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Yale University_Spatial ATAC Sequencing for Fixed Fresh Frozen Human Lymph node Tissue via DBiT-seq





Forked from Spatial Multi-omics Sequencing for Fixed Tissue via DBiT-seq

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Negin Farzad¹, Yanxiang Deng¹, Archibald Enninful¹, yao.lu.yl¹, Rong Fan¹

¹Yale University

Cellular Senescence Net...



Negin Farzad

Yale University

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Farzad N, Enninful A, Bao S, Zhang D, Deng Y, Fan R. Spatially resolved epigenome sequencing via Tn5 transposition and deterministic DNA barcoding in tissue. Nat Protoc. 2024 Jun 28. doi: 10.1038/s41596-024-01013-y. Epub ahead of print. PMID: 38943021.

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Abstract

This protocol describes the use of Deterministic Barcoding in Tissue for spatial ATAC sequencing to construct an epigenome atlas of fixed fresh frozen human lymph node tissue samples. This approach uses a microfluidic-based method to introduce combinatorial DNA oligo barcodes directly to the cells in a tissue section fixed on a glass slide. This method spatially resolved genome-wide profiling of transposase-accessible chromatin sequencing for chromatin accessibility. This technique does not directly resolve single cells but can achieve a near-single-cell resolution for spatial epigenomic analysis.



Materials

KEY RESOURCES TABLE

A	В	С
Name	Catalog num ber	Vender
Formaldehyde solution	PI28906	Thermo Fisher Scientific
Glycine	50046	Sigma-Aldrich
NaCl	AM9760G	Thermo Fisher Scientific
Digitonin	G9441	Promega
MgCl2	AM9530G	Thermo Fisher Scientific
NP40	1133247300 1	Sigma-Aldrich
EDTA Solution pH 8.0	AB00502	AmericanBio
Bovine Serum Albumin (BSA)	A8806	Sigma-Aldrich
Triton X-100	T8787	Sigma-Aldrich
T4 DNA Ligase	M0202L	New England Biola bs
T4 DNA Ligase Reaction Buffer	B0202S	New England Biola bs
NEBuffer 3.1	B7203S	New England Biola bs
DPBS	14190144	Thermo Fisher Sci
Proteinase K	E00491	Thermo Fisher Sci ntific
Ampure XP beads	A63880	Beckman Coulter
NEBNext High-Fidelity 2X PCR Master Mix	M0541L	New England Biola bs
SYBR Green I Nucleic Aci d Gel Stain	S7563	Thermo Fisher Scintific



A	В	С
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 Transcriptase (200 U/L)	EP0751	Thermo Fisher Scie ntific
dNTP mix	R0192	Thermo Fisher Scie ntific
SUPERased In RNase Inhibitor	AM2694	Thermo Fisher Scie ntific
Ampure XP beads	A63880	Beckman Coulter
Dynabeads MyOne C1	65001	Thermo Fisher Scie ntific
RNase Inhibitor	Y9240L	Enzymatics
Kapa Hotstart HiFi ReadyMix	KK2601	Kapa Biosystems
Nextera XT DNA Preparation Kit	FC-131-1024	Illumina

Table S1A. List of reagents

Oligo Name	Sequence
Ligation Linker	CGAATGCTCTGGCCTCTCAAGCACGTGGAT
P5 oligo	AATGATACGGCGACCACCGAGATCTACACTAGATCGCTCGTCGGCAGCGTCAGATGTGTATA AGAGACAG
P7 oligo (701)	CAAGCAGAAGACGCATACGAGATTCGCCTTAGTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGCAAGCGTTGGCTTCTCGCATCT
P7 oligo (702)	CAAGCAGAAGACGCATACGAGATCTAGTACGGTCTCGTGGGCTCGGAGATGTGTATAAGAG ACAGCAAGCGTTGGCTTCTCGCATCT
P7 oligo (703)	CAAGCAGAAGACGCATACGAGATTTCTGCCTGTCTCGTGGGCTCGGAGATGTGTATAAGAG ACAGCAAGCGTTGGCTTCTCGCATCT
P7 oligo (704)	CAAGCAGAAGACGCATACGAGATGCTCAGGAGTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGCAAGCGTTGGCTTCTCGCATCT
P7 oligo (705)	CAAGCAGAAGACGCATACGAGATAGGAGTCCGTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGCAAGCGTTGGCTTCTCGCATCT
P7 oligo (706)	CAAGCAGAAGACGCATACGAGATCATGCCTAGTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGCAAGCGTTGGCTTCTCGCATCT



Table S2A. List of PCR Oligo.

