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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

- Epson Connect software (Epson) for serial dilution assay picture acquisition
- Metamorph software (v7) (Universal Imaging Corporation) for cytology acquisition

Data analysis

- Trimmomatic (v0.35)
- Bowtie2 (v2.3.3)
- Samtools (v1.3.1)
- picard-tools (v2.1.0)
- deepTools (v2.0)
  - BamCompare (SES mode)
  - computeMatrix
  - plotHeatmap
- MACS2 (v2.1.1)
- IGV (v2.3.90)
- GATK HaplotypeCaller
- CNVkit (-wgs mode)
- Variant Effect Predictor (Ensembl)
- STAR (v2.2.1)
- Bioconductor (R):
  - Sushi (v1.22)
  - Rsamtools (v2.0.3)
  - GenomicFeatures (v1.36.4)
  - DESeq2 (v.1.24)
- Cutadapt (v1.17)

- SCRAM

- The complete Workflow Description Language (WDL) pipeline script used for ChIP-seq and variation analyses is available at: https://github.com/SitoTorres/Torres-Garcia-et-al.-2019

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 raw and processed reads from sequencing experiments are available at GEO with accession number GSE138436.

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

Life sciences study design

All studies must disclose on these points even when the disclosure is negative.

Sample size	No statistical measures were used to determine sample size. Sample sizes indicated below are considered standard in the field and were selected to ensure robust and statistically significant comparisons. For ChIP-qPCR and RT-qPCR experiments, biological triplicates (samples independently cultured for the experiment) were used. 2 biological replicates (samples independently cultured for the experiment) were performed for RNA-seq experiments. 1 small RNA-seq experiment was performed for each strain. 1 ChIP-seq experiment was performed for each strain and results were confirmed by ChIP-qPCR. For experiments performed to test whether specific genetic mutant strains form more caffeine-resistant colonies than wild-type cells, technical replicates were used to derive statistics. Equal volumes from a culture from each strain were plated on 20 or 40 (indicated in figure legend) caffeine-containing media plates. After 7 days, the number of caffeine-resistant colonies on each plate was counted. Sample sizes are provided in the figure legend.
Data exclusions	There were no data exclusions
Replication	Findings were reliably reproduced. For ChIP-qPCR and RT-qPCR, data are mean +/- standard deviation from 3 biological replicates. ChIP-seq experiments were performed once but results were confirmed by ChIP-qPCR. Serial dilution growth assays were repeated at least twice on different days with similar results.
Randomization	No randomization was required because the results of physical measurements of biomolecules, phenotypic analysis (e.g., drug resistance test) or sequencing of nucleic acid libraries are not affected by sample randomization.
Blinding	No blinding was required because the results of physical measurements of biomolecules, phenotypic analysis (e.g., drug resistance test), or sequencing of nucleic acid libraries are not affected by the researchers knowledge of sample identities.

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

- Anti-H3K9me2 - Mouse monoclonal 5.1.1 - for H3K9me2 ChIP-seq and ChIP-qPCR. Kindly provided by Takeshi Urano. 1 ug per ChIP-qPCR. 3 ug per ChIP-seq.
- Anti-GFP - Invitrogen - A11122 - for GFP ChIP-qPCR and cytology. 2 ug per ChIP-qPCR. 1:500 for cytology. Lot# 2083201.
- Anti-rabbit - Invitrogen - A21441 - as secondary antibody for cytology. 1:1000. Lot# 1003212.
- Anti-FLAG-HRP - Sigma - A8591 - for western analysis. 1:5000. Lot# SLCF0816
- Anti-Myc - Cell Signalling - 9B11 - for western analysis. 1:1000. Lot# 24
- Anti-alpha-tubulin - for western analysis. Kindly provided by Keith Gull. 1:15000.
- Anti-mouse - Sigma - A4416 - as secondary antibody for western analysis. 1:10000. Lot# SLCD0197
- Anti-Bip1 - for western analysis. Lab stock. 1:1000.
- Anti-rabbit - Sigma - A6154 - as secondary antibody for western analysis. 1:10000. Lot# SLCD6835
- Anti-Cdc11 - for western analysis. Kindly provided by Ken Sawin. 1:1000.
- Anti-sheep - Abcam - ab6900 - as secondary antibody for western analysis. 1:10000.

