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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.

Statistical parameters

When statistical analyses are reported, confirm that the following items are present in the relevant location (e.g. 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
☐	☒	An indication of 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 statistics 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
☐	☒	Clearly defined error bars *State explicitly what error bars represent (e.g. SD, SE, CI)*

Our web collection on statistics for biologists may be useful.

Software and code

Policy information about availability of computer code

Data collection	Raw Illumina output was converted to fastq format using Illumina Bcl2fastq v2.18.
Data analysis	All open source packages that were used to process and analyze data in this study are detailed below in the "Software" section of ChIP-seq, and include MACS2 version 2.1.0, bedGraphToBigWig from UCSC, ChIPPeakAnno v3.10.1, pybedtools, Rsubread v1.26.1, BEDtools v2.26.0, ROSE, HTSeq v0.9.1, the DiffBind v2.4.8, MEME ChIP suite, and Genomic Regions Enrichment of Annotations Tool (GREAT). Packages used to analyze RNA-seq data include STAR 2.5.2a, GFOLD version 1.1.4, DESEQ2 v1.16.1, Rsubread v1.26.1, deepTools release 2.4, Gene Set Enrichment Analysis (GSEA), and Metascape. Any scripts or code written by the authors are available upon request from the corresponding author.

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 upon request. 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

The sequencing data sets generated during the current study have been deposited in the Gene Expression Omnibus (GEO) repository under accession number GSE113042 (https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE113042). Other data sets that were previously published and used in this study have been deposited in the Gene Expression Omnibus (GEO) repository under accession numbers GSE90634 and GSE108025 available at (https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE90634) and (https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE108025) respectively.

Field-specific reporting

Please select 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/authors/policies/ReportingSummary-flat.pdf

Life sciences study design

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

Sample size	N/A. No human or animal subjects necessitating sample size calculations were used in this study.
Data exclusions	No data were excluded from analysis or reporting.
Replication	All experiments were performed in at least n=2 biologically independent experiments. For proliferation curve experiments, n=3 independent biological samples were used, enabling statistical calculations. No replicates were excluded from analyses presented, and all attempts at replication were successful.
Randomization	Not applicable as human or animal subjects were not used in this study.
Blinding	Not applicable as human or animal subjects were not used in this study.

Reporting for specific materials, systems and methods

Materials & experimental systems

n/a	Involved in the study	
☒	☐	Unique biological materials
☐	☒	Antibodies
☐	☒	Eukaryotic cell lines
☒	☐	Palaeontology
☒	☐	Animals and other organisms
☒	☐	Human research participants

Methods

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

Antibodies

Antibodies used

Antibody Clone# Company Cat# Application Dilution
SMARCA4 D1Q7F Cell Signaling Technology 49360 Western blot 1:1000
SMARCA4 G-7 Santa Cruz sc-17796 Western blot 1:1000
SMARCC1 H-76 Cell Signaling Technology 11956S Western blot 1:1000
SMARCC1 D7F8S Santa Cruz sc-10756 Western blot 1:1000
SMARCD1 23 Santa Cruz sc-135843 Western blot 1:1000
SMARCB1 A-5 Santa Cruz sc-166165 Western blot 1:1000
SMARCC2 D8O9V Cell Signaling Technology 12760S Western blot 1:1000
SMARCC2 G-12 Santa Cruz sc-166237 Western blot 1:1000

ARID1A C-7 Santa Cruz sc-373784 Western blot 1:1000
SS18 D6I4Z Cell Signaling Technology 21792S Western blot 1:1000
SS18 A10 Santa Cruz sc-365170 Western blot 1:500
BRD7 15125 Cell Signaling Technology 15125S Western blot 1:1000
BRD7 B-8 Santa Cruz sc-376180 Western blot 1:1000
ARID2 E-3 Santa Cruz sc-166117 Western blot 1:1000
BRD9 N/A abcam ab137245 Western blot 1:2000
GLTSCR1 N/A Signma-Aldrich HPA056211 Western blot 1:1000
GLTSCR1 H-10 Santa Cruz sc-515086 Western blot 1:1000
GLTSCR1L N/A Novus NBP1-86359 Western blot 1:1000
DPF2 EPR9206(B) abcam ab134942 Western blot 1:1000
PBRM1 N/A Millipore ABE70 Western blot 1:5000
SMARCE1 N/A Bethyl Laboratories A300-810A Western blot 1:1000
HA C29F4 Cell Signaling Technology 3724S Western blot 1:2000
V5 N/A Thermo Fisher R960-25 Western blot 1:5000
TBP mAbcam 51841 abcam ab51841 Western blot 1:5000
GAPDH G-9 Santa Cruz sc-365062 Western blot 1:1000