A	В
Barcode A-1	/5Phos/AGGCCAGAGCATTCGAACGTGATTTTTTTTTTTTTVN
Barcode A-2	/5Phos/AGGCCAGAGCATTCGAAACATCGTTTTTTTTTTTTVN
Barcode A-3	/5Phos/AGGCCAGAGCATTCGATGCCTAATTTTTTTTTTTTVN
Barcode A-4	/5Phos/AGGCCAGAGCATTCGAGTGGTCATTTTTTTTTTTTVN
Barcode A-5	/5Phos/AGGCCAGAGCATTCGACCACTGTTTTTTTTTTTTTVN
Barcode A-6	/5Phos/AGGCCAGAGCATTCGACATTGGCTTTTTTTTTTTTVN
Barcode A-7	/5Phos/AGGCCAGAGCATTCGCAGATCTGTTTTTTTTTTTTVN
Barcode A-8	/5Phos/AGGCCAGAGCATTCGCATCAAGTTTTTTTTTTTTTVN
Barcode A-9	/5Phos/AGGCCAGAGCATTCGCGCTGATCTTTTTTTTTTTVN
Barcode A-10	/5Phos/AGGCCAGAGCATTCGACAAGCTATTTTTTTTTTTTVN
Barcode A-11	/5Phos/AGGCCAGAGCATTCGCTGTAGCCTTTTTTTTTTTTVN
Barcode A-12	/5Phos/AGGCCAGAGCATTCGAGTACAAGTTTTTTTTTTTTVN
Barcode A-13	/5Phos/AGGCCAGAGCATTCGAACAACCATTTTTTTTTTTTVN
Barcode A-14	/5Phos/AGGCCAGAGCATTCGAACCGAGATTTTTTTTTTTTVN
Barcode A-15	/5Phos/AGGCCAGAGCATTCGAACGCTTATTTTTTTTTTTTVN
Barcode A-16	/5Phos/AGGCCAGAGCATTCGAAGACGGATTTTTTTTTTTTVN
Barcode A-17	/5Phos/AGGCCAGAGCATTCGAAGGTACATTTTTTTTTTTTVN
Barcode A-18	/5Phos/AGGCCAGAGCATTCGACACAGAATTTTTTTTTTTTVN
Barcode A-19	/5Phos/AGGCCAGAGCATTCGACAGCAGATTTTTTTTTTTTVN
Barcode A-20	/5Phos/AGGCCAGAGCATTCGACCTCCAATTTTTTTTTTTTVN
Barcode A-21	/5Phos/AGGCCAGAGCATTCGACGCTCGATTTTTTTTTTTTVN
Barcode A-22	/5Phos/AGGCCAGAGCATTCGACGTATCATTTTTTTTTTTTVN
Barcode A-23	/5Phos/AGGCCAGAGCATTCGACTATGCATTTTTTTTTTTTVN
Barcode A-24	/5Phos/AGGCCAGAGCATTCGAGAGTCAATTTTTTTTTTTTVN
Barcode A-25	/5Phos/AGGCCAGAGCATTCGAGATCGCATTTTTTTTTTTTVN
Barcode A-26	/5Phos/AGGCCAGAGCATTCGAGCAGGAATTTTTTTTTTTTVN
Barcode A-27	/5Phos/AGGCCAGAGCATTCGAGTCACTATTTTTTTTTTTTVN
Barcode A-28	/5Phos/AGGCCAGAGCATTCGATCCTGTATTTTTTTTTTTTVN
Barcode A-29	/5Phos/AGGCCAGAGCATTCGATTGAGGATTTTTTTTTTTTVN
Barcode A-30	/5Phos/AGGCCAGAGCATTCGCAACCACATTTTTTTTTTTTVN
Barcode A-31	/5Phos/AGGCCAGAGCATTCGGACTAGTATTTTTTTTTTTTVN
Barcode A-32	/5Phos/AGGCCAGAGCATTCGCAATGGAATTTTTTTTTTTTVN
Barcode A-33	/5Phos/AGGCCAGAGCATTCGCACTTCGATTTTTTTTTTTTVN
Barcode A-34	/5Phos/AGGCCAGAGCATTCGCAGCGTTATTTTTTTTTTTTVN



A	В
Barcode A-35	/5Phos/AGGCCAGAGCATTCGCATACCAATTTTTTTTTTTTTVN
Barcode A-36	/5Phos/AGGCCAGAGCATTCGCCAGTTCATTTTTTTTTTTTVN
Barcode A-37	/5Phos/AGGCCAGAGCATTCGCCGAAGTATTTTTTTTTTTTVN
Barcode A-38	/5Phos/AGGCCAGAGCATTCGCCGTGAGATTTTTTTTTTTTTVN
Barcode A-39	/5Phos/AGGCCAGAGCATTCGCCTCCTGATTTTTTTTTTTTTVN
Barcode A-40	/5Phos/AGGCCAGAGCATTCGCGAACTTATTTTTTTTTTTTVN
Barcode A-41	/5Phos/AGGCCAGAGCATTCGCGACTGGATTTTTTTTTTTTTVN
Barcode A-42	/5Phos/AGGCCAGAGCATTCGCGCATACATTTTTTTTTTTTVN
Barcode A-43	/5Phos/AGGCCAGAGCATTCGCTCAATGATTTTTTTTTTTTTVN
Barcode A-44	/5Phos/AGGCCAGAGCATTCGCTGAGCCATTTTTTTTTTTTVN
Barcode A-45	/5Phos/AGGCCAGAGCATTCGCTGGCATATTTTTTTTTTTTTVN
Barcode A-46	/5Phos/AGGCCAGAGCATTCGGAATCTGATTTTTTTTTTTTTVN
Barcode A-47	/5Phos/AGGCCAGAGCATTCGCAAGACTATTTTTTTTTTTTVN
Barcode A-48	/5Phos/AGGCCAGAGCATTCGGAGCTGAATTTTTTTTTTTTVN
Barcode A-49	/5Phos/AGGCCAGAGCATTCGGATAGACATTTTTTTTTTTTVN
Barcode A-50	/5Phos/AGGCCAGAGCATTCGGCCACATATTTTTTTTTTTTVN

Table S2B. List of DNA Barcode A Sequences.

