Supplementary information

Spatial epigenome-transcriptome coprofiling of mammalian tissues

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Spatial epigenome-transcriptome co-profiling of mammalian tissues

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Supplementary Fig. 1 Quality control metrics for spatial-ATAC-RNA-seq and spatial-CUT&Tag-RNA-seq datasets. a, Scatterplots showing the TSS enrichment score vs unique nuclear fragments per pixel. **b**, Nissl-stained image from an adjacent tissue section of P21 mouse brain. The grid has an interval of 20 μm. Scale bar, 200 μm. **c**, The insert size distribution of ATAC or CUT&Tag fragments in spatial-ATAC-RNA-seq or spatial-CUT&Tag-RNA-seq. **d**, The enrichment of ATAC or CUT&Tag reads around TSSs in spatial-ATAC-RNA-seq or spatial-CUT&Tag-RNA-seq.



Supplementary Fig. 2 Quality control metrics for spatial-ATAC-RNA-seq and spatial-CUT&Tag-RNA-seq datasets. a, Comparison of TSS fragments and fraction of mitochondrial fragments in spatial-ATAC-RNA-seq and spatial-CUT&Tag-RNA-seq. **b**, Comparison of number of unique fragments, TSS fragments, fraction of reads in peaks (FRiP), and fraction of mitochondrial fragments between biological replicates for spatial-ATAC-RNA-seq and spatial-CUT&Tag(H3K27ac)-RNA-seq. **c**, Gene and UMI count distribution between biological replicates for spatial-ATAC-RNA-seq. The box plots show the median (centre line), the first and third quartiles (box limits), and 1.5x the interquartile range (whiskers). **d**, The reproducibility of spatial-ATAC-RNA-seq between biological replicates on ATAC data (left) and RNA data (right) for P21 mouse brain. **e**, The reproducibility of spatial-CUT&Tag data (left) and RNA data (right) for P21 mouse brain.



Supplementary Fig. 3 Benchmarking of data quality in spatial-ATAC-RNA-seq. a, Comparison of transcriptional profiles between RNA in spatial-ATAC-RNA-seq and the ENCODE RNA-Seq data in brain of mouse embryo. **b**, Aggregated spatial chromatin accessibility profiles in spatial-ATAC-RNA-seq recapitulated ENCODE ATAC-seq profiles in brain of mouse embryo. **c**, Venn diagrams showing the overlap of peaks from ATAC in spatial-ATAC-RNA-seq and ENCODE ATAC-seq in brain of mouse embryo.



Supplementary Fig. 4 Further analysis of spatial-ATAC-RNA-seq for E13 mouse embryo. a, GO enrichment analysis in selected RNA clusters from spatial-ATAC-RNA-seq for E13 mouse embryo (One-sided version of Fisher's exact test, p-value was adjusted for multiple comparisons by Benjamini & Hochberg method). **b**, The number of significantly correlated peaks for each gene.



Supplementary Fig. 5 Further analysis of spatial-ATAC-RNA-seq for P22 mouse brain. a, Ribbon plot showing the relationship between ATAC and RNA clusters in spatial-ATAC-RNA-seq. **b**, Annotation of marker peaks in different clusters. **c**, GREAT enrichment analysis of marker peaks in different clusters (Binomial and hypergeometric tests).

Spatial-CUT&Tag-RNA-seq (H3K27me3)



Supplementary Fig. 6 Spatial mapping of CSS, GAS, and gene expression of selected genes in spatial-CUT&Tag-RNA-seq for P22 mouse brain. a-c, Spatial mapping of CSS or GAS, and gene expression for selected marker genes in spatial-CUT&Tag(H3K27me3)-RNA-seq (a), spatial-CUT&Tag(H3K27ac)-RNA-seq (b), and spatial-CUT&Tag(H3K4me3)-RNA-seq (c).

