Dovetail® LinkPrep™ Kit
USER GUIDE - For Non-Mammals

Version 2.0

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Dovetail® LinkPrep™ Kit Components and Storage

Note: The tube label indicates the volume sufficient for 8 reactions, however the volume supplied in the tube includes an overage to account for pipetting carryover.

LinkPrep™ Proximity Core 4°C

Components	Volume	Storage
10X Wash Buffer	15 mL	2°C to 8°C
Chromatin Capture Beads	1,200 µL	
Fragmentation Stop	8 µL	
Crosslink Reversal Buffer	800 µL	
Nuclei Prep Buffer	800 µL	

LinkPrep™ Proximity Core -20° C

Components	Volume	Storage
Fragmentation Enzyme Mix	20 µL	-30°C to - 10°C
4X Fragmentation Buffer	100 µL	
Proximity Ligation 1 Enzyme Mix	20 µL	
5X Proximity Ligation 1 Buffer	80 µL	
Proximity Ligation 2 Enzyme Mix	48 µL	
5X Proximity Ligation 2 Buffer	80 µL	
Proteinase K	24 µL	

LinkPrep™ Library Module for Illumina

Components	Volume	Storage
Library Prep 1 Enzyme Mix	12 µL	-30°C to - 10°C
5X Library Prep 1 Buffer	80 µL	
Library Prep 2 Enzyme Mix	8 µL	
2X Library Prep 2 Buffer	400 µL	
Library Prep 3 Enzyme Mix	20 µL	
HotStart PCR Ready Mix	200 µL	

LinkPrep™ Primer Module Set #1

Components	Volume	Storage
i5 Index Primer 1	30 µL	-30°C to - 10°C
i5 Index Primer 2	30 µL	
i5 Index Primer 3	30 µL	
i5 Index Primer 4	30 µL	
i7 Index Primer 1	20 µL	
i7 Index Primer 2	20 µL	
i7 Index Primer 3	20 µL	
i7 Index Primer 4	20 µL	
i7 Index Primer 5	20 µL	
i7 Index Primer 6	20 µL	

Dovetail® Cell Isolation Module

Components	Volume/Mass	Storage
Cell Isolation Enzyme Mix (powder)	45 mg	2°C to 8°C*
Reconstitution Buffer	1,700 µL	
100mM $CaCl_2$	200 µL	

***Once reconstituted, store the Cell Isolation Enzyme Mix at -20°C.**

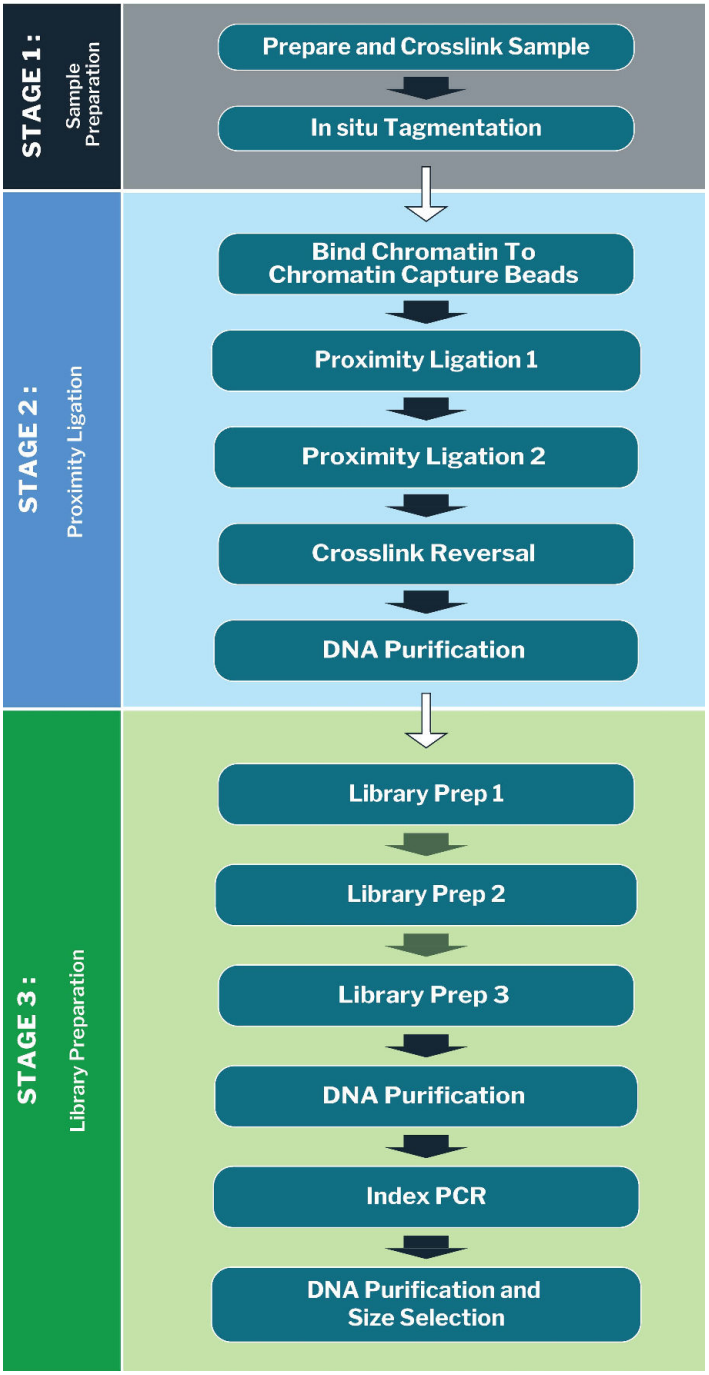
User Supplied Reagents, Consumables and Equipment

Reagents

Reagent	Supplier	Part Number
SPRIselect® Beads, 5 mL	Beckman Coulter	B23317
37% Formaldehyde Solution	Sigma-Aldrich	F8775
1X PBS, pH 7.4, 500 mL	Thermo Fisher Scientific	10010023
100% EtOH	Generic	N/A
UltraPure™ DNase / RNase-Free Distilled Water, 500 mL	Thermo Fisher Scientific	10977015
DSG (Disuccinimidyl Glutarate)	Thermo Fisher Scientific	A35392
DMSO (Dimethyl Sulfoxide, Anhydrous ≥ 99.99%)	Sigma-Aldrich	276855-100ML
TE Buffer pH 8.0	Thermo Fisher Scientific	AM9849
10% Triton X-100	Thermo Fisher Scientific	85111

Consumable/Equipment	Supplier	Part Number
1.5 mL Low binding microcentrifuge tubes	Generic	
0.2 mL PCR tubes		
Pipets and pipet tips		
Magnetic separation rack for 0.2 mL and 1.5 mL tubes		
Agitating thermal mixer		
Thermal cycler		
Vortex mixer		
Centrifuge for 0.2 mL and 1.5 mL tubes		
Hemocytometer		
Swinging bucker rotor		
MiniStrainer 70 µm mesh	pluriSelect	43-10070-46
Qubit® Fluorometer	Thermo Fisher Scientific	Q33226
Qubit® dsDNA HS Assay Kit	Thermo Fisher Scientific	Q32854
Qubit® Assay tubes	Thermo Fisher Scientific	Q32856
TapeStation System (Fragment Analyzer or Bioanalyzer)	Agilent	Various