A	В
Barcode B-1	/5Biosg/CAAGCGTTGGCTTCTCGCATCTNNNNNNNNNNNAACGTGATATCCACGTGCTTGAG
Barcode B-2	/5Biosg/CAAGCGTTGGCTTCTCGCATCTNNNNNNNNNNNAAACATCGATCCACGTGCTTGAG
Barcode B-3	/5Biosg/CAAGCGTTGGCTTCTCGCATCTNNNNNNNNNNNNATGCCTAAATCCACGTGCTTGAG
Barcode B-4	/5Biosg/CAAGCGTTGGCTTCTCGCATCTNNNNNNNNNNNAGTGGTCAATCCACGTGCTTGAG
Barcode B-5	/5Biosg/CAAGCGTTGGCTTCTCGCATCTNNNNNNNNNNNNACCACTGTATCCACGTGCTTGAG
Barcode B-6	/5Biosg/CAAGCGTTGGCTTCTCGCATCTNNNNNNNNNNNACATTGGCATCCACGTGCTTGAG
Barcode B-7	/5Biosg/CAAGCGTTGGCTTCTCGCATCTNNNNNNNNNNNNCAGATCTGATCCACGTGCTTGAG
Barcode B-8	/5Biosg/CAAGCGTTGGCTTCTCGCATCTNNNNNNNNNNNNCATCAAGTATCCACGTGCTTGAG
Barcode B-9	/5Biosg/CAAGCGTTGGCTTCTCGCATCTNNNNNNNNNNNCGCTGATCATCCACGTGCTTGAG
Barcode B-10	/5Biosg/CAAGCGTTGGCTTCTCGCATCTNNNNNNNNNNNACAAGCTAATCCACGTGCTTGAG

A	В
Barcode B-11	/5Biosg/CAAGCGTTGGCTTCTCGCATCTNNNNNNNNNNNCTGTAGCCATCCACGTGCTTGAG
Barcode B-12	/5Biosg/CAAGCGTTGGCTTCTCGCATCTNNNNNNNNNNNAGTACAAGATCCACGTGCTTGAG
Barcode B-13	/5Biosg/CAAGCGTTGGCTTCTCGCATCTNNNNNNNNNNAACAACCAATCCACGTGCTTGAG
Barcode B-14	/5Biosg/CAAGCGTTGGCTTCTCGCATCTNNNNNNNNNNNAACCGAGAATCCACGTGCTTGAG
Barcode B-15	/5Biosg/CAAGCGTTGGCTTCTCGCATCTNNNNNNNNNNNAACGCTTAATCCACGTGCTTGAG
Barcode B-16	/5Biosg/CAAGCGTTGGCTTCTCGCATCTNNNNNNNNNNAAGACGGAATCCACGTGCTGAG
Barcode B-17	/5Biosg/CAAGCGTTGGCTTCTCGCATCTNNNNNNNNNNAAGGTACAATCCACGTGCTTGAG
Barcode B-18	/5Biosg/CAAGCGTTGGCTTCTCGCATCTNNNNNNNNNNNACACAGAAATCCACGTGCTTGAG
Barcode B-19	/5Biosg/CAAGCGTTGGCTTCTCGCATCTNNNNNNNNNNNACAGCAGAATCCACGTGCTTGAG
Barcode B-20	/5Biosg/CAAGCGTTGGCTTCTCGCATCTNNNNNNNNNNNACCTCCAAATCCACGTGCTTGAG
Barcode B-21	/5Biosg/CAAGCGTTGGCTTCTCGCATCTNNNNNNNNNNNACGCTCGAATCCACGTGCTTGAG
Barcode B-22	/5Biosg/CAAGCGTTGGCTTCTCGCATCTNNNNNNNNNNNACGTATCAATCCACGTGCTTGAG
Barcode B-23	/5Biosg/CAAGCGTTGGCTTCTCGCATCTNNNNNNNNNNNACTATGCAATCCACGTGCTTGAG
Barcode B-24	/5Biosg/CAAGCGTTGGCTTCTCGCATCTNNNNNNNNNNNAGAGTCAAATCCACGTGCTTGAG
Barcode B-25	/5Biosg/CAAGCGTTGGCTTCTCGCATCTNNNNNNNNNNAGATCGCAATCCACGTGCT
Barcode B-26	/5Biosg/CAAGCGTTGGCTTCTCGCATCTNNNNNNNNNNNAGCAGGAAATCCACGTGCTGAG
Barcode B-27	/5Biosg/CAAGCGTTGGCTTCTCGCATCTNNNNNNNNNNNAGTCACTAATCCACGTGCT
Barcode B-28	/5Biosg/CAAGCGTTGGCTTCTCGCATCTNNNNNNNNNNNNATCCTGTAATCCACGTGCTTGAG
Barcode B-29	/5Biosg/CAAGCGTTGGCTTCTCGCATCTNNNNNNNNNNNATTGAGGAATCCACGTGCT
Barcode B-30	/5Biosg/CAAGCGTTGGCTTCTCGCATCTNNNNNNNNNNNCAACCACAATCCACGTGCTTGAG
Barcode B-31	/5Biosg/CAAGCGTTGGCTTCTCGCATCTNNNNNNNNNNNNGACTAGTAATCCACGTGCTTGAG
Barcode B-32	/5Biosg/CAAGCGTTGGCTTCTCGCATCTNNNNNNNNNNNCAATGGAAATCCACGTGCT
Barcode B-33	/5Biosg/CAAGCGTTGGCTTCTCGCATCTNNNNNNNNNNNCACTTCGAATCCACGTGCT



