 **BD Rhapsody™ System**
Targeted mRNA, BD® AbSeq, and
Sample Tag
Library Preparation Protocol

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Regulatory information

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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 (page 38) .
23-24124(03)	2024-11	Added the BD® OMICS-One Dual Index Kit. Added Workflows chapter. Updated Time Considerations workflow. Updated sequencing section. Added sequencing recommendation. Added BD Rhapsody™ oligo sequences to appendix.

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Introduction

This protocol provides instructions for creating single-cell Targeted mRNA, BD® AbSeq, and Sample Tag libraries after cell capture on the BD Rhapsody™ HT Single-Cell Analysis system or the BD Rhapsody™ HT Xpress System for sequencing on various sequencers. For complete instrument procedures and safety information, see the *BD Rhapsody™ HT System Instrument User Guide* or the *BD Rhapsody™ HT Xpress System Instrument User Guide for Scanner-free Workflow*.




To create the libraries, BD Rhapsody™ mRNA targets, BD® AbSeq, and Sample Tags are encoded on the BD Rhapsody™ Enhanced Cell Capture Beads and then amplified in PCR1. After PCR1, the BD® AbSeq, and Sample Tag PCR1 products are separated from the Targeted mRNA 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 Targeted mRNA, BD® AbSeq, and Sample Tag libraries requires that:

- Targeted mRNA PCR1 and Sample Tag PCR1 products undergo PCR2 amplification followed by index PCR with library index primers.
- The BD® AbSeq PCR1 products undergo a separate index PCR from Targeted mRNA and Sample Tag products with library index primers.
- After index PCR, the Targeted mRNA, BD® AbSeq, and Sample Tag libraries can be combined for sequencing.

Symbols

The following symbols are used in this guide.

Symbol	Description
	Important information for maintaining measurement accuracy or data integrity.
	Noteworthy information.
	Procedural stopping point.

Protocol kits

Before you begin, ensure that you have the correct kits for this protocol. Matching cap colors indicate you have the correct kit, along with the catalog numbers found in the [Required and recommended materials \(page 8\)](#) section.



The BD Rhapsody™ Targeted panel used is dependent on intended use.

BD Rhapsody™ Targeted mRNA and AbSeq Amplification Kit (–20 °C)

Cap Color	Name	Quantity
○	PCR master mix	1
○	Universal oligo	1
●	Elution buffer	1
●	Bead RT/PCR enhancer	1
●	Library forward primer	1
●	Library reverse primer 1–4	1 each
○	Nuclease-free water	1
●	Bead resuspension buffer	1
●	Sample Tag PCR1 primer	2
●	Sample Tag PCR2 primer	1
●	BD® AbSeq PCR1 primer	1

BD Rhapsody™ Immune Response Panel Hs (–20 °C)

Cap Color	Name	Quantity
●	PCR1 primers immune response Hs	1
●	PCR2 primers immune response Hs	1

BD Rhapsody™ Immune Response Panel Mm (–20 °C)

Cap Color	Name	Quantity
●	PCR1 primers immune response Mm	1
●	PCR2 primers immune response Mm	1

BD Rhapsody™ Onco-BC Panel Hs (-20 °C)

Cap Color	Name	Quantity
●	PCR1 primers Onco-BC Hs	1
●	PCR2 primers Onco-BC Hs	1

BD Rhapsody™ T Cell Expression Panel Hs (-20 °C)

Cap Color	Name	Quantity
●	PCR1 primers T cell expression Hs	1
●	PCR2 primers T cell expression Hs	1

BD® OMICS-One Dual Index Kit (-20 °C)

Cap Color	Name	Quantity
●	Dual index forward primer 1–8	1 each
●	Dual index reverse primer 1–8	1 each

Workflows

Targeted mRNA library amplification workflow

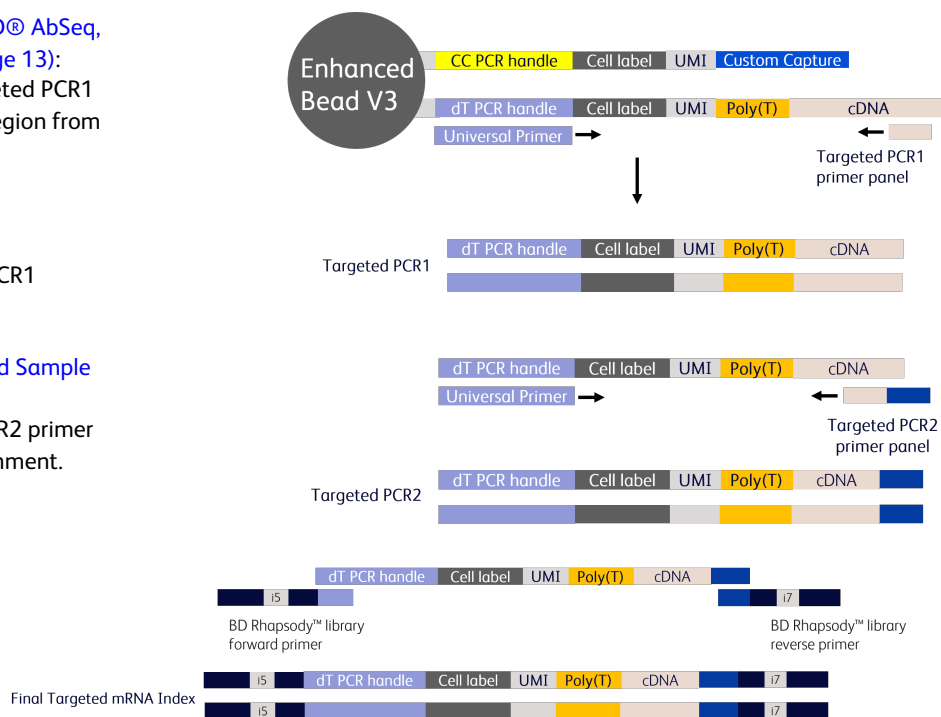
Step 1: Targeted mRNA, BD® AbSeq, and Sample Tag PCR1 (page 13): Universal primer and Targeted PCR1 primer panel copy target region from bead.

Amplify in solution. Collect supernatant as Targeted PCR1 product.

Step 4: Targeted mRNA and Sample Tag PCR2 (page 19):

Amplify using Targeted PCR2 primer panel for nested PCR enrichment.

