

Data S1

Detailed Protocol and Quality Control Results of RDD Library Construction

| | |
|--|----------|
| <i>Part I Prepare RNA enriched chromatin.....</i> | <i>2</i> |
| 1. Cell lysis and nuclei lysis | 2 |
| 2. Nuclei wash | 4 |
| 3. Sonication..... | 5 |
| 4. Preclear chromatin with C1 beads..... | 6 |
| 5. Hybridization overnight..... | 6 |
| <i>Part II Proximity ligation of chromatin DNA.....</i> | <i>9</i> |
| 6. Block beads with denatured IPB..... | 9 |
| 7. On beads end-repair, A-tailing and proximity ligation..... | 10 |
| 8. Elution of proximity ligation DNA..... | 13 |
| 9. DNA purification (Part A) | 14 |
| 10. DNA purification (Part B)..... | 15 |
| 11. Tn5 tagmentation testing and scale-up | 17 |
| 12. Prepare M280 beads for immobilization of ligated products..... | 18 |
| 13. Immobilization of DNA to streptavidin dynabeads..... | 19 |
| 14. PCR amplification of M280 enriched DNA..... | 20 |
| 15. Purify PCR product using AMPure beads (Beckman Coulter, A63881) | 21 |
| 16. Size selection for sequencing (double size selection with AMPure beads)..... | 22 |

Part I Prepare RNA enriched chromatin

Day-1

1. Cell lysis and nuclei lysis

Around 1×10^9 cells for S2-WT (non-treatment) and S2-HS (heat-shock treatment)

1.1. Thaw 2 tubes of frozen dual-crosslinking S2 cells on wet-ice for 1 hr.

0.8–1 $\times 10^9$ cells are for one library generation.

Preparation: *clean the bench and instrument with 75% ethanol and RNasezip. Use new reagents and pipettes.*

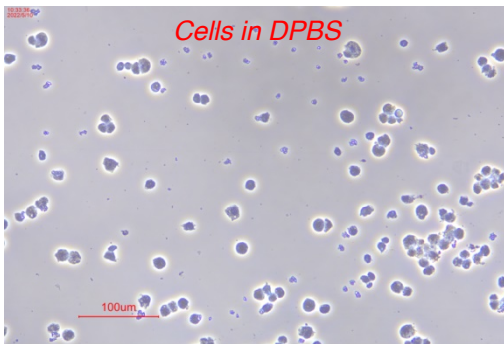
All the RNA-related buffers should be freshly set up.

1.2. Prepare 4 tubes of 50 ml of **0.1% FA lysis buffer without Triton-X100** at room temperature (RT).

| 0.1% FA lysis buffer without Triton X100 | Volume (50 ml) | Stock conc. | Catalog | Company |
|---|-----------------------|--------------------|----------------|----------------|
| 50 mM Tris-HCl pH 7 | 2.5 ml | 1 M | AM9851 | Thermo Fisher |
| 150 mM NaCl | 1.5 ml | 5 M | AM9759 | Thermo Fisher |
| 1 mM EDTA | 0.1 ml | 0.5 M | AM9261 | Thermo Fisher |
| 0.1% SDS | 0.5 ml | 10% | AM9822 | Thermo Fisher |
| ddH ₂ O | 45.4 ml | - | AM9932 | Thermo Fisher |

- *Do it during step 1.1*
- *Use RNase free tube.*
- *Mix the solution after adding each reagents*
- *Do not put lysis buffer on ice.*
- *Do not add PI (Proteinase inhibitor) and RI (RNase inhibitor) at this step.*

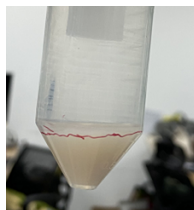
In this case: take one tube with 50 ml buffer and add 5 tablets of PI (Roche, 11836170001).



1.3. Wash cells with 50 ml **1 \times DPBS** (Thermo Fisher Scientific, 14190250) by incubating on the Intelli-Mixer (Program F1, 20 rpm) for 5 min at room temperature. Spin down at 2,000 rpm for 5 min at room temperature.

- *Combine the same treatment cells into one new RNase-free 50ml-tube.*

- *In this case: each tube adds 1 ml of DPBS, combine all the cells in one 50 ml-tube, wash with 50 ml DPBS without PI or RI (Thermo Fisher Scientific, AM2696).*



- 1.4. Spin down at 2,000 rpm for 5 min at room temperature and discard the supernatant by pouring.

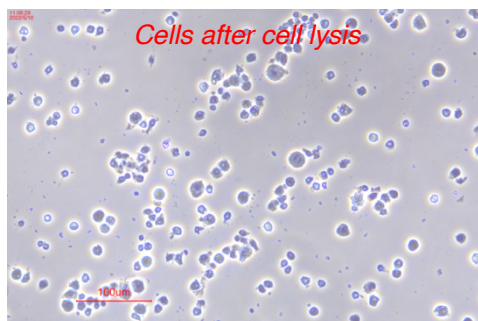
Firstly use 5 ml-pipette to remove the bubbles and then pool the supernatant, mark the size of pellets

- 1.5. Perform **cell lysis** using **20 ml of 0.1% FA lysis buffer without Triton-X100** freshly supplemented with PI, by incubating on the Intelli-Mixer (Program F1, 11 rpm) for 15 min at room temperature.

- *Add PI freshly before use at step 1.4.*
- *Do not put lysis buffer on ice.*
- *Check cells under microscope.*

In this case: firstly add 5 ml of buffer (contain PI) and use 1 ml-pipette to suspend the pellet, and then add another 5 ml buffer, finally add the remaining 10 ml buffer.

After 15 min incubation, check the cell under microscope.

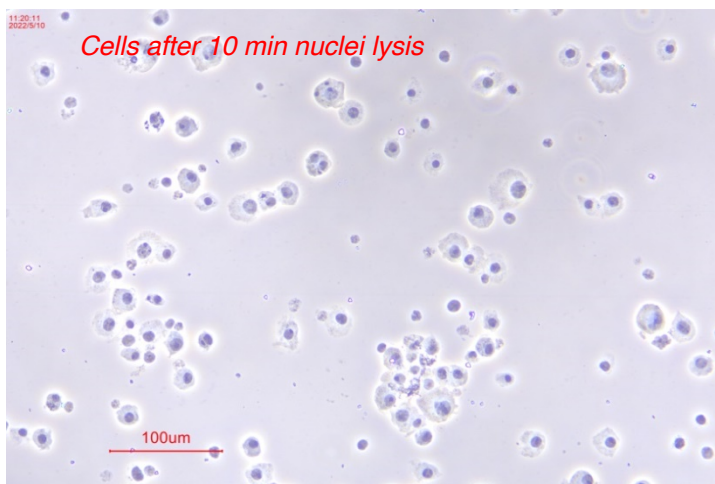


- 1.6. Perform **nuclei lysis** by adding **1.8 ml of 10% SDS** to a final concentration of **1%**, mix and incubate on the Intelli-Mixer (Program F1, 30 rpm) for 10 min at 37 °C.