Spatial-CUT&Tag(H3K27ac)-RNA-seq



b

С

Spatial-CUT&Tag(H3K27ac)-RNA-seq



Spatial-CUT&Tag(H3K4me3)-RNA-seq



Supplementary Fig. 7 Further analysis for spatial-CUT&Tag-RNA-seq with P22 mouse brain. a, Genome track visualization of marker genes with peak-to-gene links for distal regulatory elements and peak co-accessibility. b, Heatmaps of peak-to-gene links in spatial-CUT&Tag(H3K27ac)-RNA-seq. c, The layers identified by Belayer from the top right mapping region of the P22 mouse brain. Evaluate the consistency between the two Belayer results (right) by adjusted rand index (ARI): ARI = 0.915.

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Supplementary Fig. 8 GO enrichment analysis of P22 mouse brain. GO enrichment analysis of genes from Fig. 4a (One-sided version of Fisher's exact test, p-value was adjusted for multiple comparisons by Benjamini & Hochberg method).



Supplementary Fig. 9 Further analysis for epigenetic regulation of gene expression with P22 mouse brain. a, Correlation analysis of H3K27me3 CSS and RNA gene expression in striatum. b, GO enrichment analysis of genes from (a) (One-sided version of Fisher's exact test, p-value was adjusted for multiple comparisons by Benjamini & Hochberg method).



Supplementary Fig. 10 Further analysis for epigenetic regulation of gene expression with P22 mouse brain. a, Correlation analysis of H3K27me3 CSS and RNA gene expression in superficial cortical layer. b, GO enrichment analysis of genes from (a) (One-sided version of Fisher's exact test, p-value was adjusted for multiple comparisons by Benjamini & Hochberg method).



Supplementary Fig. 11 Further analysis for epigenetic regulation of gene expression with P22 mouse brain. a, Correlation analysis of H3K27me3 CSS and RNA gene expression in deeper cortical layer. b, GO enrichment analysis of genes from (a) (One-sided version of Fisher's exact test, p-value was adjusted for multiple comparisons by Benjamini & Hochberg method).



Supplementary Fig. 12 Further analysis for epigenetic regulation of gene expression with P22 mouse brain. GO enrichment analysis of genes from Fig. 4b,c (One-sided version of Fisher's exact test, p-value was adjusted for multiple comparisons by Benjamini & Hochberg method).



Supplementary Fig. 13 Further analysis for epigenetic regulation of gene expression with P22 mouse brain. a, Correlation analysis of H3K27me3 CSS and H3K27ac GAS in corpus callosum. b, GO enrichment analysis of genes from (a) (One-sided version of Fisher's exact test, p-value was adjusted for multiple comparisons by Benjamini & Hochberg method).



Supplementary Fig. 14 Further analysis for epigenetic regulation of gene expression with P22 mouse brain. a, Correlation analysis of H3K27me3 CSS and H3K4me3 GAS in corpus callosum. b, GO enrichment analysis of genes from (a) (One-sided version of Fisher's exact test, p-value was adjusted for multiple comparisons by Benjamini & Hochberg method).

Statistics and Reproducibility

Figure	Description	# of times repeated
Fig. 2b,3a	Nissl-stained image of P22 mouse brain	1
Fig. 3b,c	Nissl-stained image of P22 mouse brain	1
Fig. 5a, Extended Data Fig. 10a	Bright field image of human hippocampus	1
Extended Data Fig. 2a	H&E image of E13 mouse embryo	1
Extended Data Fig. 2d	Bright field image of E13 mouse embryo	1
Extended Data Fig. 4c,d	Bright field image of P22 mouse brain	1
Extended Data Fig. 6a,b,c	Bright field image of P21 mouse brain	1
Extended Data Fig. 6d,8d,	Nigel stained image of D21 mayor brain	1
Supplementary Fig. 1b	Nissi-stamed image of P21 mouse brain	
Extended Data Fig. 8a,b,c	Bright field image of P21 mouse brain	1

Supplementary Table 1. A list of cell type annotations in mouse brain.

