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USER MANUAL

Evercode™ WT Mini v2

SKU: ECW02115, ECW02110, and ECW02010

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U.S. Pat. No. 10,900,065
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Patents pending in the U.S. and other countries

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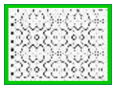
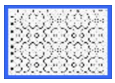
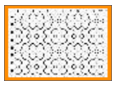
INTRODUCTION

Parts List

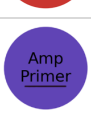
Barcoding Plates (-20°C) SP100

Label	Component	Format	Quantity	Part Number
	Round 1 Plate	96-Well Plate	1	SP101
	Round 2 Plate	96-Well Plate	1	SP102
	Round 3 Plate	96-Well Plate	1	SP103

Barcoding Reagents (-20°C) SB100

Label	Component	Format	Quantity	Part Number
	Dilution Buffer	1.5 mL tube	2	SB101
	Resuspension Buffer	5 mL tube	1	SB102
	Ligation Mix	5 mL tube	1	SB103
	Round 2 Ligation Enzyme	1.5 mL tube	1	SB104
	Round 2 Stop Mix	2 mL tube	1	SB105
	Round 3 Ligation Enzyme	1.5 mL tube	1	SB106
	Round 3 Stop Mix	5 mL tube	1	SB107
	Pre-Lyse Wash Buffer	5 mL tube	1	SB108
	Lysis Enzyme	1.5 mL tube	1	SB109

cDNA Amplification (-20°C) SC100

Label	Component	Format	Quantity	Part Number
	Lysis Neutralizer	1.5 mL tube	1	SC101
	Bead Wash Buffer	1.5 mL tube	1	SC102
	Bind Buffer A	1.5 mL tube	1	SC103
	Bind Buffer B	1.5 mL tube	1	SC104
	Bind Buffer C	1.5 mL tube	1	SC105
	Bead Storage Buffer	1.5 mL tube	1	SC106
	TS Buffer	1.5 mL tube	1	SC107
	TS Enzyme	1.5 mL tube	1	SC108
	TS Primer Mix	1.5 mL tube	1	SC109
	Amplification Master Buffer	1.5 mL tube	1	SC110
	Amplification Primer Mix	1.5 mL tube	1	SC111

Fragmentation (-20°C) SX200

Label	Component	Format	Quantity	Part Number
Frag Buf.	Fragmentation Buffer	1.5 mL tube	1	SX101
Frag Enzyme	Fragmentation Enzyme	1.5 mL tube	1	SX102
Adapt DNA	Adaptor DNA	1.5 mL tube	1	SX103
Adapt Buffer	Adaptor Ligation Buffer	1.5 mL tube	1	SX104
Adapt Ligase	Adaptor Ligase	1.5 mL tube	1	SX105
Index PCR Mix	Index PCR Mix	1.5 mL tube	1	SX106

Note: An alternative version of Evercode WT Mini v2 (ECW02010) includes SX100 instead of SX200. This configuration includes 2 single indexing primers. See Appendix D for more information.

Accessories (Room Temp) WA100

Label	Component	Format	Quantity	Part Number
	40 µm strainers	Plastic Bag	2	WA101
	Basins	Plastic Bag	2	WA102
	96 Well Plate Seal Cover	Plastic Bag	5	WA103
	Plate Sealer	Plastic Sealer	1	WA104

4°C Reagents (4°C) SA200

Label	Component	Format	Quantity	Part Number
	Spin Additive	1.5 mL tube	1	SA201
	2x Lysis Buffer	1.5 mL tube	1	SA202
	Binder Beads	1.5 mL tube	1	SA203

Materials Supplied by Parse Biosciences (Purchased Separately)

The following materials are not provided within the kit. We recommend keeping these items to use in future experiments. Any questions regarding these items can be directed to support@parsebiosciences.com.

Required Materials

Item	Supplier	Part Number	Notes
Parse Biosciences Magnetic Rack	Parse Biosciences	SB1004	Magnetic strength is critical. If 3rd party magnetic racks are used, the number of transcripts and genes detected per cell will be compromised. This magnetic rack is compatible with most 0.2 mL PCR tubes.

Optional Materials

Item	Supplier	Part Number	Notes
UDI Plate - WT	Parse Biosciences	UDI1001	48 unique dual indexes (UDIs) in a 96-well plate format. Once an individual well is pierced, it should not be reused in future experiments. However, unused wells can be used in future library preparations.

If you are using the Evercode WT Mini v2 kit (ECW02010) that includes single indexing primers, this protocol can still be used, but see Appendix D for more information.

User Supplied Equipment and Consumables

The following materials and equipment are required to perform the protocol, but are not provided within the kit. Note that this list does not include standard laboratory equipment, such as freezers. Any questions regarding these items can be directed to support@parsebiosciences.com.

Equipment

Item	Supplier	Part Number	Notes
Centrifuge with Swinging Bucket Rotors	Various Suppliers	Varies	Capable of reaching 4°C. Compatible with 15 mL centrifuge tubes and 96-well plates.
Microcentrifuge	Various Suppliers	Varies	Compatible with 1.5 mL and 0.2 mL tubes.
Heat Block	Various Suppliers	Varies	Or equivalent water bath, bead bath, or thermomixer capable of holding temperature at 37°C.
Hemocytometer	Sigma-Aldrich®	Z359629	Or other cell counting device. We recommend validating alternatives relative to a hemocytometer.
Single Channel Pipettes: P20, P200, P1000 12-channel: P20, P200	Various Suppliers	Varies	Or 8-channel pipettes can be substituted for 12-channel pipettes.
T100 Thermal Cycler	Bio-Rad Laboratories®	1861096	Or an equivalent thermocycler compatible with unskirted 96-well plates and a heated lid capable of 50-105°C.
6-Tube Magnetic Separation Rack	New England Biolabs®	S1506S	Or an equivalent magnetic rack for 1.5 mL tubes.
Vortex-Genie 2®	Scientific Industries®	SI-0236	Compatible with a vortex adapter for 96-well plates. Or a shaker set to 800-1000 RPM. Part number varies with different lab voltage and frequency requirements.
6-inch Platform	Scientific Industries	146-6005-00	Or an equivalent vortex adapter for 96-well plates.
Microplate Foam Insert	Scientific Industries	504-0235-00	Or an equivalent vortex adapter for 96-well plates.
Qubit™ Flex Fluorometer	Thermo Fisher Scientific®	Q33327	Or an equivalent fluorometer.
2100 Bioanalyzer	Agilent®	G2939BA	Choose one.
4200 TapeStation System	Agilent	G2991BA	

Consumables

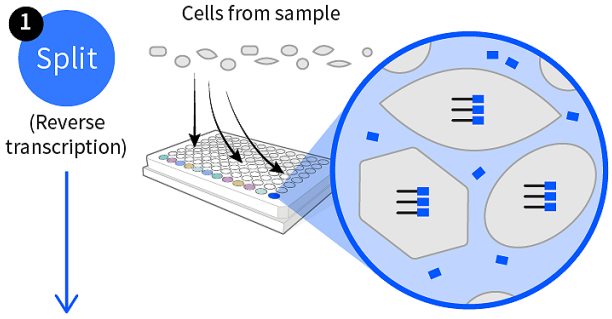
Item	Supplier	Part Number	Notes
Falcon® High Clarity PP Centrifuge Tubes, 15 mL	Corning®	352097	Or equivalent 15 mL polypropylene centrifuge tubes. Do not substitute polystyrene centrifuge tubes as it will lead to substantial cell loss.
Corning Cell Strainer (70 µm or 100 µm)	Corning	431751 (70 µm) 431752 (100 µm)	For cells larger than 40 µm, the 40 µm strainer should be replaced throughout the protocol with the appropriate size mesh (70 µm or 100 µm).
DNA LoBind® Tubes, 1.5 mL, Snap Cap	Eppendorf®	022431021	Or equivalent DNA low-binding, nuclease-free 1.5 mL tubes.
DNA LoBind Tubes, 5 mL, Snap Cap	Eppendorf	0030108310	Or equivalent DNA low-binding, nuclease-free 5 mL tubes.
TempAssure® PCR 8-Tube Strips, 0.2 mL	USA Scientific®	1402-4700	Or equivalent nuclease-free 0.2 mL PCR tubes.
Pipette Tips TR LTS 20 µL, 200 µL, 1000 µL	Rainin®	17014961 17014963 17014967	Or appropriate sterile, DNA low-binding, and filtered pipette tips. Do not use wide bore tips. Autoclaved pipette tips are not RNase and DNase free.
RNaseZap™ RNase Decontamination Solution	Thermo Fisher Scientific	AM9780	Or equivalent RNase decontamination solution.
Ethyl alcohol, Pure	Sigma-Aldrich	459844	Or equivalent 100% non-denatured ethanol.
Nuclease-Free Water	Sigma-Aldrich	W4502	Or equivalent nuclease-free water.
Trypan Blue	Various Suppliers	Varies	Or alternative dyes that can be used to assess cell viability, such as AOPI.
KAPA® Pure Beads	Roche®	KK8000 (5 mL) KK8001 (30 mL)	Choose one. We do not recommend substituting other magnetic beads, including SPRIselect (Beckman Coulter) and ProNex® (Promega®).
AMPure® XP Reagent	Beckman Coulter®	A63880 (5 mL) A63881 (60 mL)	
Qubit dsDNA HS (High Sensitivity) Assay Kit	Thermo Fisher Scientific	Q33230 (100 assays) Q33231 (500 assays)	Or equivalent DNA quantifier.
High Sensitivity DNA Kit	Agilent	5067-4626	Choose one that corresponds to chosen Bioanalyzer or TapeStation.
High Sensitivity D5000 ScreenTape and Reagents	Agilent	5067-5592 (screen tape) 5067-5593 (sample buffer and ladder)	

Background

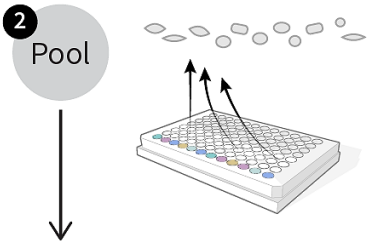
Evercode Combinatorial Barcoding Technology

Parse offers a new strategy for single cell RNA sequencing that can profile up to 20,000 cells (10,000 cells is recommended) in parallel across up to 12 samples. Our pioneering technology uses combinatorial cDNA barcoding within cells (or nuclei) themselves, and thus does not require complex cell partitioning instruments. Individual transcriptomes are uniquely labeled by passing fixed cells or nuclei through four rounds of barcoding. In each round, pooled cells are randomly distributed into different wells, and transcripts are labeled with well-specific barcodes. Using next-generation sequencing, each transcriptome is assembled by combining reads containing the same four-barcode combination. Four rounds of barcoding can yield 221,184 possible barcode combinations (three rounds of barcoding in 12x96x96 wells followed by a fourth round with 2 PCR reactions), enough to uniquely label up to 20,000 cells while avoiding doublets.

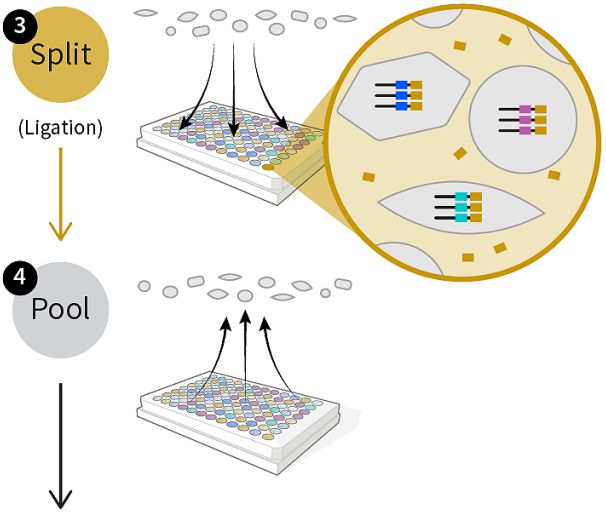
In the first round of barcoding, fixed cell samples are distributed into 12 wells, and cDNA is generated with an in-cell reverse transcription (RT) reaction using well-specific barcoded primers.



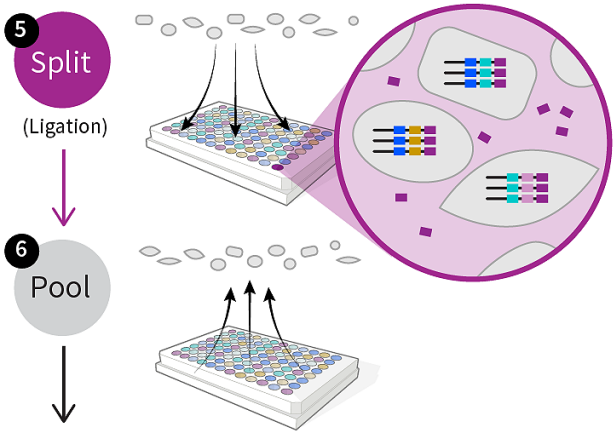
Cells from each well are pooled back together.



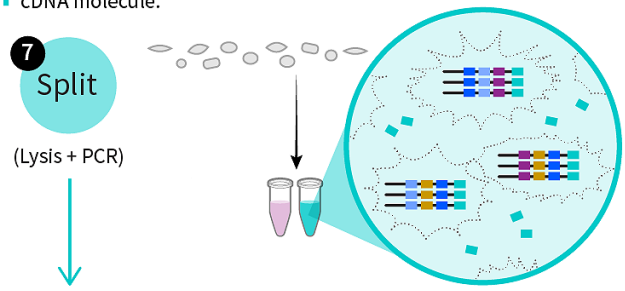
Cells are then distributed into 96 wells, and an in-cell ligation reaction appends a second well-specific barcode to the cDNA.