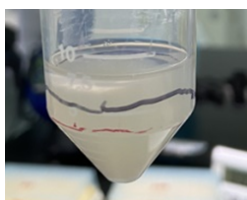
- *Do not put lysis buffer on ice.*
- *Check cells under microscope, the nuclei should be darker than step 1.5.*

Take out 5 µl samples to check the cells under microscope.

If the nuclear shows up a clear profiling, continue the nuclei wash step, if not, repeat the nuclei lysis.



- 1.7. Spin down at 3,890 rpm for 20 min at room temperature and remove the supernatant using the 5 ml-tip.

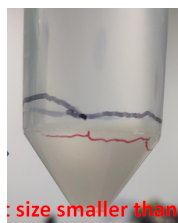


After spin down, the cell pellet tends to flow up, keep some remaining buffer in the pellet when remove the supernatant.

2. Nuclei wash

- 2.1. **Wash nuclei with 20 ml of 0.1% FA lysis buffer without Triton-X100** freshly by incubating on the Intelli-Mixer (Program F1, 20 rpm) for 5 min at room temperature.

Do not put lysis buffer on ice.



- 2.2. Spin down at 3,990 rpm for 20 min at room temperature and remove the supernatant by 5 ml-pipette.

The size of nuclei pellet after incubating with 0.1% SDS would be smaller than 1% SDS at step 1.7.

Add the sonication buffer to the nuclei pellets and put on ice until sonication.

3. Sonication

3.1. Prepare 50 ml of **0.1% FA lysis buffer with Triton-X100**.

| 0.1% FA lysis buffer with Triton-X100 | Volume (50 ml) | Stock conc. | Catalog | Company |
|--|-----------------------|--------------------|-----------------|----------------|
| 50 mM Tris-HCl pH 7 | 2.5 ml | 1 M | AM9851 | Thermo Fisher |
| 150 mM NaCl | 1.5 ml | 5 M | AM9759 | Thermo Fisher |
| 1% Triton-X100 | 2.5 ml | 20% | 327371000-100ml | Acros Organics |
| 1 mM EDTA | 0.1 ml | 0.5 M | AM9261 | Thermo Fisher |
| 0.1% SDS | 0.5 ml | 10% | AM9823 | Thermo Fisher |
| ddH ₂ O | 42.9 ml | - | AM9932 | Thermo Fisher |

- Do it during or before step 1.2.
- Use RNase free tube.
- Mix the solution after adding each reagent.
- Do not put lysis buffer on ice.
- Do not add PI and RI at this step.

In this case: after preparing 50 ml sonication buffer, keep it at 4 °C

3.2. **Clean the probe** of the sonication machine with 3~4 ml ddH₂O in 14 ml- RNase-free tube and setting the program (38%, 20 sec on/ 30 sec off, 4.5 min).

Put the tube containing ddH₂O to the tip of sonicator, and press “start” button to run 20 sec and stop, then keep the tip in ddH₂O until use.

3.3. Prepare 30 ml of **0.1% FA lysis buffer with Triton-X100** freshly supplemented with PI

15 ml for one tube of the nuclei pellet

In this case: add PI freshly in buffer before use

3.4. Resuspend nuclei pellet with 15 ml of **0.1% FA lysis buffer with Triton-X100** using 5 ml- pipette tip.

In this case: we only have two 50 ml-tubes of sample, the volume of the pellet is about 5 ml, add 5 ml buffer and suspend it, then add another 5 ml buffer, resuspended. Place it on ice until use.

3.5. **Aliquot** 1.5 ml into 14 ml-Falcon round bottom tube on ice.

Do put samples on ice.

In this case: for each treatment, aliquot 1.5 ml sonication sample to 10 tubes (14 ml-tube).

3.6. **Shearing** the nuclei by **sonication**.

- Take one of the tubes and then perform sonication, which takes about **9 min**.
- It may take half a day for sonication procedure.

- 3.7. Combine all tubes into **two** 14 ml-Falcon round bottom tubes and spin down at **3,890 rpm** for **20 min** at room temperature.



- 3.8. Transfer the supernatant into **two** 14 ml-RNase-free tube (~14 ml per tube).

- 3.9. *Prepare C1 beads* (Thermo Fisher Scientific, 65001).

Take 200 μ l of C1 beads to 1.5 ml-tube, place at magnetic rack for 1 min, remove the supernatant, wash with 200 μ l of 0.1% FA lysis buffer with Triton-X100, twice. Then suspend the beads and place it on rack for 1 min, and remove the supernatant, finally, keep beads in 100 μ l of buffer.

4. Preclear chromatin with C1 beads

- 4.1. Add 50 μ l of *pre-washed* C1 beads to the two tubes containing ~14 ml of chromatin. Incubate on the Intelli-Mixer (Program F1, 20 rpm) for 20 min at room temperature.

- 4.2. Transfer the chromatin to two new tubes.

In this case: two 50 ml-tubes, each tube contains ~13.6 ml chromatin, keep at least 10 μ l sample for QC by adding SDS with final concentration at 1%, and Proteinase K (Thermo Fisher Scientific, AM2546), then incubate at 65 °C with shaking overnight for decrosslinking.

5. Hybridization overnight

- 5.1. Prepare two tubes of **35 ml hybridization buffer**.

| Hybridization buffer | Volume (35 ml) | Stock conc. | Catalog | Company |
|----------------------|----------------|-------------|---------|---------------|
| 750 mM NaCl | 5.25 ml | 5 M | AM9759 | Thermo Fisher |
| 50 mM Tris.HCl pH 7 | 1.75 ml | 1 M | AM9851 | Thermo Fisher |
| 1 mM EDTA | 70 μ l | 0.5 M | AM9261 | Thermo Fisher |
| 1% SDS | 3.5 ml | 10% | AM9823 | Thermo Fisher |
| 15% Formamide | 5.25 ml | | AM9342 | Thermo Fisher |
| ddH ₂ O | 19.18 ml | - | | Thermo Fisher |

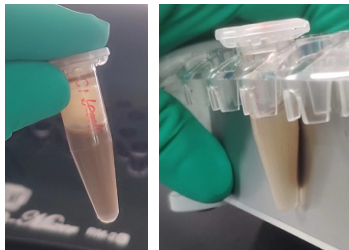
- 5.2. Add 2 volume (**26 ml**) of **freshly prepared hybridization buffer** into the **13 ml** of pre-cleared chromatin. Mix well and split them into 3 of 14 ml-RNase-free tube (*13 ml per tube, 3 tubes for S2-WT, 3 tubes for S2-HS, ~13 ml reaction solution per tube*).
- 5.3. Rotated at RT for 30 min
- 5.4. Add **biotinylated probes** into each tube. Each treatment adds **6 μ l rox2 probes (2 μ l per 14 ml tube)**. Seal the cap with film.
- 5.5. Incubate on the Intelli-Mixer (Program F1, 11 rpm) overnight at 37 °C.

