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Corresponding author(s): Brian Huntly, George Vassiliou

☐ Initial submission ☐ Revised version ☒ Final submission

Life Sciences Reporting Summary

Nature Research wishes to improve the reproducibility of the work that we publish. This form is intended for publication with all accepted life science papers and provides structure for consistency and transparency in reporting. Every life science submission will use this form; some list items might not apply to an individual manuscript, but all fields must be completed for clarity.

For further information on the points included in this form, see Reporting Life Sciences Research. For further information on Nature Research policies, including our data availability policy, see Authors & Referees and the Editorial Policy Checklist.

Experimental design

1. Sample size

Describe how sample size was determined.

Sample sizes were chosen based on power calculations of expected differences and prior experience with these types of experiments. Sample sizes of n=3 mice per genotype/cell culture were chosen for most experiments with the exception of flow cytometric analysis and mouse experiments where sample size was increased to account for variation between individuals or for the need to carry out experiments at more than one timepoint. For most of the ChIP-Seq, RNA-Seq and ATAC-Seq experiments sample size of n=2 mice per genotype were chosen in keeping with accepted practice in the field.

2. Data exclusions

Describe any data exclusions.

No data were excluded from the analysis

3. Replication

Describe whether the experimental findings were reliably reproduced.

We noted that ATAC-Seq samples for Chd4 gRNA datasets had lower replicate reproducibility score:
A_WT1_empty A_WT2_empty 0.78
A_WT1_gRNA_Chd4_1 A_WT2_gRNA_Chd4_1 0.66
We perform DiffBind analysis and obtained significant number of differentially open/closed sites however we can't exclude the possibility that we may have not adequately captured several loci regulated by Chd4.

4. Randomization

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

Animals were allocated to the study groups by genotype.

5. Blinding

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

Although the investigators were not blinded to the genotype of the animals, the animal technicians who provided the animal care, supervision and identification of sick animals on "tumor watch" (therefore making the decision to sacrifice sick animals) were blinded in order to eliminate survival bias.

Note: all studies involving animals and/or human research participants must disclose whether blinding and randomization were used.

6. Statistical parameters

For all figures and tables that use statistical methods, confirm that the following items are present in relevant figure legends (or in the Methods section if additional space is needed).

n/a	Confirmed
☐	☒ The exact sample size (*n*) for each experimental group/condition, given as a discrete number and unit of measurement (animals, litters, cultures, etc.)
☐	☒ A description of how samples were collected, noting whether measurements were taken from distinct samples or whether the same sample was measured repeatedly
☐	☒ A statement indicating how many times each experiment was replicated
☐	☒ The statistical test(s) used and whether they are one- or two-sided (note: only common tests should be described solely by name; more complex techniques should be described in the Methods section)
☐	☒ A description of any assumptions or corrections, such as an adjustment for multiple comparisons
☐	☒ The test results (e.g. *P* values) given as exact values whenever possible and with confidence intervals noted
☐	☒ A clear description of statistics including central tendency (e.g. median, mean) and variation (e.g. standard deviation, interquartile range)
☐	☒ Clearly defined error bars

See the web collection on statistics for biologists for further resources and guidance.

Software

Policy information about availability of computer code

7. Software

Describe the software used to analyze the data in this study.	GraphpadPrism, FlowJo (10), BioVenn, DESeq2(1.6.3), UCSC Genome Browser, GSEA, HOMER (4.7.2), Proteome Discoverer (1.4), Mascot (2.5), SAINTexpress, Control Freek, TopHat (2.0.13), GenomicAlignments (1.2.2), Bowtie2, SICER(1.1), DiffBind(2.6.6), MACS2(2.0.10), Living Image (4.3.1), WashU Epigenome Browser

For manuscripts utilizing custom algorithms or software that are central to the paper but not yet described in the published literature, software must be made available to editors and reviewers upon request. We strongly encourage code deposition in a community repository (e.g. GitHub). *Nature Methods* guidance for providing algorithms and software for publication provides further information on this topic.