Step 6: Targeted mRNA, BD® AbSeq, and Sample Tag index PCR (page 21): Add adapters and indices.

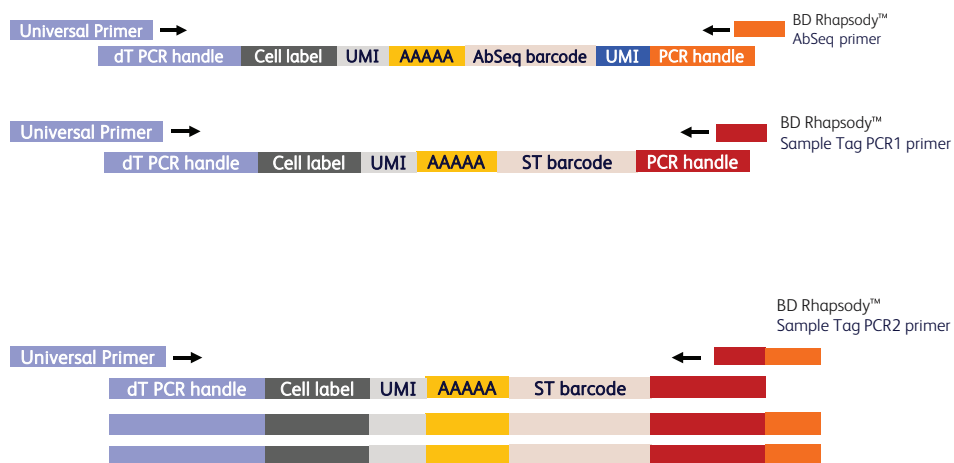


BD® AbSeq/Sample Tag library amplification workflow

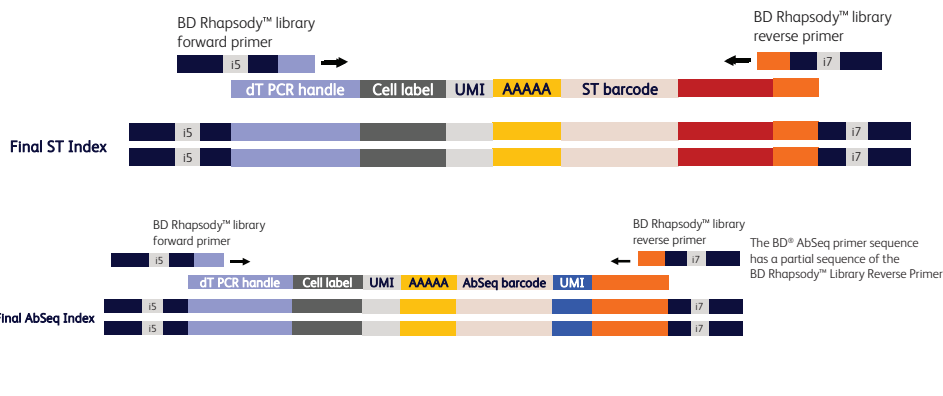
Step 1: Targeted mRNA, BD® AbSeq, and Sample Tag PCR1 (page 13):

BD® AbSeq/Sample Tag products are amplified together in PCR1.

Step 4: Targeted mRNA and Sample Tag PCR2 (page 19): Sample Tag product is further amplified in PCR2.



Step 6: Targeted mRNA, BD® AbSeq, and Sample Tag index PCR (page 21): Add Sample Tag adapters and indices.



Required and recommended materials

Required reagents

Store the reagents at the storage temperature specified on the label.

Material	Supplier	Catalog no.
BD Rhapsody™ Targeted mRNA and AbSeq Amplification Kit*	BD Biosciences	633774
BD Rhapsody™ Immune Response Panel Hs [†] †	BD Biosciences	633750
BD Rhapsody™ Immune Response Panel Mm [†] †	BD Biosciences	633753
BD Rhapsody™ Onco-BC Panel HS [†] †	BD Biosciences	633752
BD Rhapsody™ T Cell Expression Panel Hs [†] †	BD Biosciences	633751
BD® OMICS-One Dual Index Kit‡	BD Biosciences	571899
Agencourt® AMPure® XP magnetic beads	Beckman Coulter	A63880
100% ethyl alcohol, molecular biology grade	Major supplier	–
Nuclease-free water	Major supplier	–

* For processing more than four libraries, two orders of this catalog number are required.

† Dependent on targeted amplification samples used.

‡ Recommended for unique dual indexing with high-throughput (more than eight) library preparation workflows.

Recommended consumables

Material	Supplier	Part number/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*	Corning	PCR96HSC
Or, MicroAmp Optical 96-Well Reaction Plate*	Thermo Fisher Scientific	N8010560
MicroAmp Clear Adhesive Film*	Thermo Fisher Scientific	4306311
15-mL conical tube	Major supplier	–
DNA LoBind® tubes, 1.5 mL	Eppendorf	0030108051
Qubit™ Assay Tubes	Thermo Fisher Scientific	Q32856
Qubit™ dsDNA HS Assay Kit	Thermo Fisher Scientific	Q32851
Agilent High Sensitivity DNA Kit	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

* Recommended for processing high-throughput (more than eight) 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	–
PCR thermal cycler	Major supplier	–
6-tube magnetic separation rack for 1.5-mL tubes Or, 12-tube magnetic separation rack [†] Or, Invitrogen™ DynaMag™-2 magnet [†]	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‡	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
Heat block	Major supplier	–

† Recommended for processing greater than six samples.

‡ Recommended for processing high-throughput (more than eight) library preparation workflows.

Best practices

Cell capture

- For best results, ensure that cells have high viability before proceeding with cell capture.

Bead handling

- When working with BD Rhapsody™ Enhanced Cell Capture Beads, use low-retention filtered tips and LoBind® tubes.



Never vortex the beads. Pipet-mix only.

- Store BD Rhapsody™ Enhanced Cell Capture Beads at 4 °C. Do not freeze.
- Bring Agencourt® AMPure® XP magnetic beads to room temperature (15–25 °C) before use. See the *AMPure® XP User's Guide* for information.

Libraries

- BD[®] AbSeq and Sample Tag libraries can be sequenced together or separately from Targeted mRNA libraries.