A	В
Barcode B-34	/5Biosg/CAAGCGTTGGCTTCTCGCATCTNNNNNNNNNNNCAGCGTTAATCCACGTGCTTGAG
Barcode B-35	/5Biosg/CAAGCGTTGGCTTCTCGCATCTNNNNNNNNNNNNCATACCAAATCCACGTGCTTGAG
Barcode B-36	/5Biosg/CAAGCGTTGGCTTCTCGCATCTNNNNNNNNNNCCAGTTCAATCCACGTGCTTGAG
Barcode B-37	/5Biosg/CAAGCGTTGGCTTCTCGCATCTNNNNNNNNNNCCGAAGTAATCCACGTGCTTGAG
Barcode B-38	/5Biosg/CAAGCGTTGGCTTCTCGCATCTNNNNNNNNNNCCGTGAGAATCCACGTGCTTGAG
Barcode B-39	/5Biosg/CAAGCGTTGGCTTCTCGCATCTNNNNNNNNNNNCCTCCTGAATCCACGTGCTTGAG
Barcode B-40	/5Biosg/CAAGCGTTGGCTTCTCGCATCTNNNNNNNNNNNCGAACTTAATCCACGTGCTTGAG
Barcode B-41	/5Biosg/CAAGCGTTGGCTTCTCGCATCTNNNNNNNNNNNCGACTGGAATCCACGTGCTTGAG
Barcode B-42	/5Biosg/CAAGCGTTGGCTTCTCGCATCTNNNNNNNNNNCGCATACAATCCACGTGCTTGAG
Barcode B-43	/5Biosg/CAAGCGTTGGCTTCTCGCATCTNNNNNNNNNNNCTCAATGAATCCACGTGCTTGAG
Barcode B-44	/5Biosg/CAAGCGTTGGCTTCTCGCATCTNNNNNNNNNNNCTGAGCCAATCCACGTGCTTGAG
Barcode B-45	/5Biosg/CAAGCGTTGGCTTCTCGCATCTNNNNNNNNNNNCTGGCATAATCCACGTGCTTGAG
Barcode B-46	/5Biosg/CAAGCGTTGGCTTCTCGCATCTNNNNNNNNNNNNGAATCTGAATCCACGTGCTTGAG
Barcode B-47	/5Biosg/CAAGCGTTGGCTTCTCGCATCTNNNNNNNNNNNCAAGACTAATCCACGTGCTTGAG
Barcode B-48	/5Biosg/CAAGCGTTGGCTTCTCGCATCTNNNNNNNNNNNGAGCTGAAATCCACGTGCTTGAG
Barcode B-49	/5Biosg/CAAGCGTTGGCTTCTCGCATCTNNNNNNNNNNNNGATAGACAATCCACGTGCTTGAG
Barcode B-50	/5Biosg/CAAGCGTTGGCTTCTCGCATCTNNNNNNNNNNNNGCCACATAATCCACGTGCTTGAG

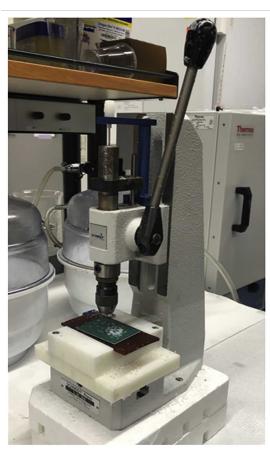
Table S2C. List of DNA Barcode B Sequences.

- This protocol requires using a microfluidic device fabricated with PDMS using soft lithography.
- A hole punching machine (SCHMIDT® Manual Press) is needed to punch the inlet and outlet holes in the PDMS chip after its fabrication.

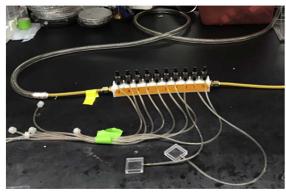


- The tissue of interest should be placed on the center of a poly-L-lysine coated glass slide. (CatLog no. 63478-AS, electron microscopy sciences).
- A custom-designed acrylic clamp with screws is needed to hold the PDMS device and the glass slide together firmly.
- The silicon wafer used for fabricating the PDMS mold is purchased from WaferPro (CatLog. No. C04004).
- The photoresist is purchased from MicroChem Laboratory (CatLog. No. SU-8 2010).
- A homemade laboratory vacuum system(See Figure Below) is needed to applying suction to move fluid in the microfluidic channels.
- Microscopy The tissue of interest can be scanned and imaged using EVOS (Thermo Fisher EVOS fl), typically at a magnification of 10×. Any suitable optical microscope can be used.
- A Laser Engraver Cutter is used to cut out the acrylic barcode and lysis clamps.
- A "humidified chamber" (See Figure Below) to prevent reagent evaporation during incubation.









Key equipment used in DBiT-seq

Hole punch machine, the key device for DBiT-seq, and the house vacuum lines. (Left) SCHMIDT® Manual Press used for hole punching 2-mm diameter holes for the inlets and outlets of Chip-A and Chip-B. (Top Right) Example of a "humidified chamber" to prevent reagent evaporation during the incubation steps. (Bottom Right) House vacuum used for pulling reagents through the microchannels.

Recipes

Critical: Prepare the RT mix, template switch mix, ligation mix, PCR mix, 1X lysis solution, flow wash buffer, PBS-RI, 80% ethanol on the same day as usage. 2X lysis buffer, 1X B&W Buffer with 0.05% Tween-20, and 2X B&W Buffer can be stored for up to 6 months at room temperature.

PBS-RI

Reagent	Volume (μL)
1X PBS	5000
RNase Inhibitor (40 U/µL) (Enzymatics)	7
Total	5007

80% Ethanol

Reagent	Volume(ml)
RNase-free water	1



Reagent	Volume(ml)
100% Ethanol	4
Total	5

RT Mixture

Reagent	Volume (μL)
5X Maxima RT buffer	50
RNase-free water	32.8
RNase Inhibitor (Enzymatics)	1.6
Superase In RNase Inhibitor (Ambion)	3.2
dNTPs (10 mM stock)	12.5
Maxima H Minus Reverse Transcriptase	25
PBS-RI	100
Total	225.1

Ligation Mix

Reagent	Volume (μL)
10X T4 Ligase Buffer	27
1X NEB buffer 3.1 with 1% RI (Enzymatics)	115.8
5% Triton-X100	5.4
RNase Inhibitor (Enzymatics)	2.2
RNase-free water	69.5
SuperaseIn RNase Inhibitor (Ambion)	0.7
T4 DNA Ligase (400 U/μL)	11
Total	231.6