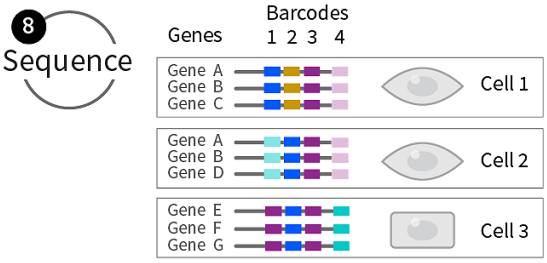
The third-round barcode, which also contains a unique molecular identifier (not depicted), is appended with another round of in-cell ligation.



After three rounds of barcoding, the cells are pooled and split into 2 distinct populations we term sublibraries. The user can choose the number of cells in each sublibrary to control the depth of sequencing. Cells will not be pooled again after this step. After this final split cells are lysed and the barcoded cDNA is isolated. A fourth sublibrary-specific barcode is introduced by PCR to each cDNA molecule.



After sequencing, each single cell transcriptome is assembled by combining reads containing the same four-barcode combination.



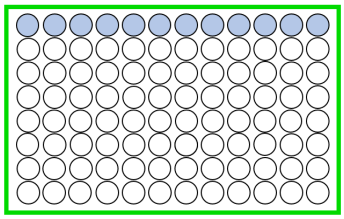
Background Continued

Unlike other scRNA-seq methods that physically separate individual cells into different compartments to label transcripts with cell-specific barcodes, Evercode WT Mini uses the cells (or nuclei) themselves as “containers” in which intracellular mRNA-transcripts are labeled using combinatorial indexing. In practice, cells are split into different wells, a well-specific barcode is appended to intracellular transcripts, and cells are then pooled back together. Repeating this process several times ensures a high likelihood that each cell travels through a unique combination of wells. Consequently, the transcriptome of each individual cell is labeled with a unique combination of well-specific barcodes. Unlike previous methods that scale linearly with the number of available compartments and barcodes, this method scales exponentially with the number of barcoding rounds, enabling a massive increase in the number of cells that can be sequenced, while minimizing doublets.

Overview of Four Rounds of Barcoding in the Evercode WT Mini

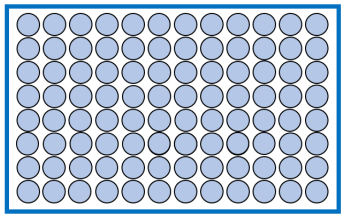
Each cell will be barcoded four times throughout the kit process, which will generate 221,184 (12 x 96 x 96 x 2) possible barcode combinations. Each barcoding round is outlined below:

Round 1 Barcoding (12 barcodes):
Cells are distributed into 12 different wells (shaded in blue) within the Round 1 Barcoding Plate. Barcodes are added through an *in situ* reverse transcription reaction using barcoded primers.
Note: Check the “WT Mini - Sample Loading Table V1.2.0” (Excel spreadsheet) to determine which sample to add to each well.



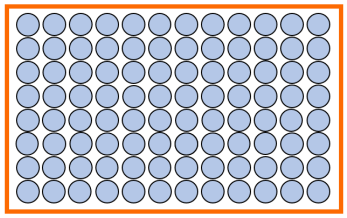
Round 2 Barcoding (96 barcodes):

Cells are distributed into 96 different wells within the Round 2 Barcoding Plate. The second barcode is added to each transcript via an *in situ* ligation reaction.



Round 3 Barcoding (96 barcodes):

Cells are distributed into 96 different wells within the Round 3 Barcoding Plate. The third barcode is added to each transcript via an *in situ* ligation reaction.



Sublibrary Barcoding (2 Illumina Indices):

Cells are distributed into 2 different tubes (sublibraries). While all the sublibraries can be processed together, each sublibrary can be sequenced separately. Different numbers of cells can be added to each sublibrary (see Section 1.5: Lysis and Sublibrary Generation) as desired by the user. Sublibraries with small cell numbers will be easier to sequence to saturation and can serve as a good QC measure before sequencing additional sublibraries with much larger cell numbers.

Unique Dual Index (UDI) Plates

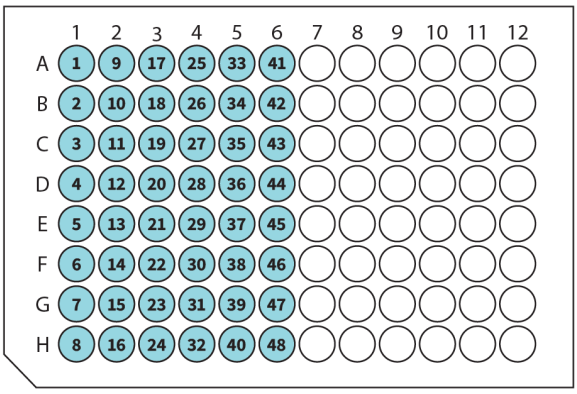
A unique dual index (UDI) provides a fourth sublibrary-specific barcode.

UDI Plate - WT should be used in Whole Transcriptome Sequencing Library preparation in Section 3.

UDI Plate - WT Configuration and Use

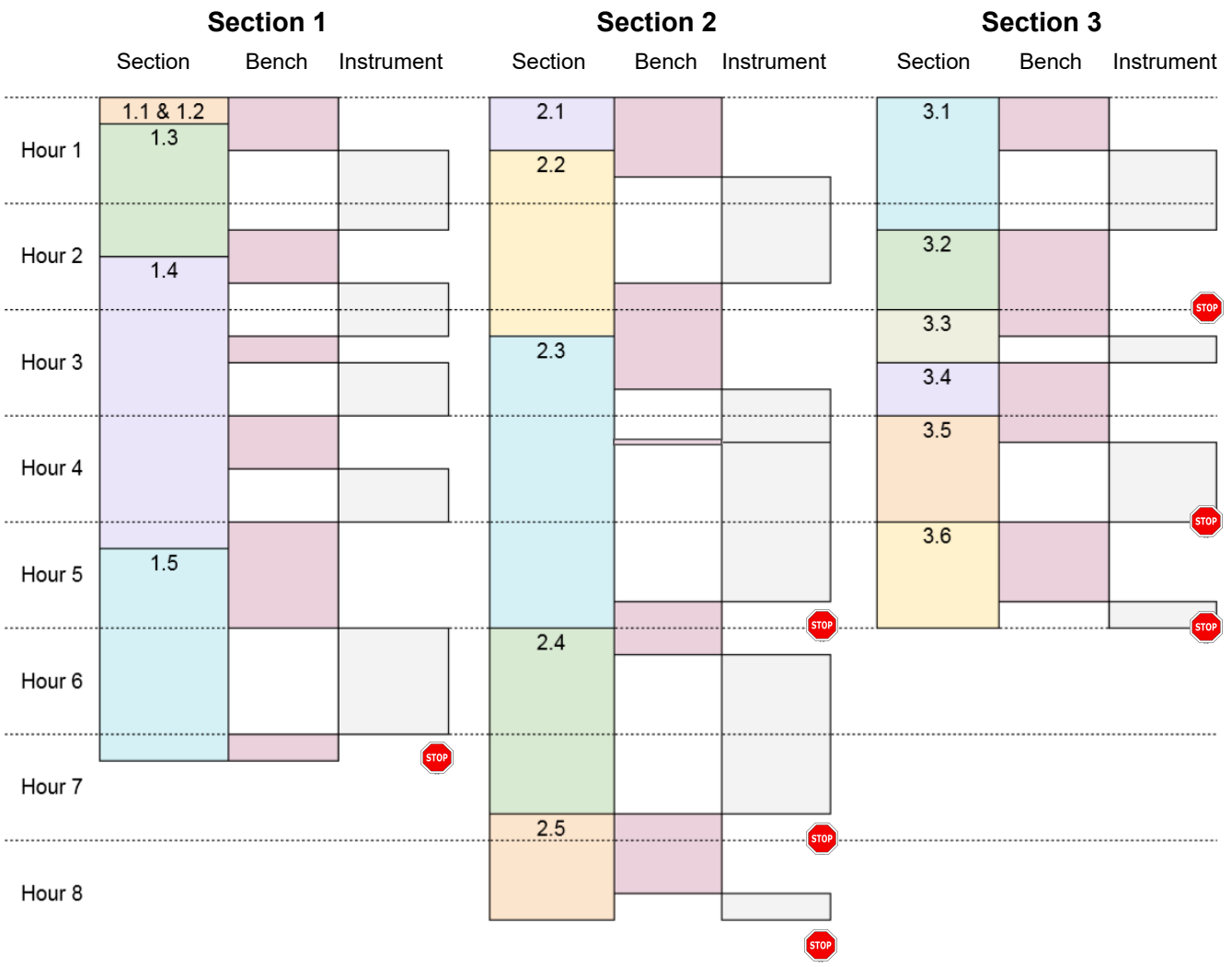
The UDI Plate - WT contains 48 UDIs in a 96-well format as shown below.

The UDI Plate - WT is sealed with a pierceable seal and each well is **single-use only** to minimize cross-contamination. The plate seal should be wiped with 70% ethanol and pierced with a new pipette tip immediately prior to use. Avoid splashing or mixing the liquid between individual wells as this could lead to cross-contamination. Once a well has been used, it should not be resealed or reused. However, unused wells can be used in future library preparations.



Note: We recommend selecting UDIs column-wise from left to right (starting with indices 1-8). UDI sequences can be found in Section 4.1.

Protocol Timing



STOP = **Optional** stopping point

Notes Before Starting

User Supplied Equipment and Consumables	Before starting an experiment, check the “User Supplied Equipment and Consumables” section and confirm that your lab has all of the supplies that are not provided by the kit. Avoid substituting custom materials for those that are provided in the kit. Each item has been deliberately chosen to attain optimal results.
Avoiding RNase Contamination	Standard precautions should be taken to avoid introducing RNases into samples or reagents throughout the workflow. Always wear proper laboratory gloves and use aseptic technique. RNases are not inactivated by ethanol or isopropanol, but can be inactivated by specific products such as RNaseZap RNase Decontamination Solution (Thermo Fisher Scientific). These can be sprayed on benchtops and used to clean pipettes. It is recommended to use pre-sterilized, filter pipette tips to reduce RNase contamination from pipettes.
Centrifuges	Use a swinging bucket centrifuge for all high speed spin steps in this protocol. Use of a fixed-angle centrifuge will lead to substantial cell loss. Although the recommended centrifugation speeds are appropriate for most sample types, they can be adjusted to improve retention.
Centrifuge Tubes	Ensure that the tubes that will be used are **polypropylene** and not polystyrene. Polystyrene tubes will lead to substantial cell loss.
Sample Handling	It is critical that cells are thoroughly resuspended after centrifugation. Resuspend cells by slowly (to prevent mechanical damage) and repeatedly pipetting up and down until no clumps are visible. Wide bore pipette tips are not recommended as they make it difficult to adequately resuspend cell pellets. Due to cell adherence to tubes, it is recommended to carefully pipette along the bottom and sides of centrifuge tubes to minimize cell loss.
Sample Loading Table	The “WT Mini - Sample Loading Table V1.2.0” (Excel spreadsheet) should be completed before starting the experimental workflow. If it is not working properly, ensure that Macros are enabled in the Sample Loading Table. Be sure to only edit the colored cells in the table to avoid disturbing the necessary formatting.

Maximizing Cell Retention During Pooling Steps	During the barcoding steps, some cells may stick to the side of the wells in the 96-well plates. To increase cell retention, it is important to pipette up and down several times in each well before removing and pooling cells. Note that additional pipetting may lead to increased bubbles while pooling. While bubbles will not affect results, we advise using caution when pipetting to prevent excess bubble formation and maintain experimental ease. We recommend the following procedure when pooling: • Set the multichannel P200 pipette to 10 µL less than the volume in each well. The volumes for Barcoding Rounds 1, 2, and 3 should be 30 µL, 50 µL, and 70 µL, respectively. This will avoid bubbles while pipetting up and down in wells. • Insert tips into the bottom of the wells. Pipette up and down 3x in the middle of the well, then pipette up and down 3x on the front side of the well, followed by 3x on the back side of the well, before proceeding with pooling cells. • Pool any remaining liquid left in the wells (should be ~10 µL).
Sealing Plates in Original Container	There are multiple steps requiring the removal and application of seals to 96-well plates. In either motion, ensure that the plate is in its original container for best support. Failure to do so may result in plate slippage and loss, or swapping, of liquid between wells.
Cell Strainers	A 40 µm cell strainer will be used in multiple steps. To maximize cell retention, press the pipette tip directly against the strainer. Ensure that ample pressure is applied to hold contact between the tip and the strainer to force liquid through in ~1 second. For cells larger than 40 µm, the 40 µm strainer should be replaced throughout the protocol with the appropriate size mesh (70 µm or 100 µm).
Lysis Buffer Precipitate	Ensure that there is no precipitate when using the 2x Lysis Buffer. Warming the 2x Lysis Buffer at 37°C for 5 minutes should resolubilize solution. If precipitate remains, warm 2x Lysis Buffer at 37°C for another 5 minutes.
Sequencing Libraries	Multiple sequencing libraries can be prepared from the same experiment. At the end of barcoding (Section 1), the recovered cells can be split across different sublibraries. The number of cells to be sequenced is determined when cells are divided into sublibraries at the lysis step. Thus, not all of the cells prepared in these steps must be sequenced together.

SECTION 1

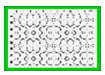
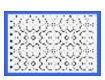
BARCODING SINGLE CELLS

1.1 Experimental Setup

1. Prepare for the first round of barcoding with the following checklist:

   - ☐ Add each of your sample names to “WT Mini - Sample Loading Table V1.2.0” (Excel spreadsheet). In Section 1.2, you will add the concentrations of each sample to this spreadsheet and use it to make appropriate dilutions to each sample. The plate configuration in this spreadsheet will also tell you which wells to add each sample to during the first round of barcoding in Section 1.3.
   - ☐ Set your swinging-bucket centrifuge to **4°C.**
   - ☐ Warm a **37°C** water bath.
   - ☐ Fill an ice bucket, large enough to hold two 96-well plates and several tubes.
   - ☐ Prepare a flow cytometer, hemocytometer, or other device for cell counting.