Master mix preparation

- Thaw reagents (except for enzymes) at room temperature.
- Keep enzymes at –25 °C to –15 °C until ready for use.
- Return reagents to correct storage temperature as soon as possible after preparing the master mix.

Supernatant handling

- Read this protocol carefully before beginning each section. Note which steps require you to keep supernatant to avoid accidentally discarding required products.
- Remove supernatants without disturbing AMPure[®] XP magnetic beads.
- Make and use fresh 80% ethyl alcohol within 24 hours. Adjust the volume of 80% ethyl alcohol depending on the number of libraries.

Bead amplification

- Do not proceed to thermal cycling until each tube is gently mixed by pipette to ensure uniform bead suspension. Start the thermocycler program immediately after mixing.




Additional documentation

- *BD Rhapsody™ HT Single-Cell Analysis System Single-Cell Capture and cDNA Synthesis Protocol* (doc ID 23-24252)
- *BD Rhapsody™ HT Xpress System Single-Cell Capture and cDNA Synthesis Protocol* (doc ID 23-24253)
- *BD Rhapsody™ System Single-Cell Labeling with BD[®] AbSeq Ab-Oligos (1 plex to 40 plex) Protocol* (doc ID 23-24262)
- *BD Rhapsody™ System Single-Cell Labeling with BD[®] AbSeq Ab-Oligos (41 plex to 100 plex) Protocol* (doc ID 23-22314)
- *BD Rhapsody™ System Single-Cell Labeling with BD[®] Single-Cell Multiplexing Kits Protocol* (doc ID 23-21340)
- *BD Rhapsody™ System Single-Cell Labeling with BD[®] Flex Single-Cell Multiplexing Kits Protocol* (doc ID 23-24311)
- *BD Rhapsody™ Sequence Analysis Pipeline User's Guide* (doc ID 23-24580)

Safety information

For safety information, refer to the *BD Rhapsody™ HT Single-Cell Analysis System Instrument User Guide* (doc ID 23-24607) or the *BD Rhapsody™ HT Xpress System Instrument User Guide for Scanner-Free Workflow* (doc ID 23-24256).

Time considerations

Station	Workflow	Timing	Stopping Point & Storage
Targeted mRNA, BD® AbSeq, and Sample Tag Library Amplification			
Post-Amplification Workspace	Step 1: Targeted mRNA, BD® AbSeq, and Sample Tag PCR1 (page 13)	100 minutes 	PCR overnight
	Step 2: Targeted mRNA, BD® AbSeq, and Sample Tag PCR1 cleanup (page 16)		<24 hours at 4 °C or <6 months at –20 °C
	Step 3: Quantifying BD® AbSeq PCR1 products (page 18)BD® AbSeq PCR1 Quality Check		<24 hours at 4 °C or <6 months at –20 °C
	Step 4: Targeted mRNA and Sample Tag PCR2 (page 19)	80 minutes 	PCR overnight
	Step 5: Targeted mRNA and Sample Tag PCR2 cleanup (page 20)		<24 hours at 4 °C or <6 months at –20 °C
	Step 6: Targeted mRNA, BD® AbSeq, and Sample Tag index PCR (page 21)	70 minutes 	PCR overnight
	Step 7: Targeted mRNA, BD® AbSeq, and Sample Tag index PCR cleanup and quality check (page 23)		<6 months at –20 °C

Procedure

Continue this procedure after staining the antibodies as described in one of the following protocols:

- *BD Rhapsody™ System Single-Cell Labeling with BD® AbSeq Ab-Oligos (1 plex to 40 plex) Protocol*
- *BD Rhapsody™ System Single-Cell Labeling with BD® AbSeq Ab-Oligos (41 plex to 100 plex) Protocol*
- *BD Rhapsody™ System Single-Cell Labeling with BD® AbSeq Ab-Oligos for Intracellular CITE-seq Protocol*
- *BD Rhapsody™ System Single-Cell Labeling with BD® Single-Cell Multiplexing Kits Protocol*
- *BD Rhapsody™ System Single-Cell Labeling with BD® Flex Single-Cell Multiplexing Kits Protocol*

Perform the experiment on the BD Rhapsody™ Single-Cell Analysis system using either of the following guides for cell capture, reverse transcription, and Exonuclease treatment:

- *BD Rhapsody™ HT Single-Cell Analysis System Single-Cell Capture and cDNA Synthesis Protocol* (doc ID 23-24252)
- *BD Rhapsody™ HT Xpress System Single-Cell Capture and cDNA Synthesis Protocol* (doc ID 23-24253)

Targeted mRNA, Sample Tag, and BD[®] AbSeq library amplification

This procedure comprises the following tasks:

- [Step 1: Targeted mRNA, BD[®] AbSeq, and Sample Tag PCR1 \(page 13\)](#)
- [Step 2: Targeted mRNA, BD[®] AbSeq, and Sample Tag PCR1 cleanup \(page 16\)](#)
- [Step 3: Quantifying BD[®] AbSeq PCR1 products \(page 18\)](#)
- [Step 4: Targeted mRNA and Sample Tag PCR2 \(page 19\)](#)
- [Step 5: Targeted mRNA and Sample Tag PCR2 cleanup \(page 20\)](#)
- [Step 6: Targeted mRNA, BD[®] AbSeq, and Sample Tag index PCR \(page 21\)](#)
- [Step 7: Targeted mRNA, BD[®] AbSeq, and Sample Tag index PCR cleanup and quality check \(page 23\)](#)

Before you begin

- Obtain Exonuclease I-treated BD Rhapsody[™] Enhanced Cell Capture Beads.
- Keep enzymes on ice or keep frozen before use.
- Thaw the reagents in the BD Rhapsody[™] Targeted mRNA and AbSeq Amplification Kit at room temperature and then place on ice.

Step 1: Targeted mRNA, BD[®] AbSeq, and Sample Tag PCR1



Before using BD Rhapsody[™] 10X PCR1 custom primers 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.

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

PCR1 reaction mix

Cap	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 master mix	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 Targeted mRNA primer panel* †	40.0	48.0	192.0	384.0
	(Optional) PCR1 panel supplement* †	(10.0)	(12.0)	(48.0)	(96.0)
●	Sample Tag PCR1 primer	1.2	1.44	5.76	11.52
●	BD® AbSeq primer	12.0	14.4	57.6	115.2
○	Nuclease-free water	14.8 (4.8)	17.76 (5.76)	71.04 (53.04)	142.08 (46.08)
	Total	200.0	240.0	960.0	1920.0

* Order from BD Biosciences.