Validation

- Mouse mAb 5.1.1: Raised in Urano Lab, validated in Nakagawachi et al (2003) Oncogone 22, 8835. Additionally, this antibody has been validated in our lab using a strain lacking the H3K9 methyltransferase.
- Anti-a-tubulin raised in Gull lab, validated in Woods et al (1989) J. Cell. Sci. 93 (Pt 3), 491–500.
- Anti-Bip1 raised and validated in Pidoux & Armstrong (1993) J. Cell. Sci. 105 (Pt 4), 1115–1120.
- Anti-Cdc11 utilized in Tong et al (2019) Nat. Commun. 10, 2343.
- All other antibodies have been extensively used for ChIP, western and cytology analyses in our laboratory and have been validated using no tag (GFP/FLAG/Myc) controls. For previous studies where these antibodies have been used see Tong et al. (2019) Nat. Commun and Bayne et al. (2010) Cell.

Eukaryotic cell lines

Policy information about cell lines

Cell line source(s)

All Schizosaccharomyces pombe strains used in this study are derivatives of 972 h- or other commonly used lab strains. Detailed genotypes are listed in Supplementary Table 2.

Strain number Name Source

143 wt Lab stock
B4411 SR-1 This study
B4412 SR-2 This study
B4413 UR-1 This study
B4414 UR-2 This study
B4415 UR-3 This study
B4416 UR-4 This study
B4417 UR-5 This study
B4418 UR-6 This study
B4419 UR-7 This study
B4420 UR-8 This study
B4421 UR-9 This study
B4422 UR-10 This study
B4423 UR-11 This study
B4424 UR-12 This study
B4425 UR-13 This study
B4426 UR-14 This study
B4427 UR-15 This study
B4428 UR-16 This study
B4429 UR-17 This study
B4430 UR-18 This study
B4431 UR-19 This study
B4432 UR-20 This study
B4433 UR-21 This study

B4434 UR-22 This study
B4435 UR-23 This study
B4436 UR-24 This study
B4437 UR-25 This study
B4438 UR-26 This study
B4439 UR-27 This study
B4440 UR-28 This study
B4441 UR-29 This study
B4442 UR-30 This study
B4443 SR-1 clr4D - 1 This study
B4444 SR-1 clr4D - 2 This study
B4445 SR-1 NAT control - 1 This study
B4446 SR-1 NAT control - 2 This study
B4447 SR-2 clr4D - 1 This study
B4448 SR-2 clr4D - 2 This study
B4449 SR-2 NAT control - 1 This study
B4450 SR-2 NAT control - 2 This study
B4451 UR-1 clr4D - 1 This study
B4452 UR-1 clr4D - 2 This study
B4453 UR-1 NAT control-1 This study
B4454 UR-1 NAT control-2 This study
B4455 UR-2 clr4D - 1 This study
B4456 UR-2 clr4D - 2 This study
B4457 UR-2 NAT control - 1 This study
B4458 UR-2 NAT control - 2 This study
B5022 UR-2 dcr1D - 1 This study
B5023 UR-2 dcr1D - 2 This study
B5024 UR-2 ago1D - 1 This study
B5025 UR-2 ago1D - 2 This study
B4352 Pap1-N424STOP This study
B4752 Clr5-Q264STOP Meu27-S100Y This study
B4459 UR-2 +14 days -CAF This study
B4460 hba1D This study
B4461 SPBC17G9.12cD This study
B4462 ncRNA.393D This study
B4463 ncRNA.394D This study
B4464 eno101D This study
B3797 TetR-Clr4* This study
B3808 4xtetO-II This study
B3813 4xtetO-I This study
B3820 4xtetO-III This study
B4707 4xtetO-IV This study
B4465 TetR-Clr4* + 4xtetO-II This study
B4466 TetR-Clr4* + 4xtetO-I This study
B4467 TetR-Clr4* + 4xtetO-III This study
B4807 TetR-Clr4* + 4xtetO-IV This study
B4885 cup1-3xDSR This study
B5005 cup1-TT This study
B4688 Cup1-L73G This study
B4690 Cup1-F99G This study
B4567 Cup1-GFP This study
B4909 Cup1-GFP Arg11-mCh This study
B4912 Arg11-mCherry This study
B4468 UR-2 (7day/+CAF) This study
B4469 UR-2 (7day/+CAF - 14 day/-CAF) This study
B4621 epe1D This study
B2835 Epe1-GFP This study
B4958 3xFLAG-Epe1 This study
B4767 TetR-Clr4* + 4xtetO-III epe1D This study
B1008 clr4D Lab stock
B3250 S. cerevisiae Sgo1-GFP Lab stock
B3111 S. octosporus wt Lab stock
B4108 Mst2-13xMyc This study
B0505 Gcn5-13xMyc Lab stock

