

Reporting Summary

Nature Portfolio 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 Portfolio 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 (<i>n</i>) 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 <i>Only common tests should be described solely by name; describe more complex techniques in the Methods section.</i>
☒	☒ 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. <i>F</i> , <i>t</i> , <i>r</i>) with confidence intervals, effect sizes, degrees of freedom and <i>P</i> value noted <i>Give P values as exact values whenever suitable.</i>
☒	☐ 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 <i>d</i> , Pearson's <i>r</i>), 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	We used Illumina Casava (v.2.19) for the sequencing data and used prefetch (v.2.8.0) to download datasets from GEO sessions.
Data analysis	No custom code was developed for this project. We used bwa (v.0.7.12), picard-tools (v.1.95), BEDtools (v.2.17.0) and MACS2 (v.2.2.7.1) for mapping and analysis of ChIP-seq. STAR (v.2.4.0h72) and featureCounts (v.2.0.1) were used for RNA-seq gene expression calculation. For Hi-ChIP and Hi-C data, paired-end reads were aligned to the hg19 genome using the HiC-Pro pipeline (v.2.7.6) and default settings. The hicchipper tool (v.0.7.7) was used for Hi-ChIP loop calling by H3K27ac ChIP-seq peaks, applying the parameters; max distance 100000000. Differential loops between siEWS-WT1 and siCTL treated cells were then identified.

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 Portfolio [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 description of any restrictions on data availability
 - For clinical datasets or third party data, please ensure that the statement adheres to our [policy](#)

NGS data generated for this study are available at the Gene Expression Omnibus (GEO) under the accession number GSE212979. It contains the datasets GSE212976

(RNA-seq), GSE212977 (ChIP-seq), GSE212978 (Hi-ChIP) and GSE242863 (HiC).

Raw data for ChIP-seq profiles for two primary samples collected prior to 2015 were deposited under restricted access in dbGAP (database of Genotypes and Phenotypes) in order to protect the privacy of research participants (accession number phs003682, https://www.ncbi.nlm.nih.gov/projects/gap/cgi-bin/study.cgi?study_id=phs003682.v1.p1). Access can be requested through dbGAP by investigators who are permanent employees of their institutions at a level equivalent to tenure-track professor or senior scientist. Requests are managed by NCI's Data Access Committee, take approximately 2 weeks for approval and provide access for 12 months.

To implement our analysis we used the following publicly available dataset EGAD00001003980.

Human research participants

Policy information about [studies involving human research participants and Sex and Gender in Research.](#)

Reporting on sex and gender	Our findings do not apply to one sex or gender, therefore there is no sex- or gender based analysis.
Population characteristics	Donors were of no specific population, samples were collected from anonymous individuals. Samples were deidentified discarded tumor material, no further information was available besides tumor type
Recruitment	Primary tumor samples were obtained under informed consent and de-identified prior to analysis. Primary patient-derived DSRCT xenografts (SJDSRCT046151_X1) were obtained from the Childhood Solid Tumor Network (Stewart et al., 2016).
Ethics oversight	Samples were collected with approval from the Commission Cantonale d'éthique de la recherche sur l'être humain (CER-VD, protocol number 260/15), and IRB from Massachusetts General Hospital (MGH, Boston, USA).

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

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 selection was based on availability (no. of primary samples) and to provide sufficient statistical power to identify significant differences (providing replicates when feasible), given our previous knowledge about sample variation for the respective technique. Sample sizes were not pre-defined based on statistical methods.
Data exclusions	None of the data were excluded from the study. The data selection criteria for each downstream analysis are stated in the manuscript.
Replication	When possible, the experiments were replicated to verify reproducibility.
Randomization	Randomization was relevant only when comparing treatment on mice. Mice were randomly selected prior to the beginning of the treatment with the drug.
Blinding	All the data of the study were analyzed without pre-established conclusions.

