

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

No software were used for data collection.

Data analysis

For RNA-Seq

Read-quality control was performed using fastQC (v0.11.7) and Rsubread38 (v1.26.1) qualityScore function. Read mapping was performed using the Rsubread align function on an indexed version of T. annulata genome assembly ASM322v1.32. RPKM values were obtained using the featureCounts function from the Rsubread package using the same ASM322v1.32 annotations. Visualisation and snapshots of bam files was performed using IGV (v2.3.91) and further modified using inkscape (v0.92.3). Kruskal-Wallis and pairwise Wilcoxon Statistical testing on RPKM values from cluster I-V was performed using the ggpubr (v0.2) R package.

ChIP-seq analysis is described below.

For image analysis:

We used ImageJ (NIH, version 1.53) and MetaMorph® Image Analysis Software (Molecular Devices®, version 7.10.2.240)

For the phylogeny and comparative genomics analysis we used the following software: mafft (v7.245), Jalview (v2.10.5), iqtree (v1.5.5) and FigTree (v1.4.3).

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

All data generated or analyzed during this study are included in this published article. The RNA-Sequencing and ChIP-Seq data have been deposited to the ENA database with the study identifier #PRJEB3379. The Zenodo access link is provided (<https://doi.org/10.5281/zenodo.3370034>) DOI number : 10.5281/zenodo.3370034. Content description : This repository provides bigwig files for ChIP and RNA sequencing experiments in *Theileria annulata*. DeepTools generated Coverage files, ReadCount normalised files and SES normalised files are provided. Also provided are genome and annotation files for visualisation with IGV software. The Mass Spectrometry proteomics data were deposited in the ProteomeXchange Consortium via the PRIDE partner repository with the dataset identifier PXD024599. Source data are provided with this paper.

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 was determined to be adequate based on the magnitude and consistency of measurable differences between groups. Sample size decisions were based on the standards used in publications in the field. For all microscopy quantification, we sampled over 50 cells and performed all experiments in triplicate.
Data exclusions	Data were only excluded for failed experiments.
Replication	All experiments were replicated at distinct dates at least three times. Replicate experiments were successful.
Randomization	After discussion with colleagues it was decided that randomization approaches were not relevant for this study.
Blinding	We considered that blinding was not relevant for most of these experiments based on data reproducibility. An exception was the quantification of induction of merogony experiments, in which two independent researchers performed quantification under blinded 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
<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 checked="" type="checkbox"/>	<input 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 type="checkbox"/>	<input checked="" 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

We used these antibodies:

anti-H3K18me1 (ab177253, Abcam), 1:5000; anti-H3K18me1 (#31259, Active Motif), 1:10000; anti-H3K18me1 (#ab177253 Mellor's laboratory, Abcam) 1:10000; anti-H3K18ac (9675 S, Cell signaling) 1:800; anti-H3K18ac (ab1191, Abcam) 1:2000; anti-H3K4me3 (pAb-003-050, Diagenode) 1:200; anti-H3K4me3 (07-473, Millipore); anti-H3K36me3 (ab9050, Abcam); anti-H3 (ab1791, Abcam) 1:10000; Alexa594-conjugated donkey anti-rabbit antibody, 1:1000. (A32754, ThermoFischer); IgG isotype control (Cell Signaling,

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 PRJEB33792 ERP116612 ERS3637548 ERX3492372 ERR3470709 06-Aug-2019 Confidential
 PRJEB33792 ERP116612 ERS3637547 ERX3492371 ERR3470708 06-Aug-2019 Confidential
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 PRJEB33792 ERP116612 ERS3637545 ERX3492369 ERR3470706 06-Aug-2019 Confidential

Bigwig files of processed data can be accessed using the Zenodo link provided. (doi : 10.5281/zenodo.3370034)

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

Theileria annulata is not available as a species at UCSC. We have provided a Zenodo download link with all the relevant files for visualisation using the IGV genome browser.