Template switch mix

Reagent	Volume (μL)
20% FicoII PM-400	44
5X Maxima RT buffer	44
dNTPs (10 mM stock)	22
RNase Inhibitor (Enzymatics)	5.5
Maxima H Minus Reverse Transcriptase	11
Template Switch Primer (100 µM stock)	5.5
RNase-free water	88
Total	220

PCR mix



Reagent	Volume (μL)
2X Kapa Hifi HotStart master mix	110
Primer1 BC_0062 (10μM)	8.8
Primer2 BC_0108 (10μM)	8.8
RNase-free water	92.4
Total	220

Flow Wash Buffer

Reagent	Volume (mL)
1X PBS	4
10 % Triton X-100	0.04
Superase In RNase Inhibitor	0.01
Total volume	4.05

1X Lysis Solution

Reagent	Volume (μL)
1X PBS	50
2X Lysis Buffer	50
Proteinase K (20mg/mL) (Thermo)	10
Total	110

2X Lysis Buffer

Reagent	Stock Concentration	Final Concentration (2X)	Volume (mL)
Tris, pH 8.0	1 M	20 mM	0.5
NaCl	5 M	400 mM	2
EDTA, pH 8.0	0.5 M	100 mM	5
SDS	10%	4.4 %	11
RNase-free Water	NA	NA	6.5
Final Volume			25

1X B&W Buffer with 0.05% Tween-20

Reagent	Volume
1M Tris-HCl pH 8.0	100 μL
EDTA, 0.5M	20 μL
5M NaCl	4 mL
Tween 20 10%	100 μL
RNase-free water	15.78 mL
Total	20 mL

2X B&W Buffer



Reagent	Volume
1M Tris-HCl pH 8.0	500 μL
EDTA, 0.5M	100 μL
5M NaCl	20 mL
RNase-free water	29.4 mL
Total	50 mL

CRITICAL: Handle all in an RNase-free area.



Before start

The protocol below describes the reagents, equipment, and specific experimental steps for using the spatial-ATAC-seq platform on fixed fresh frozen tissue slides. The 20 µm microfluidic channel width were designed and validated to provide spatial epigenomic profiles on human lymph note tissue sections.

CRITICAL: Work in an RNase-free environment when the microfluidic device is not on the tissue slide. Use RNaseZapTM or other commercially available cleaner solution and filter-tips. Clean surfaces and gloves with RNaseZapTM.

CRITICAL:Keep reagents on ice at all times.

Fabricating the Silicon Wafer Device Mold



Prepare chrome photomasks of the microfluidics chip by printing the high-resolution CAD files onto a glass substrate (Figure 1).

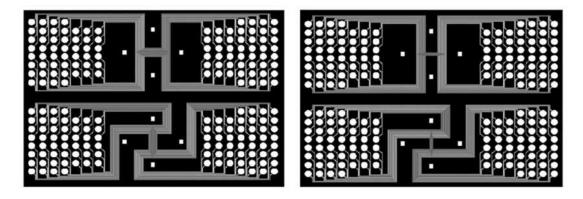


Figure 1: Microfluidic Photomask Design.

(Left) AutoCAD design for the 20 micron-width fifty channel Chip-A and Chip-B. (Right) AutoCAD design for 10 micron-width channel Chip-A and Chip-B.

NOTE: We have outsourced this step (Front Range Photomask, USA).

Using these masks, prepare a replica mold as follows:

- 2 Start the process by cleaning a 4-inch silicon wafer with 100% acetone (Aldrich) and then 100% isopropanol (Aldrich), then dry with compressed air.
 - **NOTE:** Acetone and isopropanol are mildly toxic. Use proper PPE when handling and discard waste in the appropriate containers.
- Prepare a high-resolution computer-aided-design (CAD) file with the desired microfluidics chip design. A CAD file is also available in the link provided. (https://ars.els-cdn.com/content/image/1-s2.0-S2666166721002392-mmc4.zip)
- 4 Bake the wafer at 180°C for 10 min on a hot plate to dry it out.
- Use a spin coater to evenly spread SU-8 2010 photoresist (MicroChem) for 10 μ m device or SU-8 2025 (MicroChem) for 25 μ m and 50 μ m device onto the wafer at 500 rpm for 5 seconds followed by 1100 rpm (10 μ m device), 3500 rpm (25 μ m device) or 1750 rpm (50 μ m device) for 40 seconds.
- Soft bake the wafer for 3 min at 65° C (25 µm and 50 µm device) and 4 min (10 µm device) or 6 min (25 µm and 50 µm device) at 95° C.



- 7 Expose the SU-8 on the wafer through the photomask using Mask Aligner with a dose of 150 mJ/cm2 UV.
- 8 For the post exposure bake, bake the wafer for 1 min at 65°C (25 µm and 50 µm device) and 5 min (10 µm and 25 µm device) or 6 min (50 µm device) at 95°C.
- 9 Develop the SU-8 for 4 min (10 μ m and 25 μ m device) or 5 min (50 μ m device) in a bath of ~50 mL SU-8 developer (MicroChem).
- 10 Rinse the wafer with 100% isopropanol and dry with compressed air.
- 11 Perform a hard bake by baking the wafer for 10 min at 180°C.

CRITICAL: This process needs to be carried out in a microelectronics cleanroom.

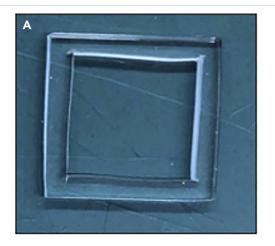
Pause Point: The replica mold can now be stored and reused indefinitely.

