567\_2T1\_TyRPB9\_HAT1KD\_0h\_ChIP\_2\_to\_HGAP3\_Tb427v9\_bwt2.sorted.bam  
 NS568\_2T1\_TyRPB9\_HAT1KD\_24h\_ChIP\_2\_to\_HGAP3\_Tb427v9\_bwt2.sorted.bam  
 NS569\_2T1\_TyRPB9\_HAT1KD\_48h\_ChIP\_2\_to\_HGAP3\_Tb427v9\_bwt2.sorted.bam  
 NS570\_2T1\_TyRPB9\_HAT1KD\_0h\_Input\_2\_to\_HGAP3\_Tb427v9\_bwt2.sorted.bam  
 NS571\_2T1\_TyRPB9\_HAT1KD\_24h\_Input\_2\_to\_HGAP3\_Tb427v9\_bwt2.sorted.bam  
 NS572\_2T1\_TyRPB9\_HAT1KD\_48h\_Input\_2\_to\_HGAP3\_Tb427v9\_bwt2.sorted.bam  
 NS573\_2T1\_TyRPB9\_HAT2KD\_0h\_ChIP\_2\_to\_HGAP3\_Tb427v9\_bwt2.sorted.bam  
 NS574\_2T1\_TyRPB9\_HAT2KD\_24h\_ChIP\_2\_to\_HGAP3\_Tb427v9\_bwt2.sorted.bam  
 NS575\_2T1\_TyRPB9\_HAT2KD\_48h\_ChIP\_2\_to\_HGAP3\_Tb427v9\_bwt2.sorted.bam  
 NS578\_2T1\_TyRPB9\_HAT2KD\_0h\_Input\_2\_to\_HGAP3\_Tb427v9\_bwt2.sorted.bam  
 NS579\_2T1\_TyRPB9\_HAT2KD\_24h\_Input\_2\_to\_HGAP3\_Tb427v9\_bwt2.sorted.bam  
 NS580\_2T1\_TyRPB9\_HAT2KD\_48h\_Input\_2\_to\_HGAP3\_Tb427v9\_bwt2.sorted.bam

RNA Pol II ChIP coverage files:

CpB\_ws1\_ss1\_ratio\_NS471\_BF\_2T1\_TyRPB9\_Input\_1\_to\_HGAP3\_Tb427v9\_bwt2.sorted\_vs\_NS470\_BF\_2T1\_TyRPB9\_ChIP\_1\_to\_HGAP3\_Tb427v9\_bwt2.sorted.wig  
 CpB\_ws1\_ss1\_ratio\_NS475\_BF\_2T1\_TyRPB9\_Input\_2\_to\_HGAP3\_Tb427v9\_bwt2.sorted\_vs\_NS474\_BF\_2T1\_TyRPB9\_ChIP\_2\_to\_HGAP3\_Tb427v9\_bwt2.sorted.wig  
 CpB\_ws1\_ss1\_ratio\_NS512\_HAT1\_KD\_TyRPB9\_0h\_Input\_1\_to\_HGAP3\_Tb427v9\_bwt2.sorted\_vs\_NS518\_HAT1\_KD\_TyRPB9\_0h\_ChIP\_1\_to\_HGAP3\_Tb427v9\_bwt2.sorted.wig  
 CpB\_ws1\_ss1\_ratio\_NS513\_HAT1\_KD\_TyRPB9\_24h\_Input\_1\_to\_HGAP3\_Tb427v9\_bwt2.sorted\_vs\_NS519\_HAT1\_KD\_TyRPB9\_24h\_ChIP\_1\_to\_HGAP3\_Tb427v9\_bwt2.sorted.wig  
 CpB\_ws1\_ss1\_ratio\_NS514\_HAT1\_KD\_TyRPB9\_48h\_Input\_1\_to\_HGAP3\_Tb427v9\_bwt2.sorted\_vs\_NS520\_HAT1\_KD\_TyRPB9\_48h\_ChIP\_1\_to\_HGAP3\_Tb427v9\_bwt2.sorted.wig  
 CpB\_ws1\_ss1\_ratio\_NS515\_HAT2\_KD\_TyRPB9\_0h\_Input\_1\_to\_HGAP3\_Tb427v9\_bwt2.sorted\_vs\_NS521\_HAT2\_KD\_TyRPB9\_0h\_ChIP\_1\_to\_HGAP3\_Tb427v9\_bwt2.sorted.wig  
 CpB\_ws1\_ss1\_ratio\_NS516\_HAT2\_KD\_TyRPB9\_24h\_Input\_1\_to\_HGAP3\_Tb427v9\_bwt2.sorted\_vs\_NS522\_HAT2\_KD\_TyRPB9\_24h\_ChIP\_1\_to\_HGAP3\_Tb427v9\_bwt2.sorted.wig  
 CpB\_ws1\_ss1\_ratio\_NS517\_HAT2\_KD\_TyRPB9\_48h\_Input\_1\_to\_HGAP3\_Tb427v9\_bwt2.sorted\_vs\_NS523\_HAT2\_KD\_TyRPB9\_48h\_ChIP\_1\_to\_HGAP3\_Tb427v9\_bwt2.sorted.wig  
 CpB\_ws1\_ss1\_ratio\_NS512\_HAT1\_KD\_TyRPB9\_0h\_Input\_1\_to\_HGAP3\_Tb427v9\_bwt2.sorted\_vs\_NS518\_HAT1\_KD\_TyRPB9\_0h\_ChIP\_1\_to\_HGAP3\_Tb427v9\_bwt2.sorted.wig  
 CpB\_ws1\_ss1\_ratio\_NS513\_HAT1\_KD\_TyRPB9\_24h\_Input\_1\_to\_HGAP3\_Tb427v9\_bwt2.sorted\_vs\_NS519\_HAT1\_KD\_TyRPB9\_24h\_ChIP\_1\_to\_HGAP3\_Tb427v9\_bwt2.sorted.wig  
 CpB\_ws1\_ss1\_ratio\_NS514\_HAT1\_KD\_TyRPB9\_48h\_Input\_1\_to\_HGAP3\_Tb427v9\_bwt2.sorted\_vs\_NS520\_HAT1\_KD\_TyRPB9\_48h\_ChIP\_1\_to\_HGAP3\_Tb427v9\_bwt2.sorted.wig  
 CpB\_ws1\_ss1\_ratio\_NS515\_HAT2\_KD\_TyRPB9\_0h\_Input\_1\_to\_HGAP3\_Tb427v9\_bwt2.sorted\_vs\_NS521\_HAT2\_KD\_TyRPB9\_0h\_ChIP\_1\_to\_HGAP3\_Tb427v9\_bwt2.sorted.wig  
 CpB\_ws1\_ss1\_ratio\_NS516\_HAT2\_KD\_TyRPB9\_24h\_Input\_1\_to\_HGAP3\_Tb427v9\_bwt2.sorted\_vs\_NS522\_HAT2\_KD\_TyRPB9\_24h\_ChIP\_1\_to\_HGAP3\_Tb427v9\_bwt2.sorted.wig  