Methodology

Replicates	Two biological replicates were used for ChIP experiment in this study. Biological replicates correlation was assessed using PCA and Spearman/Pearson correlation coefficient computation using deepTools (v3.1.1) bamCoverage, multiBamSummary and plotCorrelation tools.																																																																	
Sequencing depth	<p>Reads are all 75 bp long, single-end reads.</p> <p>mapping stats :</p> <table border="1"> <thead> <tr> <th>name</th> <th>library size</th> <th>uniquely mapped reads</th> <th>Total mapped reads</th> <th>multi mapping reads</th> </tr> </thead> <tbody> <tr> <td>TBL3_1_Input</td> <td>24'452'865</td> <td>459'003</td> <td>472'578 reads (1,9%)</td> <td>13'575</td> </tr> <tr> <td>TBL3_2_Input</td> <td>31'492'345</td> <td>865'497</td> <td>891'063 reads (2,8%)</td> <td>25'566</td> </tr> <tr> <td>TBL3_Input_H3K36_2</td> <td>26'056'479</td> <td>971'305</td> <td>999'254 reads (3,8%)</td> <td>27'949</td> </tr> <tr> <td>TBL3_Input_H3K36_1</td> <td>53'920'290</td> <td>944'560</td> <td>973'121 reads (1,8%)</td> <td>28'561</td> </tr> <tr> <td>TBL3_1_H3K4_me3</td> <td>38'998'902</td> <td>7'801'027</td> <td>7'902'032 reads (20,3%)</td> <td>101'005</td> </tr> <tr> <td>TBL3_2_H3K4_me3</td> <td>55'632'141</td> <td>12'677'213</td> <td>12'851'400 reads (23,1%)</td> <td>174'187</td> </tr> <tr> <td>TBL3_1_H3K18_me1</td> <td>41'748'547</td> <td>5'155'793</td> <td>5'285'486 reads (12,7%)</td> <td>129'693</td> </tr> <tr> <td>TBL3_2_H3K18_me1</td> <td>29'543'230</td> <td>4'838'799</td> <td>4'966'524 reads (16,8%)</td> <td>127'725</td> </tr> <tr> <td>TBL3_1_H3K18_ac</td> <td>7'215'658</td> <td>467'750</td> <td>474'769 reads (6,6%)</td> <td>7'019</td> </tr> <tr> <td>TBL3_2_H3K18_ac</td> <td>34'571'877</td> <td>2'878'572</td> <td>2'923'353 reads (8,5%)</td> <td>44'781</td> </tr> <tr> <td>TBL3_1_H3K36me3</td> <td>51'845'808</td> <td>3'262'866</td> <td>3'338'231 reads (6,4%)</td> <td>75'365</td> </tr> <tr> <td>TBL3_2_H3K36me3</td> <td>25'160'921</td> <td>3'820'804</td> <td>3'912'043 reads (15,5%)</td> <td>91'239</td> </tr> </tbody> </table>	name	library size	uniquely mapped reads	Total mapped reads	multi mapping reads	TBL3_1_Input	24'452'865	459'003	472'578 reads (1,9%)	13'575	TBL3_2_Input	31'492'345	865'497	891'063 reads (2,8%)	25'566	TBL3_Input_H3K36_2	26'056'479	971'305	999'254 reads (3,8%)	27'949	TBL3_Input_H3K36_1	53'920'290	944'560	973'121 reads (1,8%)	28'561	TBL3_1_H3K4_me3	38'998'902	7'801'027	7'902'032 reads (20,3%)	101'005	TBL3_2_H3K4_me3	55'632'141	12'677'213	12'851'400 reads (23,1%)	174'187	TBL3_1_H3K18_me1	41'748'547	5'155'793	5'285'486 reads (12,7%)	129'693	TBL3_2_H3K18_me1	29'543'230	4'838'799	4'966'524 reads (16,8%)	127'725	TBL3_1_H3K18_ac	7'215'658	467'750	474'769 reads (6,6%)	7'019	TBL3_2_H3K18_ac	34'571'877	2'878'572	2'923'353 reads (8,5%)	44'781	TBL3_1_H3K36me3	51'845'808	3'262'866	3'338'231 reads (6,4%)	75'365	TBL3_2_H3K36me3	25'160'921	3'820'804	3'912'043 reads (15,5%)	91'239
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Antibodies	anti-H3K18me1 (Abcam 177253), anti-H3K18Ac (Cell Signaling 96755), anti-H3K4me3 (Millipore 07-473), anti-H3K36me3 (ab9050) and IgG isotype control (Cell Signaling 27295).																																																																	
Peak calling parameters	<p>ChIP enrichment for each gene and upstream region was assessed by using DeepTools computeMatrix plotFingerprint and plotHeatmap functions.</p> <p>Read mapping was performed using the Rsubread align function on an indexed version of <i>Theileria annulata</i> genome assembly ASM322v1.32. Biological replicates correlation was assessed using PCA and Spearman/Pearson correlation coefficient computation using deepTools (v3.1.1) bamCoverage, multiBamSummary and plotCorrelation tools.</p> <p>Peak calling was only used to further confirm differences between H3K18me1 and H3K36me3. Peak calling was performed using macs2 using default parameters of callpeak and bdgdiff functions.</p>																																																																	
Data quality	<p>Raw reads were converted to Fastq files and their quality assessed using Aozan (version 2.2.1). Read-quality control was performed using fastQC (v0.11.7) and Rsubread (v1.26.1) qualityScore function.</p> <p>Biological replicates correlation was assessed using PCA and Spearman/Pearson correlation coefficient computation using deepTools (v3.1.1) bamCoverage, multiBamSummary and plotCorrelation tools.</p> <p>ChIP quality was assessed using DeepTools plotFingerprint function.</p>																																																																	
Software	<p>FastQC, Rsubread, IGV and DeepTools were used for ChIP-seq analysis.</p> <p>K-means clustering on H3K18me1 ChIPseq analysis was performed using the computeMatrix and plotHeatmap tools. Circos plot of ChIP-seq and RNA-seq experiment was done using circlize41 (v0.4.5).</p>																																																																	