Authentication

All strains were generated by transformation and combined using genetic crosses. Strains were verified by the presence or absence or marker genes allowing growth on selective medium and/or by PCR to determine the presence of the desired genetic alteration and/or by DNA sequencing and/or western blotting to confirm the presence of epitope tags, as

	appropriate.
Mycoplasma contamination	Not applicable - Yeast strains were not tested for mycoplasma contamination, but all cultures were observed by microscopy to be free of bacterial contamination.
Commonly misidentified lines (See ICLAC register)	No commonly misidentified lines were used. This study used the yeast Schizosaccharomyces pombe.

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.*	GSE138436
Files in database submission	K9me2_wt_input_P1.fastq.gz K9me2_wt_input_P2.fastq.gz K9me2_wt_IP_P1.fastq.gz K9me2_wt_IP_P2.fastq.gz K9me2_UR1_input_P1.fastq.gz K9me2_UR1_input_P2.fastq.gz K9me2_UR1_IP_P1.fastq.gz K9me2_UR1_IP_P2.fastq.gz K9me2_UR2_input_P1.fastq.gz K9me2_UR2_input_P2.fastq.gz K9me2_UR2_IP_P1.fastq.gz K9me2_UR2_IP_P2.fastq.gz K9me2_UR3_input_P1.fastq.gz K9me2_UR3_input_P2.fastq.gz K9me2_UR3_IP_P1.fastq.gz K9me2_UR3_IP_P2.fastq.gz K9me2_UR4_input_P1.fastq.gz K9me2_UR4_input_P2.fastq.gz K9me2_UR4_IP_P1.fastq.gz K9me2_UR4_IP_P2.fastq.gz K9me2_UR5_input_P1.fastq.gz K9me2_UR5_input_P2.fastq.gz K9me2_UR5_IP_P1.fastq.gz K9me2_UR5_IP_P2.fastq.gz K9me2_UR6_input_P1.fastq.gz K9me2_UR6_input_P2.fastq.gz K9me2_UR6_IP_P1.fastq.gz K9me2_UR6_IP_P2.fastq.gz K9me2_UR7_input_P1.fastq.gz K9me2_UR7_input_P2.fastq.gz K9me2_UR7_IP_P1.fastq.gz K9me2_UR7_IP_P2.fastq.gz K9me2_UR8_input_P1.fastq.gz K9me2_UR8_input_P2.fastq.gz K9me2_UR8_IP_P1.fastq.gz K9me2_UR8_IP_P2.fastq.gz K9me2_UR9_input_P1.fastq.gz K9me2_UR9_input_P2.fastq.gz K9me2_UR9_IP_P1.fastq.gz K9me2_UR9_IP_P2.fastq.gz K9me2_UR10_input_P1.fastq.gz K9me2_UR10_input_P2.fastq.gz K9me2_UR10_IP_P1.fastq.gz K9me2_UR10_IP_P2.fastq.gz K9me2_UR11_input_P1.fastq.gz K9me2_UR11_input_P2.fastq.gz K9me2_UR11_IP_P1.fastq.gz K9me2_UR11_IP_P2.fastq.gz K9me2_UR12_input_P1.fastq.gz K9me2_UR12_input_P2.fastq.gz

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Total_RNAseq_wt_7mM_CAF_2_forward.bw
Total_RNAseq_wt_7mM_CAF_2_reverse.bw
Total_RNAseq_wt_14mM_CAF_1_P1.fastq.gz
Total_RNAseq_wt_14mM_CAF_1_P2.fastq.gz
Total_RNAseq_wt_14mM_CAF_2_P1.fastq.gz
Total_RNAseq_wt_14mM_CAF_2_P2.fastq.gz
Total_RNAseq_wt_14mM_CAF_1_forward.bw
Total_RNAseq_wt_14mM_CAF_1_reverse.bw
Total_RNAseq_wt_14mM_CAF_2_forward.bw
Total_RNAseq_wt_14mM_CAF_2_reverse.bw

Genome browser session
(e.g. UCSC)

Not applicable. Visualized data using IGV.