† BD Rhapsody™ Targeted (pre-designed) primer panels are provided at 1X. Ensure custom and supplement panels are diluted to 1X before use.

2. Gently vortex mix, briefly centrifuge, and place back on ice.
3. Based on the sample size, complete one of the following actions:
 - If using a subsample, proceed to step 4.
 - If using the entire sample, skip to step 5.
4. To subsample 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 Exonuclease I-treated beads can be stored in bead resuspension buffer at 4 °C for up to 1 year.
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 PCR1 reaction mix. Do not vortex.

7. Ensure that the beads are fully resuspended, then pipet 50 µL of 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. Run the following PCR program on the thermal cycler.

PCR1 conditions for Targeted mRNA panel

Step	Cycles	Temperature	Time
Hot start	1	95 °C*	3 min
Denaturation	8–15 [†]	95 °C	30 seconds
Annealing		60 °C	3 min
Extension		72 °C	1 min
Final extension	1	72 °C	5 min
Hold	1	4 °C	∞

* 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 3-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 1-minute 95 °C pause step can be added immediately before the 3-minute 95 °C denaturation step.

[†] Recommended PCR cycles might require optimization for different cell types and cell number.

Recommended number of PCR cycles

Number of cells in PCR1	Recommended PCR cycles for resting PBMCs
500	15
1,000	14
2,500	13
5,000	12
10,000	11
20,000	10
40,000	9
80,000–100,000	8

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.



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 tubes 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.



Retain the supernatant in the next step.

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

Step 2: Targeted mRNA, BD® AbSeq, and Sample Tag PCR1 cleanup

This section describes how to perform double-sided AMPure cleanup to separate the shorter BD® AbSeq and Sample Tag PCR1 products (~160 bp) from the longer Targeted mRNA PCR1 products (350–800 bp).



Keep both the supernatant (BD® AbSeq and Sample Tag products) and the AMPure beads (Targeted mRNA products) for purification.



Perform PCR1 purification in the post-amplification workspace.

1. Bring the AMPure® XP magnetic beads to room temperature.
2. In a new 15-mL conical tube, prepare 5 mL of fresh 80% (v/v) ethyl alcohol by combining 4 mL absolute ethyl alcohol, molecular biology grade, with 1 mL nuclease-free water (or refer to the following table for additional libraries). Vortex the tube for 10 seconds to mix.



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 the following table are enough to cover all PCR clean ups throughout the 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

3. Vortex the AMPure® XP magnetic beads at high speed for 1 minute until the beads are fully resuspended.
4. Briefly centrifuge PCR1 products.



The final volume must be exactly 200 µL to achieve the appropriate size selection of the purified PCR1 product. If the volume is less than 200 µL, use elution buffer to achieve the final volume.

5. Pipet 140 µL of AMPure® beads into the 200 µL of Targeted mRNA, BD® AbSeq, and Sample Tag PCR1 products. Pipet-mix 10 times, then briefly centrifuge the samples.
6. Incubate at room temperature for 5 minutes.
7. Place the 1.5-mL LoBind® tube on the magnet for 5 minutes or until the supernatant is clear.

8. Keeping the tube on the magnet, transfer the 340 μL of supernatant (BD® AbSeq and Sample Tag PCR1 products) to a new 1.5-mL tube without disturbing the beads (Targeted mRNA PCR1 products).
9. Store the supernatant (step 8) on ice while purifying and eluting the Targeted mRNA products. Purify the BD® AbSeq and Sample Tag PCR1 products after purifying the Targeted mRNA PCR1 products.
10. Keeping the tube on the magnet, gently pipet 500 μL of fresh 80% ethyl alcohol into the tube and incubate for 30 seconds. Remove and discard the supernatant without disturbing the beads.
11. Repeat step 10 once for a total of two ethyl alcohol washes.
12. Keeping the tube on the magnet, use a small-volume pipette to remove and discard any residual supernatant from the tube.
13. Air-dry the beads at room temperature for 5 minutes.



Do not overdry the AMPure® beads after the ethanol washes. Overdried beads appear cracked.

14. Remove the tube from the magnet and pipet 30 μL of elution buffer to resuspend the bead pellet. Vigorously pipet-mix until the beads are uniformly dispersed. Small clumps do not affect performance.
15. Incubate at room temperature for 2 minutes and briefly centrifuge.
16. Place the tube on the magnet until the solution is clear, usually ~30 seconds.
17. Pipet the eluate (~30 μL) into a new 1.5-mL LoBind® tube (purified Targeted mRNA PCR1 products).
18. To purify BD® AbSeq and Sample Tag PCR1 products, pipet 100 μL of AMPure® beads into the tube with 340 μL supernatant from step 8. Pipet-mix 10 times, then briefly centrifuge the samples.
19. Incubate at room temperature for 5 minutes.
20. Place the 1.5-mL LoBind® tube on the magnet for 5 minutes or until the supernatant is clear. Remove and discard the supernatant without disturbing the beads.
21. Keeping the tube on the magnet, gently pipet 500 μL of fresh 80% ethyl alcohol into the tube and incubate for 30 seconds. Remove and discard the supernatant without disturbing the beads.
22. Repeat step 21 for a total of two ethyl alcohol washes.
23. Keeping the tube on the magnet, use a small-volume pipette to remove and discard any residual supernatant from the tube.
24. Air-dry the beads at room temperature for 5 minutes.



Do not overdry the AMPure® beads after the ethanol washes. Overdried beads appear cracked.

25. Remove the tube from the magnet and pipet 30 μL of elution buffer into the tube to resuspend the bead pellet. Vigorously pipet-mix until the beads are uniformly dispersed. Small clumps do not affect performance.
26. Incubate at room temperature for 2 minutes and briefly centrifuge.
27. Place the tube on the magnet until the solution is clear, usually ~30 seconds.

28. 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.

