BD Rhapsody™ System

mRNA Targeted, BD® AbSeq, and Sample Tag

Library Preparation Protocol

23-24124(02)
2022-11

For Research Use Only

Regulatory information

For Research Use Only. Not for use in diagnostic or therapeutic procedures.

History

Revision	Date	Change made
23-24124(01)	2021-12	Initial release.
23-24124(02)	2022-11	Updated for BD Rhapsody™ Enhanced Cell Capture Beads version 2.0. In the Appendix, added BD® Flex SMK sequences on page 31.

Contents

Introduction

This protocol provides instructions on creating single cell mRNA, Sample Tag, and BD® AbSeq libraries with the BD Rhapsody™ Single-Cell Analysis system or the BD Rhapsody™ Express Single-Cell Analysis system for sequencing on Illumina sequencers. For complete instrument procedures and safety information, see the *BD Rhapsody™ Single-Cell Analysis System Instrument User Guide* or the *BD Rhapsody™ Express Single-Cell Analysis System Instrument User Guide*.

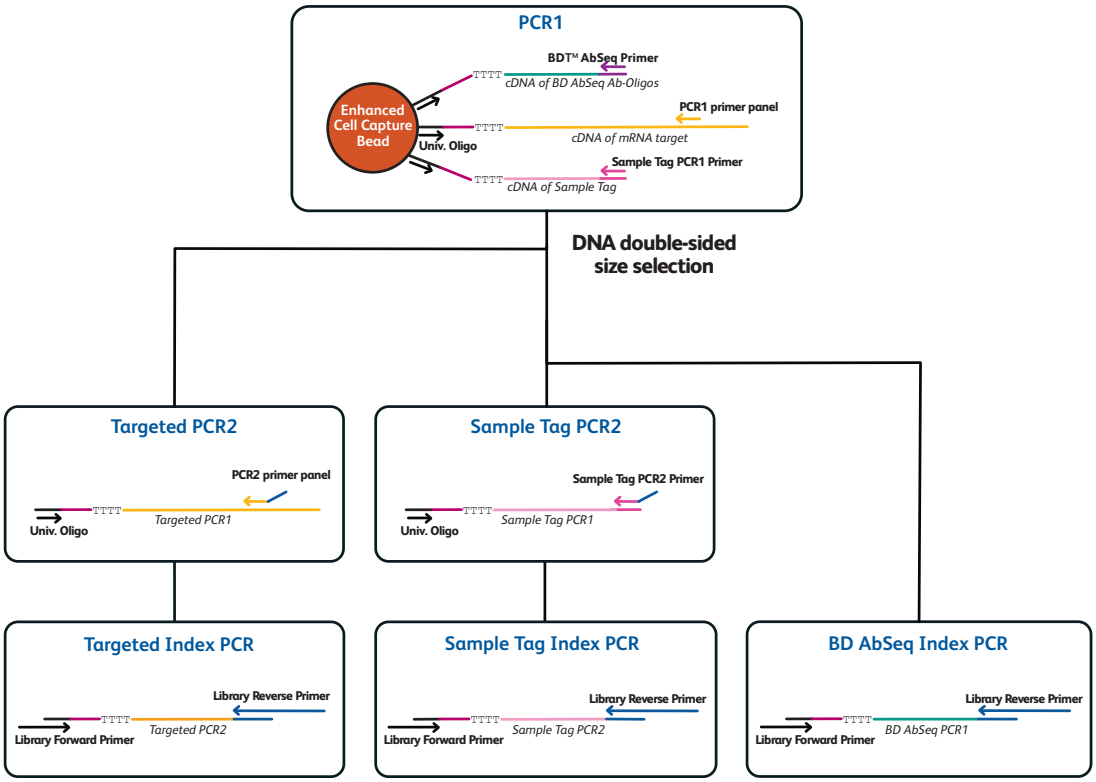
To create the libraries, the BD Rhapsody™ mRNA, Sample Tag, and BD® AbSeq targets are encoded on the BD Rhapsody™ Enhanced Cell Capture Beads and then amplified in PCR1. After PCR1, the Sample Tag and BD® AbSeq PCR1 products are separated from the mRNA targeted PCR1 products by double-sided size selection with Agencourt® AMPure® XP magnetic beads. Size selection of library molecules is achieved by specific and successive use of volume ratios between DNA samples and AMPure beads.

Successful preparation of mRNA, Sample Tag, and BD® AbSeq libraries requires that:

- The BD® AbSeq and Sample Tag PCR1 products undergo a separate index PCR from mRNA products with library index primers.
- BD Rhapsody™ mRNA targeted PCR1 products and Sample Tag PCR1 products undergo PCR2 amplification followed by index PCR with library index primers.

After index PCR, the mRNA, BD® AbSeq, and Sample Tag libraries can be combined for sequencing.

Workflow



Note: Univ. Oligo: Universal Oligo; region (dark purple) between universal oligo and poly(dT): cell label and Unique Molecular Identifier.

Required and recommended materials

Required reagents

Material	Supplier	Catalog no.
BD Rhapsody™ Targeted mRNA and AbSeq Amplification Kit[a]	BD Biosciences	633774
Targeted mRNA PCR Panel[a,b]	BD Biosciences	various
Agencourt® AMPure® XP magnetic beads	Beckman Coulter	A63880
100% ethyl alcohol	Major supplier	–
Nuclease-free water	Major supplier	–
Refer to the Technical Bulletin *Ordering Additional Indexes for the BD Rhapsody™ Library Reagent Kits* to order additional indexing primers for high throughput library preparation workflows.		
a. For processing more than four libraries, two orders of this catalog number are required. b. Examples of panels - Human or Mouse Immune Response Panel, contact your local Field Application Specialist (FAS) or scomix@bdscomix.bd.com for custom or other available panels.		

Recommended consumables

Material	Supplier	Catalog no.
Pipettes (P10, P20, P200, P1000)	Major supplier	–
Low-retention, filtered pipette tips	Major supplier	–
0.2-mL PCR 8-strip tubes	Major supplier	–
Axygen™ 96-Well PCR Microplates[a]	Corning	PCR96HSC
Or,		
MicroAmp Optical 96-Well Reaction Plate[a]	Thermo Fisher Scientific	N8010560
MicroAmp Clear Adhesive Film[a]	Thermo Fisher Scientific	4306311
DNA LoBind® tubes, 1.5-mL	Eppendorf	0030108051
DNA LoBind® tubes, 5.0-mL	Eppendorf	0030108310
Qubit™ Assay Tubes	Thermo Fisher Scientific	Q32856
Qubit™ dsDNA HS Assay Kit	Thermo Fisher Scientific	Q32851
Agilent High Sensitivity DNA	Agilent	5067-4626
Or,		
Agilent High Sensitivity D1000 ScreenTape	Agilent	5067-5584
Agilent High Sensitivity D1000 Reagents	Agilent	5067-5585
Or,		
Agilent High Sensitivity D5000 ScreenTape	Agilent	5067-5592
Agilent High Sensitivity D5000 Reagents	Agilent	5067-5593

a. Recommended for processing high throughput library preparation workflows.

Equipment

Material	Supplier	Catalog no.
Microcentrifuge for 1.5–2.0-mL tubes	Major supplier	–
Microcentrifuge for 0.2-mL tubes	Major supplier	–
Vortexer	Major supplier	–
Digital timer	Major supplier	–
Eppendorf ThermoMixer® C	Eppendorf	5382000023
6-tube magnetic separation rack for 1.5-mL tubes Or, 12-Tube Magnetic Separation Rack[a] Or, Invitrogen™ DynaMag™-2 Magnet[a]	New England Biolabs New England Biolabs Thermo Fisher Scientific	S1506S S1509S 12321D
Low-profile magnetic separation stand for 0.2-mL, 8-strip tubes	V&P Scientific, Inc.	VP772F4-1
Magnetic Stand-96[b]	Thermo Fisher Scientific	AM10027
Qubit™ 3.0 Fluorometer	Thermo Fisher Scientific	Q33216
Agilent® 2100 Bioanalyzer Or, Agilent® 4200 TapeStation System	Agilent Technologies Agilent Technologies	G2940CAG G2991AA

a. Recommended for processing greater than 6 samples.
b. Recommended for processing high throughput library preparation workflows.

For a complete list of materials, see the appropriate instrument user guide.

Before you begin

- Obtain Exonuclease I-treated and inactivated BD Rhapsody™ Enhanced Cell Capture Beads.
- Thaw reagents in the BD Rhapsody™ Targeted mRNA and AbSeq Amplification Kit at room temperature (15–25 °C), and then place on ice.

Best practices

- Use low-retention filtered pipette tips.
- When working with BD Rhapsody™ Enhanced Cell Capture Beads, use low-retention filtered tips and LoBind® tubes. **Never vortex the beads. Pipet-mix only.**
- Bring AMPure XP magnetic beads to room temperature before use.
- Remove supernatants without disturbing AMPure XP magnetic beads.