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 and archaeology
☐	☒ Animals and other organisms
☒	☐ Clinical data
☒	☐ Dual use research of concern

Methods

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

Antibodies

Antibodies used	HA (clone 3F10, cat#11867423001, Roche) used at a final 1:1000 dilution V5 for western blot (SV5-Pk1, cat#ab27671, Abcam) used at a final 1:1000 dilution β -actin (AC-15, cat#ab6276, Abcam) used at a final 1:10 000 dilution WT1 (cat#12609-1-AP, Proteintech) used at a final 1:1000 dilution WT1 (C19, cat#sc-192, Santa Cruz Biotechnology) used at a final 1:200 dilution EWSR1 (G5, cat# sc-28327 Santa Cruz Biotechnology) used at a final 1:500 dilution GAPDH (HRP-conjugated: clone GAPDH-71.1, cat#G9295, Sigma) used at a final 1:10 000 dilution GAPDH (clone 6C5, cat# MAB374, Millipore) used at a final 1:10 000 dilution
Validation	V5/HA antibodies by western blot and ChIPseq of V5/HA construct overexpression vs control cells. The other antibodies have been validated by the manufacturers for the application used: https://www.sigmaaldrich.com/CH/fr/product/roche/roahaha https://www.cellsignal.com/products/primary-antibodies/v5-tag-d3h8q-rabbit-mab/13202 https://www.abcam.com/v5-tag-antibody-sv5-pk1-ab27671.html https://www.abcam.com/beta-actin-antibody-ac-15-ab6276.html https://www.merckmillipore.com/CH/en/product/Anti-Tubulin-Mouse-mAb-DM1A,EMD_BIO-CP06 https://www.ptglab.com/products/WT1-Antibody-12609-1-AP.htm https://www.scbt.com/p/wt1-antibody-c-19 https://www.sigmaaldrich.com/CH/fr/product/sigma/g9295 https://www.merckmillipore.com/CH/en/product/Anti-Glyceraldehyde-3-Phosphate-Dehydrogenase-Antibody-clone-6C5,MM_NF-MAB374 https://www.scbt.com/p/ews-antibody-g-5 https://www.cellsignal.com/products/primary-antibodies/tri-methyl-histone-h3-lys27-c36b11-rabbit-mab/9733 https://www.merckmillipore.com/CH/de/product/Anti-trimethyl-Histone-H3-Lys27-Antibody,MM_NF-07-449 https://www.abcam.com/histone-h3-acetyl-k9-antibody-chip-grade-ab4441.html https://www.abcam.com/histone-h3-mono-methyl-k4-antibody-chip-grade-ab8895.html https://www.activemotif.com/catalog/details/39133/histone-h3-acetyl-lys27-antibody-pab https://www.merckmillipore.com/CH/de/product/Anti-trimethyl-Histone-H3-Lys4-Antibody,MM_NF-07-473

Eukaryotic cell lines

Policy information about [cell lines and Sex and Gender in Research](#)

Cell line source(s)	MeT-5A (CRL-9444) and Lentix HEK293T (Takara #632180) were obtained from ATCC and Takara respectively. The JN-DSRCT1 cell line was a generous gift from Daniel Haber (Massachusetts General Hospital Cancer Center and Harvard Medical School, Charlestown, USA)
Authentication	We periodically evaluated the JN-DSRCT cell line for EWSR1-WT1 expression by immunoblotting.
Mycoplasma contamination	All cell cultures were periodically tested negative for mycoplasma contamination by PCR-based methods.
Commonly misidentified lines (See ICLAC register)	No commonly misidentified cell lines were used.

Animals and other research organisms

Policy information about [studies involving animals](#); [ARRIVE guidelines](#) recommended for reporting animal research, and [Sex and Gender in Research](#)

Laboratory animals	5-7 weeks old NOD/SCID c Gamma (NSG) mice were purchased from Jackson Laboratory, USA (stock number 005557). Light cycle (7AM-7PM) and humidity was controlled at all times. Temperatures varied between 20°C to 23°C. Food and water was accessible at all times, autoclaved or irradiated prior use. When needed, mice were fed with doxycycline-containing food (SAFE, U8200P Version 0115, A03 at 0.625 g/kg Doxycycline, irradiated). Mice were handle as little as possible. Nevertheless, all mice were monitored three times a week for tumor development, and
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sacrificed using CO₂ inhalation and cervical dislocation, when the tumor reached a maximum of 1500 mm³ volume or at the end of the experiment.

Wild animals

No wild animals were used.

Reporting on sex

Our findings do not apply to one sex or gender, therefore there is no sex- or gender based analysis.

Field-collected samples

No field collected samples were used in the study.

Ethics oversight

All mice experiments were approved by the Cantonal Veterinary Office, authorization number VD3021 and VD3437.

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

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.