Materials and reagents

Policy information about availability of materials

8. Materials availability

Indicate whether there are restrictions on availability of unique materials or if these materials are only available for distribution by a for-profit company.	No unique materials were used. All antibodies used in the study were obtained commercially.

9. Antibodies

Describe the antibodies used and how they were validated for use in the system under study (i.e. assay and species).

Antibody used for ChIP-Seq, ChIP-qPCR, IP, WB:

H3K4Me1 (Diagenode, #pAb-194-050, lot: A1862D),
H3K27Me3 (Abcam, #Ab6002,lot GR137554-2),
H3K27Ac (Diagenode, #pAb-196-050, lot: A1723-0041D).
PU.1 (Santa Cruz Biotechnology, sc-352x, lot: F2713).
UTX (Bethyl, A302-374A)
UTX (GeneTex, GTX121246, lot: 41563)
CHD4 (Abcam, ab72418, lot: GR300277-1)
BRG1 (Santa Cruz Biotechnology, sc-10768, clone: H-88, lot: L3115)
IgG (Santa Cruz Biotechnology, sc-2027, lot: L2414)
α-tubulin (Sigma, T6074, clone: B-5-1-2, lot: 103M4773)
HRP-linked donkey anti-rabbit (GE Healthcare UK, NA934V, lot: 9593792)
ECL HRP-linked anti-mouse (Santa Cruz Biotechnology, sc-2005, lot: D1614)
ACITN (Santa Cruz Biotechnology, sc-1616, lot: L0414)

Antibody used for FACS:
CD4 (Biolegend, #100514, clone: RM4-5, lot: B171933)
CD5 (Biolegend, #100610, clone: 53-7.3, lot: B178256)
CD8a (Biolegend, # 100710, clone: 53-6.7, lot: B166422)
CD11b (Biolegend, #101210, clone: M1/70, lot: B167424)
B220 (Biolegend, #103210, clone: RA3-6B2, lot: E07569-1635)
TER-119 (Biolegend, #116210, clone: TER-119, lot: B169021)
GR-1 (Biolegend, #108410, clone: RB6-8C5, lot: B179158)
SCA-1 (Biolegend, #122520, clone: E13-161.7, lot: B174209)
CD117 (eBioscience, # 47-1171-82, clone: 2B8, lot: E08461-1637)
CD48 (Biolegend, #103411, clone: HM-48-1, lot: B214727)
CD150 (Biolegend, #115913, clone: TC15-12F12.2, lot: B172059)
CD34 (BD Pharmigen, #553733, clone: RAM34, lot: 4319145)
FLT3 (BD Pharmigen, #553842, clone: A2F10.1, lot: 6148682)
MAC1 (BD Pharmigen, #52-01712J, lot: 6169944)
GR1 (BD Pharmigen, #51-01212J, lot: 6169943)
CD3 (BD Pharmigen, #51-01082J, lot: 6169941)
B220 (BD Pharmigen, #51-01122J, lot: 6169942)
TER119 (BD Pharmigen, #51-09082J, lot: 6169946)
IL7Ra (Biolegend, #135008, clone: A7R34, lot:B190405)
IL7Ra (Biolegend, #121103, clone: SB/199, lot: B176923)
Streptavidin (Biolegend, #405206, lot: B182997)
CD16/32 (BD Pharmigen, #553145, clone: 2.4G2, lot: 3123812)
c-KIT (BioLegend, #105812, clone: 2B8, lot: B217855)
NK (LSBio, LS-C62548, lot: 44694)
CD45 (BD Pharmigen, #563891, clone: 30-F11, lot: 4276708)
CD11b (BD Pharmigen, #557657, clone: M1/70, lot: 4275513)
GR1 (BD Pharmigen, #560603, clone: 1A8, lot: 4290881)
TER119 (BD Pharmigen, #557915, clone: TER-119, lot: 7100737)
CD3e (eBioscience, #12-0031-82, clone: 145-2C11, lot: 4308509)

Antibodies used in this study were previously validated and published in multiple studies. Additionally, for each experiment we had relevant controls to ensure correct interpretation of results. For ChIP-Seq studies, we performed comparison of each antibody to IgG control (either by conducting control experiments - e.g., validation of antibody by immunoblot; small scale sequencing). Our datasets were also compared to publicly available data, where available, for corroboration.