Dovetail® LinkPrep™ Protocol Overview



Good Practices

- Read the entire guide before use, including Before You Begin and the Notes.
- The sample input amount will influence the efficiency of the fragmentation reaction. Refer to the input amounts recommended in the User Guide.
- **Ensure the centrifuge is set to 500 x g or 500 x rcf (NOT rpm).**
- To ensure efficient crosslinking, a new or recently opened solution of formaldehyde should be used. Formaldehyde solution containing white precipitates should not be used.
- Keep all enzymes and master mixes on ice during setup and use. Promptly move reagents back to the indicated storage.
- Fully thaw buffers, place on ice and thoroughly mix before use.
- Always add the reagents to the master mix in the specified order throughout the protocol.
- When preparing master mixes, scale the volume of each reagent as appropriate, using 10% excess volume to compensate for pipetting loss.
- When working with beads, such as Chromatin Capture, you should:
    a. Equilibrate the beads to room temperature before use.
    b. Thoroughly vortex the beads immediately before use and ensure they are a homogeneous slurry.
    c. After placing the tube in the magnetic rack, always wait until the solution looks clear before removing the supernatant carefully and slowly to allow the beads to fully separate. This helps minimize bead/ sample loss throughout the protocol.
    d. Do not let the beads dry out during washing steps. Keep the beads in buffer until ready to resuspend them for the next step.
    e. After washing the SPRIselect beads with 80% ethanol during DNA purification, do not let the beads over-dry before proceeding with elution. Over-drying the beads may result in lower recovery of DNA.
- Cantata Bio's list of validated sample types includes, but is not limited to:

Validated non-mammalian samples
Fish
Insects
Marine worms
Mollusks
Cnidarians
Crustaceans

Things To Consider

- We recommend shallow sequencing the Dovetail® LinkPrep™ library to run a QC analysis prior to deep sequencing to determine the long-range information and complexity in the library. While recommended, the shallow sequencing for QC analysis is not required. The QC assessment is based on shallow sequenced data (1M - 10M read pairs 2 x 150 bp) generated by a **MiSeq or MiniSeq** platform. If you don't have access to a MiSeq or MiniSeq, you can shallow sequence the library on an alternative platform to assess mappability and long-range information. However, you may not be able to accurately assess the duplication rate. The kit is accompanied by a QC analysis pipeline, which is documented on readthedocs and accessible to all users of the kit. Click on the links below to access the QC analysis pipeline that corresponds to your application of interest.
    - **Genome Assembly**, click here
    - **3D Genomics**, click here
    - **Somatic Variant Detection**, click here

- Each library can be sequenced up to 300M read pairs (2 x 150 bp). The depth and number of libraries depend on the application of interest. The tables below list recommendations for the genomic coverage, sequencing depth and number of libraries for each of the kit supported applications.

    - **Genome Assembly:**

Genome Size	Genomic Coverage	# of Read Pairs (2 x 150 bp)	# of Libraries
≤ 3 Gb	30X	≤300 Million	1
3 - 6 Gb	30X	300 - 600 Million	2
6 - 9 Gb	30X	600 - 900 Million	3
> 9 Gb	30X	> 900 Million	> 3

    - **3D Genomics:**

Topological Feature	Genomic Coverage	# of Read Pairs (2 x 150 bp)	# of Libraries
A/B Compartments	10X	100 Million	1
TADs	30X	300 Million	1
Loops	80X	800 Million	3

    - **Somatic Variant Detection:**

Variant*	Tumor Fraction	Genomic Coverage	# of Read Pairs (2 x 150 bp)	# of Libraries
SVs	>50%	10X	100 Million	1
SVs, SNVs, Indels, CNVs	>50%	30X	300 Million	1
SVs	20-50%	30X	300 Million	1
SVs, SNVs, Indels, CNVs	20-50%	80X	800 Million	3

*Detection of Low VAF events are dependent on sequence depth

- You can prepare multiple libraries (up to 3) from the proximity ligated DNA recovered at the end of Stage 2: Proximity Ligation. If you plan to generate multiple libraries from the proximity ligated DNA recovered at the end of Stage 2 to support your application of interest, split the Stage 2 DNA evenly between library preps. **We recommend a minimum input of 150 ng per library.**

Stage 1A: Sample Preparation - Fresh Frozen Non-Mammalian Animal Tissues

As you prepare for Stage 1, keep the following in mind:

- Tissue sample preparation takes ~ 2 hours.

Before You Begin

- The 10X Wash Buffer and Fragmentation Stop might have precipitated in storage. **Incubate these solutions at 50°C for 15 minutes** or until the precipitate is no longer visible. Vortex to mix prior to use.
- **Dilute the 10X Wash Buffer to 1X** with UltraPure™ Water. Store at room temperature. 1X Wash Buffer is stable at room temperature for 2 months. You need ~2 mL of 1X Wash Buffer per sample for the entire protocol.
- **Prepare 0.3 M DSG in DMSO** (anhydrous) by dissolving 1 mg of DSG in 10.22 µL DMSO. DSG is water-insoluble and moisture-sensitive. Prepare immediately before use. Do not store DSG in solution.
- **Check out this video which showcases proper grinding and correct consistency of the ground tissue in step 2.**
- **Prewarm the Nuclei Prep Buffer at 62°C for 10 minutes before use.** Make sure there is no precipitate visible. Vortex to mix prior to use.
- If working with multiple samples, you may choose **step 11 as a SAFE HOLD** step to enable you to proceed with processing the samples in parallel for the remaining steps.
- **Reconstitute Cell Isolation Enzyme Mix** as follows: on ice, transfer 850 µL of Reconstitution Buffer to the tube containing Cell Isolation Enzyme Mix powder. Pipet up and down to mix. Transfer an additional 800 µL of Reconstitution Buffer, so the powder is now resuspended in a total of 1,650 µL buffer. Pipet up and down to mix. Incubate on ice for 30 minutes. Pipet mix again before use. **Reconstituted Cell Isolation Enzyme Mix should be stored at -20°C. It is stable for 1 year after reconstitution. Thaw reconstituted cell isolation enzyme mix on ice as it is temperature sensitive. To expedite thawing, Reconstituted Cell Isolation Enzyme Mix may be aliquoted into single use 50 µL aliquots in 1.5 mL tubes and stored at -20°C.**

Follow the steps below for Sample Preparation:

1. Weigh 10 mg - 20 mg of frozen tissue.

> NOTE Expected lysate amounts vary between tissues and organisms. For some samples, 5 mg of tissue generates sufficient lysate quantities to proceed through Stage 2.

2. Disrupt the tissue by grinding it to a **fine powder** with a mortar and pestle **in liquid nitrogen**.
3. Transfer the ground tissue to a 1.5 mL tube.

> NOTES
>
> - You may choose to freeze your ground/disrupted tissue pellet at -80°C at this stage. Otherwise, proceed with the protocol.
> - All crosslinking reactions (steps 5 – 11) should be carried out at room temperature.