Day-2

- 5.6. **Block** C1 beads with iBlock buffer.
- 5.6.1. Take **800 μ l** C1 beads to a 1.5 ml-tube.
- 5.6.2. Place it on magnetic rack and remove the supernatant.



- 5.6.3. Wash the beads three times with 800 μ l (per tube) of **0.1% FA lysis buffer without Triton-X100**.
- *In this case: after adding wash buffer, mix beads by flick and invert the tubes (may introduce some bubbles), spin briefly and place the tube on magnetic rack, keep tube on rack for 1 min before removed the supernatant.*
 - *Wash step: do not need rotation.*
- 5.6.4. Add 800 μ l iBlock (Thermo Fisher Scientific, T2015), incubate on the Intelli-Mixer (Program F8, 20 rpm) for 30 min at room temperature. Then place the tube on magnetic rack for 7~10 min.



5.6.5. Wash beads three times with 800 μ l (per tube) of **0.1% FA lysis buffer without Triton-X100**.

Wash step: do not need rotation, just invert tube to mix beads.

5.6.6. Resuspend beads to original volume with corresponding hybridization reaction buffer.

In this case, resuspend beads in 600 μ l of Hybridization buffer (for 6 tubes)

5.7. **Immobilize** the probe-chromatin to C1 beads. Add iBlock treated C1 beads to the corresponding hybridization chromatin. 300 μ l C1 beads for S2-WT and 300 μ l for S2-HS (100 μ l per 14 ml-tube). Incubate on the Intelli-Mixer (Program F1, 11 rpm) for 2.5 hrs at room temperature.

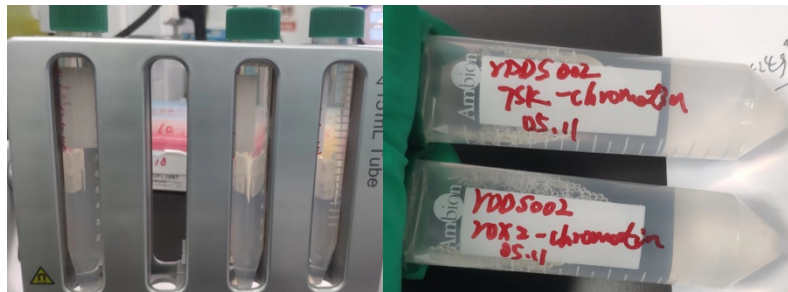
In this case, take 100 μ l of iBlock treated C1 beads to each 14 ml-tube of corresponding hybridization chromatin.

5.8. Prepare 50 ml of **Wash buffer** and pre-warm at 37 °C.

| Wash buffer | Volume (50 ml) | Stock conc. | Catalog | Company |
|--------------------|----------------|-------------|---------|---------------|
| 2 \times SSC | 5 ml | 20% | AM9770 | Thermo Fisher |
| 1% SDS | 2.5 ml | 10% | AM9823 | Thermo Fisher |
| ddH ₂ O | 42.5 ml | - | AM9932 | Thermo Fisher |

5.9. Transfer C1 beads bounded chromatin from the 14 ml-tube to 1.5 ml-tubes using magnetic rack (two 1.5 ml-tubes, one for S2-WT, one for S2-HS).

In this case: Place the 14 ml-tube on magnetic rack for 5 min, remove the supernatant. Take 1 ml of Wash buffer to suspend the beads and transfer to a new 1.5 ml-tube. Repeat and combine other beads from 14 ml-tube of same treatment to the 1.5 ml-tube, and then wash the 14 ml-tube with Wash buffer, collect them into the 1.5 ml-tube.

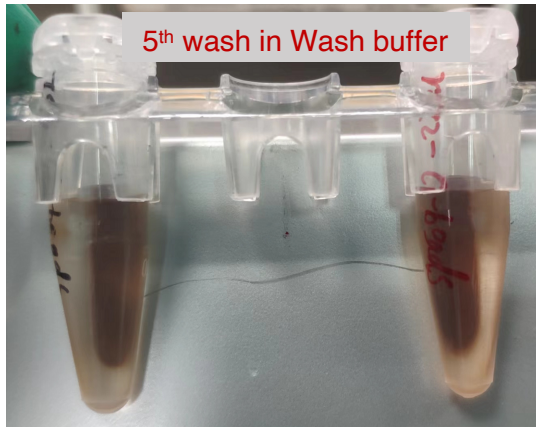
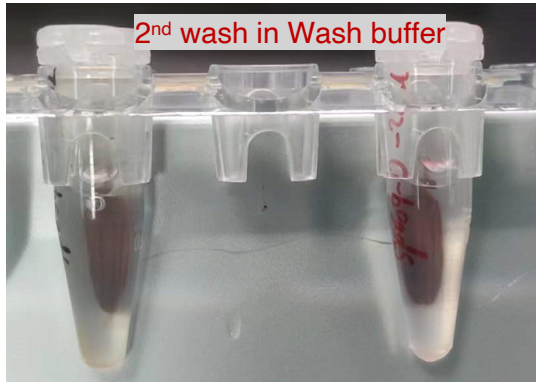


- Keep the supernatant into to RNA-free 50 ml-tubes in case for trouble shooting.
- When transferring, perform tube by tube, place one tube on magnetic rack, remove the supernatant, repeat.

5.10. Take 10 ml **Wash buffer** and 10 ml **TE buffer** (Thermo Fisher Scientific, AM9849) that supplemented with PI

- *In this case: Wash buffer do not need add PI or RI (because they contained 1% SDS), TE buffer need add PI before use.*
- *This period should start to prepare the IPB (weight IPB).*

5.1.1. **Wash beads** with 800 μ l of **freshly prepared Wash buffer** for 5 times (*rotation for 5 min*), then wash with 800 μ l **TE buffer** for 3 times. At the last wash step, keep the tube at room temperature in TE buffer (1000 μ l).



- During the wash step of TE buffer, beads tend to be scatter and sticky, place the tube on the rack for 2 min before remove supernatant.
- Attention: 30 min before completed the wash step, we need start to prepare IPB solution and β -ME solution.
- For each wash step with Wash buffer, just flick then spin down briefly.

Part II Proximity ligation of chromatin DNA

6. Block beads with denatured IPB

6.1. Prepare the denatured IPB during beads wash at step 5.10.

6.1.1. Weight 4.8 mg of IPB (Thermo Fisher Scientific, 11821334) and dissolve them into 400 μ l of **IPB wash buffer**, incubate on the Intelli-Mixer (Program F1, 11 rpm) for 15 min at room temperature. Avoid of light using foil.