Additional documentation

- *BD Rhapsody™ Single-Cell Analysis System Instrument User Guide*
- *BD Rhapsody™ Express Single-Cell Analysis System Instrument User Guide*
- *BD® Single-Cell Multiomics Bioinformatics Handbook*

Safety information

For safety information, see the *BD Rhapsody™ Single-Cell Analysis Instrument User Guide* or the *BD Rhapsody™ Express Single-Cell Analysis System Instrument User Guide*.

Procedure

Perform the experiment on the BD Rhapsody™ Single-Cell Analysis system following either the *BD Rhapsody™ Single-Cell Analysis System Instrument User Guide* or the *BD Rhapsody™ Express Single-Cell Analysis System Instrument User Guide* for cell capture, reverse transcription, and Exonuclease treatment.

Performing PCR1

1 In the pre-amplification workspace, pipet the following reagents into a new 1.5-mL LoBind® tube on ice.

Note: Before use of BD Rhapsody™ 10X PCR1 Custom primers and/or BD Rhapsody™ 10X PCR1 Supplement primers, dilute 1 part of the 10X PCR primer stock to 9 parts of IDTE buffer to prepare a 1X primer solution. BD Rhapsody™ targeted (pre-designed) primer panels are provided at 1X concentration and should not be diluted.

PCR1 reaction mix

Component	For 1 library (µL)	For 1 library with 20% overage (µL)	For 4 libraries with 20% overage (µL)	For 8 libraries with 20% overage (µL)
PCR MasterMix	100.0	120.0	480.0	960.0
Universal Oligo	20.0	24.0	96.0	192.0
Bead RT/PCR Enhancer	12.0	14.4	57.6	115.2
PCR1 primer panel[a,b]	40.0	48.0	192.0	384.0
(Optional) PCR1 panel supplement[a,b]	(10.0)	(12.0)	(48.0)	(96.0)
Sample Tag PCR1 Primer	1.2	1.4	5.8	11.5
BD® AbSeq Primer	12.0	14.4	57.6	115.2
Nuclease-free water	Up to 14.8	Up to 17.8	Up to 71.0	Up to 142.1
Total	**200.0**	**240.0**	**960.0**	**1,920.0**

a. Order from BD Biosciences.

b. BD Rhapsody™ targeted (pre-designed) primer panels are provided at 1X. Ensure custom panels are diluted to 1X before use.

2 Gently vortex mix, briefly centrifuge, and place back on ice.

3 Proceed as follows:

- Entire sample: Skip to **step 5**.
- Sub-sample: Proceed to **step 4**.

4 Sub-sample the Exonuclease I-treated beads:

a Based on the number of wells with viable cells and a bead detected by the BD Rhapsody™ scanner or the number of cells targeted for capture in the cartridge, determine the volume of beads to sub-sample for targeted sequencing.

b Pipet-mix to completely resuspend the beads, and pipet the calculated volume of bead suspension into a new 1.5-mL LoBind® tube.

The remaining beads can be stored at 2–8 °C for up to 3 months.

5 Place the tube of Exonuclease I-treated beads in Bead Resuspension Buffer on a 1.5-mL magnet for <2 minutes.

Remove and discard the supernatant.

6 Remove the tube from the magnet, and resuspend the beads in 200 µL of the PCR1 reaction mix. Do not vortex.

7 Ensuring that the beads are fully resuspended, pipet 50 µL of the PCR1 reaction mix with beads into each of four 0.2-mL PCR tubes.

Transfer any residual mix to one of the tubes.

8 Bring the reaction mix to the post-amplification workspace.

9 Program the thermal cycler. Do not use fast cycling mode.

Program thermal cycler

Step	Cycles	Temperature	Time
Hot start	1	95 °C[a]	3 min
Denaturation	11-15[b]	95 °C	30 s
Annealing		60 °C	3 min
Extension		72 °C	1 min
Final extension	1	72 °C	5 min
Hold	1	4 °C	∞

a. To avoid beads settling due to prolonged incubation time on the thermal cycler before the denaturation step, it is critical to pause the instrument at 95 °C before loading the samples. Different thermal cyclers might have different pause time settings. In certain brands of thermal cyclers, however, we have observed a step-skipping error with the pause/unpause functions. To ensure that the full three-minute denaturation is not skipped, verify that the pause/unpause functions are working correctly on your thermal cycler. To avoid the step-skipping problem, a one-minute 95 °C pause step can be added immediately before the three-minute 95 °C denaturation step.

b. Suggested PCR cycles might need to be optimized for different cell types, number of antibodies in BD® AbSeq panel, and cell number.

Suggested number of PCR cycles

Number of cells in PCR1	Suggested PCR cycles for resting PBMCs
1,000	14
2,500	13
5,000	12
10,000	11
20,000	10

10 Ramp the heated lid and heat block of the post-amplification thermal cycler to ≤95 °C by starting the thermal cycler program and then pausing it.

Note: Do not proceed to thermal cycling until each tube is gently mixed by pipette to ensure uniform bead suspension.

11 For each 0.2-mL PCR tube, gently pipet-mix, immediately place the tube in thermal cycler, and unpause the thermal cycler program.

STOPPING POINT: The PCR can run overnight, but proceed with purification within 24 hours after PCR.

12 After PCR, briefly centrifuge the tubes.

13 Pipet-mix and combine the four reactions from the same sample into a new 1.5-mL LoBind® tube.

Note: Retain the supernatant in the next step.

14 Place the 1.5-mL tube on the magnet for 2 minutes, and carefully pipet the supernatant (PCR1 products) into the new 1.5-mL LoBind® tube without disturbing the beads.

Note: (Optional) Remove the tube with the BD Rhapsody™ Enhanced Cell Capture Beads from the magnet, and pipet 200 µL cold Bead Resuspension Buffer into the tube. Pipet-mix. Do not vortex. Store beads at 2–8 °C in the post-amplification workspace.

Purifying PCR1 products by double-sided size selection

Perform double-sided AMPure bead purification to separate the shorter BD® AbSeq and Sample Tag PCR1 products (~160 bp) from the longer mRNA targeted PCR1 products (350–800 bp).

In the protocol, keep both the supernatant (BD® AbSeq and Sample Tag products) and the AMPure beads (mRNA targeted products) during purification workflow.

Note: Perform the purification in the post-amplification workspace.

Separating BD® AbSeq and Sample Tag PCR1 products from mRNA targeted PCR1 products

1 In a new 5.0-mL LoBind® tube, prepare 5 mL of fresh 80% (v/v) ethyl alcohol by combining 4.0 mL absolute ethyl alcohol, molecular biology grade (major supplier) with 1.0 mL nuclease-free water (major supplier). Vortex the tube for 10 seconds to mix.

Note: Make fresh 80% ethyl alcohol, and use it within 24 hours. The 80% ethyl alcohol volume should be adjusted depending on the number of libraries. Volumes provided in following table are enough to cover all PCR clean ups throughout protocol.

80% Ethyl Alcohol

Component	For 1 library (mL)	For 4 libraries (mL)	For 8 libraries (mL)
100% Ethyl Alcohol	4	16	32
Nuclease Free Water	1	4	8
Total	**5**	**20**	**40**

2 Bring AMPure XP magnetic beads to room temperature. Vortex at high speed for 1 minute until the beads are fully resuspended.

3 Pipet 140 µL AMPure XP beads into a tube with 200 µL PCR1 products (**step 14** of Performing PCR1). Pipet-mix 10 times.

4 Incubate at room temperature for 5 minutes.

5 Place the 1.5-mL LoBind® tube on the magnet for 5 minutes.

6 Keeping the tube on the magnet, transfer the 340 µL supernatant (Sample Tag PCR1 products) to a new 1.5-mL tube without disturbing beads (mRNA targeted PCR1 products).

7 Store the supernatant (**step 6**) at room temperature while purifying and eluting mRNA targeted PCR1 products in Purifying BD® AbSeq and Sample Tag PCR1 products on page 14. Purify the BD® AbSeq and Sample Tag PCR1 products after purifying the mRNA targeted PCR1 products.

Purifying mRNA targeted PCR1 products

1 Keeping the tube on the magnet, gently add 500 µL fresh 80% ethyl alcohol into the tube of AMPure beads bound with mRNA targeted PCR1 products, and incubate 30 seconds. Remove and discard the supernatant.

2 Repeat **step 1** once for a total of two washes.

3 Keeping the tube on the magnet, use a small-volume pipette to remove and discard any residual supernatant from the tube.

4 Air-dry the beads at room temperature for 5 minutes.

5 Remove the tube from the magnet, and resuspend the bead pellet in 30 µL of Elution Buffer into the tube. Vigorously pipet-mix until beads are uniformly dispersed. AMPure bead clumping is normal at this step and does not affect performance.