			E13 mouse embryo (50 barcodes, 50 μm pixel size)	P22 mouse brain (100 barcodes , 20 μm pixel size)	P21 mouse brain (replica 1, 50 barcodes, 20 μm pixel size)	P21 mouse brain (replica 2, 50 barcodes, 20 μm pixel size)	Human brain (50 barcodes, 50 µm pixel size)
		Number of Unique fragments	18,079	14,284	10,857	14,385	9,898
ATAO Spatial- ATAC- RNA- seq RNA	ATAC	TSS fragments	16%	19%	20%	19%	15%
		FRiP	11%	26%	24%	26%	11%
		Mitochondrial fragments	0.96%	4.6%	9%	8.4%	20%
		Averagenumberofgenesperpixel	1,255	1,073	1,005	1,600	1,200
	RNA	Average number of UMIs per pixel	3,603	2,358	2,391	3,811	2,809
		Number of unique genes present	20,900	22,914	19,859	20,046	29,293
		Pixels on tissue	2,187	9,215	2,373	2,498	2,500

Supplementary Table 2. Summary of metrics for ATAC and RNA in spatial-ATAC-RNA-seq for all the samples.

			P22 mouse brain (H3K27m e3) (100 barcodes, 20 μm pixel size)	P22 mouse brain (H3K27 ac) (100 barcodes , 20 μm pixel size)	P22 mouse brain (H3K4m e3) (100 barcodes , 20 μm pixel size)	P21 mouse brain (H3K27ac , replica 1) (50 barcodes, 20 μm pixel size)	P21 mouse brain (H3K27ac , replica 2) (50 barcodes, 20 μm pixel size)
Spatial-	CUT&T	Number of Unique fragments	10,644	10,002	2,507	4,756	5,022
CUT&Tg ag-RNA- seq	ag	TSS fragments	12%	17% 210/	67% 540/	19%	20%
		Mitochondrial fragments	0.2%	0.3%	3.6%	0.1%	0.02%
		Average number of genes per pixel	2,011	1,513	1,329	1,145	752
	RNA	Average number of UMIs per pixel	4,734	3,580	2,885	2,938	1,890
		Number of unique genes present	25,881	23,415	22,731	19,831	18,718
		I IACIS OII LISSUE	9,152	9,570	2,540	2,307	2,477

Supplementary Table 3. Summary of metrics for CUT&Tag and RNA in spatial-CUT&Tag-RNA-seq for all the samples.

RT primer	/5Phos/CATCGGCGTACGACTNNNNNNNNNNN/iBiodT/TTTTTTTTTTTTTT VN
Ligation linker 1	AGTCGTACGCCGATGCGAAACATCGGCCAC
Ligation linker 2	CGAATGCTCTGGCCTCTCAAGCACGTGGAT
PCR Primer 1	CAAGCGTTGGCTTCTCGCATCT
PCR Primer 2	AAGCAGTGGTATCAACGCAGAGT
N501	AATGATACGGCGACCACCGAGATCTACACTAGATCGCTCGTCGGCAGCG
N301	TCAGATGTGTATAAGAGACAG
N/701	CAAGCAGAAGACGGCATACGAGATTCGCCTTAGTCTCGTGGGCTCGGAG
IN /01	ATGTGTATAAGAGACAGCAAGCGTTGGCTTCTCGCATCT
N702	CAAGCAGAAGACGGCATACGAGATCTAGTACGGTCTCGTGGGCTCGGAG
	ATGTGTATAAGAGACAGCAAGCGTTGGCTTCTCGCATCT
N/702	CAAGCAGAAGACGGCATACGAGATTTCTGCCTGTCTCGTGGGCTCGGAG
N/03	ATGTGTATAAGAGACAGCAAGCGTTGGCTTCTCGCATCT
N704	CAAGCAGAAGACGGCATACGAGATGCTCAGGAGTCTCGTGGGCTCGGA
N/04	GATGTGTATAAGAGACAGCAAGCGTTGGCTTCTCGCATCT
N/705	CAAGCAGAAGACGGCATACGAGATAGGAGTCCGTCTCGTGGGCTCGGA
IN /05	GATGTGTATAAGAGACAGCAAGCGTTGGCTTCTCGCATCT
N706	CAAGCAGAAGACGGCATACGAGATCATGCCTAGTCTCGTGGGCTCGGAG
IN / 00	ATGTGTATAAGAGACAGCAAGCGTTGGCTTCTCGCATCT
N707	CAAGCAGAAGACGGCATACGAGATGTAGAGAGGTCTCGTGGGCTCGGA
	GATGTGTATAAGAGACAGCAAGCGTTGGCTTCTCGCATCT