4. Resuspend the tissue pellet in 1 mL of 1X PBS and pipet up and down to ensure no clumps are present.
5. Add 10 µL of 0.3 M DSG. Pipet to mix.
6. Rotate the tube for 10 minutes at room temperature. Sample should not settle.
7. Add 27 µL of 37% formaldehyde.
8. Rotate the tube for 10 minutes at room temperature. Sample should not settle.
9. Spin the tube at 500 x g for 5 minutes in a swinging bucket rotor. Carefully remove and discard the supernatant, taking care not to disturb the pellet. To minimize cell loss, remove the supernatant SLOWLY from the TOP DOWN, using a P200 pipette.

NOTES

- The centrifugation steps must be carried out in a **swinging bucket rotor**. Using a swinging bucket rotor reduces cell loss and generates the expected QC results.
- **To minimize cell loss, remove the supernatant SLOWLY from the TOP DOWN, using a P200 pipette.**
- If the sample does not seem to pellet, increase the speed to 1,000 x g throughout the preparation. If still not pelleting, increase the speed to 2,500 x g.

10. Wash the tissue pellet with 500 µL of 1 X Wash Buffer, pipet up and down to break up clumps and fully resuspend the pellet.

NOTE **If working with insects,** filter the sample through a 70 µm MiniStrainer. Place a MiniStrainer in a 1.5 mL 1.5 mL microfuge tube. Pipet the sample (resuspended in Wash Buffer) into the MiniStrainer. Quick spin at 500 x g for 5 seconds. Debris should be retained in the filter and discarded. You will proceed to step 11 with the filtrate collected in the tube.

11. Spin the tube at 500 *x* g for 5 minutes in a swinging bucket rotor. Carefully remove and discard the supernatant, taking care not to disturb the pellet.

NOTES

- **To minimize cell loss, remove the supernatant SLOWLY from the TOP DOWN, using a P200 pipette.**
- This is a SAFE HOLD step: after discarding the supernatant, you can leave your tube on ice if you need to continue processing other samples before moving to step 12 with all samples in parallel.

12. Resuspend the pellet in 100 µL Nuclei Prep Buffer, pipet up and down to break up clumps and fully resuspend the pellet.
13. Incubate the tube in a thermal mixer WITHOUT SHAKING as follows:

Temperature	Time
62°C	10 minutes

14. Spin the tube at 500 *x g* for 5 minutes in a swinging bucket rotor. Carefully remove and discard the supernatant, taking care not to disturb the pellet.

NOTE **To minimize cell loss, remove the supernatant SLOWLY from the TOP DOWN, using a P200 pipette.**

15. Resuspend the pellet in 52.5 µL of the fragmentation master mix containing the following reagents **added in the order listed:**

Reagent	Volume Per Reaction
UltraPure Water	37.5 µL
4X Fragmentation Buffer	12.5 µL
Fragmentation Enzyme Mix	2.5 µL
Total	**52.5 µL**

16. Pipet up and down to fully mix. Incubate the tube in a thermal mixer WITHOUT SHAKING as follows:

Temperature	Time
55°C	20 minutes

NOTE Precipitation may occur during this reaction, this is normal.

17. Quick spin the tube. Stop the reaction by adding 1 µL of **Fragmentation Stop**. **Pipet the entire volume up and down to fully mix**.
18. Incubate the tube in the thermal mixer WITHOUT SHAKING as follows:

Temperature	Time
65°C	5 minutes

19. Quick spin the tube. Add 6 µL of 10% Triton. **Pipet the entire volume up and down to fully mix.**
20. Incubate the tube on benchtop (at room temperature/no shaking) for 5 minutes. This tube now contains your **LYSATE**.
21. Aliquot 2.5 µL of the sample into a new tube labeled QC tube and **store at -80°C**. Proceed with the rest of your sample to Proximity Ligation (Stage 2).

NOTE The QC tube containing the 2.5 µL aliquot can be stored at -80°C for 6 months and used in troubleshooting, if needed.

Stage 1B: Sample Preparation - Fresh Frozen Plant Leaves

As you prepare for Stage 1, keep the following in mind:

- Tissue sample preparation takes ~ 2 hours.

Before You Begin

- The 10X Wash Buffer and Fragmentation Stop might have precipitated in storage. **Incubate these solutions at 50°C for 15 minutes** or until the precipitate is no longer visible. Vortex to mix prior to use.
- **Dilute the 10X Wash Buffer to 1X** with UltraPure™ Water. Store at room temperature. 1X Wash Buffer is stable at room temperature for 2 months. You need ~2 mL of 1X Wash Buffer per sample for the entire protocol.
- **Prepare 0.3 M DSG in DMSO** (anhydrous) by dissolving 1 mg of DSG in 10.22 µL DMSO. DSG is water-insoluble and moisture-sensitive. Prepare immediately before use. Do not store DSG in solution.
- **Prewarm the Nuclei Prep Buffer at 62°C for 10 minutes before use**. Make sure there is no precipitate visible. Vortex to mix prior to use.
- **Check out this video which showcases the correct consistency of the ground tissue in step 2.**
- If working with multiple samples, you may choose **step 12 as a SAFE HOLD** step to enable you to proceed with processing the samples in parallel for the remaining steps.

Follow the steps below for Sample Preparation:

1. Weigh 30 mg of frozen leaves.
2. Disrupt the tissue by grinding it to a **fine powder** with a mortar and pestle **in liquid nitrogen**.
3. Transfer the ground tissue to a 1.5 mL tube.

NOTES

You may choose to freeze your ground/disrupted tissue pellet at -80°C at this stage. Otherwise, proceed with the protocol.

All crosslinking reactions (steps 5 – 12) should be carried out at room temperature.

4. Resuspend the tissue pellet in 1 mL of 1X PBS at room temperature and pipet up and down using **wide bore pipet tips** to ensure no clumps are present.
5. Add 10 µL of 0.3 M DSG. Pipet to mix.
6. Rotate the tube for 10 minutes at room temperature. Sample should not settle.
7. Add 27 µL of 37% formaldehyde.
8. Rotate the tube for 10 minutes at room temperature. Sample should not settle.
9. Spin the tube at 1,000 x g for 5 minutes in a swinging bucket rotor. Carefully remove and discard the supernatant. **To minimize cell loss, remove the supernatant SLOWLY from the TOP DOWN, using a P200 pipette**. Be careful to not disturb the pellet.

NOTES

- The centrifugation steps must be carried out in a **swinging bucket rotor**. Using a swinging bucket rotor reduces cell loss and generates the expected QC results.

10. Resuspend the tissue pellet with 700 µL of 1 X Wash Buffer, pipet up and down with **wide bore pipet tips** to break up clumps and fully resuspend the pellet.

11. Filter your sample through a 70 µm MiniStrainer. Place a MiniStrainer in a 1.5 mL microfuge tube. Pipet the sample (resuspended in Wash Buffer) into the MiniStrainer. Quick spin for 5 seconds. Debris should be retained in the filter and discarded. You will proceed to step 12 with the filtrate collected in the tube.

