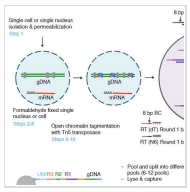

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Oct 22, 2021

SNARE-seq2 V.3

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Human Cell Atlas Method Development Community BICCN

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University of California, San Diego

To study the heterogeneity of complex tissues by joint profiling of gene expression and its regulation, we require an accurate and high-throughput method. Here we described improved high-throughput combinatorial indexing-based single-nucleus chromatin accessibility and mRNA expression sequencing 2 (SNARE-Seq2) co-assay. This protocol involves fixing and permeabilizing the nucleus followed by tagmentation, chromatin barcode ligation, reverse transcription, pooling and splitting for the next rounds of cell barcode ligation into cDNA and accessible chromatin (AC) on the same nucleus. The captured cDNA and AC are co-amplified before splitting and enrichment into single-nucleus RNA and single-nucleus AC sequencing libraries. The protocol can also be applied to both nuclei and whole cells to capture mRNA in the cytoplasm. This improvement allows us to generate hundreds of thousands of data set of each assay and can be scaled up to half a million cells from a single experiment. The entire procedure can be complete in 3.5 d for generating joint single-nucleus RNA and single-nucleus ATAC sequencing libraries.

SNARE-seq2 Oligos.xlsx

DOI

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Nongluk Plongthongkum, Dinh H Diep, Song Chen, Blue Lake, Kun Zhang 2021. SNARE-seq2. **protocols.io**
https://dx.doi.org/10.17504/protocols.io.bzdrp256
Dinh Diep

protocol

Plongthongkum N, Diep D, Chen S, Lake BB, Zhang K. Scalable dual-omics profiling with single-nucleus chromatin accessibility and mRNA expression sequencing 2 (SNARE-seq2). Nat Protoc. 2021 Oct 14. doi: 10.1038/s41596-021-00507-3. Epub ahead of print. PMID: 34650278.

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Oct 22, 2021

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MATERIALS
In-house Tn5 transposase or alternatively,
☒ Tagmentase
(Unloaded) **Diagenode Catalog #C01070010-20**
☒ T4 DNA Ligase Reaction Buffer - 6.0 ml **New England Biolabs Catalog #B0202S**
☒ NEBuffer 3.1 - 5.0 ml **New England Biolabs Catalog #B7203S**
☒ Hemo KlenTaq - 1,000 rxns **New England Biolabs Catalog #M0332L**
☒ T7 DNA Ligase - 750,000 units **New England Biolabs Catalog #M0318L**
☒ PMSF **Sigma Aldrich Catalog #P7626**
☒ T4 DNA Ligase **New England Biolabs Catalog #M0202**
☒ Tween 20 **Sigma Aldrich Catalog #P9416-50ML**
☒ Microseal® 'B' Adhesive Seals **BioRad Sciences Catalog #MSB-1001**
☒ DNA LoBind Tube 1.5ml **Eppendorf Catalog #022431021**
☒ RNAse Inhibitor **Enzymatics Catalog #Y9240L**
☒ Tango Buffer **Thermo Fisher Scientific Catalog #BY5**
☒ twin.tec PCR Plate 96 LoBind semi-shirted clear 25 pcs. **Eppendorf Catalog #30129504**
☒ Dynabeads MyOne Streptavidin C1 **Invitrogen - Thermo Fisher Catalog #65001**
☒ Ficoll PM-400 20% in H2O **Sigma Aldrich Catalog #F5415-50ML**
☒ Qubit assay tubes **Thermo Fisher Scientific Catalog #Q32856**

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Qubit dsDNA HS Assay Kit **Thermo Fisher Scientific Catalog #Q32854**

cOmplete™ Protease Inhibitor Cocktail **Sigma Aldrich Catalog #11697498001**

Low DNA Mass Ladder **Thermo Fisher Catalog #10068013**

UltraPure™ DNase/RNase-Free Distilled Water **Thermo Fisher Catalog #10977015**

Pierce™ 16% Formaldehyde (w/v), Methanol-free **Thermo Fisher Catalog #28906**

SUPERase• In™ RNase Inhibitor (20 U/µL) **Thermo Fisher Catalog #AM2696**

GlycoBlue™ Coprecipitant (15 mg/mL) **Thermo Fisher Catalog #AM9515**

ATP Solution (100 mM) **Thermo Fisher Catalog #R0441**

Bovine Albumin Fraction V (7.5% solution) **Gibco, ThermoFisher Catalog #15260037**

PBS **Gibco - Thermo Fischer Catalog # 10010023**

Polyethylene Glycol 6000 (PEG 6000) **Sigma Aldrich Catalog #81255-1KG**

Tris hydrochloride (1M) pH 8.0 **Thermo Fisher Scientific Catalog #15568025**

Magnesium chloride solution for molecular biology (1.00 M) **Sigma – Aldrich Catalog #M1028**

Potassium chloride (2M) **Thermo Fisher Scientific Catalog #AM9640G**

5 M Sodium chloride (NaCl) **Sigma Aldrich Catalog #S5150-1L**

NN-Dimethylformamide (DMF) **Sigma Aldrich Catalog #227056**

Advantage UltraPure dNTP combination kit (100 mM each dNTP) **Clontech Catalog #639132**

DL-Dithiothreitol **Sigma Aldrich Catalog #10708984001**

Sodium dodecyl sulfate solution **Thermo Fisher Scientific Catalog #AM9822**

Citation: Nongluk Plongthongkum, Dinh H Diep, Song Chen, Blue Lake, Kun Zhang SNARE-seq2 https://dx.doi.org/10.17504/protocols.io.bzdrp256

Maxima H Minus Reverse Transcriptase (200 U/uL) **Thermo Fisher Scientific Catalog #EP0753**

Bovine Serum Albumin (20 mg/mL) Molecular Biology Grade **New England Biolabs Catalog #B9000S**

EDTA (0.5 M) pH 8.0 **Sigma Aldrich Catalog #20158**

Triton X-100 **Sigma Aldrich Catalog #X100-100ML**

Proteinase K solution (20mg/mL) RNA grade **Thermo Fisher Scientific Catalog #25530049**

SSC Buffer (20X) **Sigma Aldrich Catalog #S6639**

KAPA HiFi HotStart ReadyMix (2X) **Kapa Biosystems Catalog #KK2602**

EvaGreen® Dye, 20x in Water **Gold Biotechnology Catalog #E-670**

SYBR Gold (10000x) **Thermo Fisher Scientific Catalog #S11494**

Sodium acetate (3M) pH 5.5 **Thermo Fisher Scientific Catalog #AM9740**

2-Propanol or Isopropanol for molecular biology **Sigma Aldrich Catalog #I9516-500mL**

Ethanol Pure 200 proof for molecular biology **Sigma Aldrich Catalog #E7023-500mL**

DNA Clean & Concentrator-5 (capped) **Zymo Research Catalog #D4014**

Tris-borate-EDTA buffer (10X) **Thermo Fisher Scientific Catalog #15581044**

DNA LoBind Tubes 2.0 mL **Eppendorf Catalog #30108078**

DNA LoBind Tubes 5mL **Eppendorf Catalog #30108310**

8-strip PCR tube without cap (0.2mL) **VWR Scientific Catalog #20170-002**

8-strip PCR tube with individually attached bubble **VWR Scientific Catalog #53509-304**

Corning polypropylene tube (15mL) **Fisher Scientific Catalog #0553859B**

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Corning polypropylene tube (50mL) **Fisher Scientific Catalog #0553868**

Reservoir for 8 channel pipetters (25mL) individually wrapped **Contributed by users Catalog #28-132**

Millex-GP syringe filter unit (0.22 µm) **Merck Millipore Catalog #SLGP033RS**

Nanosep 0.2 µm column **Pall Catalog #ODM02C35**

CELLTRICS 30 µm strainer **Fisher Scientific Catalog #NC9682496**

Scalpel blade **Integra Catalog #4-410**

Dual-chambered counting slide **Bio-rad Laboratories Catalog #145-0011**

Equipments List:

- Eppendorf ThermoMixer C with Thermo Top (Eppendorf, cat. no.2231000574)
- IKA MS3 digital orbital shaker, with MS 1.32 tube insert (Coleparmer, cat. no. UX-04304-04)
- Tube revolver/rotator (Thermo Fisher Scientific, cat. no. 88881001)
- 0.2 mL PCR Strip / 1.5 mL Microfuge magnetic separator (Permagen Labware, cat. no. SKU: MSR1224B)
- MiSeq (Illumina)
- MiSeq reagent kit v2 (300 cycles) (Illumina, cat. no. MS-102-2002)
- MiSeq reagent kit v3 (150 cycles) (Illumina, cat. no. MS-102-3001)
- Qubit 3.0 fluorometer (Thermo Fisher Scientific, cat. no. Q33216)
- E1-ClipTip multichannel pipette, 12 channel, 0.5-12.5 µL, 1-30 µL and 2-125 µL (Fisher Scientific, cat. no. 14-387-972TI, 14-387-973TI and 14-387-974TI)
- ClipTip 384 12.5 µL, 30 µL and 125 µL multichannel pipette tip, racked, filter, sterile (Thermo Fisher Scientific, cat. no. 94420053, 94420103 and 94420153)
- Refrigerated centrifuge (Eppendorf)
- Bench top centrifuge (Eppendorf)
- mySPIN mini centrifuge (Thermo Fisher Scientific, cat. no. 75004061)
- CFX96 Touch deep well real-time PCR detection system (BIO-RAD)
- T100 Thermocycler (BIO-RAD, cat. no. 1861096)
- TC20 Automated cell counter (BIO-RAD, cat. no.1450102)
- Dual-chambered counting slide (BIO-RAD, cat. no. 145-0011)
- Eppendorf PCR cooler (Eppendorf, cat. no. 022510525)
- XCell SureLock mini-cell electrophoresis system (Thermo Fisher Scientific, cat. no. EI0001)
- UV transilluminator

Reagent setup 3h

1 **40% (wt/vol) PEG 6000.** Weigh 16.0 g of PEG 6000 in 50 mL tube. Add nuclease-free water and bring the total volume to 40 mL. Rotate the tube at room temperature until PEG 6000 completely dissolved. Spin down the tube at 200 g for 2 min, at room temperature to remove the tiny bubble. CRITICAL: 40% (wt/vol) of PEG 6000 is very viscous and difficult to filter through a 0.22 µm filter. We suggest preparing 40% PEG freshly before making GLR buffer. When PEG is diluted in 4x GLR buffer, it is easier to filter.

2 **4x GLR buffer.** To prepare 40 mL of 4x GLR buffer, Add 2.64 mL of nuclease-free water, 10.56 mL of 1

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https://dx.doi.org/10.17504/protocols.io.bzdrp256

M Tris-HCl, pH 8.0, 0.8 mL of 1 M MgCl2 and 4 mL of 2 M KCl into 50 mL tube. Gently mix well by vortexing. Add 22 mL of 40% (wt/vol) PEG 6000 and gently mix well by vortexing. Filter through 0.22 µm into a new 50 mL tube and briefly spin the tube at room temperature for 30 s. Aliquot 1.8 mL into 2 mL tubes to minimize contamination from each use and store at 4 ºC.

3 **10% (vol/vol) Triton X-100.** Slowly aspirate 2.0 mL of Triton X-100 liquid with low retention pipette tip and slowly dispend into 18.0 mL nuclease-free water in 50 mL tube. Dissolve Triton X-100 by slowly rotate the tube until the solution is clear. Filter 10% Triton X-100 solution through 0.22 µm syringe filter into a new 50 mL tube and store at room temperature. CRITICAL: If it's difficult to pipette Triton X-100 accurately as it's a viscous liquid, we may warm it at 37 ºC before pipetting

4 **10% (vol/vol) Tween 20.** Tween 20 is very viscous liquid and difficult to pipette accurately. We convert the volume in cm3 into grams using the density of tween 20 at 25 ºC is 1.1 cm3. To prepare 20 mL of 10% (vol/vol) Tween 20, weigh 2.2 g of Tween 20 in 50 mL tube. Add 18.0 mL of nuclease-free water and invert or rotate the tube slowly at room temperature until Tween 20 is completely dissolved in water. Filter 10% Tween 20 solution through 0.22 µm syringe filter into a new 50 mL tube and store at room temperature.

5 **25 mM dNTP mix.** Mix 250 µL each of 100 mM dATP, dCTP, dGTP and dTTP in 1.5 mL tube. Mix well by vortexing and briefly spin the tube at room temperature for 5 s. Aliquot 250 µL into each of 1.5 mL tube and store at -20 ºC for a couple of years

6 **2x Lysis buffer.** To prepare 25 mL of 2x Lysis buffer, add 6.5 mL of nuclease-free water into 50 mL tube. Add 0.5 mL of 1 M Tris-HCl, pH 8.0, 2 mL of 5 M NaCl, 5 mL of 0.5 M EDTA and 11 mL of 10% (wt/vol) SDS. Gently mix and aliquot 1.8 mL into 2 mL tubes and store at room temperature.

7 **1x B&W-T buffer.** To prepare 40 mL of 1x B&W-T, add 31.56 mL of nuclease-free water into 50 mL tube. Add 200 µL of 1 M Tris-HCl, pH 8.0, 8 mL of 5 M NaCl, 40 µL of 0.5 M EDTA and 200 µL of 10% (vol/vol) Tween 20. Gently mix by vortexing and store at room temperature.

8 **2x B&W buffer.** To prepare 25 mL of 1x B&W, add 14.7 mL of nuclease-free water into 50 mL tube. Add 250 µL of 1 M Tris-HCl, pH 8.0, 10 mL of 5 M NaCl, and 50 µL of 0.5 M EDTA. Mix well by vortexing and store at room temperature.

9 **0.1 M PMSF.** Weigh 34.8 mg of PMSF and transfer into 2 mL microtube. Add 100% isopropanol to 2 mL and vortex vigorously to dissolve PMSF. Quick spin the tube down and transfer all solution into 3 mL syringe. Filter through a 0.22 µm syringe filter to a new 2 mL tube. Aliquot 50 µL per 0.2 mL PCR tube and store at -20 ºC for up to 4 months. CRITICAL: To maintain the activity of PMSF in solution, store PMSF in single-use aliquots.

10 **Transposon preparation.** Resuspend Nextera adapter 1, 5P-Nextera adapter 2 and mosaic end (ME) oligos with nuclease-free water to 100 µM. Mix 500 µL of 100 µM Nextera adapter 1 and 500 µL of 100 µM ME in 1.5 mL DNA LoBind microtube, aliquot 30 µL of non-annealed transposons into each of 0.2 mL PCR tube and store at -20 ºC for up to 1-2 years. Prepare 5P-Nextera adapter 2 and ME the same way as Nextera adapter 1. All sequences of oligos can be found in the attached tables.