2. Gather the following items and handle as indicated below:

Item	Location	Quantity	Format	After taking out
Adhesive 96-well plate cover	Accessories (Room Temp)	1	With white protector	Keep at room temperature.
 Spin Additive	4°C Reagents (4°C)	1	1.5 mL tube	Keep at room temperature.
 Dilution Buffer	Barcoding Reagents (-20°C)	1	1.5 mL tube	Thaw, then place on ice.
 Resuspension Buffer	Barcoding Reagents (-20°C)	1	5 mL tube	Thaw, then place on ice.
 Ligation Mix	Barcoding Reagents (-20°C)	1	5 mL tube	Thaw, then place on ice.
 Round 2 Ligation Enzyme	Barcoding Reagents (-20°C)	1	1.5 mL tube	Place directly on ice.
 Round 1 Plate	Barcoding Plates (-20°C)	1	96-well plate	Place directly on ice.
 Round 2 Plate	Barcoding Plates (-20°C)	1	96-well plate	Place directly on ice.

CRITICAL! Only proceed if you have completed the checklist in step 1 and taken out all the items listed in step 2.

3. To thaw, place the **Round 1 Plate** into a thermocycler and set the following protocol below. The heated lid will force any liquid on the plastic plate seal back down into the well. Proceed to the next step while the thermocycler is running.

Round 1 Plate Thaw Protocol		
Run Time	**Lid Temperature**	**Sample Volume**
10 min	70°C	26 µL
Step	**Time**	**Temperature**
1	10 min	25°C
2	Hold	4°C

1.2 Sample Counting and Loading Setup

1. Thaw the fixed cell samples in a **37°C** water bath until all ice crystals dissolve, then place on ice. It is important to fully thaw samples before placing on ice.
2. Using an automated cell counter, hemocytometer, or flow cytometer, count the number of cells in each sample.
3. Fill out the cell concentrations of each sample in the "WT Mini - Sample Loading Table V1.2.0" (Excel spreadsheet).

Dilution Buffer

4. Dilute samples in **Dilution Buffer** according to the Sample Loading Table and place on ice.

1.3 Reverse Transcription Barcoding

During this section, cDNA will be reverse transcribed from RNA with barcoded RT primers specific to each well. It is critical to add the samples to the wells specified in the plate configuration within the "WT Mini - Sample Loading Table V1.2.0" document.

1. Gently remove the **Round 1 Plate** from the thermocycler and place into the original green plastic plate holder. Centrifuge the plate at **100 x *g*** for **1 minute**.
2. Place the plate (and holder) on a flat surface and remove the plastic seal. Store on ice.

   Note: Plate seals may be difficult to remove. Carefully peel the plate seal while applying downward pressure to keep the plates from moving (to minimize cross-contamination of wells).

3. **Add diluted samples to wells in the Round Plate 1.**

   Note: To prevent sample loss, mix cells as indicated below. Additionally, this step requires at least 12 unused 20 µL tips.

   Follow the Sample Loading Table during this step to determine which samples to add to each well. Using a P20 pipette, add **14 µL** cells to each of the top 12 wells in the **Round 1 Plate**. Immediately after dispensing cells, mix gently by pipetting up and down exactly 3x. When pipetting the same sample into many wells, the sample should be periodically mixed by gentle pipetting to avoid cells from settling. Do not vortex your cells.

CRITICAL! Different tips must be used when pipetting cells into the 96-well plate. Never place a tip that has entered one of the 96 wells into a different well.

4. Remove the **Round 1 Plate** and holder from the ice bucket and place on a flat surface. Seal the **Round 1 Plate** with an adhesive 96-well plate seal cover.

   Note: A plate sealer in included in the Accessories box.

~40 min

5. **Start the reverse transcription reaction.** Put the **Round 1 Plate** with cells into a thermocycler with the following thermocycling protocol:

Round 1 Plate Barcoding Protocol		
Run Time	**Lid Temperature**	**Sample Volume**
~40 min	70°C	40 µL
Step	**Time**	**Temperature**
1	10 min	50°C
	Begin Cycling	
2	12 sec	8°C
3	45 sec	15°C
4	45 sec	20°C
5	30 sec	30°C
6	2 min	42°C
7	3 min	50°C
	Go to step 2, repeat 2 times (3 cycles total)	
8	5 min	50°C
9	Hold	4°C

6. Transfer the **Round 1 Plate** from the thermocycler back to the original green plate holder and place on ice.

7. Thaw the **Round 2 Plate** by transferring the plate from the ice bucket into the thermocycler and running the following protocol. Proceed directly to the next step.

Round 2 Plate Thaw Protocol		
Run Time	**Lid Temperature**	**Sample Volume**
10 min	70°C	10 µL
Step	**Time**	**Temperature**
1	10 min	25°C
2	Hold	4°C

8. Place the **Round 1 Plate** (and holder) on a flat surface and remove adhesive seal. Place back on ice.

9. **Pool all wells from the Round 1 Plate into a single 15 mL centrifuge tube on ice.**

   Note: Proper mixing is required to prevent substantial cell loss during pooling. See "Maximizing Cell Retention During Pooling Steps" in Notes Before Starting.

   With a single channel pipette set to 30 µL, pool Row A into a 15 mL centrifuge tube. To maximize cell retention while pooling, pipette up and down 3x in the middle of the well, 3x on the front side of the well, and 3x on the back side of the well before transferring the volume of Row A into the 15 mL tube. Recover residual liquid from Row A using the single channel pipette set to 10 µL. Do not be concerned if there are a few µL of residual volume in the wells after pooling.

   Note: Bubbles may form while pooling. They will not affect the quality of the experiment.

CRITICAL! Both the Round 1 Plate and the 15 mL falcon tube with pooled cells should be kept on ice during the pooling step.

10. Discard the **Round 1 Plate**.

Spin Additive

11. Add **2.4 µL** of **Spin Additive** to the 15 mL tube with pooled cells. Gently invert the tube once to mix.

CRITICAL! Do NOT discard the **Spin Additive** as it will be needed in another step.

12. Centrifuge the pooled cells in a swinging bucket centrifuge cooled to **4°C** for **10 minutes** at **200 x *g***.

CRITICAL! Move to the next step as soon as the centrifuge finishes and handle the tube gently to avoid dislodging the cell pellet. Waiting too long to aspirate supernatant increases the risk of dislodging the pellet.

13. Using a P200 pipette, aspirate supernatant such that about ~40 µL of liquid remains above the pellet (see image on right for estimate of 40 µL). Do not disturb the pellet. Depending on the number of starting cells and cell types, the pellet may not be visible.

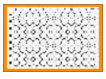
14. *Note: To prevent substantial cell loss during resuspension, see "Sample Handling" in Notes Before Starting.*

Resusp. Buffer

Gently resuspend cells with **1 mL** of **Resuspension Buffer**. Once cells are fully resuspended, add an **additional 1 mL** of **Resuspension Buffer** for a total volume of 2 mL. Keep this solution on ice and proceed to Ligation Barcoding.

1.4 Ligation Barcoding

1. Gather the following items and handle as indicated below:

Item	Location	Quantity	Format	After taking out
Adhesive 96-well plate cover	Accessories (Room Temp)	3	With white protector	Keep at room temperature.
 40 µm strainer	Accessories (Room Temp)	2	In plastic bag	Keep at room temperature.
 Basins	Accessories (Room Temp)	6	In plastic bag	Keep at room temperature.
 Round 2 Stop Mix	Barcoding Reagents (-20°C)	1	2 mL tube	Thaw, then place on ice.
 Round 3 Stop Mix	Barcoding Reagents (-20°C)	1	5 mL tube	Thaw, then place on ice.
 Pre-Lyse Wash Buffer	Barcoding Reagents (-20°C)	1	5 mL tube	Thaw, then place on ice.
 Round 3 Ligation Enzyme	Barcoding Reagents (-20°C)	1	1.5 mL tube	Place directly on ice.
 Round 3 Plate	Barcoding Plates (-20°C)	1	96-well plate	Place directly on ice.

2. Lightly centrifuge the **Round 2 Ligation Enzyme** and add **20 µL** of **Round 2 Ligation Enzyme** directly into the cold **Ligation Mix** tube to make **Ligation Mix + Enzyme**.

3. Using a P1000 pipette, add **2 mL** of cells in **Resuspension Buffer** into the **Ligation Mix + Enzyme** tube. Mix 10x with a P1000 set to 1000 µL and place back on ice.

CRITICAL! Do NOT vortex the **Ligation Mix + Enzyme** tube.

4. Transfer the **Round 2 Plate** from the thermocycler back to its original blue plate holder and keep at room temperature. Centrifuge the plate at **100 x *g*** for **1 minute**. Place the plate (and holder) on a flat surface and remove the seal. Keep at room temperature.

   Note: Plate seals may be difficult to remove. Carefully peel the plate seal while applying downward pressure to keep the plates from moving (to minimize cross-contamination of wells).

5. Using a P1000 pipette, add the entirety of cells in the **Ligation Mix + Enzyme** to a basin.

6. **Add pooled cells to the Round 2 Plate.**

   Note: To prevent sample loss, mix cells as indicated below. Additionally, this step requires a new box of 200 µL tips.

   Using a multichannel P200 pipette, add **40 µL** of mix in the basin to each of the 96 wells in the **Round 2 Plate**. As you add the 40 µL to each well, pipette up and down exactly 2x to ensure proper mixing**.** To avoid cells settling in the basin, also gently pipette up and down 2x with the multichannel pipette in the basin before transferring the cells from the basin to each row.

   Note: Using a single channel pipette and tilting the basin may be required to fill the last row if volume in the basin is low. If volume is insufficient to fill every well, a few wells can be left empty without impacting experimental results.

CRITICAL! Different tips must be used when pipetting cells into the 96-well plate. Never place a tip that has entered one of the 96 wells back into the basin.

7. Reseal the **Round 2 Plate** with an adhesive seal.

30 min

8. **Start the second round of barcoding.** Incubate the **Round 2 Plate** in a thermocycler with the following protocol:

Round 2 Ligation Barcoding Protocol		
Run Time	**Lid Temperature**	**Sample Volume**
30 min	50°C	50 µL
Step	**Time**	**Temperature**
1	30 min	37°C
2	Hold	4°C

R2 Stop Mix

9. Vortex the **Round 2 Stop Mix** briefly (2-3 sec) and using a P1000 pipette, add the entirety (~1.4 mL) to a new basin.

10. Transfer the **Round 2 Plate** from the thermocycler back to its original blue plate holder and remove the seal. Keep the plate at room temperature.

R2 Stop Mix

11. **Add Round 2 Stop Mix to each well.**

    Note: This step requires a new box of 20 µL tips.

    Using a multichannel P20 pipette, add **10 µL** of the **Round 2 Stop Mix** in the basin to each of the 96 wells of the **Round 2 Plate**. Pipette up and down exactly 3x to ensure proper mixing after adding **Round 2 Stop Mix** to each well.

CRITICAL! Different tips must be used when pipetting **Round 2 Stop Mix** into the 96-well plate. Never place a tip that has entered one of the 96 wells back into the basin.

12. Reseal the **Round 2 Plate** with an adhesive seal.

30 min

13. Incubate the **Round 2 Plate** in a thermocycler with the following protocol:

Round 2 Stop Protocol		
Run Time	**Lid Temperature**	**Sample Volume**
30 min	50°C	60 µL
Step	**Time**	**Temperature**
1	30 min	37°C
2	Hold	4°C

14. Transfer the **Round 2 Plate** from the thermocycler to its original blue plate holder. Keep at room temperature.

15. Thaw the **Round 3 Plate** by transferring it from the ice bucket into the thermocycler and running the following protocol. Proceed directly to the next step.

Round 3 Plate Thaw Protocol		
Run Time	**Lid Temperature**	**Sample Volume**
10 min	70°C	10 µL
Step	**Time**	**Temperature**
1	10 min	25°C
2	Hold	4°C

16. Remove the seal on the **Round 2 Plate**.

17. **Pool all wells from the Round 2 Plate into a new basin.**

    Note: Proper mixing is required to prevent substantial cell loss during pooling. See "Maximizing Cell Retention During Pooling Steps" in Notes Before Starting.

    With the multichannel pipette set to 50 µL, pool volume from each well into a new basin. To maximize cell retention while pooling, pipette up and down 3x in the middle of the well, 3x on the front side of the well, and 3x on the back side of the well before transferring the volume of rows A-H to the basin. Recover residual liquid across all rows using the multichannel pipette. Do not be concerned if there are a few µL of residual volume in the wells after pooling.

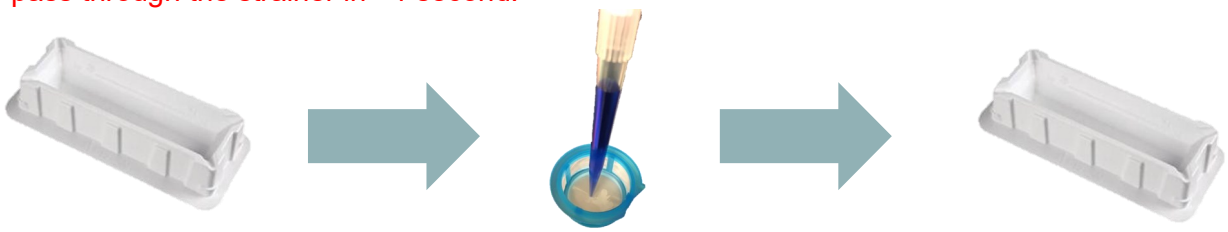
    Note: Bubbles may form while pooling. They will not affect the quality of the experiment.

18. Discard the **Round 2 Plate**.

19. Remove the 40 µm strainer from the packaging and carefully hold the strainer using the outside casing without touching the mesh. Using a P1000 pipette set to 1000 µL, pass all cells from this basin through the 40 µm strainer into a new basin. Mix cells in the basin between passages. The original basin must be tilted in order to pipette the final volume.