12. Spin the tube at 1,000 *x g* for 5 minutes in a swinging bucket rotor. Carefully remove and discard the supernatant, taking care not to disturb the pellet.

NOTES

- Minimizing cell loss during sample preparation is important to the success of the assay. To minimize cell loss, remove the supernatant SLOWLY from the TOP DOWN, using a P200 pipette.

- Step 12 is a SAFE HOLD step: after discarding the supernatant, you can leave your tube on ice if you need to continue processing other samples before moving to step 13 with all samples in parallel.

13. Resuspend the pellet in 100 µL Nuclei Prep Buffer, pipet up and down to break up clumps and fully resuspend the pellet.
14. Incubate the tube in a thermal mixer WITHOUT SHAKING as follows:

Temperature	Time
62°C	10 minutes

15. Spin the tube at 1,000 *x g* for 5 minutes in a swinging bucket rotor. Carefully remove and discard the supernatant. Be careful to not disturb the pellet.

NOTE **To minimize cell loss, remove the supernatant SLOWLY from the TOP DOWN, using a P200 pipette.**

16. Resuspend the pellet in 52.5 µL of the fragmentation master mix containing the following reagents **added in the order listed:**

Reagent	Volume Per Reaction
UltraPure Water	37.5 µL
4X Fragmentation Buffer	12.5 µL
Fragmentation Enzyme Mix	2.5 µL
Total	**52.5 µL**

17. Pipet up and down to fully mix. Incubate the tube in a thermal mixer WITHOUT SHAKING as follows:

Temperature	Time
55°C	20 minutes

NOTE Precipitation may occur during this reaction, this is normal.

18. Quick spin the tube. Stop the reaction by adding 1 µL of **Fragmentation Stop**. **Pipet the entire volume up and down to fully mix**.
19. Incubate the tube in the thermal mixer WITHOUT SHAKING as follows:

Temperature	Time
65°C	5 minutes

20. Quick spin the tube. Add 6 µL of 10% Triton. **Pipet the entire volume up and down to fully mix.**
21. Incubate the tube on benchtop (at room temperature/no shaking) for 5 minutes. This tube now contains your **LYSATE**.
22. Mix well then aliquot 2.5 µL of the sample into a new tube labeled QC tube and **store at -80°C**. Proceed with the rest of your sample to Proximity Ligation (Stage 2).

N O T E The QC tube containing the 2.5 µL aliquot can be stored at -80°C for 6 months and used in troubleshooting, if needed.

Stage 2: Proximity Ligation

As you prepare for Stage 2, keep the following in mind:

- Proximity ligation takes ~ 1.5 hour.
- Follow best practices when working with beads (see Good Practices). The below protocol uses 0.2 mL strip tubes and corresponding magnetic rack. However, the below protocol is compatible with 1.5 mL tubes and corresponding magnetic rack.

Before You Begin

- Equilibrate Chromatin Capture Beads to room temperature.
- The Crosslink Reversal Buffer might have precipitated in storage**. Incubate at 50°C for 15 minutes** or until the precipitate is no longer visible. Vortex prior to use.
- Thaw 5X Proximity Ligation 1 Buffer and 5X proximity Ligation 2 Buffer at room temperature. Leave on ice once thawed. Vortex to mix prior to use.

2.1 Bind Chromatin to Chromatin Capture Beads

Follow the steps below for Binding Chromatin to Chromatin Capture Beads:

1. Equilibrate the Chromatin Capture Beads to room temperature and vortex thoroughly (>30 seconds) to resuspend.
2. Transfer 100 µL of resuspended Chromatin Capture Beads to a **new** 0.2 mL PCR tube.
3. Add your lysate to the Chromatin Capture Beads aliquoted above.
4. Pipet up and down to fully mix. Incubate at room temperature, off the magnetic rack, for 10 minutes.
5. Place the tube in the magnetic rack for 5 minutes (or until the solution looks clear). Discard the supernatant.
6. Remove the tube from the magnetic rack and wash the beads with 150 µL 1X Wash Buffer. Pipet up and down to resuspend the beads, place the tube in the magnetic rack for 1 minute and discard the supernatant.
7. Remove the tube from the magnetic rack and resuspend the beads in 150 µL 1X Wash Buffer. Pipet up and down to fully resuspend the beads. **Leave the tube on the bench while you prepare for the next reaction.**

2.2 Proximity Ligation 1

Follow the steps below for Proximity Ligation 1:

1. Prepare the proximity ligation 1 master mix containing the following reagents **added in the order listed**:

Reagent	Volume Per Reaction
UltraPure Water	40 µL
5X Proximity Ligation 1 Buffer	10 µL
Proximity Ligation 1 Enzyme Mix	2.5 µL
Total	**52.5 µL**

2. Place the tube from step 7 in Stage 2.1 in the magnetic rack for 1 minute (or until the solution looks clear). Discard the supernatant and immediately proceed to the next step (**do not let the beads dry out**).
3. Remove the tube from the magnetic rack and **immediately** add to the beads 52.5 µL of the proximity ligation 1 master mix.

4. Pipet up and down to fully mix. Incubate in an agitating thermal mixer set at 1,500 rpm as follows:

Temperature	Time
25°C	15 minutes

5. Quick spin the tube and place the tube in the magnetic rack for 1 minute (or until the solution looks clear). Discard the supernatant.
6. Remove the tube from the magnetic rack and resuspend the beads in 150 µL 1X Wash Buffer. Pipet up and down to fully resuspend the beads. **Leave the tube on the bench while you prepare for the next reaction.**

2.3 Proximity Ligation 2

Follow the steps below for Proximity Ligation 2:

1. Prepare the proximity ligation 2 master mix containing the following reagents **added in the order listed**:

Reagent	Volume Per Reaction
UltraPure Water	40 µL
5X Proximity Ligation 2 Buffer	10 µL
Proximity Ligation 2 Enzyme Mix	6 µL
Total	**56 µL**

2. Place the tube from step 6 in Stage 2.2 in the magnetic rack for 1 minute (or until the solution looks clear). Discard the supernatant and immediately proceed to the next step (**do not let the beads dry out**).
3. Remove the tube from the magnetic rack and **immediately** add to the beads 56 µL of the proximity ligation 2 master mix.
4. Pipet up and down to fully mix. Incubate in an agitating thermal mixer set at 1,500 rpm as follows:

Temperature	Time
37°C	15 minutes

5. Quick spin the tube and place the tube in the magnetic rack for 1 minute (or until the solution looks clear). Discard the supernatant.

2.4 Crosslink Reversal

Follow the steps below for Crosslink Reversal:

1. Remove the tube from the magnetic rack and add to the beads 51.5 µL of a master mix containing the following reagents **added in the order listed**:

Reagent	Volume Per Reaction
Crosslink Reversal Buffer	50 µL
Proteinase K	1.5 µL
Total	**51.5 µL**

2. Pipet up and down to fully mix. Incubate in an agitating thermal mixer set at 1,500 rpm as follows:

Temperature	Time
78°C	10 minutes
25°C Note: secure the tube lid to prevent opening during incubation.	Hold

3. Quick spin the tube and place it in the magnetic rack for 1 minute. **Transfer 50 µL of the SUPERNATANT** to a new 0.2 mL PCR tube. Discard the beads.