Round 1 DNA barcoding plates generation 1h

11 Accessible chromatin (AC) Round 1 barcoded oligos preparation (Plate A). Prepare 50 µL of 25 µM

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https://dx.doi.org/10.17504/protocols.io.bzdrp256

accessible chromatin (AC) Round 1 barcoded oligos annealed with 23 µM accessible chromatin (AC) Round 1 linker oligos (BC_0100)

11.1 Resuspend AC Round 1 linker (BC_0100) with nuclease-free water to final concentration of 1 mM

11.2 Prepare 2.5 mL of 30.67 µM AC Round 1 linker by adding 76.68 µL of 1 mM of AC Round 1 linker to 2,423.32 µL of nuclease-free water in 5 mL tube and mix well by vortexing

11.3 Add 12.5 µL of 100 µM AC Round 1 barcoded oligos into 96-well plate (total 48 wells, rows A - D) with multichannel pipette

11.4 Transfer AC Round 1 linker oligos into 25 mL reservoir

11.5 Add 37.5 µL of 30.67 µM AC Round 1 linker into each well of AC Round 1 barcodes with multichannel pipette and mix well by pipetting 12 times (mixing volume 45 µL)

11.6 CRITICAL STEP: Seal and spin down the plate on 96-well plate swinging bucket rotor at 160 g for 1min, 4 ºC.

11.7 Anneal AC Round 1 barcoded oligos and AC linker oligos on thermocycler using the following annealing program: 95 ºC for 2 min, slowly cool down to 20 ºC (0.1 ºC/s) and hold at 4 ºC. CRITICAL STEP: After annealing oligonucleotides in the plate, we recommend spinning down the plate and use a sterile needle to punch the holes on the sealing film to release the pressure in every single well. Otherwise, the liquid inside the well will be pulled up to the top of the well when the film is unsealed, and this can lead to barcode cross-contamination. PAUSE POINT: If do not want to continue to mix these annealed oligos in the next step, store that plate at -20 ºC

12 RNA reverse transcription (RT) Round 1 barcoded oligos preparation (Plate B). Prepare 50 µL of 25 µM of oligo (dT)15 and 25 µM of random hexamer (N6) RT barcoded oligos (see attached tables) mix in each of 48 wells. CRITICAL STEP: 100 µM of dT and N6 reverse transcription barcoded oligos are ordered in row A-D and row E-H of oligo plate, respectively.

12.1 Transfer 12.5 µL of 100 µM of rows A-D (dT) in the RT barcoded oligos plate to rows A-D of a new 96-well DNA LoBind plate. CRITICAL STEP If use electronic multichannel pipette, add 1 µL of air after aspirating to avoid cross-contamination of barcoded oligos. This can be applied to other steps when we have to transfer barcoded oligos from stock plate to a new plate. Make sure that oligos are delivered to the bottom of the well.

Transfer 12.5 µL of 100 µM of rows E-H oligos (N6) in RT barcoded oligos plate to rows A-

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12.2 D (row E to row A, row F to row B, row G to row C, row H to row D) of 96-well plate that contains dT barcoded oligos above

12.3 Pipette 2 mL of nuclease-free water into 25 mL reservoir

12.4 Add 25 µL of nuclease-free water to row A-D of RNA Round 1 stock plate and mix well by pipetting 12 times (mixing volume 45 µL)

12.5 Seal and spin down the plate at 160 g for 1 min, 4 ºC and leave the plate on ice or PCR cool rack

13 AC Round 1 barcoded oligos and RT Round 1 barcoded oligos mix. The final concentration of each oligo (dT, N6, AC) in the oligo mix is 12.5 µM.

13.1 Transfer 50 µL of oligos in plate B (RT Round 1 barcoded oligos) into plate A that contain 50 µL of annealed AC Round 1 barcoded oligos and linker at identical well IDs (rows A-D) and mix well by pipetting 12 times (mixing volume 90 µL)

13.2 Spin down the plate at 160 g for 1 min, 4 ºC and put the plate on PCR cool rack

13.3 Aliquot 4 µL of mixed Round 1 barcoded oligos (rows A-D) into 10-25 of 96-well plates as “working plates”

13.4 Spin down working plates at 160 g for 1 min, 4 ºC and store at -20 ºC for up to a couple of years. Store the left over Round 1 stock plate at -20 ºC.

Round 2 DNA barcoding plates generation 1h

14 Ligation Round 2 barcoded oligos. Prepare stock plate of 100 µL of 18 µM ligation Round 2 barcoded oligos annealed with 16.5 µM ligation Round 2 linker (BC_0215).

15 Resuspend ligation Round 2 linker (BC_0215) with nuclease-free water to final concentration of 1 mM

16 Prepare 9 mL of 20.12 µM ligation Round 2 linker by adding 181.08 µL of 1 mM round 2 linker to 8,818.9

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https://dx.doi.org/10.17504/protocols.io.bzdrp256

µL of nuclease-free water in 15 mL tube and mix well by vortexing

17 Add 18 µL of 100 µM of ligation round 2 barcoded oligos into 96-well plate (rows A-H)

18 Transfer ligation Round 2 linker into 25 mL reservoir

19 Add 82 µL of 20.12 µM ligation Round 2 linker to each well of ligation Round 2 barcoded oligos with and mix well by pipetting 10 times (mixing volume 90 µL)

20 Seal and spin down the plate at 160 g for 1min, 4 ºC

21 Anneal ligation Round 2 barcoded oligos and Round 2 linker on thermocycler using the annealing program for Round 1 barcoded oligos and keep on ice

22 Spin down the plate at 160 g for 1min, 4 ºC and keep on ice

23 Aliquot 10 µL of annealed ligation Round 2 barcoded/linker oligos into 10 of 96-well plate as “working plate”

24 Spin down the working plate at 160 g for 1min, 4 ºC before store at -20ºC for up to a couple of year

Round 3 DNA barcoding plates generation 1h

25 Ligation Round 3 barcoded oligos. Prepare stock plate of 100 µL of 21 µM Round 3 barcoded oligos annealed with 19.5 µM ligation Round 3 linker (BC_0060).

26 Resuspend ligation Round 3 linker (BC_0060) with nuclease-free water to final concentration of 1 mM

27 Prepare 8.5 mL of 24.68 µM ligation Round 3 linker by adding 209.8 µL of 1 mM Round 3 linker to 8,290.2 µL of nuclease-free water in 15 mL tube and mix well by vortexing

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28 Add 21 µL of 100 µM of ligation Round 3 barcoded oligos into 96-well plate (rows A-H)

29 Transfer ligation Round 3 linker into 25 mL reservoir

30 Add 79 µL of 24.68 µM ligation Round 3 linker to each well of ligation Round 3 barcoded oligos and mix well by pipetting 12 times (mixing volume 90 µL)

31 Seal and spin down the plate at 160 g for 1min, 4 ºC

32 Anneal ligation Round 3 barcoded oligos and Round 3 linker on thermocycler using the annealing program for Round 1 barcoded oligos and keep on ice

33 Spin down the plate at 160 g for 1min, 4 ºC and keep on ice

34 Aliquot 10 µL of annealed ligation Round 3 barcoded/linker oligos into 10 of 96-well plate as “working plate”

35 Spin down the working plate at 160 g for 1min, 4 ºC before store at -20ºC for up to a couple of year

Transposase preparation 2h

36

Convert Tn5 transposase (EZ-Tn5 Transposase, Lucigen #TNP92110, or expressed/purified with an in house protocol) concentration from mg/mL to µM unit. For example, if the concentration of unloaded Tn5 is 0.40 mg/mL, the monomer concentration in uM is 7.55 µM based on molar mass of monomer Tn5 ~53,000 g/mol [0.4 mg/mL * (1 mol/53,000 g)]. CRITICAL STEP: Anneal transposons and load Tn5 on the day of experiment 1-2 h prior experiment starts. Combine transposons and mix well before adding Tn5 to make sure that both transposons are sufficiently homogeneous prior to mixing with Tn5. Avoid generating bubbles when mixing Tn5 with transposons by pipetting slowly and do not fill pipette tip with air. If the experiment is not ready, store loaded Tn5 at -20 ºC.

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37 Thaw non-annealed transposons (Nextera adapter 1/ME and 5P-Nextera adapter 2/ME) on ice. Briefly vortex and quick spin the tube. Anneal transposons on thermocycler using following program: 95 ºC 5 min, slowly cool down to 65 ºC (0.1 ºC/s), 65 ºC 5 min, slowly cool down to 4 ºC (0.1 ºC/s) and hold at 4 ºC.

38 Load transposons 1.5x molar ratio to Tn5. The volume of each transposon is calculated by [7.54 µM monomer Tn5 * 75 µL of monomer Tn5 * (1.5x / 50 µM transposons)] / 2 = ~8.5 µL. The amount below is sufficient for tagmenting ~ 1 million nuclei/cells.

75 µL 7.54 uM monomer Tn5

8.5 µL 50 uM Annealed Nextera adapter 1/ME

8.5 µL 50 uM Annealed 5P-Nextera adapter 2/ME

Add annealed Nextera adapter 1/ME and annealed 5P-Nextera adapter 2/ME into the bottom of 1.5 mL DNA LoBind microtube, mix well by pipetting 10 times or gently vortexing and briefly spin the tube on mini centrifuge for 3 s. Addunloaded Tn5 and mix by gently pipetting 20 times (set the volume of p200 pipette to 80 µL). Quick spin the tube and incubate at 25 ºC for 1 h, 350 rpm. **The final concentration of loaded Tn5 is 6.15 µM** (monomer Tn5 concentration).