 CpB\_ws1\_ss1\_ratio\_NS517\_HAT2\_KD\_TyRPB9\_48h\_Input\_1\_to\_HGAP3\_Tb427v9\_bwt2.sorted\_vs\_NS523\_HAT2\_KD\_TyRPB9\_48h\_ChIP\_1\_to\_HGAP3\_Tb427v9\_bwt2.sorted.wig  
 CpB\_ws1\_ss1\_ratio\_NS570\_2T1\_TyRPB9\_HAT1KD\_0h\_Input\_2\_to\_HGAP3\_Tb427v9\_bwt2.sorted\_vs\_NS567\_2T1\_TyRPB9\_HAT1KD\_0h\_ChIP\_2\_to\_HGAP3\_Tb427v9\_bwt2.sorted.wig  
 CpB\_ws1\_ss1\_ratio\_NS571\_2T1\_TyRPB9\_HAT1KD\_24h\_Input\_2\_to\_HGAP3\_Tb427v9\_bwt2.sorted\_vs\_NS568\_2T1\_TyRPB9\_HAT1KD\_24h\_ChIP\_2\_to\_HGAP3\_Tb427v9\_bwt2.sorted.wig  
 CpB\_ws1\_ss1\_ratio\_NS572\_2T1\_TyRPB9\_HAT1KD\_48h\_Input\_2\_to\_HGAP3\_Tb427v9\_bwt2.sorted\_vs\_NS569\_2T1\_TyRPB9\_HAT1KD\_48h\_ChIP\_2\_to\_HGAP3\_Tb427v9\_bwt2.sorted.wig  
 CpB\_ws1\_ss1\_ratio\_NS570\_2T1\_TyRPB9\_HAT1KD\_0h\_Input\_2\_to\_HGAP3\_Tb427v9\_bwt2.sorted\_vs\_NS567\_2T1\_TyRPB9\_

HAT1KD\_0h\_ChIP\_2\_to\_HGAP3\_Tb427v9\_bwt2.sorted.wig  
 CpB\_ws1\_ss1\_ratio\_NS571\_2T1\_TyRPB9\_HAT1KD\_24h\_Input\_2\_to\_HGAP3\_Tb427v9\_bwt2.sorted\_vs\_NS568\_2T1\_TyRPB9\_HAT1KD\_24h\_ChIP\_2\_to\_HGAP3\_Tb427v9\_bwt2.sorted.wig  
 CpB\_ws1\_ss1\_ratio\_NS572\_2T1\_TyRPB9\_HAT1KD\_48h\_Input\_2\_to\_HGAP3\_Tb427v9\_bwt2.sorted\_vs\_NS569\_2T1\_TyRPB9\_HAT1KD\_48h\_ChIP\_2\_to\_HGAP3\_Tb427v9\_bwt2.sorted.wig  
 CpB\_ws1\_ss1\_ratio\_NS578\_2T1\_TyRPB9\_HAT2KD\_0h\_Input\_2\_to\_HGAP3\_Tb427v9\_bwt2.sorted\_vs\_NS573\_2T1\_TyRPB9\_HAT2KD\_0h\_ChIP\_2\_to\_HGAP3\_Tb427v9\_bwt2.sorted.wig  
 CpB\_ws1\_ss1\_ratio\_NS579\_2T1\_TyRPB9\_HAT2KD\_24h\_Input\_2\_to\_HGAP3\_Tb427v9\_bwt2.sorted\_vs\_NS574\_2T1\_TyRPB9\_HAT2KD\_24h\_ChIP\_2\_to\_HGAP3\_Tb427v9\_bwt2.sorted.wig  
 CpB\_ws1\_ss1\_ratio\_NS580\_2T1\_TyRPB9\_HAT2KD\_48h\_Input\_2\_to\_HGAP3\_Tb427v9\_bwt2.sorted\_vs\_NS575\_2T1\_TyRPB9\_HAT2KD\_48h\_ChIP\_2\_to\_HGAP3\_Tb427v9\_bwt2.sorted.wig  
 CpB\_ws1\_ss1\_ratio\_NS578\_2T1\_TyRPB9\_HAT2KD\_0h\_Input\_2\_to\_HGAP3\_Tb427v9\_bwt2.sorted\_vs\_NS573\_2T1\_TyRPB9\_HAT2KD\_0h\_ChIP\_2\_to\_HGAP3\_Tb427v9\_bwt2.sorted.wig  
 CpB\_ws1\_ss1\_ratio\_NS579\_2T1\_TyRPB9\_HAT2KD\_24h\_Input\_2\_to\_HGAP3\_Tb427v9\_bwt2.sorted\_vs\_NS574\_2T1\_TyRPB9\_HAT2KD\_24h\_ChIP\_2\_to\_HGAP3\_Tb427v9\_bwt2.sorted.wig  
 CpB\_ws1\_ss1\_ratio\_NS580\_2T1\_TyRPB9\_HAT2KD\_48h\_Input\_2\_to\_HGAP3\_Tb427v9\_bwt2.sorted\_vs\_NS575\_2T1\_TyRPB9\_HAT2KD\_48h\_ChIP\_2\_to\_HGAP3\_Tb427v9\_bwt2.sorted.wig