Methodology

Replicates

1 ChIP-seq was performed for each strain. Results were confirmed by ChIP-qPCR.

Sequencing depth

All libraries were sequenced by 75 bp paired-end reads. We did not calculate number of uniquely mapped reads, since Bowtie2 default options do not do so. Heterochromatin regions/sequences are repetitive and the number of uniquely mapped reads is not informative. Number of total reads for each fastq file are provided below:

Sample Total reads
K9me2_wt_input_P1.fastq.gz 4657568
K9me2_wt_input_P2.fastq.gz 4657568
K9me2_wt_IP_P1.fastq.gz 11558824
K9me2_wt_IP_P2.fastq.gz 11558824
K9me2_UR1_input_P1.fastq.gz 24492873
K9me2_UR1_input_P2.fastq.gz 24492873
K9me2_UR1_IP_P1.fastq.gz 23508431
K9me2_UR1_IP_P2.fastq.gz 23508431
K9me2_UR2_input_P1.fastq.gz 1470372
K9me2_UR2_input_P2.fastq.gz 1470372
K9me2_UR2_IP_P1.fastq.gz 7862615
K9me2_UR2_IP_P2.fastq.gz 7862615
K9me2_UR3_input_P1.fastq.gz 28636264
K9me2_UR3_input_P2.fastq.gz 28636264
K9me2_UR3_IP_P1.fastq.gz 22145255
K9me2_UR3_IP_P2.fastq.gz 22145255
K9me2_UR4_input_P1.fastq.gz 1742547
K9me2_UR4_input_P2.fastq.gz 1742547
K9me2_UR4_IP_P1.fastq.gz 8439033
K9me2_UR4_IP_P2.fastq.gz 8439033
K9me2_UR5_input_P1.fastq.gz 2007651
K9me2_UR5_input_P2.fastq.gz 2007651
K9me2_UR5_IP_P1.fastq.gz 8024785
K9me2_UR5_IP_P2.fastq.gz 8024785
K9me2_UR6_input_P1.fastq.gz 1842928
K9me2_UR6_input_P2.fastq.gz 1842928
K9me2_UR6_IP_P1.fastq.gz 8120241
K9me2_UR6_IP_P2.fastq.gz 8120241
K9me2_UR7_input_P1.fastq.gz 2653694
K9me2_UR7_input_P2.fastq.gz 2653694
K9me2_UR7_IP_P1.fastq.gz 8632643
K9me2_UR7_IP_P2.fastq.gz 8632643
K9me2_UR8_input_P1.fastq.gz 7639839
K9me2_UR8_input_P2.fastq.gz 7639839
K9me2_UR8_IP_P1.fastq.gz 15412350
K9me2_UR8_IP_P2.fastq.gz 15412350
K9me2_UR9_input_P1.fastq.gz 4554001
K9me2_UR9_input_P2.fastq.gz 4554001
K9me2_UR9_IP_P1.fastq.gz 11021688
K9me2_UR9_IP_P2.fastq.gz 11021688
K9me2_UR10_input_P1.fastq.gz 5176464
K9me2_UR10_input_P2.fastq.gz 5176464
K9me2_UR10_IP_P1.fastq.gz 13223029
K9me2_UR10_IP_P2.fastq.gz 13223029
K9me2_UR11_input_P1.fastq.gz 4636366
K9me2_UR11_input_P2.fastq.gz 4636366
K9me2_UR11_IP_P1.fastq.gz 12148357
K9me2_UR11_IP_P2.fastq.gz 12148357
K9me2_UR12_input_P1.fastq.gz 5608106
K9me2_UR12_input_P2.fastq.gz 5608106
K9me2_UR12_IP_P1.fastq.gz 12336535
K9me2_UR12_IP_P2.fastq.gz 12336535
K9me2_UR13_input_P1.fastq.gz 1632034
K9me2_UR13_input_P2.fastq.gz 1632034
K9me2_UR13_IP_P1.fastq.gz 7052099
K9me2_UR13_IP_P2.fastq.gz 7052099
K9me2_UR14_input_P1.fastq.gz 1638982
K9me2_UR14_input_P2.fastq.gz 1638982
K9me2_UR14_IP_P1.fastq.gz 8411534
K9me2_UR14_IP_P2.fastq.gz 8411534