Supplementary Table 4. DNA oligos used for PCR and preparation of sequencing library.

Barcode A	Sequence
Barcode A-1	/5Phos/AGGCCAGAGCATTCGAACGTGATGTGGCCGATGTTTCG
Barcode A-2	/5Phos/AGGCCAGAGCATTCGAAACATCGGTGGCCGATGTTTCG
Barcode A-3	/5Phos/AGGCCAGAGCATTCGATGCCTAAGTGGCCGATGTTTCG
Barcode A-4	/5Phos/AGGCCAGAGCATTCGAGTGGTCAGTGGCCGATGTTTCG
Barcode A-5	/5Phos/AGGCCAGAGCATTCGACCACTGTGTGGCCGATGTTTCG
Barcode A-6	/5Phos/AGGCCAGAGCATTCGACATTGGCGTGGCCGATGTTTCG
Barcode A-7	/5Phos/AGGCCAGAGCATTCGCAGATCTGGTGGCCGATGTTTCG
Barcode A-8	/5Phos/AGGCCAGAGCATTCGCATCAAGTGTGGCCGATGTTTCG
Barcode A-9	/5Phos/AGGCCAGAGCATTCGCGCTGATCGTGGCCGATGTTTCG
Barcode A-10	/5Phos/AGGCCAGAGCATTCGACAAGCTAGTGGCCGATGTTTCG
Barcode A-11	/5Phos/AGGCCAGAGCATTCGCTGTAGCCGTGGCCGATGTTTCG
Barcode A-12	/5Phos/AGGCCAGAGCATTCGAGTACAAGGTGGCCGATGTTTCG
Barcode A-13	/5Phos/AGGCCAGAGCATTCGAACAACCAGTGGCCGATGTTTCG
Barcode A-14	/5Phos/AGGCCAGAGCATTCGAACCGAGAGTGGCCGATGTTTCG
Barcode A-15	/5Phos/AGGCCAGAGCATTCGAACGCTTAGTGGCCGATGTTTCG
Barcode A-16	/5Phos/AGGCCAGAGCATTCGAAGACGGAGTGGCCGATGTTTCG
Barcode A-17	/5Phos/AGGCCAGAGCATTCGAAGGTACAGTGGCCGATGTTTCG
Barcode A-18	/5Phos/AGGCCAGAGCATTCGACACAGAAGTGGCCGATGTTTCG
Barcode A-19	/5Phos/AGGCCAGAGCATTCGACAGCAGAGTGGCCGATGTTTCG
Barcode A-20	/5Phos/AGGCCAGAGCATTCGACCTCCAAGTGGCCGATGTTTCG
Barcode A-21	/5Phos/AGGCCAGAGCATTCGACGCTCGAGTGGCCGATGTTTCG
Barcode A-22	/5Phos/AGGCCAGAGCATTCGACGTATCAGTGGCCGATGTTTCG
Barcode A-23	/5Phos/AGGCCAGAGCATTCGACTATGCAGTGGCCGATGTTTCG
Barcode A-24	/5Phos/AGGCCAGAGCATTCGAGAGTCAAGTGGCCGATGTTTCG
Barcode A-25	/5Phos/AGGCCAGAGCATTCGAGATCGCAGTGGCCGATGTTTCG
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Barcode A-39	/5Phos/AGGCCAGAGCATTCGCCTCCTGAGTGGCCGATGTTTCG
Barcode A-40	/5Phos/AGGCCAGAGCATTCGCGAACTTAGTGGCCGATGTTTCG
Barcode A-41	/5Phos/AGGCCAGAGCATTCGCGACTGGAGTGGCCGATGTTTCG

