

tapestri



tapestri



# Tapestri<sup>®</sup> Single-Cell DNA + Protein Sequencing

User Guide

AML | CLL | Myeloid  
Tumor Hotspot | Custom

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*Moving precision medicine FORWARD.*



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# Introduction

The *Mission Bio Tapestri® Platform* uses microfluidic droplet technology to combine cell lysate with barcoding beads anchored to gene specific primers to deliver a high-throughput single-cell genomics workflow for targeted DNA sequencing. Users can produce sequencing-ready libraries starting from a single cell suspension in as few as 2 days. This User Guide describes the experimental procedure in detail.

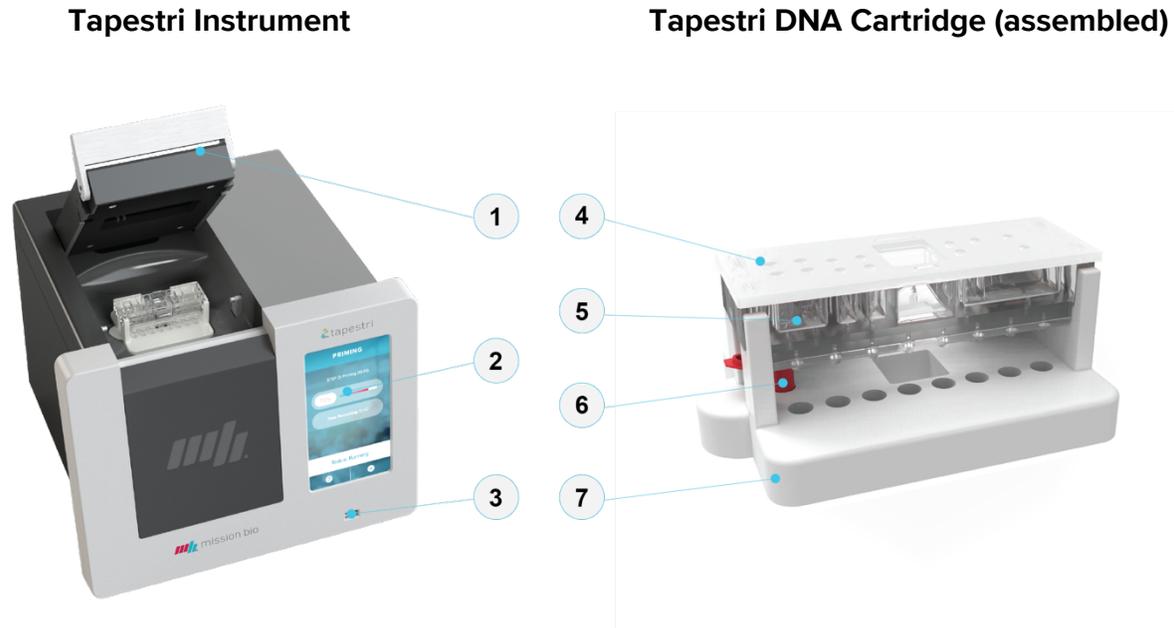
## About This Guide

This User Guide describes the experimental procedure when using the *Mission Bio Tapestri Platform* for DNA/Protein applications.

## Tapestri Platform Overview

The *Tapestri Platform* consists of the instrument itself, the DNA cartridge, which represents the microfluidics device, and reagents. The cartridge is equipped with reservoirs that are used to load reagents required for automated cell processing. Pressure supplied by the instrument drives the fluidics from the reservoirs through the microfluidic device out to PCR collection tubes that are mounted below the cartridge. The assembled cartridge and tubes can be loaded and unloaded from the instrument and disposed after the completion of the workflow.

The Tapestri Instrument is designed to receive the loaded cartridge and drive the fluidics with programmed, pressurized air. The instrument seals the cartridge using a lid over the top of a loaded cartridge via a rubber gasket and levered handle. The user interacts with the instrument via a touch screen interface, which can be used to select programs, monitor the status of running programs, and more.



**Figure 1.** Tapestri Platform: Instrument and Assembled DNA Cartridge (Tapestri Single-Cell DNA AML Kit not shown, instrument color may vary)

- 1 Lid**  
Levered lid to open and close the instrument and install the DNA Cartridge.
- 2 Touchscreen**  
To interface with the instrument's software and select programs.
- 3 USB Port** (*on back panel in some instruments*)  
To export diagnostics data.
- 4 Tapestri DNA Gasket**  
To seal the instrument lid.
- 5 Tapestri DNA Cartridge**  
Microfluidics device to load with reagents and cells.
- 6 Collection Tubes**  
To collect emulsions.
- 7 Base Plate**  
Foundation to mount DNA Cartridge and collection tubes.

# Materials

## Tapestri Single-Cell DNA + Protein Core Kit Configuration

| Component Name                               | Part Number |     |     |        | Storage |
|--|-------------|-----|-----|--------|---------|
|  | AML         | MYE | THP | Custom |         |
| Tapestri Single-Cell DNA Core Ambient Kit v2 | MB51-0007   |     |     |        | RT      |
| Tapestri Single-Cell DNA Core -20 Kit v2     | MB51-0010   |     |     |        | -20°C   |
| Tapestri Single-Cell DNA Bead Kit            | MB51-0009   |     |     |        | 4°C     |
| Tapestri Protein Staining Kit                | MB51-0017   |     |     |        | 4°C     |

## Tapestri Single-Cell DNA Oligo Pools

| Component Name  | Part Number | Storage |
|---|-------------|---------|
| Tapestri Single-Cell DNA AML Oligo Pool   | MB03-0035   | -20°C   |
| Tapestri Single-Cell DNA CLL Oligo Pool   | MB03-0038   | -20°C   |
| Tapestri Single-Cell DNA MYE Oligo Pool   | MB03-0036   | -20°C   |
| Tapestri Single-Cell DNA THP Oligo Pool   | MB03-0037   | -20°C   |
| Tapestri Single-Cell DNA 1-100 Amplicons Oligo Pool (Quantity for 4 Tapestri Core Kits)   | MB03-0039   | -20°C   |
| Tapestri Single-Cell DNA 101-200 Amplicons Oligo Pool (Quantity for 4 Tapestri Core Kits) | MB03-0040   | -20°C   |
| Tapestri Single-Cell DNA 201-300 Amplicons Oligo Pool (Quantity for 4 Tapestri Core Kits) | MB03-0041   | -20°C   |
| Tapestri Single-Cell DNA 301-400 Amplicons Oligo Pool (Quantity for 4 Tapestri Core Kits) | MB03-0042   | -20°C   |
| Tapestri Single-Cell DNA 401-500 Amplicons Oligo Pool (Quantity for 4 Tapestri Core Kits) | MB03-0043   | -20°C   |
| Tapestri Single-Cell DNA Custom Amplicons Oligo Pool (Quantity for 4 Tapestri Core Kits)  | MB03-0044   | -20°C   |

## Tapestri Single-Cell DNA Core/Custom Kit Components

| Component Name                       | Kit                                       | Storage |
|--------------------------------------|---|---------|
| Cell Buffer                          | Tapestri Single-Cell DNA Core Ambient Kit | RT      |
| Encapsulation Oil                    |   | RT      |
| Electrode Solution                   |   | RT      |
| Barcoding Oil                        |   | RT      |
| ● Extraction Agent (green cap)       |   | RT      |
| ● Lysis Buffer (brown cap)           | Tapestri Single-Cell DNA Core -20 Kit     | -20°C   |
| Barcoding Mix V2                     |   | -20°C   |
| Library Mix V2                       |   | -20°C   |
| ● V2 Index Primer 1 – 8 (purple cap) |   | -20°C   |
| ● DNA Clean up Buffer                |   | -20°C   |
| ● Clean up Enzyme                    |   | -20°C   |
| ● Barcoding Beads (blue cap)         | Tapestri Single-Cell DNA Bead Kit         | 4°C     |
| ● Fwd Primer Pool (white cap)        | AML, MYE, THP, CLL, Custom                | -20°C   |
| ● Rev Primer Pool (black cap)        |   |         |
| Tapestri DNA Cartridge (2 x 4x)      | Tapestri Single-Cell DNA Cartridge Kit    | RT      |
| Tapestri DNA Gasket (2 x 4x)         |   | RT      |

**NOTE** Make sure to use non-frost free freezers for all -20°C reagent storage.

**NOTE** Please contact Mission Bio Support ([support@missionbio.com](mailto:support@missionbio.com)) when interested in Custom Kit Reagents.

## Tapestri Protein Staining Kit Reagents

| Component Name                            | Kit                           | Storage |
|---|-------------------------------|---------|
| ● Blocking Buffer (orange cap)            | Tapestri Protein Staining Kit | 4°C     |
| ● Antibody Tag Primer (red cap)           |                               | 4°C     |
| ● Biotin Oligo (blue cap)                 |                               | 4°C     |
| ● Streptavidin Beads (brown cap)          |                               | 4°C     |
| 2x Wash Buffer                            |                               | 4°C     |
| ● Protein Primer Indices 1-8 (yellow cap) |                               | 4°C     |

## Required Third Party Consumable Reagents

| Component Name  | Suggested Supplier (Part Number)                                     | Protocol Step             |
|---|--|---------------------------|
| TotalSeq™-D Heme Oncology Cocktail  | BioLegend (399906)   | Cell Staining             |
| Human TruStain FcX (Fc Receptor Blocking Solution)                          | BioLegend (422301)   | Cell Staining             |
| Cell Staining Buffer  | BioLegend (420201)   | Cell Staining             |
| AMPure XP Reagent   | Beckman Coulter (A63880)   | Targeted PCR, Library PCR |
| Qubit® dsDNA HS Assay Kit   | Qubit® (Q32851)  | Targeted PCR              |
| Ethanol, Molecular Biology Grade  | Sigma (E7023)  | AMPure purification       |
| Agilent DNA 1000 Kit<br>Agilent DNA High Sensitivity Kit                    | Agilent Technologies (5067-1504)<br>Agilent Technologies (5067-4626) | Library PCR               |
| Trypan Blue   | Thermo Fisher (15250061)   | Dead cell staining        |
| Propidium Iodide  | Thermo Fisher (P3566)  | Dead cell staining        |
| TipOne RPT ultra low retention filter tip                                   | USA Scientific (1180-8810) or<br>Approved Supplier                   | Liquid handling           |
| 200 µL Wide bore tip, rack, sterile<br>1000 µL Wide bore tip, rack, sterile | USA Scientific (1011-8410)<br>USA Scientific (1011-9410)             | Cell handling             |
| Flowmi™ Cell Strainers for 1000 µL pipette tips, 40 µm                      | Fisher Scientific (14-100-150)                                       | Cell handling             |

## Required Third Party Consumable Reagents (continued)

|   |   |                       |
|---|---|-----------------------|
| 1.5 mL DNA low-bind Microcentrifuge Tubes   | Eppendorf (0030108035)                          | Cell/Reagent handling |
| 0.2 mL PCR Tubes  | USA Scientific (1402-8120) or Approved Supplier | Non-emulsion PCR      |
| * 0.2 mL Axygen MAXYmum Recovery PCR Tubes  | Axygen (PCR-02-L-C)                             | Emulsion handling     |
| Axygen Gel Tips   | Axygen (TGL200RD57R) or Approved Supplier       | Emulsion handling     |
| Qubit Assay Tubes   | Thermo Fisher (Q32856)                          | Post PCR quantitation |
| 15 mL DNA low-bind conical tubes  | Eppendorf (30122208)                            | Protein               |
| 1.5 mL Protein low-bind tubes   | Eppendorf (22431081)                            | Protein               |
| KAPA Library Quantification Kit Illumina Platforms (OPTIONAL)   | KAPA (KK4873)                                   | Sequencing            |
| Sequencing Reagent Kit 300 cycles (150bp PE) (MiSeq, HiSeq 2500, HiSeq 4000, NextSeq 550/1000/2000, NovaSeq 6000) | Illumina  | Sequencing            |

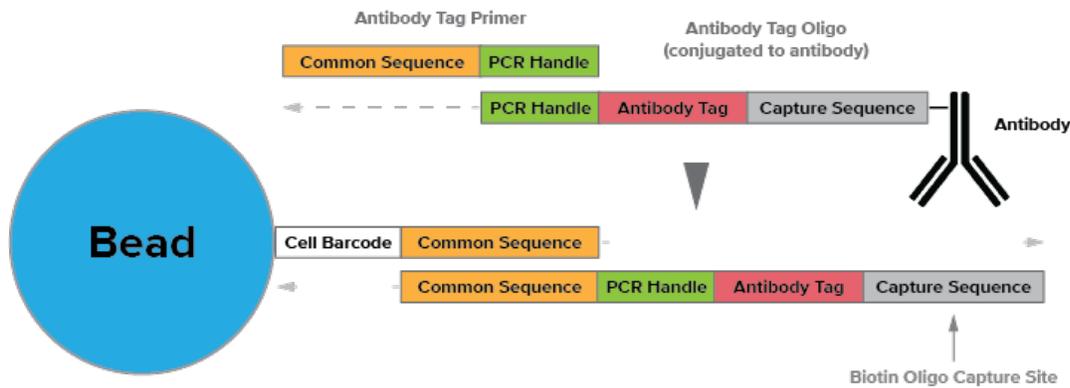
**NOTE** \* *These consumables are used for handling emulsion samples and must not be substituted. Only listed consumables have been validated by Mission Bio.*

