nature research

Corresponding author(s): Zhijie Liu

Last updated by author(s): Mar 10, 2020

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	Illumina output was converted to fastq format using Bcl2fastq v2.17.
Data analysis	MS data were analyzed by MaxQuant (version 1.6.0.16), statistical analysis was performed by Perseus (version 1.6.0.7). STAR (version 2.5.2b), featureCounts (version 1.5.1) and DESeq2 (version 1.14.1) were used to analyze RNA-seq data. Bowtie (version 1.1.2), MACS2 (version 2.1.1), ChIPseeker (version 1.10.3), and GREAT (version 3.0.0) were used to analyze ChIP-seq data. and HOMER (version 4.8) and FIMO (version 4.11.2) were used to search and scan motifs. ROSE (version 0.1) was used to identify super enhancers. Cutadapt (version 1.11) was used to trim adapters and bowtie (version 1.1.2) was used to map the reads for ATAC-seq data. bowtie and HOMER (version 4.8) were used to analyze GRO-seq data. JAVA GSEA tool (version 3.0) was used to conduct gene set enrichment analysis. GSVA (version 1.28.0) was used to conduct gene set variation analysis. The methylation percentage of each interrogated CpG site was calculated by PyroMark CpG software (version 1.0.11). http://kmplot.com/ was used to compare the survival rate (Relapse free survival curve).

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 deep sequencing raw data supporting the findings of this study have been deposited in the Gene Expression Omnibus (GEO) under accession code: GSE128460. Previous published DNA methylation data for different cell lines including MCF7, TamR, MCF7X and FASR were retrieved from GEO website (GSE69118). All BioID proteomic data from MCF7 and TamR cell lines have been deposited in the Proteomexchange repository under the accession number PXD014015. All other data supporting the findings of this study are available from the corresponding author upon reasonable request.

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 sample size calculations were performed. The sample size was determined based on our experience as well as literature reporting in terms of specific experiment. For animal experiment has at least n=4 independent mice per group. Unless explicitly stated, 3 independent experiments were performed to achieve two-sided t-test analysis.
Data exclusions	No data was excluded from the study.
Replication	Multiple independent repeats were included for related experiments. Each experiment was performed for at least twice to make sure similar results are reproducible. All attempts at replication were successful.
Randomization	5-6 week female nude mice were chosen as xenograft hosts, and all these mice were randomly allocated into experimental groups.
Blinding	For cell-based experiments including Western blotting and immunostaining, cell types were known when prepared the samples or started to treat cells at the beginning of experiments. Data measurement for cell viability or photo capture were blinded to different person who processed assay at the time. ChIP-seq, RNA-seq, GRO-seq, ATAC-seq and mass spectrometry analysis were blinded before analysis.

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	Primary antibodies specific for KRT8(TS1) (Thermo Fisher, MA5-14428, 1:1000 for WB), KRT18(DC10) (Thermo Fisher, MA5-12104,1:100 for IF,1:1000 for WB), KRT19(A53-B/A2.26 (Ks19.1))(Thermo Fisher, MA5-12663, 1:1000 for WB), FOXI1 (Thermo Fisher, PA5-30031, 1:1000 for WB), Mouse IgG Isotype Control (Thermo Fisher, 02-6502, 3 µg per IP), ERα (HC-20) (Santa Cruz, sc-543, 1:4000 for WB, 5 µg per ChIP), AP-2γ (H-77)(Santa Cruz, sc-8977, 1:1000 for WB), p300(C-20)(Santa Cruz, sc-585, 5 µg per ChIP), PR(C-19)(Santa Cruz, sc-538, 1:2000 for WB), GAPDH(FL-335)(Santa Cruz, sc-25778, 1:1000 for WB), BCL2(C-2)(Santa Cruz, sc-7382, 1:1000 for WB), CXCL8(C-11)(Santa Cruz, sc-376750, 1:1000 for WB), SOX2(E-4)(Santa Cruz, sc-365823, 1:1000 for WB), MUC1(VU4H5)(Santa Cruz, sc-7313, 1:1000 for WB), S100P(B-10)(Santa Cruz, sc-374547, 1:1000 for