10. Eukaryotic cell lines

a. State the source of each eukaryotic cell line used.

All cancer cell lines were obtained from the Sanger Institute Cancer Cell Collection.

b. Describe the method of cell line authentication used.

Cell lines used in the study had known mutation patterns. We performed q-PCR for UTX and UTY as validation.

c. Report whether the cell lines were tested for mycoplasma contamination.

All cell lines tested negative for Mycoplasma

d. If any of the cell lines used are listed in the database of commonly misidentified cell lines maintained by ICLAC, provide a scientific rationale for their use.

No commonly misidentified cell lines were used in the study.

Animals and human research participants

Policy information about studies involving animals; when reporting animal research, follow the ARRIVE guidelines

11. Description of research animals

Provide details on animals and/or animal-derived materials used in the study.

The Utx mouse model, C57/Bl6, was developed at the Sanger Institute. Utxf/f mice were crossed with Rosa-Flpe mice and then with Mx1-Cre mice. Cre expression was induced by intra-peritoneal injection of 5- to 6-week-old mice with pIpC (Sigma #P1530, 400 µg/mouse; 5 doses over a period of 10 days). All preleukemic experiments were performed 4-6 weeks post pIpC injection. Additional blood analysis was performed at 36-weeks post pIpC. For spontaneous tumor formation mice were aged for 22 months. Cas9-expressing mice (C57/Bl6) were reported previously (Tzelepis et al., 2016).

Policy information about studies involving human research participants

12. Description of human research participants

Describe the covariate-relevant population characteristics of the human research participants.

The study did not involved human research participants

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Flow Cytometry Reporting Summary

Form fields will expand as needed. Please do not leave fields blank.

Data presentation

For all flow cytometry data, confirm that:

☒ 1. The axis labels state the marker and fluorochrome used (e.g. CD4-FITC).

☒ 2. The axis scales are clearly visible. Include numbers along axes only for bottom left plot of group (a 'group' is an analysis of identical markers).

☒ 3. All plots are contour plots with outliers or pseudocolor plots.

☒ 4. A numerical value for number of cells or percentage (with statistics) is provided.

Methodological details

5. Describe the sample preparation.	These informations are provided in the supplementary materials and methods
6. Identify the instrument used for data collection.	Flow cytometry analysis was performed using the LSRFortessa instrument (BD)
7. Describe the software used to collect and analyze the flow cytometry data.	The data were analysed using FlowJo software
8. Describe the abundance of the relevant cell populations within post-sort fractions.	NA
9. Describe the gating strategy used.	Cells were gated according to physical parameters in order to discard cell debris (FSC/SSC) and cell clumps (width vs. Height). Gating strategy for progenitor population are provided in Fig.S2 of the manuscript

Tick this box to confirm that a figure exemplifying the gating strategy is provided in the Supplementary Information. ☒

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ChIP-seq Reporting Summary

Form fields will expand as needed. Please do not leave fields blank.

Data deposition

1. For all ChIP-seq data:

☒ a. Confirm that both raw and final processed data have been deposited in a public database such as GEO.

☒ b. Confirm that you have deposited or provided access to graph files (e.g. BED files) for the called peaks.