<https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=gse212979>

Files in database submission

DSRCT1.H3K27ac
 DSRCT1.H3K27me3
 DSRCT1.H3K4m1
 DSRCT1.H3K4m3
 DSRCT1.H3K9ac
 DSRCT1.INPUT
 DSRCT2.H3K27ac
 DSRCT2.H3K27me3
 DSRCT2.H3K4me1
 DSRCT2.H3K4me3
 DSRCT2.H3K9ac
 DSRCT2.INPUT
 DSRCT3.H3K27ac
 DSRCT3.H3K27me3
 DSRCT3.H3K4me1
 DSRCT3.H3K4me3
 DSRCT3.H3K9ac
 DSRCT3.INPUT
 DSRCT4.H3K27ac
 DSRCT4.H3K27me3
 DSRCT4.H3K4me1
 DSRCT4.H3K4me3
 DSRCT4.H3K9ac
 DSRCT4.INPUT
 JN-DSRCT1.H3K27ac
 JN-DSRCT1.H3K27me3
 JN-DSRCT1.H3K4me1
 JN-DSRCT1.H3K4me3
 JN-DSRCT1.H3K9ac
 JN-DSRCT1.INPUT
 JN-DSRCT1.shEWSWT1.H3K27ac.1
 JN-DSRCT1.shEWSWT1.H3K27ac.2
 JN-DSRCT1.shEWSWT1.H3K4me1.1
 JN-DSRCT1.shEWSWT1.H3K4me1.2
 JN-DSRCT1.shEWSWT1.INPUT.1
 JN-DSRCT1.shEWSWT1.INPUT.2
 JN-DSRCT1.shEWSWT1.WT1.1
 JN-DSRCT1.shEWSWT1.WT1.2.a
 JN-DSRCT1.shEWSWT1.WT1.2.b
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 MeT-5A.control.H3K27ac.4
 MeT-5A.control.H3K27ac.5
 MeT-5A.control.H3K27ac.6
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 MeT-5A.control.HA.2
 MeT-5A.control.V5.1
 MeT-5A.control.V5.2
 MeT-5A.control.V5.3
 MeT-5A.control.V5.4
 MeT-5A.control.V5.5
 MeT-5A.control.V5.6
 MeT-5A.EV.INPUT
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 MeT-5A.EWSWT1+KTS.H3K27ac.1
 MeT-5A.EWSWT1-KTS.H3K27ac.2
 MeT-5A.EWSWT1+KTS.H3K27ac.2
 MeT-5A.EWSWT1-KTS.HA.1
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 MeT-5A.EWSWT1-KTS.V5.2
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 MeT-5A.EWS.YS37.WT1-KTS.V5.6
 MeT-5A.EWS.YS37.WT1+KTS.YS37.H3K27ac.5
 MeT-5A.EWS.YS37.WT1+KTS.YS37.H3K27ac.6
 MeT-5A.EWS.YS37.WT1+KTS.YS37.V5.5
 MeT-5A.EWS.YS37.WT1+KTS.YS37.V5.6
 MeT-5A.WT1-KTS.H3K27ac.3
 MeT-5A.WT1+KTS.H3K27ac.3
 MeT-5A.WT1-KTS.H3K27ac.4
 MeT-5A.WT1+KTS.H3K27ac.4
 MeT-5A.WT1-KTS.V5.3
 MeT-5A.WT1+KTS.V5.3
 MeT-5A.WT1-KTS.V5.4
 MeT-5A.WT1+KTS.V5.4

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

Provide a link to an anonymized genome browser session for "Initial submission" and "Revised version" documents only, to enable peer review. Write "no longer applicable" for "Final submission" documents.

Methodology

Replicates

There are four replicates from primary tumors. In addition, there are at least two replicates for JN-DSRCT1 and MeT-5A ChIP-seq samples.

Sequencing depth

Sample	Sequence_depth	Uniquely_mapped_reads	Mapping_ratio	Read_length	Single_read
DSRCT1.H3K27ac	16879805	13742566	0.814142462	50	Single
DSRCT1.H3K27me3	17113637	13134951	0.767513709	50	Single
DSRCT1.H3K4m1	14055200	11815758	0.84066808	50	Single
DSRCT1.H3K4m3	16316756	13783360	0.84473654	50	Single
DSRCT1.H3K9ac	15638883	12737407	0.814470381	50	Single
DSRCT1.INPUT	17873674	13952678	0.780627307	50	Single
DSRCT2.H3K27ac	18285565	16836520	0.920754705	50	Single