WB), FN1(EP5)(Santa Cruz, sc-8422, 1:1000 for WB), EGR1(S-25)(Santa Cruz, sc-101033, 1:1000 for WB), SERPINE1(C-9)(Santa Cruz, sc-5297, 1:500 for WB), ERα(D-12)(Santa Cruz, sc-8005, 1:1000 for WB, 3 µg per IP), PRLR(D4A9)(Cell Signaling, 13552, 1:1000 for WB), RHOB (Cell Signaling, 2098T, 1:1000 for WB), EGFR(D38B1)(Cell Signaling, 4267T, 1:50 for IF,1:1000 for WB), AGR2(D9V2F)(Cell Signaling, 13062T, 1:1000 for WB), PAK1 (Cell Signaling, 2602T, 1:1000 for WB), c-JUN(60A8)(Cell Signaling, 9165S, 1:1000 for WB, 1:50 for ChIP), GATA3(D13C9)(Cell Signaling, 5852S, 1:1000 for WB, 1:100 for ChIP), FOXA1(D7P9B)(Cell Signaling, 58613, 1:1000 for WB), Phospho-c-Jun (Ser73)(D47G9)(Cell Signaling, 3270S, 1:1000 for WB), Phospho-c-Jun (Ser63) (54B3) (Cell Signaling, 2361S, 1:1000 for WB), RUNX2 (D1H7) (Cell Signaling, 8486S, 1:1000 for WB), c-JUN (BD Transduction Laboratories, 610326, 1:1000 for WB, 5 µg per ChIP), H3K27ac (Abcam, ab4729, 5 µg per ChIP), H3K4me1 (Abcam, ab8895, 5 µg per ChIP), BRG1 (Abcam, ab4081, 5 µg per ChIP), FOXA1 (Abcam, ab5089, 5 µg per ChIP), HA (Abcam, ab9110, 1:4000 for WB), ARID1B (Bethyl Laboratories, A301-046A, 5 µg per ChIP), ERα (Bethyl Laboratories, A300-495A, 5 µg per ChIP), P300 (NM11) (Active motif, 61401, 5 µg per ChIP), α-Tubulin(DM1A) (Sigma, T9026, 1:1000 for WB), FLAG(M2) (Sigma, F1804, 1:1000 for WB), H3 (GenScript, A01502, 1:2000 for WB), Rabbit TrueBlot®: Anti-Rabbit IgG HRP (Monoclonal eB182) (Rockland, 18-8816-33, 1:1000 for WB), HRP-conjugated Streptavidin (Jackson ImmunoResearch, 016-030-084, 1:5000 for WB), FITC-conjugated AffiniPure Donkey Anti-Rabbit IgG (H+L) (Jackson ImmunoResearch, 711-095-152, 1:500 for IF), Alexa Fluor 488-conjugated AffiniPure Fab Fragment Goat Anti-mouse IgG (H+L) (Jackson ImmunoResearch, 115-547-003, 1:500 for IF). The more detailed information is provided in the Supplementary Table 2.