## Required Benchtop Equipment

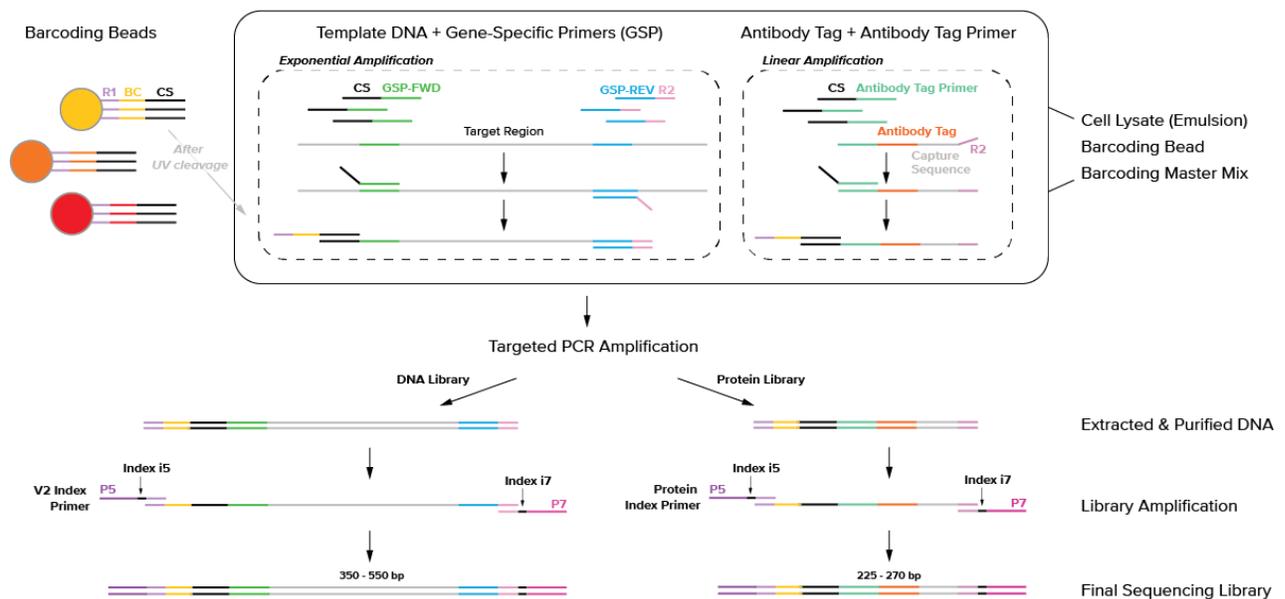
| Required Equipment  | Suggested Supplier (Part Number)            |
|---|---|
| MB Tapestri Instrument  | Mission Bio (191335)                        |
| Countess® II Automated Cell Counter or equivalent   | Thermo Fisher (AMQAX1000)                   |
| Fluorescence microscope (optional)  | Thermo Fisher or Approved Supplier          |
| Centrifuge with temperature control and swinging bucket (needs to support 15 mL conical tubes)    | Eppendorf (5810 R) or Alternative Supplier  |
| Agilent 2100 Bioanalyzer or Tapestation   | Bioanalyzer: Agilent (G2939BA)              |
| Qubit Fluorometer   | Qubit: Thermo Fisher (Q33216)               |
| Pipettes, 1 µL – 1000 µL  | Mettler-Toledo, Rainin Pipettes             |
| Microcentrifuge (1.5 mL, 0.2 mL PCR tubes) with temperature control                               | Thermo Fisher (75004081)                    |
| Tube Vortexer   | Thermo Fisher (88880017TS)                  |
| Thermal cycler with heated lid (100 µL volume, needs to support ramp rates between 1°C/s – 4°C/s) | Thermo Fisher (A24811) or Approved Supplier |
| ThermoMixer   | Eppendorf (5382000023) or Approved Supplier |
| Rotating Shaker (Hulamixer)   | Thermo Fisher (15920D)                      |
| 0.2 mL 8-strip PCR tube Magnetic Separation Stand   | Seqmatic (TM-700) or Approved Supplier      |
| 6-Tube Magnetic Separation Rack   | New England Biolabs (S1506S)                |
| MiSeq Sequencing Instrument [Optional]  | Illumina                                    |
| HiSeq 2500 Sequencing Instrument [Optional]   | Illumina                                    |
| HiSeq 4000 Sequencing Instrument [Optional]   | Illumina                                    |
| NextSeq 550 Sequencing Instrument [Optional]  | Illumina                                    |
| NovaSeq 6000 Sequencing Instrument [Optional]   | Illumina                                    |

# Protocol Overview

Single cells stained with oligo-tagged antibodies are individually partitioned into sub-nanoliter droplets. Barcoding Beads and PCR reagents are introduced using the Mission Bio Tapestry Instrument and DNA Cartridge. Cell lysis, protease digestion, cell barcoding and targeted amplification using multiplexed PCR occur within the droplets. Droplets are then disrupted, and barcoded DNA is extracted for Library Amplification. The Protein library is separated from the DNA library by biotinylated oligo pull-out. Protein and DNA libraries are indexed and amplified separately. Final libraries are purified and can be sequenced on one of the supported Illumina Sequencer instruments.



**Figure 2.** Antibody Tag Oligo construct.



**Figure 3.** Overview of library construction. R1: Read 1, BC: barcode, CS: common sequence GSP-FWD: gene-specific forward primer, GSP-REV = gene-specific reverse primer, P5: P5 Illumina adapter, P7: P7 Illumina adapter.

# Best Practices: Emulsion & DNA Cartridge

## Cell Culture, Pre- and Post-PCR areas

- All cell sample preparation must be conducted in a designated area that is restricted to cell culture work.
- All Pre-PCR steps (encapsulation, barcoding, PCR master mix preparation) must be conducted in a lab space that is physically separated from amplified genetic material.
- All Post-PCR (amplified material) steps (library PCR, library purification, DNA quantification, sample pooling) must be conducted in a lab space that is physically separated from the unamplified genetic material.
- Do not transfer material (gloves, pipettes, tubes) or equipment from the Post-PCR area to the Pre-PCR area.
- Carefully clean bench areas and pipettes with 5% bleach before starting any protocol.

## Cross-contamination

- When pipetting samples, change tips between samples.
- Use aerosol-resistant (filtered) pipette tips to reduce the risk of reagent carryover and sample-to-sample cross-contamination.

## Suggestions for working with emulsions

- Consumables (gel tips, emulsion safe PCR tubes) have been carefully tested and specified. Do not substitute.
- Pipette emulsions very slowly and carefully and only when necessary.
- Avoid sources of static and any excess handling of emulsion samples
- Handle emulsion sample tubes carefully. Avoiding direct contact with the sidewall of the tube, where emulsions directly interface and hold tubes on the lid instead.

## Cell Recovery

If the number of cells after staining and cell washing is below the recommended minimum concentration of 3,000 cells/ $\mu$ L, we suggest optimizing the workflow by following any of the adjustments listed below:

- Verify 1 million cells were used by counting the cells with an alternate method.
- Increase the **time of centrifugation** for washes 2 – 4 from 5 minutes to **7 – 10 minutes**.
- Always pipette slowly and carefully when removing the supernatant and leave at least 0.5 mL of residual volume in the tube between the washing steps.

## Suggestions for working with the Tapestri Instrument and DNA Cartridge

The DNA cartridge is equipped with microfluidics channels that are as small as 40  $\mu\text{m}$  and are used to transport reagents and cells. Care should be taken to avoid introduction of particles, fibers or clumped cells into cartridge that may potentially clog the cartridge. Minimize exposure of the instrument, reagents, cartridges, gaskets to sources of particles and fibers, such as open reagent reservoirs, laboratory wipes, clothing that easily sheds fibers, and dusty surfaces. Place DNA cartridges into original packaging after Encapsulation or Barcoding is completed. Lower the instrument lid when DNA cartridges are mounted on the instrument and are not in use.

Pay attention to the timing of loading the DNA cartridge and running the Encapsulation or Barcoding programs. Experimental steps should be executed successively as outlined in the protocol without delays.

Ensure that the instrument is not placed near a ventilation system or similar sources of high airflow. For additional information about requirements of the instrument's placement consult the **Tapestri Instrument Site Requirements Guide (PN 65307)**.

# Gene Panels

## AML Panel (20 Genes, 127 Amplicons)

|        |       |      |        |       |
|--------|-------|------|--------|-------|
| ASXL1  | GATA2 | KIT  | PTPN11 | TP53  |
| DNMT3A | IDH1  | KRAS | RUNX1  | U2AF1 |
| EZH2   | IDH2  | NPM1 | SF3B1  | WT1   |
| FLT3   | JAK2  | NRAS | SRSF2  | TET2  |

## CLL Panel (32 Genes, 274 Amplicons)

|        |        |        |        |       |       |
|--------|--------|--------|--------|-------|-------|
| ATM    | CD79B  | EZH2   | MED12  | POT1  | XPO1  |
| BCOR   | CHD2   | FAT1   | MYD88  | RPS15 | ZMYM3 |
| BIRC3  | CREBBP | FBXW7  | NFKBIE | SETD2 |       |
| BRAF   | CXCR4  | KRAS   | NOTCH1 | SF3B1 |       |
| BTK    | DDX3X  | LRP1B  | NRAS   | SPEN  |       |
| CARD11 | EGR2   | MAP2K1 | PLCG2  | TP53  |       |

## Myeloid Panel (45 Genes, 312 Amplicons)

|       |        |       |        |        |       |
|-------|--------|-------|--------|--------|-------|
| ASXL1 | DNMT3A | IDH2  | MYD88  | RAD21  | TET2  |
| ATM   | ERG    | JAK2  | NF1    | RUNX1  | TP53  |
| BCOR  | ETV6   | KDM6A | NPM1   | SETBP1 | U2AF1 |
| BRAF  | EZH2   | KIT   | NRAS   | SF3B1  | WT1   |
| CALR  | FLT3   | KMT2A | PHF6   | SMC1A  | ZRSR2 |
| CBL   | GATA2  | KRAS  | PPM1D  | SMC3   |       |
| CHEK2 | GNAS   | MPL   | PTEN   | STAG2  |       |
| CSF3R | IDH1   | MYC   | PTPN11 | STAT3  |       |

## Tumor Hotspot Panel (59 Genes, 244 Amplicons)

|        |        |       |        |        |         |
|--------|--------|-------|--------|--------|---------|
| ABL1   | CSF1R  | FGFR1 | IDH2   | MLH1   | RB1     |
| AKT1   | CTNNB1 | FGFR2 | JAK1   | MPL    | RET     |
| ALK    | DDR2   | FGFR3 | JAK2   | MTOR   | SMAD4   |
| APC    | EGFR   | FLT3  | JAK3   | NOTCH1 | SMARCB1 |
| AR     | ERBB2  | GNA11 | KDR    | NRAS   | SMO     |
| ATM    | ERBB3  | GNAQ  | KIT    | PDGFRA | SRC     |
| BRAF   | ERBB4  | GNAS  | KRAS   | PI3KCA | STK11   |
| CDH1   | ESR1   | HNF1A | MAP2K1 | PTEN   | TP53    |
| CDK4   | EZH2   | HRAS  | MAP2K2 | PTPN11 | VHL     |
| CDKN2A | FBXW7  | IDH1  | MET    | RAF1   |         |

# Thermal Cycling Programs

Always use a properly calibrated thermal cycler suited for 0.2 mL tubes with a maximum reaction volume of 100  $\mu$ L for all incubations. Program all four thermal cycling protocols from **Tables I1** into the instrument. For all protocols, use a heated lid set to 100  $^{\circ}$ C – 105  $^{\circ}$ C. For specific instrument operation, follow the instructions provided by the manufacturer.

| 1. Cell Lysis and Protein Digest |                 |        | 3. Enzymatic Cleanup |                 |        | 4. Library PCR |                 |        |                       |
|----------------------------------|-----------------|--------|----------------------|-----------------|--------|----------------|-----------------|--------|-----------------------|
| Step                             | Temperature     | Time   | Step                 | Temperature     | Time   | Step           | Temperature     | Time   | Cycle                 |
| 1                                | 50 $^{\circ}$ C | 60 min | 1                    | 37 $^{\circ}$ C | 60 min | 1              | 95 $^{\circ}$ C | 3 min  |                       |
| 2                                | 80 $^{\circ}$ C | 10 min | 2                    | 4 $^{\circ}$ C  | HOLD   | 2              | 98 $^{\circ}$ C | 20 sec | DNA   10<br>PROT   20 |
| 3                                | 4 $^{\circ}$ C  | HOLD   |                      |                 |        | 3              | 62 $^{\circ}$ C | 20 sec |                       |
|                                  |                 |        |                      |                 |        | 4              | 72 $^{\circ}$ C | 45 sec |                       |
|                                  |                 |        |                      |                 |        | 5              | 72 $^{\circ}$ C | 2 min  |                       |
|                                  |                 |        |                      |                 |        | 6              | 4 $^{\circ}$ C  | HOLD   |                       |

| 2. Targeted PCR |                  |                                  |          |           |           |        |       |
|-----------------|------------------|----------------------------------|----------|-----------|-----------|--------|-------|
| Amplicon Number |                  |                                  | 20 – 100 | 101 – 200 | 201 – 300 | > 300  |       |
| Catalog Panel   |                  |                                  | N/A      | AML       | THP/CLL   | MYE    |       |
| Step            | Ramp Rate        | Temperature                      | Time     | Time      | Time      | Time   | Cycle |
| 1               | 4 $^{\circ}$ C/s | 98 $^{\circ}$ C                  | 6 min    | 6 min     | 6 min     | 6 min  |       |
| 2               | 1 $^{\circ}$ C/s | 95 $^{\circ}$ C                  | 30 sec   | 30 sec    | 30 sec    | 30 sec | 11    |
| 3               |                  | 72 $^{\circ}$ C                  | 10 sec   | 10 sec    | 10 sec    | 10 sec |       |
| 4               |                  | <b>61 <math>^{\circ}</math>C</b> | 3 min    | 4.5 min   | 6 min     | 9 min  |       |
| 5               |                  | 72 $^{\circ}$ C                  | 20 sec   | 20 sec    | 20 sec    | 20 sec |       |
| 6               | 1 $^{\circ}$ C/s | 95 $^{\circ}$ C                  | 30 sec   | 30 sec    | 30 sec    | 30 sec | 13    |
| 7               |                  | 72 $^{\circ}$ C                  | 10 sec   | 10 sec    | 10 sec    | 10 sec |       |
| 8               |                  | <b>48 <math>^{\circ}</math>C</b> | 3 min    | 4.5 min   | 6 min     | 9 min  |       |
| 9               |                  | 72 $^{\circ}$ C                  | 20 sec   | 20 sec    | 20 sec    | 20 sec |       |
| 10              | 4 $^{\circ}$ C/s | 72 $^{\circ}$ C                  | 2 min    | 2 min     | 2 min     | 2 min  |       |
| 11              |                  | 4 $^{\circ}$ C                   | HOLD     | HOLD      | HOLD      | HOLD   |       |

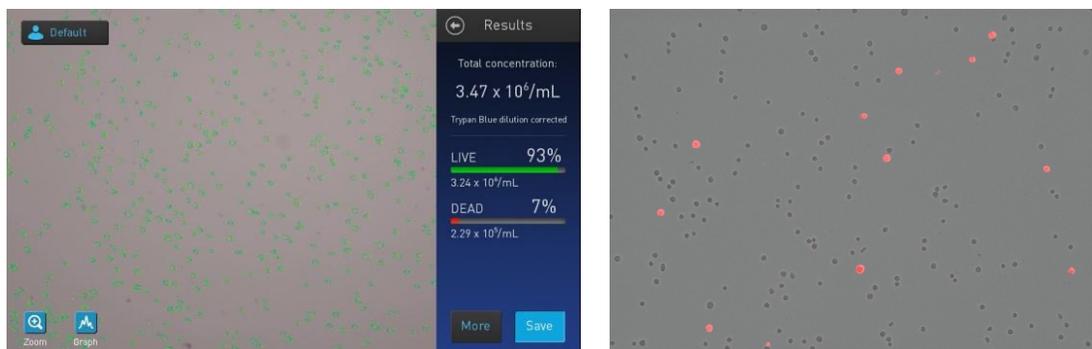
**Tables I1.** Thermal cycling programs.

# Cell Handling Guidelines

The steps provided in this protocol are applicable to non-adherent cells from culture, bone marrow aspirates and buffy coat fractions. If other cell types will be used, contact [support@missionbio.com](mailto:support@missionbio.com) for additional support. Different cell types may require revised procedures including cell dissociation, washing, re-suspension or quantitation.