DSRCT2.H3K27me3 23950957 20758805 0.866721317 50 Single
 DSRCT2.H3K4me1 18656409 15455564 0.828431881 50 Single
 DSRCT2.H3K4me3 17393805 15910898 0.914745106 50 Single
 DSRCT2.H3K9ac 12740176 11683071 0.917025872 50 Single
 DSRCT2.INPUT 22561365 19570962 0.867454695 50 Single
 DSRCT3.H3K27ac 18226186 16590910 0.91027876 50 Single
 DSRCT3.H3K27me3 20313654 17591337 0.865985854 50 Single
 DSRCT3.H3K4me1 22127691 20337507 0.919097569 50 Single
 DSRCT3.H3K4me3 16393037 14876518 0.907490052 50 Single
 DSRCT3.H3K9ac 18974637 17199781 0.906461662 50 Single
 DSRCT3.INPUT 22380862 19262360 0.860662114 50 Single
 DSRCT4.H3K27ac 22055380 19930325 0.903649132 50 Single
 DSRCT4.H3K27me3 23611756 19939668 0.844480521 50 Single
 DSRCT4.H3K4me1 31024705 28107990 0.905987341 50 Single
 DSRCT4.H3K4me3 16552353 14974402 0.904669082 50 Single
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 DSRCT4.INPUT 39372076 33419028 0.848800251 50 Single
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 JN-DSRCT1.shEWSWT1.H3K4me1.1 27319475 25365775 0.928486913 50 Single
 JN-DSRCT1.shEWSWT1.H3K4me1.2 26661995 22452279 0.842107989 50 Single
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 MeT-5A.EWSWT1+KTS.H3K27ac.1 21724057 20014618 0.921311245 50 Single
 MeT-5A.EWSWT1-KTS.H3K27ac.2 28247812 26145474 0.925575191 50 Single
 MeT-5A.EWSWT1+KTS.H3K27ac.2 26819995 24670987 0.919872916 50 Single
 MeT-5A.EWSWT1-KTS.HA.1 31973947 28032519 0.876730014 50 Single
 MeT-5A.EWSWT1+KTS.HA.1 50184267 42881977 0.854490452 50 Single
 MeT-5A.EWSWT1-KTS.HA.2 27035019 23874365 0.883090373 50 Single
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 MeT-5A.EWSWT1+KTS-KTS.H3K27ac.1 24977572 22874324 0.915794538 50 Single
 MeT-5A.EWSWT1+KTS-KTS.H3K27ac.2 25624386 23469176 0.915892229 50 Single