Step 3: Quantifying BD® AbSeq PCR1 products

1. Measure the yield of the largest peak of the BD® AbSeq 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 PCR1 sample bioanalyzer high-sensitivity DNA trace

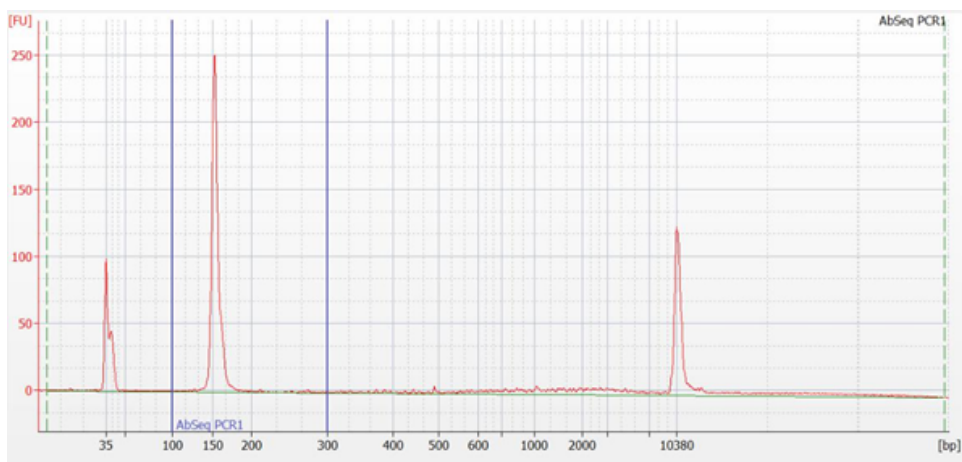
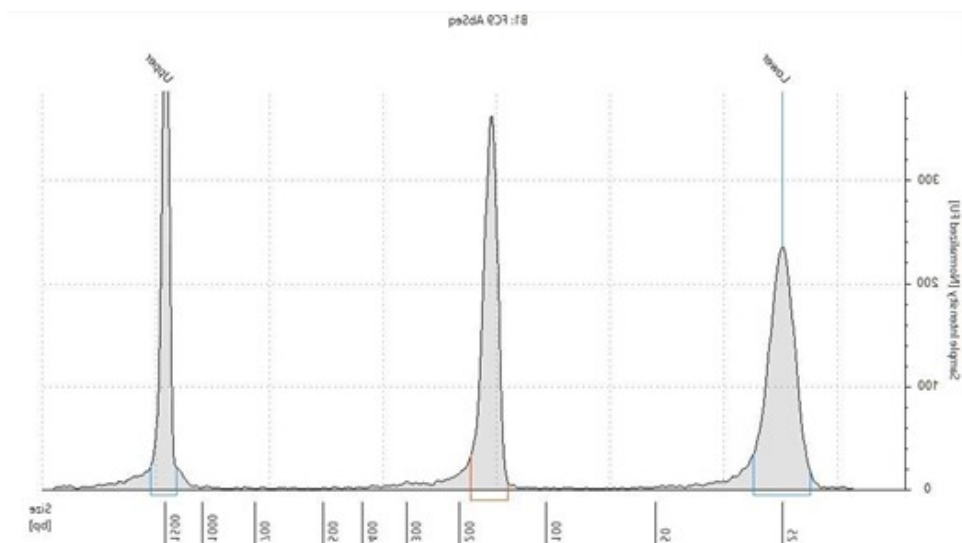


Figure 2 BD® AbSeq PCR1 sample TapeStation high-sensitivity D1000 trace



2. Dilute an aliquot of BD® AbSeq products to 0.1–1.1 ng/ μL with elution buffer before index PCR of BD® AbSeq PCR1 products.

Step 4: Targeted mRNA and Sample Tag PCR2



Before using BD Rhapsody™ 10X PCR1 Custom primers 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.



Only the Targeted mRNA and Sample Tag PCR1 products require PCR2 amplification. The BD® AbSeq PCR1 products require only index PCR.

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

Targeted mRNA PCR2 reaction mix

Cap	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 master mix	25.0	30.0	120.0	240.0
○	Universal oligo	2.0	2.4	9.6	19.2
●	PCR2 primer panel* †	10.0	12.0	48.0	96.0
	(Optional) PCR2 panel supplement* †	(2.5)	(3.0)	(12.0)	(24.0)
○	Nuclease-free water	8.0 (5.5)	9.6 (6.6)	38.4 (26.4)	76.8 (52.4)
	Total	45.0	54.0	216.0	432.0

* Order from BD Biosciences.

† 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

Cap	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 master mix	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. Pipet 45 μL of PCR2 reaction mix into one 0.2-mL PCR tube for each library and place back on ice.
3. Bring the PCR2 reaction mixes to the post-amplification workspace.
4. In two separate and new 0.2-mL PCR tubes:

- Targeted mRNA PCR1 products: Pipet 5.0 µL products into 45.0 µL Targeted mRNA PCR2 reaction mix.
 - 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. Run the following PCR program on the thermal cycler.

PCR2 conditions for Targeted mRNA

Step	Cycles	Temperature	Time
Hot start	1	95 °C	3 min
Denaturation	10	95 °C	30 seconds
Annealing		60 °C	3 min
Extension		72 °C	1 min
Final extension	1	72 °C	5 min
Hold	1	4 °C	∞

PCR2 conditions for Sample Tag


Step	Cycles	Temperature	Time
Hot start	1	95 °C	3 min
Denaturation	10	95 °C	30 seconds
Annealing		66 °C	30 seconds
Extension		72 °C	1 min
Final extension	1	72 °C	5 min
Hold	1	4 °C	∞



STOPPING POINT: The PCR can run overnight.

Step 5: Targeted mRNA and Sample Tag PCR2 cleanup

Perform PCR2 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.
 -  The final volume must be exactly 50 µL to achieve the appropriate size selection of the purified PCR2 product. If the volume is less than 50 µL, use elution buffer to achieve the final volume.
3. To 50 µL of the PCR2 products, pipet AMPure® beads as follows:
 - Targeted mRNA library: 40 µL of AMPure® beads
 - Sample Tag library: 60 µL AMPure® beads

4. Pipet-mix 10 times and incubate at room temperature for 5 minutes.
5. Place the suspension on the 0.2-mL strip tube magnet for 3 minutes or until the supernatant is clear. Remove and discard the supernatant without disturbing the beads.
6. Keeping the tube on the magnet, gently add 200 μ L of fresh 80% ethyl alcohol into the tube and incubate for 30 seconds. Remove and discard the supernatant without disturbing the beads.
7. Repeat step 6 once for a total of two alcohol washes.
8. Keeping the 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.