2. Provide all necessary reviewer access links.
The entry may remain private before publication.

http://www.ncbi.nlm.nih.gov/projects/geo/query/acc.cgi?acc=GSE86490,
https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE101307

3. Provide a list of all files available in the database submission.

Raw files

KAMX52-WT1-H3K27Me3.bam
KAMX52-WT2-H3K27Me3.bam
KAMX52-KO1-H3K27Me3.bam
KAMX52-KO2-H3K27Me3.bam
KDM6A-H3K27Ac-WT1.bam
KDM6A-H3K27Ac-WT2.bam
KDM6A-H3K27Ac-KO1.bam
KDM6A-H3K27Ac-KO2.bam
KAMX34-4C-UTX-BETHYL-WT.bam
UTX-IP-BETHYL-C-WT.bam
BCOR-IP-IgG-Control.bam
KDM6A-H3K27Ac-INPUT.bam
UTX-IP-IgG-D-Control.bam
UTX_INPUT_A.bam
KAMX-WT1.bam
KAMX-WT2.bam
KAMX-WT3.bam
KAMX-KO1.bam
KAMX-KO2.bam
KAMX-KO3.bam
B_KO1_empty.cram
B_KO1_gRNA_Smarca4_2.cram
B_KO2_empty.cram
B_KO2_gRNA_Smarca4_2.cram
B_WT1_empty.cram
B_WT1_gRNA_Smarca4_2.cram
B_WT2_empty.cram
B_WT2_gRNA_Smarca4_2.cram
Input_10RT_KO1.cram
Input_10RT_WT1.cram
KAMX52_KO1_1F_H3K4me1.cram
KAMX52_KO2_1I_H3K4me1.cram
KAMX52_WT1_1G_H3K4me1.cram
KAMX52_WT2_1H_H3K4me1.cram
PU1_KO1_F.cram
PU1_KO2_F.cram
PU1_KO3_F.cram
PU1_WT1_F.cram

PU1_WT2_F.cram
PU1_WT3_F.cram
A_WT1_empty.cram
A_WT2_empty.cram
A_WT1_gRNA_Chd4_1.cram
A_WT2_gRNA_Chd4_1.cram

Processed files
KAMX52-WT1-H3K27Me3.bw
KAMX52-WT2-H3K27Me3.bw
KAMX52-KO1-H3K27Me3.bw
KAMX52-KO2-H3K27Me3.bw
KDM6A-H3K27Ac-WT1.bw
KDM6A-H3K27Ac-WT2.bw
KDM6A-H3K27Ac-KO1.bw
KDM6A-H3K27Ac-KO2.bw
KAMX34-4C-UTX-BETHYL-WT.bw
UTX-IP-BETHYL-C-WT.bw
BCOR-IP-IgG-Control.bw
KDM6A-H3K27Ac-INPUT.bw
UTX-IP-IgG-D-Control.bw
UTX_INPUT_A.bw
KAMX_1.bw
KAMX_2.bw
KAMX_3.bw
KAMX_4.bw
KAMX_5.bw
KAMX_6.bw
KAMX52_WT1_1G_H3K4me1.bw
KAMX52_WT2_1H_H3K4me1.bw
KAMX52_KO1_1F_H3K4me1.bw
KAMX52_KO2_1I_H3K4me1.bw
PU1_WT1_F.bw
PU1_WT2_F.bw
PU1_WT3_F.bw
PU1_KO1_F.bw
PU1_KO2_F.bw
PU1_KO3_F.bw
Input_10RT_WT1.bw
Input_10RT_KO1.bw
B_WT1_empty.bw
B_WT1_gRNA_Smarca4_2.bw
B_WT2_empty.bw
B_WT2_gRNA_Smarca4_2.bw
B_KO1_empty.bw
B_KO1_gRNA_Smarca4_2.bw
B_KO2_empty.bw
B_KO2_gRNA_Smarca4_2.bw
A_WT1_empty.bw
A_WT2_empty.bw
A_WT1_gRNA_Chd4_1.bw
A_WT2_gRNA_Chd4_1.bw

BED files

KAMX52-WT1-H3K27Me3.bed
KAMX52-WT2-H3K27Me3.bed
KAMX52-KO1-H3K27Me3.bed
KAMX52-KO2-H3K27Me3.bed