Nuclei isolation and fixation 3h

39 Isolate nuclei from tissue following tissue-specific nuclei extraction protocol (dx.doi.org/10.17504/protocols.io.ufketkw) with 0.1 U/µL of SUPERase In RNase Inhibitor and 0.2 U/µL of Enzymatics RNase Inhibitor. For cell lines, nuclei can be extracted with ATAC Lysis buffer with 0.1% NP-40 as previously described with the addition of RNase inhibitors, and increase lysis volume proportional to the number of input cells.

40 Prepare 1x PBS + RI (1 mL per sample) and keep on ice.

1000 µL PBS, pH 7.4

2.5 µL SUPERase In (20 U/uL)

1.25 µL Enzymatics Rnase In (40 U/uL)

41 Prepare 1% (wt/vol) formaldehyde in 1x PBS (1 mL per sample) and keep on ice. CRITICAL: formaldehyde solution should be in 1x PBS and methanol free.

937.5 µL PBS, pH 7.4

62.5 µL Formaldehyde, 16% wt/vol

42 Resuspend 1-2 million nuclei with 1 mL 1x PBS + RI and keep on ice.

43 Add 1 mL of 1% formaldehyde to nuclei suspension and pipette gently 8 times. Leave the tube on ice for 10 minutes.

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00:10:00 **Fixation**

44 Pellet nuclei at 900 g for 8 min at 4C using bucket rotor centrifuge.

45 Prepare 1x PBS + 0.1% (wt/vol) BSA + RI (1 mL per sample) and leave on ice.

- **1000 µL PBS, pH 7.4**
- **13.4 µL BSA, 7.5% wt/vol**
- **1.5 µL SUPERase In (20 U/uL)**
- **0.75 µL Enzymatics RNase In (40 U/uL)**

46 Prepare 1x Tango Buffer + RI (1 mL per ~ 3 million nuclei/cells) and leave on ice.

- **100 µL Tango Buffer, 10x**
- **160 µL DMF, 100%**
- **5 µL SUPERase In (20U/uL)**
- **2.5 µL Enzymatics RNase In (40 U/uL)**
- **732.5 µL Nuclease-free water**

47 Aspirate the supernatant and resuspend pelleted nuclei with 1 mL of 1x PBS + 0.1% BSA + RI to wash.

48 Pellet nuclei at 900 g for 8 min at 4C using bucket rotor centrifuge.

49 Aspirate the supernatant and resuspend with 1x Tango Buffer + RI to have a minimum concentration of 3,400 nuclei per microliter.

50 Count the nuclei using cell counter and resuspend the nuclei solution with additional 1x Tango Buffer + RI to obtain 3,400 nuclei per microliter.

Tagmentation 1h

51 Set up tagmentation mix per reaction as follows (1 reaction per 150,000 nuclei/cells). Minimum 4 reactions for 1 sample per plate (48 wells of round 1).

- **3 µL Tango Buffer, 10x**
- **4.8 µL DMF, 100%**

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9.77 µL Loaded Tn5, 6.15uM

1.5 µL SUPERase In (20 U/uL)

0.75 µL Enzymatics RNase In (40 U/uL)

10.18 µL Nuclease-free water

52 Prepare 150,000 nuclei in 45 µL of 1x Tango Buffer and mix with 30 µL of tagmentation mix. The final concentration of Tn5 and DMF in final reaction is 0.8 µM and 16% (vol/vol), respectively. The ratio of nuclei suspension and tagmentation mix is 3 : 2 or 45 µL : 30 µL. Add nuclei into 1.5 mL DNA LoBind tube then add tagmentation mix and mix gently by pipetting 10 times. Briefly spin the tube on mini centrifuge at room temperature for 3 s and aliquot 75 µL of tagmentation reaction into 1.5 mL DNA LoBind tube.

53 CRITICAL STEP: Set up 4 tubes of tagmentation reactions to have enough nuclei for Round 1 barcoding (8,000 nuclei/well x total 48 wells = 384,000 nuclei). Set up the reactions on ice. Do not incubate tagmentation reaction in large volume to make sure that nuclei are distributed evenly in the reaction not sitting on the bottom of the tube when incubating during tagmentation.

54 Place the tubes on thermomixer and incubate at 37 ºC for 30 min, 300 rpm.

00:30:00 Tagmentation

55 Before incubation is complete, prepare 1x PBS + 0.1% (wt/vol) BSA + RI (1 mL per 400 µL tagmented nuclei) and keep on ice

1000 µL PBS, pH 7.4

13.33 µL BSA, 7.5% wt/vol

1.5 µL SUPERase In (20 U/uL)

0.75 µL Enzymatics RNase In (40 U/uL)

56 Remove the tubes from thermomixer and place on ice. Then pool tagmented nuclei of the same sample into the same tube.

57 Add 2.5x volume of 1x PBS + 0.1% (wt/vol) BSA + RI (1000 µL to 400 µL tagmented nuclei) to pooled tagmented nuclei and mix by pipetting gently 5 times and centrifuge at 900 g for 8 min, 4 ºC with swinging bucket rotor

58 During centrifugation, prepare 0.5x PBS + RI (1 mL per 1 million nuclei/cells) and keep on ice

500 µL PBS, pH 7.4

500 µL Nuclease free water

2.5 µL SUPERase In (20 U/uL)

1.25 µL Enzymatics Rnase In (40 U/uL)

59 CRITICAL STEP Aspirate supernatant and resuspend nuclei with 300 µL of 0.5x PBS + RI to have a minimum concentration of nuclei not lower than 1,000 nuclei/µL. If different numbers of nuclei in

Citation: Nongluk Plongthongkum, Dinh H Diep, Song Chen, Blue Lake, Kun Zhang SNARE-seq2
https://dx.doi.org/10.17504/protocols.io.bzdrp256

tagmentation are used, adjust suspension volume. Pipetette gently to resuspend

60 Count nuclei concentration with cell counter and dilute nuclei to 1,000 nuclei/µL with 0.5x PBS + RI.

Accessible chromatin (AC) oligo ligation 45m

61 Thaw Round 1 AC/RT oligo working plate on ice and spin the plate on swinging bucket at 200 g for 1 min, 4 ºC and leave the plate on ice. Note: Can leave in 4C at the beginning of Day 1 to thaw.

62 Prepare GLR-A mix following table below. CRITICAL STEP: Prepare GLR-A mix during washing tagmented nuclei, but add ATP, RNase inhibitor and T7 DNA Ligase just before ready to load into Round 1 barcoding plate

- **260 µL GLR Buffer, 4x**
- **20.8 µL ATP, 100mM**
- **52 µL dNTPs, 25 mM each**
- **13 µL SUPERase In (20U/uL)**
- **6.76 µL Enzymatics RNase In, (40U/uL)**
- **10.4 µL DTT, 1M**
- **78 µL T7 DNA Ligase (3000U/uL)**
- **1.04 µL Nuclease-free water**

63 Add 8 µL of nuclei to each well (row A – D) with a multichannel pipette.

64 Aliquot 73 µL of GLR-A into 6 tube-strip on PCR cool rack and add 8.5 µL of GLR-A mix to each well with a multichannel pipette.