Supplementary Table 5. DNA barcode A sequences.

Barcode A-42	/5Phos/AGGCCAGAGCATTCGCGCATACAGTGGCCGATGTTTCG
Barcode A-43	/5Phos/AGGCCAGAGCATTCGCTCAATGAGTGGCCGATGTTTCG
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Barcode B	Sequence
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Barcode B-37	CAAGCGTTGGCTTCTCGCATCTCCGAAGTAATCCACGTGCTTGAG
Barcode B-38	CAAGCGTTGGCTTCTCGCATCTCCGTGAGAATCCACGTGCTTGAG
Barcode B-39	CAAGCGTTGGCTTCTCGCATCTCCTCCTGAATCCACGTGCTTGAG
Barcode B-40	CAAGCGTTGGCTTCTCGCATCTCGAACTTAATCCACGTGCTTGAG
Barcode B-41	CAAGCGTTGGCTTCTCGCATCTCGACTGGAATCCACGTGCTTGAG

Supplementary Table 6. DNA barcode B sequences.

Barcode B-42	CAAGCGTTGGCTTCTCGCATCTCGCATACAATCCACGTGCTTGAG
Barcode B-43	CAAGCGTTGGCTTCTCGCATCTCTCAATGAATCCACGTGCTTGAG
Barcode B-44	CAAGCGTTGGCTTCTCGCATCTCTGAGCCAATCCACGTGCTTGAG
Barcode B-45	CAAGCGTTGGCTTCTCGCATCTCTGGCATAATCCACGTGCTTGAG
Barcode B-46	CAAGCGTTGGCTTCTCGCATCTGAATCTGAATCCACGTGCTTGAG
Barcode B-47	CAAGCGTTGGCTTCTCGCATCTCAAGACTAATCCACGTGCTTGAG
Barcode B-48	CAAGCGTTGGCTTCTCGCATCTGAGCTGAAATCCACGTGCTTGAG
Barcode B-49	CAAGCGTTGGCTTCTCGCATCTGATAGACAATCCACGTGCTTGAG
Barcode B-50	CAAGCGTTGGCTTCTCGCATCTGCCACATAATCCACGTGCTTGAG
Barcode B-51	CAAGCGTTGGCTTCTCGCATCTGCGAGTAAATCCACGTGCTTGAG
Barcode B-52	CAAGCGTTGGCTTCTCGCATCTGCTAACGAATCCACGTGCTTGAG
Barcode B-53	CAAGCGTTGGCTTCTCGCATCTGCTCGGTAATCCACGTGCTTGAG
Barcode B-54	CAAGCGTTGGCTTCTCGCATCTGGAGAACAATCCACGTGCTTGAG
Barcode B-55	CAAGCGTTGGCTTCTCGCATCTGGTGCGAAATCCACGTGCTTGAG
Barcode B-56	CAAGCGTTGGCTTCTCGCATCTGTACGCAAATCCACGTGCTTGAG
Barcode B-57	CAAGCGTTGGCTTCTCGCATCTGTCGTAGAATCCACGTGCTTGAG