KDM6A-H3K27Ac-WT1.bed
KDM6A-H3K27Ac-WT2.bed
KDM6A-H3K27Ac-KO1.bed
KDM6A-H3K27Ac-KO2.bed
KAMX34-4C-UTX-BETHYL.bed
UTX-IP-BETHYL-C-WT.bed
KAMX_1_p1e-11.bed
KAMX_2_p1e-11.bed
KAMX_3_p1e-11.bed
KAMX_4_p1e-11.bed
KAMX_5_p1e-11.bed
KAMX_6_p1e-11.bed
KAMX52_WT1_1G_H3K4me1_peaks.bed
KAMX52_WT2_1H_H3K4me1_peaks.bed
KAMX52_KO1_1F_H3K4me1_peaks.bed
KAMX52_KO2_1I_H3K4me1_peaks.bed
PU1_WT1_F_peaks.bed
PU1_WT2_F_peaks.bed
PU1_WT3_F_peaks.bed
PU1_KO1_F_peaks.bed
PU1_KO2_F_peaks.bed
PU1_KO3_F_peaks.bed
B_WT1_empty_peaks.bed
B_WT1_gRNA_Smarca4_2_peaks.bed
B_WT2_empty_peaks.bed
B_WT2_gRNA_Smarca4_2_peaks.bed
B_KO1_empty_peaks.bed
B_KO1_gRNA_Smarca4_2_peaks.bed
B_KO2_empty_peaks.bed
B_KO2_gRNA_Smarca4_2_peaks.bed
A_WT1_empty_p1e-9_peaks.bed
A_WT2_empty_p1e-9_peaks.bed
A_WT1_gRNA_Chd4_1_p1e-9_peaks.bed
A_WT2_gRNA_Chd4_1_p1e-9_peaks.bed

4. If available, provide a link to an anonymized genome browser session (e.g. UCSC).

Methodological details

5. Describe the experimental replicates.

All experiments were performed with biological replicates

Replicate1 Replicate2 spearman correlation
KAMX52-WT1-H3K27Me3 KAMX52-WT2-H3K27Me3 0.91
KAMX52-KO1-H3K27Me3 KAMX52-KO2-H3K27Me3 0.88
KDM6A-H3K27Ac-WT1 KDM6A-H3K27Ac-WT2 0.84
KDM6A-H3K27Ac-KO1 KDM6A-H3K27Ac-KO2 0.85
KAMX-WT1 KAMX-WT2 0.87
KAMX-WT2 KAMX-WT3 0.87
KAMX-WT3 KAMX-WT1 0.88
KAMX-KO1 KAMX-KO2 0.84
KAMX-KO2 KAMX-KO3 0.85
KAMX-KO3 KAMX-KO1 0.84
KAMX52_WT1_1G_H3K4me1 KAMX52_WT2_1H_H3K4me1 0.91
KAMX52_KO1_1F_H3K4me1 KAMX52_KO2_1I_H3K4me1 0.85
PU1_WT1_F PU1_WT2_F 0.93
PU1_WT2_F PU1_WT3_F 0.94
PU1_WT3_F PU1_WT1_F 0.92

PU1_KO1_F PU1_KO2_F 0.93
PU1_KO2_F PU1_KO3_F 0.93
PU1_KO3_F PU1_KO1_F 0.95
B_WT1_empty B_WT2_empty 0.88
B_WT1_gRNA_Smarca4_2 B_WT2_gRNA_Smarca4_2 0.92
B_KO1_empty B_KO2_empty 0.94
B_KO1_gRNA_Smarca4_2 B_KO2_gRNA_Smarca4_2 0.9
A_WT1_empty A_WT2_empty 0.78
A_WT1_gRNA_Chd4_1 A_WT2_gRNA_Chd4_1 0.66