Antibody Clone# Company Cat# Application
BRD9 N/A abcam ab137245 Immunoprecipitation
GLTSCR1L N/A Novus NBP1-86359 Immunoprecipitation
GLTSCR1 H-10 Santa Cruz sc-240516 Immunoprecipitation
BRD7 D9K2T Cell Signaling Technology 14910 Immunoprecipitation
ARID1A D2A8U Cell Signaling Technology 12354S Immunoprecipitation
SMARCA4 EPNCIR111A abcam ab110641 Immunoprecipitation
SMARCA4 Cell Signaling Technology 49360 Immunoprecipitation
V5 D3H8Q Cell Signaling Technology 13202 Immunoprecipitation
Rabbit IgG N/A Santa Cruz sc-2027 Immunoprecipitation
Goat IgG N/A Santa Cruz sc-2028 Immunoprecipitation

Cell Line Antibody Clone# Company Cat# Lot# Amount
EoL-1 BRD9 N/A abcam ab137245 GR257571-14 3ug
EoL-1 BRD9 N/A abcam ab66443 GR144569-1 3ug
EoL-1 GLTSCR1 S-16 Santa Cruz SC-240516 A2313 15ul
EoL-1 BRD7 D9K2T Cell Signaling Technology 14910 Lot 1 15ul
EoL-1 DPF2 EPR9206(B) abcam ab134942 YJ031611CS 3ug
EoL-1 SMARCC1 fx 2, 4-11 homemade N/A 3/9/15 3ug
EoL-1 SMARCA4 EPNCIR111A abcam ab110641 GR150844-12 5ul
EoL-1 CTCF D31H2 Cell Signaling Technology 3418S Lot 3 3ug
EoL-1 H3K27Ac N/A abcam ab4729 GR238017-2 3ug
EoL-1 H3K4me1 N/A abcam ab8895 GR159018-1 3ug
EoL-1 H3K4me3 15-10C-E4 Millipore 05745R 2326998 3ul
MOLM-13 BRD9 N/A abcam ab137245 GR257571-14 3ug
MOLM-13 GLTSCR1 S-16 Santa Cruz SC-240516 A2313 15ul
MOLM-13 BRD7 D9K2T Cell Signaling Technology 14910 Lot 1 15ul
MOLM-13 DPF2 EPR9206(B) abcam ab134942 YJ031611CS 3ug
MOLM-13 SMARCA4 EPNCIR111A abcam ab110641 GR150844-12 5ul
MOLM-13 CTCF D31H2 Cell Signaling Technology 3418S Lot 3 3ug
SYO-1 BRD9 N/A abcam ab137245 GR257571-20 3ug
SYO-1 CTCF D31H2 Cell Signaling Technology 3418S Lot 3 3ug
SYO-1 SS18 D6I4Z Cell Signaling Technology 21792s Lot 1 3ul
TTC1240 BRD9 N/A abcam ab137245 GR257571-20 3ug
TTC1240 BRD9 N/A abcam ab137245 GR257571-23 3ug
TTC1240 SMARCA4 EPNCIR111A abcam ab110641 GR3208604-3 5ul
TTC1240 CTCF D31H2 Cell Signaling Technology 3418S Lot 3 3ug
Aska BRD9 N/A abcam ab137245 GR257571-20 3ug
Jurkat BRD9 N/A abcam ab137245 GR257571-20 3ug

Validation

All antibodies used in this study have been thoroughly validated by our laboratory to be specific (using IP-mass-spectrometry in wild-type and KO cell lines, and using immunoblot in wild-type and KO cell lines).

Eukaryotic cell lines

Policy information about cell lines

Cell line source(s)

Cell Line Source
HEK-293T, Gift from Dr. Gerald Crabtree at Stanford
EoL-1, Gift from Dr. Jay Bradner at DFCI
MOLM-13, Gift from Dr. Jay Bradner at DFCI
TTC1240, Gift from Dr. Timothy Triche
G401, ATCC
ES-X, ATCC
IMR-90, ATCC
CRL7250, Gift from Drs. Berkeley Gryder and Javed Khan at NCI

NCIH-1437, CCLE, Broad Institute
ES-2, Gift from Dr. Charles Roberts at DFCI
RD, CCLE
HCT116, CCLE
Calu-6, CCLE
Aska, RIKEN
SYO-1, RRID:CVCL_7146
HSSYII, RRID:CVCL_8719

Authentication	All cell lines were routinely checked for mycoplasma contamination and confirmed negative. All cell lines were subjected to routine fingerprinting analyses to confirm identity.
Mycoplasma contamination	All cell lines used in the study tested negative for mycoplasma.
Commonly misidentified lines (See ICLAC register)	No cell lines used in this study were found in the database of commonly misidentified cell lines that is maintained by ICLAC and NCBI Biosample.