    Note: For cells larger than 40 µm, the 40 µm strainer should be replaced throughout the protocol with the appropriate size mesh (70 µm or 100 µm). Additionally, bubbles may form while straining. They will not affect the quality of the experiment.

CRITICAL! To ensure that all of the liquid passes through the strainer, press the tip of the pipette against the filter and press the pipette plunger down steadily. All of the liquid should pass through the strainer in ~1 second.



R3 Lig. Enzyme

20. Add **20 µL** of **Round 3 Ligation Enzyme** to the basin with strained cells and mix by gently pipetting up and down ~20x with a P1000 pipette set to 1000 µL.

21. Transfer the **Round 3 Plate** from the thermocycler back to its original orange plate holder. Centrifuge the plate at **100 x *g*** for **1 minute.** Place the plate (and holder) on a flat surface and remove the seal. Keep at room temperature.

    Note: Plate seals may be difficult to remove. Carefully peel the plate seal while applying downward pressure to keep the plates from moving (to minimize cross-contamination of wells).

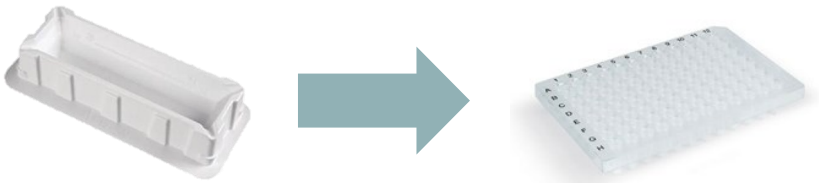
22. **Add pooled cells to the Round 3 Plate.**

    Note: To prevent sample loss, mix cells as indicated below. Additionally, this step requires a new box of 200 µL tips.

    Using a multichannel P200 pipette, add **50 µL** of the mix in the basin to each of the 96 wells in the **Round 3 Plate**. As you add the 50 µL to each well, pipette up and down exactly 2x to ensure proper mixing**.** To avoid cells settling, also gently pipette up and down 2x with the multichannel pipette in the basin before transferring the cells from the basin to each row.

    Note: Using a single channel pipette and tilting the basin may be required to fill the last row if volume in the basin is low. If volume is insufficient to fill every well, a few wells can be left empty without impacting experimental results.

CRITICAL! Different tips must be used when pipetting cells into the 96-well plate. Never place a tip that has entered one of the 96 wells back into the basin.



23. Reseal the **Round 3 Plate** with an adhesive seal.

30 min

24. Start the third round of barcoding. Incubate the **Round 3 Plate** in a thermocycler with the following protocol:

Round 3 Ligation Barcoding Protocol		
Run Time	**Lid Temperature**	**Sample Volume**
30 min	50°C	60 µL
Step	**Time**	**Temperature**
1	30 min	37°C
2	Hold	4°C

25. Remove the **Round 3 Plate** from the thermocycler, place it in its original orange plate holder on a flat surface and remove the seal. Keep at room temperature.

R3 Stop Mix

26. Vortex the **Round 3 Stop Mix** briefly (2-3 sec) and using a P1000 pipette, add the entirety of the Round 3 Stop Mix to a new basin.

R3 Stop Mix

27. Add Round 3 Stop Mix to each well.

Note: This step requires a new box of 20 µL tips.

Using a multichannel P20 pipette, add **20 µL** of the **Round 3 Stop Mix** in the basin to each of the 96 wells of the **Round 3 Plate**. Pipette up and down exactly 3x to ensure proper mixing after adding **Round 3 Stop Mix** to each well. No incubation required after this step, proceed directly to the next step.

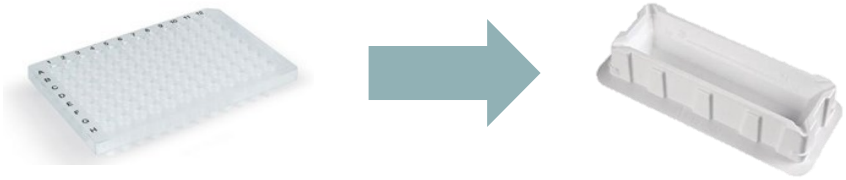
CRITICAL! Different tips must be used when pipetting stop mix into the 96-well plate. Never place a tip that has entered one of the 96 wells back into the basin.

28. Pool all wells from the Round 3 Plate into a new basin.

Note: Proper mixing is required to prevent substantial cell loss during pooling. See "Maximizing Cell Retention During Pooling Steps" in Notes Before Starting.

With the multichannel pipette set to 70 µL, pool volume from each well into a new basin. To maximize cell retention while pooling, pipette up and down 3x in the middle of the well, 3x on the front side of the well, and 3x on the back side of the well before transferring the volume of rows A-H to the basin. Recover residual liquid across all rows using the multichannel pipette. Do not be concerned if there are a few µL of residual volume in the wells after pooling.

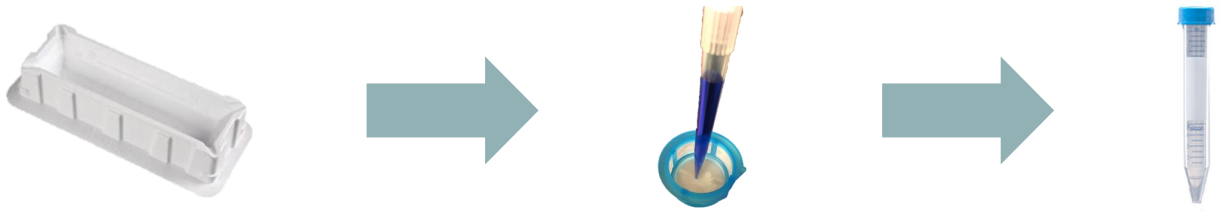
Note: Bubbles may form while pooling. They will not affect the quality of the experiment.



29. Discard the **Round 3 Plate**.

30. Remove a 40 µm strainer from the packaging and carefully hold the strainer using the outside casing without touching the mesh. Using a P1000 pipette set to 1000 µL, pass all cells from this basin through a 40 µm strainer into a new 15 mL tube on ice. Mix cells in the basin between passages. The basin must be tilted in order to pipette the final volume. Keep the 15 mL tube on ice and proceed to lysis.

    Note: Bubbles may form while straining. They will not affect the quality of the experiment.



1.5 Lysis and Sublibrary Generation

1. Gather the following items and handle as indicated below:

Item	Location	Quantity	Format	After taking out
2x Lysis Buffer	4°C Reagents (4°C)	1	1.5 mL tube	Keep warm at 37°C until use.
Lysis Enzyme	Barcoding Reagents (-20°C)	1	1.5 mL tube	Place directly on ice.
Dilution Buffer	Barcoding Reagents (-20°C)	1	1.5 mL tube	Thaw, then place on ice.

Spin Additive

2. Add **70 µL** of **Spin Additive** to your cells in a 15 mL centrifuge tube. Gently invert the tube once to mix.

3. Use a swinging bucket centrifuge to spin down the cells for **10 minutes** at **200 x *g*** at **4°C**.

4. Using a P1000 pipette for the first 6 mL, then a P200 pipette for the remaining volume, aspirate supernatant such that ~40 µL of liquid remains above the pellet (see image on right for estimate of 40 µL). Do not disturb the pellet. Depending on the number of starting cells and cell types, the pellet may not be visible.

Pre-Lyse Wash

5. *Note: To prevent substantial cell loss during resuspension, see "Sample Handling" in Notes Before Starting.*

    Gently resuspend cells with **1 mL** of **Pre-Lyse Wash Buffer**. When resuspending the pellet, pipette slowly to prevent mechanical damage to cells. Once cells are fully resuspended, add an **additional 3 mL** of **Pre-Lyse Wash Buffer** for a total volume of 4 mL.

6. Use a swinging bucket centrifuge to spin down for **10 minutes** at **200 x *g*** at **4°C**.

7. Using a P1000 pipette for the first 3 mL, then a P200 pipette for the remaining volume, aspirate supernatant such that ~40 µL of liquid remains above the pellet (see image on right for estimate of 40 µL). Do not disturb the pellet. Depending on the number of starting cells and cell types, the pellet may not be visible.

8. *Note: To prevent substantial cell loss during resuspension, see "Sample Handling" in Notes Before Starting.*

   Dilution Buffer

   Using a P200 pipette, gently resuspend the cell pellet with the remaining supernatant in the 15 mL tube. When resuspending the pellet, pipette slowly to prevent mechanical damage to cells. **Measure the volume of the resuspended cells with a P200 pipette**. Add **Dilution Buffer** to a total volume of 60 µL. If 60 µL or more are measured of remaining cell suspension, proceed without adding **Dilution Buffer**.

CRITICAL! Do NOT add **Dilution Buffer** to a volume greater than 60 µL. This may result in a concentration that is too low to load sublibraries.

CRITICAL! Do NOT discard **Dilution Buffer** as it will be needed in another step.

9. Using a P200 pipette set to 50 µL, gently pipette up and down 5x and immediately use **5 µL** of the mixed cells to count using a hemocytometer. Keep the 15 mL tube on ice.

   *Note: When using a hemocytometer, dilute **5 µL** of the mixed cell solution into **5 µL** of Trypan Blue. Mix well and load onto hemocytometer. Some level of debris is normal at this step. Alternatively, cells can be counted via flow cytometry, but using a hemocytometer is strongly recommended.*

   Choosing Sublibrary Sizes: In the following step, cells will be aliquoted into different sublibraries that will be prepared for sequencing. At the end of library prep, each sublibrary will have its own sublibrary index, making it possible to sequence each sublibrary with different numbers of reads. It is also possible to add different numbers of cells to each sublibrary. In practice it can be useful to have at least one sublibrary with very few cells (200-500) that can be sequenced deeply (>50,000 reads per cells) with a limited number of overall reads. This sublibrary then provides a good estimate of gene and transcript detection per cell that would be expected if the other sublibraries were also sequenced deeply. The maximum number of cells that can eventually be sequenced will be the sum of the number of cells across all sublibraries.

10. **Determine sublibrary size(s) and dilutions**. Up to 2 sublibraries, of varying sizes, can be made. Use the "Sublibrary Generation Table" (Appendix A) to determine the volume of cells and **Dilution Buffer** to add to each sublibrary (dependent on desired sublibrary size and the concentration of cells measured in the previous step). Give each sublibrary a unique label. Make sure to record which sublibrary sizes correspond to what labels. Label both the top and side of the PCR tube with those labels.

CRITICAL! Do NOT overload a sublibrary. The recommended loading is up to 5,000 cells/ sublibrary, with a maximum of 10,000 cells/sublibrary. Overloading a sublibrary with too many cells will result in increased doublets.

11. Dilution Buffer

    Using a P200 pipette set to 45 µL, gently pipette up and down 5x. Aliquot the determined volume of cells (from the previous step) to each correctly labelled sublibrary PCR tube and add **Dilution Buffer** to bring to total volume to 25 µL. Between each aliquot, gently pipette mix the cells to avoid settling. Store sublibraries on ice.

12. Make a **Lysis Master Mix.** Ensure there is no precipitate present in the **2x Lysis Buffer**. Add **55 µL** of **2x Lysis Buffer** to **11 µL** of **Lysis Enzyme** in a 1.5 mL tube.

CRITICAL! Do NOT place **Lysis Master Mix** on ice, as a precipitate will form.

13. **Add Lysis Master Mix to sublibraries**. Add **30 µL** of **Lysis Master Mix** to each tube, bringing the total volume to 55 µL. Keep sublibraries at room temperature.

14. Vortex samples for 10 sec to initiate lysis. Be sure to keep caps closed on tubes. Briefly centrifuge tubes (~2 sec).


1 hr

15. Incubate the sublibrary lysates in a thermocycler with the following protocol:

Sublibrary Lysis Protocol		
Run Time	**Lid Temperature**	**Sample Volume**
60 min	80°C	55 µL
Step	**Time**	**Temperature**
1	60 min	65°C
2	Hold	4°C

16. Freeze sublibrary lysate(s) at -80°C. Sublibrary lysates can be stored for up to 6 months.

[STOPPING POINT]

SECTION 2

AMPLIFICATION OF BARCODED cDNA

Any number of sublibraries (1-2) can be chosen for processing, where each sublibrary will ultimately be barcoded a fourth time with a sublibrary index. **Take care not to cross-contaminate any sublibraries for the remainder of the experiment**.

Setup

- ☐ Fill an ice bucket.
- ☐ Take out a magnetic rack for 1.5 mL tubes.
- ☐ Take out the Parse Biosciences magnetic rack for 0.2 mL PCR tubes.
- ☐ Ensure you have at least 79 µL of SPRI beads (Ampure XP or KAPA Pure Beads) per sublibrary.

Gather the following items and handle as indicated below:

Note: Do NOT remove sublibrary lysates from the freezer until the beginning of Section 2.2.

Item	Location	Quantity	Format	After taking out
 Binder Beads	4°C Reagents (4°C)	1	1.5 mL tube	Keep at room temperature.
 Bead Wash Buffer	cDNA Amplification (-20°C)	1	1.5 mL tube	Keep at room temperature.
 Bind Buffer A	cDNA Amplification (-20°C)	1	1.5 mL tube	Keep at room temperature.
 Bind Buffer B	cDNA Amplification (-20°C)	1	1.5 mL tube	Keep at room temperature.
 Bind Buffer C	cDNA Amplification (-20°C)	1	1.5 mL tube	Keep at room temperature.
 Bead Storage Buffer	cDNA Amplification (-20°C)	1	1.5 mL tube	Keep at room temperature.
 TS Buffer	cDNA Amplification (-20°C)	1	1.5 mL tube	Thaw, then place on ice.
 Lysis Neutralization	cDNA Amplification (-20°C)	1	1.5 mL tube	Place directly on ice.