6. Describe the sequencing depth for each experiment.

filename readlength Single/Paired Total reads Uniquely mapped reads
KAMX52_WT1_1G_H3K4me1.cram 75 Paired 45408980 17214691
KAMX52_WT2_1H_H3K4me1.cram 75 Paired 45384755 19771043
KAMX52_KO1_1F_H3K4me1.cram 75 Paired 47570450 16220312
KAMX52_KO2_1I_H3K4me1.cram 75 Paired 51755680 24136397
PU1_WT1_F.cram 75 Paired 33533075 26102629
PU1_WT2_F.cram 75 Paired 37291482 28878852
PU1_WT3_F.cram 75 Paired 37252414 28965498
PU1_KO1_F.cram 75 Paired 40331995 31308279
PU1_KO2_F.cram 75 Paired 37420073 27408137
PU1_KO3_F.cram 75 Paired 37019325 28063223
Input_10RT_WT1.cram 75 Paired 40225812 27467687
Input_10RT_KO1.cram 75 Paired 41679214 28074519
B_WT1_empty.cram 75 Paired 37782992 17685362
B_WT1_gRNA_Smarca4_2.cram 75 Paired 33439995 20887328
B_WT2_empty.cram 75 Paired 37729109 21866047
B_WT2_gRNA_Smarca4_2.cram 75 Paired 35188441 22405984
B_KO1_empty.cram 75 Paired 38224099 16228832
B_KO1_gRNA_Smarca4_2.cram 75 Paired 43073551 17988332
B_KO2_empty.cram 75 Paired 39537397 19326627
B_KO2_gRNA_Smarca4_2.cram 75 Paired 36704028 19414033
KAMX52-WT1-H3K27Me3.bam 75 Paired 27263312 8656937
KAMX52-WT2-H3K27Me3.bam 75 Paired 24653639 6856589
KAMX52-KO1-H3K27Me3.bam 75 Paired 38173458 10730203
KAMX52-KO2-H3K27Me3.bam 75 Paired 28218085 9378647
KDM6A-H3K27Ac-WT1.bam 75 Paired 69928720 52708581
KDM6A-H3K27Ac-WT2.bam 75 Paired 64425283 50088674
KDM6A-H3K27Ac-KO1.bam 75 Paired 72368820 56091052
KDM6A-H3K27Ac-KO2.bam 75 Paired 61919322 46437231
KDM6A-H3K27Ac-INPUT.bam 75 Paired 66175531 41464655
KAMX34-4C-UTX-BETHYL-WT.bam 75 Paired 36950737 18493439
UTX-IP-BETHYL-C-WT.bam 75 Paired 53360163 32268969
BCOR-IP-IgG-Control.bam 75 Paired 42399198 22803111
UTX-IP-IgG-D-Control.bam 75 Paired 45791654 29770523
UTX_INPUT_A.bam 75 Paired 13948916 8822846
KAMX-WT1.bam 75 Paired 48753591 25372707
KAMX-WT2.bam 75 Paired 60308700 29131936
KAMX-WT3.bam 75 Paired 68031961 33275425
KAMX-KO1.bam 75 Paired 57770887 29929684
KAMX-KO2.bam 75 Paired 52716067 27014876
KAMX-KO3.bam 75 Paired 47436123 23713391
A_WT1_empty.cram 75 Paired 21180047 8999272
A_WT2_empty.cram 75 Paired 18424778 9328023
A_WT1_gRNA_ChD4_1 75 Paired 21488460 10371973
A_WT2_gRNA_Chd4_1 75 Paired 22939317 11635522

7. Describe the antibodies used for the ChIP-seq experiments.

Antibody used for ChIP-Seq:
H3K4Me1 (Diagenode, #pAb-194-050, lot: A1862D),

H3K27Me3 (Abcam, #Ab6002,lot GR137554-2),
H3K27Ac (Diagenode, #pAb-196-050, lot: A1723-0041D).
PU.1 (Santa Cruz Biotechnology, sc-352x, lot: F2713).
UTX (Bethyl, A302-374A, lot not provided)
Validation:
The antibody used in the study were recommended for ChIP-Seq application and are reported in several publication listed in the links below. Additionally all ChIP-Seq data provided in the manuscript were compared to IgG control (background control) in the study.
https://www.diagenode.com/en/p/h3k4me1-polyclonal-antibody-premium-50-mg-54-ml#
https://www.diagenode.com/en/p/h3k27ac-polyclonal-antibody-premium-sample-size-10-ug
http://www.abcam.com/histone-h3-tri-methyl-k27-antibody-mabcam-6002-chip-grade-ab6002-references.html
https://www.scbt.com/scbt/product/pu-1-antibody-t-21
https://www.bethyl.com/product/A302-374A