2.5 DNA Purification

Follow the steps below for DNA Purification:

1. Vortex the SPRIselect beads thoroughly (>30 seconds) to resuspend.
2. Add 90 µL of resuspended SPRIselect beads to the 0.2 mL PCR tube containing your sample.
3. Vortex to mix thoroughly. Quick spin the tube (make sure to spin down only briefly and to stop before the beads start to settle).
4. Incubate the tube at room temperature, off the magnetic rack, for 5 minutes.
5. Quick spin the tube and place it in the magnetic rack for 5 minutes. Discard the supernatant.
6. Leave the tube in the magnetic rack and wash the beads **twice** with 200 µL fresh 80% ethanol. Do not resuspend the beads for these washes. Add the ethanol, wait for 1 minute then discard the ethanol supernatant.
7. After the last wash, quick spin the tube and place it in the magnetic rack for 1 minute. Use a 10 µL pipet tip to remove all traces of ethanol.
8. Air dry the beads for 3 minutes in the magnetic rack until no residual ethanol remains. **Do not over dry the beads**.
9. Off the magnetic rack, resuspend the beads in 42 µL TE Buffer pH 8.0.
10. Vortex to mix thoroughly. Quick spin the tube (make sure to spin down only briefly and to stop before the beads start to settle).
11. Incubate at room temperature, off the magnetic rack, for 2 minutes.
12. Quick spin the tube and place it in the magnetic rack for 1 minute.
13. **Transfer** 40 µL of the **SUPERNATANT** (purified DNA) to a new tube. Discard the beads.
14. Quantify the purified DNA using a Qubit Fluorometer and Qubit dsDNA HS Kit.

- We expect a yield ≥ 150 ng.
- If the yield you recover is **≥ 150 ng**, proceed to Library Preparation (Stage 3).
- If the yield you recover is **< 150 ng**, you should expect a lower complexity library which may be insufficient to support sequencing up to 300M read pairs. You have the following options:

  1. Continue with the Library Preparation (Stage 3), generate a library and shallow sequence it for QC analysis (see QC Analysis & Sequencing) to assess if the library you generated has sufficient complexity to support sequencing up to 300M read pair depth or if additional library is needed .
  2. Perform the Lysate QC and determine the lysate yield/your sample chromatin content (Refer to Appendix 2: Troubleshooting Guide For Yields).

SAFE STOP Purified DNA sample can be stored at -20°C for up to 6 months.

Stage 3: Library Preparation

As you prepare for Stage 3, keep the following in mind:

- The library preparation protocol does not require sonication.
- The library preparation protocol takes ~ 3 hours.
- Follow best practices when working with beads (see Good Practices)

Before You Begin

- Thaw 5X Library Prep 1 Buffer, 5X Library Prep 2 Buffer, HotStart PCR Ready Mix and Primers at room temperature. Leave on ice once thawed. Mix by inversion and quick spin prior to use.

NOTES

- The protocol from here onwards is per **1 LIBRARY** prep. If you are preparing more than 1 library simultaneously, scale the reactions proportional to the number of libraries.
- The number of libraries needed per sample depends on the application of interest. **Refer to Things To Consider (page 9) for recommendations regarding the number of libraries per application.**
- If you plan to generate multiple libraries (up to 3) from the proximity ligated DNA recovered at the end of Stage 2 to support your application of interest, split the Stage 2 DNA evenly between library preps. **We recommend a minimum input of 150 ng per library.**
- LinkPrep Library Module **must be used** for library preparation. Other library preparation kits are **NOT** compatible.

3.1 Library Prep 1

Follow the steps below for Library Prep 1:

1. Place **up to 1,000 ng of purified DNA** from step 13 Stage 2.5 in a new 0.2 mL PCR tube and bring the volume to 40 µL with UltraPure Water.

2. Add to the tube the following reagents **in the order listed**:

Reagent	Volume Per Reaction
5X Library Prep 1 Buffer	10 µL
Library Prep 1 Enzyme Mix	1.5 µL
Total	**11.5 µL**

3. Pipet up and down to fully mix. Incubate in a thermal cycler as follows (lid at 75°C):

Temperature	Time
25°C	15 minutes
68°C	15 minutes

3.2 Library Prep 2

Follow the steps below for Library Prep 2:

1. Quick spin the tube. To the tube containing the reaction from library prep 1, add the following reagents **in the order listed:**

Reagent	Volume Per Reaction
2X Library Prep 2 Buffer	50 µL
Library Prep 2 Enzyme Mix	1 µL
Total	**51 µL**

2. Pipet up and down to fully mix. Incubate in a thermal cycler as follows (lid at 75°C):

Temperature	Time
25°C	15 minutes

3.3 Library Prep 3

Follow the steps below for Library Prep 3:

1. Quick spin the tube. To the tube containing the reaction from library prep 2, **add 2.5 µL of Lib Prep 3 Enzyme Mix.**

2. Pipet up and down to fully mix. Incubate in a thermal cycler as follows (lid at 75°C):

Temperature	Time
37°C	15 minutes

NOTE Thorough pipet mixing of the sample after addition of the Lib Prep 3 Enzyme Mix is very important. Pipet carefully as the solution is viscous.

3.4 DNA Purification

Follow the steps below for DNA Purification:

1. Vortex the SPRIselect beads thoroughly (>30 seconds) to resuspend.
2. Add 85 µL of resuspended SPRIselect beads to the 0.2 mL PCR tube containing your sample.
3. Vortex to mix thoroughly. Quick spin the tube (make sure to spin down only briefly and to stop before the beads start to settle).
4. Incubate the tube at room temperature, off the magnetic rack, for 5 minutes.
5. Quick spin the tube and place it in the magnetic rack for 5 minutes. Discard the supernatant.
6. Leave the tube in the magnetic rack and wash the beads **twice** with 200 µL fresh 80% ethanol. Do not resuspend the beads for these washes. Add the ethanol, wait for 1 minute then discard the ethanol supernatant.
7. After the last wash, quick spin the tube and place it in the magnetic rack for 1 minute. Use a 10 µL pipet tip to remove traces of ethanol.
8. Air dry the beads for 3 minutes in the magnetic rack until no residual ethanol remains. **Do not over dry the beads**.
9. Off the magnetic rack, resuspend the beads in 16 µL UltraPure Water.
10. Vortex to mix thoroughly. Quick spin the tube (make sure to spin down only briefly and to stop before the beads start to settle).
11. Incubate at room temperature, off the magnetic rack, for 2 minutes.
12. Quick spin the tube and place it in the magnetic rack for 1 minute.
13. **Transfe**r 15 µL of the **SUPERNATANT** (purified DNA) to a new 0.2ml tube. Discard the beads.

SAFE STOP The library can be stored at -20°C for up to 6 months.