Barcode B-58	CAAGCGTTGGCTTCTCGCATCTGTCTGTCAATCCACGTGCTTGAG
Barcode B-59	CAAGCGTTGGCTTCTCGCATCTGTGTTCTAATCCACGTGCTTGAG
Barcode B-60	CAAGCGTTGGCTTCTCGCATCTTAGGATGAATCCACGTGCTTGAG
Barcode B-61	CAAGCGTTGGCTTCTCGCATCTTATCAGCAATCCACGTGCTTGAG
Barcode B-62	CAAGCGTTGGCTTCTCGCATCTTCCGTCTAATCCACGTGCTTGAG
Barcode B-63	CAAGCGTTGGCTTCTCGCATCTTCTTCACAATCCACGTGCTTGAG
Barcode B-64	CAAGCGTTGGCTTCTCGCATCTTGAAGAGAATCCACGTGCTTGAG
Barcode B-65	CAAGCGTTGGCTTCTCGCATCTTGGAACAAATCCACGTGCTTGAG
Barcode B-66	CAAGCGTTGGCTTCTCGCATCTTGGCTTCAATCCACGTGCTTGAG
Barcode B-67	CAAGCGTTGGCTTCTCGCATCTTGGTGGTAATCCACGTGCTTGAG
Barcode B-68	CAAGCGTTGGCTTCTCGCATCTTTCACGCAATCCACGTGCTTGAG
Barcode B-69	CAAGCGTTGGCTTCTCGCATCTAACTCACCATCCACGTGCTTGAG
Barcode B-70	CAAGCGTTGGCTTCTCGCATCTAAGAGATCATCCACGTGCTTGAG
Barcode B-71	CAAGCGTTGGCTTCTCGCATCTAAGGACACATCCACGTGCTTGAG
Barcode B-72	CAAGCGTTGGCTTCTCGCATCTAATCCGTCATCCACGTGCTTGAG
Barcode B-73	CAAGCGTTGGCTTCTCGCATCTAATGTTGCATCCACGTGCTTGAG
Barcode B-74	CAAGCGTTGGCTTCTCGCATCTACACGACCATCCACGTGCTTGAG
Barcode B-75	CAAGCGTTGGCTTCTCGCATCTACAGATTCATCCACGTGCTTGAG
Barcode B-76	CAAGCGTTGGCTTCTCGCATCTAGATGTACATCCACGTGCTTGAG
Barcode B-77	CAAGCGTTGGCTTCTCGCATCTAGCACCTCATCCACGTGCTTGAG
Barcode B-78	CAAGCGTTGGCTTCTCGCATCTAGCCATGCATCCACGTGCTTGAG
Barcode B-79	CAAGCGTTGGCTTCTCGCATCTAGGCTAACATCCACGTGCTTGAG
Barcode B-80	CAAGCGTTGGCTTCTCGCATCTATAGCGACATCCACGTGCTTGAG
Barcode B-81	CAAGCGTTGGCTTCTCGCATCTATCATTCCATCCACGTGCTTGAG
Barcode B-82	CAAGCGTTGGCTTCTCGCATCTATTGGCTCATCCACGTGCTTGAG
Barcode B-83	CAAGCGTTGGCTTCTCGCATCTCAAGGAGCATCCACGTGCTTGAG
Barcode B-84	CAAGCGTTGGCTTCTCGCATCTCACCTTACATCCACGTGCTTGAG