Genome browser session  
 (e.g. [UCSC](#))

Not used

## Methodology

### Replicates

Only one H2A.Z-MNase-ChIP-seq experiment in WT cells was performed to reproduce previous findings.  
 H2A.Z-MNase-ChIP-seq experiments in HAT1-depleted cells were performed in replicates (0h: n=4; 24h: n=2; 48h: n=4) with an input control for each experiment.  
 H2A.Z-MNase-ChIP-seq experiments in HAT2-depleted cells were performed in replicates (0h: n=4; 24h: n=2; 48h: n=4; 72h: n=2) with an input control for each experiment, except for replicate 1.  
 H2A.Z-MNase-ChIP-seq experiments in HAT2-depleted cells were performed in replicates (0h: n=4; 24h: n=2; 48h: n=4; 72h: n=2) with an input control for each experiment.  
 TY-H2A-MNase-ChIP-seq experiments were performed in duplicates with an input control for each experiment.  
 RPB9-ChIP-seq experiments in HAT1 and HAT2 depleted cells were performed in duplicates with an input control for each experiment.

### Sequencing depth

"NS263\_WT\_ChIP\_H2AZ\_R1.fq.bz2; NS263\_WT\_ChIP\_H2AZ\_R2.fq.bz2 ";Illumina NextSeq 500, paired-end, 2x76 bp;sequenced reads: 3015378;Bowtie2 version 2.2.9, local;mapping rate: 99.08%  
 "NS276\_2T1\_HAT2\_KD\_ChIP\_0h\_1\_R1.fq.gz; NS276\_2T1\_HAT2\_KD\_ChIP\_0h\_1\_R2.fq.gz";Illumina NextSeq 500, paired-end, 2x76 bp;sequenced reads: 3380265;Bowtie2 version 2.2.9, local;mapping rate: 97.95%  
 "NS277\_2T1\_HAT2\_KD\_ChIP\_24h\_1\_R1.fq.gz; NS277\_2T1\_HAT2\_KD\_ChIP\_24h\_1\_R2.fq.gz";Illumina NextSeq 500, paired-end, 2x76 bp;sequenced reads: 3357305;Bowtie2 version 2.2.9, local;mapping rate: 98.39%  
 "NS278\_2T1\_HAT2\_KD\_ChIP\_48h\_1\_R1.fq.gz; NS278\_2T1\_HAT2\_KD\_ChIP\_48h\_1\_R2.fq.gz";Illumina NextSeq 500, paired-end, 2x76 bp;sequenced reads: 3453220;Bowtie2 version 2.2.9, local;mapping rate: 98.62%  
 "NS283\_HAT2\_KD\_2T1\_ChIP\_0h\_2\_R1.fq.gz; NS283\_HAT2\_KD\_2T1\_ChIP\_0h\_2\_R2.fq.gz";Illumina NextSeq 500, paired-end, 2x76 bp;sequenced reads: 2619228;Bowtie2 version 2.2.9, local;mapping rate: 97.67%  
 "NS284\_HAT2\_KD\_2T1\_ChIP\_24h\_2\_R1.fq.gz; NS284\_HAT2\_KD\_2T1\_ChIP\_24h\_2\_R2.fq.gz";Illumina NextSeq 500, paired-end, 2x76 bp;sequenced reads: 2695096;Bowtie2 version 2.2.9, local;mapping rate: 96.62%  
 "NS285\_HAT2\_KD\_2T1\_ChIP\_48h\_2\_R1.fq.gz; NS285\_HAT2\_KD\_2T1\_ChIP\_48h\_2\_R2.fq.gz";Illumina NextSeq 500, paired-end, 2x76 bp;sequenced reads: 2276000;Bowtie2 version 2.2.9, local; mapping rate: 95.92%  
 "NS286\_HAT2\_KD\_2T1\_ChIP\_72h\_1\_R1.fq.gz; NS286\_HAT2\_KD\_2T1\_ChIP\_72h\_1\_R2.fq.gz";Illumina NextSeq 500, paired-end, 2x76 bp;sequenced reads: 1080736;Bowtie2 version 2.2.9, local;mapping rate: 96.91%  
 "NS287\_HAT2\_KD\_2T1\_ChIP\_72h\_2\_R1.fq.gz; NS287\_HAT2\_KD\_2T1\_ChIP\_72h\_2\_R2.fq.gz";Illumina NextSeq 500, paired-end, 2x76 bp; sequenced reads: 7344525;Bowtie2 version 2.2.9, local;mapping rate: 97.61%  
 "NS291\_HAT2\_KD\_2T1\_Input\_0h\_2\_R1.fq.gz; NS291\_HAT2\_KD\_2T1\_Input\_0h\_2\_R2.fq.gz ";Illumina NextSeq 500, paired-end, 2x76 bp;sequenced reads: 2788620;Bowtie2 version 2.2.9, local;mapping rate: 93.45%  
 "NS292\_HAT2\_KD\_2T1\_Input\_24h\_2\_R1.fq.gz; NS292\_HAT2\_KD\_2T1\_Input\_24h\_2\_R2.fq.gz";Illumina NextSeq 500, paired-end, 2x76 bp;sequenced reads: 2709181;Bowtie2 version 2.2.9, local;mapping rate: 96.05%  
 "NS293\_HAT2\_KD\_2T1\_Input\_48h\_2\_R1.fq.gz; NS293\_HAT2\_KD\_2T1\_Input\_48h\_2\_R2.fq.gz";Illumina NextSeq 500, paired-end, 2x76 bp;sequenced reads: 3004490;Bowtie2 version 2.2.9, local;mapping rate: 94.67%  
 "NS294\_HAT2\_KD\_2T1\_Input\_72h\_1\_R1.fq.gz; NS294\_HAT2\_KD\_2T1\_Input\_72h\_1\_R2.fq.gz";Illumina NextSeq 500, paired-end, 2x76 bp;sequenced reads: 2816922;Bowtie2 version 2.2.9, local;mapping rate: 95.57%  
 "NS295\_HAT2\_KD\_2T1\_Input\_72h\_2\_R1.fq.gz; NS295\_HAT2\_KD\_2T1\_Input\_72h\_2\_R2.fq.gz";Illumina NextSeq 500, paired-end, 2x76 bp;sequenced reads: 2084397;Bowtie2 version 2.2.9, local;mapping rate: 91.39%  
 "NS476\_2T1\_HAT1\_KD\_24h\_Input\_1\_R1.fq.gz; NS476\_2T1\_HAT1\_KD\_24h\_Input\_1\_R2.fq.gz";Illumina NextSeq 500, paired-end, 2x76 bp;sequenced reads: 7211097;Bowtie2 version 2.2.9, local;mapping rate: 97.38%  
 "NS477\_2T1\_HAT1\_KD\_48h\_Input\_1\_R1.fq.gz; NS477\_2T1\_HAT1\_KD\_48h\_Input\_1\_R2.fq.gz";Illumina NextSeq 500, paired-end, 2x76 bp;sequenced reads: 6611792;Bowtie2 version 2.2.9, local;mapping rate: 96.91%  
 "NS484\_2T1\_HAT1\_KD\_0h\_ChIP\_1\_R1.fq.gz; NS484\_2T1\_HAT1\_KD\_0h\_ChIP\_1\_R2.fq.gz";Illumina NextSeq 500, paired-end, 2x76 bp;sequenced reads: 8091270;Bowtie2 version 2.2.9, local;mapping rate: 97.65%  
 "NS485\_2T1\_HAT1\_KD\_24h\_ChIP\_1\_R1.fq.gz; NS485\_2T1\_HAT1\_KD\_24h\_ChIP\_1\_R2.fq.gz";Illumina NextSeq 500, paired-end, 2x76 bp;sequenced reads: 8246854;Bowtie2 version 2.2.9, local;mapping rate: 97.97%  
 "NS486\_2T1\_HAT1\_KD\_48h\_ChIP\_1\_R1.fq.gz; NS486\_2T1\_HAT1\_KD\_48h\_ChIP\_1\_R2.fq.gz";Illumina NextSeq 500, paired-



end, 2x76 bp;sequenced reads: 11620011;Bowtie2 version 2.2.9, local;mapping rate: 97.97%

"NS487\_2T1\_HAT1\_KD\_0h\_Input\_1\_R1.fq.gz; NS487\_2T1\_HAT1\_KD\_0h\_Input\_1\_R2.fq.gz";illumina NextSeq 500, paired-end, 2x76 bp;sequenced reads: 10018772;Bowtie2 version 2.2.9, local;mapping rate: 97.73%

"NS491\_2T1\_HAT1\_KD\_0h\_ChIP\_2\_R1.fq.gz; NS491\_2T1\_HAT1\_KD\_0h\_ChIP\_2\_R2.fq.gz";illumina NextSeq 500, paired-end, 2x76 bp;sequenced reads: 3980805;Bowtie2 version 2.2.9, local;mapping rate: 97.99%

"NS492\_2T1\_HAT1\_KD\_24h\_ChIP\_2\_R1.fq.gz; NS492\_2T1\_HAT1\_KD\_24h\_ChIP\_2\_R2.fq.gz";illumina NextSeq 500, paired-end, 2x76 bp;sequenced reads: 4484259;Bowtie2 version 2.2.9, local;mapping rate: 99.1%