## Cell counting

- Mission Bio strongly recommends the use of an automated cell counter, such as the Countess II Automated Cell Counter (Thermo Fisher).
- Optimal concentration range for cell counting with the Countess II ranges from  $1 \times 10^5$  to  $4 \times 10^6$  cells/mL.
- Final cell suspensions are measured at least twice. Concentrations found must agree within 10%.
- Cell suspensions must have > 90% viability. Mission Bio recommends Propidium Iodide, rather than Trypan Blue for measuring viability (see below).
- Final cell concentration values are based on the **total (live + dead)** cell counts.
- Avoid the use of samples containing significant debris, dead cells, or fragments of lysed cells.
- Example images of a well-prepared single cell suspension quantified with Trypan Blue (left) and PI (right) are shown below.



**Figure 5.** Representative images of high-quality cell suspension measured with Trypan Blue (left) and PI (right).

## Cell death assessment using Propidium Iodide (PI)

Mission Bio strongly recommends the use of fluorescent exclusion reagents such as Propidium Iodide (PI) to determine cell death/viability. PI-based assays compared to Trypan Blue-based assays may be more robust in accurately determining the percentage of dead/viable cells. Please follow manufacturer's instructions when using PI-based viability assays.



# **DNA + Protein Protocol**

1 Prepare Cell Suspension

# Genomic Protocol

## 1 Prepare Cell Suspension

This section describes the steps required to prepare a single-cell suspension, count cells, assess cell viability and cell suspension quality, and stain cells with oligo-tagged antibodies. The workflow is optimized for a starting cell concentration of between 6,000 and 10,000 cells/ $\mu\text{L}$  at greater than 90% viability in DPBS (w/o  $\text{Ca}^{2+}/\text{Mg}^{2+}$ ) with a minimum volume of 100  $\mu\text{L}$ . Some cell loss is to be expected throughout the antibody staining and washing procedure and therefore a recommended  $\sim 6,000 - 10,000$  cells/ $\mu\text{L}$  ensures a minimum cell concentration of 3,000 – 4,000 cells/ $\mu\text{L}$  in 35  $\mu\text{L}$  needed for encapsulation.

- NOTE**
- **Thaw reagents at room temperature unless directed to thaw them on ice.**
  - **Store reagents according to manufacturer's storage recommendations as soon as they are received. Vortex and then centrifuge reagents as directed.**
  - **The following procedure assumes cell lines or PBMCs to be cryopreserved in 2 mL cryovials in a total volume of 0.5 mL and stored in liquid nitrogen or  $-80^{\circ}\text{C}$ .**

### Thaw Cells

- 1.1 Retrieve all reagents required for preparing the cell suspension:
  - Cell Buffer (Ambient Kit)
  - Human TruStain FcX (on ice)
  - Blocking Buffer (●) ( $4^{\circ}\text{C}$ , Protein Staining Kit) (on ice)
  - Cell Staining Buffer (BioLegend, 420201) (at RT)
  - Reconstituted TotalSeq™-D Heme Oncology Cocktail (at RT)
  - Flowmi Cell Strainer
- 1.2 **Warm thawing media** (for instance 40% FBS + 60% base media) to  $37^{\circ}\text{C}$ .
- 1.3 Remove cryovial of cells from liquid nitrogen or the  $-80^{\circ}\text{C}$  freezer, **immediately transfer** to a biosafety hood, twist the cap a quarter to relieve pressure, and immediately retighten.
- 1.4 **Immediately transfer to a  $37^{\circ}\text{C}$  water bath**, quickly thaw the vial by gently swirling the tube until a small amount of ice remains ( $< 1$  minute). Ensure to avoid submerging the tube completely.
- 1.5 Remove tube and clean with 70% ethanol.
- 1.6 Using aseptic techniques, add **1 mL of thawing media drop wise** to the cryovial. Transfer the entire contents of the vial to a 15 mL conical tube.
- 1.7 Using a wide bore P-1000, **wash** the vial with **1 mL of pre-warmed thawing media**.
- 1.8 Transfer wash from vial to the 15 mL tube, drop by drop, making sure to pipette against the wall. Gently shake tube while adding.

- 1.9** Add **2 mL of thawing media** to 15 mL, drop by drop, making sure to pipette against the wall, and gently shake the tube while adding.
- 1.10** Add **0.5 mL of thawing media** to 15 mL tube **every few seconds until 12 mL total volume** is reached. Gently mix the tube by hand after each addition.
- 1.11** Centrifuge at **400 x g for 5 minutes** at room temperature.
- 1.12** Immediately aspirate supernatant, leaving 0.5 mL to 1 mL of washing media behind. **Do not disturb the cell pellet.**
- 1.13** Using a wide bore tip, gently **resuspend the cell pellet** in remaining thawing media by pipetting up and down ~5x.
- 1.14** Add **10 mL of thawing media.**
- 1.15** Centrifuge at **400 x g for 5 minutes** at room temperature.
- 1.16** Aspirate all supernatant.
- 1.17** Resuspend the cells in 1 mL of Cell Staining Buffer (BioLegend, 420201) (CSB).
- 1.18** Centrifuge at **400 x g for 5 minutes** at room temperature.
- 1.19** Aspirate supernatant.
- 1.20** Resuspend the cells in **250 µL of CSB.**
- 1.21** Quantify the cells using an automated cell counter or hemocytometer following best practices and the manufacturer's instructions.
- 1.22** Dilute cell suspension to **25,000 cells/µL using CSB** in a **minimum volume of 40 µL.**
- 1.23** **Store the cells on ice** until used for staining the cells (**Stain Cells**) and proceed **immediately** to Step **1.24.**

**IMPORTANT** *Cells must not be stored longer than 30 minutes as a subset of cells (e.g., monocytes) are prone to stick to the tube plastic and may be unrecoverable.*

## Reconstitute Antibody-Oligo Conjugate (AOC) Panel

The TotalSeq™-D Heme Oncology Cocktail (BioLegend) is supplied lyophilized in single reaction vials. The panel needs to be reconstituted prior to staining the cells.

- 1.24** Retrieve a vial of the lyophilized TotalSeq™-D Heme Oncology Cocktail (BioLegend, 399906) from 4°C and **equilibrate to room temperature for 5 minutes.**
- 1.25** Centrifuge the tube at **10,000 x g for 30 seconds** at room temperature.
- 1.26** **Resuspend** the lyophilized panel in **60 µL of Cell Staining Buffer** (BioLegend, 420201). Close the tube with the original cap and vortex for 10 seconds.
- 1.27** Incubate at **room temperature for 5 minutes.**
- 1.28** **Vortex** the tube for **10 seconds** and centrifuge at **10,000 x g for 30 seconds** at room temperature.
- 1.29** **Transfer the entire volume (60 µL)** of reconstituted panel to a **Protein low-bind** Eppendorf tube (Eppendorf, 22431081).
- 1.30** Centrifuge the tube at **14,000 x g for 15 minutes at 4° C.** Once completed, the reconstituted TotalSeq™-D Heme Oncology Cocktail must be used immediately in Step **1.33.**

## Stain Cells

**1.31** In a 15 mL **low-bind** conical Eppendorf tube add the following reagents:

| Reagent                                   | Volume (μL) |
|---|-------------|
| Human TruStain FcX                        | 5.0         |
| Blocking Buffer (●)                       | 5.0         |
| Cell Suspensions in CSB (25,000 cells/μL) | 40.0        |
| <b>Total Volume</b>                       | <b>50.0</b> |

**1.32** Gently mix with a 200 μL wide bore tip and **incubate the solution for 15 minutes on ice.**

**1.33** **Aspirate 50 μL** of the reconstituted TotalSeq™-D Heme Oncology Cocktail and **add to the blocked cell suspension.** Total volume is 100 μL.

**IMPORTANT** *Avoid touching the bottom or sides of the tube containing the reconstituted TotalSeq™-D Heme Oncology Cocktail with pipette tip to avoid pelleted protein aggregates. Aggregates are not visible.*

**1.34** Gently mix with a 200 μL wide bore tip.

**1.35** Incubate for 30 minutes on ice.

**1.36** Add 14 mL of pre-chilled CSB to the cell staining solution.

**1.37** Centrifuge at **400 x g for 10 minutes at 4° C** in a swinging bucket.

**1.38** Carefully **aspirate and discard 13.5 mL** of supernatant using a serological pipette.

**IMPORTANT** *Aspirate from the top of the solution and avoid touching the bottom and sides of the tube. Leave at least 0.5 mL of supernatant behind. Do not disturb or resuspend the cell pellet. Cell pellet may not be visible.*

**1.39** Repeat steps **1.36 to 1.38** for two additional washes, centrifuging at **400 x g for 5 minutes each at 4° C.**

**1.40** **Remove and discard supernatant, leaving ~100 μL:** Aspirate all but 1 mL of supernatant using a serological pipette, then switch to a P1000 pipette to remove the remaining supernatant (~100 μL).

**1.41** **Add 900 μL of Cell Staining Buffer** to the cell pellet and resuspend by gently pipetting up and down several times using a 1 mL wide bore tip.

**1.42** **Filter the cells with a 40 μm Flowmi cell strainer:** Aspirate 1 mL of the cell suspension, insert the filter onto the same sample tube, and release the filtered suspension through the filter into the tube.

**1.43** **Transfer** the cell suspension to a 1.5 mL DNA low-bind Eppendorf tube.

**1.44** Centrifuge at **400 x g for 5 minutes at 4° C.**

**1.45** Inspect the cell pellet and carefully remove all supernatant. **Do not disturb the cell pellet.** Use a P-200 or P-20 to remove all the supernatant.

**IMPORTANT** *Failure to remove all Cell Staining Buffer from the cell pellet may reduce the stability of emulsions during cell encapsulation.*

**1.46** Resuspend the pellet in **60 µL of Cell Buffer (Mission Bio)** by pipetting up and down several times.

**1.47** **Count the cells** using an automated cell counter and dead-cell exclusion dye (e.g., Trypan Blue or Propidium iodide) according to the manufacturer's instructions. **Assess both single cell suspension quality and cell viability.**

**1.48** Dilute cell suspension to **3,000 – 4,000 cells/µL** using Cell Buffer.

**IMPORTANT** *Mission Bio's Cell Buffer contains density gradient medium. Cells that are resuspended in Cell Buffer are difficult to pellet via centrifugation.*

**IMPORTANT** *Use of cell concentrations outside the range of 3,000 – 4,000 cells/µL or viability 90% may adversely affect results. If the minimum concentration of 3,000 cells/µL cannot be met in a total volume of 50 µL, the total volume of Cell Suspension may be reduced to as low as 35 µL.*

**1.49** Place cell suspension on ice until required in [Section 2 – Encapsulate Cells](#). Do not keep cell suspensions on ice for longer than 30 minutes before proceeding to encapsulation.



# **DNA + Protein**

## **Protocol**

### 2 Encapsulate Cells

## 2 Encapsulate Cells

In this step, cells are encapsulated with Lysis Buffer and Protease to create a cell emulsion. For input cell concentrations of 3,000 – 4,000 cells/ $\mu\text{L}$ , approximately 5% of all emulsion droplets will contain a cell.

### IMPORTANT

- **Handle emulsions with caution, avoiding sources of static and pipetting slowly and carefully.**
- **Use only the consumables (sample tubes and pipette tips) validated by Mission Bio (see *Tapestri Instrument and DNA Cartridge and list of Required Third Party Consumable Reagents*).**

**2.1** Turn on the Tapestri Instrument at least 5 minutes prior to use.

**2.2** Retrieve all reagents required for cell encapsulation:

- Tapestri DNA Cartridge
- Tapestri DNA Gasket
- Lysis Buffer (●) (-20 °C Kit)
- Reverse Primer Pool (●) (-20 °C Kit)
- Encapsulation Oil (Ambient Kit)
- Cell Suspension (prepared in [Section 1 – Prepare Cell Suspension](#))

Thaw Lysis Buffer and Reverse Primer Pool on ice.

**2.3** In the Pre-PCR area, carefully open a new Tapestri DNA Cartridge.

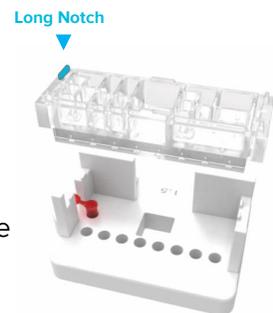
### IMPORTANT

- **Avoid dust and debris at all times when handling the DNA cartridge.**
- **Each DNA cartridge is packaged with one DNA Gasket to be used throughout the run. Store both DNA cartridge and DNA Gasket in protective packaging when not in use during the experiment. Use within 24 hours after opening.**

**2.4** Mount the Base Plate onto the Tapestri Instrument. Pre-label and **place a 0.2 mL Axygen MAXYmum Recovery PCR tube into the middle of the slot at the left of the Base Plate** for collecting the encapsulation emulsion product. Position the tube with the open lid facing left.

*Avoid sources of static.*

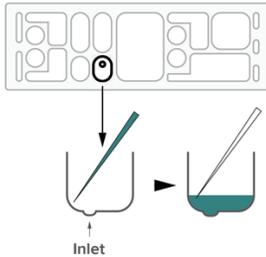
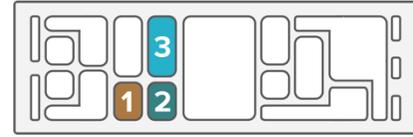
**2.5** **Place the DNA Cartridge onto the Base Plate** with the long notch on the side of the cartridge oriented on the top left, as shown, and place in instrument.



### IMPORTANT

**Minimize electrostatic sources. Only the Axygen MAXYmum Recovery PCR tubes have been validated by Mission Bio as nuclease-free and emulsion-safe. Do not substitute with other PCR tubes.**

- 2.6** In a new tube, prepare **Lysis Mix** by adding **7.3  $\mu$ L of Reverse Primer Pool (●)** into **92.7  $\mu$ L of Lysis Buffer (●)**, vortex and briefly centrifuge.
- 2.7** Pipette 90  $\mu$ L of **Lysis Mix** into **reservoir 1**.
- 2.8** Pipette 35  $\mu$ L of **Cell Suspension** into **reservoir 2**.



Pipette slowly into the bottom of the reservoir where the inlet is located. Raise the pipette tip as the liquid level in the reservoir is rising, keeping the tip slightly submerged.

The total volume of **Cell Suspension** may be as low as 35  $\mu$ L. Ensure that the inlet is fully covered with **Cell Suspension** before starting the Cell Encapsulation program.

- 2.9** Pipette 200  $\mu$ L of **Encapsulation Oil** into **reservoir 3**.