Do not overdry the AMPure[®] beads after the ethanol washes. Overdried beads appear cracked.

10. Remove the tube from the magnet and pipet 30 μ L of elution buffer into the tube. Pipet-mix at least 10 times to completely resuspend the AMPure[®] XP magnetic beads.
11. Incubate the sample at room temperature for 2 minutes.
12. Place the tube on the magnet until the solution is clear, usually ~30 seconds.
13. Pipet the entire eluate (~30 μ L) of each sample into two separate and new 1.5-mL LoBind[®] tubes (purified Targeted mRNA 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. Quantify the concentration of the Targeted mRNA and Sample Tag PCR2 products with a Qubit[™] Fluorometer using the Qubit[™] dsDNA HS Assay Kit. Follow the manufacturer's instructions.

Step 6: Targeted mRNA, BD[®] AbSeq, and Sample Tag index PCR

This section describes how to generate Targeted mRNA, BD[®] AbSeq, and Sample Tag libraries compatible with various sequencing platforms, by adding full-length sequencing adapters and indices through PCR.



If additional unique or combinatorial indexing is needed, use the BD[®] OMICS-One Dual Index Kit primers.

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

Targeted mRNA, BD® AbSeq, and Sample Tag index PCR mix

Cap	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 master mix	25.0	30.0	120.0	240.0
●	Library forward primer	2.0	2.4	9.6	19.2
●	Library reverse primer 1–4* †	2.0	2.4	–	–
○	Nuclease-free water	18.0	21.6	86.4	172.8
	Total	47.0	56.4	216.0	432.0

* For more than one library, use different library reverse primers for each library. For recommendations about how to index libraries, contact your local Field Application Specialist or go to scomix@bdscomix.bd.com.

† For more than four libraries, use the BD® OMICS-One Dual Index Kit.

For sequencing on Illumina systems, refer to the Illumina guidelines for preparing libraries with balanced index combinations.

2. Gently vortex mix and briefly centrifuge. Pipet 47 µL of Targeted mRNA, BD® AbSeq or Sample Tag index PCR mix into one 0.2-mL PCR tube for each library, and place back on ice.
3. Bring the Index PCR mixes to post-amplification workspace.
4. In separate and new 0.2-mL PCR tubes:
 - Targeted mRNA PCR2 products: Pipet 3.0 µL of 0.2–2.7 ng/µL products into 47.0 µL index PCR mix.
 - Sample Tag PCR2 products: Pipet 3.0 µL of 0.1–1.1 ng/µL products into 47.0 µL index PCR mix.
 - BD® AbSeq PCR1 products: Pipet 3.0 µL of 0.1–1.1 ng/µL products into 47.0 µL index PCR mix
5. Gently vortex, and briefly centrifuge.
6. Run the following PCR program on the thermal cycler.

Index PCR conditions for Targeted mRNA

Step	Cycles	Temperature	Time
Hot start	1	95 °C	3 min
Denaturation	6–8*	95 °C	30 seconds
Annealing		60 °C	30 seconds
Extension		72 °C	30 seconds
Final extension	1	72 °C	1 min
Hold	1	4 °C	∞

* See suggested PCR cycles.

Suggested PCR cycles

Concentration index PCR input for mRNA Targeted libraries (ng/μL)	Concentration index PCR input for BD® AbSeq and Sample Tag 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.

Step 7: Targeted mRNA, BD® AbSeq, and Sample Tag index PCR cleanup and quality check



Perform PCR 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 the index PCR products.



The final volume must be exactly 50 μL to achieve the appropriate size selection of the purified PCR1 product. If the volume is less than 50 μL, use elution buffer to achieve the final volume.

3. To 50 μL of the index PCR products, pipet AMPure® beads as follows:
 - Targeted mRNA library: 35 μL AMPure® beads
 - BD® AbSeq and Sample Tag library: 40 μL AMPure® beads
4. Pipet-mix the PCR products 10 times, then briefly centrifuge the samples.
5. Incubate at room temperature for 5 minutes.
6. Place the suspension on the 0.2-mL strip tube magnet for 3 minutes or until the supernatant is clear. Remove and discard the supernatant without disturbing the beads.
7. Keeping the tube on the magnet, gently add 200 μL of fresh 80% ethyl alcohol into the tube and incubate for 30 seconds. Remove and discard the supernatant without disturbing the beads.
8. Repeat step 7 for a total of two ethyl alcohol washes.
9. Keeping the tube on the magnet, use a small-volume pipette to remove and discard the residual supernatant from the tube.
10. Air-dry the beads at room temperature for 2 minutes.



Do not overdry the AMPure® beads after the ethanol washes. Overdried beads appear cracked.

11. Remove the tube from the magnet and pipet 30 μL of elution buffer into the tube. Pipet-mix at least 10 times to fully resuspend the AMPure® XP magnetic beads.

12. Incubate at room temperature for 2 minutes.
13. Place the tube on the magnet until the solution is clear, usually ~30 seconds.
14. Pipet the eluate (~30 µL) into a new 1.5-mL LoBind® tube (final sequencing library).



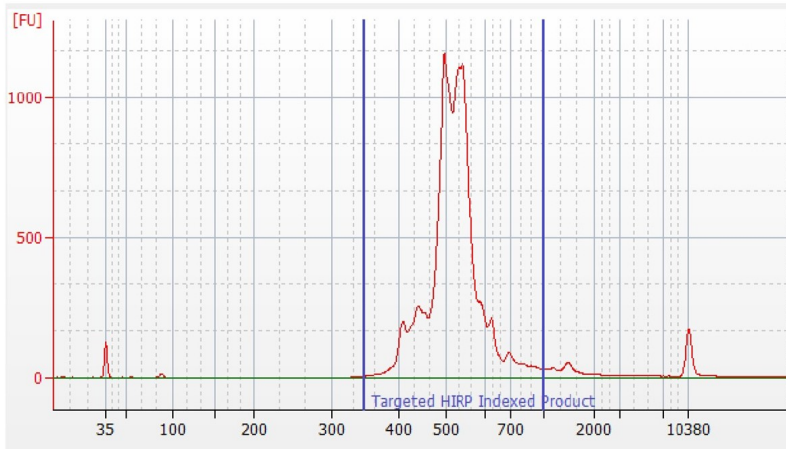
STOPPING POINT: Store at –25 °C to –15 °C for up to 6 months until sequencing.