3.5 Index PCR

Follow the steps below for Index PCR:

1. Add 25 µL of the HotStart PCR Ready Mix to the tube from step 13 in Stage 3.4.
2. Add 5 µL of i5 Index Primer to the PCR reaction (see Appendix 1: Dual Index Primers).
3. Add 5 µL of i7 Index Primer to the PCR reaction (see Appendix 1: Dual Index Primers).

4. Pipet up and down to fully mix. Quick spin the tube, place the tube into the thermal cycler (lid temp: 105°C) and run the following program:

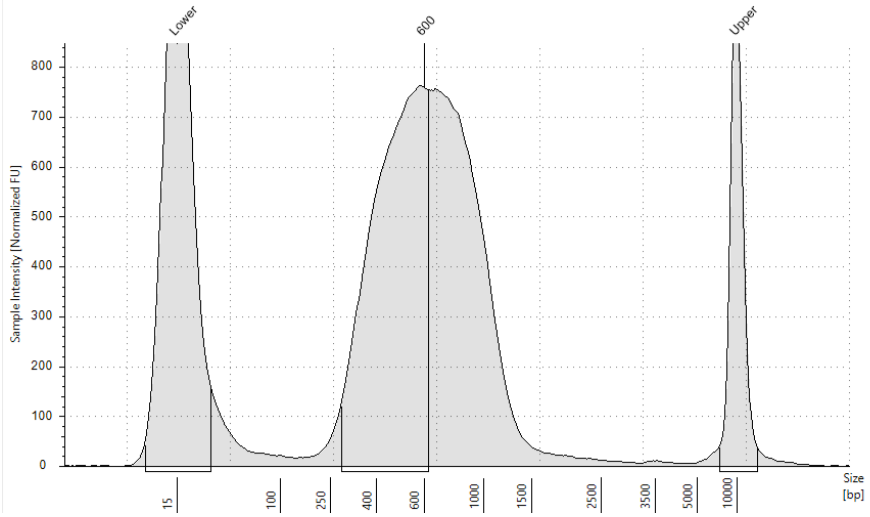
Step	Temperature	Time	Cycles
Enzyme Activation	98°C	3 minutes	1
Denature	98°C	20 seconds	
Anneal	60°C	30 seconds	12
Extend	72°C	30 seconds	
Extend	72°C	1 minute	1
	12°C	Hold	

3.6 Size Selection

Follow the steps below for Size Selection:

1. Quick spin the tube, add 50 µL of TE Buffer pH 8.0 to the tube to bring the volume of the sample in the tube to 100 µL.
2. Vortex the SPRIselect beads thoroughly (>30 seconds) to resuspend.
3. Add 50 µL of resuspended SPRIselect beads to the tube containing your sample.
4. Vortex to mix thoroughly. Quick spin the tube (make sure to spin down only briefly and to stop before the beads start to settle).
5. Incubate the tube at room temperature, off the magnetic rack, for 5 minutes.
6. Quick spin the tube and place it in the magnetic rack for 5 minutes.
7. **Transfer 145 µL of the SUPERNATANT** to a new 0.2 mL PCR tube. Discard the beads.
8. Add 30 µL of resuspended SPRIselect beads to the 0.2 mL PCR tube containing your sample.
9. Vortex to mix thoroughly. Quick spin the tube (make sure to spin down only briefly and to stop before the beads start to settle).
10. Incubate the tube at room temperature, off the magnetic rack, for 5 minutes.
11. Quick spin the tube and place it in the magnetic rack for 5 minutes. Discard the supernatant.
12. Leave the tube in the magnetic rack and wash the beads **twice** with 200 µL fresh 80% ethanol. Do not resuspend the beads for these washes. Add the ethanol, wait for 1 minute then discard the ethanol supernatant.
13. Quick spin the tube and place it in the magnetic rack for 1 minute. Use a 10 µL pipet tip to remove traces of ethanol.
14. Air dry the beads for 3 minutes in the magnetic rack until no residual ethanol remains. **Do not over dry the beads.**
15. Off the magnetic rack, resuspend the beads in 32 µL TE Buffer pH 8.0.
16. Vortex to mix thoroughly. Quick spin the tube (make sure to spin down only briefly and to stop before the beads start to settle).
17. Incubate the tube at room temperature, off the magnetic rack, for 2 minutes.
18. Quick spin the tube and place it in the magnetic rack for 1 minute.
19. **Transfer** 30 µL of the **SUPERNATANT** to a new 0.2 mL PCR tube. The supernatant is your size selected library. Discard the beads.
20. Quantify your size selected library using a Qubit Fluorometer and Qubit dsDNA HS Kit. We expect a final library yield > 200 ng if you used >150 ng input into library preparation. If the yield is < 200 ng, refer to the Troubleshooting Guide For Yields (Appendix 2).
21. Use a TapeStation or Bioanalyzer to verify the size distribution of your size selected library. The size range is expected to be between 350 bp and 1,000 bp (figure 2).

Figure 2. Expected final library profile, as analyzed on HS D5000 ScreenTape



SAFE STOP The library can be stored at -20°C for up to 6 months.

QC Analysis & Sequencing

Dovetail® LinkPrep™ libraries are sequenced via Illumina® sequencers in paired-end mode. Each library can be deep sequenced to 300M read pairs (2 x 150 bp).

The depth and number of libraries depend on the application of interest. Refer to Things to Consider (page 9) for recommendations on the genomic coverage, sequencing depth and number of libraries for each of the kit supported applications.

We recommend shallow sequencing the library to run a QC analysis prior to deep sequencing to determine the long-range information and complexity in the library. While this is recommended, the shallow sequencing for QC analysis is not required. The QC assessment is based on shallow sequenced data (1M - 10M read pairs 2 x 150 bp) generated by a **MiSeq** or **MiniSeq** platform. If you don't have access to a MiSeq or MiniSeq, you can shallow sequence the library on an alternative sequencing platform to assess mappability and long-range information. However, you may not be able to accurately assess the duplication rate and library complexity. The kit is accompanied by a QC analysis pipeline, which is documented on readthedocs and accessible to all users of the kit. Refer to Things to Consider (page 9) to access the QC analysis pipeline that corresponds to your application of interest.