2.1 Preparing Binder Beads

Binder Beads

1. Vortex **Binder Beads** until fully mixed and add a volume to an empty 1.5 mL tube according to the number of sublibrary lysates that you plan to process:

	Volume to Add by Number of Sublibrary Lysates (µL)	
# Sublibrary Lysates	1	2
Binder Beads (µL)	44	88

2. Capture the **Binder Beads** to a magnet using a magnetic rack (for 1.5 mL tubes) and wait until liquid becomes clear (~2 min).
3. Remove the clear supernatant with a pipette and discard.

Bead Wash

4. Remove the tube from the magnetic rack and resuspend beads with the appropriate volume of **Bead Wash Buffer** (see table below). Ensure that all beads are fully resuspended and not stuck to the side of the tube.

	Volume to Add by Number of Sublibrary Lysates (µL)	
# Sublibrary Lysates	1	2
Bead Wash Buffer (µL)	50	100

5. Capture the **Binder Beads** to a magnet using a magnetic rack (for 1.5 mL tubes) and wait until liquid becomes clear (~2 min).
6. Remove the clear supernatant with a pipette and discard.
7. Repeat steps 4-6 twice more for a total of three washes.

Bind Buf. A

8. Remove the tube from the magnetic rack and resuspend beads in the appropriate volume of **Bind Buffer A** (see table below). Keep beads at room temperature and proceed to Section 2.2.

	Volume to Add by Number of Sublibrary Lysates (µL)	
# Sublibrary Lysates	1	2
Bind Buffer A (µL)	55	110

2.2 Applying Binder Beads to Sublibrary Lysates

5 min

1. Remove the desired sublibrary lysates from the -80°C freezer and incubate at **37°C** for **5 minutes**, ensuring that no precipitate is present before proceeding. If precipitate is still present, incubate at 37°C for 5 more minutes.

Lysis Neut

2. Briefly centrifuge sublibrary lysates (~2 sec).
3. Gently centrifuge the **Lysis Neutralizer**, mix gently with a pipette, and add **2.5 µL** to each sublibrary lysate. Mix 5x with a P200 pipette (set to 40 µL), taking care not to lose any volume. Briefly centrifuge (~2 sec), and incubate at room temperature for **10 minutes**.

10 min

4. **Add Binder Beads to sublibrary lysates.** First mix the **Binder Beads** suspended in **Bind Buffer A** by pipetting up and down. Then add **50 µL** to each sublibrary lysate. Mix 5x with a P200 pipette (set to 90 µL), taking care not to lose any volume. Discard the tube with any excess **Binder Beads.**

60 min

5. Agitate the sublibrary lysates with **Binder Beads** at room temperature for **60 minutes**. Place the tubes in a 96-well plastic plate holder (press tubes securely into the holder) with the lid on and then put the plastic holder into a foam attachment for a vortexer. Vortex on 2 (out of 10) for the duration of the 60 minute incubation (~800-1000 RPM).
6. Take the tubes off of the vortexer (beads may have settled somewhat). Vortex briefly (~5 sec) and then briefly centrifuge (~1 sec) without letting beads collect at the bottom of the tubes.
7. Place the tubes against a magnetic rack (for 0.2 mL tubes) on the high position (with magnets closest to the top) and wait for all the beads to bind to the magnet (~2 min).

CRITICAL! The supernatant should be clear before proceeding. The cDNA is unamplified at this step, so discarding any beads in the supernatant will result in a reduction of transcripts and genes detected per cell.

8. Remove the clear supernatant with a pipette and discard, while still keeping the tubes in the magnetic rack.

Bind Buf. B

9. Remove tubes from the magnetic rack and resuspend beads with **125 µL** of **Bind Buffer B**.
10. Keep tubes at room temperature for **1 minute**.

11. Place the tubes against a magnetic rack (high setting) and wait for all the beads to bind to the magnet (~2 min: liquid should be clear).
12. Remove the clear supernatant with a pipette and discard, while still keeping the tubes in the magnetic rack.
13. Repeat steps 9-12 for a second wash using **Bind Buffer B**.
14. Remove tubes from magnetic rack and resuspend beads with **125 µL Bead Storage Buffer**.
15. Keep tubes at room temperature for **1 minute**.
16. Proceed directly to Section 2.3: Template Switch.

2.3 Template Switch

1. Gather the following items and handle as indicated below:

Item	Location	Quantity	Format	After taking out
TS Primer Mix	cDNA Amplification (-20°C)	1	1.5 mL tube	Thaw, then place on ice.
TS Enzyme	cDNA Amplification (-20°C)	1	1.5 mL tube	Place directly on ice.

2. Ensure that the **TS Buffer** is fully thawed and has no white precipitate before proceeding.
3. In a new 1.5 mL tube, make the **Template Switch Mix** by adding the following volumes of **TS Buffer**, **TS Primer Mix**, and **TS Enzyme** together. Mix well and store on ice.

		Volume to Add by Number of Sublibraries (µL)	
# Sublibraries		**1**	**2**
TS Buffer	TS Buffer	101.75	203.5
TS Primer	TS Primer Mix	2.75	5.5
TS Enzyme	TS Enzyme	5.5	11
Total		**110**	**220**

4. Place the sublibrary tubes against a magnetic rack (for 0.2 mL tubes) on the high position and wait for all the beads to bind to the magnet (~2 min: liquid should be clear).

CRITICAL! The supernatant should be clear before proceeding. The cDNA is unamplified at this step, so discarding any beads in the supernatant will result in a reduction of transcripts and genes detected per cell.

5. Remove the clear supernatant with a pipette and discard while still keeping the tubes in the magnetic rack.

Bind Buf. C

6. Without resuspending beads, add **125 µL** of **Bind Buffer C** and wait **1 minute.**

CRITICAL! Do NOT discard the supplied stock tube of **Bind Buffer C** as it will be needed in another step.

7. Without removing tubes (still in magnetic rack), remove and discard **Bind Buffer C** from each tube using a pipette.

8. Remove tubes from the magnetic rack and resuspend beads with **100 µL** of **Template Switch Mix**.

   *Note: **Template Switch Mix** is a viscous solution. Ensure that beads are fully resuspended and mixed well before proceeding.*

9. Centrifuge tubes very briefly (~1 sec). Longer centrifugation will cause beads to settle.

30 min

10. Incubate sublibraries at room temperature for **30 minutes**.

90 min

11. Mix sublibraries by pipetting 5x, ensuring that beads that may have settled are resuspended. Be careful to prevent any losses of bead volumes while pipetting. Incubate sublibraries in a thermocycler with the following protocol:

Sublibrary Template Switching		
Run Time	**Lid Temperature**	**Sublibrary Volume**
90 min	70°C	100 µL
Step	**Time**	**Temperature**
1	90 min	42°C
2	Hold	4°C

STOP

12. If you would like to stop and store sublibraries, proceed with the following steps. If you are continuing the protocol, proceed directly to Section 2.4: cDNA Amplification.

    Note: You may need to pipette mix to resuspend settled beads.

    a. Place the tubes against a magnetic rack (high position) and wait for all the beads to bind to the magnet (~2 min: liquid should be clear).

    b. Remove the clear supernatant with a pipette and discard, while still keeping the tubes in the magnetic rack.

Bead Storage

    c. Resuspend beads in **125 µL** of **Bead Storage Buffer**.

    d. Store tubes at 4°C overnight. Do not freeze sublibraries.

[STOPPING POINT]

2.4 cDNA Amplification

Multiple thermocyclers may be needed for this section depending on your sample types and sublibrary sizes. Refer to step 2.4.8 (next page) to determine how many thermocyclers are needed.

1. Gather the following items and handle as indicated below:

Item	Location	Quantity	Format	After taking out
Amp Master Amplification Master Buffer	cDNA Amplification (-20°C)	1	1.5 mL tube	Thaw, then place on ice.
Amp Primer Amplification Primer Mix	cDNA Amplification (-20°C)	1	1.5 mL tube	Thaw, then place on ice.

2. In a new 1.5 mL tube, make the **Amplification Reaction Solution** by adding the following volumes of **Amplification Master Buffer** and **Amplification Primer Mix**. Mix well and store on ice.

	Volume to Add by Number of Sublibraries (µL)	
# Sublibraries	**1**	**2**
Amp Master Amplification Master Buffer	60.5	121
Amp Primer Amplification Primer Mix	60.5	121
Total	**121**	**242**

3. Place the tubes against a magnetic rack (high setting) and wait for all the beads to bind to the magnet (~2 min: liquid should be clear).
4. Remove the clear supernatant with a pipette and discard while still keeping the tubes in the magnetic rack.
5. Bind Buf. C Without removing tubes (still in magnetic rack), add **125 µL** of **Bind Buffer C** and wait **1 minute.** Do not remove the tubes from the magnetic rack during this time.
6. Remove the clear supernatant with a pipette and discard.
7. Remove tubes from magnetic rack and resuspend beads in each tube with **100 µL** of the **Amplification Reaction Solution**. Place tubes with **Amplification Reaction Solution** on ice.

8. For each sublibrary, determine the cDNA amplification cycling conditions. Only the number of 2nd cycles (**X**) changes with cell type and sublibrary size. Below are recommended cycling conditions for commonly used cell types.

	Number of Cells/Nuclei in Individual Sublibrary	Number of 1st Cycles (PCR Steps 2-4)	Number of 2nd Cycles (X) (PCR Steps 5-7)
Mammalian Cell Lines	200-1,000	5	12
	1,000-2,000	5	10
	2,000-6,000	5	8
	6,000-10,000	5	6
Nuclei	200-1,000	5	13
	1,000-2,000	5	11
	2,000-6,000	5	9
	6,000-10,000	5	7
Immune Cells (PBMCs)	200-1,000	5	14
	1,000-2,000	5	12
	2,000-6,000	5	10
	6,000-10,000	5	8

Note: 1-2 cycles may need to be added (to 2nd cycling) to account for cells with low RNA content. The cycling protocol may need to be optimized for your sample type.

60-100 min

9. Start cDNA amplification. Group sublibraries with the same cycling conditions in their own thermocycler with the following protocol, adjusting the number of 2nd cycles (**X**), according to the table on step 2.4.8 (previous page).

Note: For primer annealing, steps 3 and 6 below (*) have different time and temperature settings. Double check the settings inputted into the thermocycler before starting the amplification protocol.

Amplification Protocol		
Run Time	**Lid Temperature**	**Sublibrary Volume**
50-70 min	105°C	100 µL
Step	**Time**	**Temperature**
1	3 min	95°C
	Begin 1st Cycling	
2	20 sec	98°C
3	***45 sec**	***65°C**
4	3 min	72°C
	Go to step 2, repeat 4 times (5 cycles total)	
	Begin 2nd Cycling	
5	20 sec	98°C
6	***20 sec**	***67°C**
7	3 min	72°C
	*Go to step 5, repeat **X - 1** times (**X** cycles total)*	
8	5 min	72°C
9	Hold	4°C

*Example: If you had 500 cells (with medium to high RNA content), your cycling conditions would be: 5 (first cycling) and 12 (second cycling). In this scenario, you would "Go to step 2, repeat 4 times (5 cycles total)" and "Go to step 5, repeat **11** times (**12** cycles total)".*

10. Remove tubes from the thermocycler. Sublibraries can be stored at this point at 4°C overnight. If you wish to continue, proceed directly to Section 2.5: Post-Amplification SPRI Clean Up.

[STOPPING POINT]

2.5 Post-Amplification SPRI Clean Up

1. Place the sublibrary tubes against a magnetic rack (for 0.2 mL tubes) on the high position and wait for all the beads to bind to the magnet (~2 min: liquid should be clear).

CRITICAL! Do NOT discard the supernatant at this step.

2. Transfer 90 µL of the clear supernatant into new 200 µL PCR tubes. Discard the original tubes with the magnetic beads.

3. Remove SPRI beads (Ampure XP or KAPA Pure Beads) from the 4°C fridge and aliquot the following amount into a 1.5 mL tube (this accounts for 10% extra volume):

	Volume to Add by Number of Sublibraries (µL)	
# Sublibraries	**1**	**2**
SPRI Beads Needed	79	158

4. Prepare a fresh 85% ethanol solution (400 µL) for each sublibrary.

5. Add **72 µL** of SPRI beads to each sublibrary (90 µL) for a total volume of 162 µL.

6. Close the tops of all the tubes securely, vortex (~5 sec), then centrifuge briefly (~2 sec).

7. Incubate at room temperature for **5 minutes.**

8. Place the tubes against a magnetic rack on the high position and wait for all the beads to bind to the magnet (~2 min: liquid should be clear).

9. With SPRI beads still against the magnetic rack, aspirate and discard the clear supernatant with a pipette.

10. Without resuspending beads, add **180 µL** of 85% ethanol and wait for **1 minute**.

11. Using a pipette, aspirate and discard the ethanol from each tube.

12. Without resuspending beads, add another **180 µL** of 85% ethanol and wait for **1 minute**.

13. Using a pipette, aspirate and discard all of the ethanol from each tube (it may be necessary to remove the final few drops with a P20 pipette). With the tube still on the rack, air dry the beads (~2 min).

CRITICAL! Do NOT over-dry the beads. Over-drying of beads can lead to substantial losses in yield. “Cracking” of the beads is a sign of over-drying.

14. Remove the tubes from the magnetic rack and resuspend beads from each tube in **20 µL** of molecular biology grade water.

15. Incubate the tubes at **37°C** for **10 minutes** to maximize elution of amplified cDNA.

16. Place the tubes against a magnetic rack on the low position (with magnets closest to the bottom) and wait for all the beads to bind to the magnet (~2 min: liquid should be clear).

17. Transfer **20 µL** of the eluted DNA into new PCR tubes with a P200 pipette. Discard the tubes with the SPRI beads. The amplified cDNA is now ready to be quantified.

    Note: Label the new PCR tubes as cDNA to avoid confusion in subsequent steps.

18. Measure the concentration of the cDNA using the Qubit dsDNA HS protocol.

    Note: Be sure to record sample concentrations as they will be needed for further downstream steps (Section 3.5: Sublibrary Index PCR).