Barcode B-85	CAAGCGTTGGCTTCTCGCATCTCCATCCTCATCCACGTGCTTGAG
Barcode B-86	CAAGCGTTGGCTTCTCGCATCTCCGACAACATCCACGTGCTTGAG
Barcode B-87	CAAGCGTTGGCTTCTCGCATCTCCTAATCCATCCACGTGCTTGAG
Barcode B-88	CAAGCGTTGGCTTCTCGCATCTCCTCTATCATCCACGTGCTTGAG
Barcode B-89	CAAGCGTTGGCTTCTCGCATCTCGACACACATCCACGTGCTTGAG
Barcode B-90	CAAGCGTTGGCTTCTCGCATCTCGGATTGCATCCACGTGCTTGAG
Barcode B-91	CAAGCGTTGGCTTCTCGCATCTCTAAGGTCATCCACGTGCTTGAG
Barcode B-92	CAAGCGTTGGCTTCTCGCATCTGAACAGGCATCCACGTGCTTGAG
Barcode B-93	CAAGCGTTGGCTTCTCGCATCTGACAGTGCATCCACGTGCTTGAG
Barcode B-94	CAAGCGTTGGCTTCTCGCATCTGAGTTAGCATCCACGTGCTTGAG
Barcode B-95	CAAGCGTTGGCTTCTCGCATCTGATGAATCATCCACGTGCTTGAG
Barcode B-96	CAAGCGTTGGCTTCTCGCATCTGCCAAGACATCCACGTGCTTGAG
Barcode B-97	CAAGCGTTGGCTTCTCGCATCTCGGAAGAAATCCACGTGCTTGAG
Barcode B-98	CAAGCGTTGGCTTCTCGCATCTGTGACAAGATCCACGTGCTTGAG
Barcode B-99	CAAGCGTTGGCTTCTCGCATCTGAACCAGAATCCACGTGCTTGAG
Barcode B-100	CAAGCGTTGGCTTCTCGCATCTTTGCTGGAATCCACGTGCTTGAG

Name	Catalog number	Vender
Formaldehyde solution	PI28906	Thermo Fisher Scientific
HEPES pH 7.5	BBH-75-250	Boston BioProducts
Glycine	50046	Sigma-Aldrich
NaCl	AM9760G	Thermo Fisher Scientific
Digitonin	G9441	Promega
MgCl ₂	AM9530G	Thermo Fisher Scientific
Spermidine	S0266	Sigma-Aldrich
EDTA-free Protease Inhibitor Cocktail	11873580001	Millipore Sigma
NP40	11332473001	Sigma-Aldrich
EDTA Solution pH 8.0	AB00502	AmericanBio
Bovine Serum Albumin (BSA)	A8806	Sigma-Aldrich
Anti-H3K27ac antibody	ab177178	Abcam
Anti-H3K27me3 antibody	9733	Cell Signaling Technology
Histone H3K4me3 antibody	39159	Active Motif
Secondary antibody (Guinea Pig anti-	ABIN101961	Antibodies-Online
Rabbit IgG)		
pA-Tn5 Transposase – unloaded	C01070002	Diagenode
Triton X-100	T8787	Sigma-Aldrich
T4 DNA Ligase	M0202L	New England Biolabs
T4 DNA Ligase Reaction Buffer	B0202S	New England Biolabs
NEBuffer 3.1	B7203S	New England Biolabs
DPBS	14190144	Thermo Fisher Scientific
Proteinase K	EO0491	Thermo Fisher Scientific
Ampure XP beads	A63880	Beckman Coulter
NEBNext High-Fidelity 2X PCR	M0541L	New England Biolabs
Master Mix		
SYBR Green I Nucleic Acid Gel Stain	S7563	Thermo Fisher Scientific
DNA Clean & Concentrator-5	D4014	Zymo Research
Tn5 Transposase - unloaded	C01070010	Diagenode
Tagmentation Buffer (2x)	C01019043	Diagenode
Sodium dodecyl sulfate	71736	Sigma-Aldrich
Maxima H Minus Reverse	EP0751	Thermo Fisher Scientific
Transcriptase (200 U/L)		
dNTP mix	R0192	Thermo Fisher Scientific
SUPERased In RNase Inhibitor	AM2694	Thermo Fisher Scientific
Ampure XP beads	A63880	Beckman Coulter
Dynabeads MyOne C1	65001	Thermo Fisher Scientific
RNase Inhibitor	Y9240L	Enzymatics
Kapa Hotstart HiFi ReadyMix	KK2601	Kapa Biosystems
Nextera XT DNA Preparation Kit	FC-131-1024	Illumina

Supplementary Table 7. Chemicals and reagents.