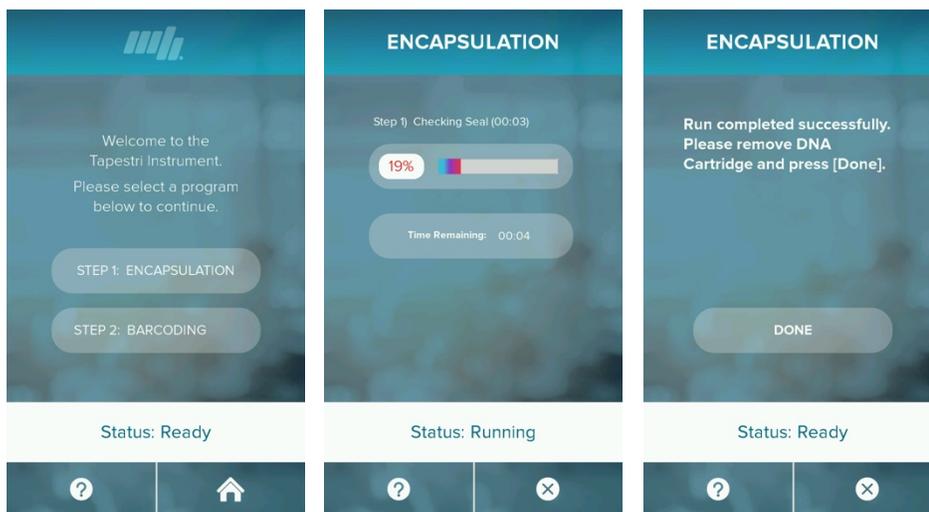
**IMPORTANT** *Make sure to apply the DNA Gasket and start the program within 1 minute after loading the Encapsulation Oil.*

- 2.10** **Apply the Tapestri DNA Gasket** to the top of the cartridge. Ensure that it is oriented correctly.

- 2.11** Firmly **close the instrument lid**, until the lid handle is level and flush with the top of the lid and instrument.



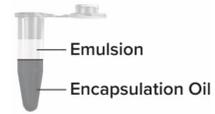
- 2.12** Run the **Encapsulation** program by pressing **Step 1:** **Encapsulation** on the Tapestri Instrument touchscreen. Press **NEXT** and confirm to start the run. The program runs for about 5 minutes.



**Figure 6.** Touchscreen displays show main menu (left), screen after selecting 'Step 1:

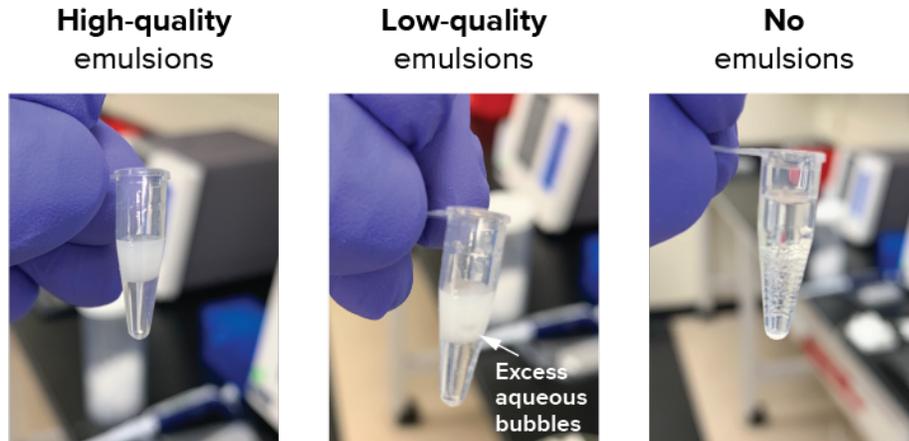
Encapsulation' program (middle), and final screen after Encapsulation is completed (right).

- 2.13** When the touchscreen displays **DONE**, carefully open the lid and **remove the cartridge from the Base Plate. Remove the gasket from the lid and set aside.**
- 2.14** **Carefully transfer the emulsion sample tube to a 96-well plate holder** and assess emulsion quality. Encapsulated cells appear as a white layer.
- 2.15** **Return the cartridge back onto the Base Plate** seated inside the instrument and close the lid to protect it from environmental debris.
- 2.16** The sample tube contains 50 – 80  $\mu\text{L}$  of cell emulsion (top layer) and 80 – 120  $\mu\text{L}$  encapsulation oil (bottom layer) for a total volume of 130 – 200  $\mu\text{L}$ .
- 2.17** Use a **gel loading tip** to carefully **remove up to 100  $\mu\text{L}$  of oil** from the bottom layer of the sample. *Aspirate oil very slowly, as to avoid emulsion sticking to walls of tube and inspect emulsion for uniformity.*



**IMPORTANT** **Hold the tube by the lid. Remove oil only. Make sure the gel loading tip is at the very bottom of the sample tube and wait ~5 seconds before removing oil. This will minimize removal of cell emulsion.**

**After removal, ~70  $\mu\text{L}$  of cell emulsion and ~5  $\mu\text{L}$  of oil remain at the bottom of the tube. Make sure the entire tube volume does not exceed the maximum volume specified in the thermal cycler manufacturer's instructions (typically 100  $\mu\text{L}$ ).**



If low-quality or no emulsions are detectable, please contact [support@missionbio.com](mailto:support@missionbio.com).



# **DNA + Protein Protocol**

3 Lyse and Digest Cells

### 3 Lyse and Digest Cells

In this step, cells are lysed, and DNA binding proteins are enzymatically digested to make DNA accessible for downstream target amplification.

- 3.1** Run the “Lysis/Digest” protocol on the thermal cycler according to the manufacturer's instructions, using the following parameters:

| Step | Temperature | Time   |
|------|-------------|--------|
| 1    | 50 °C       | 60 min |
| 2    | 80 °C       | 10 min |
| 3    | 4 °C        | HOLD   |

**Table 2.** Thermal cycling protocol for ‘Lysis/Digest’.

- 3.2** When the run completes, **store the lysed and digested samples at 4 °C** until required in [Section 4 – Barcode Cells](#). The volume of oil at the bottom of the tube is expected to increase slightly after thermal cycling.

**NOTE** We strongly recommend proceeding through [Section 4 – Barcode Cells](#) on day 1.



# **DNA + Protein**

## **Protocol**

4 Barcode Cells

## 4 Barcode Cells

In this step, the drops containing encapsulated cell lysate are combined with drops containing both Barcoding Master Mix and Barcoding Beads. These newly generated drops are then distributed into 8 PCR collection tubes, to create 8 cell-barcoding emulsion samples.

- 4.1** Retrieve all reagents required for Cell Barcoding:
- Barcoding Mix V2 (-20 °C Kit)
  - Barcoding Beads (●) (4 °C Barcoding Bead Kit) → *thaw at RT, protected from light*
  - Forward Primer Pool (●) (-20 °C Primer Pools Kit)
  - Barcoding Oil (Ambient Kit)
  - Electrode Solution (Ambient Kit)
  - AbTag Primer (30 μM)

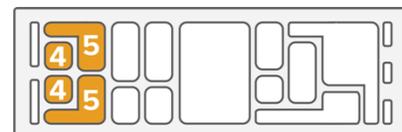
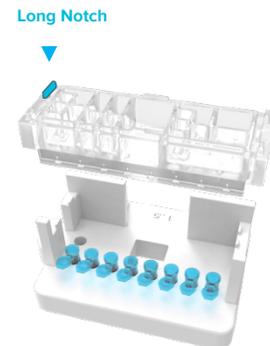
**Thaw all -20 °C reagents on ice**, except for the Barcoding Beads.

**IMPORTANT** *Protect Barcoding Beads from light and thaw at room temperature.*

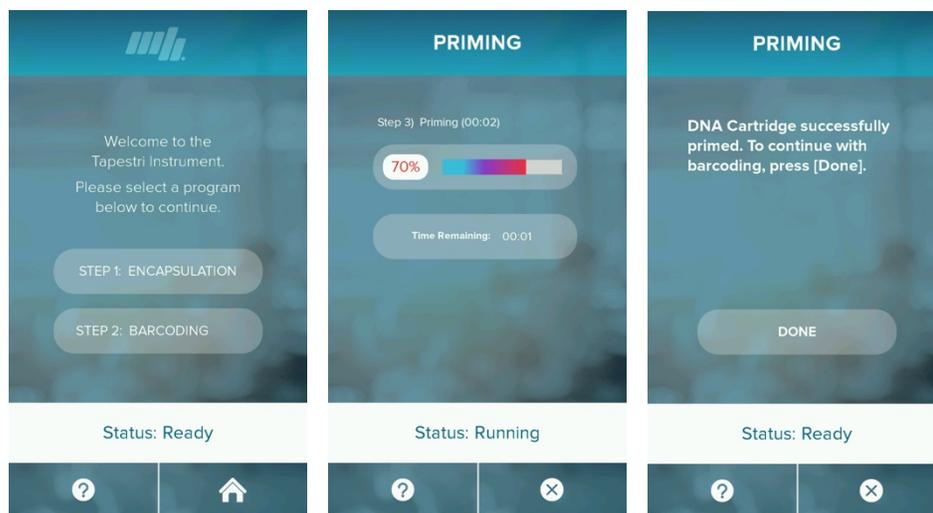
### Prime the DNA Cartridge for Barcoding

**IMPORTANT** *Use emulsion-safe PCR tubes (Axygen MAXYmum Recovery).*

- 4.2** Label eight 0.2 mL emulsion-safe PCR tubes with the sample number and **load them into the eight bottom slots of the Tapestri Base Plate** with the open lids toward you.
- 4.3** Retrieve Tapestri DNA Cartridge from its packaging and mount onto Base Plate (used during Cell Encapsulation).
- 4.4** Pipette **200 μL** of **Electrode Solution** into each of the two **reservoir 4** of the cartridge.
- 4.5** Pipette **500 μL** of **Electrode Solution** into each of the two **reservoir 5** of the cartridge.
- 4.6** **Apply the DNA Gasket** and firmly close the instrument lid, until the lid handle is level and flush with the top of the lid and instrument.



- 4.7** Run the **Priming** program by pressing **Step 2: Barcoding** on the Tapestri Instrument touchscreen. Press **NEXT** and confirm to start the program. The **program runs for about 20 minutes** before automatically pausing to allow for loading of the remaining reagents.



**Figure 7.** Touchscreen displays show main menu (left), screen after selecting ‘Step 2: Barcoding’ program (middle), and final screen after Priming is completed (right).

## Prepare Barcoding Master Mix

- 4.8** Ensure reagents are completely thawed. Vortex and centrifuge prior to mixing.
- 4.9** **Prepare 300  $\mu$ L Barcoding Master Mix Solution** as shown in the following table.  
*A total of 250  $\mu$ L will be used for Barcoding.*

| Reagent                 | Volume ( $\mu$ L) |
|-------------------------|-------------------|
| Barcoding Mix V2        | 293.0             |
| Forward Primer Pool (●) | 5.0               |
| Antibody Tag Primer (●) | 2.0               |
| <b>Total</b>            | <b>300.0</b>      |

**Table 3.** Reagents for Barcoding Master Mix

- 4.10** **Briefly vortex the Barcoding Master Mix** and centrifuge to collect the contents and store on ice.

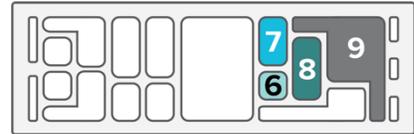
**IMPORTANT** After the Priming program has completed the Barcoding program must be started within 30 minutes.

## Load the DNA Cartridge

- 4.11 When the touchscreen displays DONE, retrieve the emulsion containing the encapsulated cell lysate from the thermal cycler at 4 °C (see [Section 2 – Encapsulate Cells](#)).
- 4.12 Open the instrument lid and pipette all of the contents of the encapsulated emulsion (~80 µL) – including 5 – 10 µL Encapsulation Oil at the bottom of the tube – into reservoir 6.

**IMPORTANT** Remember to avoid sources of static and pipette slowly and carefully when handling emulsions.

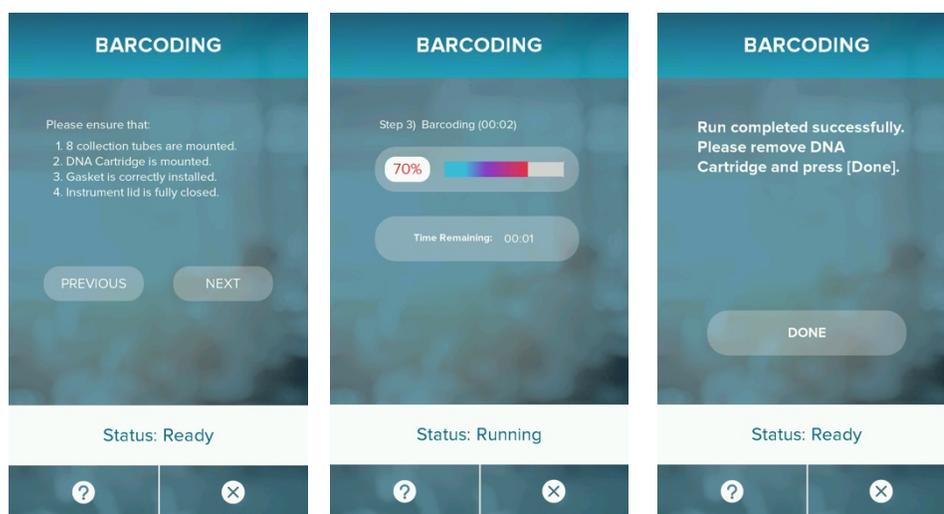
- 4.13 Retrieve the Barcoding Beads (●) and vortex tube for 1 minute at high speed.
- 4.14 Carefully pipette 200 µL of Barcoding Beads (●) into reservoir 7. *Pipette slowly and do not introduce bubbles.*
- 4.15 Pipette 250 µL of Barcoding Master Mix into reservoir 8.
- 4.16 Pipette 1.25 mL of Barcoding Oil into the reservoir 9. Be careful not to spill oil into surrounding reservoirs while loading the cartridge.



**IMPORTANT** Make sure to apply the DNA Gasket and start the Cell Barcoding program within 1 minute of loading the oil.

- 4.17 Apply the DNA Gasket and firmly close the instrument lid, until the lid handle is level and flush with the top of the lid and instrument.
- 4.18 Run the Barcoding program by pressing NEXT on the Tapestry Instrument touchscreen in the following figure. This program will complete in 35 minutes. In Tapestry instruments with serial numbers MBT-2020 or higher the Barcoding program will complete in 45 minutes (35 minutes barcoding + 10 minutes UV treatment). See [Section 5 – UV Treatment and Targeted PCR Amplification](#) for additional information.



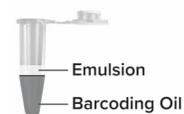


**Figure 8.** Touchscreen displays before the second part of Barcoding (left), the status during Barcoding (middle), and final screen after Barcoding is completed (right).

- 4.19** When the screen displays Run completed successfully, press DONE, carefully open the lid and **remove the Base Plate together with the cartridge to collect the eight tubes** containing the barcoded emulsion. Place the cartridge on the bench.
- 4.20** Remove the cartridge from the Base Plate.

**NOTE** *The volumes of oil and emulsion may vary across all 8 tubes. If more than 100  $\mu\text{L}$  of Barcoding Beads or more than 15  $\mu\text{L}$  of emulsions remain in reservoirs proceed with the workflow and contact [support@missionbio.com](mailto:support@missionbio.com).*

- 4.21** Visually evaluate the emulsion quality. The barcoded DNA emulsions are visible as a **white solid layer** on top of the oil layer ( $\sim 20 \mu\text{L}$ ).
- 4.22** Using a **gel loading pipette tip** carefully remove up to 90  $\mu\text{L}$  of **Barcoding Oil** from the bottom of each tube. The volume of the oil should be  $\sim 10\text{-}15 \mu\text{L}$  per tube and the total volume in each tube must be no more than 100  $\mu\text{L}$ . Place sample tubes back onto the Base Plate.