65 Seal and quick spin the plate at 160 g for 15 s, 4 ºC. Gently mix reaction mix, Round 1 barcoded oligos and nuclei 5 times (mixing volume 18 µL)

66 Seal and quick spin the plate at 160 g for 10 s, 4 ºC and incubate the plate on thermomixer at 25 ºC for 30 min, 300 rpm

00:30:00 AC oligo ligation

Reverse transcription 45m

67 Aliquot 20 µL of Maxima H Minus Reverse Transcriptase into 6 tubes of PCR strip tube

120 µL Maxima H Minus RT (200 U/uL)

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https://dx.doi.org/10.17504/protocols.io.bzdrp256

68 Remove Round 1 barcoding plate from thermomixer, put on PCR cool rack, and add 2.2 µL of Maxima H Minus Reverse Transcriptase to each well with a multichannel pipette. CRITICAL STEP: To get accurate volumes, set the speed of multichannel pipette to be very slow for aspirating and dispensing as the enzyme is very viscous

69 Seal and quick spin the plate at 160 g for 15 s, 4 ºC to bring enzyme to the bottom of the well and mix by gently pipetting 5 times (mixing volume 18 µL). Seal and quick spin the plate at 160 g for 10 s, 4ºC

70 Incubate the plate on thermocycler using the program: 50ºC for 10 min, 3 cycles of (8ºC for 12 s, 15ºC for 45 s, 20ºC for 45 s, 30ºC 30 s, 42ºC for 2 min, 50ºC for 3 min), 50ºC for 5 min.

Round 2 DNA barcoding 1h 30m

71 Before reverse transcription finishes, prepare 3 mL of 1x PBS + 0.1% BSA + RI

- **3000 µL PBS, pH 7.4**
- **40 µL BSA, 7.5% wt/vol**
- **4.5 µL SUPERase In (20 U/uL)**
- **2.25 µL Enzymatics RNase In (40 U/uL)**

72 Remove the plate from thermocycler and put on ice or PCR cool rack then pool all reactions into a chilled 25 mL reservoir and transfer pooled reaction into a chilled 5 mL DNA LoBind tube. CRITICAL STEP: Before pooling, pipette Round 1 barcoding plate 2 times to kick up nuclei from the bottom of the well and make sure that you transfer all reactions from the well by aspirating slowly and set pipette volume to 26 µL. This technique should be done for all pooling steps. Also keep reactions on ice all the time when handling samples or reaction mixes to prevent RNA degradation and preserve enzyme activity or temperature sensitive reagents like ATP.

73 Add 2.8 mL of 1x PBS + 0.1% (wt/vol) BSA + RI (2.5x volume) to rinse the basin and transfer buffer to the tube

74 Add 19.5 µL of 10% (vol/vol) Triton X-100 (final concentration of Triton X-100 is 0.05% (vol/vol)) and mix by inverting the tube 5 times before centrifuge at 900 g for 8 min, 4 ºC

- **19.5 µL Triton X-100, 10% vol/vol**

75 Thaw Round 2 barcoded oligos working plate on ice and spin the plate at 200 g, for 1 min, 4 ºC and leave the plate on ice. Note: Can leave in 4C at the beginning of Day 1 to thaw.

76 Prepare 1x Buffer 3.1 as follows:

- **210 µL NEBuffer 3.1, 10x**

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21 µL Enzymatics RNase In (40U/uL)

1890 µL Nuclease free water

77 Prepare Ligation Mix as follows:

510 µL T4 DNA Ligase Buffer, 10x

40.8 µL Enzymatics RNase In (40U/uL)

12.75 µL SUPERase In (20U/uL)

51 µL BSA (20 mg/mL)

127.5 µL T4 DNA Ligase (400U/uL)

1338.8 µL Nuclease free water

78 Remove supernatant as much as possible (~20 µL left) and resuspend nuclei with 2.02 mL of 1x Buffer 3.1 and add 2.04 mL of Ligation mix and mix by pipetting 10 times

79 Transfer nuclei in ligation mix into 25 mL reservoir and add 40 µL of nuclei suspension into each well of Round 2 barcoding plate and mix gently by pipetting 5 times (mixing volume 45 µL)

80 Seal the plate with sealing film and quick spin the plate at 160 g for 10 s, 4 ºC

81 Incubate the plate on thermomixer at 37 ºC for 30 min, 300 rpm

00:30:00 Round 2 barcoding

82 Prepare Round 2 blocking solution as follows:

47.52 µL BC_0216, 1000 uM

300 µL T4 DNA Ligase Buffer, 10x

852.5 µL Nuclease free water

83 Remove Round 2 DNA barcoding plate from thermomixer and quick spin at 160 g for 10 s, 4 ºC. Add 10 µL of Round 2 blocking solution to each well with multichannel pipette and mix by pipetting gently 5 times (mixing volume 55 µL)

84 Seal the plate with sealing film and quick spin at 160 g for 10 s, 4ºC then incubate the plate on thermomixer at 37 ºC for 30 min, 300 rpm

00:30:00 Round 2 blocking

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Round 3 DNA barcoding 1h

85 Thaw Round 3 barcoded oligos working plate on ice, spin the plate on swinging bucket at 200 g for 1 min, 4 ºC and leave the plate on ice

86 Place Round 2 DNA barcoding plate on PCR cool rack and pool into 25 mL reservoir. Add 100 µL of T4 DNA Ligase (400 U/µL) into the basin with nuclei from Round 2 barcoding plate and mix well by gently pipetting 10 times and rock the basin from side-to-side 10 times

100 µL T4 DNA Ligase, (400 U/uL)

87 Add 50 µL of nuclei suspension to each well of Round 3 DNA barcoding plate and mix gently by pipetting 5 times (mixing volume 55 µL).

88 Seal the plate with sealing film and briefly spin the plate at 160 g for 10 s, 4ºC. Incubate the plate on thermomixer at 37 ºC for 30min, 300 rpm

00:30:00 Round 3 barcoding

89 Prepare Round 3 blocking solution as follows:

41.4 µL BC_0066, 1000 uM

600 µL EDTA, 500mM

1758.6 µL Nuclease free water

90 Remove Round 3 DNA barcoding plate from thermomixer and add 20 µL of Round 3 blocking solution to each well and gently mix by pipetting 3 times (mixing volume 75 µL)

91 Without incubation, pool the reaction into 25 mL reservoir placed on ice, transfer supernatant into 15 mL tube and centrifuge at 1,000 g for 8 min, 4ºC. OPTIONAL: EDTA in the reaction inhibits ligase activity, therefor there is no need to change the pipette tips when pooling Round 3 ligation reaction. Set pipetting volume 85 µL when pooling nuclei.

92 In parallel, prepare chilled wash buffer as follows.

4000 µL PBS, pH 7.4

40 µL Triton X-100, 10% vol/vol

10 µL SUPERase In (20U/uL)

92.1 Also in parallel, thaw 2X Lysis buffer at 37C for ~15 minutes if previously prepped. If not see step 6 for recipe.

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93 Remove supernatant and add 4 mL of wash buffer. Pipette gently 5 times with p1000 pipette then centrifuge at 1,000 g for 8 min, 4 ºC

94 Carefully remove supernatant as much as possible and resuspend nuclei with 300 µL of 1x PBS + RI

500 µL PBS, pH 7.4

5 µL SUPERase In (20 U/uL)

2.5 µL Enzymatics Rnase In (40 U/uL)

95 Count nuclei concentration with cell counter and aliquot nuclei at required number in each pool in 1.5 mL DNA LoBind tube and adjust total volume of nuclei to 50 µL with 1x PBS + RI. CRITICAL STEP: To sequence all nuclei, recommend using ≤20,000 cells per pool by splitting 50 µL of nuclei suspension into 6 - 12 tubes per plate.

Nuclei lysis 2h

96 Add 50 µL of 2x Lysis buffer and 10 µL of 20 mg/mL Proteinase K to each pool, mix well by gently vortexing and brief spin the tube down at room temperature for 10 s to collect all nuclei suspension to the bottom of the tube and incubate on thermomixer at 55 ºC for 2 h, 350 rpm to lyse nuclei and reverse crosslink formaldehyde fixation.

02:00:00 Nuclei lysis

97 Put nuclei lysate at -80 ºC to inactivate Proteinase K before continue to day 2 experiment. CRITICAL STEP: Lysis buffer tends to precipitate at room temperature or low temperature. Redissolve by incubating the tube at 37 ºC until it completely dissolves before adding to nuclei suspension. PAUSE POINT: Nuclear or cell lysate can be store at -80 ºC for up to 6 months before continue to day 2 experiment.