6 Incubate at room temperature for 2 minutes, and briefly centrifuge.

7 Place the tube on the magnet until the solution is clear, usually within 30 seconds.

8 Pipet the eluate (~30 µL) into a new 1.5-mL LoBind® tube (purified mRNA targeted PCR1 products).

STOPPING POINT: Store at 2–8 °C before proceeding within 24 hours or at –25 °C to –15 °C for up to 6 months.

Purifying BD® AbSeq and Sample Tag PCR1 products

1 Pipet 100 µL AMPure XP beads into the tube with 340 µL BD® AbSeq and Sample Tag PCR1 products from **step 6** of Separating BD® AbSeq and Sample Tag PCR1 products from mRNA targeted PCR1 products on page 13. Pipet-mix 10 times.

2 Incubate at room temperature for 5 minutes.

3 Place on magnet for 5 minutes.

4 Keeping the tube on the magnet, remove and discard the supernatant.

5 Keeping the tube on the magnet, gently add 500 µL of fresh 80% ethyl alcohol, and incubate for 30 seconds. Remove and discard the supernatant.

6 Repeat **step 5** once for a total of two washes.

7 Keeping the tube on the magnet, use a small-volume pipette to remove and discard the residual supernatant from the tube.

8 Air-dry beads at room temperature for 5 minutes.

9 Remove the tube from the magnet, and resuspend the bead pellet in 30 µL of Elution Buffer. Vigorously pipet-mix until beads are uniformly dispersed. AMPure bead clumping is normal at this step and does not affect performance.

10 Incubate at room temperature for 2 minutes, and briefly centrifuge.

11 Place the tube on the magnet until the solution is clear, usually within 30 seconds.

12 Pipet the eluate (~30 µL) into a new 1.5-mL LoBind® tube (purified BD® AbSeq and Sample Tag PCR1 products).

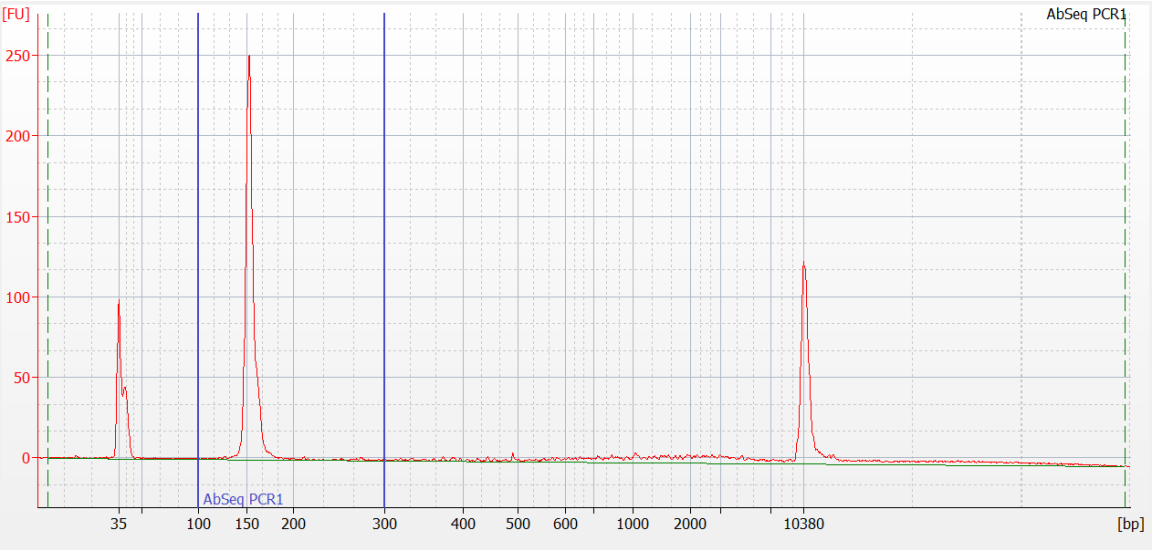
STOPPING POINT: Store at 2–8 °C before proceeding within 24 hours or at –25 °C to –15 °C for up to 6 months.

Quantifying BD® AbSeq and Sample Tag PCR1 products

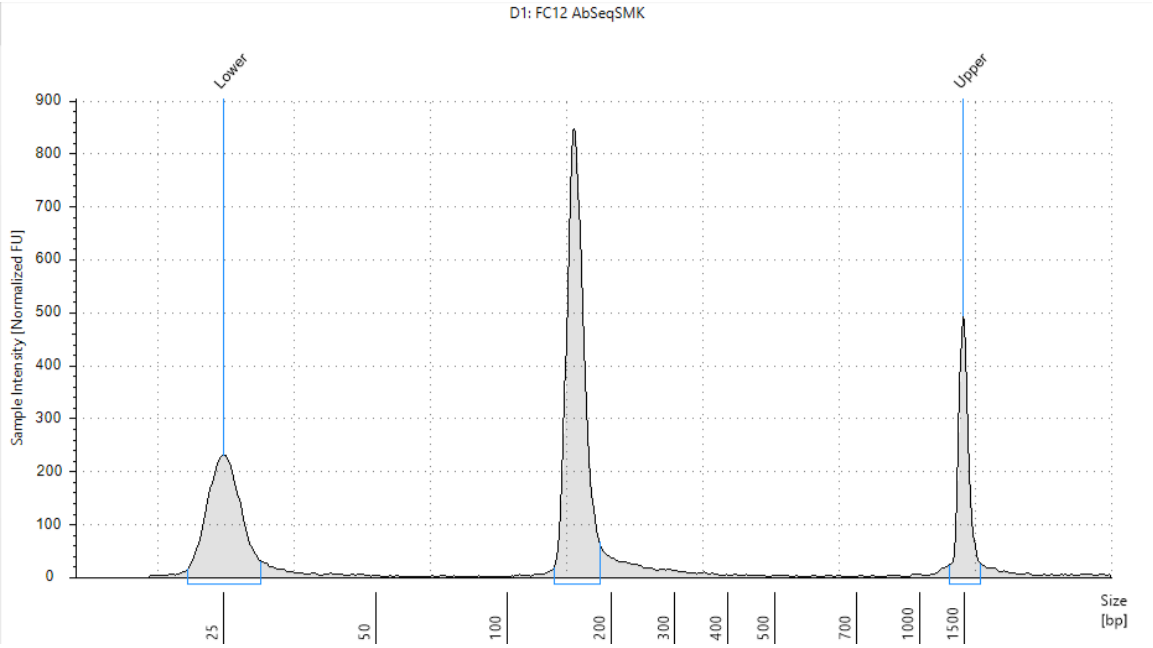
1 Measure the yield of the largest peak of the BD® AbSeq and Sample Tag PCR1 products (~160 bp) by using the Agilent Bioanalyzer with the High Sensitivity Kit or Agilent TapeStation. Follow the manufacturer's instructions. Peak sizes may vary depending on instrumentation or assay used for measurement.

Figure 1 BD® AbSeq and Sample Tag PCR1

A. Sample Bioanalyzer high-sensitivity DNA trace



B. Sample TapeStation high-sensitivity D1000 trace



2 Dilute an aliquot of BD® AbSeq or Sample Tag PCR1 products to 0.1–1.1 ng/µL with Elution Buffer before index PCR of BD® AbSeq PCR1 products. Use undiluted PCR1 products for Sample Tag PCR2 amplification.

Performing PCR2

Note: Only the mRNA targeted PCR1 products and Sample Tags require PCR2 amplification. The BD® AbSeq PCR1 products require only index PCR.

1 In the pre-amplification workspace, pipet reagents into a new 1.5-mL LoBind® tube on ice.

Note: Before use of BD Rhapsody™ 10X PCR2 Custom primers and/or BD Rhapsody™ 10X PCR2 Supplement primers, dilute 1 part of the 10X PCR primer stock to 9 parts of IDTE buffer to prepare a 1X primer solution. BD Rhapsody™ targeted (pre-designed) primer panels are provided at 1X concentration and should not be diluted.

mRNA targeted PCR2 reaction mix

Component	For 1 library (µL)	For 1 library with 20% overage (µL)	For 4 libraries with 20% overage (µL)	For 8 libraries with 20% overage (µL)
PCR MasterMix	25.0	30.0	120.0	240.0
Universal Oligo	2.0	2.4	9.6	19.2
PCR2 primer panel[a,b]	10.0	12.0	48.0	96.0
(Optional) PCR2 panel supplement[a,b]	(2.5)	(3.0)	(12.0)	(24.0)
Nuclease-free water	Up to 8.0	Up to 9.6	Up to 38.4	Up to 76.8
Total	**45.0**	**54.0**	**216.0**	**432.0**

a. Order from BD Biosciences.

b. BD Rhapsody™ targeted (pre-designed) primer panels are provided at 1X. Ensure custom panels are diluted to 1X before use.