Appendix 1: Dual Index Primers

LinkPrep™ Primer Module Set # 1 includes four i5 index primers and six i7 index primers. **Verify that the indexes selected for pooling have the appropriate color balance for your sequencing instrument.**

NOTE LinkPrep Primer Module Set #1 contains sufficient index primers to support multiplexing up to 24 libraries, where each library is prepared by combining a unique i5 Index Primer with a unique i7 Index Primer in steps 2 and 3 of Stage 3.5 Index PCR. For example, 6 libraries can be prepared by setting up 6 individual PCR reactions as follows:

- Library 1: i5 Index Primer 1 and i7 Index Primer 1
- Library 2: i5 Index Primer 1 and i7 Index Primer 2
- Library 3: i5 Index Primer 1 and i7 Index Primer 3
- Library 4: i5 Index Primer 1 and i7 Index Primer 4
- Library 5: i5 Index Primer 1 and i7 Index Primer 5
- Library 6: i5 Index Primer 1 and i7 Index Primer 6

NOTE Refer to the first page in the following Illumina Guide for how to enter the i5 in forward or reverse complement orientation on the **sample sheet**: https://support-docs.illumina.com/SHARE/AdapterSequences/Content/SHARE/AdapterSeq/Overview.htm#Index.

i5 Index Name	Bases in Adapter	Bases for Sample Sheet in Forward Orientation	Bases for Sample Sheet in Reverse Complement Orientation
i5 Index Primer 1	GCGTAAGA	GCGTAAGA	TCTTACGC
i5 Index Primer 2	CTCTCTAT	CTCTCTAT	ATAGAGAG
i5 Index Primer 3	TATCCTCT	TATCCTCT	AGAGGATA
i5 Index Primer 4	CGTCTAAT	CGTCTAAT	ATTAGACG

i7 Index Name	Bases in Adapter	Bases for Sample Sheet
i7 Index Primer 1	TCGCCTTA	TAAGGCGA
i7 Index Primer 2	CTAGTACG	CGTACTAG
i7 Index Primer 3	TTCTGCCT	AGGCAGAA
i7 Index Primer 4	CAGCCTCG	CGAGGCTG
i7 Index Primer 5	AGGAGTCC	GGACTCCT
i7 Index Primer 6	CATGCCTA	TAGGCATG

Appendix 2: Troubleshooting Guide For Yields

- This guide enables users to troubleshoot:
  - Purified DNA yield (end of Stage 2) < 150 ng.
  - Library yield (end of Stage 3) < 200 ng.

Troubleshooting Purified DNA Yield (End of Stage 2) < 150 ng

Reason: Insufficient input material (used less than recommended starting amount or chromatin content in the sample is low).
Recommendation: Perform the Lysate QC (Appendix 3) to quantity the chromatin content recovered from the sample and check the fragmentation size distribution.

Fragmentation profile *within* specification and lysate yield < 300 ng	Fragmentation profile *outside* of specification and lysate yield < 300 ng
Redo the sample preparation with **double** the input amount. NOTE • You may choose to combine the purified DNA at the end of Stage 2 for library conversion at Stage 3 (refer to Appendix 5 for how to combine samples for library preparation). • You may choose to produce two technical replicate libraries to pool for deep sequencing to 300M read pairs.	Refer to Appendix 4: Troubleshooting Guide For Fragmentation Profile and redo the sample preparation with **double** the input amount.

Troubleshooting Library Yield (End of Stage 3) < 200 ng

Reason	Recommendation
1. You started the library preparation with < 150 ng.	1. Shallow sequence the library and run a QC analysis to assess long-range and complexity. If needed, generate another library to pool for deep sequencing.
2. The chromatin was not properly fragmented.	2. If the sample was under-fragmented, insufficient proximity ligated molecules are available for library conversion. Perform Lysate QC (Appendix 3) and check the fragment size distribution. Refer to Troubleshooting Guide for under-fragmented samples to improve the fragmentation profile.
3. Low proximity ligation efficiency.	3. Besides a user error during the preparation, impurities found in some samples can lower the efficiency of the reactions. Filtering the lysate at the end of Stage 1 through a MiniStrainer before proceeding with proximity ligation can help.

Appendix 3: Lysate QC

- This guide enables users to troubleshoot unexpected yields at Stage 2 or Stage 3 by:
    - Quantifying the lysate yield recovered at the end of sample preparation (Stage 1).
    - Confirming that the chromatin was properly fragmented in Stage 1.
- The QC protocol below is written for the TapeStation; however, it is also compatible with the Bioanalyzer System and Fragment Analyzer. Please refer to the table below for the recommended kits for each system.

System	Recommended Kits
TapeStation	HS D5000
Bioanalyzer System	HS DNA
Fragment Analyzer	DNF-488 HS Genomic DNA

Before You Begin

- The Crosslink Reversal Buffer might have precipitated in storage. **Incubate at 50°C for 15 minutes** or until the precipitate is no longer visible. Vortex prior to use.
- Equilibrate the Chromatin Capture Beads to room temperature.

Follow the steps below for Lysate QC:

1. Equilibrate the Chromatin Capture Beads to room temperature and vortex thoroughly (>30 seconds) to resuspend.
2. Thaw the QC tube that was stored at -80°C (see Note at the end of Stage 1). Pipet mix the 2.5 µL aliquot.
3. Transfer 50 µL of the resuspended Chromatin Capture Beads to the QC tube containing the 2.5 µL aliquot.
4. Pipet up and down to fully mix. Incubate the QC tube at room temperature, off the magnetic rack, for 10 minutes.
5. Place the tube in the magnetic rack for 5 minutes (or until the solution looks clear). Discard the supernatant.
6. Remove the tube from the magnetic rack and wash the beads with 150 µL 1X Wash Buffer. Pipet up and down to resuspend the beads, place the tube in the magnetic rack for 1 minute and discard the supernatant.
7. Repeat step 6 once, for a total of 2 washes.
8. After removing the last wash, add to the QC tube 51.5 µL of a master mix containing the following reagents **added in the order listed**:

Reagent	Volume Per Reaction
Crosslink Reversal Buffer	50 µL
Proteinase K	1.5 µL
Total	**51.5 µL**

9. Pipet up and down to fully mix. Incubate the tube in an agitating thermal mixer set at 1,200 rpm as follows:

Temperature	Time
78°C	10 minutes
25°C Note: secure the tube lid to prevent opening during incubation	Hold