- In this case, take 7.8 mg IPB, and dissolve them into 650 μ l wash buffer.
- Make sure the IPB was dissolved before rotation.

| IPB wash buffer | Volume (10 ml) | Stock conc. | Catalog | Company |
|---------------------|----------------|-------------|---------|---------------|
| 50 mM Tris-HCl pH 8 | 0.5 ml | 1 M | AM9851 | Thermo Fisher |
| 50 mM NaCl | 0.1 ml | 5 M | AM9759 | Thermo Fisher |
| 1 mM EDTA | 0.02 ml | 0.5 M | AM9261 | Thermo Fisher |
| ddH ₂ O | 9.38 ml | - | | Thermo Fisher |

6.1.2. At the same time, take 1 μ l of β -ME (Sigma, M6250) to 312 μ l of H₂O. Incubate on the Intelli-Mixer (Program F1, 11 rpm) for 15 min at room temperature. Vortex briefly for 10 times before rotation.

Add the β -ME (stored at 4 °C) at chemical fume hood to avoid of the foul smell.

6.1.3. Take 44 μ l β -ME solution into 400 μ l IPB solution, mix and incubate on the Intelli-Mixer (Program F1, 11 rpm) for 15 min at room temperature to denature the IPB.

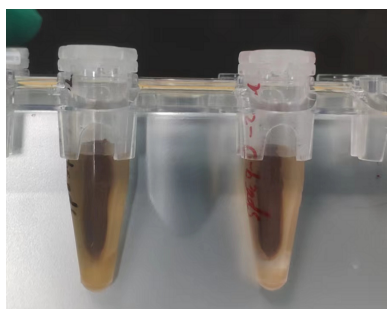
Attention: IPB should pre-warm at room temperature at least 1 hr before weighting. Both IPB and β -ME should be avoid of light.

6.2. Add 220 μ l of the **denatured IPB** to the 1000 μ l beads in TE. Incubate on the Intelli-Mixer (Program F1, 10 rpm) for 15 min at room temperature.

Attention: Keep the tubes to avoid light during rotation by packaging them with foil.

6.3. Rinse the beads once and wash beads with **TE (added PI freshly)** for five times (*rotation for 5 min at RT with F8, 10 rpm*)

Attention: the beads are sticky, should rinse the tips before using it to remove the supernatant. Some beads may float up during the wash step with TE buffer. Keep the beads in TE buffer for next step.



7. On beads end-repair, A-tailing and proximity ligation

7.1. Put buffer and dNTP on ice for end-repair.

7.2. Prepare 50 ml ChIA-PET wash buffer. Take out **10** ml and add **25** μ l RI **and 1 tablet of PI**.

| ChIA-PET wash buffer | Volume (50 ml) | Stock conc. | Catalog | Company |
|----------------------|----------------|-------------|---------|---------------|
| 10 mM Tris.HCl pH 7 | 0.25 ml | 1 M | AM9851 | Thermo Fisher |
| 10 mM Tris.HCl pH 8 | 0.25 ml | 1 M | AM9856 | Thermo Fisher |
| 1 mM EDTA | 100 μ l | 0.5 M | AM9261 | Thermo Fisher |
| 150 mM NaCl | 1.5 ml | 5 M | AM9759 | Thermo Fisher |
| ddH ₂ O | 47.9 ml | - | AM9937 | Thermo Fisher |

This buffer should be stored at 4 °C.

- 7.3. Prepare two times of volume of End-Blunt Mix **on ice**. When adding dNTPs and RI, then flick, vortex, and spin down briefly each time to mix well.

| End-Blunt Mix | 1 × | 2.2 × | Catalog | Company |
|---------------------|-------------|----------------|---------|---------------|
| Nuclease-free water | 613 μ l | 1348.6 μ l | AM9937 | Thermo Fisher |
| NEB 10 X Buffer 2.1 | 70 μ l | 154 μ l | | NEB |
| 10 mM dNTPs | 7 μ l | 15.4 μ l | N0447S | NEB |
| 0.1 U/ μ l RI | 3 μ l | 6.6 μ l | AM2696 | Invitrogen |

Notice: Prepare all solution (2.2 ×) in one 2 ml-tube and then use 693 μ l volume for one reaction.

- 7.4. Place tube at magnetic rack. Remove the supernatant in step 7.3, and add 693 μ l End-Blunt Mix into the beads. Flick it to mix.

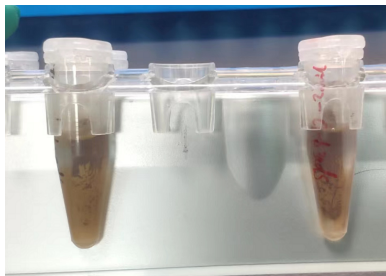
- 7.5. Add 7 μ l of T4 DNA Polymerase (NEB, M0203S). Flick it to mix.

In this case: incubate the reaction at 12 °C on Thermomixer for 30 min with 800 rpm shaking, and then transfer to the 16 °C- incubator for 15 min with rotation (F8, 10 rpm).

- 7.6. Thaw buffer and dATP for A-tailing on ice.

- 7.7. Take out the End-repair chromatin and spin down briefly. Then put on the magnetic rack and discard the supernatant. Wash beads with 800 μ l ice-cold ChIA-PET buffer (*supplemented with PI and RI*) three times.

In this case: the wash steps do not need rotation, just by flick to mix beads, then place tube on magnetic rack for 2 min, rinse the pipette before removed the supernatant (The beads are very sticky).



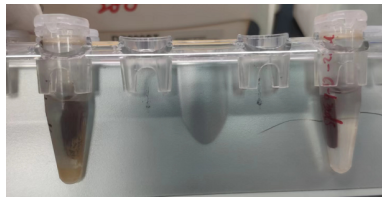
- 7.8. Add 800 μ l TE buffer, flick to mix, spin down briefly, put it at RT.

- 7.9. Prepare two times of volume of A-tailing Mix. When adding dATPs and RI, flick, vortex and spin down briefly each time to mix.

| A-tailing Mix | 1 × | 2.2 × | Catalog | Company |
|---------------------|--------|-----------|----------|---------------|
| Nuclease-free water | 613 µl | 1348.6 µl | AM9937 | Thermo Fisher |
| 10 X NEB Buffer 2 | 70 µl | 154 µl | B7002S | NEB |
| 10 mM dATPs | 7 µl | 15.4 µl | 18252015 | Thermo Fisher |
| 0.1 U/µl RI | 3 µl | 6.6 µl | AM2696 | Invitrogen |

Notice: Prepare all solution (2.2 ×) in one 2 ml-tube and then use 693 µl volume for one reaction.