Validation

All antibodies used in our study were validated by the respective commercial source for the application used. Some of them have also been validated by our experiments as shown in this manuscript using either overexpression or knockdown strategies.
KRT8(TS1), https://www.thermofisher.com/antibody/product/Cytokeratin-8-Antibody-clone-TS1-Monoclonal/MA5-14428;
KRT18(DC10), https://www.thermofisher.com/antibody/product/Cytokeratin-18-Antibody-clone-DC10-Monoclonal/MA5-12104;
KRT19(A53-B/A2.26 (Ks19.1)), https://www.thermofisher.com/antibody/product/Cytokeratin-19-Antibody-clone-A53-B-A2-26-Ks19-1-Monoclonal/MA5-12663;
FOXI1, https://www.thermofisher.com/antibody/product/FOXI1-Antibody-Polyclonal/PA5-30031;
Mouse IgG Isotype Control, https://www.thermofisher.com/antibody/product/Mouse-IgG-Isotype-Control/02-6502;
ERα(HC-20), https://www.scbt.com/scbt/product/eralpha-antibody-hc-20;
AP-2γ (H-77), https://www.scbt.com/scbt/product/ap-2gamma-antibody-h-77;
P300(C-20), https://www.scbt.com/scbt/product/p300-antibody-c-20;
PR(C-19), https://www.scbt.com/scbt/product/pr-antibody-c-19;
GAPDH(FL-335), https://www.scbt.com/scbt/product/gapdh-antibody-fl-335;
BCL2(C-2), https://www.scbt.com/scbt/product/bcl-2-antibody-c-2;
CXCL8(C-11), https://www.scbt.com/scbt/product/il-8-antibody-c-11;
SOX2(E-4),https://www.scbt.com/scbt/product/sox-2-antibody-e-4;
MUC1(VU4H5), https://www.scbt.com/scbt/product/mucin-1-antibody-vu4h5;
S100P(B-10), https://www.scbt.com/scbt/product/s-100p-antibody-b-10;
FN1(EP5), https://www.scbt.com/scbt/product/fibronectin-antibody-ep5;
EGR1(S-25), https://www.scbt.com/scbt/product/egr-1-antibody-s-25;
SERPINE1(C-9), https://www.scbt.com/scbt/product/pai-1-antibody-c-9;
ERα(D-12), https://www.scbt.com/scbt/product/eralpha-antibody-d-12;
PRLR(D4A9), https://www.cellsignal.com/products/primary-antibodies/prolactin-receptor-d4a9-rabbit-mab/13552;
RHOB, https://www.cellsignal.com/products/primary-antibodies/rhob-antibody/2098;
EGFR(D38B1), https://www.cellsignal.com/products/primary-antibodies/egf-receptor-d38b1-xp-rabbit-mab/4267;
AGR2(D9V2F), https://www.cellsignal.com/products/primary-antibodies/agr2-d9v2f-xp-rabbit-mab/13062;
PAK1, https://www.cellsignal.com/products/primary-antibodies/pak1-antibody/2602;
c-JUN(60A8), https://www.cellsignal.com/products/primary-antibodies/c-jun-60a8-rabbit-mab/9165;
GATA3(D13C9), https://www.cellsignal.com/products/primary-antibodies/gata-3-d13c9-xp-rabbit-mab/5852;
FOXA1(D7P9B), https://www.cellsignal.com/products/primary-antibodies/foxa1-hnf3a-d7p9b-rabbit-mab/58613;
Phospho-c-Jun (Ser73) (D47G9), https://www.cellsignal.com/products/primary-antibodies/phospho-c-jun-ser73-d47g9-xp-rabbit-mab/3270;
Phospho-c-Jun (Ser63)(54B3), https://www.cellsignal.com/products/primary-antibodies/phospho-c-jun-ser63-54b3-rabbit-mab/2361?site-search-type=Products;
c-JUN, http://www.bdbiosciences.com/us/applications/research/stem-cell-research/cancer-research/human/purified-mouse-anti-jun-3jun/p/610326;
RUNX2 (D1H7), https://www.cellsignal.com/products/primary-antibodies/runx2-d1h7-rabbit-mab/8486;
H3K27ac, https://www.abcam.com/histone-h3-acetyl-k27-antibody-chip-grade-ab4729.html;
H3K4me1, https://www.abcam.com/histone-h3-mono-methyl-k4-antibody-chip-grade-ab8895.html;
BRG1, https://www.abcam.com/brg1-antibody-ab4081.html;
FOXA1, https://www.abcam.com/foxa1-antibody-chip-grade-ab5089.html;
HA, https://www.abcam.com/ha-tag-antibody-chip-grade-ab9110.html;
ARID1B, https://www.bethyl.com/product/A301-046A/ARID1B+Antibody;
ERα, https://www.bethyl.com/product/A300-495A?referrer=search;
P300, https://www.activemotif.com/catalog/details/61401/p300-antibody-mab-clone-nm11;
α-Tubulin(DM1A), https://www.sigmaaldrich.com/catalog/product/sigma/t9026;
FLAG(M2), https://www.sigmaaldrich.com/catalog/product/sigma/f1804;
H3, https://www.genscript.com/antibody/A01502-Histone_H3_antibody_pAb_Rabbit.html;
Rabbit TrueBlot®: Anti-Rabbit IgG HRP, https://rockland-inc.com/Product.aspx?id=42150;
HRP-conjugated Streptavidin, https://www.jacksonimmuno.com/catalog/products/016-030-084;
FITC-conjugated AffiniPure Donkey Anti-Rabbit IgG (H+L), https://www.jacksonimmuno.com/catalog/products/711-095-152;
Alexa Fluor 488-conjugated AffiniPure Fab Fragment Goat Anti-mouse IgG (H+L), https://www.jacksonimmuno.com/catalog/products/115-547-003.