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.

The sequencing data sets generated and/or analyzed during the current study have been deposited in the Gene Expression Omnibus (GEO) repository under accession number GSE113042 (https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE113042).

Files in database submission

fastq and bigWig files for the following ChIP-Seq samples were deposited in the Gene Expression Omnibus, they can be accessed using the link above:
GSM3094366 EOL1_Input_Naive_ChIP-Seq
GSM3094367 EOL1_SMARCA4_Naive_ChIP-Seq
GSM3094368 EOL1_BRD9_137245_Naive_ChIP-Seq
GSM3094369 EOL1_BRD9_66443_Naive_ChIP-Seq
GSM3094370 EOL1_GLTSCR1_Naive_ChIP-Seq
GSM3094371 EOL1_SMARCC1_Naive_ChIP-Seq
GSM3094372 EOL1_BRD7_Naive_ChIP-Seq
GSM3094373 EOL1_DPF2_Naive_ChIP-Seq
GSM3094374 EOL1_H3K27Ac_Naive_ChIP-Seq
GSM3094375 EOL1_CTCF_Naive_ChIP-Seq
GSM3094376 MOLM13_Input_DMSO_ChIP-Seq
GSM3094377 MOLM13_SMARCA4_DMSO_ChIP-Seq
GSM3094378 MOLM13_BRD9_DMSO_ChIP-Seq
GSM3094379 MOLM13_BRD7_DMSO_ChIP-Seq
GSM3094380 MOLM13_DPF2_DMSO_ChIP-Seq
GSM3094381 MOLM13_GLTSCR1_DMSO_ChIP-Seq
GSM3094382 MOLM13_CTCF_DMSO_ChIP-Seq
GSM3094383 EOL1_H3K4me1_Naive_ChIP-Seq
GSM3094384 EOL1_H3K4me3_Naive_ChIP-Seq
GSM3094385 SYO1_Input_shControl_ChIP-Seq
GSM3094386 SYO1_SS18_shControl_ChIP-Seq
GSM3094387 SYO1_BRD9_shControl_ChIP-Seq
GSM3094388 SYO1_CTCF_shControl_ChIP-Seq
GSM3094389 SYO1_Input_shSSX_ChIP-Seq
GSM3094390 SYO1_SS18_shSSX_ChIP-Seq
GSM3094391 SYO1_BRD9_shSSX_ChIP-Seq
GSM3094394 JURKAT_Input_Naive_ChIP-Seq
GSM3094395 JURKAT_BRD9_Naive_ChIP-Seq
GSM3094396 JURKAT_CTCF_Naive_ChIP-Seq
GSM3094397 TTC1240_BRD9_N106_Empty_ChIP-Seq
GSM3094398 TTC1240_BRD9_N106_SMARCB1_ChIP-Seq
GSM3326008 TTC1240_BRD9_dBRD9_ChIP-Seq
GSM3326009 TTC1240_BRD9_DMSO_ChIP-Seq
GSM3326010 TTC1240_CTCF_Empty_ChIP-Seq
GSM3326011 TTC1240_Input_dBRD9_ChIP-Seq
GSM3326012 TTC1240_Input_DMSO_ChIP-Seq
GSM3326013 TTC1240_SMARCA4_Rep1_dBRD9_ChIP-Seq
GSM3326014 TTC1240_SMARCA4_Rep1_DMSO_ChIP-Seq
GSM3326015 TTC1240_SMARCA4_Rep2_dBRD9_ChIP-Seq
GSM3326016 TTC1240_SMARCA4_Rep2_DMSO_ChIP-Seq
GSM3326017 Aska_BRD9_shScr_ChIP-Seq

GSM3326018 Aska_BRD9_shSSX1_ChIP-Seq
GSM3326021 MOLM13 (AML)_SMARCA4_dBRD9_ChIP-Seq

Genome browser session (e.g. UCSC)

N/A

Methodology

Replicates

For profiling subcomplex localization in AML, BRD9 ChIPs were done in biological duplicate with multiple independent antibodies in both MOLM13 and EOL-1. All other BAF subunit ChIPs were performed at least once in the independent cell lines EOL1 and MOLM13, with at least 2 antibodies targeting the each subcomplex. In the TTC1240 dBRD9 and DMSO treatment, SMARCA4 ChIP-Seq was performed in biological replicate and these replicates were used to determine differential localization. TTC1240 +SMARCB1 ChIP BRD9 ChIP was also done in biological replicate, however one sample was removed due to insufficient quality (low number of peaks). For synovial sarcoma experiments, fusion and non-fusion complexes were targeted with at least 3 independent antibodies.