**IMPORTANT** *Hold tubes by the lid. Insert pipette tip only once when removing oil. Aspirate very slowly.*

## Clean Electrode Pins

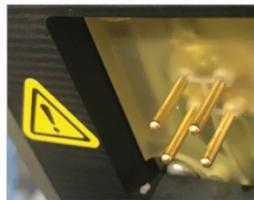
**NOTE** *The electrode pins on the bottom of the instrument lid are in direct contact with the Electrode Solution during Priming and Cell Barcoding. Gradual buildup of salt deposits might eventually hinder instrument function. Electrodes are disabled when the instrument lid is open.*

**4.23** With a dust-free cloth and deionized water **clean all four electrode pins** on the bottom of the instrument lid.

**4.24** **Dry the electrode pins** using a dry dust-free cloth.



**Dirty (salt deposits)**



**Clean**



# **DNA + Protein Protocol**

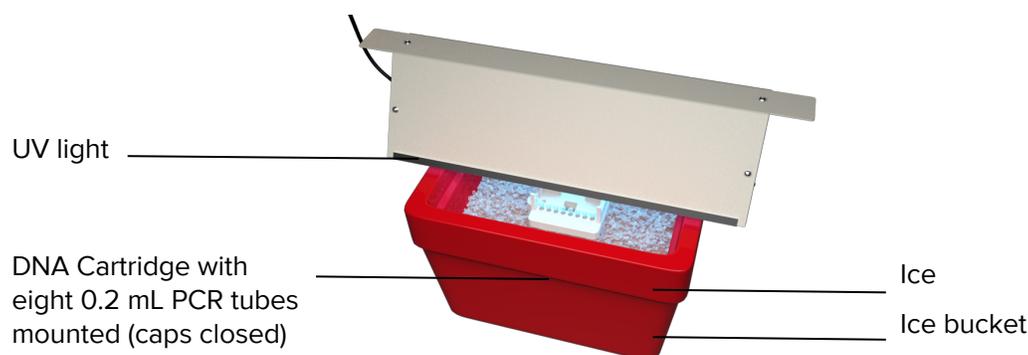
5 UV Treatment and  
Targeted PCR Amplification

## 5 UV Treatment and Targeted PCR Amplification

In this step, emulsions containing cell lysate, barcoding beads, and PCR reagents are exposed to UV light to cleave off barcode-containing forward primers from the barcoding beads prior to targeted PCR amplification.

**IMPORTANT** *Tapestri Instruments with serial numbers MBT-2020 (located on back panel of instrument) are equipped with a UV light source, which is automatically turned on in the last 10 minutes of the Barcoding program. Therefore, skip the instructions provided in this section (Steps 5.1 – 5.2) and proceed to Step 5.3.*

- 5.1** Place the entire Base Plate with tubes containing barcoded DNA on ice.



- 5.2** Place a UV light on top of the ice bucket and **expose the samples to UV light for 8 minutes**. The distance between sample and UV light must not exceed 5 inches.

**IMPORTANT** *Make sure to use the Analytik Jena Blak-Ray XX-15L UV light source.*

- 5.3** After UV exposure, remove the Base Plate from the ice, **transfer the samples to the thermal cycler, and run the “Targeted PCR” protocol** according to the manufacturer's instructions.

Make sure to select the correct thermal cycling program with the **correct annealing/extension times (Steps 4 and 8, see Table 4 below)** that are compatible with the targeted gene panel you processed your samples with.

**IMPORTANT** *Ensure that the emulsions in all eight tubes (white top layer) sit within the height of the block of the thermal cycler that is temperature controlled. Use a skirt or empty PCR tubes placed at the corners of the thermal cycling block to maximize even heat transfer.*

## 5 UV Treatment and Targeted PCR Amplification

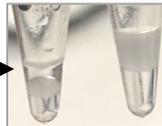
|                 |        |             | 2. Targeted PCR |                |              |              |       |
|-----------------|--------|-------------|-----------------|----------------|--------------|--------------|-------|
| Amplicon Number |        |             | 20 – 100        | 100 – 200      | 200 – 300    | > 300        |       |
| Panel           |        |             | Custom*         | AML V2         | THP/CLL      | Myeloid      |       |
| Step            | Ramp   | Temperature | Time            | Time           | Time         | Time         | Cycle |
| 1               | 4 °C/s | 98 °C       | 6 min           | 6 min          | 6 min        | 6 min        |       |
| 2               | 1 °C/s | 95 °C       | 30 sec          | 30 sec         | 30 sec       | 30 sec       | 11    |
| 3               |        | 72 °C       | 10 sec          | 10 sec         | 10 sec       | 10 sec       |       |
| 4               |        | 61 °C       | <b>3 min</b>    | <b>4.5 min</b> | <b>6 min</b> | <b>9 min</b> |       |
| 5               |        | 72 °C       | 20 sec          | 20 sec         | 20 sec       | 20 sec       |       |
| 6               | 1 °C/s | 95 °C       | 30 sec          | 30 sec         | 30 sec       | 30 sec       | 13    |
| 7               |        | 72 °C       | 10 sec          | 10 sec         | 10 sec       | 10 sec       |       |
| 8               |        | 48 °C       | <b>3 min</b>    | <b>4.5 min</b> | <b>6 min</b> | <b>9 min</b> |       |
| 9               |        | 72 °C       | 20 sec          | 20 sec         | 20 sec       | 20 sec       |       |
| 10              | 4 °C/s | 72 °C       | 2 min           | 2 min          | 2 min        | 2 min        |       |
| 11              |        | 4 °C        | HOLD            | HOLD           | HOLD         | HOLD         |       |

**Table 4.** Thermal cycling programs for Targeted PCR.

\*Please contact [support@missionbio.com](mailto:support@missionbio.com) for additional information.

**IMPORTANT** *Ensure that ramp rate is set to 1 °C/s for emulsion stability. If you observe an aqueous layer on top of the white-appearing emulsion layer, please contact [support@missionbio.com](mailto:support@missionbio.com).*

*Emulsions not intact  
Targeted PCR  
unsuccessful*



*Emulsions intact  
Targeted PCR  
successful*

## Break Emulsions and Pool Tubes

- 5.4** Retrieve the following reagents needed for PCR product purification:
- Extraction Agent (●)
  - Nuclease-free water
- 5.5** Add **10  $\mu\text{L}$  of Extraction Agent (●) to each sample tube**. Vortex and spin for 20 seconds.
- 5.6** **Incubate at room temperature for 3 minutes** until the entire emulsion changes from white to clear in color. *If emulsions don't lose their white appearance, add 5  $\mu\text{L}$  of additional Extraction Agent, vortex and spin for 20 more seconds.*
- 5.7** Add **45  $\mu\text{L}$  of nuclease-free water to each tube**. Mix by briefly vortexing and then spinning for 10 seconds in a benchtop centrifuge to separate the aqueous and oil layers.
- 5.8** Pipette **42  $\mu\text{L}$**  of each of the aqueous top layers from **tubes 1 – 4** into a **first 1.5 mL** low-bind Eppendorf tube (this Eppendorf tube should now contain 168  $\mu\text{L}$ ). Pipette **42  $\mu\text{L}$**  of the aqueous top layer from each of **tubes 5 – 8** into a **second 1.5 mL** low-bind Eppendorf tube. *Do not transfer any oil (bottom phase) or Barcoding Beads (interphase).*
- 5.9** Store samples at 4 °C or proceed to **Section 6 – Cleanup PCR Products**.

### STOPPING POINT

*This is a good place to stop in the protocol if there is not adequate time to continue to clean up the libraries in one day (~ 1 hr).  
The amplified PCR products can be stored at 4 °C for < 24 hours or -20 °C for > 24 hours.*



# **DNA + Protein Protocol**

6 Cleanup PCR Products

## 6 Cleanup PCR Products

### Digest PCR Product

- 6.1** Retrieve all reagents required for digesting the PCR product:
- DNA Clean up Buffer (●) (-20 °C Kit)
  - Clean up Enzyme (●) (-20 °C Kit)
- 6.2** For each of the two pooled samples prepare a 200  $\mu\text{L}$  **Digestion Mix** by adding **20  $\mu\text{L}$  DNA Clean up Buffer (●)** and **12  $\mu\text{L}$  Clean up Enzyme (●)**.

| Reagent                 | Volume ( $\mu\text{L}$ ) |
|-------------------------|--------------------------|
| Pooled sample           | 168.0                    |
| DNA Clean up Buffer (●) | 20.0                     |
| Clean up Enzyme (●)     | 12.0                     |
| <b>Total</b>            | <b>200.0</b>             |

**Table 5.** Reagents for Digestion Mix.

- 6.3** Briefly vortex and quick-spin the tubes.
- 6.4** **Split each sample into two new tubes**, each containing 100  $\mu\text{L}$  (a total of 4 tubes), and place on thermocycler to **digest at 37 °C for 60 minutes**.
- 6.5** Remove from thermal cycler, store at room temperature and continue with AMPure XP Library Cleanup.

### AMPure XP Library Cleanup

- 6.6** Thoroughly **vortex AMPure XP reagent for 45 seconds** at high-speed. Equilibrate the **AMPure XP reagent to room temperature**.
- 6.7** Prepare **5 mL fresh 80% ethanol** using nuclease-free water.

**NOTE** *Measure volumes for 100% ethanol and nuclease-free water separately. Make sure to tightly close all ethanol containers when not in use, since ethanol can absorb water over time, leading to lower concentrations.*

- 6.8** **Recombine contents** of sample tubes into **two** new 1.5 mL low-bind Eppendorf tubes.
- 6.9** Thoroughly **vortex AMPure XP reagent** at high speed immediately prior to usage.
- 6.10** For each 200  $\mu\text{L}$  sample tube, **add 140  $\mu\text{L}$  (0.7 X) of AMPure XP reagent**.
- 6.11** **Vortex for 10 seconds** and quick-spin to collect contents.

- 6.12** Incubate the tubes at **room temperature for 5 minutes**, and then place the tubes on the magnet.
- 6.13** Allow at least **5 minutes** for the AMPure beads to separate from solution.

**IMPORTANT** *Do not discard the supernatant from the tubes as it contains the Protein Library.*

- 6.14** Without removing the tubes from the magnet, **transfer the supernatant (~340 µL) from each tube** to two new 1.5 mL low-bind Eppendorf tubes and set aside at room temperature for **Protein Library Cleanup I** in **Step 6.34**. *The DNA library is bound to the beads.*
- 6.15** Proceed with **DNA Library Cleanup I** followed by **Protein Library Cleanup I**.

### DNA Library Cleanup I

- 6.16** In each tube, **wash AMPure bead pellets** while keeping the tubes on the magnet:
- Carefully **add 800 µL** of the freshly prepared **80% ethanol**.
  - Wait **30 seconds**.
  - Remove ethanol** without disturbing the AMPure beads.
  - Repeat Steps a. – c.** once, for a total of two wash cycles.
- 6.17** Keeping the tubes on the magnet, using a P-10 pipette, **remove all residual ethanol** from each tube without disturbing the AMPure beads.
- 6.18** **Dry AMPure bead pellets** in the tubes on the magnet by incubating at room temperature for **4 – 6 minutes**. *Over-dried beads may be more difficult to suspend.*
- 6.19** Remove the tubes from the magnet.
- 6.20** **Add 60 µL** of nuclease-free water into each tube.
- 6.21** **Vortex each tube for 10 seconds**, quick-spin to collect the contents, and incubate the tubes at room temperature for **2 minutes**.
- 6.22** Place the tubes onto the magnet and **wait for at least 2 minutes** or until solutions are clear.
- 6.23** **Transfer and combine 50 µL** of purified PCR product from each tube to a **single** new 0.2 mL PCR tube each for a total of 100 µL. *Avoid transfer of AMPure beads.*
- 6.24** [OPTIONAL] If AMPure beads persist in the supernatant, place the 0.2 mL PCR tubes onto a 96-well magnet stand, wait 5 minutes and transfer 50 µL of purified PCR products to a new 0.2 mL PCR tubes.
- 6.25** **Quantify 1 µL of purified PCR product**, using the **High Sensitivity dsDNA 1X Qubit Kit** (or equivalent assay) according to the manufacturer's instructions.

**NOTE** *The DNA may vary between 0.2 ng/µL to 4.0 ng/µL. If yields are outside this range, contact [support@missionbio.com](mailto:support@missionbio.com) for additional support.*

- 6.26** Store purified PCR product samples at 4° C until proceeding to the next step or -20° C for long-term storage.

## Protein Library Cleanup I

### Prepare Streptavidin Beads

- 6.27** Retrieve all reagents required for cleaning up the protein library:
- Streptavidin Beads (●) (4°C, Protein Staining Kit)
  - 2X Wash Buffer (4°C, Protein Staining Kit)
  - Biotin Oligo (●) (4°C, Protein Staining Kit)
- 6.28** Equilibrate the **Streptavidin Beads (●)** to room temperature.
- 6.29** Thoroughly **vortex Streptavidin Beads (●)** at high speed immediately prior to usage.
- 6.30** Transfer **100 µL of Streptavidin Beads (●)** to a new 1.5 mL low-bind Eppendorf tube.
- 6.31** Place on magnet and wait for 2 minutes for beads to separate from solution.
- 6.32** Remove the supernatant and discard.
- 6.33** Wash the beads while keeping the tube on the magnet:
- a. Carefully add **1 mL of 2X Wash Buffer**.
  - b. Wait **1 minute** for solution to clear.
  - c. **Remove 2X Wash Buffer** without disturbing the beads.
- a. **Repeat Steps a. – c.** once, for a total of two wash cycles.
- 6.34** Resuspend the beads **690 µL of 2X Wash Buffer** and set aside until later usage in **Step 6.39**.

### Isolate Antibody Tags

- 6.35** Retrieve the two tubes with the supernatant from **Step 6.14** of the **Clean Up PCR Product section**.
- 6.36** To each tube add **2 µL of Biotin Oligo (●)** to the supernatant, vortex and spin down.
- 6.37** Incubate at **96 °C for 5 minutes**.
- 6.38** Transfer tubes immediately onto ice and incubate for 5 minutes.
- 6.39** Add and mix **342 µL of Streptavidin Beads** resuspended in 2X Wash Buffer – **from Step 6.34 above** – to each Biotin Oligo-treated sample tube.
- 6.40** Incubate for **20 minutes** on a shaker at room temperature.
- 6.41** Quick-spin to collect contents.
- 6.42** Place on magnet and wait **5 minutes** for the beads to separate from solution.
- 6.43** While waiting, prepare **3 mL of 1X Wash Buffer** by mixing 1.5 mL of 2X Wash Buffer with 1.5 mL of nuclease-free water.
- 6.44** Remove the supernatant, wash the Streptavidin Beads while keeping the tube on the magnet:
- a. Carefully add **1 mL of 1X Wash Buffer**.
  - b. Wait **1 minute** for solution to clear.
  - c. **Remove 1X Wash Buffer** without disturbing the beads.
- 6.45** Remove the tube from magnet and wash a second time with **1 mL nuclease-free water** by pipetting up and down five times.
- 6.46** Place on magnet and wait **3 minutes** for the beads to separate from solution.
- 6.47** Remove the supernatant and in each tube resuspend the beads in **25 µL of nuclease-free water**. Transfer and combine into a new 0.2 mL PCR tube for a total of **50 µL**.