	MeT-5A.EWSWT1+KTS-KTS.HA.1 32973576 28478226 0.863668108 50 Single MeT-5A.EWSWT1+KTS-KTS.HA.2 32308899 28496327 0.881996226 50 Single MeT-5A.EWSWT1+KTS-KTS.V5.1 33420515 29209674 0.874004305 50 Single MeT-5A.EWSWT1+KTS-KTS.V5.2 29296718 25869634 0.883021573 50 Single MeT-5A.EWSWT1-KTS.V5.1 39750178 33983109 0.854917153 50 Single MeT-5A.EWSWT1+KTS.V5.1 29490661 25788877 0.874476059 50 Single MeT-5A.EWSWT1-KTS.V5.2 30480350 26548353 0.870998955 50 Single MeT-5A.EWSWT1+KTS.V5.2 29369143 25966752 0.884150825 50 Single MeT-5A.EWS.YS37.WT1-KTS.H3K27ac.5 25509397 19403918 0.760657651 50 Single MeT-5A.EWS.YS37.WT1-KTS.H3K27ac.6 24935098 18917405 0.758665757 50 Single MeT-5A.EWS.YS37.WT1-KTS.V5.5 24803403 18281913 0.737072772 50 Single MeT-5A.EWS.YS37.WT1-KTS.V5.6 26894298 19114526 0.710727828 50 Single MeT-5A.EWS.YS37.WT1+KTS.YS37.H3K27ac.5 18803629 14910941 0.792982089 50 Single MeT-5A.EWS.YS37.WT1+KTS.YS37.H3K27ac.6 23591657 18013716 0.763562983 50 Single MeT-5A.EWS.YS37.WT1+KTS.YS37.V5.5 25136556 18669909 0.742739339 50 Single MeT-5A.EWS.YS37.WT1+KTS.YS37.V5.6 24799146 17942146 0.723498543 50 Single MeT-5A.WT1-KTS.H3K27ac.3 20376542 16224774 0.796247666 50 Single MeT-5A.WT1+KTS.H3K27ac.3 20545567 16457325 0.801015859 50 Single MeT-5A.WT1-KTS.H3K27ac.4 18811473 15045677 0.799813869 50 Single MeT-5A.WT1+KTS.H3K27ac.4 21248703 17053417 0.802562726 50 Single MeT-5A.WT1-KTS.V5.3 21219832 16694052 0.786719329 50 Single MeT-5A.WT1+KTS.V5.3 24491531 18778840 0.76674831 50 Single MeT-5A.WT1-KTS.V5.4 25161653 19326636 0.768098821 50 Single MeT-5A.WT1+KTS.V5.4 21147695 16166377 0.764451019 50 Single
Antibodies	HA (clone 3F10, cat#11867423001, Roche): 3ug per 3-5 million cells V5 (D3H8Q, cat#13202, Cell signaling): 3ug per 3-5 million cells WT1 (cat#12609-1-AP, Proteintech): 5ug per 3-5 million cells WT1 (C19, cat#sc-192, Santa Cruz Biotechnology): 5ug per 3-5 million cells H3K4me3 (cat#07-473, Millipore): 5ug per 3-5 million cells H3K27ac (cat#39133, Active motif): 5ug per 3-5 million cells H3K4me1 (cat#ab8895, Abcam): 5ug per 3-5 million cells H3K27me3 (C36B11, cat#9733, Cell signaling or cat#07-449, EMD Millipore): 5ug per 3-5 million cells H3K9ac (cat#ab4441, Abcam): 5ug per 3-5 million cells H3K36me3 (cat#ab9050, Abcam): 5ug per 3-5 million cells
Peak calling parameters	For ChIP-seq, peaks were first called with MACS2 version 2.2.7.1 with an FDR of 1e-4. MACS peaks were then subjected to a second round of selection using the method described in Methods.
Data quality	Sample enrichment FDR DSRCT1.H3K27ac 2603 46333 DSRCT1.H3K27me3 93 681 DSRCT1.H3K4m1 374 83937 DSRCT1.H3K4m3 12456 26467 DSRCT1.H3K9ac 1831 28407 DSRCT1.INPUT 252 535 DSRCT2.H3K27ac 2978 68788 DSRCT2.H3K27me3 86 681 DSRCT2.H3K4me1 153 80068 DSRCT2.H3K4me3 12547 36363 DSRCT2.H3K9ac 2179 53107 DSRCT2.INPUT 272 666 DSRCT3.H3K27ac 2218 74338 DSRCT3.H3K27me3 80 752 DSRCT3.H3K4me1 148 144843 DSRCT3.H3K4me3 9837 34945 DSRCT3.H3K9ac 2536 55529 DSRCT3.INPUT 256 619 DSRCT4.H3K27ac 4870 66871 DSRCT4.H3K27me3 88 1004 DSRCT4.H3K4me1 344 162946 DSRCT4.H3K4me3 14586 42300 DSRCT4.H3K9ac 4757 70967 DSRCT4.INPUT 245 889 JN-DSRCT1.H3K27ac 10687 61723 JN-DSRCT1.H3K27me3 116 2894 JN-DSRCT1.H3K4me1 401 134269 JN-DSRCT1.H3K4me3 18874 42731 JN-DSRCT1.H3K9ac 11677 55255