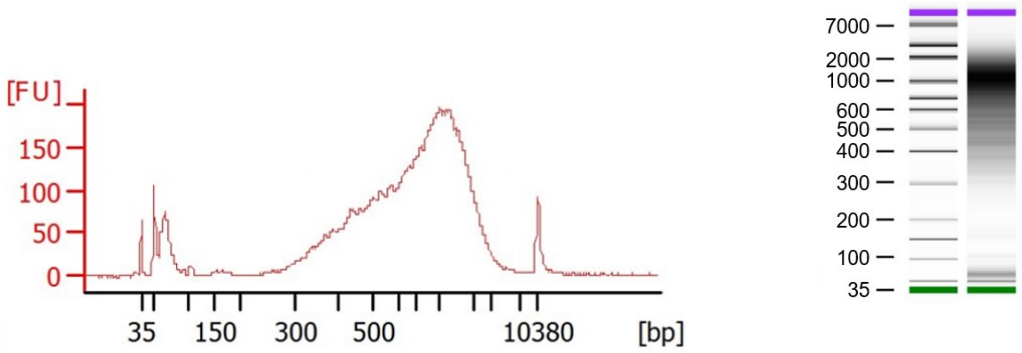
19. Run 1 µL of the cDNA on a Bioanalyzer or TapeStation. Use the concentration obtained from the Qubit to determine the appropriate dilution necessary (check manufacturer specifications, 1:10 dilution is generally appropriate). See Figure 1 (next page) for the expected cDNA size distribution.

20. Sublibraries can be stored at this point at 4°C for up to 2 days or at -20°C for up to 3 months. If you wish to continue, proceed directly to Section 3: Preparing Libraries for Sequencing.

[STOPPING POINT]

.

A



B

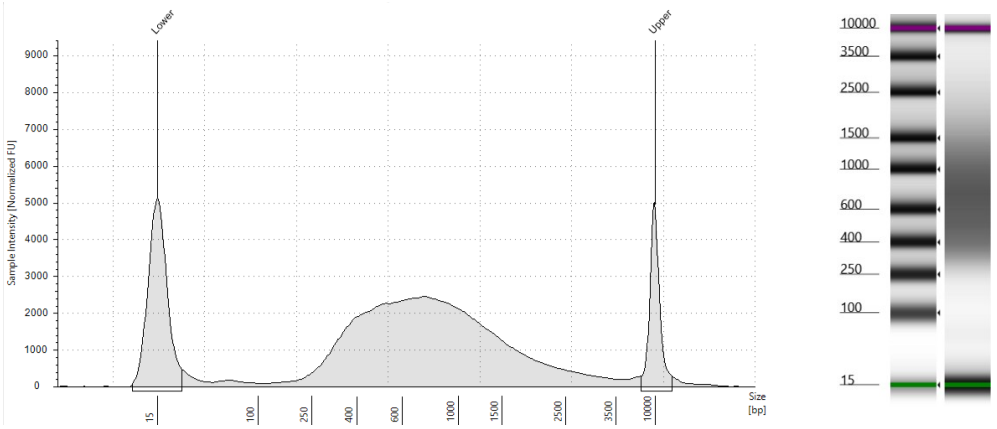


Fig. 1: Expected cDNA Size Distribution after cDNA Amplification. (A) Example trace of cDNA run on a Bioanalyzer. (B) Example trace of cDNA run on a TapeStation (it is normal for libraries to be shifted to the left on a TapeStation relative to a Bioanalyzer).

Note: The traces above are representative of typical Bioanalyzer and TapeStation cDNA traces. The shape and prominence of the trace is dependent on cell type, sublibrary size, and amount of DNA loaded into the Bioanalyzer or TapeStation. Sublibraries with minor deviations can still produce high quality data.

SECTION 3

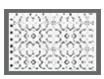
PREPARING LIBRARIES FOR SEQUENCING

Setup

- ☐ Prepare ~1.2 mL 85% ethanol per sublibrary lystate (e.g. 2.4 mL for 2 sublibraries).
- ☐ Fill an ice bucket.
- ☐ Take out the Parse Biosciences magnetic rack for 0.2 mL PCR tubes.
- ☐ Ensure you have at least 176 µL SPRI beads (Ampure XP or KAPA Pure Beads) per sublibrary. These will be used throughout Section 3.
- ☐ Obtain recorded cDNA concentrations from step 2.5.18.

Note: If using an already opened UDI - WT plate, confirm you have at least 2 unused UDI wells remaining before starting the protocol.

Gather the following items and handle as indicated below:

Item	Location	Quantity	Format	After taking out
 Fragmentation Buffer	Fragmentation (-20°C)	1	1.5 mL tube	Thaw, then place on ice.
 Adaptor DNA	Fragmentation (-20°C)	1	1.5 mL tube	Thaw, then place on ice.
 Index PCR Mix	Fragmentation (-20°C)	1	1.5 mL tube	Thaw, then place on ice.
 Adaptor Ligation Buffer	Fragmentation (-20°C)	1	1.5 mL tube	Thaw, then place on ice.
 Fragmentation Enzyme	Fragmentation (-20°C)	1	1.5 mL tube	Place directly on ice.
 Adaptor Ligase	Fragmentation (-20°C)	1	1.5 mL tube	Place directly on ice.
 UDI Plate - WT (SKU: UDI1001)	UDI Plate - WT (-20°C)	1	96-well plate	Thaw, then place on ice.

3.1 Fragmentation, End Repair, and A-Tailing

1. Vortex amplified cDNA briefly (2-3 sec). Be sure to keep caps closed on tubes. Briefly centrifuge tubes (~2 sec).
2. For each sublibrary to be sequenced, aliquot out **100 nanograms** into a PCR strip tube and bring the total volume to **35 µL** using molecular biology grade water. Ensure that concentrations obtaining from the Qubit, not the Bioanalyzer, are used to aliquot 100 ng. Store any remaining cDNA at -20°C to be used for future experiments.

   Note 1: Keep these tubes on ice.

   Note 2: If you have less than 100 ng of cDNA for a given sublibrary, add the entire amount of cDNA at this step. This will not affect the quality of your libraries. Successful libraries can be prepared from as little as 10 ng of cDNA. Record the amount added to each tube as subsequent PCR cycles will have to be adjusted based on cDNA concentration.
3. Set the thermocycler to the following program:

Sublibrary Fragmentation, End Repair, and A-Tailing		
Run Time	**Lid Temperature**	**Sublibrary Volume**
40 min	70°C	50 µL
Step	**Time**	**Temperature**
1	Hold	4°C
2	10 min	32°C
3	30 min	65°C
4	Hold	4°C

4. Initiate the thermocycling program such that the machine is pre-cooled to 4°C.
5. Vortex the **Fragmentation Buffer** followed by a brief centrifugation (~2 sec) and confirm it is fully thawed (no precipitate).
6. Using a new 1.5 mL tube, combine the **Fragmentation Buffer** and **Fragmentation Enzyme** to make the **Fragmentation Mix**. Mix well by pipetting 10x and store on ice.

		Volume to Add by Number of Sublibraries (µL)	
# Sublibraries		1	2
Frag Buf.	Fragmentation Buffer	5.5	11
Frag Enzyme	Fragmentation Enzyme	11	22
Total		**16.5**	**33**

7. Add **15 µL** of **Fragmentation Mix** to each sublibrary, bringing the total volume to 50 µL, and keep on ice.
8. Mix sublibraries 10x with a P200 multichannel pipette set to 40 µL. Briefly centrifuge sublibraries (~2 sec) and place back on ice.

40 min

9. Place tubes in the chilled thermocycler and press “skip” or similar option to allow the machine to proceed to next step. Confirm that the thermocycler has elevated to 32°C and has proceeded to the rest of the protocol before leaving the machine.
10. Proceed directly to Section 3.2 after the thermocycling protocol finishes.

3.2 Post-Fragmentation Double-Sided SPRI Selection

1. Remove your SPRI beads (Ampure XP or KAPA Pure Beads) from the 4°C fridge and aliquot the following amount into a 1.5 mL tube (this accounts for 10% extra volume):

	Volume to Add by Number of Sublibraries (µL)	
# Sublibraries	**1**	**2**
SPRI Beads Needed	44	88

2. Add **30 µL** of SPRI beads to the 50 µL of fragmented sublibraries and vortex briefly (2-3 sec) followed by a brief centrifugation (~2 sec).
3. Incubate at room temperature for **5 minutes.**
4. Place the sublibrary tubes against a magnetic rack (for 0.2 mL tubes) on the high position (with magnets closest to the top) and wait for all the beads to bind to the magnet (~2 min: liquid should be clear).

CRITICAL! Do NOT discard the supernatant at this step.

5. With SPRI beads still against the magnetic rack, transfer **75 µL** of the clear supernatant into new 200 µL PCR tubes. Discard the tubes with the SPRI beads.
6. Add **10 µL** of SPRI beads to the 75 µL of supernatant and vortex briefly (2-3 sec) followed by a brief centrifugation (~2 sec).
7. Incubate at room temperature for **5 minutes.**

8. Place the tubes against a magnetic rack on the high position and wait for all the beads to bind to the magnet (~2 min: liquid should be clear).

CRITICAL! This may take longer than other SPRI bead binding due to the low volume of beads. Ensure that all of the beads have bound before proceeding.

9. With SPRI beads still against the magnetic rack, aspirate and discard the clear supernatant with a pipette.

10. Without resuspending beads, add **180 µL** of 85% ethanol and wait for **1 minute**.

11. Using a pipette, aspirate and discard the ethanol from each tube.

12. Without resuspending beads, add **180 µL** of 85% ethanol and wait for **1 minute**.

13. Using a pipette, aspirate and discard all of the ethanol from each tube (it may be necessary to remove the final few drops with a P20 pipette). Air dry the beads (only ~30 seconds due to the small amount of beads).

CRITICAL! Do NOT over-dry the beads. Over-drying of beads can lead to substantial losses in yield. “Cracking” of the beads is a sign of over-drying.

14. Remove the tubes from the magnetic rack and resuspend beads from each tube in **50 µL** of molecular biology grade water.

15. Incubate the tubes at room temperature for **5 minutes** to elute fragmented DNA.

16. Place the tubes against a magnetic rack on the high position and wait for all the beads to bind to the magnet (~2 min: liquid should be clear).

17. Transfer exactly **50 µL** of the eluted DNA into new PCR tubes. Discard the tubes with SPRI beads.

18. Sublibraries can be stored at this point at 4°C overnight or at -20°C for up to 2 weeks. If you wish to continue, proceed directly to section 3.3: Adaptor Ligation.

[STOPPING POINT]

3.3 Adaptor Ligation

1. Make the **Adaptor Ligation Mix**, in the order shown below. Ensure that all reagents are fully thawed and mixed well before using. Mix the **Adaptor Ligation Mix** by pipetting and store on ice.

		Volume to Add by Number of Sublibraries (µL)	
# Sublibraries		**1**	**2**
Water	Nuclease-free water (not supplied)	19.25	38.5
Adapt Buffer	Adaptor Ligation Buffer	22	44
Adapt Ligase	Adaptor Ligase	11	22
Adapt DNA	Adaptor DNA	2.75	5.5
Total		**55**	**110**

2. Add **50 µL** of the **Adaptor Ligation Mix** to the 50 µL of the eluted DNA (from the end of Section 3.2).
3. Mix sublibraries 10x with a P200 pipette set to 80 µL. Briefly centrifuge sublibraries (~2 sec).
4. Put the tubes into a thermocycler with the following protocol:

15 min

Sublibrary Adaptor Ligation		
Run Time	**Lid Temperature**	**Sublibrary Volume**
15 min	30°C	100 µL
Step	**Time**	**Temperature**
1	15 min	20°C
2	Hold	4°C
Proceed Directly to Next Step		

5. Proceed directly to the next step. Do NOT leave the tube in the thermocycler for longer than the indicated time.

3.4 Post-Ligation SPRI Clean Up

1. Remove SPRI beads (Ampure XP or KAPA Pure Beads) from the 4°C fridge and aliquot the following amount into a 1.5 mL tube (this accounts for 10% extra volume):

	Volume to Add by Number of Sublibraries (µL)	
# Sublibraries	**1**	**2**
SPRI Beads Needed	88	176

2. Add **80 µL** of SPRI beads to each sublibrary (100 µL) to a total volume of 180 µL. Ensure the caps are secured and then vortex briefly (2-3 sec) followed by a brief centrifugation (~2 sec).
3. Incubate at room temperature for **5 minutes.**
4. Place the sublibrary tubes against a magnetic rack (for 0.2 mL tubes) on the high position and wait for all the beads to bind to the magnet (~2 min: liquid should be clear).
5. With SPRI beads still against the magnetic rack, aspirate and discard the clear supernatant with a pipette.
6. Without resuspending beads, add **180 µL** of 85% ethanol and wait for **1 minute**.
7. Using a pipette, aspirate and discard the ethanol from each tube.
8. Without resuspending beads, add another **180 µL** of 85% ethanol and wait for **1 minute**.
9. Using a pipette, aspirate and discard all of the ethanol from each tube (it may be necessary to remove the final few drops with a P20 pipette). Air dry the beads (~3 min).

CRITICAL! Do NOT over-dry the beads. Over-drying of beads can lead to substantial losses in yield. “Cracking” of the beads is a sign of over-drying.

10. Remove the tubes from the magnetic rack and resuspend beads from each tube in **23 µL** of molecular biology grade water.
11. Incubate the tubes at room temperature for **5 minutes** to elute DNA.
12. Place the tubes against a magnetic rack on the low position (with magnets closest to the bottom) and wait for all the beads to bind to the magnet (~2 min: liquid should be clear).
13. Transfer exactly **21 µL** of the eluted DNA into new PCR tubes. Discard the tubes with the SPRI beads.