- 7.10. Place tube on magnetic rack, remove supernatant, add 693 µl A-tailing mix, flick to mix and spin down briefly.
- 7.11. Add 7 µl of Klenow fragment (3'-5' exo-) (NEB, M0212L). Flick to mix. Incubate at 37 °C for 50 min with rotation (F1, 11 rpm).
- 7.12. Put linker and buffer for ligation on ice.
- 7.13. Spin down the A-tailing chromatin briefly. Then put on the magnetic rack and discard the supernatant. Wash beads with 800 µl ice-cold ChIA-PET wash buffer three times (*do not need rotation*).

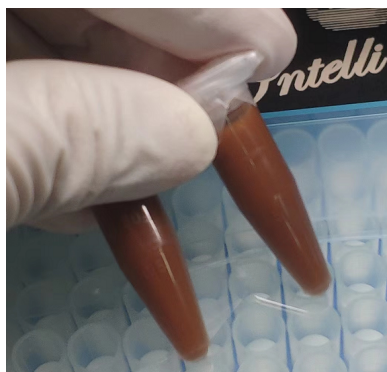


- 7.14. Add 800 µl **EB** buffer (Qiagen, 19086), flick to mix, spin down briefly, then keep it at RT.
- 7.15. Prepare the Proximity Ligation Mix. When adding linker, flick, and upside down to mix. When adding buffer and RI, flick, vortex to mix each time.

| Proximity Ligation Mix | 1 × | Catalog | Company |
|--------------------------------------|---------|---------|---------------|
| Nuclease-free water | 1243 µl | AM9937 | Thermo Fisher |
| Bridge Linker (133 ng/µl) (In-house) | 6 µl | - | IDT |
| 10 X T4 DNA Ligase Buffer | 140 µl | M0202s | NEB |
| 0.1 U/µl RI | 5 µl | AM2696 | Thermo Fisher |

Notice: Here prepare one tube (1.394 ml) and then add all of them into the reaction tube. Rotated the tube at RT with rotation (F8, 10 rpm).

- 7.16. Place tube at magnetic rack, remove supernatant, add 1394 μ l of Proximity Ligation Mix, Flick to mix and spin down briefly.
- 7.17. Put tubes on shaker (F8, 30 rpm).
- 7.18. Take out one tube from the shaker and add **10 μ l** T4 DNA ligase (NEB, M0202S), flick, upside down and put it on shaker again. Then add enzyme to another tube. ***Incubate at RT for 50 min with rotation (F1, 20 rpm).*** After that seal the tube with film.



- 7.19. Then incubate overnight at 16 °C with rotation (F1, 20 rpm).

Day-3

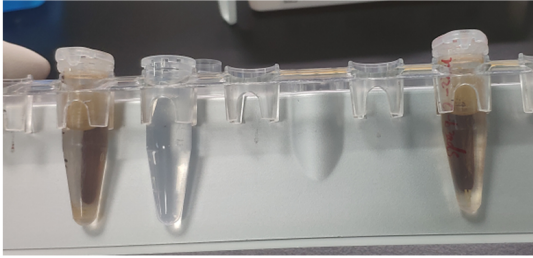
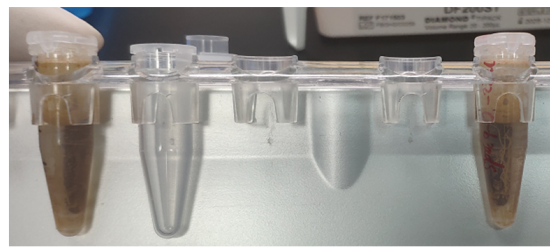
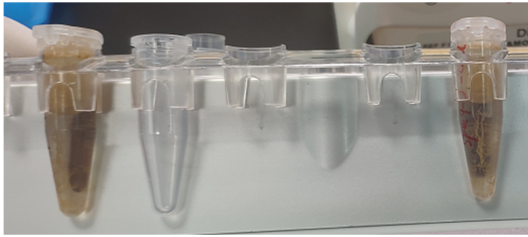
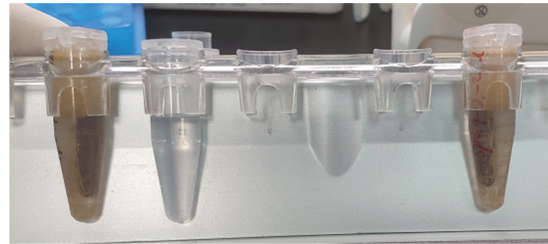
8. Elution of proximity ligation DNA

- 8.1. Prepare 10 ml **low salt concentration (LC) ChIP elution buffer**. Do not place them on ice.

| LC ChIP Elution Buffer | 10 ml | 50 ml | Stock conc. | Catalog | Company |
|------------------------|---------|---------|-------------|---------|---------------|
| 50 mM Tris.HCl pH 7 | 0.25 ml | 1.25 ml | 1 M | AM9851 | Thermo Fisher |
| 50 mM Tris.HCl pH 8 | 0.25 ml | 1.25 ml | 1 M | AM9856 | Thermo Fisher |
| 0.5 % SDS | 0.5 ml | 2.5 ml | 10% | AM9823 | Thermo Fisher |
| ddH ₂ O | 9 ml | 45 ml | - | AM9932 | Thermo Fisher |

- 8.2. Wash beads with 800 μ l of ChIA-PET wash buffer three times, and TE buffer twice.

Notice: Flick the tube once and upside down to mix in the rest procedures. Upside down for mixing, spin down briefly and keep on magnetic rack for removing the supernatant. When upside down for mixing, the beads were sticky, and may remain something on the beads.

After 2nd Wash in ChIA-PET wash bufferAfter 3rd Wash in ChIA-PET wash bufferAfter 1st Wash in TE bufferAfter 2nd Wash in TE buffer

- In this case: Place ChIA-PET wash buffer on ice.
- Wash step: rotated at RT with program (F8, 10 rpm) for 5 min during each wash step. Beads are easy spreading on the magnetic rack. The beads are sticky to the tips, and some beads may bind at the tube, hard to wash both in ChIA-PET wash buffer and TE buffer.

- 8.3. Add 480 μ l LC ChIP elution buffer into the beads bounded with ligated DNA. Mix and add 20 μ l of 20 mg/ml Proteinase K (Thermo Fisher Scientific, AM2546).

Notice: Just upside down to mix in case of introducing bubbles (elution buffer contains SDS, beads in bubbles may not be fully eluted). Working concentrations of the proteinase K is from 50 to 250 μ g/ml.

- 8.4. Incubate at 65 °C on Thermomixer (Eppendorf) with 950 rpm overnight.

Notice: Do not put the tube to the Thermomixer until the temperature reach to 65 °C.

Day-4

9. DNA purification (Part A)

- 9.1. Put the ligated products with beads on magnetic rack.

Notice: The products include: 10 μ l input DNA; 20 μ l beads after Hybridization for rox2 or 7sk respectively; 800 μ l beads after ligation for rox2 or 7sk respectively.