"NS493\_2T1\_HAT1\_KD\_48h\_ChIP\_2\_R1.fq.gz; NS493\_2T1\_HAT1\_KD\_48h\_ChIP\_2\_R2.fq.gz";illumina NextSeq 500, paired-end, 2x76 bp;sequenced reads: 12761757;Bowtie2 version 2.2.9, local;mapping rate: 97.75%

"NS494\_2T1\_HAT1\_KD\_0h\_Input\_2\_R1.fq.gz; NS494\_2T1\_HAT1\_KD\_0h\_Input\_2\_R2.fq.gz";illumina NextSeq 500, paired-end, 2x76 bp;sequenced reads: 5350241;Bowtie2 version 2.2.9, local;mapping rate: 96.52%

"NS495\_2T1\_HAT1\_KD\_24h\_Input\_2\_R1.fq.gz; NS495\_2T1\_HAT1\_KD\_24h\_Input\_2\_R2.fq.gz";illumina NextSeq 500, paired-end, 2x76 bp;sequenced reads: 5922089;Bowtie2 version 2.2.9, local; mapping rate: 96.69%

"NS496\_2T1\_HAT1\_KD\_48h\_Input\_2\_R1.fq.gz; NS496\_2T1\_HAT1\_KD\_48h\_Input\_2\_R2.fq.gz";illumina NextSeq 500, paired-end, 2x76 bp;sequenced reads: 5596528;Bowtie2 version 2.2.9, local;mapping rate: 97.81%

"NS531\_HAT1KD\_0h\_H2AZ\_ChIP\_3\_R1.fq.bz2; NS531\_HAT1KD\_0h\_H2AZ\_ChIP\_3\_R2.fq.bz2";illumina NextSeq 500, paired-end, 2x76 bp;sequenced reads: 2967118;Bowtie2 version 2.2.9, local;mapping rate: 98.04%

"NS532\_HAT1KD\_0h\_H2AZ\_ChIP\_4\_R1.fq.bz2; NS532\_HAT1KD\_0h\_H2AZ\_ChIP\_4\_R2.fq.bz2";illumina NextSeq 500, paired-end, 2x76 bp;sequenced reads: 3597753;Bowtie2 version 2.2.9, local;mapping rate: 98.24%

"NS533\_HAT1KD\_48h\_H2AZ\_ChIP\_3\_R1.fq.bz2; NS533\_HAT1KD\_48h\_H2AZ\_ChIP\_3\_R2.fq.bz2";illumina NextSeq 500, paired-end, 2x76 bp;sequenced reads: 3738898;Bowtie2 version 2.2.9, local;mapping rate: 98.14%

"NS534\_HAT1KD\_48h\_H2AZ\_ChIP\_4\_R1.fq.bz2; NS534\_HAT1KD\_48h\_H2AZ\_ChIP\_4\_R2.fq.bz2";illumina NextSeq 500, paired-end, 2x76 bp;sequenced reads: 3015430;Bowtie2 version 2.2.9, local;mapping rate: 97.86%

"NS535\_HAT1KD\_0h\_H2AZ\_Input\_3\_R1.fq.bz2; NS535\_HAT1KD\_0h\_H2AZ\_Input\_3\_R2.fq.bz2";illumina NextSeq 500, paired-end, 2x76 bp;sequenced reads: 3587464;Bowtie2 version 2.2.9, local;mapping rate: 97.15%

"NS536\_HAT1KD\_0h\_H2AZ\_Input\_4\_R1.fq.bz2; NS536\_HAT1KD\_0h\_H2AZ\_Input\_4\_R2.fq.bz2";illumina NextSeq 500, paired-end, 2x76 bp;sequenced reads: 3176148;Bowtie2 version 2.2.9, local;mapping rate: 97.31%

"NS537\_HAT1KD\_48h\_H2AZ\_Input\_3\_R1.fq.bz2; NS537\_HAT1KD\_48h\_H2AZ\_Input\_3\_R2.fq.bz2";illumina NextSeq 500, paired-end, 2x76 bp;sequenced reads: 3429705;Bowtie2 version 2.2.9, local;mapping rate: 97.86%

"NS538\_HAT1KD\_48h\_H2AZ\_Input\_4\_R1.fq.bz2; NS538\_HAT1KD\_48h\_H2AZ\_Input\_4\_R2.fq.bz2";illumina NextSeq 500, paired-end, 2x76 bp;sequenced reads: 2808329;Bowtie2 version 2.2.9, local;mapping rate: 96.6%

"NS539\_HAT2KD\_0h\_H2AZ\_ChIP\_3\_R1.fq.bz2; NS539\_HAT2KD\_0h\_H2AZ\_ChIP\_3\_R2.fq.bz2";illumina NextSeq 500, paired-end, 2x76 bp;sequenced reads: 2060120;Bowtie2 version 2.2.9, local; mapping rate: 95.11%

"NS540\_HAT2KD\_0h\_H2AZ\_ChIP\_4\_R1.fq.bz2; NS540\_HAT2KD\_0h\_H2AZ\_ChIP\_4\_R2.fq.bz2";illumina NextSeq 500, paired-end, 2x76 bp;sequenced reads: 3065918;Bowtie2 version 2.2.9, local;mapping rate: 95.45%