15. Quantify the concentration of the final sequencing library with a Qubit™ Fluorometer using the Qubit™ dsDNA HS Kit. Follow the manufacturer's instructions. The expected concentration of the libraries is >1.5 ng/µL.

16. Measure the average fragment size of the Targeted mRNA, BD® AbSeq, and Sample Tag libraries within the size range of 200–1,000 bp by using the Agilent Bioanalyzer with the High Sensitivity Kit for 50–7,000 bp, 5–1,000 pg/μL or the Agilent TapeStation. Follow the manufacturer's instructions.

Figure 3 Targeted mRNA index PCR product

A. Sample bioanalyzer high-sensitivity DNA trace - BD Rhapsody™ Immune Response Panel HS



B. Sample TapeStation high-sensitivity D5000 trace - BD Rhapsody™ Immune Response Panel HS

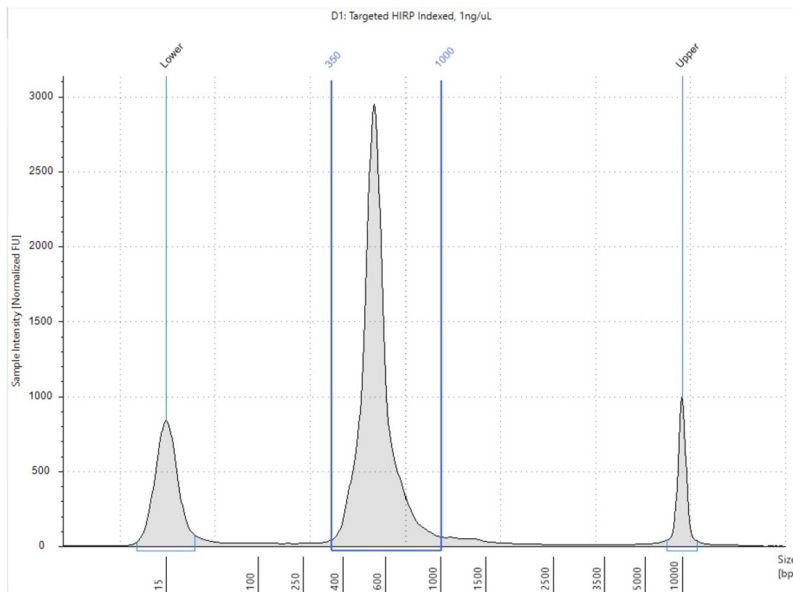
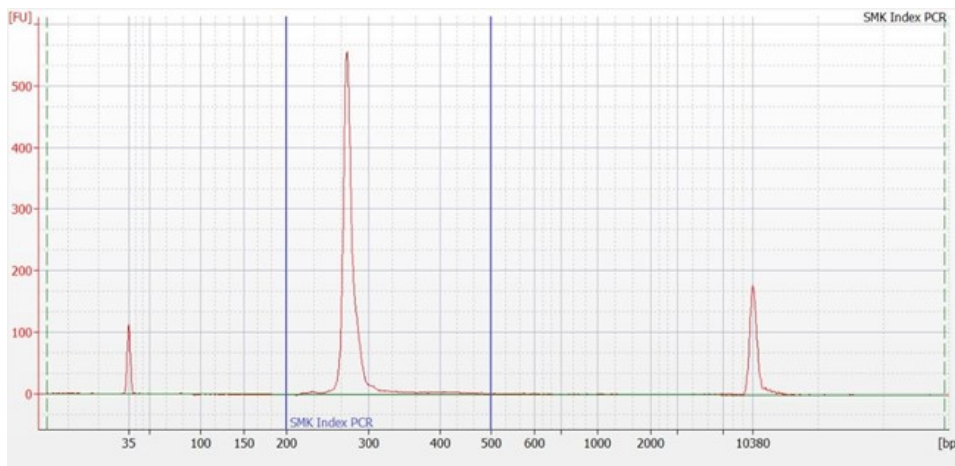
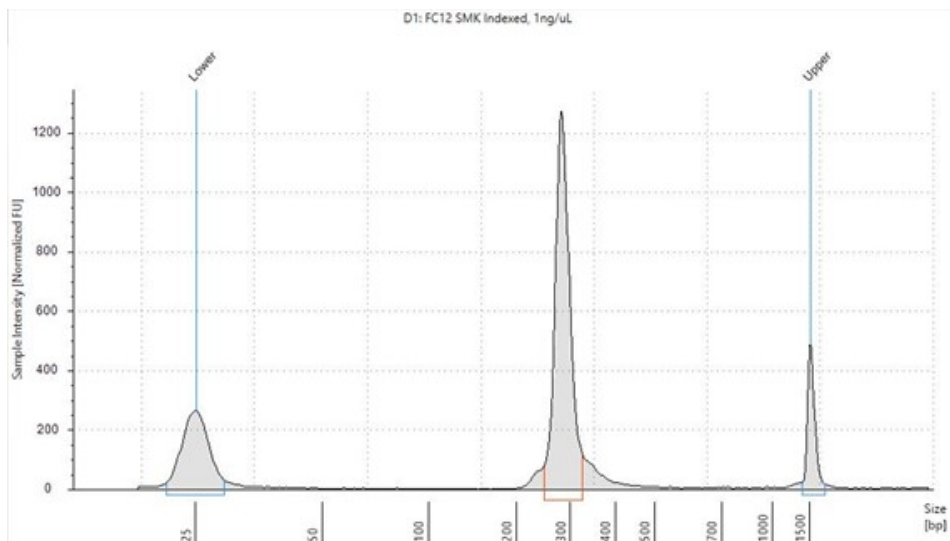
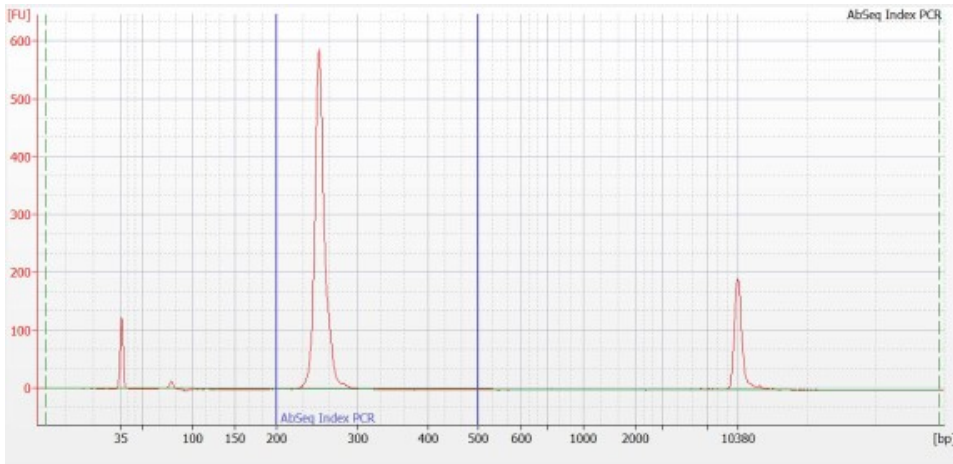
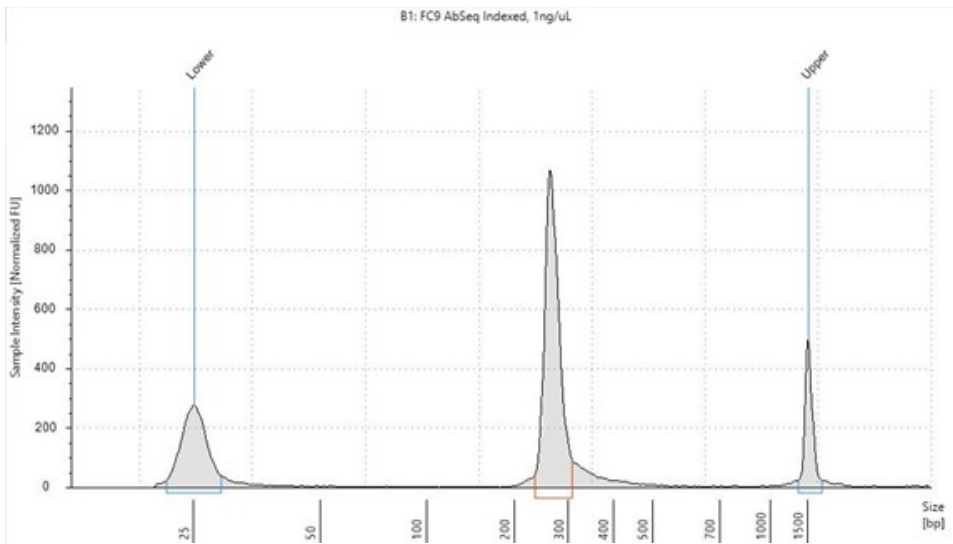