8. Describe the peak calling parameters.

Sequences were aligned to the mouse reference genome (assembly mm10) using Bowtie software (version 2.1.0). The identification of ChIP-seq enriched regions (peaks) was performed using SICER for Broad peaks with parameters W200 and G600. For ATAC sequencing, peaks were called with MACS2 with –nomodel and –nolambda parameters

9. Describe the methods used to ensure data quality.

Sample P-valuecutoff no. of peaks
KAMX52-WT1-H3K27Me3.bed 1.00E-08 18854
KAMX52-WT2-H3K27Me3.bed 1.00E-08 20417
KAMX52-KO1-H3K27Me3.bed 1.00E-08 15754
KAMX52-KO2-H3K27Me3.bed 1.00E-08 14674
KDM6A-H3K27Ac-WT1.bed 1.00E-08 29668
KDM6A-H3K27Ac-WT2.bed 1.00E-08 32171
KDM6A-H3K27Ac-KO1.bed 1.00E-08 30148
KDM6A-H3K27Ac-KO2.bed 1.00E-08 26488
KAMX34-4C-UTX-BETHYL.bed 1.00E-08 14508
UTX-IP-BETHYL-C-WT.bed 1.00E-08 3579
KAMX_1_p1e-11.bed 1.00E-11 57405
KAMX_2_p1e-11.bed 1.00E-11 57917
KAMX_3_p1e-11.bed 1.00E-11 57622
KAMX_4_p1e-11.bed 1.00E-11 45260
KAMX_5_p1e-11.bed 1.00E-11 50249
KAMX_6_p1e-11.bed 1.00E-11 44576
KAMX52_WT1_1G_H3K4me1_peaks.bed 1.00E-08 51394
KAMX52_WT2_1H_H3K4me1_peaks.bed 1.00E-08 54654
KAMX52_KO1_1F_H3K4me1_peaks.bed 1.00E-08 44089
KAMX52_KO2_1I_H3K4me1_peaks.bed 1.00E-08 43706
PU1_WT1_F_peaks.bed 1.00E-08 143628
PU1_WT2_F_peaks.bed 1.00E-08 143183
PU1_WT3_F_peaks.bed 1.00E-08 137850
PU1_KO1_F_peaks.bed 1.00E-08 171535
PU1_KO2_F_peaks.bed 1.00E-08 138373
PU1_KO3_F_peaks.bed 1.00E-08 161605
B_WT1_empty_peaks.bed 1.00E-09 50845
B_WT1_gRNA_Smarca4_2_peaks.bed 1.00E-09 42015
B_WT2_empty_peaks.bed 1.00E-09 50927
B_WT2_gRNA_Smarca4_2_peaks.bed 1.00E-09 46191
B_KO1_empty_peaks.bed 1.00E-09 40477
B_KO1_gRNA_Smarca4_2_peaks.bed 1.00E-09 35975
B_KO2_empty_peaks.bed 1.00E-09 41024
B_KO2_gRNA_Smarca4_2_peaks.bed 1.00E-09 29930

A_WT1_empty_p1e-9_peaks.bed 1.00E-09 48687
A_WT1_gRNA_Chd4_1_p1e-9_peaks.bed 1.00E-09 34429
A_WT2_empty_p1e-9_peaks.bed 1.00E-09 41480
A_WT2_gRNA_Chd4_1_p1e-9_peaks.bed 1.00E-09 24833

10. Describe the software used to collect and analyze the ChIP-seq data.

Differential binding was performed using DIffBind