Sample Tag PCR2 reaction mix

Component	For 1 library (µL)	For 1 library with 20% overage (µL)	For 4 libraries with 20% overage (µL)	For 8 libraries with 20% overage (µL)
PCR MasterMix	25.0	30.0	120.0	240.0
Universal Oligo	2.0	2.4	9.6	19.2
Sample Tag PCR2 Primer	3.0	3.6	14.4	28.8
Nuclease-free water	15.0	18.0	72.0	144.0
Total	**45.0**	**54.0**	**216.0**	**432.0**

2 Gently vortex mix, briefly centrifuge, and place back on ice.

3 Bring the PCR2 reaction mixes into the post-amplification workspace.

4 In two separate and new 0.2-mL PCR tubes:

- **a** mRNA targeted PCR1 products: Pipet 5.0 µL of products into 45 µL of mRNA targeted PCR2 reaction mix.
- **b** Sample Tag PCR1 products: Pipet 5.0 µL products into 45.0 µL Sample Tag PCR2 reaction mix.

5 Gently vortex, and briefly centrifuge.

6 For mRNA targeted PCR2 products, program the thermal cycler. **Do not use fast cycling mode**.

Program thermal cycler – mRNA targeted PCR2 products

Step	Cycles	Temperature	Time
Hot start	1	95 °C	3 min
Denaturation	10[a]	95 °C	30 s
Annealing		60 °C	3 min
Extension		72 °C	1 min
Final extension	1	72 °C	5 min
Hold	1	4 °C	∞
a. Cycle number might require optimization according to cell number and type.			

For Sample Tag PCR2, program the thermal cycler. **Do not use fast cycling mode**.

Program thermal cycler – Sample Tag PCR2 products

Step	Cycles	Temperature	Time
Hot start	1	95 °C	3 min
Denaturation	10[a]	95 °C	30 s
Annealing		66 °C	30 s
Extension		72 °C	1 min
Final extension	1	72 °C	5 min
Hold	1	4 °C	∞
a. Cycle number might require optimization according to cell number and type.			

STOPPING POINT: Both PCR programs can run overnight.

Purifying mRNA targeted and Sample Tag PCR2 products

Note: Perform purification in the post-amplification workspace.

1. Bring AMPure XP beads to room temperature, and vortex at high speed for 1 minute until beads are fully resuspended.
2. Briefly centrifuge the PCR2 products.
3. To 50.0 µL PCR2 products, pipet:
   - mRNA targeted PCR2 products: 40 µL AMPure beads.
   - Sample Tag PCR2 products: 60 µL AMPure beads.
4. Pipet-mix 10 times, and incubate at room temperature for 5 minutes.
5. Place the tube on the strip tube magnet for 3 minutes. Remove and discard the supernatant.
6. Keeping the tubes on the magnet, for each tube, gently add 200 µL of fresh 80% ethyl alcohol into the tube, and incubate for 30 seconds. Remove and discard the supernatant.
7. Repeat **step 6** once for a total of two washes.
8. Keeping each tube on the magnet, use a small-volume pipette to remove and discard any residual supernatant from the tube.

9 Air-dry the beads at room temperature for 3 minutes.

10 Remove the tubes from the magnet, and resuspend each bead pellet in 30 µL of Elution Buffer. Pipet-mix until the beads are fully resuspended.

11 Incubate at room temperature for 2 minutes, and briefly centrifuge.

12 Place each tube on the magnet until the solution is clear, usually within 30 seconds.

13 Pipet the entire eluate (~30 µL) of each sample into two separate new 1.5-mL LoBind® tubes (purified mRNA targeted PCR2 and Sample Tag PCR2 products).

STOPPING POINT: Store at 2–8 °C before proceeding on the same day, or at –25 °C to –15 °C for up to 6 months.

14 Estimate the concentration of each sample by quantifying 2 µL of the PCR2 products with a Qubit™ Fluorometer using the Qubit dsDNA HS Assay Kit.

15 Dilute an aliquot of the products with Elution Buffer:

- mRNA targeted PCR2 products: 0.2–2.7 ng/µL.
- Sample Tag PCR2 products: 0.1–1.1 ng/µL.

Performing index PCR to prepare final libraries

1 In pre-amplification workspace, prepare the final amplification mix for each of the three products. Pipet reagents into a new 1.5-mL LoBind® tube on ice.

Index PCR mix

Component	For 1 library (µL)	For 1 library with 20% overage (µL)	For 4 libraries with 20% overage (µL)	For 8 libraries with 20% overage (µL)
PCR MasterMix	25.0	30.0	120.0	240.0
Library Forward Primer	2.0	2.4	9.6	19.2
Library Reverse Primer 1-4[a]	2.0	2.4	–	–
Nuclease-free water	18.0	21.6	86.4	172.8
Total	**47.0**	**56.4**	**216.0**	**432.0**

a. For more than one library, use different Library Reverse Primers for each library. For recommendations of how to index libraries, please contact your local Field Application Specialist (FAS) or scomix@bdscomix.bd.com.

2 Gently vortex mix, briefly centrifuge, and place back on ice.

3 Bring index PCR mixes into the post-amplification workspace.

4 In three separate and new 0.2-mL PCR tubes:

- **a** mRNA targeted PCR2 products: Pipet 3.0 µL of 0.2–2.7 ng/µL products into 47.0 µL index PCR mix.
- **b** Sample Tag PCR2 products: Pipet 3.0 µL of 0.1–1.1 ng/µL products into 47.0 µL index PCR mix.
- **c** BD® AbSeq PCR1 products: Pipet 3.0 µL of 0.1–1.1 ng/µL products into 47.0 µL index PCR mix.

4 Gently vortex, and briefly centrifuge.

5 Program the thermal cycler. **Do not use fast cycling mode**.

Program thermal cycler

Step	Cycles	Temperature	Time
Hot start	1	95 °C	3 min
Denaturation	6-8[a]	95 °C	30 s
Annealing		60 °C	30 s
Extension		72 °C	30 s
Final extension	1	72 °C	1 min
Hold	1	4 °C	∞

a. Suggested PCR cycles.

Suggested PCR cycles

Concentration index PCR input for mRNA targeted libraries (ng/µL)	Concentration Index PCR input for Sample Tag and BD® AbSeq libraries (ng/µL)	Suggested PCR cycles
1.2–2.7	0.5–1.1	6
0.6–1.2	0.25–0.5	7
0.2–0.6	0.1–0.25	8

STOPPING POINT: The PCR can run overnight.

Purifying index PCR products

Note: Perform the purification in the post-amplification workspace.

1. Bring AMPure XP beads to room temperature, and vortex at high speed for 1 minute until the beads are fully resuspended.
2. Briefly centrifuge all of the index PCR products.
3. To 50.0 µL of the index PCR products, pipet:
   - mRNA targeted library: 35 µL AMPure beads.
   - BD® AbSeq and Sample Tag libraries: 40 µL AMPure beads.
4. Pipet-mix 10 times, and incubate at room temperature for 5 minutes.
5. Place the tubes on the strip tube magnet for 3 minutes. Remove and discard the supernatant.
6. Keeping the tubes on the magnet, for each tube, gently add 200 µL of fresh 80% ethyl alcohol into the tube, and incubate for 30 seconds. Remove and discard the supernatant.
7. Repeat **step 6** once for a total of two washes.
8. Keeping the tubes on the magnet, use a small-volume pipette to remove and discard the residual supernatant from the tube.
9. Air-dry the beads at room temperature for 3 minutes.
10. Remove the tubes from the magnet and resuspend each bead pellet in 30 µL of Elution Buffer. Pipet-mix until the beads are fully resuspended.
11. Incubate at room temperature for 2 minutes, and briefly centrifuge.
12. Place the tubes on the magnet until the solution is clear, usually within 30 seconds.
13. For each tube, pipet the entire eluate (~30 µL) into three separate new 1.5-mL LoBind® tubes (final sequencing libraries).
14. Perform quality control before freezing samples. See Performing quality control on the final sequencing libraries on page 20.

STOPPING POINT: Store at –25 °C to –15 °C for up to 6 months until sequencing.