3.5 Sublibrary Index PCR

If using the alternative version of Evercode WT Mini v2 (ECW02010) that includes SX100 instead of SX200, follow the protocol modifications described in Appendix D.

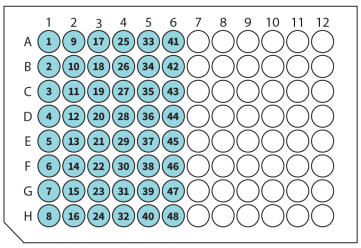
Multiple thermocyclers may be needed for this section depending on the amount of cDNA added to each sublibrary during the fragmentation reaction. Refer to step 3.5.6.

1. Ensure that each well of the **UDI Plate - WT** is properly thawed. Centrifuge the plate at ***100 x g*** for **1 minute**.

CRITICAL! Double-check the label on the plate as specific plates are used in different protocols.

2. Thoroughly wipe the **UDI Plate - WT** seal with 70% ethanol and allow it to dry completely.

Note: Before proceeding, ensure the UDI Plate is properly orientated. The notched corner should be in the bottom left (see image on the right). Only wells from columns 1-6, and only one well/sublibrary can be used.



3. Add well-specific index primers from the **UDI Plate - WT** to your sublibraries as follows:

   - Using a multichannel P20 pipette set to 4 µL, pierce new, unused wells of the **UDI Plate - WT**. Mix 5x then transfer **4 µL** of the index primer solution into your sublibraries.

     Note: Ensure that no two sublibraries contain index primers from the same well. To minimize cross-contamination, use a new pipette tip for each sublibrary and avoid splashing or mixing the liquid between individual wells.

   - For each sublibrary, record the **UDI Plate - WT's** well position (e.g., 'A1', 'B1') and sublibrary index ID (see Section 4.1) for sequencing and demultiplexing purposes.

4. If the **UDI Plate - WT** has unused wells, store it at -20°C for future use.

Index PCR Mix

5. Add **25 µL** of the **Index PCR Mix** to each sublibrary, bringing the total volume to 50 µL. Pipette up and down 10x with the pipette set to 25 µL to ensure proper mixing, followed by brief centrifugation (~2 sec).

CRITICAL! Different tips must be used when pipetting **Index PCR Mix** into each sublibrary. Never place a tip that has entered a sublibrary back into the **Index PCR Mix**.

~30 min

6. Place the sample(s) into a thermocycler and run the program below. The number of cycles (**X**) should be adjusted based on the amount of cDNA added to the fragmentation reaction.

Sublibrary Index Amplification		
Run Time	**Lid Temperature**	**Sublibrary Volume**
~30 min	105°C	50 µL
Step	**Time**	**Temperature**
1	3 min	95°C
	Begin Cycling	
2	20 sec	98°C
3	20 sec	67°C
4	1 min	72°C
	*Go to step 2, repeat **X-1** times (**X** cycles total)*	
5	5 min	72°C
6	Hold	4°C

	PCR Cycles based on cDNA in Fragmentation			
cDNA in Fragmentation (ng)	**10-24**	**25-49**	**50-99**	**100+**
Total PCR Cycles Required (**X**)	13	12	11	10

Note: The amount of cDNA per sublibrary inputted into the fragmentation reaction was recorded in step 3.1.2.

7. Sublibraries can be stored at this point at 4°C overnight. If you wish to continue, proceed directly to Section 3.6: Post-Amplification Double-Sided Size Selection.

[STOPPING POINT]

3.6 Post-Amplification Double-Sided SPRI Selection

1. Remove SPRI beads (Ampure XP or KAPA Pure Beads) from the 4°C fridge and aliquot the following amount into a 1.5 mL tube (this accounts for 10% extra volume):

	Volume to Add by Number of Sublibraries (µL)	
# Sublibraries	**1**	**2**
SPRI Beads Needed	44	88

2. For each sublibrary, add **30 µL** of SPRI beads to the 50 µL of fragmented sublibraries (80 µL total volume). Vortex briefly (2-3 sec) followed by a brief centrifugation (~2 sec).
3. Incubate at room temperature for **5 minutes.**
4. Place the tubes against a magnetic rack (for 0.2 mL tubes) on the high position and wait for all the beads to bind to the magnet (~2 min: liquid should be clear).

CRITICAL! Do NOT discard the supernatant at this step.

5. With SPRI beads still against the magnetic rack, transfer **75 µL** of the clear supernatant into new PCR tubes. Discard the tubes with the SPRI beads.
6. Add **10 µL** of SPRI beads to the 75 µL of supernatant. Vortex briefly (2-3 sec) followed by a brief centrifugation (~2 sec).
7. Incubate at room temperature for **5 minutes.**
8. Place the tubes against a magnetic rack on the high position and wait for all the beads to bind to the magnet (~2 min: liquid should be clear).

CRITICAL! This may take longer than other SPRI bead binding due to the low volume of beads. Ensure that all of the beads have bound before proceeding.

9. With SPRI beads still against the magnetic rack, aspirate and discard the clear supernatant with a pipette.
10. Without resuspending beads, add **180 µL** of 85% ethanol and wait for **1 minute**.
11. Using a pipette, aspirate and discard the ethanol from each tube.
12. Without resuspending beads, add another **180 µL** of 85% ethanol and wait for **1 minute**.

13. Using a pipette, aspirate and discard all of the ethanol from each tube (it may be necessary to remove the final few drops with a P20 pipette). Air dry the beads (as little as 30 seconds due to the small amount of beads).

CRITICAL! Do NOT over-dry the beads. Over-drying of beads can lead to substantial losses in yield. “Cracking” of the beads is a sign of over-drying.

14. Remove tubes from magnet and resuspend beads from each tube in **20 µL** of molecular biology grade water.

15. Incubate the tube at room temperature for **5 minutes** to elute DNA.

16. Place the tubes against a magnetic rack (**low setting**) and wait for all the beads to bind to the magnet (~2 min: liquid should be clear).

17. Transfer the elutant into new PCR tubes. Discard the tubes with the SPRI beads. The products are now ready to be quantified for sequencing.

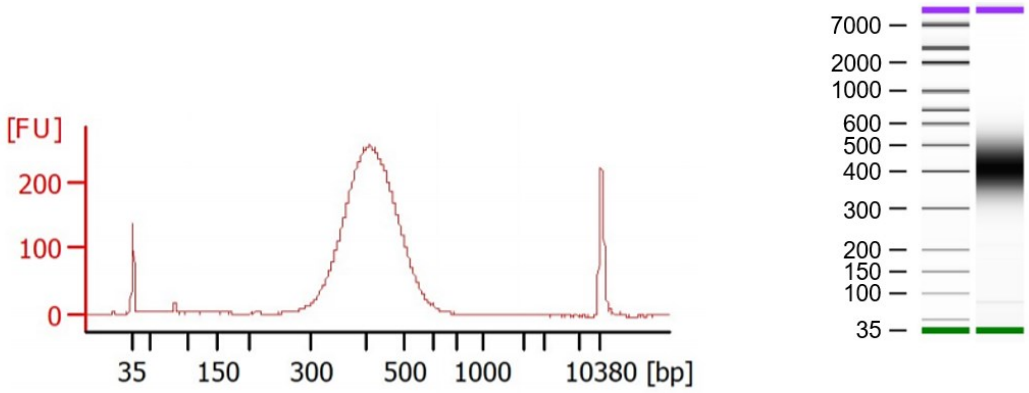
18. Measure the concentration of the fragmented cDNA using the Qubit dsDNA HS protocol.

19. Run 1 µL of the elutant on a Bioanalyzer or TapeStation. Use the concentrations obtained from the Qubit to determine the appropriate dilution necessary (check manufacturer specifications, 1:10 dilution is generally appropriate). There should be a peak between 400-500 bp. See Figure 2 (next page) for the expected DNA size distribution.

20. Sublibraries can be stored at this point at -20°C for up to 3 months. If you wish to continue, proceed directly to Section 4: Sequencing Libraries.

[STOPPING POINT]

A



B

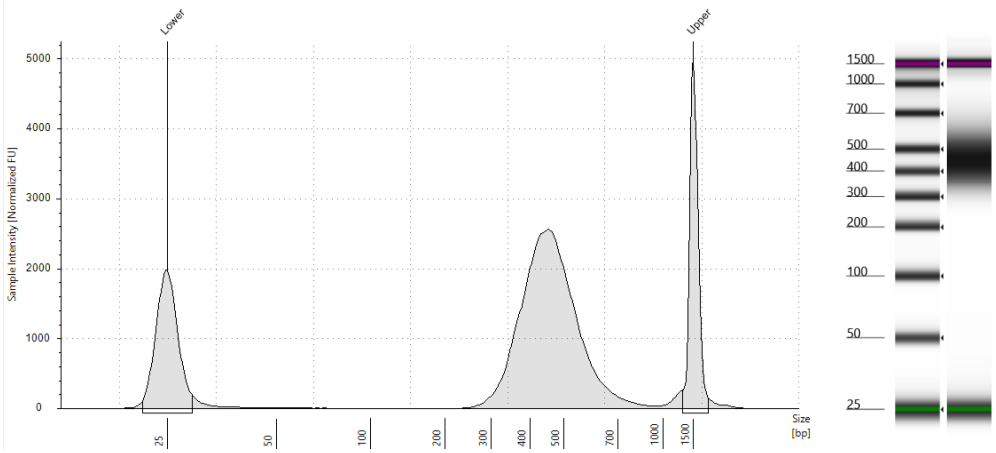


Fig. 2: Expected Size Distribution before Illumina Sequencing (A) Example trace of DNA from indexed sublibraries run on a Bioanalyzer. (B) Example trace of DNA from indexed sublibraries run on a TapeStation.

Note: The traces above are representative of typical Bioanalyzer and TapeStation of DNA from indexed sublibraries. There should be a peak between 400-500 bp. The prominence of the trace is dependent on amount of DNA loaded into the Bioanalyzer or TapeStation. Sublibraries with minor deviations can still produce high quality data.

Bioanalyzer Note: There may be an additional peak present on the Bioanalyzer. This typically occurs if products are overamplified, but should not impact sequencing or data quality (assuming there is still a peak present at 400-500 bp). Do not use this additional peak when estimating amplicon size.

SECTION 4

SEQUENCING LIBRARIES

4.1 ILLUMINA RUN CONFIGURATION

4.1 Illumina Run Configuration

If single indexing primers were used in Section 3, see Appendix D2. Otherwise, use the following UDI-specific Illumina run configuration and sequence information.

Evercode sequencing libraries should be diluted and denatured according to the instruction for the relevant sequencing instrument. We strongly recommend adding 5% PhiX for optimal sequencing quality. Libraries should be sequenced with paired reads using the following read structure.

Read	Cycles
Read 1	66
i7 Index (Index 1)	8
i5 Index (Index 2)	8
Read 2	86

The fourth barcode that tags each sublibrary acts as a standard Illumina UDI with i7 and i5 indexes. Please refer to the following table to demultiplex Whole Transcriptome sublibraries with UDIs that were sequenced together in the same run.

Sublibrary Index ID	Well Position	i7 Forward Sequence (For Sample Sheet)	i5 Reverse Complementary Sequence	i5 Forward Sequence
UDI_WT_1	A1	CAGATCAC	ATGTGAAG	CTTCACAT
UDI_WT_2	B1	ACTGATAG	GTCCAACC	GGTTGGAC
UDI_WT_3	C1	GATCAGTC	AGAGTCAA	TTGACTCT
UDI_WT_4	D1	CTTGTAAT	AGTTGGCT	AGCCAACT
UDI_WT_5	E1	AGTCAAGA	ATAAGGCG	CGCCTTAT
UDI_WT_6	F1	CCGTCCTA	CCGTACAG	CTGTACGG
UDI_WT_7	G1	GTAGAGTA	CATTCATG	CATGAATG
UDI_WT_8	H1	GTCCGCCT	AGATACGG	CCGTATCT
UDI_WT_9	A2	GTGAAACT	TACAGACT	AGTCTGTA
UDI_WT_10	B2	TCATTCCT	AATGCCTG	CAGGCATT
UDI_WT_11	C2	GGTAGCAT	TGCTTGCC	GGCAAGCA
UDI_WT_12	D2	ACTTGATC	TTTGGGTG	CACCCAAA
UDI_WT_13	E2	ATGAGCAT	GAATCTGA	TCAGATTC
UDI_WT_14	F2	GCGCTATC	CGACTGGA	TCCAGTCG
UDI_WT_15	G2	TGACCAGT	ACATTGGC	GCCAATGT
UDI_WT_16	H2	TATAATCA	ACCACTGT	ACAGTGGT
UDI_WT_17	A3	CAAAAGTC	CGGTTGTT	AACAACCG
UDI_WT_18	B3	CGATGTCA	CATGAGGA	TCCTCATG