*The Protein PCR products are bound to the streptavidin beads (brown).*

**STOPPING POINT**

*This is a good place to stop in the protocol if there is not adequate time to continue to Library PCR (~ 1 hr).*

*The purified DNA PCR products can be stored at 4 °C for < 24 hours or -20 °C long-term and will be stable for up to six months.*

*The amplified Protein PCR products can be stored at 4 °C overnight.  
Do not store at -20 °C.*



# **DNA + Protein Protocol**

## 7 PCR Target Library

## 7 PCR Target Library

During Target Library PCR the P5 and P7 adapter (Illumina) sequences are added to the amplicons required for sequencing. Each V2 Index Primer includes two unique index sequences.

Use the following V2 Index Primer combination when indexing your DNA libraries.

| # of Samples | Option 1                              | Option 2                              | Option 3 | Option 4 |
|--------------|---------------------------------------|---------------------------------------|----------|----------|
| 1            | Any index                             |                                       |          |          |
| 2            | 1 + 4                                 | 2 + 3                                 | 5 + 7    | 6 + 8    |
| 3            | 1 + 2 + 3                             | 4 + 6 + 8                             |          |          |
| 4            | 1 + 2 + 3 + 4                         | 5 + 6 + 7 + 8                         |          |          |
| 5            | 1 + 2 + 3 + 4<br>+ one from (6, 7, 8) | 5 + 6 + 7 + 8<br>+ one from (1, 3, 4) |          |          |
| 6            | 1 + 2 + 3 + 4<br>+ two from (6, 7, 8) | 5 + 6 + 7 + 8<br>+ two from (1, 3, 4) |          |          |
| 7            | 1 + 2 + 3 + 4 + 6 + 7 + 8             |                                       |          |          |
| 8            | 1 + 2 + 3 + 4 + 5 + 6 + 7 + 8         |                                       |          |          |
| > 8          | Contact Mission Bio                   |                                       |          |          |

**Table 6.** V2 Index Primer combinations for different sample multiplexing schemes.

- 7.1** Retrieve the following reagents required for Library PCR
- Purified PCR products (DNA and Protein) (from [Section 6](#))
  - V2 Index Primer 1 – 8 (●) (-20 °C Kit) *DNA Library*
  - Protein Library Indices 1-8 (●) (+4 °C Kit) *Protein Library*
  - Library Mix V2 (-20 °C Kit)
  - Nuclease-free water (Ambient Kit)
- 7.2** In a Pre-PCR area **label two new 0.2 mL PCR tubes** with the index numbers of the V2 Index Primer.
- 7.3** **Set up two different Library PCR reactions: one for the DNA Library and one for the Protein Library as follows:**

**IMPORTANT** Ensure V2 index primers (●) are used for DNA and Protein index primers (●) are used for protein. Record the index number used for each sample. Make sure to avoid cross-contamination when handling the Indices.

|   | DNA Library        | Protein Library |
|---|--------------------|-----------------|
| <b>Reagent</b>  | <b>Volume [μL]</b> |                 |
| Library Mix V2  | 25                 | 25              |
| V2 Index Primer (●)                                     | 10                 | -               |
| Protein Index Primer (●)                                | -                  | 10              |
| Targeted DNA PCR product                                | 15                 | -               |
| Resuspended Streptavidin Beads containing Antibody Tags |                    | 15              |
| Total Volume  | 50                 | 50              |

**Table 7.** Library Mix

- 7.4** Vortex and quick-spin the tubes to collect contents.
- 7.5** Transfer the samples to the thermal cycler, then **run the Library PCR protocol** according to the manufacturer's instructions, using the following parameters:

| Step | Temperature | Time   | Cycles   |
|------|-------------|--------|--|
| 1    | 95 °C       | 3 min  |  |
| 2    | 98 °C       | 20 sec | <b>10</b> for DNA Library<br><b>20</b> for Protein Library |
| 3    | 62 °C       | 20 sec |  |
| 4    | 72 °C       | 45 sec |  |
| 5    | 72 °C       | 2 min  |  |
| 6    | 4 °C        | HOLD   |  |

**Table 8.** Thermal cycling program for Library PCR.

- 7.6** Remove the samples from thermal cycler and store at room temperature.

## Library cleanup

- 7.7** Thoroughly vortex AMPure XP reagent for **15 seconds** at high-speed. Equilibrate the AMPure XP reagent to room temperature.
- 7.8** Prepare **5 mL fresh 80% ethanol** using nuclease-free water.

**NOTE** Measure volumes for 100% ethanol and nuclease-free water separately. Make sure to tightly close all ethanol containers when not in use, since ethanol can absorb water over time, leading to lower concentrations.

## DNA Library Cleanup II

- 7.9** Thoroughly **vortex AMPure XP reagent** at high-speed immediately prior to usage.
- 7.10** Add **50  $\mu$ L** of **nuclease-free water to the sample tube.**
- 7.11** **Add 69  $\mu$ L (0.69 X) of AMPure XP reagent** to the 100  $\mu$ L sample.
- 7.12** **Vortex for 5 seconds** and quick-spin to collect contents.
- 7.13** Incubate the tube at **room temperature for 5 minutes**, and then place the tube on the magnet.
- 7.14** Allow at least **2 minutes** for the AMPure beads to separate from solution.
- 7.15** Without removing the tube from the magnet, **remove the clear liquid** and discard.  
*The DNA is bound to the beads.*
- 7.16** **Wash AMPure bead pellets** while keeping the tube on the magnet:
- Carefully **add 200  $\mu$ L** of the freshly prepared **80% ethanol**.
  - Wait **30 seconds**.
  - Remove ethanol** without disturbing the AMPure beads.
  - Repeat Steps 7.16 a. – c.** once, for a total of two wash cycles.
- 7.17** Keeping the tube on the magnet, **remove all residual ethanol** without disturbing the AMPure beads.
- 7.18** **Dry AMPure bead pellets** in the tube on the magnet by incubating at room temperature for at least **2 minutes**. *Over-dried beads may be more difficult to suspend.*
- 7.19** Remove the tube from the magnet.
- 7.20** **Add 100  $\mu$ L** of nuclease-free water into the tube.
- 7.21** **Vortex tube for 5 seconds**, quick-spin to collect the contents, and incubate at room temperature for **2 minutes**.
- 7.22** Place the tube onto the magnet and **wait for at least 2 minutes** or until solutions are clear.
- 7.23** **Transfer 100  $\mu$ L** of purified PCR product from the tube to a new 0.2 mL PCR tube.  
*Avoid transfer of AMPure beads.*
- 7.24** **Add 72  $\mu$ L (0.72 X) of AMPure XP reagent** to the 100  $\mu$ L sample.
- 7.25** **Vortex for 5 seconds** and quick-spin to collect contents.
- 7.26** Incubate the tube at **room temperature for 5 minutes**, and then place the tube on the magnet.
- 7.27** Allow at least **2 minutes** for the AMPure beads to separate from solution.
- 7.28** Without removing the tube from the magnet, **remove the clear liquid** and discard.  
*The DNA is bound to the beads.*
- 7.29** **Wash AMPure bead pellets** while keeping the tube on the magnet:
- Carefully **add 200  $\mu$ L** of the freshly prepared **80% ethanol**.
  - Wait **30 seconds**.
  - Remove ethanol** without disturbing the AMPure beads.
  - Repeat Steps 7.29 a. – d.** once, for a total of two wash cycles.
- 7.30** Keeping the tube on the magnet, **remove all residual ethanol** without disturbing the AMPure beads.
- 7.31** **Dry AMPure bead pellets** in the tube on the magnet by incubating at room temperature for at least **2 minutes**. *Over-dried beads may be more difficult to suspend.*
- 7.32** Remove the tube from the magnet.

- 7.33** Add **15  $\mu\text{L}$**  of nuclease-free water into the tube.
- 7.34** **Vortex tube for 5 seconds**, quick-spin to collect the contents, and incubate at room temperature for **2 minutes**.
- 7.35** Place the tube onto the magnet and **wait for at least 2 minutes** or until solutions are clear.
- 7.36** **Transfer 12  $\mu\text{L}$**  of purified PCR product from the tube to a new 0.2 mL PCR tube.  
*Avoid transfer of AMPure beads.*
- 7.37** Store purified PCR product samples at  $-20\text{ }^{\circ}\text{C}$  until proceeding to the next step.

### Protein Library Cleanup II

- 7.38** Place tube on magnet and wait for **2 minutes** for Streptavidin Beads to separate from the solution.
- 7.39** Without removing the tube from the magnet, transfer **50  $\mu\text{L}$  of supernatant** in to a new 0.2 mL PCR tube.
- 7.40** **Add 45  $\mu\text{L}$  (0.9 X) of AMPure XP reagent** to the 50  $\mu\text{L}$  sample.
- 7.41** **Vortex for 10 seconds** and quick-spin to collect contents.
- 7.42** Incubate the tube at **room temperature for 5 minutes**, and then place the tube on the magnet.
- 7.43** Allow at least **2 minutes** for the AMPure beads to separate from solution.
- 7.44** Without removing the tube from the magnet, **remove the supernatant** and discard.
- 7.45** **Wash AMPure bead pellets** while keeping the tube on the magnet:
- Carefully **add 200  $\mu\text{L}$**  of the freshly prepared **80% ethanol**.
  - Wait **30 seconds**.
  - Remove ethanol** without disturbing the AMPure beads.
  - Repeat Steps 7.45 a. – d.** once, for a total of two wash cycles.
- 7.46** Keeping the tube on the magnet, **remove all residual ethanol** with a P-10 pipette without disturbing the AMPure beads.
- 7.47** **Dry AMPure bead pellets** in the tube on the magnet by incubating at room temperature for at least **2 minutes**. *Over-dried beads may be more difficult to suspend.*
- 7.48** Remove the tube from the magnet.
- 7.49** **Add 17  $\mu\text{L}$**  of nuclease-free water into the tube.
- 7.50** **Vortex tube for 5 seconds**, quick-spin to collect the contents, and incubate at room temperature for **2 minutes**.
- 7.51** Place the tube onto the magnet and **wait for at least 2 minutes** or until solutions are clear.
- 7.52** **Transfer 15  $\mu\text{L}$**  of purified PCR product from the tube to a new 0.2 mL PCR tube.  
*Avoid transfer of AMPure beads.*

**STOPPING POINT** *This is a good place to stop in the protocol if there is not adequate time to finish in one day (~ 1 hr). The purified Library PCR products can be stored at  $-20\text{ }^{\circ}\text{C}$ .*



# **DNA + Protein Protocol**

8 Quantify and Normalize  
Sequencing Library

## 8 Quantify and Normalize Sequencing Library

- 8.1** Retrieve the following for library quantitation:
- Purified sample libraries (DNA library and protein library)
  - Agilent DNA High Sensitivity Kit or Agilent DNA 1000 kit

### Quantify Using Agilent Bioanalyzer

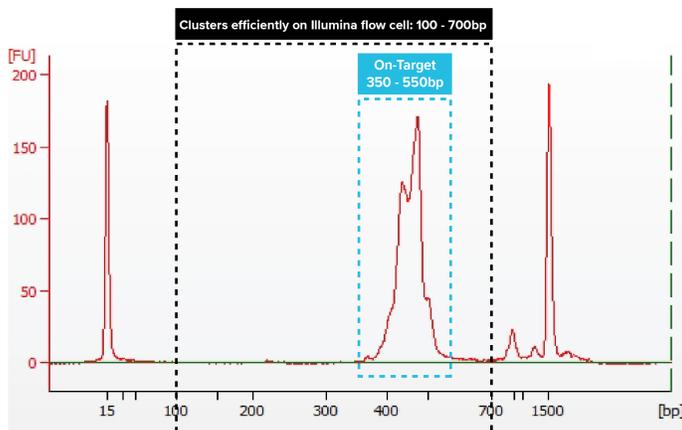
**NOTE** *Agilent TapeStation 2200/4200 or Fragment Analyzer (Advanced Analytical) may be used if an Agilent Bioanalyzer 2100 is not available.*

- 8.2** Use **1  $\mu$ L of a 1:10 dilution of the DNA and Protein Library** and follow Agilent's protocol instructions to prime, load, and run DNA samples from all tubes on a DNA 1000 chip.
- 8.3** Verify the DNA and Protein Library product sizes and purity and quantify following manufacturer's instructions.

**NOTE** *A final concentration of on-target product between 2 – 50 ng/ $\mu$ L can be expected for the DNA Library with a peak at ~460bp. A final concentration of on-target product between 1 – 30 ng/ $\mu$ L can be expected for the Protein Library with a peak at ~250bp.*

#### AML Libraries

Libraries generated with the AML panel in general produce high-quality on-target amplicons (**blue rectangle**) with only a few off-target fragments (e.g., primer dimers).

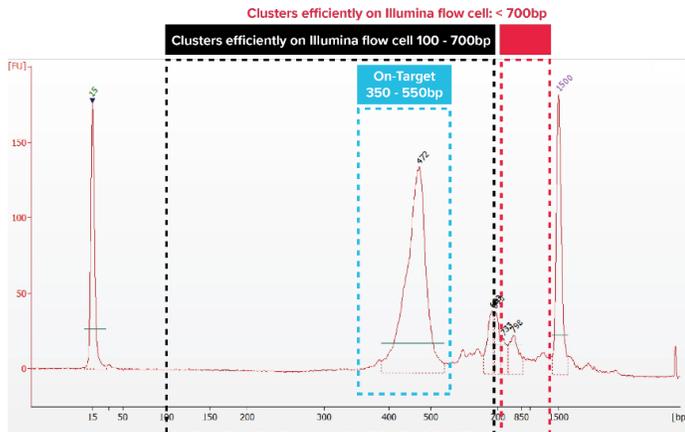


- 8.4** Quantify the concentration of the libraries based on a range of 100 – 700bp (**black rectangle**) to include products that may efficiently cluster on the Illumina flow cell. This minimizes the potential to over-cluster when sequencing the libraries. Use this value in **Step 8.7**.