Performing quality control on the final sequencing libraries

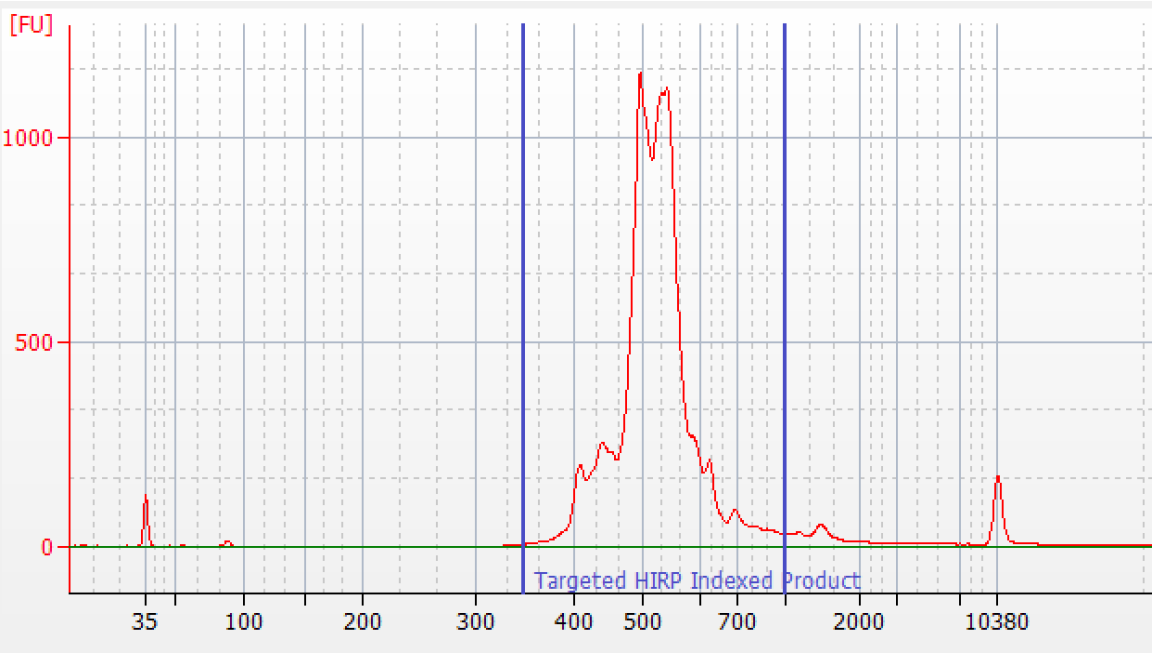
1. Estimate the concentration by quantifying 2 µL of the final sequencing library with a Qubit Fluorometer using the Qubit dsDNA HS Kit to obtain an approximate concentration of PCR products to dilute for quantification on an Agilent 2100 Bioanalyzer or Agilent 4200 TapeStation. Follow the manufacturer's instructions. The expected concentration of the libraries is >1.5 ng/µL.

2. Measure the average fragment size of the mRNA targeted library within the size range of 350–1,000 bp by using the Agilent Bioanalyzer with the High Sensitivity Kit for 50–7,000 bp, 5–1,000 pg/µL. The Bioanalyzer is used to calculate molarity for the targeted library because of the distribution of fragment sizes for this library type. Follow the manufacturer's instructions.

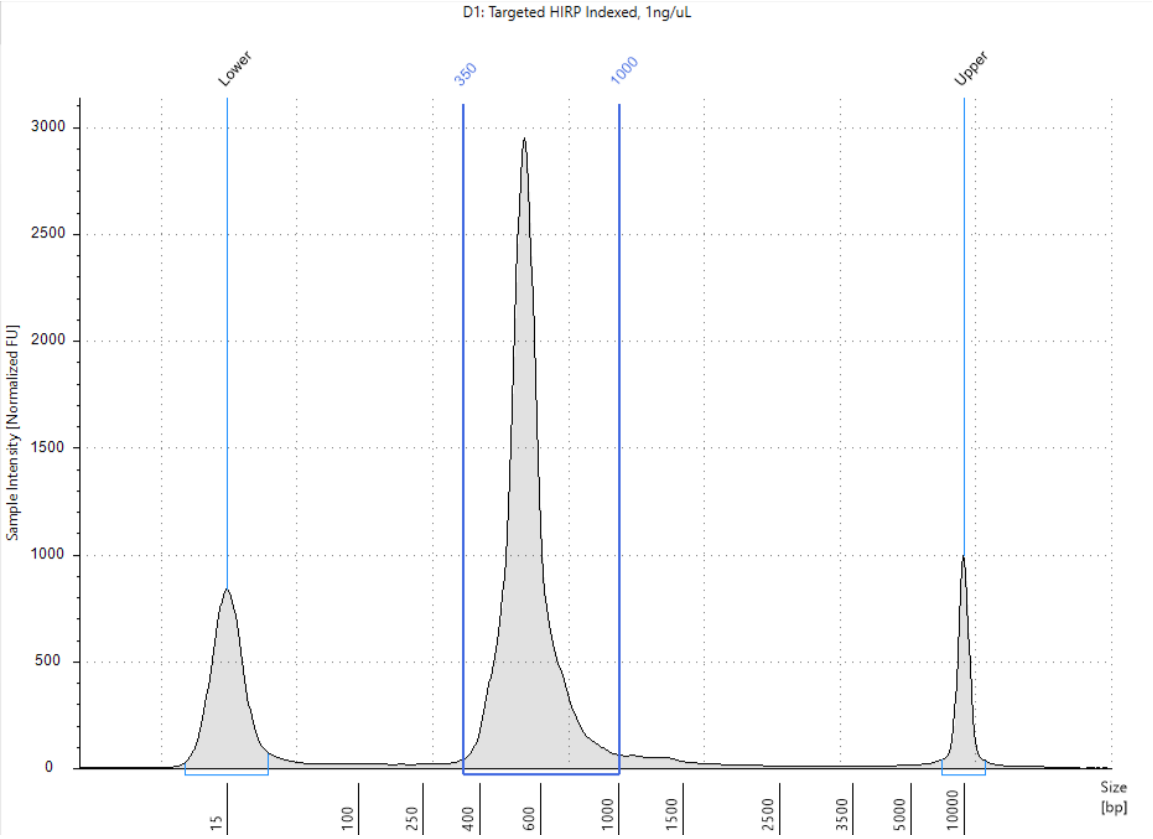
The final mRNA targeted library should show a fragment distribution that depends on the panel used. For example, with peripheral blood mononuclear cells (PBMCs):

Figure 2 Targeted human immune response panel (HIRP) indexed product

A. Sample Bioanalyzer high-sensitivity DNA trace



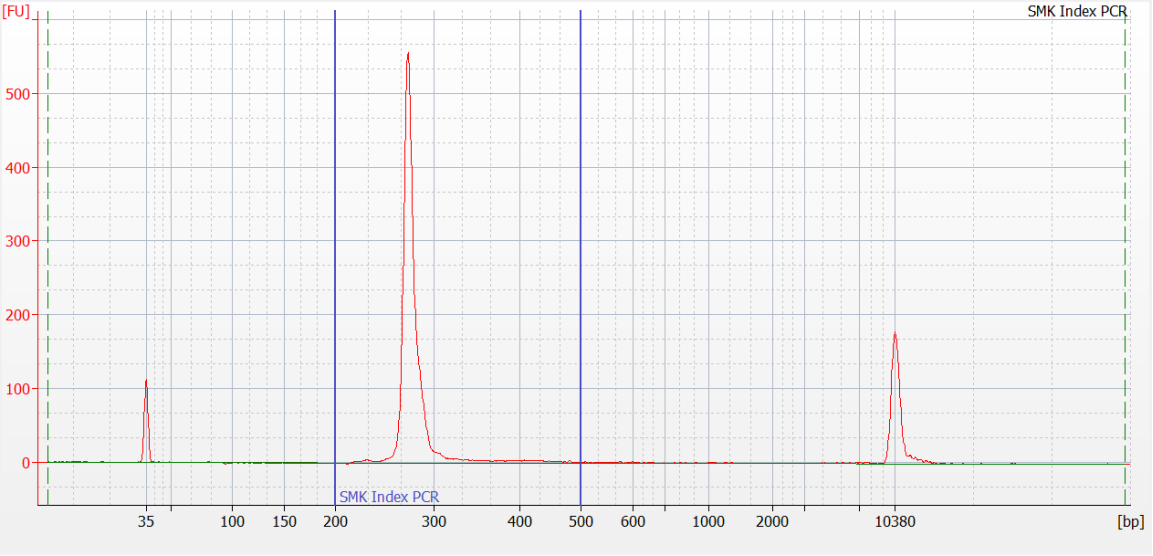
B. Sample TapeStation high-sensitivity D5000 trace



The expected size of Sample Tag index PCR product is 276 bp. You might observe a smaller peak of ~264 bp, which corresponds to BD® AbSeq products (as shown). Peak sizes may vary depending on instrumentation or assay used for measurement.