- 9.2. Centrifuge the MaXtract High Density Tube (Qiagen, 129046) at 12,000 rpm for 2 min at RT.

- 9.3. Add the de-crosslinked products (500 μ l) into the MaXtract tube.
- 9.4. Then transfer 500 μ l Phenol:Chloroform:IAA (Solarbio, P1012) to the MaXtract tube using a 5 ml-pipette tip in fume hood. Mix gently by hand.
- 9.5. Spin down at 12,000 rpm for 6 min at RT.
- 9.6. During step 9.5, prepare the reagents: add 52 μ l of 3 M Sodium Acetate pH 5.5 (Ambion, AM9740) to the bottom of a 1.5 ml-tube, and add 1 μ l of GlycoBlue (ThermoFisher, AM9516) to the cap of tube. Do not mix. Do not close the cap. Transfer the supernatant from the MaXtract tube into the 1.5 ml-tube quickly.
- 9.7. Add 520 μ l ice-cold isopropanol (Sigma, I9516) to the 1.5 ml-tube. Mix gently. Put it at -80 °C overnight.

In this case: first we add 1.5 μ l GlycoBlue to the cap of tube, secondly add 50 μ l of 3 M Sodium Acetate pH 5.5 (Ambion, cat. AM9740) to the bottom, and then transfer the supernatant of MaXtract tube by pouring, finally added the 500 μ l of isopropanol (RT) into the tube. Mix by inverting the tubes and put it at -80 °C overnight.



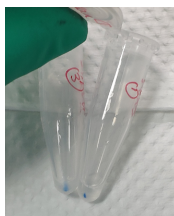
Day-5

10. DNA purification (Part B)

- 10.1. Take out the mixture from -80 °C and thaw at RT (*about 10 min*), then spin down at 12,000 rpm for about 1 hr at 4 °C to precipitate DNA.

In this case: we centrifuge for 1 hr.

There will have a blue pellet:



10.2. Wash DNA pellet with 75% ethanol: carefully remove the supernatant. Add 800 μ l of 70% ice-cold ethanol (Sigma, E7023), spin down at 12,000 rpm for 5 min at 4 °C, remove the supernatant. Repeat it once.

Notice:

a. Once after the centrifuge, remove the supernatant quickly by tips (first use 1 ml-tips following by 100 μ l-tips).

b. Do it just nearby the centrifuge, do not take all of them out. If the temperature recovers, the blue pellet may not stick to the tube wall.

In this case: first we pour out the supernatant quickly, and then add 1 ml of ice-cold 75% ethanol to rinse the pellet and pour out the supernatant quickly. After 1st rinse, add 1 ml of ice-cold 75% ethanol, and flick the tube to make the pellet float up. Then spin down at 12,000 rpm for 10 min at 4 °C, remove the supernatant. Repeat it once.

10.3. Spin down the tube at 12,000 rpm for **10** min at 4 °C to collect the extra ethanol at the bottom of the tube. Then remove the rest ethanol.

10.4. Dry the DNA pellet by Vacuum (from 1 min 30 sec to 2 min generally).

10.5. Resuspend DNA pellet in 10 μ l Qiagen elution buffer for 1~2 hrs at RT.

In this case: S2-WT and S2-HS samples were dissolved in 30 μ l of EB buffer, input DNA was dissolved in 100 μ l of EB buffer. Place the tube at RT for 2 hrs, flick the tube several times during the dissolved step.

10.6. Calculate the concentration using Qubit.

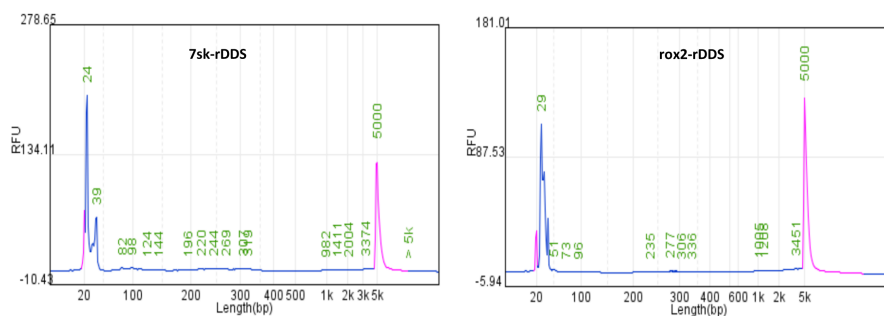
| Sample ID | Factor | Elution volume (μ l) | Concentration (ng/ μ l) | Elution DNA Amount (ng) |
|-------------------------|--------|---------------------------|-----------------------------|-------------------------|
| rox2-original tube | rox2 | 30 | 12.8 | 384 |
| 7sk-original tube | 7sk | 30 | 12 | 360 |
| input DNA-original tube | | 100 | 86.8 | 8680 |

10.7. Put the DNA on ice when perform Qubit. Then store them at -20 °C for later library construction.

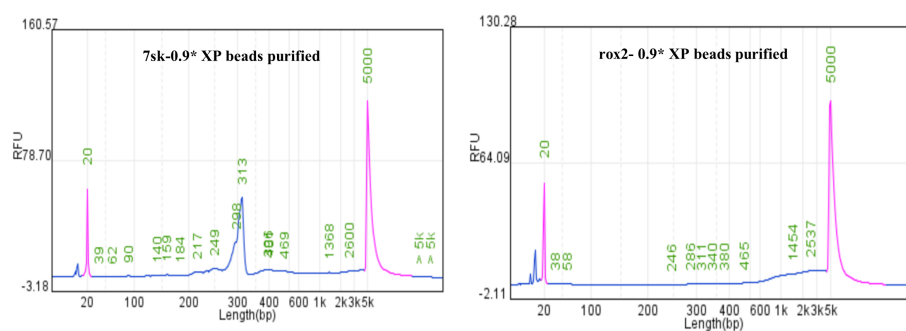
In this case, the samples are aliquot for Tn5 testing and scale-up tagmentation directly.

10.8. Check DNA size and profiling using Qsep.

rDDS002 Qsep results



After 0.9* Ampure XP beads purification



DNA amount after 0.9× Ampure XP beads purification:

| NO. | Sample ID | Elution volume (μl) | Concentration (ng/μl) | Elution DNA Amount (ng) | Remaining Volume (μl) | Remaining DNA Amount (ng) |
|-----|-----------|------------------------|--------------------------|----------------------------|-----------------------------|---------------------------------|
| 1 | rox2-rDD | 20 | 1.16 | 23.2 | 16.9 | 19.6 |
| 2 | 7sk-rDD | 20 | 1.97 | 39.4 | 17.4 | 34.28 |

11. Tn5 tagmentation testing and scale-up

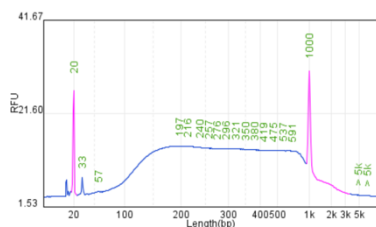
11.1. Prepare the reaction in a PCR tube on ice as below, add water in advance, followed by DNA sample, 4× THS TD buffer, then mix 10-20 times by pipetting with setting at 30 µl, briefly spin down, finally add Tn5, mix 10-20 times by pipetting with setting at 30 µl, spin down briefly, and make sure there is no bubble.