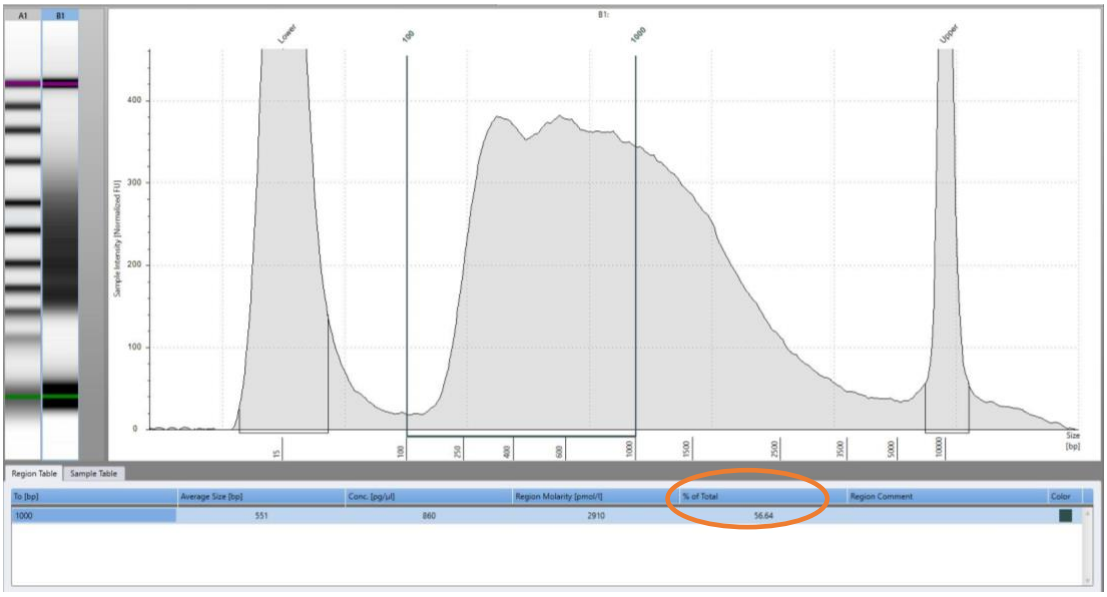
10. Quick spin the tube and place it on the magnetic rack for 1 minute (or until the solution looks clear). **Transfer the SUPERNATANT** to a new 1.5 mL tube for DNA purification. Discard the beads.
11. Vortex the SPRIselect beads thoroughly (>30 seconds) to resuspend.
12. Add 90 µL of resuspended SPRIselect beads to the 1.5 mL tube containing your sample.
13. Vortex to mix thoroughly. Quick spin the tube (make sure to spin down only briefly and to stop before the beads start to settle).
14. Incubate the tube at room temperature, off the magnetic rack, for 5 minutes.
15. Quick spin the tube and place it in the magnetic rack for 5 minutes. Discard the supernatant.
16. Leave the tube in the magnetic rack and wash the beads **twice** with 200 µL fresh 80% ethanol. Do not resuspend the beads for these washes. Add the ethanol, wait for 1 minute then discard the ethanol supernatant.
17. After the last wash, quick spin the tube and place it in the magnetic rack for 1 minute. Use a 10 µL pipet tip to remove traces of ethanol.
18. Air dry the beads for 3 minutes in the magnetic rack until no residual ethanol remains. **Do not over dry the beads**.
19. Off the magnetic rack, resuspend the beads in 10 µL TE Buffer pH 8.0.
20. Vortex to mix thoroughly. Quick spin the tube (make sure to spin down only briefly and to stop before the beads start to settle).
21. Incubate at room temperature, off the magnetic rack, for 2 minutes.
22. Quick spin the tube and place it in the magnetic rack for 1 minute.
23. Transfer 8 µL of the **SUPERNATANT** (purified DNA) to a new tube. Discard the beads.
24. Quantify the purified DNA using a Qubit Fluorometer and Qubit dsDNA HS Kit.
    a. Based on the Qubit concentration, the total lysate amount (ng) can be calculated as follows: Total Lysate (ng) = Qubit reading ng/µL x 10 µL (elution volume) x 23.8 (dilution factor)
    b. We expect a yield > 300 ng. Refer to Appendix 2: Troubleshooting Guide For Yields if the yield you obtain is < 300 ng.
25. Check the fragment size distribution of your purified QC sample on a TapeStation HS D5000 ScreenTape. Make sure your sample is diluted to 1 ng/µL.

- The fragmentation profile should **contain DNA in the range of 100 – 1,000 bp as specified in the Table below.** On the TapeStation System, create a region from 100 – 1,000 bp (see figure 3 below). Creating this region will automatically generate a '% of total' value. This value should be ≥ 40%. Refer to Appendix 4: Troubleshooting Guide For Fragmentation Profile if the value you obtain is outside of the specification for the analysis system you are using.

N O T E The '% of total' cut-off value varies between analytical instruments. Please refer to the table below for the recommended **fragmentation cut-off value** for the system you are using.

System	**DNA in the range of 100 – 1,000 bp (% of total value)**
TapeStation	≥40%
Bioanalyzer	≥30%
Fragment Analyzer	≥60%

Figure 3. Expected (QC Pass) fragmentation profile, as analyzed on HS D5000 ScreenTape



Appendix 4: Troubleshooting Guide For Fragmentation Profile

- This guide enables users to troubleshoot a fragmentation profile that contains **less** than recommended DNA in the 100 – 1,000 bp region (under-fragmented sample).

Troubleshooting under-fragmented tissue samples

If the profile is under-fragmented (i.e. below the recommended lower limit), re-start the sample preparation (Stage 1A) and incorporate the following two modifications:

1. Perform steps a, b, and c below **before the Nuclei Prep** (i.e before step 12 in Stage 1A) .

   a. Resuspend the tissue pellet in 105 µL of cell isolation master mix containing the following reagents. Pipet up and down to break up clumps and fully resuspend the pellet.

Reagent	Volume Per Reaction
Reconstituted Cell Isolation Enzyme Mix (see Before You Begin in Stage 1B)	100 µL
100 mM $CaCl_2$	5 µL
Total	**105 µL**

   b. Incubate the tube in a thermal mixer WITHOUT SHAKING as follows:

Temperature	Time
37°C	**30** minutes

   c. Spin the tube at 500 x g for 5 minutes in a swinging bucket rotor. Carefully remove and discard the supernatant, taking care not to disturb the pellet.

   NOTE **To minimize cell loss, remove the supernatant SLOWLY from the TOP DOWN, using a P200 pipette.**

   d. Proceed to Step 12 in Stage 1A: Fresh frozen non-mammalian animal tissue.

2. Filter the sample through the 70 µm MiniStrainer at the end of Stage 1 (after completing Step 20).
   Place a MiniStrainer in a 1.5 mL microfuge tube. Pipet the sample into the MiniStrainer. Quick spin at 500 x g for 5 seconds. The aggregates should be retained in the filter and discarded. You will be proceeding with Stage 2 with the filtrate collected in the tube.

Appendix 5: Combining Samples For Library Preparation

- This guide enables users to:
    - Concentrate their sample if they are combining purified DNA from end of Stage 2 from two proximity ligation reactions for library conversion.

1. Combine the purified DNA from end of stage 2 from two proximity ligation reactions (total volume 80 µL) in a 1.5 mL tube.
2. Vortex the SPRIselect beads thoroughly (> 30 seconds) to resuspend.
3. Add 145 µL of resuspended SPRIselect beads to the 1.5 mL tube containing the combined purified DNA sample.
4. Vortex to mix thoroughly. Quick spin the tube (make sure to spin down only briefly and to stop before the beads start to settle).
5. Incubate the tube at room temperature, off the magnetic rack, for 10 minutes.
6. Quick spin the tube and place it in the magnetic rack for 5 minutes. Discard the supernatant.
7. Leave the tube in the magnetic rack and wash the beads **twice** with 200 µL **fresh** 80% ethanol. Do not resuspend the beads for these washes. Add the ethanol, wait for 1 minute then discard the ethanol supernatant.
8. After the last wash, quick spin the tube and place it in the magnetic rack for 1 minute. Use a 10 µL pipet tip to remove traces of ethanol.
9. Air dry the beads for 5 minutes in the magnetic rack until no residual ethanol remains. Do not over dry the beads.
10. Off the magnetic rack, resuspend the beads in 42 µL TE Buffer pH 8.0.
11. Vortex to mix thoroughly. Quick spin the tube (make sure to spin down only briefly and to stop before the beads start to settle).
12. Incubate at room temperature, off the magnetic rack, for 5 minutes.
13. Quick spin the tube and place it in the magnetic rack for 1 minute.
14. Transfer 40 µL of the **SUPERNATANT** (purified DNA) to a new tube. Discard the beads.