Figure 3 Final Sample Tag library

A. Sample Bioanalyzer high-sensitivity DNA trace



B. Sample TapeStation high-sensitivity D1000 trace

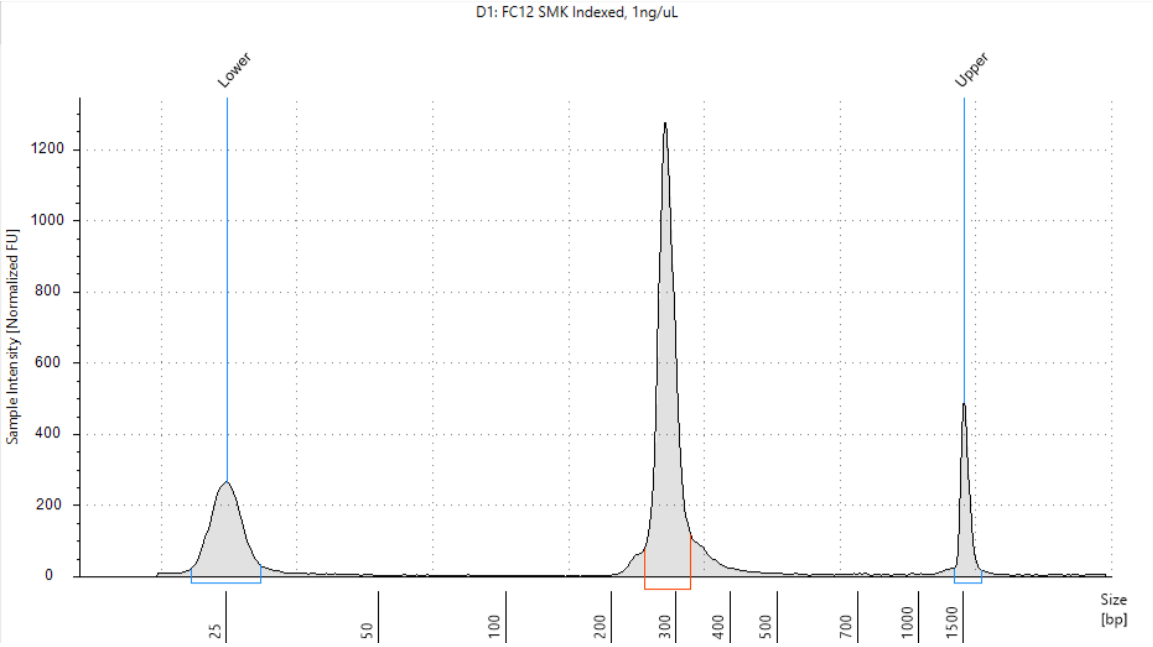
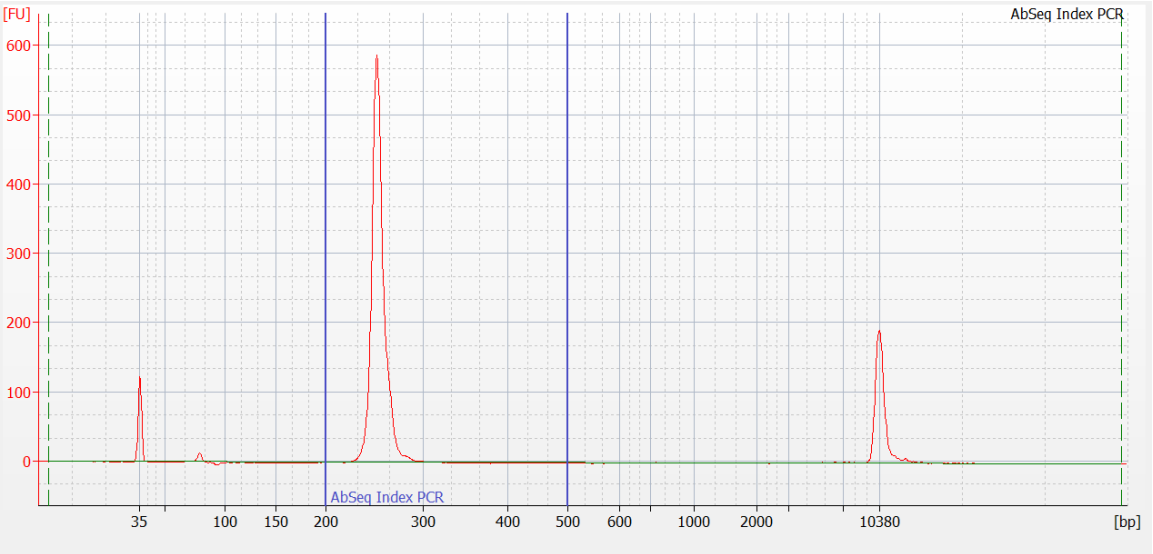
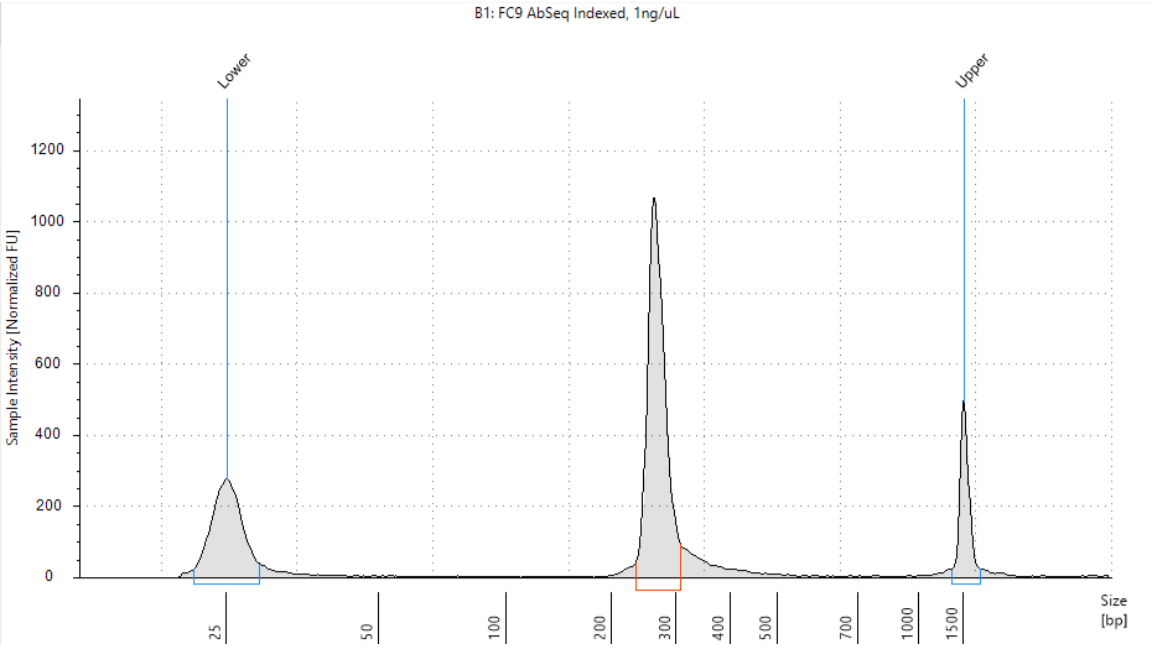


Figure 4 Final BD® AbSeq library

A. Sample Bioanalyzer High Sensitivity DNA trace



B. Sample TapeStation High Sensitivity D1000 trace



Note: If the concentration or size of the library is outside of the expected range, see Library preparation on page 25 or contact your local Field Application Specialist (FAS) or scomix@bdscomix.bd.com.

Sequencing

Sequencing depth is dependent on application. For cell type clustering, shallow sequencing is sufficient. For in-depth analysis, such as comparison across multiple libraries, deep sequencing is recommended. We recommend meeting the requirement for recursive substitution error correction (RSEC) sequencing depth of ≤6 in order to reach the threshold of sequencing saturation where most molecules of the library have been recovered. RSEC sequencing depth is reported by the analysis pipeline. The actual sequencing reads/cell required to achieve this depth can vary because it depends on the chosen gene panel, number of cells, and sequencing run quality.

Requirements

For a NextSeq High or Mid Output run and MiniSeq High or Mid Output run, load the flow cell at a concentration between 1.5-1.8 pM with 1% PhiX for a sequencing run.

Run setup for Illumina® BaseSpace and sample sheet sequencing. Enter the pooled libraries as one sample if both libraries were made with the same Library Reverse primer or if both libraries share the same i7 index.

Required parameters

Parameter	Requirement
Platform	Illumina[a]
Paired-end reads	Recommend Read 1: 51 cycles; Read 2: 71 cycles
PhiX	1% recommended
Analysis	See the *BD® Single-Cell Multiomics Bioinformatics Handbook*

a. To review Illumina Index 1 (i7) sequences, see Appendix on page 29.