Dynabeads MyOne streptavidin beads preparation 20m

98 Prepare 3.5 mL of 1x B&W-T + RI for bead washing:

3500 µL B&W-T, 1x

5 µL SUPERase In (20U/uL)

99 Vortex the bottle of Dynabeads MyOne C1 thoroughly and aliquot required volume (44 µL/pool * number of pool) into 1.5 mL tube. Add 800 µL of 1x B&W-T + RI, mix by vortexing and pulse spin on mini centrifuge at room temperature for 3 s

44 µL MyOne C1 beads

100 Place the tubes onto the magnetic rack until liquid is clear; Remove supernatant with p1000 pipette

101 Resuspend the beads with 800 µL of 1x B&W-T + RI, vortex and pulse spin on mini centrifuge at room temperature for 3 s

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102 Place the tubes onto the magnetic rack until solution is clear and remove supernatant with p1000 pipette

103 Repeat washes two more times (total of 3 washes)

104 Resuspend the beads with 100 µL of 2x B&W + RI per pool:

100 µL 2x B&W-T

2 µL SUPERase In (20U/uL)

cDNA/DNA capture 1h 30m

105 During bead preparation, take the tubes of lysate out of -80 ºC and place onto thermomixer set at 55 ºC for 2 min until lysate is completely thawed

106 Add 5 µL of 0.1 M PMSF (from -20 ºC) to each tube, pulse vortex for 10 s and pulse spin on mini centrifuge at room temperature for 5 s and incubate at room temperature for 10 min with no shaking

5 µL PMSF, 100 mM

00:10:00

107 Add 100 µL of streptavidin beads in 2x B&W + RI to each tube of lysate (no pipetting required) then agitate the tubes on mixer at room temperature for 1 h, 1,200 rpm. CRITICAL STEP: We recommend to use orbital shaker for microtubes. The speed of mixer can be adjusted as long as the beads do not settle on the bottom of the tube

01:00:00 Binding to beads

108 Pulse spin the tubes on mini centrifuge at room temperature for 5 s, place onto magnetic rack until solution is clear and remove supernatant with p200 pipette. CRITICAL STEP: Every time before placing the tube back to the magnet, quick spin the tubes on mini centrifuge for 3-5 s to collect all supernatant/lysate/buffer and beads to the bottom of the tube. Use p200 pipette to remove supernatant to avoid disturbing the beads and prevent bead loss.

109 Prepare 1 mL of 1x B&W-T + RI (750 uL per lysate) for bead washing as follows:

1000 µL B&W-T, 1x

1.4 µL SUPERase In (20U/uL)

110 Add 250 µL of 1 x B&W-T + RI and agitate the bead at room temperature for 5 min, 1,500 rpm to wash the beads

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00:05:00 wash with 1x B&W-T + RI

111 Place the tube onto magnetic rack until solution is clear and remove supernatant. Continue to template switching oligo blocking on AC DNA immediately.

Blocking template switching oligo 30m

112 During working on Steps 109-110, prepare Nextera adapter 1 blocking solution per pool:

250 µL SSC, 6x

2.5 µL Nextera adapter 1 blocker, 100 uM

1 µL SUPERase In (20U/uL)

113 Add 250 µL of 6x SSC to each tube without bead suspension and wait until the supernatant is clear then remove supernatant with p200 pipette

250 µL SSC, 6x

114 Add 250 µL of Nextera adapter 1 blocking solution to each tube and agitate the tubes on mixer at room temperature for 1 min, 1,500 rpm then reduce the speed to 500 rpm for 14 min. CRITICAL STEP: Agitate the tubes at high speed 1,500 rpm for 1 min to make sure the beads are resuspended well, then shake gently at 500 rpm for 14 min to allow hybridization of Nextera adapter 1 blocker and Nextera adpter 1 on AC DNA and make sure that the beads do not settle.

00:15:00 incubate with Nextera Blocking Solution

115 Place the tube onto magnetic rack until solution is clear and remove supernatant with p200 pipette.

116 Wash the beads twice with 1x B&W-T + RI as described above at room temperature for 5 min each round.

00:05:00 wash with 1x B&W-T + RI

00:05:00 wash #2 with 1x B&W-T + RI

117 In parallel, prepare Tris-T + RI during second bead wash

250 µL Tris-HCl, pH 8.0, 10 mM

2.5 µL Tween 20, 10% vol/vol

0.63 µL SUPERase In (20U/uL)

118 Wash the beads with 250 µL of Tris-T + RI (5 min) the same way as 1x B&W-T + RI wash (at room temperature for 5 min, 1,500 rpm). In parallel, prepare GLR-B mix. CRITICAL STEP: If GLR-B mix is not ready, leave the beads in the tube with Tris-T + RI on ice until GLR-B mix is ready

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00:05:00 wash with Tris-T + RI

Gap filling, ligation and complete reverse transcription 2h 15m

119 During washing, prepare GLR-B mix as follows:

- **50 µL GLR buffer, 4x**
- **4 µL ATP, 100mM**
- **20 µL Ficoll PM 400, 20% wt/vol**
- **10 µL dNTPs, 25 mM each**
- **5 µL SUPERase In (20U/uL)**
- **2 µL DTT , 1M**
- **12.5 µL Hemo Klentag**
- **2.5 µL T7 DNA Ligase (3000U/uL)**
- **89 µL Nuclease free water**

120 Place the tubes onto magnetic rack until solution is clear, remove supernatant with p200 pipette and add 250 µL of nuclease-free water to each tube without bead suspension

- **250 µL Nuclease free water**

121 Remove water and resuspend the beads with 195 µL of GLR-B mix by gently vortexing and quick spin the tubes on mini centrifuge for 3 s

122 Rotate the tubes in incubator at 37 ºC with slow speed for 15 min to allow for gap filling on AC DNA and ligate Nextera adapter 1 blocker to the AC DNA. OPTIONAL: For any step required rotator, thermomixer can be alternatively used as long as the tube is shaken gently and the beads do not settle.

00:15:00 Gap filling and ligation

123 Remove the tubes from incubator and add each tube with 5 µL of 100 µM TSO and 5 µL of Maxima H Minus reverse transcriptase and mix well by gently vortexing.

- **5 µL TSO oligo, 100 uM**
- **5 µL Maxima H Minus RT, (200 U/uL)**

124 Continue to incubate at room temperature for 30 min with slow rotation.

00:30:00 complete reverse transcription

125 Incubate at 42 ºC for 90 min with slow rotation.

01:30:00 complete reverse transcription

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126 PAUSE POINT: The beads can be stored in Tris-T buffer at 4 ºC overnight before continuing to 1st PCR (Remove supernatant and replace with Tris-T buffer). However, we recommend to continue to the 1st PCR immediately if possible.

First PCR, cDNA/DNA amplification 1h 30m

127 Before finishing 42C incubation, set up the first PCR mix to amplify both cDNA and accessible chromatin (AC) DNA and prepare PCR strip tubes with individual hinged cap (4 tubes per pool):

- **110 µL KAPA HiFi HotStart ReadyMix, 2x**
- **8.8 µL BC_0108, 10 uM**
- **17.6 µL BC_0062, 10 uM**
- **8.8 µL BC_0082, 10 uM**
- **74.8 µL Nuclease free water**

128 After finishing incubation at 42 ºC for 90 min, place the tubes onto the magnetic rack until liquid is clear and remove supernatant with p200 pipette

129 Add 250 µL of nuclease-free water to each tube without bead resuspension. Once liquid is clear, remove supernatant.

- **250 µL Nuclease free water**

130 Resuspend the beads with 220 µL of first PCR mix, quick spin and aliquot 55 µL of bead suspension in PCR mix to each of 4 PCR strip tubes. Transfer all the leftover beads to 4 PCR tubes equally. CRITICAL STEP: Transfer the beads in PCR mix directly to the bottom of the tube, so there is no need to spin the tube before placing on thermocycler. Try to transfer PCR mix with the beads into PCR strip tubes as quick as possible to minimize bead settling before the reaction starts.