"NS541\_HAT2KD\_48h\_H2AZ\_ChIP\_3\_R1.fq.bz2; NS541\_HAT2KD\_48h\_H2AZ\_ChIP\_3\_R2.fq.bz2";illumina NextSeq 500, paired-end, 2x76 bp;sequenced reads: 3308527;Bowtie2 version 2.2.9, local;mapping rate: 98.65%

"NS542\_HAT2KD\_48h\_H2AZ\_ChIP\_4\_R1.fq.bz2; NS542\_HAT2KD\_48h\_H2AZ\_ChIP\_4\_R2.fq.bz2";illumina NextSeq 500, paired-end, 2x76 bp;sequenced reads: 3561204;Bowtie2 version 2.2.9, local;mapping rate: 98.5%

"NS543\_HAT2KD\_0h\_H2AZ\_Input\_3\_R1.fq.bz2; NS543\_HAT2KD\_0h\_H2AZ\_Input\_3\_R2.fq.bz2";illumina NextSeq 500, paired-end, 2x76 bp;sequenced reads: 2884766;Bowtie2 version 2.2.9, local;mapping rate: 94.38%

"NS544\_HAT2KD\_0h\_H2AZ\_Input\_4\_R1.fq.bz2; NS544\_HAT2KD\_0h\_H2AZ\_Input\_4\_R2.fq.bz2";illumina NextSeq 500, paired-end, 2x76 bp;sequenced reads: 2783881;Bowtie2 version 2.2.9, local;mapping rate: 95.24%

"NS545\_HAT2KD\_48h\_H2AZ\_Input\_3\_R1.fq.bz2; NS545\_HAT2KD\_48h\_H2AZ\_Input\_3\_R2.fq.bz2";illumina NextSeq 500, paired-end, 2x76 bp;sequenced reads: 2961602;Bowtie2 version 2.2.9, local;mapping rate: 97.52%

"NS546\_HAT2KD\_48h\_H2AZ\_Input\_4\_R1.fq.bz2; NS546\_HAT2KD\_48h\_H2AZ\_Input\_4\_R2.fq.bz2";illumina NextSeq 500, paired-end, 2x76 bp;sequenced reads: 2643620;Bowtie2 version 2.2.9, local;mapping rate: 95.74%

"NS470\_BF\_2T1\_TyRPB9\_ChIP\_1\_R1.fq.gz; NS470\_BF\_2T1\_TyRPB9\_ChIP\_1\_R2.fq.gz";illumina NextSeq 500, paired-end, 2x76 bp;sequenced reads: 13626619;Bowtie2 version 2.2.9, local;mapping rate: 95.48%

"NS471\_BF\_2T1\_TyRPB9\_Input\_1\_R1.fq.gz; NS471\_BF\_2T1\_TyRPB9\_Input\_1\_R2.fq.gz";illumina NextSeq 500, paired-end, 2x76 bp;sequenced reads: 12737249;Bowtie2 version 2.2.9, local;mapping rate: 95.55%

"NS474\_BF\_2T1\_TyRPB9\_ChIP\_2\_R1.fq.gz; NS474\_BF\_2T1\_TyRPB9\_ChIP\_2\_R2.fq.gz";illumina NextSeq 500, paired-end, 2x76 bp;sequenced reads: 12737249;Bowtie2 version 2.2.9, local;mapping rate: 94.08%

"NS475\_BF\_2T1\_TyRPB9\_Input\_2\_R1.fq.gz; NS475\_BF\_2T1\_TyRPB9\_Input\_2\_R2.fq.gz";illumina NextSeq 500, paired-end, 2x76 bp;sequenced reads: 11622367;Bowtie2 version 2.2.9, local;mapping rate: 94.25%

"NS512\_HAT1\_KD\_TyRPB9\_0h\_Input\_1\_R1.fq.bz2; NS512\_HAT1\_KD\_TyRPB9\_0h\_Input\_1\_R2.fq.bz2";illumina NextSeq 500, paired-end, 2x76 bp;sequenced reads: 6396887;Bowtie2 version 2.2.9, local;mapping rate: 97.72%

"NS513\_HAT1\_KD\_TyRPB9\_24h\_Input\_1\_R1.fq.bz2; NS513\_HAT1\_KD\_TyRPB9\_24h\_Input\_1\_R2.fq.bz2";illumina NextSeq 500, paired-end, 2x76 bp;sequenced reads: 8439618;Bowtie2 version 2.2.9, local;mapping rate: 97.68%

"NS514\_HAT1\_KD\_TyRPB9\_48h\_Input\_1\_R1.fq.bz2; NS514\_HAT1\_KD\_TyRPB9\_48h\_Input\_1\_R2.fq.bz2";illumina NextSeq 500, paired-end, 2x76 bp;sequenced reads: 8144610;Bowtie2 version 2.2.9, local;mapping rate: 96.54%

"NS515\_HAT2\_KD\_TyRPB9\_0h\_Input\_1\_R1.fq.bz2; NS515\_HAT2\_KD\_TyRPB9\_0h\_Input\_1\_R2.fq.bz2";illumina NextSeq 500, paired-end, 2x76 bp;sequenced reads: 7919934;Bowtie2 version 2.2.9, local;mapping rate: 97.7%

"NS516\_HAT2\_KD\_TyRPB9\_24h\_Input\_1\_R1.fq.bz2; NS516\_HAT2\_KD\_TyRPB9\_24h\_Input\_1\_R2.fq.bz2";illumina NextSeq 500, paired-end, 2x76 bp;sequenced reads: 7887257;Bowtie2 version 2.2.9, local;mapping rate: 98.03%