Sequencing recommendations

Read requirements for libraries

Gene panel	Read requirement for data analysis
BD Rhapsody™ Targeted	~2,000-20,000 reads/cell[a]
BD Rhapsody™ AbSeq	1,000 reads/cell/AbSeq[b]
Sample Tag: samples from the same type of cell (combining different donor PBMCs)	120 reads/cell
Sample Tag: samples from different type of cells (combining cells lines with PBMCs)	600 reads/cell

a. 2,000 reads/cell can be sufficient for cell-type clustering and classification. For deeply saturated sequencing (RSEC depth >6), use 20,000 reads/cell.

b. The amount of sequencing needed for BD® AbSeq libraries will vary depending on the application, BD® AbSeq panel plexy, and cell type. We have observed that using 40,000 sequencing reads per cell for 40-plex BD® AbSeq libraries prepared from resting PBMCs achieves an RSEC sequencing depth of ~2.

Note: Avoid pooling greater than 60% total BD® AbSeq in final sequencing pool as it may impact sequencing quality of targeted mRNA libraries.

Note: For additional assistance and to determine the ratio of the BD Rhapsody™ targeted mRNA library to BD® AbSeq library to Sample Tag library to pool for sequencing, contact your local Field Application Specialist (FAS) or scomix@bdscomix.bd.com for a sequencing calculator.

Troubleshooting

Library preparation

Observation	Possible causes	Recommended solutions
PCR2 product yield too low.	PCR1 and PCR2 primers might have been swapped by mistake.	• Ensure that the correct primers are used for each step.
	cDNA synthesis might have failed due to incomplete washing of Lysis Buffer.	• Avoid leaving behind Lysis Buffer or bubbles after removing Lysis Buffer from the tube during bead wash after retrieval from the cartridge. • Use new tubes for each wash step, as described in the protocol.
	cDNA synthesis might have failed due to thermomixer not shaking during reverse transcription.	• Samples need to be on the thermomixer in shake mode. • Where applicable, ensure that a SmartBlock™ Thermoblock is installed on the thermomixer for 1.5-mL tubes so that the reaction can proceed at the designated temperature.
	BD Rhapsody™ Enhanced Cell Capture Beads not fully resuspended immediately before PCR1.	• Gently pipet-mix BD Rhapsody™ Enhanced Cell Capture Beads in PCR1 reaction mix immediately before starting PCR1 thermal cycling to ensure uniform bead suspension.
	Thermal cycler mis-programming.	• Ensure that the correct thermal cycling program is used.
	Too few PCR1 cycles.	• Optimize the number of PCR cycles for the specific sample type.
	Incorrect volume of Agencourt AMPure XP magnetic beads used during PCR2 cleanup.	• Use the specified volume of AMPure XP beads.
	Incorrect solution or incorrect concentration of 80% ethyl alcohol used for washing Agencourt AMPure XP magnetic beads, resulting in premature elution of PCR products from beads.	• Use 80% ethyl alcohol for washing AMPure XP beads.

Observation	Possible causes	Recommended solutions
Concentration of final mRNA sequencing library too low.	Issue with PCR2 product yield or quality.	1. Determine the product size range: – Load 1 µL of purified PCR2 product at 1 ng/µL in a High Sensitivity DNA Chip on the Agilent Bioanalyzer. – Follow the manufacturer's instructions. 2. Confirm that the mRNA targeted PCR2 products should show an average size range of 350–600 bp and the Sample Tag PCR2 products should show an average size of ~182 bp. 3. If the products pass quality control, proceed to Performing index PCR to prepare final libraries on page 19. Repeat the index PCR. If the products do not pass quality control, contact your local Field Application Specialist (FAS) or scomix@bdscomix.bd.com.
	Thermal cycler mis-programming.	• Ensure that the correct thermal cycling program is used.
Final sequencing product size too large.	• Over-amplification during index PCR. • Input amount of PCR2 products too high.	• Repeat the index PCR with a lower input of mRNA targeted PCR2 products.
	Upper and lower markers on the Agilent Bioanalyzer are incorrectly called.	• Ensure that markers are correct. • Follow manufacturer's instructions.
	Incorrect volume of Agencourt AMPure XP magnetic beads used.	• Use volume specified in protocol.

Observation	Possible causes	Recommended solutions
BD® AbSeq PCR1 product size too low.	• BD® AbSeq Primer not added to PCR1. • Too few PCR1 cycles. • Incorrect volumes of AMPure XP beads used during double-sided selection and/or volumes of AMPure XP beads swapped for mRNA and Sample Tag and BD® AbSeq products.	• Contact BD Biosciences technical support at scomix@bdscomix.bd.com.
Yield of Sample Tag library too low after index PCR (<1 ng/µL).	Sample Tag labeling incubation time too short.	• Ensure that the cells were labeled with Sample Tags correctly and that the correct incubation time was used.
	PCR1 and PCR2 primers swapped.	• Ensure that correct primer is used for each step.
	Only one primer (Library Forward or Library Reverse primer) added to index PCR mix.	• Ensure that both the Library Forward Primer and Library Reverse Primer are added to the index PCR mix, and repeat index PCR.
	Too few index PCR cycles.	• Increase the number of index PCR cycles.
Yield of BD® AbSeq library too low after index PCR, but yield of BD® AbSeq PCR1 products is sufficient.	Too few index PCR cycles.	• Increase the number of cycles for index PCR.
	Only one primer (Library Forward or Library Reverse primer) added to index PCR mix.	• Ensure that both the Library Forward Primer and Library Reverse Primer are added to the index PCR mix, and repeat index PCR.

Observation	Possible causes	Recommended solutions
Expected size of Sample Tag products is too short (<280 bp).	Upper and lower markers on the Agilent Bioanalyzer are incorrectly called.	• Ensure that the markers are correct. Follow the manufacturer's instructions.
	Inefficient Sample Tag labeling.	• Ensure that the cells were labeled with Sample Tags correctly and that the correct incubation time was used.
	Sample Tags were not amplified in PCR steps due to incorrect primers used.	• Perform PCR2 again. See Performing PCR2 on page 15. Analyze products using the Agilent Bioanalyzer and look for a ~182 bp peak that corresponds to Sample Tag PCR2 products. Note that a ~160 bp peak might be present that corresponds to BD® AbSeq products. If the ~182 bp peak is observed, proceed to index PCR. See Performing index PCR to prepare final libraries on page 19. If the ~182 bp peak is not observed, contact your local Field Application Specialist (FAS) or scomix@bdscomix.bd.com.

Sequencing

Observation	Possible causes	Recommended solutions
Over-clustering on the Illumina flow cell due to under-estimation of the library.	Inaccurate measurement of the library concentration.	• Quantitate library according to instructions in the protocol.
Low sequencing quality.	Suboptimal cluster density, and/or library denaturation.	• See troubleshooting in Illumina documentation.
High proportion of undetermined Sample Tag calls in sequencing results.	Insufficient sequencing of the Sample Tag library.	1. Set: – Pooled samples of the same cell type: 120 reads/cell. – Pooled samples of different cell types: 600 reads/cell. 2. Repeat sequencing. If issue persists, contact your local Field Application Specialist (FAS) or scomix@bdscomix.bd.com.
	Insufficient washes after labeling cells with Sample Tags.	• Follow the washing steps in this protocol.
	BD Rhapsody™ Cartridge overloaded with cells.	• Follow the cell loading steps in the instrument user guides.

Appendix

Sample Tag sequences

Human Sample Tag

Each Human Sample Tag is a human universal antibody conjugated with a unique oligonucleotide sequence to allow for sample identification. Each Sample Tag has common 5' and 3' ends and the Sample Tag sequence:

GTTGTCAAGATGCTACCGTTCAGAG[**Sample Tag sequence**]AAAAAAAAAAAAAAAAAAAAAAAA

Sample tag	Sample tag sequence
Sample Tag 1 — Human	ATTCAAGGGCAGCCGCGTCACGATTGGATACGACTGTTGGACCGG
Sample Tag 2 — Human	TGGATGGGATAAGTGCGTGATGGACCGAAGGGACCTCGTGGCCGG
Sample Tag 3 — Human	CGGCTCGTGCTGCGTCGTCTCAAGTCCAGAAACTCCGTGTATCCT
Sample Tag 4 — Human	ATTGGGAGGCTTTCGTACCGCTGCCGCCACCAGGTGATACCCGCT
Sample Tag 5 — Human	CTCCCTGGTGTTCAATACCCGATGTGGTGGGCAGAATGTGGCTGG
Sample Tag 6 — Human	TTACCCGCAGGAAGACGTATACCCCTCGTGCCAGGCGACCAATGC
Sample Tag 7 — Human	TGTCTACGTCGGACCGCAAGAAGTGAGTCAGAGGCTGCACGCTGT
Sample Tag 8 — Human	CCCCACCAGGTTGCTTTGTCGGACGAGCCCGCACAGCGCTAGGAT
Sample Tag 9 — Human	GTGATCCGCGCAGGCACACATACCGACTCAGATGGGTTGTCCAGG
Sample Tag 10 — Human	GCAGCCGGCGTCGTACGAGGCACAGCGGAGACTAGATGAGGCCCC
Sample Tag 11 — Human	CGCGTCCAATTTCCGAAGCCCCGCCCTAGGAGTTCCCCTGCGTGC
Sample Tag 12 — Human	GCCCATTCATTGCACCCGCCAGTGATCGACCCTAGTGGAGCTAAG