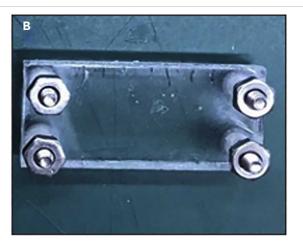
Creating the Acrylic Clamps

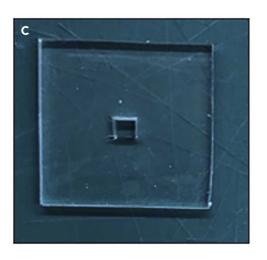
30m

- 12 Prepare the pattern and dimensions for the barcoding clamp and lysis clamp.
- 13 Peel covering of acrylic sheet and place it in the laser cutting machine.
- 14 Select the program dimensions and cut two pieces for the top and bottom of the barcoding clamp.
- 15 Place the top blank piece into the laser cutter and select the pattern to cut out the four holes in the corner for the screws and nuts.
- 16 Remove cut-out scraps with a pipet tip or a similar pointed tool.
- 17 Repeat steps 15 and 16 for the bottom blank piece.
- 18 Repeat steps 13 to 17 for the lysis clamp using the correct dimensions and pattern with an additional hole in the center of the top piece (Example shown in Figure 2).









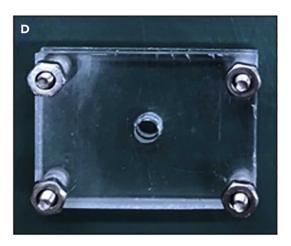


Figure 2. Key parts for setup. PDMS reservoirs and acrylic clamps used in DBiT-seq. (A) Inlet Reservoir. (B) Barcoding Clamp. (C) Lysis Reservoir. (D) Lysis Clamp.

NOTE: The acrylic clamps can be reused indefinitely.

Preparing the Microfluidic Device and reagent reservoirs

3h

19 Thoroughly mix polydimethylsiloxane (PDMS) elastomer base and curing agent (these come together) at a 10:1 ratio (See Figure 3).



Chronological steps for preparing the PDMS chip from left to right. The liquid PDMS mix is poured into the replica mold, degassed and baked. The solidified PDMS is then cut out and assembled into the microfluidics chip by punching inlet and outlet holes and attaching to a glass slide. Detailed steps are available in the text.







Weigh out PDMS base and curing agent in a 1:10 mass ratio



Mix PDMS base and curing agent thoroughly



Transfer PDMS mixture to the mold



Degas PDMS mixture with vacuum desiccator



Bake at 65-70 ° C for 2



Cut out PDMS using scalpel and gently peel from the mold



Cover the PDMS device with scotch tape to protect from dust and debris



Punch inlet and outlet holes using SCHMIDT press hole puncher



Cover the final PDMS device with scotch tape

Figure 3: Step-by-step visual guide for making Chip-A and Chip-B.

20 Pour the mixture into the silicon device mold.

NOTE: Aim for a chip height of about 5mm.

- 21 Place in a vacuum desiccator until all bubbles dissipate from the mixture about 30-60 min.
- 22 Cure in an oven at 65-70°C for a minimum of 2 hours and up to overnight.

NOTE: Make sure to place on an even surface to prevent uneven curing!

23 Cut out the cured device and hole punch each of the 50 inlets and outlets for the channels.

NOTE: Cut both Chip-A and Chip-B in the approximate size of a glass slide.

NOTE: Make sure there are no PDMS pieces left in the inlets or outlets.

- Thoroughly clean the surface of the device with scotch tape.
- Pour mixture in a container large enough to cut out two roughly 25x25x5mm PDMS pieces.
- For the barcoding reservoir, cut out a 20x20mm piece in the center, barely large enough to surround the inlets of the chips when placed above.



For the lysis reservoir, depending on the device size used, cut out the center to barely surround the barcoded region of the tissue (1x1mm for the 10µm channel device, 2.5x2.5mm for the 25µm channel device).

NOTE: The reservoirs are reusable. Thoroughly wash with 70% ethanol after each use.

CRITICAL: Be careful when cutting out the Chips A and B. Make sure not to cut across any patterned areas of the silicon wafer mold, otherwise it will need to be replaced and refabricated.

Preparing Barcodes (A and B).

1h

- Thoroughly mix the ligation linker 1 with each barcode A_{1-50} at and ligation linker 2 with each barcode B_{1-50} at a 1:1 ratio.
- 29 Place the 50 mixes in a thermal cycle and heat to 97°C to anneal.
- 30 Slowly cool to room temperature at a rate of -0.1°C/sec.

Store at -20°C for up to 6 months.

Preparing the Tissue Slide

1d

- 31 25% sucrose overnight bath.
- 32 Embed in OCT frozen on dry ice.
- 33 Section at \sim 7 µm thickness for the 25µm channel device and \sim 5 µm thickness for the 10 µm channel device onto Poly-L-lysine slides.
- 34 Store slides at -80°C for up to 6 months until use.

CRITICAL: Ensure that the tissue is sectioned as evenly as possible, otherwise the risk of cross-flow between the microfluidic channels will be increased. Tissue section should be placed at the center of a glass slide to the greatest extent.

Transposome assembly preparation

35

Prepare the transposome assembly annealing buffer (The Tn5 annealing buffer contains 400 μ l of 1 M Tris-HCl pH 8.0, 100 μ l of Nacl 5 M and 9.5 ml water. This annealing buffer is used to resuspend each oligos of Tn5-Rev, Tn5-A and Tn5-B in this annealing buffer to stock concentrations of 100 μ M.