131 Place the tubes on thermocycler and run following program: 95 ºC for 3 min, 9 cycles of (98 ºC for 20 s, 58 ºC for 45 s, 72 ºC for 3 min), 72 ºC for 5 min, 4 ºC hold.

132 PAUSE POINT PCR reaction can be stored at -20 ºC for a month or 4 ºC for a week.

133 Place strip tubes onto 0.2 mL magnetic rack until supernatant is clear and pool 1st round PCR products from 4 strip tubes of the same pool into 1.5 mL DNA LoBind tube

134 Vortex the tube and quick spin on mini centrifuge for 3 s before splitting PCR products into two parts (100 µL each), “AC” for chromatin accessibility (AC) library preparation and “R” for RNA library preparation. Note: AC and R in this step are the same PCR products but will be bead size-selected at different bead volume ratio.

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sn/scATAC libraries: purifiation and validation 1h

135 Perform one round of 1.2x KAPA Pure Beads purification following manufacturer's instructions by using 120 µL of KAPA Pure Beads with 100 µL of PCR products and elute with 40 µL of nuclease-free water

1. Binding

120 µL KAPA Pure Beads **00:08:00**

2. Washing

180 µL Ethanol, 100% **00:00:30**

3. 2nd wash

180 µL Ethanol, 100% **00:00:30**

4. Drying

00:01:00 **37 °C**

5. Elution

40 µL Nuclease free water **00:10:00** **37 °C**

136 Transfer eluent into new PCR strip tubes. The resultant is called AC-A.

137 Use 2 µL of AC-A product to determine DNA concentration with Qubit dsDNA HS assay kit following manufacturer's instruction

138 Verify ~10 ng of AC-A in 6% TBE gel and run in 1x TBE buffer at 250 volts for 23 min with 0.5 µL of Low DNA Mass Ladder as reference

sn/scATAC libraries: 2nd PCR and library preparation 6h 30m

139 In PCR strip tubes, use 5 ng of AC-A as template for enrichment of AC DNA over cDNA and adjust volume of template to 10 µL with nuclease-free water and quick spin down the tubes. CRITICAL STEP: If the concentration of PCR product is higher than 5 ng/µL, it tends to have high error to pipette the volume smaller than 1 µL. We recommend to aliquot AC-A, dilute into 0.5 ng/µL in total 30-50 µL and use 10 µL as template for AC 2nd PCR.

10 µL AC-A DNA (total 5 ng)

140 Prepare PCR mix as follows:

25 µL KAPA HiFi HotStart ReadyMix, 2x

2.5 µL SPLiT_N701, 10 uM

2.5 µL EvaGreen, 20x

7.5 µL Nuclease free water

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141 Add 37.5 µL of PCR mix and 2.5 µL of 10 µM Ad1_N50X (attached tables) into the tube with AC-A template

2.5 µL Ad1_N5XX, 10 uM

142 Mix by gently vortexing, quick spin PCR tubes on mini centrifuge at room temperature for 3 s and run qPCR on real-time PCR machine: 95 ºC for 3 min, 12 (or fewer) cycles of (98 ºC for 20 s, 58 ºC for 45 s, 72 ºC for 1 min), 72 ºC for 5 min, 4 ºC hold.

143 PAUSE POINT: PCR reaction can be stored at -20 ºC for a month or 4 ºC for a week.

144 Purify PCR product with DNA Clean & Concentrator following manufacturer's instructions and elute with 40 µL of DNA Elution Buffer. Resultant is called AC-B

145 Use 2 µL of AC-B to determine DNA concentration with Qubit dsDNA HS assay kit following manufacturing's instruction

146 Verify ~10 ng of AC-B in 6% TBE gel and run in 1x TBE buffer at 250 volts for 23 min with 0.5 µL of Low DNA Mass Ladder as a reference in separate lane. CRITICAL STEP: We expect to see nucleosome pattern with larger size (~125 bp larger) compare to standard ATAC-seq due to the presence of cell barcodes and linker sequences

147 Pool equimolar ratio of AC-B libraries (~200-250 ng/pool) and perform PAGE size-selection at the size between 300-1,000 bp.

148 Use 2 µL of AC sequencing libraries to determine for DNA concentration with Qubit dsDNA HS assay

149 Verify ~5 -10 ng of AC sequencing libraries in 6% TBE gel and run in 1x TBE buffer at 250 volts for 23 min or by TapeStation

sn/scATAC libraries: Quality validation by MiSeq sequencing 1d

150 Validate AC sequencing libraries with MiSeq sequencing using v2 reagent kit by loading at 20 pm based on Qubit dsDNA HS quantification with at least 5% PhiX spike in following Illumina loading guide. The sequencing configuration is 75 cycles for read 1, 94 cycles for index 1, 8 cycles for index 2, and 75 cycles for read 2.

CRITICAL STEP: For MiSeq sequencing, quantification of sequencing library concentration by Qubit

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and determination of average library size is sufficient. For high-throughput sequencing, we recommend to run sequencing libraries on Bioanalyzer, TapeStation or equivalent instrument that can determine accurate average library size and contamination of adapter dimers peaks at approximately 125-175 bp. We recommend to run qPCR to quantify sequencing library concentration using the average library size derived from TapeStation. For a two-channel sequencing system such as NovaSeq, we recommend to spike-in with minimum of 10% PhiX or consult sequencing core.

151 Mix 1:1 ratio of "SN2-AC R1" sequencing primer pairs for sequencing read 1 on Illumina workflow A (HiSeq 2500, MiSeq, NovaSeq 6000 platforms).

3 µL SNARE2_Read1, 100 uM

3 µL PhiX_Read1, 100 uM

594 µL Hybridization buffer, HT1

152 Mix 1:1 ratio of "SN2-AC R2" sequencing primer pairs for sequencing index 1 on Illumina workflow A (HiSeq 2500, MiSeq, NovaSeq 6000 platforms).

3 µL SNARE2-AC_BCread, 100 uM

3 µL PhiX_Read1, 100 uM

594 µL Hybridization buffer, HT1

153 Mix 1:1 ratio of "SN2-AC R4" sequencing primer pairs for sequencing read 2 on Illumina workflow A (HiSeq 2500, MiSeq, NovaSeq 6000 platforms).

3 µL SNARE2-AC_Read2, 100 uM

3 µL PhiX_Read2, 100 uM

594 µL Hybridization buffer, HT1

sn/scRNA libraries: purification and validation 1h

154 Perform 1 round of 0.8x KAPA Pure Beads purification following manufacturer's instructions by mixing 100 µL of 1st PCR product + with 80 µL of KAPA Pure Beads and elute with 40 µL of nuclease-free water. Resultant is called R-A.

1. Binding

80 µL KAPA Pure Beads **00:08:00**

2. Washing

180 µL Ethanol, 100% **00:00:30**

3. 2nd wash

180 µL Ethanol, 100% **00:00:30**

4. Drying

00:01:00 **37 °C**

5. Elution

40 µL Nuclease free water **00:10:00**

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155 Use 2 µL of R-A to determine DNA concentration with Qubit dsDNA HS assay following manufacturer's instructions

156 Verify 5-10 ng of R-A in 6% TBE gel and run in 1x TBE buffer at 250 volts for 23 min with 0.5 µL of Low DNA Mass Ladder as a reference

sn/scRNA libraries: 2nd PCR, purification, and validation 2h

157 In PCR strip tubes, use 5 ng of R-A as template for enrichment of cDNA over AC DNA and adjust the volume of template to 10 µL with nuclease-free water and quick spin down the tubes. CRITICAL STEP: If the concentration of PCR product is higher than 5 ng/µL, it tends to have high error to pipette the volume smaller than 1 µL. We recommend to aliquot R-A, dilute into 0.5 ng/µL in total 30-50 µL and use 10 µL as template for RNA 2nd PCR

158 Prepare PCR mix for second round amplification of cDNA as follows:

25 µL KAPA HiFi HotStart ReadyMix, 2x

2 µL BC_0108, 10 uM

2 µL BC_0062, 10 uM

2.5 µL EvaGreen, 20x

8.5 µL Nuclease free water

159 Add 40 µL of PCR mix to each tube, gently vortex and quick spin PCR tubes on mini centrifuge at room temperature for 3 s

160 Run the reactions on real-time PCR using following program: 95 ºC for 3 min, 12 (or fewer) cycles of (98 ºC for 20 s, 67 ºC for 45 s, 72 ºC for 3 min), 72 ºC for 5 min, 4 ºC hold.