Mouse Immune Sample Tag

Each Mouse Immune Sample Tag is an Anti-Mouse CD45, Clone 30-F11 antibody conjugated with a unique oligonucleotide sequence to allow for sample identification. Each Sample Tag has common 5' and 3' ends and the Sample Tag sequence:

GTTGTCAAGATGCTACCGTTCAGAG[**Sample Tag sequence**]AAAAAAAAAAAAAAAAAAAAAAAA

Sample tag	Sample tag sequence
Sample Tag 1 — Mouse Immune	AAGAGTCGACTGCCATGTCCCCTCCGCGGGTCCGTGCCCCCCAAG
Sample Tag 2 — Mouse Immune	ACCGATTAGGTGCGAGGCGCTATAGTCGTACGTCGTTGCCGTGCC
Sample Tag 3 — Mouse Immune	AGGAGGCCCCGCGTGAGAGTGATCAATCCAGGATACATTCCCGTC
Sample Tag 4 — Mouse Immune	TTAACCGAGGCGTGAGTTTGGAGCGTACCGGCTTTGCGCAGGGCT
Sample Tag 5 — Mouse Immune	GGCAAGGTGTCACATTGGGCTACCGCGGGAGGTCGACCAGATCCT
Sample Tag 6 — Mouse Immune	GCGGGCACAGCGGCTAGGGTGTTCCGGGTGGACCATGGTTCAGGC
Sample Tag 7 — Mouse Immune	ACCGGAGGCGTGTGTACGTGCGTTTCGAATTCCTGTAAGCCCACC
Sample Tag 8 — Mouse Immune	TCGCTGCCGTGCTTCATTGTCGCCGTTCTAACCTCCGATGTCTCG
Sample Tag 9 — Mouse Immune	GCCTACCCGCTATGCTCGTCGGCTGGTTAGAGTTTACTGCACGCC
Sample Tag 10 — Mouse Immune	TCCCATTCGAATCACGAGGCCGGGTGCGTTCTCCTATGCAATCCC
Sample Tag 11 — Mouse Immune	GGTTGGCTCAGAGGCCCCAGGCTGCGGACGTCGTCGGACTCGCGT
Sample Tag 12 — Mouse Immune	CTGGGTGCCTGGTCGGGTTACGTCGGCCCTCGGGTCGCGAAGGTC

Illumina index 1 (i7) sequences

Library reverse primer	Sequence
1	GCTACGCT
2	CGAGGCTG
3	AAGAGGCA
4	GTAGAGGA

BD® Flex SMK sequences

Each Flex Sample Tag is an anti-PE antibody conjugated with a unique oligonucleotide sequence to allow for sample identification. Each Sample Tag has common 5' and 3' ends and the Sample Tag sequence:

GTTGTCAAGATGCTACCGTTCAGAG**[Sample Tag sequence]**AAAAAAAAAAAAAAAAAAAAAAAA

BD® Flex Single-Cell Multiplexing Kit A (Cat. No. 633849)

Note: Not Compatible with Hu SMK Tags 1-6 (Cat. No. 633781)

Sample Tag	Sample Tag Sequence	Notes
Sample Tag 1 – Flex	ATTCAAGGGCAGCCGCGTCACGATTGGATACGACTGTTGGACCGG	Barcode sequence is the same as human SMK Sample Tag 1
Sample Tag 2 – Flex	TGGATGGGATAAGTGCGTGATGGACCGAAGGGACCTCGTGGCCGG	Barcode sequence is the same as human SMK Sample Tag 2
Sample Tag 3 – Flex	CGGCTCGTGCTGCGTCGTCTCAAGTCCAGAAACTCCGTGTATCCT	Barcode sequence is the same as human SMK Sample Tag 3
Sample Tag 4 – Flex	ATTGGGAGGCTTTCGTACCGCTGCCGCCACCAGGTGATACCCGCT	Barcode sequence is the same as human SMK Sample Tag 4
Sample Tag 5 – Flex	CTCCCTGGTGTTCAATACCCGATGTGGTGGGCAGAATGTGGCTGG	Barcode sequence is the same as human SMK Sample Tag 5
Sample Tag 6 – Flex	TTACCCGCAGGAAGACGTATACCCCTCGTGCCAGGCGACCAATGC	Barcode sequence is the same as human SMK Sample Tag 6

BD® Flex Single-Cell Multiplexing Kit B (Cat. No. 633850)

Note: Not Compatible with Hu SMK Tags 7-12 (Cat. No. 633781)

Sample Tag	Sample Tag Sequence	Notes
Sample Tag 7 – Flex	TGTCTACGTCGGACCGCAAGAAGTGAGTCAGAGGCTGCACGCTGT	Barcode sequence is the same as human SMK Sample Tag 7
Sample Tag 8 – Flex	CCCCACCAGGTTGCTTTGTCGGACGAGCCCGCACAGCGCTAGGAT	Barcode sequence is the same as human SMK Sample Tag 8
Sample Tag 9 – Flex	GTGATCCGCGCAGGCACACATACCGACTCAGATGGGTTGTCCAGG	Barcode sequence is the same as human SMK Sample Tag 9
Sample Tag 10 – Flex	GCAGCCGGCGTCGTACGAGGCACAGCGGAGACTAGATGAGGCCCC	Barcode sequence is the same as human SMK Sample Tag 10
Sample Tag 11 – Flex	CGCGTCCAATTTCCGAAGCCCCGCCCTAGGAGTTCCCCTGCGTGC	Barcode sequence is the same as human SMK Sample Tag 11
Sample Tag 12 – Flex	GCCCATTCATTGCACCCGCCAGTGATCGACCCTAGTGGAGCTAAG	Barcode sequence is the same as human SMK Sample Tag 12

BD® Flex Single-Cell Multiplexing Kit C (Cat. No. 633851)

Note: Not Compatible with Ms SMK Tags 1-6 (Cat. No. 633793)

Sample Tag	Sample Tag Sequence	Notes
Sample Tag 13 – Flex	AAGAGTCGACTGCCATGTCCCCTCCGCGGGTCCGTGCCCCCCAAG	Barcode sequence is the same as mouse SMK Sample Tag 1
Sample Tag 14 – Flex	ACCGATTAGGTGCGAGGCGCTATAGTCGTACGTCGTTGCCGTGCC	Barcode sequence is the same as mouse SMK Sample Tag 2
Sample Tag 15 – Flex	AGGAGGCCCCGCGTGAGAGTGATCAATCCAGGATACATTCCCGTC	Barcode sequence is the same as mouse SMK Sample Tag 3
Sample Tag 16 – Flex	TTAACCGAGGCGTGAGTTTGGAGCGTACCGGCTTTGCGCAGGGCT	Barcode sequence is the same as mouse SMK Sample Tag 4
Sample Tag 17 – Flex	GGCAAGGTGTCACATTGGGCTACCGCGGGAGGTCGACCAGATCCT	Barcode sequence is the same as mouse SMK Sample Tag 5
Sample Tag 18 – Flex	GCGGGCACAGCGGCTAGGGTGTTCCGGGTGGACCATGGTTCAGGC	Barcode sequence is the same as mouse SMK Sample Tag 6

BD® Flex Single-Cell Multiplexing Kit D (Cat. No. 633852)

Note: Not Compatible with Ms SMK Tags 7-12 (Cat. No. 633793)

Sample Tag	Sample Tag Sequence	Notes
Sample Tag 19 – Flex	ACCGGAGGCGTGTGTACGTGCGTTTCGAATTCCTGTAAGCCCACC	Barcode sequence is the same as mouse SMK Sample Tag 7
Sample Tag 20 – Flex	TCGCTGCCGTGCTTCATTGTCGCCGTTCTAACCTCCGATGTCTCG	Barcode sequence is the same as mouse SMK Sample Tag 8
Sample Tag 21 – Flex	GCCTACCCGCTATGCTCGTCGGCTGGTTAGAGTTTACTGCACGCC	Barcode sequence is the same as mouse SMK Sample Tag 9
Sample Tag 22 – Flex	TCCCATTCGAATCACGAGGCCGGGTGCGTTCTCCTATGCAATCCC	Barcode sequence is the same as mouse SMK Sample Tag 10
Sample Tag 23 – Flex	GGTTGGCTCAGAGGCCCCAGGCTGCGGACGTCGTCGGACTCGCGT	Barcode sequence is the same as mouse SMK Sample Tag 11
Sample Tag 24 – Flex	CTGGGTGCCTGGTCGGGTTACGTCGGCCCTCGGGTCGCGAAGGTC	Barcode sequence is the same as mouse SMK Sample Tag 12

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