Sublibrary Index ID	Well Position	i7 Forward Sequence (For Sample Sheet)	i5 Reverse Complementary Sequence	i5 Forward Sequence
UDI_WT_19	C3	CTCAGAGT	TGGAGAGT	ACTCTCCA
UDI_WT_20	D3	TAATCGAC	TGACTTCG	CGAAGTCA
UDI_WT_21	E3	CATTTTCT	GGAAGGAT	ATCCTTCC
UDI_WT_22	F3	CTATACTC	TGTTCGAG	CTCGAACA
UDI_WT_23	G3	CACTCACA	AAGGCTGA	TCAGCCTT
UDI_WT_24	H3	CTCGAACA	CTCGAGTG	CACTCGAG
UDI_WT_25	A4	CTCTATCG	ATCGGTGG	CCACCGAT
UDI_WT_26	B4	TCCTCATG	AGGTCTTG	CAAGACCT
UDI_WT_27	C4	AACAACCG	AGGAAGCG	CGCTTCCT
UDI_WT_28	D4	GCCAATGT	ACATGTGT	ACACATGT
UDI_WT_29	E4	TGGTTGTT	ATACAGTT	AACTGTAT
UDI_WT_30	F4	TCTGCTGT	ATCGCCTT	AAGGCGAT
UDI_WT_31	G4	TTGGAGGT	TTCGACGC	GCGTCGAA
UDI_WT_32	H4	TCGAGCGT	TGTCGTTC	GAACGACA
UDI_WT_33	A5	TGCGATCT	TCCATAGC	GCTATGGA
UDI_WT_34	B5	TTCCTGCT	TAAGTGTC	GACACTTA
UDI_WT_35	C5	TTCCATTG	CTGGCATA	TATGCCAG
UDI_WT_36	D5	TAACGCTG	CTGAGCCA	TGGCTCAG
UDI_WT_37	E5	TTGGTATG	CTCAATGA	TCATTGAG
UDI_WT_38	F5	TGAACTGG	CGCATACA	TGTATGCG
UDI_WT_39	G5	TCCAGTCG	CCGAAGTA	TACTTCGG
UDI_WT_40	H5	TGTATGCG	CCAGTTCA	TGAACTGG
UDI_WT_41	A6	TGGCTCAG	CAGCGTTA	TAACGCTG
UDI_WT_42	B6	TATGCCAG	CAATGGAA	TTCCATTG
UDI_WT_43	C6	GGTTGGAC	ATCCTGTA	TACAGGAT
UDI_WT_44	D6	GACACTTA	AGCAGGAA	TTCCTGCT
UDI_WT_45	E6	GAACGACA	ACGCTCGA	TCGAGCGT
UDI_WT_46	F6	AAGGCGAT	ACAGCAGA	TCTGCTGT
UDI_WT_47	G6	ATGCTTGA	ACAAGCTA	TAGCTTGT
UDI_WT_48	H6	AGTATCTG	CATCAAGT	ACTTGATG

APPENDIX

Appendix A: Sublibrary Generation Table

Green text (top): Volume of cell suspension (from step 1.5.8) to add to each sublibrary
Purple text (bottom): Volume of Dilution Buffer to add to each sublibrary
Blue Shading: Serial dilution of cell stock is required to improve sublibrary cell count accuracy
Red Shading: Insufficient cell stock concentration for target sublibrary cell count

Cell Stock Conc. (cells/µL)	Target Sublibrary Cell Count (cells/sublibrary)							
	200	500	1,000	2,000	3,000	4,000	5,000	10,000*
50	4	10	20	N/A	N/A	N/A	N/A	N/A
	21	15	5	N/A	N/A	N/A	N/A	N/A
100	2	5	10	20	N/A	N/A	N/A	N/A
	23	20	15	5	N/A	N/A	N/A	N/A
200	Dilute	2.5	5	10	15	20	25	N/A
	N/A	22.5	20	15	10	5	0	N/A
300	Dilute	Dilute	3.33	6.67	10	13.33	16.67	N/A
	N/A	N/A	21.67	18.33	15	11.67	8.33	N/A
400	Dilute	Dilute	2.5	5	7.5	10	12.5	25
	N/A	N/A	22.5	20	17.5	15	12.5	0
500	Dilute	Dilute	2	4	6	8	10	20
	N/A	N/A	23	21	19	17	15	5
600	Dilute	Dilute	Dilute	3.33	5	6.67	8.33	16.67
	N/A	N/A	N/A	21.67	20	18.33	16.67	8.33
700	Dilute	Dilute	Dilute	2.86	4.29	5.71	7.14	14.29
	N/A	N/A	N/A	22.14	20.71	19.29	17.86	10.71
800	Dilute	Dilute	Dilute	2.5	3.75	5	6.25	12.5
	N/A	N/A	N/A	22.5	21.25	20	18.75	12.5
900	Dilute	Dilute	Dilute	2.22	3.33	4.44	5.56	11.11
	N/A	N/A	N/A	22.78	21.67	20.56	19.44	13.89
1,000	Dilute	Dilute	Dilute	2	3	4	5	10
	N/A	N/A	N/A	23	22	21	20	15
1,100	Dilute	Dilute	Dilute	Dilute	2.73	3.64	4.55	9.09
	N/A	N/A	N/A	N/A	22.27	21.36	20.45	15.91
1,200	Dilute	Dilute	Dilute	Dilute	2.5	3.33	4.17	8.33
	N/A	N/A	N/A	N/A	22.5	21.67	20.83	16.67
1,300	Dilute	Dilute	Dilute	Dilute	2.31	3.08	3.85	7.69
	N/A	N/A	N/A	N/A	22.69	21.92	21.15	17.31
1,400	Dilute	Dilute	Dilute	Dilute	2.14	2.86	3.57	7.14
	N/A	N/A	N/A	N/A	22.86	22.14	21.43	17.86
1,500	Dilute	Dilute	Dilute	Dilute	2	2.67	3.33	6.67
	N/A	N/A	N/A	N/A	23	22.33	21.67	18.33

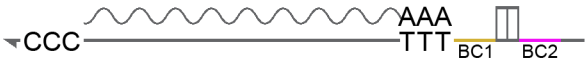
*10,000 cells/sublibrary will have about twice the doublet rate as 5,000 cells/sublibrary, the recommended maximum sublibrary size.

Appendix B: Molecular Mechanisms

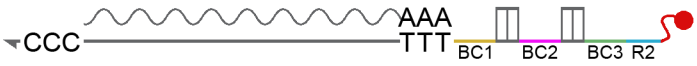
Barcoding mRNA in Single Cells

Polyadenylated mRNA

Reverse Transcription
Poly T and random hexamer primers anneal to mRNA within single cells. Each primer contains a barcode and a DNA linker. Reverse transcriptase extends cDNA to form a cDNA/mRNA hybrid.



R2 Ligation
A cDNA adaptor ligates to the DNA linker. The adaptor contains a second barcode and an additional DNA linker.



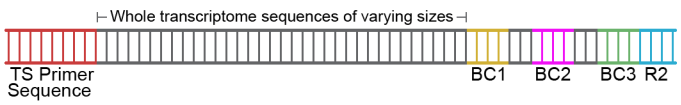
R3 Ligation
A second adaptor ligates to the growing cDNA. The adaptor contains a third barcode, an Illumina adaptor, and a biotin molecule.

Cell Lysis

cDNA Amplification

Apply Binder Beads
After cell lysis, the biotinylated cDNA/mRNA hybrid binds to a streptavidin binder bead. Molecules lacking biotin are lost.

Template Switch
A template switch reaction appends a primer binding site to the 3' end of the cDNA molecule.



cDNA Amplification PCR
A PCR reaction amplifies the cDNA using the TS primer and R2 Illumina primer. cDNA is now double stranded.

Quantify DNA

Preparing Sequencing Libraries

Fragmentation

Sublibrary cDNA is fragmented to a size compatible with Illumina sequencing.

Adaptor Ligation

A second Illumina adaptor ligates to the fragmented end of the cDNA.

Sublibrary Index PCR with UDIs

A final PCR amplifies the fragmented cDNA and appends the fourth DNA barcodes, UDIs from the UDI Plate - WT, as well as the P5 and P7 adaptors.

OR

Sublibrary Index PCR

A final PCR amplifies the fragmented cDNA and appends the fourth DNA barcode as well as the P5 and P7 adaptors.

Note: See Appendix D for more

Quantify DNA and Sequence

Appendix C: Troubleshooting

Assessing Quality of Fixed Samples

Several steps throughout your experiment require counting the cells or nuclei in your sample before progressing. If you are counting manually using a hemocytometer, it can be difficult to judge the quality of your sample. Below we provide examples of varying sample quality:

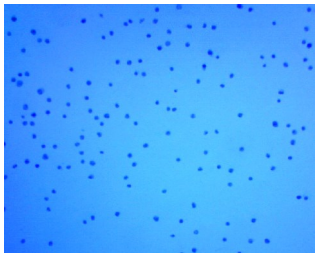
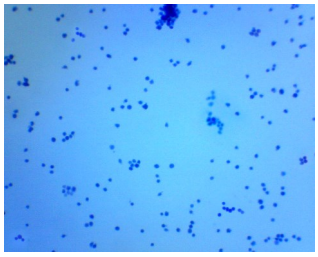
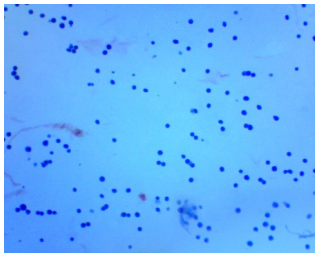
High Quality Sample		Single cells are easily distinguishable and no debris can be seen. Count each cell and proceed with your experiment as instructed.
Cell Clumps Have Formed		High quality cell samples should consist of >95% single cells. Lower fractions of single cells may lead to elevated doublets.
Presence of Cell Debris		This is not a cause for concern assuming single cells are visible and debris is not causing cells to aggregate. Do not include any debris in your counting and continue your experiment as instructed.

Fig. 3: Photos Representative of Varying Qualities of Cell Samples Observed While Counting in the Presence of the Trypan Blue Stain.

Sample Loading Table

A situation may arise in which a cell sample is not concentrated enough according to the "WT Mini - Sample Loading Table V1.2.0" (Excel spreadsheet). The corrective action depends on your experimental goals. Some users will require constant ratios of all cell samples, while other users may allow for a decreased fraction in particular samples. Here we outline our recommended actions for each case:

A. If you require constant ratios for cell samples, you should decrease the "Max number barcoded cells" until the Sample Loading Table no longer gives an error.

B. If your experiment allows for a decreased fraction for the less concentrated samples, do not dilute these samples any further. Simply add 14 µL of undiluted sample into each designated well of the Round 1 Plate. This will result in fewer cells for the given sample, but the total number of barcoded cells will be greater than for option A.

Appendix D: Single Indexing

If using the alternative version of Evercode WT Mini v2 (ECW02010) that includes SX100 instead of SX200, follow the protocol modifications described here.

Protocol Adjustments with Single Indexing	
Original Section	**Replacement Section**
3.5: Sublibrary Index PCR with UDIs	Appendix D1: Sublibrary Index PCR (see protocol on the next page)
4.1: Illumina Run Configuration with UDIs	Appendix D2: Illumina Run Configuration with Single Indexing

Appendix D1: Part List

Fragmentation (-20˚C) SX100				
Label	**Component**	**Format**	**Quantity**	**Part Number**
	Fragmentation Buffer	1.5 mL tube	1	SX101
	Fragmentation Enzyme	1.5 mL tube	1	SX102
	Adaptor DNA	1.5 mL tube	1	SX103
	Adaptor Ligation Buffer	1.5 mL tube	1	SX104
	Adaptor Ligase	1.5 mL tube	1	SX105
	Index PCR Mix	1.5 mL tube	1	SX106
	Universal Index Primer	1.5 mL tube	1	SX107
	Sublibrary Index Primer 1	1.5 mL tube	1	SX108
	Sublibrary Index Primer 2	1.5 mL tube	1	SX109

Appendix D2: Sublibrary Single Index PCR

If using unique dual indexes (UDIs) instead of sublibrary single index primers for indexing, see Section 3.5. Otherwise, replace the entirety of Section 3.5 with the following steps.

Multiple thermocyclers may be needed for this section depending on the amount of cDNA added to each sublibrary during the fragmentation reaction. Refer to step next page to determine how many thermocyclers are needed.

1. Using a new 1.5 mL tube, combine the **Universal Index Primer** and **Index PCR Mix** to make the **Sublibrary Amplification Mix**. Mix well by pipetting and store on ice.

	Volume to Add by Number of Sublibraries (µL)	
# Sublibraries	**1**	**2**
 Index PCR Mix	27.5	55
 Universal Index Primer	2.2	4.4
Total	**29.7**	**59.4**

2. **Add 2 µL of different index primers to each sublibrary** ensuring that no two sublibraries contain the same sublibrary index primer. Make sure to record which sublibrary contains which index primer.

3. Add **27 µL** of the **Sublibrary Amplification Mix** to the 23 µL sublibrary from the previous step. Pipette up and down 10x with the pipette set to 27 µL to ensure proper mixing, followed by brief centrifugation (~2 sec).

~30 min

4. Place the sample(s) into a thermocycler and run the program below. The number of cycles (**X**) should be adjusted based on the amount of cDNA added to the fragmentation reaction.

Sublibrary Index Amplification		
Run Time	**Lid Temperature**	**Sublibrary Volume**
~30 min	105°C	50 µL
Step	**Time**	**Temperature**
1	3 min	95°C
	Begin Cycling	
2	20 sec	98°C
3	20 sec	67°C
4	1 min	72°C
	*Go to step 2, repeat **X-1** times (**X** cycles total)*	
5	5 min	72°C
6	Hold	4°C

	PCR Cycles based on cDNA in Fragmentation			
cDNA in Fragmentation (ng)	**10-24**	**25-49**	**50-99**	**100+**
Total PCR Cycles Required (**X**)	13	12	11	10

Note: cDNA concentration was recorded in step 2.5.18, and 10 µL from each sublibrary should have been added into the fragmentation reaction (step 3.1.2).

5. Sublibraries can be stored at this point at 4°C overnight. If you wish to continue, proceed directly to Section 3.6: Post-Amplification Double-Sided SPRI Selection.

[STOPPING POINT]

Appendix D3: Illumina Run Configuration

If unique dual indexes (UDIs) instead of sublibrary index primers were used for indexing, see Section 4.1. Otherwise, use the following single index Illumina run configuration and sequence information.

Evercode sequencing libraries should be diluted and denatured according to the instruction for the relevant sequencing instrument. We strongly recommended adding 5% PhiX for optimal sequencing quality. Libraries should be sequenced with paired reads using the following read structure.

Read	Cycles
Read 1	74
i7 Index (Index 1)	6
i5 Index (Index 2)	0
Read 2	86

The fourth barcode that tags each sublibrary acts as a standard Illumina index. Please refer to the following table to demultiplex sublibraries that have been sequenced together in the same run.

Sublibrary Index	Forward Sequence (For Sample Sheet)
1	CAGATC
2	ACTTGA

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