"NS517\_HAT2\_KD\_TyRPB9\_48h\_Input\_1\_R1.fq.bz2; NS517\_HAT2\_KD\_TyRPB9\_48h\_Input\_1\_R2.fq.bz2";illumina NextSeq 500, paired-end, 2x76 bp;sequenced reads: 4348814;Bowtie2 version 2.2.9, local;mapping rate: 97.4%

"NS518\_HAT1\_KD\_TyRPB9\_0h\_ChIP\_1\_R1.fq.bz2; NS518\_HAT1\_KD\_TyRPB9\_0h\_ChIP\_1\_R2.fq.bz2";illumina NextSeq 500, paired-end, 2x76 bp;sequenced reads: 9739561;Bowtie2 version 2.2.9, local;mapping rate: 95.54%

"NS519\_HAT1\_KD\_TyRPB9\_24h\_ChIP\_1\_R1.fq.bz2; NS519\_HAT1\_KD\_TyRPB9\_24h\_ChIP\_1\_R2.fq.bz2";illumina NextSeq 500, paired-end, 2x76 bp;sequenced reads: 9440267;Bowtie2 version 2.2.9, local;mapping rate: 97.55%

"NS520\_HAT1\_KD\_TyRPB9\_48h\_ChIP\_1\_R1.fq.bz2; NS520\_HAT1\_KD\_TyRPB9\_48h\_ChIP\_1\_R2.fq.bz2";illumina NextSeq 500, paired-end, 2x76 bp;sequenced reads: 8647732;Bowtie2 version 2.2.9, local;mapping rate: 93.72%

"NS521\_HAT2\_KD\_TyRPB9\_0h\_ChIP\_1\_R1.fq.bz2; NS521\_HAT2\_KD\_TyRPB9\_0h\_ChIP\_1\_R2.fq.bz2";illumina NextSeq 500, paired-end, 2x76 bp;sequenced reads: 11248028;Bowtie2 version 2.2.9, local;mapping rate: 90.78%

"NS522\_HAT2\_KD\_TyRPB9\_24h\_ChIP\_1\_R1.fq.bz2; NS522\_HAT2\_KD\_TyRPB9\_24h\_ChIP\_1\_R2.fq.bz2";illumina NextSeq 500, paired-end, 2x76 bp;sequenced reads: 9259488;Bowtie2 version 2.2.9, local;mapping rate: 97.02%

"NS523\_HAT2\_KD\_TyRPB9\_48h\_ChIP\_1\_R1.fq.bz2; NS523\_HAT2\_KD\_TyRPB9\_48h\_ChIP\_1\_R2.fq.bz2";illumina NextSeq 500, paired-end, 2x76 bp;sequenced reads: 7396188;Bowtie2 version 2.2.9, local;mapping rate: 91.75%

"NS567\_2T1\_TyRPB9\_HAT1KD\_0h\_ChIP\_2\_R1.fq.bz2; NS567\_2T1\_TyRPB9\_HAT1KD\_0h\_ChIP\_2\_R2.fq.bz2";illumina NextSeq 500, paired-end, 2x76 bp;sequenced reads: 4848659;Bowtie2 version 2.2.9, local;mapping rate: 12.33%

"NS568\_2T1\_TyRPB9\_HAT1KD\_24h\_ChIP\_2\_R1.fq.bz2; NS568\_2T1\_TyRPB9\_HAT1KD\_24h\_ChIP\_2\_R2.fq.bz2";illumina NextSeq 500, paired-end, 2x76 bp;sequenced reads: 1494552;Bowtie2 version 2.2.9, local;mapping rate: 12.32%

"NS569\_2T1\_TyRPB9\_HAT1KD\_48h\_ChIP\_2\_R1.fq.bz2; NS569\_2T1\_TyRPB9\_HAT1KD\_48h\_ChIP\_2\_R2.fq.bz2";illumina NextSeq 500, paired-end, 2x76 bp;sequenced reads: 3314592;Bowtie2 version 2.2.9, local;mapping rate: 6.83%

"NS570\_2T1\_TyRPB9\_HAT1KD\_0h\_Input\_2\_R1.fq.bz2; NS570\_2T1\_TyRPB9\_HAT1KD\_0h\_Input\_2\_R2.fq.bz2";illumina NextSeq 500, paired-end, 2x76 bp;sequenced reads: 2378211;Bowtie2 version 2.2.9, local;mapping rate: 85.8%

"NS571\_2T1\_TyRPB9\_HAT1KD\_24h\_Input\_2\_R1.fq.bz2; NS571\_2T1\_TyRPB9\_HAT1KD\_24h\_Input\_2\_R2.fq.bz2";illumina NextSeq 500, paired-end, 2x76 bp;sequenced reads: 2024278;Bowtie2 version 2.2.9, local;mapping rate: 83.29%

"NS572\_2T1\_TyRPB9\_HAT1KD\_48h\_Input\_2\_R1.fq.bz2; NS572\_2T1\_TyRPB9\_HAT1KD\_48h\_Input\_2\_R2.fq.bz2";illumina NextSeq 500, paired-end, 2x76 bp;sequenced reads: 2469782;Bowtie2 version 2.2.9, local;mapping rate: 87.63%