K9me2_UR15_input_P1.fastq.gz 1328085
K9me2_UR15_input_P2.fastq.gz 1328085
K9me2_UR15_IP_P1.fastq.gz 7511500
K9me2_UR15_IP_P2.fastq.gz 7511500
K9me2_UR16_input_P1.fastq.gz 1574195
K9me2_UR16_input_P2.fastq.gz 1574195
K9me2_UR16_IP_P1.fastq.gz 7552346
K9me2_UR16_IP_P2.fastq.gz 7552346
K9me2_UR17_input_P1.fastq.gz 1906114
K9me2_UR17_input_P2.fastq.gz 1906114
K9me2_UR17_IP_P1.fastq.gz 8182937
K9me2_UR17_IP_P2.fastq.gz 8182937
K9me2_UR18_input_P1.fastq.gz 1684998
K9me2_UR18_input_P2.fastq.gz 1684998
K9me2_UR18_IP_P1.fastq.gz 4860918
K9me2_UR18_IP_P2.fastq.gz 4860918
K9me2_UR19_input_P1.fastq.gz 1875542
K9me2_UR19_input_P2.fastq.gz 1875542
K9me2_UR19_IP_P1.fastq.gz 7053803
K9me2_UR19_IP_P2.fastq.gz 7053803
K9me2_UR20_input_P1.fastq.gz 1755882
K9me2_UR20_input_P2.fastq.gz 1755882
K9me2_UR20_IP_P1.fastq.gz 7803452
K9me2_UR20_IP_P2.fastq.gz 7803452
K9me2_UR21_input_P1.fastq.gz 1854096
K9me2_UR21_input_P2.fastq.gz 1854096
K9me2_UR21_IP_P1.fastq.gz 7963343
K9me2_UR21_IP_P2.fastq.gz 7963343
K9me2_UR22_input_P1.fastq.gz 1534548
K9me2_UR22_input_P2.fastq.gz 1534548
K9me2_UR22_IP_P1.fastq.gz 7713816
K9me2_UR22_IP_P2.fastq.gz 7713816
K9me2_UR23_input_P1.fastq.gz 1786133
K9me2_UR23_input_P2.fastq.gz 1786133
K9me2_UR23_IP_P1.fastq.gz 7886760
K9me2_UR23_IP_P2.fastq.gz 7886760
K9me2_UR24_input_P1.fastq.gz 1623522
K9me2_UR24_input_P2.fastq.gz 1623522
K9me2_UR24_IP_P1.fastq.gz 8527474
K9me2_UR24_IP_P2.fastq.gz 8527474
K9me2_UR25_input_P1.fastq.gz 1664888
K9me2_UR25_input_P2.fastq.gz 1664888
K9me2_UR25_IP_P1.fastq.gz 8235632
K9me2_UR25_IP_P2.fastq.gz 8235632
K9me2_UR26_input_P1.fastq.gz 1674916
K9me2_UR26_input_P2.fastq.gz 1674916
K9me2_UR26_IP_P1.fastq.gz 6584663
K9me2_UR26_IP_P2.fastq.gz 6584663
K9me2_UR27_input_P1.fastq.gz 1591681
K9me2_UR27_input_P2.fastq.gz 1591681
K9me2_UR27_IP_P1.fastq.gz 7201369
K9me2_UR27_IP_P2.fastq.gz 7201369
K9me2_UR28_input_P1.fastq.gz 1700557
K9me2_UR28_input_P2.fastq.gz 1700557
K9me2_UR28_IP_P1.fastq.gz 8257483
K9me2_UR28_IP_P2.fastq.gz 8257483
K9me2_UR29_input_P1.fastq.gz 1697044
K9me2_UR29_input_P2.fastq.gz 1697044
K9me2_UR29_IP_P1.fastq.gz 8492861
K9me2_UR29_IP_P2.fastq.gz 8492861
K9me2_UR30_input_P1.fastq.gz 1539579
K9me2_UR30_input_P2.fastq.gz 1539579
K9me2_UR30_IP_P1.fastq.gz 7862112
K9me2_UR30_IP_P2.fastq.gz 7862112
K9me2_SR1_input_P1.fastq.gz 5049507
K9me2_SR1_input_P2.fastq.gz 5049507
K9me2_SR1_IP_P1.fastq.gz 11333792
K9me2_SR1_IP_P2.fastq.gz 11333792