Eukaryotic cell lines

Policy information about cell lines

Cell line source(s)	HEK-293T and regular MCF7, T47D and ZR75-1 cell lines were obtained from American Type Culture Collection (ATCC). Paired tamoxifen-sensitive and -resistant MCF7 (MCF7P vs TamR) and T47D (T47DP vs T47D-TamR) cell lines were provided by Dr. Rachel Schiff at Baylor College of Medicine.
Authentication	Cell lines were not authenticated.
Mycoplasma contamination	All cell lines tested negative for mycoplasma contamination.
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.

Animals and other organisms

Policy information about studies involving animals; ARRIVE guidelines recommended for reporting animal research

Laboratory animals	5 to 6-week-old athymic nude female mice were purchased from the Jackson Laboratory (#002019). For orthotopic xenograft studies, tumor cells resuspended in 100 µl of 1:1 mix of growth media and Matrigel were injected into the fourth mammary fat pads of the mice. The hormone-independent HBCx-124 ED PDX mouse model was established from a HBCx-124 PDX model that gained resistance to endocrine therapy after 3 months of estrogen deprivation (ED) treatment.
Wild animals	No wild animals involved in this study.
Field-collected samples	This study didn't involve samples collected from field.
Ethics oversight	All xenograft experiments were performed in accordance with a protocol approved by the Institutional Animal Care and Use Committee (IACUC) at the UTHSCSA. The study is compliant with all relevant ethical regulations regarding animal research. Care and housing of PDX mouse models were in accordance with institutional guidelines and rules of the French Ethics Committee (Project Authorization no. 02163.02)

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

Human research participants

Policy information about studies involving human research participants

Population characteristics	21 breast cancer cases that were estrogen receptor (ER)-positive, human epidermal growth receptor 2 (HER2)-negative were chosen from the Chinese Breast Cancer Study Group (CBCSG) 036 trial. Immunohistochemistry and fluorescence in situ hybridization were used to identify the ER-positive and HER2-negative cases. The 21 patients used in this paper were all from neoadjuvant chemoendocrine therapy (NCET) group and were found unable to achieve pathological complete remission (PCR) after surgery. Thus, these 21 breast cancer patients are considered as therapy-resistant. In the NCET group, postmenopausal patients were treated with 2.5 mg of aromatase inhibitor (AI) letrozole daily accompanied with neoadjuvant chemotherapy, whereas premenopausal women received 2.5 mg of letrozole daily and a 3.75 mg subcutaneous injection of the gonadotropin-releasing hormone analogue (GnRH-a) leuprorelin (Takeda Pharmaceutical Company) every month concomitant with neoadjuvant chemotherapy (Ovarian suppression by GnRH-a combined with an AI has been found to be highly effective among premenopausal patients with endocrine-sensitive breast cancer). For chemotherapy, patients aged ≤60 years received a regimen of 90 mg/m2 of epirubicin (E) and 600 mg/m2 of cyclophosphamide (C) every 2 weeks followed by 100 mg/m2 of docetaxel (T) every 2 weeks (EC*4-T*4 regimen). For patients aged >60 years, they received 500 mg/m2 of 5-fluorouracil(F), 90 mg/m2 of E, and 500 mg/m2 of C every 3 weeks, followed by 80 to 100 mg/m2 of T every 3 weeks (FEC*3-T*3 regimen) due to reduced tolerance among this age group. For all cases, pre-treatment and post-treatment fresh frozen tumor tissues were obtained. These tissues were macrodissected to avoid the influence of stromal tissues (<30% stromal tissue). High quality RNA were extracted to perform RNA-seq assay.
Recruitment	Parents concented to Chinese Breast Cancer Study Group (CBCSG) 036 trial. The 21 participants included in our study were randomly selected from non-PCR (pathological complete remission) patients post NECT (neoadjuvant chemoendocrine therapy). Briefly, 125 patients were randomly selected from a pool of patients and assigned to NECT group. 116 out of the 125 patients were found unable to achieve pathological complete remission (PCR). Of these 116 patients, 54 patients had adequate pre-treatment and post-treatment freshly-frozen tumor tissues for RNA extraction. From these 54 patients, we randomly selected 21 patients (ER-positive and HER2-negative cases) and obtained 21 pairs of samples (before and after receiving NECT), followed by RNA sequencing and subsequent analyses.
Ethics oversight	The current study was approved by the institutional ethics committee of 4 centers in China within the CBCSG. Four centers that approved the study protocol are Fudan University Shanghai Cancer Center, Obstetrics and Gynecology Hospital of Fudan University, the First Maternity and Infant Health Hospital, and Zhongshan Hospital.