11.2. Then incubate at 55 °C for 10 min, and keep at 4 °C in PCR instrument.

PCR instrument setting:

| Temperature | Time |
|-------------|--------------|
| 70 °C | Heat the lid |
| 55 °C | 10 min |
| 4 °C | Hold |

This is quality control, and the majority of DNA fragments should fall into the range of 200-bp to 1-kb (shown as below).



11.3. According to Tn5 testing result, the rest products were scale-up with the same condition.

11.4. Then release Tn5 from DNA template: take out the sample from PCR instrument and place on ice. Spin down briefly, put at RT for 2 min, then add 5.5 μ l 10% SDS to the sample (finally concentration is 1%), mix 10-20 times by pipetting with setting at 30 μ l, avoid bubbles and spin down briefly, incubate in PCR instrument at 37 °C for 15 min at least.

12. Prepare M280 beads for immobilization of ligated products

12.1. Prepare M280 beads (Thermo Fisher Scientific, 11205D): take 40 μ l of M280 (for 2 samples), wash with 200 μ l of 1 \times B&W buffer twice.

Wash step: suspend the M280 beads with pipette, spin down briefly, then put on the tube on magnetic rack, rinse the tip in the supernatant for 5 times, keep the tube staying on magnetic rack for 30 sec, then remove the supernatant

| 1 \times B&W buffer (10 ml) | | |
|-------------------------------|---------------------|-----------------|
| Component (Stock) | Final concentration | Amount for 10ml |
| 1M Tris-HCl pH 7.0 | 5 mM | 0.025 |
| 1M Tris-HCl pH 8.0 | 5 mM | 0.025 |
| 5M NaCl | 1 M | 2 |
| 0.5M EDTA | 0.5mM | 0.01 |
| Water (Molecular Grade) | | 7.94 |

12.2. Resuspend beads in 200 μ l of iBlock Buffer, mix and incubate at RT from 45 min on rotating Intelli-Mixer (F1,12).

12.3. Briefly spin down and keep the tube on magnetic rack for about 15 min, remove the iBlock buffer, then wash beads with 500 μ l of 2 \times B&W buffer twice.

| 2 \times B&W buffer (10 ml) | | |
|-------------------------------|---------------------|-----------------|
| Component (Stock) | Final concentration | Amount for 10ml |
| 1M Tris-HCl pH 7.0 | 5 mM | 0.05 |
| 1M Tris-HCl pH 8.0 | 5 mM | 0.05 |
| 5M NaCl | 1 M | 4 |
| 0.5M EDTA | 0.5mM | 0.02 |
| Water (Molecular Grade) | | 5.88 |

12.4. Add 100 μ l 2 \times B&W buffer to suspend the M280 beads, then add 100 μ l of genomic DNA mixture (around 1,000 ng), mix well with the iBlocked beads, then incubate on Intelli-Mixer with rotation for at least 30 min (UU 50rpm) at RT for at least 30 min.

12.5. Briefly spin down the tube and place tube on magnetic rack for 15 min, discard iBlock buffer, and then wash beads with 200 μ l of 1 \times B&W buffer twice.

Wash step: add 200 μ l of 1 \times B&W, mix by pipette, and then rotate at RT with program (uu 70 rpm) for 2~5min, then place on magnetic rack, discard the supernatant.

12.6. Add 40 μ l of 1 \times B&W buffer and stay on RT, aliquot to 2 tubes for 2 samples (20 μ l per tube).

13. Immobilization of DNA to streptavidin dynabeads

13.1. Remove the remaining buffer in M280 beads, add 50 μ l of 2 \times B&W buffer, transfer all the 50 μ l of fragmented DNA library product from PCR tube to the M280 beads, then rinse the PCR tube with 55 μ l 1 \times B&W buffer, and collect them to M280 beads. Mix well and incubate on Intelli-Mixer at RT for 45min (UU, 50 rpm).

13.2. Briefly spin down the tube, place the tube on magnetic rack, discard supernatant, wash beads with 500 µl of 0.5% SDS/ 2× SSC buffer at 37 °C for five times.

Wash step: rotating the tube at 37°C for 5 min with program (F8 30 rpm, uu 20 rpm, UU 30 rpm), Buffer was pre-warmed at 37°C.

0.5% SDS/ 2× SSC

| Wash buffer | Volume (10 ml) | Stock conc. | Catalog | Company |
|--------------------|----------------|-------------|---------|---------------|
| 2 × SSC | 1 ml | 20% | AM9770 | Thermo Fisher |
| 0.5% SDS | 0.5 ml | 10% | AM9823 | Thermo Fisher |
| ddH ₂ O | 8.5 ml | - | AM9932 | Thermo Fisher |

13.3. Add 500 µl of 1× B&W buffer, rotate at 37°C for 5 min (F8, 30 rpm, uu 20, UU 30) and discard the supernatant. Then add 200 µl of 1× B&W buffer, rotate at 37 °C for 5 min (UU50). Place the tube on the magnetic rack for 1 min, then use 200 µl-pipet to mix the buffer on the bottom of tube to allow all the beads attaching to the wall of tubes. Then discard the supernatant. Add 30 µl of EB buffer to the beads and store at -20°C.

14. PCR amplification of M280 enriched DNA

14.1. Prepare PCR reaction (according to the manual of Vazyme TD501 kit)

14.2. Thaw the samples and reagents on ice. All the preparation steps for PCR should be on ice.

14.3. Set up PCR reaction mixture as follow

| Solution Name | Component (Stock) | ×1 (µl) |
|---------------|---------------------------------|---------|
| PCR mix | High-Fidelity 2X PCR Master Mix | 25.00 |
| | PPM (dilute 5 times) | 1 |
| | N5XX (dilute 5 times) | 1 |
| | N7XX (dilute 5 times) | 1 |
| | M280 beads (1/3) | 10 |
| | H2O | 12 |
| | Total | 50.00 |

14.4. Transfer the PCR tubes to PCR machine and set up the program.

| Temperature | Time | Cycles |
|-------------|--------------|--------|
| 105 °C | Heat the lid | |
| 72 °C | 3 min | |
| 98 °C | 30 sec | |
| 98 °C | 15 sec | x |
| 60 °C | 30 sec | |
| 72 °C | 2 min | |
| 72 °C | 5 min | |
| 4 °C | Hold | |

The PCR amplification cycle is important; the more PCR cycles used; the lower complexity of the library obtained. Thus, the optimal number of PCR amplification cycles needs to be determined empirically. Generally, do not perform more than 15 cycles.