K9me2_UR2_7_days_CAF_input_P1.fastq.gz 1590914
K9me2_UR2_7_days_CAF_input_P2.fastq.gz 1590914
K9me2_UR2_7_days_CAF_IP_P1.fastq.gz 8276251
K9me2_UR2_7_days_CAF_IP_P2.fastq.gz 8276251
K9me2_UR2_7_days_CAF_14_days_no_CAF_input_P1.fastq.gz 1668325
K9me2_UR2_7_days_CAF_14_days_no_CAF_input_P2.fastq.gz 1668325
K9me2_UR2_7_days_CAF_14_days_no_CAF_IP_P1.fastq.gz 7837845
K9me2_UR2_7_days_CAF_14_days_no_CAF_IP_P2.fastq.gz 7837845
K9me2_wt_no_treat_input_P1.fastq.gz 2484101
K9me2_wt_no_treat_input_P2.fastq.gz 2484101
K9me2_wt_no_treat_IP_P1.fastq.gz 7881079
K9me2_wt_no_treat_IP_P2.fastq.gz 7881079
K9me2_wt_7mM_CAF_input_P1.fastq.gz 2606829
K9me2_wt_7mM_CAF_input_P2.fastq.gz 2606829
K9me2_wt_7mM_CAF_IP_P1.fastq.gz 9212592
K9me2_wt_7mM_CAF_IP_P2.fastq.gz 9212592
K9me2_wt_14mM_CAF_input_P1.fastq.gz 2472114
K9me2_wt_14mM_CAF_input_P2.fastq.gz 2472114
K9me2_wt_14mM_CAF_IP_P1.fastq.gz 7870676
K9me2_wt_14mM_CAF_IP_P2.fastq.gz 7870676
K9me2_wt_1mM_H2O2_input_P1.fastq.gz 6680370
K9me2_wt_1mM_H2O2_input_P2.fastq.gz 6680370
K9me2_wt_1mM_H2O2_IP_P1.fastq.gz 10697650
K9me2_wt_1mM_H2O2_IP_P2.fastq.gz 10697650
K9me2_clr5meu27_input_P1.fastq.gz 6748422
K9me2_clr5meu27_input_P2.fastq.gz 6748422
K9me2_clr5meu27_IP_P1.fastq.gz 30064927
K9me2_clr5meu27_IP_P2.fastq.gz 30064927
K9me2_epe1D_input_P1.fastq.gz 1542750
K9me2_epe1D_input_P2.fastq.gz 1542750
K9me2_epe1D_IP_P1.fastq.gz 5929968
K9me2_epe1D_IP_P2.fastq.gz 5929968

Antibodies

Mouse mAb 5.1.1 anti-H3K9me2 for H3K9me2 ChIP-seq

Peak calling parameters

macs2 callpeak -f BAMPE -t sample.bam -c sample.bam --broad -g 14e6 --broad-cutoff 0.05 -n sample

Data quality

MACS2 was used to call peaks from paired-end ChIP-seq reads

Software

- Trimmomatic (v0.35)
- Bowtie2 (v2.3.3)
- Samtools (v1.3.1)
- picard-tools (v2.1.0)
- deepTools (v2.0)
  - BamCompare (SES mode)
  - computeMatrix
  - plotHeatmap
- MACS2 (v2.1.1)
- IGV (v2.3.90)
- Bioconductor (R):
  - Sushi (v1.22)
- The complete Workflow Description Language (WDL) pipeline script used for ChIP-seq and variation analyses is available at: https://github.com/SitoTorres/Torres-Garcia-et-al.-2019