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=GSE128460
token=sdgxsgawdfkblih

Files in database submission

MCF7_Full_ER.bw
TamR_Full_ER.bw
MCF7_K4me1.bw
MCF7_K27ac_rep1.bw
TamR_K4me1.bw
TamR_K27ac_rep1.bw
MCF7_K27ac_rep2.bw
TamR_K27ac_rep2.bw
MCF7_input.bw
TamR_input.bw
MCF7_FOXA1.bw
TamR_FOXA1.bw
TamR_shCtrl_ER.bw
TamR_shJUN_ER.bw
TamR_shCtrl_K27ac.bw
TamR_shJUN_K27ac.bw
MCF7_shCtrl_ER.bw
MCF7_shGATA3_ER.bw
MCF7_shCtrl_K27ac.bw
MCF7_shGATA3_K27ac.bw
MCF7_P300.bw
TamR_P300.bw
MCF7_oeCtrl_ER.bw
MCF7_oeJUN_ER.bw
TamR_oeCtrl_K27ac.bw
TamR_oeGATA3_K27ac.bw
MCF7_oeCtrl_K27ac.bw
MCF7_oeJUN_K27ac.bw
TamR_shCtrl_ARID1B.bw
TamR_shJUN_ARID1B.bw
TamR_shCtrl_BRG1.bw
TamR_shJUN_BRG1.bw
TamR_shCtrl_P300.bw
TamR_shJUN_P300.bw
MCF7_GATA3.bw
TamR_GATA3.bw
MCF7_shCtrl_noDox_K27ac.bw
MCF7_shCtrl_Dox_K27ac.bw
MCF7_shGATA3_noDox_K27ac.bw
MCF7_shGATA3_Dox_K27ac.bw
MCF7_JUN_CST9165.bw
TamR_JUN_CST9165.bw
MCF7_JUN_BD610326.bw
TamR_JUN_BD610326.bw
T47D_Ctrl_K27ac.bw
T47D_oeJUN_K27ac.bw
T47D_shGATA3_K27ac.bw
T47D_Both_K27ac.bw
ZR75_Ctrl_K27ac.bw
ZR75_oeJUN_K27ac.bw
ZR75_shGATA3_K27ac.bw
ZR75_Both_K27ac.bw

Genome browser session
(e.g. UCSC)