JN-DSRCT1.INPUT.253.511
 JN-DSRCT1.shEWSWT1.H3K27ac.1.11096.79444
 JN-DSRCT1.shEWSWT1.H3K27ac.2.11326.58939
 JN-DSRCT1.shEWSWT1.H3K4me1.1.355.196656
 JN-DSRCT1.shEWSWT1.H3K4me1.2.339.184359
 JN-DSRCT1.shEWSWT1.INPUT.1.284.710
 JN-DSRCT1.shEWSWT1.INPUT.2.193.407
 JN-DSRCT1.shEWSWT1.WT1.1.8844.14931
 JN-DSRCT1.shEWSWT1.WT1.2.a.1089.1472
 JN-DSRCT1.shEWSWT1.WT1.2.b.12167.16657
 JN-DSRCT1.shGFP.H3K27ac.1.9312.87726
 JN-DSRCT1.shGFP.H3K27ac.2.10005.65775
 JN-DSRCT1.shGFP.H3K4me1.1.198.206919
 JN-DSRCT1.shGFP.H3K4me1.2.419.190418
 JN-DSRCT1.shGFP.INPUT.1.272.698
 JN-DSRCT1.shGFP.INPUT.2.174.337
 JN-DSRCT1.shGFP.WT1.1.27025.41243
 JN-DSRCT1.shGFP.WT1.2.a.8804.10451
 JN-DSRCT1.shGFP.WT1.2.b.29899.44628
 JN-DSRCT1.WT1.1.11779.15118
 JN-DSRCT1.WT1.2.28251.40090
 MeT-5A.control.H3K27ac.1.17852.81866
 MeT-5A.control.H3K27ac.2.7596.70321
 MeT-5A.control.H3K27ac.3.9350.71079
 MeT-5A.control.H3K27ac.4.8958.71403
 MeT-5A.control.H3K27ac.5.8380.68437
 MeT-5A.control.H3K27ac.6.8279.70571
 MeT-5A.control.HA.1.341.775
 MeT-5A.control.HA.2.333.746
 MeT-5A.control.V5.1.551.2404
 MeT-5A.control.V5.2.659.2467
 MeT-5A.control.V5.3.1092.3186
 MeT-5A.control.V5.4.2752.6588
 MeT-5A.control.V5.5.3678.12162
 MeT-5A.control.V5.6.2126.6723
 MeT-5A.EV.INPUT.489.2247
 MeT-5A.EWSWT1-KTS.H3K27ac.1.13890.106434
 MeT-5A.EWSWT1+KTS.H3K27ac.1.12343.97222
 MeT-5A.EWSWT1-KTS.H3K27ac.2.5536.95486
 MeT-5A.EWSWT1+KTS.H3K27ac.2.4765.92321
 MeT-5A.EWSWT1-KTS.HA.1.80468.109583
 MeT-5A.EWSWT1+KTS.HA.1.245.898
 MeT-5A.EWSWT1-KTS.HA.2.59530.92824
 MeT-5A.EWSWT1+KTS.HA.2.325.741
 MeT-5A.EWSWT1+KTS-KTS.H3K27ac.1.9950.104312
 MeT-5A.EWSWT1+KTS-KTS.H3K27ac.2.4240.95940
 MeT-5A.EWSWT1+KTS-KTS.HA.1.57119.90919
 MeT-5A.EWSWT1+KTS-KTS.HA.2.36781.82603
 MeT-5A.EWSWT1+KTS-KTS.V5.1.37796.77705
 MeT-5A.EWSWT1+KTS-KTS.V5.2.36224.83457
 MeT-5A.EWSWT1-KTS.V5.1.561.2564
 MeT-5A.EWSWT1+KTS.V5.1.37562.69317
 MeT-5A.EWSWT1-KTS.V5.2.433.1613
 MeT-5A.EWSWT1+KTS.V5.2.41222.78071
 MeT-5A.EWS.YS37.WT1-KTS.H3K27ac.5.8795.75117
 MeT-5A.EWS.YS37.WT1-KTS.H3K27ac.6.8500.74085
 MeT-5A.EWS.YS37.WT1-KTS.V5.5.13117.34625
 MeT-5A.EWS.YS37.WT1-KTS.V5.6.19644.45754
 MeT-5A.EWS.YS37.WT1+KTS.YS37.H3K27ac.5.9495.70684
 MeT-5A.EWS.YS37.WT1+KTS.YS37.H3K27ac.6.9040.73107
 MeT-5A.EWS.YS37.WT1+KTS.YS37.V5.5.13210.32247
 MeT-5A.EWS.YS37.WT1+KTS.YS37.V5.6.10020.25625
 MeT-5A.WT1-KTS.H3K27ac.3.8791.70092
 MeT-5A.WT1+KTS.H3K27ac.3.9223.69779
 MeT-5A.WT1-KTS.H3K27ac.4.9610.72914
 MeT-5A.WT1+KTS.H3K27ac.4.9161.71557
 MeT-5A.WT1-KTS.V5.3.42526.71570
 MeT-5A.WT1+KTS.V5.3.9900.25518

MeT-5A.WT1-KTS.V5.4 48344 78251
MeT-5A.WT1+KTS.V5.4 9181 21987

We used BWA v.0.7.12 to map the sequenced reads, picard-tools v.1.95 to remove duplicates and MACS2 v.2.2.7.1 to call peaks.