#### Myeloid, Tumor Hot Spot, and CLL Libraries

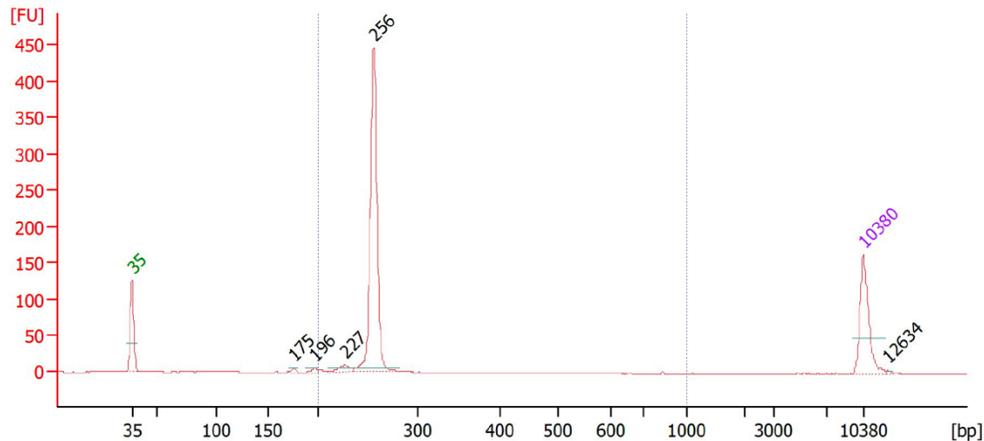
## 8 Quantify and Normalize Sequencing Library

Libraries generated with 250+ amplicon panels (e.g., Myeloid, Tumor Hot Spot, CLL) may produce large-size off-target fragments that need to be taken into account when quantifying the concentration of the libraries.



- 8.5 Quantify the concentration of the libraries based on a range of 100 – 700 bp (**black rectangle**) to include products that may efficiently cluster on the Illumina flow cell.  
Use this value in **Step 8.7**.
- 8.6 Quantify the concentration of the libraries based on a range of 700 – 1,200 bp (**red rectangle**) to record the fraction of products that will impact the final concentration of the pooled library when quantifying with a Qubit Fluorometer.

### Protein Libraries



**NOTE** If primer dimers (~220 bp) are detectable (> 5% for DNA Library, > 10% for Protein library, based on molarity) it is recommended to clean the libraries again using the protocols outlined in the **Appendix – Removing Excess Amounts of Primer Dimers**.  
If > 25% of primer dimers are detectable, contact [support@missionbio.com](mailto:support@missionbio.com) for additional support.

### Normalize and Pool Libraries

- 8.7** For the DNA libraries use the *Tapestri Sample Quantification Tool (PN 40678)* to dilute each sample DNA library.
- 8.8** **Pool 5 nM of each of the libraries equimolar.** The final concentration of DNA in the pooled library will be ~ 5 nM (0.9 – 1.3 ng/μL).
- 8.9** **Re-quantify the pooled library** with a Qubit Fluorometer.

#### AML Libraries

The final concentration of the library will be between **0.9 – 1.3 ng/μL**.

#### Myeloid, Tumor Hot Spot, and CLL Libraries

The final concentration of the library will be between **0.9 – 1.6 ng/μL**. The products quantified between 700 – 1,200 bp account for the increased concentration > 1.3 ng/μL. Ensure that the relative fraction of large-size off-target products as measured in **Steps 8.5 – 8.6** is consistent with the Qubit measurement.

#### Protein Libraries

The final concentration of the library will be between **0.8 – 0.9 ng/μL**.

**NOTE** *Alternatively pooled libraries may be quantified using quantitative PCR (KAPA Library Quantification Kit Illumina Platforms, PN KK4873).*



# **DNA + Protein Protocol**

9 Sequence Library

## 9 Sequence Library

| Parameter                                    | Specification  |
|--|--|
| Final library size                           | <b>DNA Library: 350 bp – 550 bp</b> with peak at ~460 bp<br><b>Protein Library: 225 bp – 270 bp</b> with peak at ~250 bp   |
| Supported sequencers                         | MiSeq, HiSeq 2500, NextSeq 1000/2000, NextSeq 550, HiSeq 3000/4000, NovaSeq 5000/6000  |
| Supported sequencing chemistries             | See <b>Table 9</b> on next page.   |
| Index 1 (i7)                                 | <b>Yes (8nt)</b> . Index 1 – 8 sequences are different from Illumina's Indices.<br><i>Illumina Indices may be used (4 μM).</i>   |
| Index 2 (i5)                                 | <b>Yes (8nt)</b> . Index 1 – 8 sequences are different from Illumina's Indices.<br><i>Illumina Indices may be used (4 μM).</i>   |
| Number of unique i7/i5 index pair per sample | <b>1</b>   |
| Custom sequencing primer?                    | <b>No</b>  |
| Sequencing chemistry                         | <b>2 x 150 bp</b> (in some cases 500 cycle kits may be used with 300 cycle runs programmed)  |
| PhiX %                                       | <b>5 % – 20 %</b> see <b>Table 9</b> on next page  |
| Compatible with non-Tapestry libraries?      | <b>Yes</b> , if libraries are of similar size.   |
| Number of expected FASTQ files per sample    | <b>2: one Read 1/Read 2 pair representing one unique i7/i5 combination</b><br>If the library is distributed across more than one flow cell lane, please merge lane-specific FASTQ files that belong to one sample. |
| Recommended coverage per sample              | <b>AML (~67M read pairs), Myeloid (~173M read pairs)</b><br><b>CLL (~144M read pairs), THP (~128M read pairs)</b>  |

Please refer to the Illumina User Guides listed in **Table 10**.

The following table provides guidance on how many samples maximally may be multiplexed and sequenced together on one flow cell. Please note that the recommended number of samples refers to the **DNA libraries only**.

For **Protein libraries** please refer to the next page to obtain additional information on sequencing requirements.

| Sequencer                   | Final Library Input [pM] | PhiX % | Cluster Density [K/mm <sup>2</sup> ] | # of Lanes | Samples (DNA library only) / Sequencing Run / Flow Cell |         |         |         |                 | Sequencing Chemistry  | # of Read Pairs*** [10 <sup>6</sup> ] |
|-----------------------------|--------------------------|--------|--------------------------------------|------------|---|---------|---------|---------|-----------------|-----------------------|---------------------------------------|
|                             |                          |        |                                      |            | Panel (# of amplicons)                                  |         |         |         |                 |                       |                                       |
|                             |                          |        |                                      |            | AML 127   | MYE 312 | THP 244 | CLL 274 | Custom variable |                       |                                       |
| MiSeq V3*                   | 20 – 22                  | 5 %    | 1,200 – 1,500                        | 1          | 0   | 0       | 0       | 0       | Varies          | V3 Paired End         | 25 – 30                               |
| HiSeq 2500**                | 8 – 10                   | 10 %   | 750 – 900                            | 2          | 4   | 2       | 2       | 2       | Varies          | V2 SBS Rapid Mode     | 300 – 350                             |
| NextSeq 500/550 Mid-Output  | 1.8 – 2                  | 20 %   | 150 – 175                            | 4          | 2   | 1^      | 1^      | 1^      | Varies          | V2.5 Paired End       | 120 – 140                             |
| NextSeq 500/550 High-Output | 1.8 – 2                  | 20 %   | 150 – 175                            | 4          | 5   | 2       | 3       | 2       | Varies          | V2.5 Paired End       | 360 – 420                             |
| HiSeq 4000                  | 250 – 300                | 15 %   | 1,350 – 1,550                        | 8          | 33  | 13      | 17      | 15      | Varies          | Standard SBS          | 4,000 – 5,000                         |
| NovaSeq 6000 SP             | 300 – 400                | 15 %   | 600 – 800                            | 1          | 10  | 4       | 5       | 5       | Varies          | SP Reagent 300 cycles | 650 – 800                             |
| NovaSeq 6000 S1             | 300 – 400                | 15 %   | > 80% occupancy                      | 2          | 21  | 9       | 11      | 10      | Varies          | S1 Reagent 300 cycles | 1,300 – 1,600                         |
| NovaSeq 6000 S2             | 300 – 400                | 15 %   | > 80% occupancy                      | 2          | 53  | 21      | 27      | 24      | Varies          | S2 Reagent 300 cycles | 3,300 – 4,000                         |
| NovaSeq 6000 S4             | 300 – 400                | 15 %   | > 80% occupancy                      | 4          | 133   | 53      | 68      | 61      | Varies          | S4 Reagent 300 cycles | 8,000 – 10,000                        |

**Table 9.** Recommended sequencing specifications and sample multiplexing for DNA Library.

\*MiSeq V3 kit is only available as 600 cycle kit which needs to be run with 2x150bp paired end sequencing

\*\*HiSeq 2500 V2 SBS Rapid Mode kit is only available as 500 cycle kit which needs to be run with 2x150bp paired end sequencing

\*\*\*Paired-end sequencing required      ^With 10,000 cell output, coverage may be below recommendations.

## DNA Library

- Recommended coverage (per cell, per amplicon) = **60 – 80X**
- Formula:
  - **Total read pairs needed = number of expected cells x number of amplicons x coverage**
  - **Example:** AML (127 amplicons) and 5,000 cells
  - $5,000 \times 127 \times 70 = \mathbf{67M}$  read pairs

## Protein Library

- Recommended coverage (per cell) = **30,000X**
- Formula:
  - **Total read pairs needed = number of expected cells x coverage**
  - Example:  $5,000 \times 30,000 = \mathbf{150M}$  read pairs

**NOTE** *DNA Libraries and Protein Libraries may be pooled and sequenced together. However, note that the average sizes differ between both libraries and particular care needs to be taken care when normalizing and pooling DNA and Protein libraries together for sequencing to ensure sufficient read coverage.*

*If using a patterned sequencing flowcell (eg. Nextseq2000), reduce Protein library input by 25% by volume to ensure sufficient DNA library reads. Contact [support@missionbio.com](mailto:support@missionbio.com) for additional support.*

| User Guide  | MiSeq   | HiSeq 2500  |
|---|---|---|
| System Guide                                      | MiSeq System Guide (PN 1000000061014)                             | HiSeq 2500 System Guide (PN 15035786)                             |
| Denaturing and Diluting Libraries Reference Guide | MiSeq System – Denature and Dilute Libraries Guide (PN 15039740)  | HiSeq Systems – Denature and Dilute Libraries Guide (PN 15050107) |
| Custom Primer Guide                               | MiSeq System – Custom Primers Guide (PN 15041638)                 | HiSeq System – Custom Primers Guide (PN 15061846)                 |
| cBot System                                       | -   | cBot System Guide (PN 15006165)                                   |
| User Guide  | HiSeq 4000  | NovaSeq 6000  |
| System Guide                                      | HiSeq 4000 System Guide (PN 15066496)                             | NovaSeq 6000 System Guide (PN 1000000019358)                      |
| Denaturing and Diluting Libraries Reference Guide | HiSeq Systems – Denature and Dilute Libraries Guide (PN 15050107) | NovaSeq 6000 System Guide (PN 1000000019358)                      |
| Custom Primer Guide                               | HiSeq System – Custom Primers Guide (PN 15061846)                 | NovaSeq Series – Custom Primers Guide (PN 1000000022266)          |

**Table 10.** Illumina User Guides

# Troubleshooting

| Step                 | Problem  | Potential Cause  | Recommended Action   |
|----------------------|--|--|--|
| <b>Instrument</b>    | Instrument lid does not close.   | DNA cartridge and/or Gasket not properly installed.    | Check correct orientation of DNA cartridge and ensure that the Gasket is properly seated on DNA Cartridge. |
|                      |  | Multiple Gaskets installed.                            | Make sure no second Gasket is still attached under the lid before closing.                                 |
|                      |  | One or both pins on the side of the chip door missing. | Ensure that both pins are on either side. Contact Support.   |
|                      | Instrument reports sealing error message.  | Gasket and/or manifold not clean.                      | Check that the Gasket and manifold are clean and free of dust.   |
|                      |  | DNA cartridge and/or Gasket not properly installed.    | Check correct orientation of DNA cartridge and ensure that the Gasket is properly seated on DNA cartridge. |
|                      |  | Multiple Gaskets installed.                            | Make sure no second Gasket is still attached under the lid before closing.                                 |
|                      | Touch screen becomes unresponsive.   | Instrument operating system under-powered.             | Power cycle instrument by turning it off, wait 20 seconds, and turning it back on.                         |
| <b>Encapsulation</b> | Volumes of cell emulsion and/or oil are too low.                                   | Clogged channel on the DNA cartridge.                  | Contact Support.   |
|                      |  | Reagents loaded incorrectly on DNA cartridge.          | Ensure proper cartridge reagent loading according to the instructions.                                     |
|                      |  | Instrument lid broken.                                 | Ensure that both pins are on either side. Contact Support.   |
| <b>Barcoding</b>     | Volumes of cell emulsion and/or oil are too low in all or a subset of eight tubes. | Subset of channels clogged on the DNA cartridge.       | Contact Support.   |
|                      |  | DNA cartridge and/or Gasket not properly installed.    | Check correct orientation of DNA cartridge and ensure that the Gasket is properly seated on DNA cartridge. |

|                     |   |   |  |
|---------------------|---|---|--|
|                     | If only a subset is affected, you may proceed the workflow with the unaffected tubes. | Incorrect reagent loading on DNA cartridge.             | Ensure proper cartridge reagent loading following the instructions.  |
|                     |   | Instrument lid broken.                                  | Ensure that both pins are on either side. Contact Support.   |
| <b>Targeted PCR</b> | Low DNA yield < 0.2 ng/μL.  | UV cleave step omitted.                                 | Repeat the protocol with a fresh aliquot of sample. If the problem persists, contact Support.  |
|                     |   | Sample lost during AMPURE cleanup.                      | Ensure to use fresh 80% EtOH and follow protocol instructions.   |
|                     |   | Incorrectly prepared Barcoding Master Mix.              | Ensure barcoding master mix and primers are completely thawed and mix thoroughly via vortexing and centrifuging.   |
| <b>Library PCR</b>  | Low DNA yield < 1.0 ng/μL.  | Lost sample during AMPURE cleanup.                      | Ensure to use fresh 80% EtOH and follow protocol instructions.   |
|                     |   | Incorrectly prepared Library PCR Master Mix.            | Ensure to correctly prepare the Library PCR Master Mix with 5 μL of Library Prep Primer and 5 μL of one of the eight Library P7 Indices 1 - 8 per sample.  |
| <b>Sequencing</b>   | No sequencing data generated/Over clustering  | Incorrect library quantification/<br>Forgot to add PhiX | Requantify library using BioAnalyzer traces, with smear analysis set to 350bp-550bp. Alternatively, run qPCR using Kapa library quantification kit. Ensure PhiX is freshly diluted and included in final loading pool. |

# Appendices

## Frequently Asked Questions (FAQs)

### **Can I use Tapestri to measure mRNA transcripts in single cells?**

No. Tapestri is currently available only for genomic (DNA) single cell analysis.

### **Can I use my own Library and Targeted PCR reagents?**

No. Only the reagents supplied with the Tapestri Single Cell DNA AML, CLL, Myeloid, THP or Custom Bead Kit are fully validated and supported.

### **Can I analyze more cells by increasing my cell sample concentration?**

The Tapestri workflow and instrumentation have been optimized for cell concentrations between 3,000 and 4,000 cells/ $\mu$ L. Working with cell concentrations outside of this range is not recommended.