Fig3e: https://genome.ucsc.edu/cgi-bin/hgTracks?db=hg19&lastVirtModeType=default&lastVirtModeExtraState=&virtModeType=default&virtMode=0&nonVirtPosition=&position=chr18%3A60747650%2D61038071&hgsid=727398247_SbofHYfhZnVIAaa0VXY4yflJ5mL0
Fig5b:https://genome.ucsc.edu/cgi-bin/hgTracks?db=hg19&lastVirtModeType=default&lastVirtModeExtraState=&virtModeType=default&virtMode=0&nonVirtPosition=&position=chr18%3A60757155%2D61149224&hgsid=727398363_URMsk872RY9rtdaPmWKf2abknVaV
Fig6e:https://genome.ucsc.edu/cgi-bin/hgTracks?db=hg19&lastVirtModeType=default&lastVirtModeExtraState=&virtModeType=default&virtMode=0&nonVirtPosition=&position=chr7%3A55055068%2D55478759&hgsid=727398381_CMpVAIGLAtAPy0MUUxLjtQZhVOab
Fig7d:https://genome.ucsc.edu/cgi-bin/hgTracks?db=hg19&lastVirtModeType=default&lastVirtModeExtraState=&virtModeType=default&virtMode=0&nonVirtPosition=&position=chr7%3A55057685%2D55340145&hgsid=727398411_KSfiQ0yTS6y3QaAlBikj9rlAFWZ4
Fig7g: https://genome.ucsc.edu/cgi-bin/hgTracks?db=hg19&lastVirtModeType=default&lastVirtModeExtraState=&virtModeType=default&virtMode=0&nonVirtPosition=&position=chr7%3A55064109%2D55346569&hgsid=793217981_AWi6E0rkyQ78Nm3SspNMH4u8YYWZ

Methodology

Replicates

For H3K27ac and JUN ChIP-seq data, we did two replicates for each cell line.

Sequencing depth

Sample	Total reads	Total Unique reads	Unique mapped ratio
MCF7_Full_ER	40,852,531	36,290,407	88.83%
TamR_Full_ER	25,877,630	23,313,428	90.09%
MCF7_K4me1	22,392,643	18,936,604	84.57%
MCF7_K27ac_rep1	33,364,499	29,601,295	88.72%
TamR_K4me1	20,719,201	17,872,057	86.26%
TamR_K27ac_rep1	27,897,063	24,687,274	88.49%
MCF7_K27ac_rep2	28,526,996	25,329,518	88.79%
TamR_K27ac_rep2	25,481,252	22,551,942	88.50%
MCF7_input	24,898,739	21,339,988	85.71%
TamR_input	25,850,495	21,966,383	84.97%
MCF7_FOXA1	14,763,676	12,380,950	83.86%
TamR_FOXA1	14,924,070	12,796,149	85.74%
TamR_shCtrl_ER	19,549,394	16,262,619	83.19%
TamR_shJUN_ER	9,029,745	7,194,551	79.68%
TamR_shCtrl_K27ac	22,266,445	19,696,688	88.46%
TamR_shJUN_K27ac	14,804,876	12,939,341	87.40%
MCF7_shCtrl_ER	14,894,836	12,084,245	81.13%
MCF7_shGATA3_ER	10,281,937	8,002,311	77.83%
MCF7_shCtrl_K27ac	15,015,910	12,968,411	86.36%
MCF7_shGATA3_K27ac	13,770,429	11,875,200	86.24%
MCF7_P300	15,034,150	11,838,236	78.74%
TamR_P300	15,724,869	12,837,072	81.64%
MCF7_oeCtrl_ER	19,897,362	16,498,169	82.92%
MCF7_oeJUN_ER	15,343,907	12,616,919	82.23%
TamR_oeCtrl_K27ac	13,522,266	12,140,114	89.78%
TamR_oeGATA3_K27ac	17,758,003	15,754,603	88.72%
MCF7_oeCtrl_K27ac	35,409,818	32,193,406	90.92%
MCF7_oeJUN_K27ac	22,630,846	20,504,807	90.61%
TamR_shCtrl_ARID1B	8,373,484	6,783,094	81.01%
TamR_shJUN_ARID1B	15,559,152	13,002,753	83.57%
TamR_shCtrl_BRG1	7,339,938	5,997,503	81.71%
TamR_shJUN_BRG1	9,559,767	7,740,785	80.97%
TamR_shCtrl_P300	15,295,852	12,667,876	82.82%
TamR_shJUN_P300	20,769,920	17,629,428	84.88%
MCF7_GATA3	16,141,996	13,294,294	82.36%
TamR_GATA3	11,739,766	9,405,087	80.11%
MCF7_shCtrl_noDox_K27ac	22,331,543	19,755,297	88.46%
MCF7_shCtrl_Dox_K27ac	27,816,537	24,841,421	89.30%
MCF7_shGATA3_noDox_K27ac	20,077,829	17,821,808	88.76%
MCF7_shGATA3_Dox_K27ac	22,034,110	19,515,636	88.57%
MCF7_JUN_CST9165	12,352,709	10,143,615	82.12%
TamR_JUN_CST9165	10,234,424	8,403,809	82.11%
MCF7_JUN_BD610326	15,241,619	11,078,130	72.68%
TamR_JUN_BD610326	17,794,556	14,889,577	83.67%
T47D_Ctrl_K27ac	14194888	12407771	87.41%
T47D_oeJUN_K27ac	20705973	18419416	88.96%
T47D_shGATA3_K27ac	17976242	15910330	88.51%
T47D_Both_K27ac	18636587	16464847	88.35%
ZR75_Ctrl_K27ac	20929411	18254170	87.22%
ZR75_oeJUN_K27ac	17238248	14756124	85.60%
ZR75_shGATA3_K27ac	28015795	24642228	87.96%
ZR75_Both_K27ac	17850307	15516689	86.93%