"NS573\_2T1\_TyRPB9\_HAT2KD\_0h\_ChIP\_2\_R1.fq.bz2; NS573\_2T1\_TyRPB9\_HAT2KD\_0h\_ChIP\_2\_R2.fq.bz2";illumina NextSeq 500, paired-end, 2x76 bp;sequenced reads: 3295209;Bowtie2 version 2.2.9, local;mapping rate: 15.08%

"NS574\_2T1\_TyRPB9\_HAT2KD\_24h\_ChIP\_2\_R1.fq.bz2; NS574\_2T1\_TyRPB9\_HAT2KD\_24h\_ChIP\_2\_R2.fq.bz2";illumina NextSeq 500, paired-end, 2x76 bp;sequenced reads: 3306559;Bowtie2 version 2.2.9, local;mapping rate: 8.75%

"NS575\_2T1\_TyRPB9\_HAT2KD\_48h\_ChIP\_2\_R1.fq.bz2; NS575\_2T1\_TyRPB9\_HAT2KD\_48h\_ChIP\_2\_R2.fq.bz2";illumina NextSeq 500, paired-end, 2x76 bp;sequenced reads: 8180258;Bowtie2 version 2.2.9, local;mapping rate: 7.88%

"NS578\_2T1\_TyRPB9\_HAT2KD\_0h\_Input\_2\_R1.fq.bz2; NS578\_2T1\_TyRPB9\_HAT2KD\_0h\_Input\_2\_R2.fq.bz2";illumina NextSeq 500, paired-end, 2x76 bp;sequenced reads: 2331259;Bowtie2 version 2.2.9, local;mapping rate: 84.82%

"NS579\_2T1\_TyRPB9\_HAT2KD\_24h\_Input\_2\_R1.fq.bz2; NS579\_2T1\_TyRPB9\_HAT2KD\_24h\_Input\_2\_R2.fq.bz2";illumina NextSeq 500, paired-end, 2x76 bp;sequenced reads: 3043255;Bowtie2 version 2.2.9, local;mapping rate: 86%

"NS580\_2T1\_TyRPB9\_HAT2KD\_48h\_Input\_2\_R1.fq.bz2; NS580\_2T1\_TyRPB9\_HAT2KD\_48h\_Input\_2\_R2.fq.bz2";illumina NextSeq 500, paired-end, 2x76 bp;sequenced reads: 3042335;Bowtie2 version 2.2.9, local;mapping rate: 91.39%

"NS563\_SM\_TyH2A\_ChIP\_1\_R1.fq.bz2; NS563\_SM\_TyH2A\_ChIP\_1\_R2.fq.bz2";illumina NextSeq 500, paired-end, 2x76 bp;sequenced reads: 3867340;Bowtie2 version 2.2.9, local;mapping rate: 98.15%

"NS564\_SM\_TyH2A\_ChIP\_2\_R1.fq.bz2; NS564\_SM\_TyH2A\_ChIP\_2\_R2.fq.bz2";illumina NextSeq 500, paired-end, 2x76 bp;sequenced reads: 2877590;Bowtie2 version 2.2.9, local;mapping rate: 98.08%

"NS565\_SM\_TyH2A\_Input\_1\_R1.fq.bz2; NS565\_SM\_TyH2A\_Input\_1\_R2.fq.bz2";illumina NextSeq 500, paired-end, 2x76 bp;sequenced reads: 3189383;Bowtie2 version 2.2.9, local;mapping rate: 96.89%

"NS566\_SM\_TyH2A\_Input\_2\_R1.fq.bz2; NS566\_SM\_TyH2A\_Input\_2\_R2.fq.bz2";illumina NextSeq 500, paired-end, 2x76 bp;sequenced reads: 1159079;Bowtie2 version 2.2.9, local; mapping rate:94.65%

## Antibodies

## BB2 antibody

Bastin, P., Bagherzadeh, A., Matthews, K. R. & Gull, K. A novel epitope tag system to study protein targeting and organelle biogenesis in *Trypanosoma brucei*. *Mol. Biochem. Parasitol.* 77, 235-239 (1996).

## H2A.Z antibody

Wedel, C., Förstner, K. U., Derr, R. & Siegel, T. N. GT-rich promoters can drive RNA pol II transcription and deposition of H2A.Z in African trypanosomes. *EMBO J* 36, 2581-2594 (2017).

## Peak calling parameters

For all datasets, sequencing reads were mapped using Bowtie2 local, converted to BAM files using samtools-1.8 view -b, sorted using samtools-1.8 sort and indexed using samtools index. Coverage plots were generated using COVERNant version 0.3.2 (<https://github.com/bgbrink/COVERnant>) and visualized using GraphPad Prism version 7.0c.

## Data quality

FDR5% were not determined as no peak calling was performed in this study.

## Software

Bowtie 2 (version 2.2.9): Langmead, B. & Salzberg, S.L. Fast gapped-read alignment with Bowtie 2. *Nat Methods* 9(4):357-9 (2012)

SAMtools (version 1.8): Li, H. et al. The Sequence Alignment/Map format and SAMtools. *Bioinformatics* 25(16):2078-9. (2009)

Python (version 3.6): van Rossum, G. & de Boer, J. Interactively Testing Remote Servers Using the Python Programming Language. *CWI Quarterly* 4(4):283-303. (1991)

COVERnant (version 0.3.2): <https://github.com/bgbrink/COVERnant>

GraphPad Prism version 7.0c (GraphPad Software, USA)