15. Purify PCR product using AMPure beads (Beckman Coulter, A63881)

15.1. Transfer the PCR product to a new 1.5 ml-tube. Add 20 µl EB buffer to rinse the PCR tube, then collect the EB buffer to the 1.5 ml-tube and place tube on magnetic rack.

15.2. Transfer the supernatant (about 100 µl) to a new 1.5ml-tube. Add 100 µl (1× volume) of AMPure XP beads (pre-warmed at RT) to the 1.5 ml-tube (details are described as the manual)

15.3. Finally, vacuum samples about 1 min. Then elute the DNA from beads with 12 µl EB buffer.

15.4. DNA quantification by Qubit.

15.5. According to the concentration of purified DNA, the optimal PCR cycle is determined, and the rest sample is amplified for size selection.

| Sample | PCR index | PCR index | Tn5 input | 1/3 PCR cycle | 1/3 Amount (ng) | 1/3 Remained (ng) | 2/3 PCR cycle | Estimated 2/3PCR product (ng) | Estimated all PCR product (ng) |
|--------|-----------|-----------|-----------|---------------|-----------------|-------------------|---------------|-------------------------------|--------------------------------|
| 7sk | N505 | N703 | 34.2ng | 15 | 14.3 | 11.44 | 14 | 14.3 | 25 |
| rox2 | N505 | N704 | 19.6ng | 15 | 7.2 | 5.76 | 15 | 14.4 | 20 |

16. Size selection for sequencing (double size selection with AMPure beads)

- 16.1. Use Ampure XP beads for size selection. Generally, DNA size range of 250~600 bp is suitable for Illumina sequencing.
- 16.2. Take out Ampure XP beads and keep at RT for at least 30 min. Thaw the PCR samples (~50 μ l per tube, 2 tubes) and purified DNA (1/3 of M280-bounded DNA for testing, ~8 μ l) on ice. Spin down the samples briefly.
- 16.3. Combine the PCR product (2 tubes) and purified DNA in a 1.5 ml-tube. Place the tube on magnetic rack for 1 min. Use a new 50 μ l-tip to transfer the 100 μ l of supernatant to a new 1.5 ml-tube and evaluate the volume (in this case, 120 μ l in total).
- 16.4. Add 73.2 μ l (0.61 \times) Ampure XP beads to the above tubes. Vortex 10 times softly. Rotate at RT for 10 min with rotation (F8, 12rpm). Spin down briefly, and place on magnetic rack for 5min. Transfer 193.2 μ l of supernatant to a new tube.
- 16.5. Then add 22.8 μ l (0.8-0.61 \times) Ampure beads to the 193.2 μ l of supernatant, vortex 10 times softly. Rotate at RT for 10 min with rotation (F8, 12rpm). Spin down briefly, and place on magnetic rack for 5 min. Wash the beads with 80% ethanol twice, dry beads by vacuum. Elute DNA from beads with 12 μ l EB buffer for 10 min with rotation (UU 70 rpm), and then obtain 8 μ l of supernatant and transfer to a new tube.
- 16.6. Take 1 μ l for the concentration test by Qubit. And take samples to run Qsep for size distribution analysis (details are refer to the manual of Qsep).

| Samples | Conc. (ng/ μ l) | | | Amount (ng) | | | Remained double-size volume (μ l) | Remained Amount (ng) | | |
|---------|---------------------|---------------------|----------------------|-------------|-------|--------|--|----------------------|-------|--------|
| | Large-(ng/ μ l) | Small-(ng/ μ l) | Double-(ng/ μ l) | Large | Small | Double | | Large | Small | Double |
| 7sk | 0.7 | 0.77 | 0.61 | 7 | 7.7 | 6.1 | 8 | 5.2 | 5.7 | 4.88 |
| rox2 | 0.42 | 0.54 | 0.46 | 4.2 | 5.4 | 4.6 | 8 | 3.1 | 4 | 3.68 |

**The Qsep profile of the size distribution should be at length of 250~ 600 bp. In addition, 10~30 ng of library would be obtained.*

- 16.7. The double size selected library is ready for Illumina Novaseq sequencing with length of 2 \times 150 bp.

Attach: Time schedule for RDD experiments

| Time Schedule | | In Solution RDD Experiments | Time course |
|---------------|-------------|--|-------------|
| DAY 1 | 08:50-12:00 | Thaw cells on ice | 60 min |
| | | Wash cells in DPBS | 15 min |
| | | Cell lysis | 15 min |
| | | Nucleus lysis | 25 min |
| | | Repeat nuclei lysis | 25 min |
| | | Wash nuclei | 20 min |
| | 13:00-18:30 | Aliquot nuclei to Falcon tube | 10 min |
| | | Sonication | 250 min |
| | | Preclear chromatin with C1 beads | 20 min |
| | | Prepare for Hybridization | 20 min |
| | | Hybridization overnight | O/N |
| DAY 2 | 09:00-11:00 | Block C1 beads with iBlock buffer | 60 min |
| | | Immobilize chromatin to C1 beads | 150 min |
| | 13:30-20:30 | Transfer C1 beads bounded chromatin to 1.5 ml-tube | 40 min |
| | | Wash C1 beads | 40 min |
| | | Prepare denatured IPB | 40 min |
| | | Block C1 beads with denatured IPB | 20 min |
| | | Wash C1 beads with TE buffer | 40 min |
| | | On beads end repair | 60 min |
| | | Wash beads | 15 min |
| | | A-tailing | 60 min |
| | | Prepare reaction for proximity ligation | 30 min |
| | | Ligation overnight | O/N |
| DAY 3 | 14:30-16:00 | Wash beads | 60 min |
| | | Decrosslinking overnight | O/N |
| DAY 4 | 14:30-15:30 | DNA purification (Part A) | 40 min |
| DAY 5 | 10:00-16:00 | DNA purification (Part B) | 120 min |
| | | Qsep test | 30 min |
| | | Qubit test | 30 min |
| DAY 6 | 09:00-11:30 | Tn5 testing | 120 min |
| | | Proximity ligation product tagmentation | 30 min |
| | 13:30-21:00 | Prepare streptavidin dynabeads M280 | 120 min |
| | | Immobilization of DNA to M280 | 60 min |
| | | Wash M280 beads | 120 min |
| | | PCR cycle test (use 1/3 M280 bounded DNA) | 60 min |
| | | Purify PCR product using AMPure beads | 60 min |
| | | DNA quantification by Qubit | 30 min |
| DAY 7 | 09:30-11:00 | PCR amplification (2/3 M280 bounded DNA) | 90 min |
| | 14:00-17:00 | Double size selection | 180 min |