161 PAUSE POINT PCR reaction can be stored at -20 ºC for a month or 4 ºC for a week.

162 Purify PCR products with 1 round of 0.8x KAPA Pure Beads and elute with 40 µL of nuclease-free water. The resultant purified DNA is called R-B

1. Binding

40 µL KAPA Pure Beads **00:08:00**

2. Washing

180 µL Ethanol, 100% **00:00:30**

3. 2nd wash

180 µL Ethanol, 100% **00:00:30**

4. Drying

00:01:00 **37 °C**

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5. Elution

40 µL Nuclease free water **00:10:00** **37 °C**

163 Determine DNA concentration with Qubit dsDNA HS assay using 2 µL of R-B

164 Verify ~5-10 ng of R-B in 6% TBE gel by running at 250 volts for 23 min with 0.5 µL of Low DNA Mass Ladder as a reference. CRITICAL STEP: If the smear of R-B is between 375 bp and above, continue to cDNA tagmentation. If there is strong smear smaller than 375 bp, repeat another round of 0.8x KAKA Pure Beads and elute with 40 µL of nuclease-free water.

sn/scRNA libraries: cDNA tagmentation and library preparation 3h

165 Mix ME and Nextera Adapter 1 (Ad1) oligos 1:1 for final 50 uM each. Briefly vortex and quick spin the tube. Anneal transposons on thermocycler using following program: 95 ºC 5 min, slowly cool down to 65 ºC (0.1 ºC/s), 65 ºC 5 min, slowly cool down to 4 ºC (0.1 ºC/s) and hold at 4 ºC.

166 Load Tn5 (In-house, 11.32 uM)

20 µL Tn5, (In-house, 11.32 uM)

6.8 µL 50 uM, Nextera Adapter 1/ME

1h

167 Incubate 1 hour at room temperate with gentle shaking.

01:00:00

168 Prepare Tagmentation mix as follows in 1.5 mL tube and aliquot 18 µL per pool into 0.2 mL PCR strip tubes with hinged cap.

2 µL Tango Buffer, 10X

2 µL DMF, 100%

12 µL Nuclease free water

2 µL Loaded Tn5, 8.44 uM

169 Transfer 2 µL of diluted cDNA (total 10-20 ng) with multichannel pipette into tagmentation mix, mix by pipetting 10 times, gently vortex and quick spin on mini centrifuge at room temperature for 5 s

7m

170 Place the tubes on thermocycler that set at 55 ºC for 7 min with the heated lid

00:07:00

171 Remove the tube from thermocycler and stop reaction by adding 5 µL of 0.2 % (wt/vol) SDS, mix by pipetting 5 times, gently spin down the tubes on mini centrifuge for 5 s and incubate at room temperature

Citation: Nongluk Plongthongkum, Dinh H Diep, Song Chen, Blue Lake, Kun Zhang SNARE-seq2
https://dx.doi.org/10.17504/protocols.io.bzdrp256

for 5 min

5 µL 0.2% SDS

00:05:00

172 Set up Tagmentation PCR mix during incubation

25 µL KAPA Hifi Hotstart ReadyMix, 2X

2.5 µL BC_0118, 10 uM

2.5 µL EvaGreen, 20X

7.5 µL Nuclease free water

173 Add 2.5 SPLiT_N7XX (attached tables) primers to 10 uL tagmented cDNA, then 37.5 of Tagmentation PCR mix respectively, mix well and gently spin down the tube on mini centrifuge for 3 s

2.5 µL SPLiT_N7XX, 10 uM

10 µL tagmented cDNA

37.5 µL Tagmentation PCR Mix

174 Run PCR on thermocycler using program follows: 72 ºC for 3 min, 98 ºC for 30 s, 9-12 cycles of (98 ºC for 30 s, 63 ºC for 30 s, 72 ºC for 45 s), 72 ºC for 3 min, 4 ºC hold. Terminate the reaction when it reaches mid-exponential growth. 20m

175 Purify PCR products at least two rounds of 0.7x KAPA Pure beads to make sure that no adapter dimers are leftover in the sequencing libraries. Elute the last round of bead purified RNA libraries with 30 µL of nuclease-free water. CRITICAL STEP: Adapter dimers can cluster more efficiently than regular sequencing libraries and is more sensitive on the patterned flow cell such as NovaSeq S4. This can lead to the reduction of sequencing output and sequencing quality

1. Binding

35 µL KAPA Pure Beads **00:08:00**

2. Washing

180 µL Ethanol, 100% **00:00:30**

3. 2nd wash

180 µL Ethanol, 100% **00:00:30**

4. Drying

00:01:00 **37 °C**

5. Elution

50 µL Nuclease free water **00:10:00** **37 °C**

6. Binding

35 µL KAPA Pure Beads **00:08:00**

7. Washing

180 µL Ethanol, 100% **00:00:30**

8. 2nd wash

Citation: Nongluk Plongthongkum, Dinh H Diep, Song Chen, Blue Lake, Kun Zhang SNARE-seq2
https://dx.doi.org/10.17504/protocols.io.bzdrp256

180 µL Ethanol, 100% **00:00:30**

9. Drying

00:01:00 **37 °C**

10. Elution

30 µL Nuclease free water **00:10:00** **37 °C**

176 Use 1 µL of RNA sequencing libraries to determine for DNA concentration with Qubit dsDNA HS assay

177 Verify ~ 5 ng of RNA libraries in 6% TBE gel at 250 volts for 23 min with 0.5 µL of Low DNA Mass Ladder as a reference

sn/scRNA libraries: Quality validation by MiSeq sequencing 1d

178 Validate sequencing libraries with MiSeq sequencing using v3 reagent kit by loading at 22 pm based on Qubit dsDNA HS quantification with at least 5% PhiX spike. The sequencing configuration is 70 cycles for read 1, 6 cycles for index, and 102 cycles for read 2.a

CRITICAL STEP: For MiSeq sequencing, quantification of sequencing library concentration by Qubit and determination of average library size is sufficient. For high-throughput sequencing, we recommend to run sequencing libraries on Bioanalyzer, TapeStation or equivalent instrument that can determine accurate average library size and contamination of adapter dimers peaks at approximately 125-175 bp. We recommend running qPCR to quantify sequencing library concentration using the average library size derived from TapeStation. For a two-channel sequencing system such as NovaSeq, we recommend spike-in with a minimum of 10% PhiX or consult sequencing core.

179 Mix 1:1 ratio of "SN2-R R1" sequencing primer pairs for sequencing read 1 on Illumina workflow A (HiSeq 2500, MiSeq, NovaSeq 6000 platforms).

3 µL SNARE2_Read1, 100 uM

3 µL PhiX_Read1, 100 uM

594 µL Hybridization buffer, HT1

180 Mix 1:1 ratio of "SN2-R Index1" sequencing primer pairs for sequencing index 1 on Illumina workflow A (HiSeq 2500, MiSeq, NovaSeq 6000 platforms).

3 µL SNARE2-R_Index1

3 µL PhiX_Read1

594 µL Hybridization buffer, HT1

Citation: Nongluk Plongthongkum, Dinh H Diep, Song Chen, Blue Lake, Kun Zhang SNARE-seq2
https://dx.doi.org/10.17504/protocols.io.bzdrp256

181 Mix 1:1 ratio of "SN2-R R2" sequencing primer pairs for sequencing read 2 on Illumina workflow A (HiSeq 2500, MiSeq, NovaSeq 6000 platforms).

- **3 µL SNARE2-R_Read2**
- **3 µL PhiX_Read2**
- **594 µL Hybridization buffer, HT1**

Citation: Nongluk Plongthongkum, Dinh H Diep, Song Chen, Blue Lake, Kun Zhang SNARE-seq2
https://dx.doi.org/10.17504/protocols.io.bzdrp256