Sequencing depth

All ChIP-Seq samples were single-end sequenced, the raw and mapped read number for each are below:
Sample Name Raw Reads Mapped Reads
EOL1_Input_Naive_ChIP-Seq 42699075 40669502
EOL1_SMARCA4_Naive_ChIP-Seq 42341658 40326539
EOL1_BRD9_137245_Naive_ChIP-Seq 43447352 40728707
EOL1_BRD9_66443_Naive_ChIP-Seq 42280285 40193228
EOL1_GLTSCR1_Naive_ChIP-Seq 46796897 44237227
EOL1_SMARCC1_Naive_ChIP-Seq 47561828 45205765
EOL1_BRD7_Naive_ChIP-Seq 41626359 39680595
EOL1_DPF2_Naive_ChIP-Seq 21669829 20808853
EOL1_H3K27Ac_Naive_ChIP-Seq 74052071 66199250
EOL1_CTCF_Naive_ChIP-Seq 40528536 39213478
MOLM13_Input_DMSO_ChIP-Seq 93329733 89605195
MOLM13_SMARCA4_DMSO_ChIP-Seq 57070615 54925351
MOLM13_BRD9_DMSO_ChIP-Seq 63412810 59467859
MOLM13_BRD7_DMSO_ChIP-Seq 49599144 47390911
MOLM13_DPF2_DMSO_ChIP-Seq 31158535 29961930
MOLM13_GLTSCR1_DMSO_ChIP-Seq 17825260 16942277
MOLM13_CTCF_DMSO_ChIP-Seq 49433582 48148480
EOL1_H3K4me1_Naive_ChIP-Seq 82356833 80809430
EOL1_H3K4me3_Naive_ChIP-Seq 50558228 49324772
SYO1_Input_shControl_ChIP-Seq 70319926 67773771
SYO1_SS18_shControl_ChIP-Seq 52043986 50297551
SYO1_BRD9_shControl_ChIP-Seq 51564898 49073866
SYO1_CTCF_shControl_ChIP-Seq 50839866 49248273
SYO1_Input_shSSX_ChIP-Seq 60286800 58197355
SYO1_SS18_shSSX_ChIP-Seq 47256134 45975755
SYO1_BRD9_shSSX_ChIP-Seq 43844159 42111274
JURKAT_Input_Naive_ChIP-Seq 51476102 50131147
JURKAT_BRD9_Naive_ChIP-Seq 24082851 22286692
JURKAT_CTCF_Naive_ChIP-Seq 45704160 44472440
TTC1240_BRD9_N106_Empty_ChIP-Seq 40508291 39040020
TTC1240_BRD9_N106_SMARCB1_ChIP-Seq 37321904 35886274
TTC1240_CTCF_Empty_ChIP-Seq 30451167 29859369
TTC1240_Input_DMSO_ChIP-Seq 28267013 27586551
TTC1240_BRD9_DMSO_ChIP-Seq 35453747 31754443
TTC1240_SMARCA4_Rep1_DMSO_ChIP-Seq 32074909 26965363
TTC1240_SMARCA4_Rep2_DMSO_ChIP-Seq 26794147 21150749
TTC1240_Input_dBRD9_ChIP-Seq 30672294 29974187
TTC1240_BRD9_dBRD9_ChIP-Seq 33762508 28773196
TTC1240_SMARCA4_Rep1_dBRD9_ChIP-Seq 28977197 22765324
TTC1240_SMARCA4_Rep2_dBRD9_ChIP-Seq 31275737 25903044
Aska_BRD9_shScr_ChIP-Seq 45980542 43309210
Aska_BRD9_shSSX1_ChIP-Seq 46476740 44060369
MOLM13_SMARCA4_dBRD9_ChIP-Seq 27453257 26423192

Antibodies

Sample Name: Antibody Catalog Number
EOL1_SMARCA4_Naive_ChIP-Seq: Abcam EPNCIR111A
EOL1_BRD9_137245_Naive_ChIP-Seq: Abcam 137245
EOL1_BRD9_66443_Naive_ChIP-Seq: Abcam 66443
EOL1_BRD7_Naive_ChIP-Seq: CST 14910
EOL1_DPF2_Naive_ChIP-Seq: Abcam ab134942
EOL1_H3K27Ac_Naive_ChIP-Seq: Abcam ab4729
EOL1_CTCF_Naive_ChIP-Seq: CST 3418S
MOLM13_SMARCA4_DMSO_ChIP-Seq: Abcam EPNCIR111A
MOLM13_BRD9_DMSO_ChIP-Seq: Abcam ab137245
MOLM13_BRD7_DMSO_ChIP-Seq: CST 14910
MOLM13_DPF2_DMSO_ChIP-Seq: Abcam ab134942
MOLM13_CTCF_DMSO_ChIP-Seq: CST 3418