### **Can I store my emulsions after Cell Encapsulation or Cell Barcoding for a few days before continuing with the protocol?**

The Cell Encapsulation emulsions (1 tube) may be stored at 4 °C overnight. The Cell Barcoding emulsions (8 tubes) must be processed immediately to ensure efficient PCR amplification of targets.

### **Can I use the Nanodrop for both Targeted PCR and Library PCR quantification?**

For targeted PCR product quantification we strongly suggest using the Qubit Fluorometer and/or Agilent Bioanalyzer. Quantification of the products after Library PCR must be performed with a method that measures the quantity and size of PCR products (i.e., Bioanalyzer, TapeStation). We do not recommend using the Nanodrop to quantify PCR products as concentration measurements may be inaccurate.

### **How should I pool my samples for sequencing?**

Please follow the instructions in the *Tapestri Sample Quantification Tool (PN 40676)*. Individual sample-tube libraries are pooled equimolar yielding a 5 nM pooled library.

### **Can I pool my Tapestri samples with other Illumina Indexed samples for sequencing?**

Yes. Please refer to the Appendix of this document for additional information.

### **Can I run my Tapestri Single-Cell DNA Library on a NextSeq or HiSeq or NovaSeq?**

Yes, Mission Bio currently supports MiSeq, HiSeq 2500, HiSeq 4000, NextSeq 550 and NovaSeq 6000 platforms.

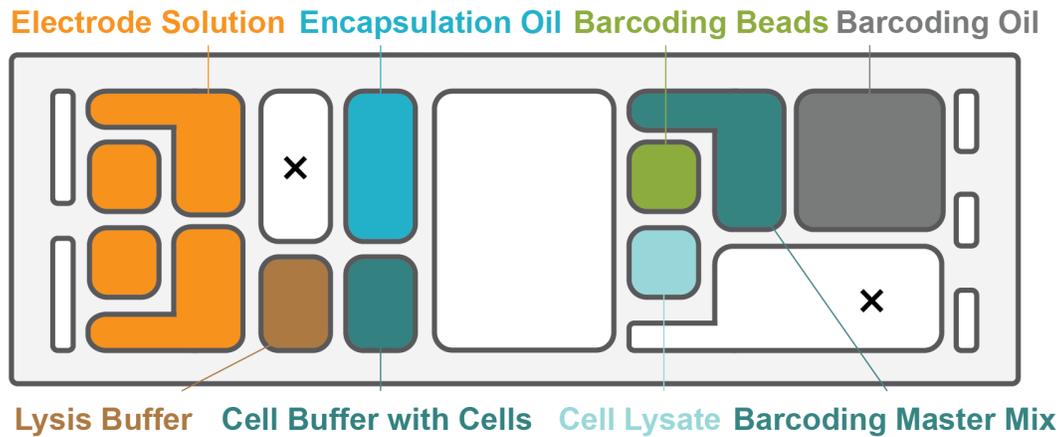
### **What sequencing depth is required, per cell, per amplicon?**

Please refer to the *Table 8 - Recommended sequencing specifications and sample multiplexing* on page 44.

### **Can I design my own primers for the Tapestri Platform?**

Yes. Please contact [support@missionbio.com](mailto:support@missionbio.com) to learn more about our Custom Panel Program.

## Cartridge Map



## Sequence Information for V2 Index Primer 1 – 8

| Primer | Sequence i7 | Sequence i5 |
|--------|-------------|-------------|
| 1      | CTGATCGT    | ATATGCGC    |
| 2      | ACTCTCGA    | TGGTACAG    |
| 3      | TGAGCTAG    | AACCGTTC    |
| 4      | GAGACGAT    | TAACCGGT    |
| 5      | CTTGTCGA    | GAACATCG    |
| 6      | TTCCAAGG    | CCTTGTAG    |
| 7      | CGCATGAT    | TCAGGCTT    |
| 8      | ACGGAACA    | GTTCTCGT    |

**Table A1.** Sequence nucleotide information for V2 Index Primer 1 – 8. Sequences are unique to Mission Bio and do not overlap with Illumina’s i7 indices (N701 to N729).

## Sequence Information for Protein Index Primer 1 – 8

| Primer | Sequence i7 | Sequence i5 |
|--------|-------------|-------------|
| 1      | TAAGGCGA    | ATATGCGC    |
| 2      | CGTACTAG    | TGGTACAG    |
| 3      | AGGCAGAA    | AACCGTTC    |
| 4      | TCCTGAGC    | TAACCGGT    |
| 5      | GGACTCCT    | GAACATCG    |
| 6      | TAGGCATG    | CCTTGTAG    |
| 7      | CTCTCTAC    | TCAGGCTT    |
| 8      | CAGAGAGG    | GTTCTCGT    |

**Table A2.** Sequence nucleotide information for V2 Index Primer 1 – 8. Sequences are unique to Mission Bio and do not overlap with Illumina’s i7 indices (N701 to N729).

**Note, i5 sequences 1 – 8 are identical to the i5 sequences 1 – 8 of the DNA libraries.**

## Removing Excess Amounts of Primer Dimers

### DNA Library

- 1.1** Quantify the amount of primer dimers by measuring the molarity of **the low-size off-target products between 100 – 350 bp (dimer molarity)**. Quantify the molarity of the **on-target products between 350 – 520 bp (on-target molarity)**.
- 1.2** Calculate the % of primer dimers as follows:  $(\text{dimer molarity} / \text{on-target molarity}) \times 100$   
If the % of primer dimers is > 5 %, follow the steps below:
- 1.3** Add **90 µL of nuclease-free water** to 10 µL sample for a total volume of 100 µL.
- 1.4** Mix and quick-spin the tube to collect the contents.
- 1.5** **Add 72 µL of AMPure XP reagent**, at room temperature and well-mixed, to the above sample.
- 1.6** **Vortex the tube for 5 seconds** and quick-spin to collect the contents.
- 1.7** Incubate the tube at room temperature for **5 minutes**.
- 1.8** Place on the magnet and **wait 5 minutes** for the beads to separate from the solution.
- 1.9** Without removing the tube from the magnet, **remove the clear liquid** from the tube and discard.
- 1.10** **Add 200 µL of the freshly prepared 80 % ethanol**, wait 30 seconds, and remove 200 µL of ethanol without disturbing the AMPure beads.
- 1.11** **Repeat Step 1.10 once** for a total of two wash cycles.
- 1.12** **Remove all residual ethanol** from the tube. Take the tube off the magnet and quick-spin.

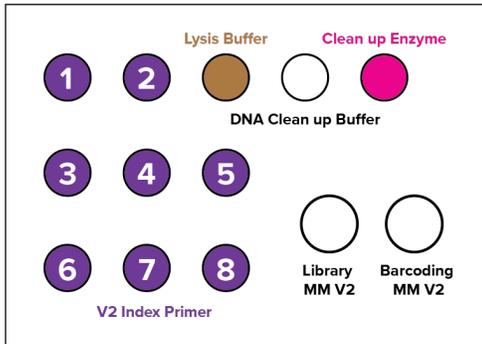
- Place the tube back on the magnet with the caps open and remove any residual ethanol.
- 1.13 Dry the AMPure bead pellets in the tubes on the magnet by **incubating at room temperature for 2 – 5 minutes**. *Avoid overdrying the beads.*
  - 1.14 Remove the tube from the magnet. **Add 10 µL of nuclease-free water** into the tube. Vortex and quick-spin to collect the contents.
  - 1.15 Incubate the tubes at room temperature for **2 minutes**.
  - 1.16 Place the tube onto the magnet and wait for at least 2 minutes or until the solutions are clear.
  - 1.17 **Transfer 8 µL** of purified PCR product from the tube to a new 0.2 mL PCR.
  - 1.18 Use **1 µL of a 1:10 dilution of the DNA library** and follow Agilent's protocol instructions to prime, load, and run DNA samples from all tubes on a DNA 1000 chip.
  - 1.19 Verify the DNA library product sizes and purity and quantify following manufacturer's instructions.

### Protein Library

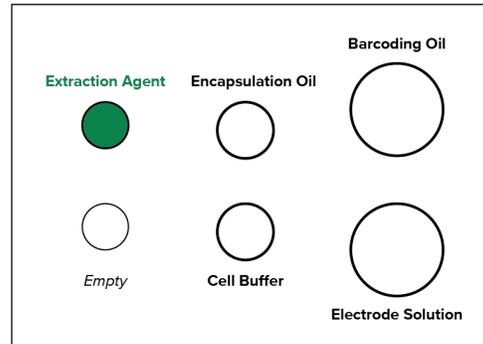
- 1.20 Quantify the amount of primer dimers by measuring the molarity of the **low-size off-target products between 100 – 225 bp (dimer molarity)**. Quantify the molarity of the **on-target products between 220 – 270 bp (on-target molarity)**.
- 1.21 Calculate the % of primer dimers as follows:  $(\text{dimer molarity} / \text{on-target molarity}) \times 100$   
If the % of primer dimers is > 10 %, follow the steps below:
- 1.22 Add **88 µL of nuclease-free water** to 12 µL sample for a total volume of 100 µL.
- 1.23 Mix and quick-spin the tube to collect the contents.
- 1.24 **Add 97 µL of AMPure XP reagent**, at room temperature and well-mixed, to the above sample.
- 1.25 **Vortex the tube for 5 seconds** and quick-spin to collect the contents.
- 1.26 Incubate the tube at room temperature for **5 minutes**.
- 1.27 Place on the magnet and **wait 5 minutes** for the beads to separate from the solution.
- 1.28 Without removing the tube from the magnet, **remove the clear liquid** from the tube and discard.
- 1.29 **Add 200 µL of the freshly prepared 80 % ethanol**, wait 30 seconds, and remove 150 µL of ethanol without disturbing the AMPure beads.
- 1.30 **Repeat Step 1.29 once** for a total of two wash cycles.
- 1.31 **Remove all residual ethanol** from the tube. Take the tube off the magnet and quick-spin. Place the tube back on the magnet with the caps open and remove any residual ethanol.
- 1.32 Dry the AMPure bead pellets in the tubes on the magnet by **incubating at room temperature for 2 – 5 minutes**. *Avoid overdrying the beads.*
- 1.33 Remove the tube from the magnet. **Add 15 µL of nuclease-free water** into the tube. Vortex and quick-spin to collect the contents.
- 1.34 Incubate the tubes at room temperature for **2 minutes**.
- 1.35 Place the tube onto the magnet and wait for at least 2 minutes or until the solutions are clear.
- 1.36 **Transfer 12 µL** of purified PCR product from the tube to a new 0.2 mL PCR.
- 1.37 Use **1 µL of a 1:10 dilution of the DNA library** and follow Agilent's protocol instructions to prime, load, and run DNA samples from all tubes on a DNA 1000 chip.
- 1.38 Verify the DNA library product sizes and purity and quantify following manufacturer's instructions.

## Kit Contents

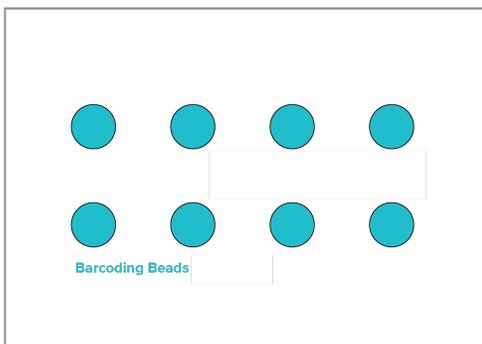
### TAPESTRI SINGLE-CELL DNA CORE -20°C KIT



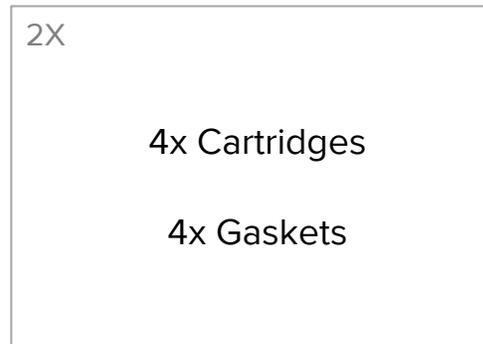
### TAPESTRI SINGLE-CELL DNA CORE AMBIENT KIT



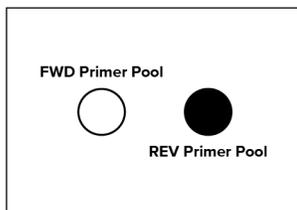
### TAPESTRI SINGLE-CELL DNA BEAD KIT



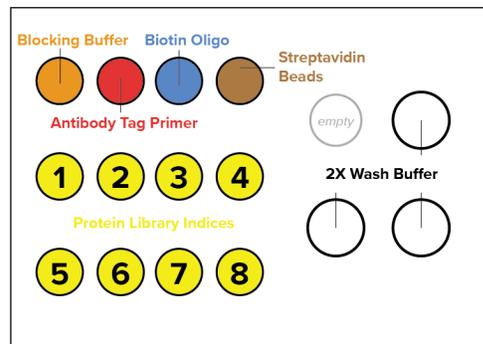
### CARTRIDGE KIT



### PRIMER POOL KIT



### PROTEIN STAINING KIT



## References

1. Lgr6 is a stem cell marker in mouse skin squamous cell carcinoma. P.Y. Huang et al., *Nature Genetics* 49(11):1624-1632 (2017).
2. RNA-Seq following PCR-based sorting reveals rare cell transcriptional signatures. M. Pellegrino, A. Sciambi, J.L. Yates, J. Mast, C. Silver, D.J. Eastburn, *BMC Genomics* 17:361 (2016).
3. Ultrahigh-Throughput Mammalian Single-Cell Reverse-Transcriptase Polymerase Chain Reaction in Microfluidic Drops. D.J. Eastburn, A. Sciambi, A.R. Abate, *Analytical Chemistry* 85, 8016 (2013).
4. Microfluidic droplet enrichment for targeted sequencing. D.J. Eastburn, Y. Huang, M. Pellegrino, A. Sciambi, L. Ptáček, A. Abate, *Nucleic Acids Research* Jul 27; 43(13):e86. (2015).
5. Picoinjection enables digital detection of RNA with droplet rt-PCR. D.J. Eastburn, A. Sciambi, A.R. Abate, *PLoS ONE* 8(4): e62961 (2013).
6. Identification and genetic analysis of cancer cells with PCR-activated cell sorting. D.J. Eastburn, A. Sciambi, A.R. Abate, *Nucleic Acids Research* 42, e128 (2014).

## Tapestri Instrument Specifications

- Model: Tapestri Instrument
- Part Number (PN): 191335
- Mains Voltage: 115 VAC
- Frequency: 50/60 Hz
- Current: 2.0 A Max.
- Circuit Breaker: 16 Amp
- Ambient Temperature Range: 15 °C to 30 °C (59 °F – 86 °F)
- Relative Humidity (Non-Condensing): 5% to 85%
- Maximum Altitude: 6,562 ft (2,000 m)
- HV Cable Length: 59" (1500 mm)
- Overall Dimensions. H/W/D: 12.5"/31.75 cm x 11.75"/29.85 cm x 12.25"/31.10 cm



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