- Resuspend the oligos (Tn5Erev, Tn5ME-A , and Tn5ME-B) in Annealing Buffer to stock concentration of 100 μ M.
- 37 In a PCR tube, mix 10 μl of oligo Rev with 10 μl of oligo A.
- 38 In a separate PCR tube, mix 10 µl of oligo Rev with 10 µl of oligo B
- Vortex the tubes and place them in a thermocycler, and run the thermocycler with the following program:

Temperatur e	Time
95 °C	5 min
Cool to 65 C	-0.1C/ second
65 °C	5 min
Cool to 4 °C	-0.1 C/sec ond

The Annealed linker oligos can be stored at -20 C.

40 Mix 5 μl of each prepared oligo A/oligo Rev and oligo B/oligo Rev at the ratio of 1:1 in a pcr tube.

41 Add10 µl of unloaded Tn5 transposome (Diagnode Tagmentase) to the mixture of oligo A/oligo Rev and oligo B/oligo Rev.

After vortexing the mixture briefly, incubate the tube at 23 °C for 30 minutes in a thermocycler. The product can be use at the same day or stored in -20 °C with 10 µl glycerol up to 60 days.

Tissue Preparation

- 42 Remove stored sections from the freezer and allow to warm to room temperature for 10 minutes.
- 43 Clean sections by pipetting 2 mL of PBS-RI across the tissue.
- 44 If sections are not yet fixed, then fix here with 1 mL 0.2% PFA, without methanol in 1X PBS, by applying on top of the tissue and incubate for 5 min at room temperature.
- 45 Remove the formaldehyde by pipetting it off and quench the tissue with 1mL 1.25M glycine for min at room temperature.
- 46 Wash the slides with 1 mL of PBS for 1 minute and then dip the slide in a 50 mL falcon tube with DI water.
- 47 Dry the section with gentle air flow.
- 48 Take a full pre-scan image of the section at the desired optical resolution (Figure 4A).

Recommended 10X resolution.



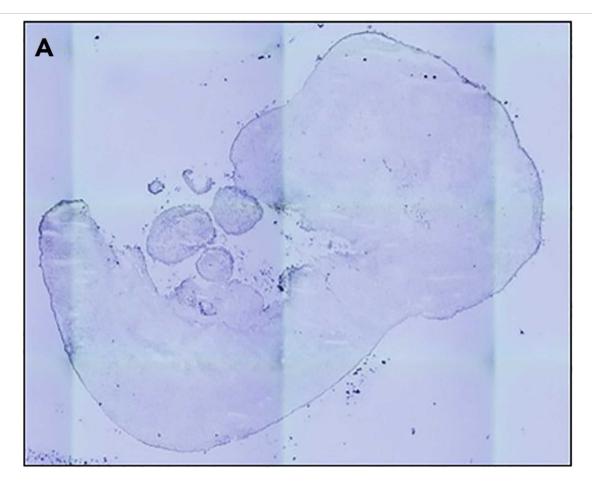


Figure 4: Example scanning of the tissue slide. (A) Initial full scan of the tissue section prior to DBiT-seq.

49 Attach the Antibody PDMS reservoir and 12mm diameter clamp to the tissue.

50 Permeabilize the tissue with 500uL 0.1 Xlysis buffer and incubate at room temperature for 15 min

Make sure to prepare 0.1x lysis buffer fresh each time. using the following reagents: 1X Lysis Buffer (10 mM Tris-HCl, pH 8.0; 10 mM NaCl; 3 mM MgCl2; 0.1% Tween-20; 0.1% NP-40; 0.01% Digitonin; 1% BSA) Dilute down to 0.1X with lysis dilution buffer (10 mM Tris-HCl, pH 8.0; 10 mM NaCl; 3 mM MgCl2; 1% BSA)



51 Wash the tissue with 500uL wash buffer for 5 min make sure to prepare wash buffer fresh each time:

Wash Buffer (10 mM Tris-HCl pH 8.0; 10 mM NaCl; 3 mM MgCl2; 1% BSA; 0.1% Tween-20)

52 Prepare the transposition mix with the loaded Tn5 transposon and add 100uL to the tissue.

make sure to prepare the Tn5 mix fresh each time

A	В	С	D
Volume (200 u l/chip)	Volume (300 ul)	Volume (400 ul)	Reagent (50 ul/reaction)
100 ul	150 ul	200 ul	2X TD Buffer (25 ul)
66 ul	99 ul	132 ul	1X PBS (16.5 ul)
2 ul	3 ul	4 ul	10% Tween-20 (final 0.1% v/v) (0.5 ul)
2 ul	3 ul	4 ul	1% Digitonin (final 0.01% v/v) (0.5 ul)
10 ul	15 ul	20 ul	Transposome (2.5 ul)
20 ul	30 ul	40 ul	Nuclease-free H2O (5 ul)

- 53 Incubate the tissue at 37 °C for 30 min
- 54 Stop the tagmentation reaction by adding 500 µL of 40 mM EDTA onto the tissue and incubating at room temperature for 5 min.
- 55 Dip in a 50 mL falcon tube with DI water and gently dry with air flow.



DBiT-seq assembly and Barcoding

56 Refer to https://www.protocols.io/view/spatial-multi-omics-sequencing-for-fixed-tissue-vi- 3byl4j2kolo5/v1

Lysis

- 57 Take a small PDMS solution reservoir and place it on the tissue slide so that the reservoir opening is directly over the barcoded ROI.
- 58 Load the slide into a lysis clamping device and tighten screws as much as possible by hand.
- 59 Image the lysis chip on the ROI using a 10x objective lens.
- 60 Prepare the reverse crosslinking lysis solution.

Reagent	Volume	Stock Concentratio n	Final Concentratio n
Tris-HCl (pH 8.	7.5 µL	1M	50 mM
EDTA	0.3 μL	0.5M	1 mM
SDS	15 µL	10%	1%
NaCl	6 μL	5M	200 mM
proteinase K	3 µL	20mg/mL	0.4 mg/mL
dH2O	118.2 µL	-	-

61 Add approximately 50-100µL of the reverse crosslinking lysis solution into the lysis chip. CRITICAL STEP Make sure to record the volume added of the lysis solution for the remaining steps.