EOL1_H3K4me1_Naive_ChIP-Seq: Abcam ab8895
EOL1_H3K4me3_Naive_ChIP-Seq: Millipore 05745R
SYO1_SS18_shControl_ChIP-Seq: CST 21792s
SYO1_BRD9_shControl_ChIP-Seq: Abcam ab137245
SYO1_CTCF_shControl_ChIP-Seq: CST 3418S
SYO1_SS18_shSSX_ChIP-Seq: CST 21792s
SYO1_BRD9_shSSX_ChIP-Seq: Abcam ab137245
JURKAT_BRD9_Naive_ChIP-Seq: Abcam 137245
JURKAT_CTCF_Naive_ChIP-Seq: CST 3418
TTC1240_BRD9_N106_Empty_ChIP-Seq: Abcam 137245
TTC1240_BRD9_N106_SMARCB1_ChIP-Seq: Abcam 137245
TTC1240_BRD9_dBRD9_ChIP-Seq: Abcam 137245
TTC1240_BRD9_DMSO_ChIP-Seq: Abcam 137245
TTC1240_CTCF_Empty_ChIP-Seq: CST 3418S
TTC1240_SMARCA4_Rep1_dBRD9_ChIP-Seq: Abcam EPNCIR111A
TTC1240_SMARCA4_Rep1_DMSO_ChIP-Seq: Abcam EPNCIR111A
TTC1240_SMARCA4_Rep2_dBRD9_ChIP-Seq: Abcam EPNCIR111A
TTC1240_SMARCA4_Rep2_DMSO_ChIP-Seq: Abcam EPNCIR111A
Aska_BRD9_shScr_ChIP-Seq: Abcam 137245
Aska_BRD9_shSSX1_ChIP-Seq: Abcam 137245
MOLM13_SMARCA4_dBRD9_ChIP-Seq: Abcam EPNCIR111A

Peak calling parameters

In EOL1, TTC1240, MOLM13 and Jurkat, narrow peaks were called for all BAF subunits and CTCF against an input using MACS2 'callpeak' with a -q value cutoff of 1e-3 and the --nomodel option. Broad peaks were called for all histone marks using MACS2 'callpeak' with a -q value of 1e-3, and the options --broad_cutoff --broad --nomodel --SPMR. In the synovial sarcoma cell lines SYO1 and Aska, histone marks and BAF subunits peaks were called using the broadPeak options above, while CTCF peaks were again called using the narrowPeak options.

Data quality

For all samples, peaks were called using a qvalue cutoff of 1e-3 against an input. Excepting particular disease or experimental conditions (such as BRD9 peaks after BRD9 degradation with dBRD9) all samples had >6000 peaks, most far higher (20,000+), a full list of peak numbers for each sample is available in Supp.Table 6. Read coverage in peaks was calculated to ensure quality as well. For the TTC1240 DMSO and dBRD9 treatment, a spike-in control was done to normalize read levels between samples.

Software

ChIP-Seq Data was aligned using Bowtie2, version 2.1.0 to the hg19 reference genome with the parameter k -1. MACS2 version 2.1.0 was used to call peaks against input with a cutoff of q = .001. Duplicates were removed from reads files using samtools rmdup with the -b option. (SAMtools v1.3.1)

Overlaps for ChIP venn diagrams were created using the bioconductor package ChIPPeakAnno v3.10.1, peak files were read in using the toGRanges() command, values were determined using the getVennCounts() function with maxgap=0. Data was visualized using matplotlib. Read count across peak sets of interest were calculated by calling the Rsubread v1.26.1 bioconductor package function featur0.9eCounts() on duplicate removed bam files. Metagene plots and heatmaps were generated created using HTSeq v0.9.1. Peak distance from TSS elements was determined using bedtools closest function with the hg19 ref Flat TSS annotation. Intersection of peaks was determined using bedtools intersect. (bedtools v2.26.0)Determination of super enhancers was performed using ROSE. Differential occupancy of SMARCA4 in TTC1240 upon dBRD9 treatment was determined using the DiffBind v2.4.8 bioconductor package, with all default settings. Motif analysis on these sequences was done was done using the MEME-ChIP suite.