Antibodies

ERα(HC-20)(Santa Cruz, sc-543),
p300(C-20)(Santa Cruz, sc-585),
c-JUN(60A8)(Cell Signaling, 9165S),
GATA3(D13C9)(Cell Signaling, 5852S),
c-JUN (BD Transduction Laboratories, 610326),
H3K27ac (Abcam, ab4729),
H3K4me1 (Abcam, ab8895),
BRG1 (Abcam, ab4081),
FOXA1 (Abcam, ab5089),
ERα (Bethyl Laboratories, A300-495A),
ARID1B (Bethyl Laboratories, A301-046A),
P300 (Active motif, 61401).

Peak calling parameters

macs2 callpeak -t sample.bam -c input.bam -n sample -g hs --outdir macs2 -p 1e-5

Data quality

FastQC (v0.11.5) was used for reads quality control.
P < 1e-5 was used as cutoff to identify peaks with MACS2 (v2.1.1).

Sample	Peak count
MCF7_Full_ER	57354
TamR_Full_ER	62910
MCF7_K4me1	58870
MCF7_K27ac_rep1	35260
TamR_K4me1	68831
TamR_K27ac_rep1	36422
MCF7_K27ac_rep2	33965
TamR_K27ac_rep2	36648
MCF7_FOXA1	14752
TamR_FOXA1	21913
TamR_shCtrl_ER	9335
TamR_shJUN_ER	726
TamR_shCtrl_K27ac	35435
TamR_shJUN_K27ac	18723
MCF7_shCtrl_ER	6654
MCF7_shGATA3_ER	1032
MCF7_shCtrl_K27ac	31180
MCF7_shGATA3_K27ac	31481
MCF7_P300	5160
TamR_P300	18148
MCF7_oeCtrl_ER	7216
MCF7_oeJUN_ER	6425
TamR_oeCtrl_K27ac	34219
TamR_oeGATA3_K27ac	44215
MCF7_oeCtrl_K27ac	34856
MCF7_oeJUN_K27ac	35303
TamR_shCtrl_ARID1B	3778
TamR_shJUN_ARID1B	4061
TamR_shCtrl_BRG1	4342
TamR_shJUN_BRG1	3433
TamR_shCtrl_P300	4469
TamR_shJUN_P300	9752
MCF7_GATA3	19270
TamR_GATA3	6955
MCF7_shCtrl_noDox_K27ac	27562
MCF7_shCtrl_Dox_K27ac	34429
MCF7_shGATA3_noDox_K27ac	28186
MCF7_shGATA3_Dox_K27ac	35835
MCF7_JUN_CST9165	3514
TamR_JUN_CST9165	18903
MCF7_JUN_BD610326	3903
TamR_JUN_BD610326	15017
T47D_Ctrl_K27ac	26176
T47D_oeJUN_K27ac	36330
T47D_shGATA3_K27ac	29954
T47D_Both_K27ac	36344
ZR75_Ctrl_K27ac	36733
ZR75_oeJUN_K27ac	34981
ZR75_shGATA3_K27ac	47373
ZR75_Both_K27ac	39297

Software

bowtie v1.1.2; MACS2 v2.1.1; bedtools v2.26.0; R v3.3.2;