- 62 Cover the ROI hole using parafilm and load the slide into a humidifying chamber.
- Incubate tissue the slide with PDMS reservoir and Lysis Solution at 58 °C for 2 hours to reverse formaldehyde crosslinks.
- After incubation, collect the lysate in a 200µL PCR tube (or 1.5mL tube) and seal the tube with parafilm.
- 65 Incubate the lysate at 65 °C with rotation overnight.

Purification and Library Generation

- If necessary, transfer the lysate to a 1.5mL microcentrifuge tube.
- During this transfer, carefully use a P200 pipette to measure the volume of the lysate, for an accurate PCR product: DNA fragment ratio in the Zymo purification.
- Purify the lysate with the Zymo DNA Clean & Concentrator-5 according to the kit protocol:

 a. Follow the 5:1 DNA Binding Buffer: DNA Sample

 Use a pipette to accurately determine the initial volume of the PCR Product

 b.For the final elution, elute with 100 uL of DNA Elution buffer

PCR

2h

- Prepare the PCR solution:
 - **a.** 21uL purified DNA
 - **b.** 2.5uL 25uM Universal or barcoded i5 primer
 - c. 2.5uL 25uM Universal or barcoded i7 primer

(using different indices if needed)

d. 25uL 2X NEBNext Master Mix

Pipette up and down to mix once you have added everything.

Briefly vortex and spin down the tubes.

Place the tube in the NEW thermocycler and run the following protocol with a heated lid:

a. Lid should be heated at 105°C



b. Used default ramp rate

Steps	Temperature	Time	Cycles
Initial Denaturation	72°C	5 min	1
Denaturation	98°C	30 sec	
Denaturation	98°C	10 sec	5
Annealing	63°C	30 sec	
Extension	72°C	1 min	

PCR Cycling Conditions

70 **Determine Additional Cycles**

1. Prepare preliminary qPCR solution:

- Pre-amplified library , 5uL
- Pre-amplified solution,0.5uL
- 25uM Universal or barcoded i5 primer, 0.5uL
- 25uM Universal or barcoded i7 primer (using different indices if needed), 5uL
- NEBNext Master Mix, 3.25uL
- Fuclease-free water, 0.75uL
- For a final concentration of 1X EvaGreen Dye, 0.75 uL

Pipette up and down to mix once you have added everything.

Briefly vortex and spin down the tubes.

Place the tube in the NEW thermocycler and run the following protocol with a heated lid:

- Lid should be heated at 105°C
- Use default ramp rate

Denaturation	98°C	30 sec	
Denaturation	98°C	10 sec	20 cylces
Annealing	63°C	30 sec	
Extension	72°C	1 min	

2. Use the qPCR data in Excel to determine the cycle where you reach 1/3 of the saturated signal in qPCR

- Graph the qPCR fluorescence values
- It's a good run if it plateaus in less than 10 cycles
- ((fluorescence value at cycle 20 fluorescence value at cycle 1)/3) + fluorescence value at cycle 1 = 1/3 Saturated Signal Fluorescence Value



 Determine how many cycles it takes to get to this 1/3 Saturated Signal Fluorescence Value. If in the middle of two cycles, always take the lower.

Note: Sometimes, all the graphed values may be negative if the amount of DNA Is very high. This is fine, and just proceed to determine the number of cycles.

71 Repeat step 68 PCR protocol to amplify the remaining product with the cycles determined in step 69

Ampure Purification

40m

- 72 Perform a 1X SPRI purification by adding 45uL Ampure XP beads to the sample. Mix thoroughly by pipetting or vortexing.
- 73 Mix thoroughly by pipetting.
- 74 Keep the tubes on the magnet and add 200 µL of 80% ethanol.
- 75 Carefully remove and discard the supernatant.
- 76 Incubate the tubes at room temperature for at least 30 sec.
- 77 Carefully remove and discard the ethanol.
- 78 Repeat steps 70-75.
- 79 Remove the tubes from the magnet and resuspend the beads in 15-20 µL of PCR-grade water or elution buffer depending on downstream application.
- 80 Incubate the tubes at room temperature for at least 10 min to elute the cDNA off the beads.
- 81 Place the tubes back on the magnet and incubate until the liquid is fully clear.



- Transfer the clear supernatant to a new tube.
- Perform Bioanalyzer QC to obtain cDNA length profile and concentration.

Pause Point: Stop here for the second day. Store at 4°C for 1-2 weeks or up to 6 months at -20°C.

Sequencing

Send the samples for 100 million reads (30 Gb) and 150 bp paired end sequencing.

Data Processing

- Transfer the two filtered sequences from Step 125 to Cell Ranger ATAC format (10x Genomics)
- Align the filtered reads to the reference genome (e.g., mouse reference (mm10) or human reference (GRCh38) genome)
- Adjust the reads for the Tn5 offset and generate an HTML report with per-base quality scores from which the overall sequencing quality of the library can be inferred. This step provides adjusted reads to correct the Tn5 enzyme's tendency to insert sequencing adapters from true chromatin accessibility sites at positions offset.
- Perform peak calling and generate the number of Tn5 insertion events and fragments, generating a matrix with spatial barcodes. This step generates a BED-like fragment files for data visualization through Seurat packages.
- 89 Evaluate the molecular mechanism of binding and transposition by the Tn5 transposase dimer by generating fragment size distribution plots.
- The Snakemake workflow management system (v5.28.0) pretreatment pipeline was created and used for preprocessing data, including trimming and alignment, and it is publicly available on GitHub at https://github.com/dyxmvp/Spatial_ATAC-seq.