Figure 4 Sample Tag index PCR product**A.** Sample bioanalyzer high-sensitivity DNA trace**B.** Sample TapeStation high-sensitivity D1000 trace

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. This does not affect the quality of the final Sample Tag library. Peak sizes may vary depending on instrumentation or assay used for measurement.

Figure 5 Final BD® AbSeq library**A. Sample bioanalyzer high-sensitivity DNA trace****B. Sample TapeStation high-sensitivity D1000 trace**

17. If the concentration or size of the library is outside of the expected range, see [Troubleshooting \(page 30\)](#) or contact your local Field Application Specialist or go to scomix@bdscomix.bd.com.

Sequencing

The sequencing depth for each library is dependent on application. For cell-type clustering, shallow sequencing is sufficient. However, for in-depth analysis such as comparison across multiple samples, deep sequencing is advised. We recommend meeting the requirement for recursive substitution error correction (RSEC) sequencing depth of ≥ 6 to reach the threshold of sequencing saturation where most molecules of the library have been recovered, approximately 80%. The RSEC sequencing depth and sequencing saturation are both reported by the analysis pipeline. The actual sequencing reads/cell required to achieve this depth can vary as it is dependent on the gene expression levels, number of cells, and sequencing run quality. The following reads/cell are recommended for Targeted mRNA, Sample Tag, and BD® AbSeq libraries.

Sequencing depth of the Targeted mRNA libraries can vary depending on whether the sample contains high or low-content RNA cells. For resting PBMCs, we recommend:

Read requirements for libraries

Gene panel	Read requirement for data analysis
BD Rhapsody™ Targeted	~2,000–20,000 reads/cell*
BD® AbSeq	1,000 reads/cell/AbSeq†
Sample Tag	600 reads/cell

* 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.

† 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 .

Required parameters

Parameter	Requirement
Platform	Illumina*
Paired-end reads	Recommend Read 1: 51 cycles; Read 2: 71 cycles; Index 1 (i5): 8 cycles; Index 2 (i7): 8 cycles
PhiX	1% recommended
Analysis	See the <i>BD® Single-Cell Multiomics Bioinformatics Handbook</i>

* To review Illumina Index 1 (i7) sequences, see the [Appendix \(page 34\)](#).

Sequencing recommendations

- 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 and 1.8 pM with 1% PhiX for a sequencing run.
- For Novaseq:

Sequencing platform	Cycles	Recommended loading concentration
NovaSeq 6000 S Prime (Single Lane)	2×50, 2×100, 2×150, 2×250*	180–250 pM (XP workflow)
NovaSeq 6000 S Prime (Single Flow Cell)	2×50, 2×100, 2×150, 2×250*	350–650 pM (standard workflow)
NovaSeq 6000 S1 (Single Lane)	2×50, 2×100, 2×150*	180–250 pM (XP workflow)
NovaSeq 6000 S1 (Single Flow Cell)	2×50, 2×100, 2×150*	350–650 pM (standard workflow)
NovaSeq 6000 S2 (Single Flow Cell)	2×50, 2×100, 2×150*	350–650 pM (standard workflow)
NovaSeq 6000 S4 (Single Lane)	2×100, 2×150	180–250 pM (XP workflow)
NovaSeq 6000 S4 (Single Flow Cell)	2×100, 2×150	350–650 pM (standard workflow)
NovaSeq X 10B	2×100, 2×150	Contact local Field Application Specialist (FAS)

* NovaSeq 100 cycle kit (v1.0 or v1.5) can be used. The 100-cycle kit contains enough reagents for up to 130 cycles.

- For other sequencing platforms (e.g. Element AVITI System), follow the manufacturer's sequencing recommendations.



Avoid pooling greater than 60% total BD[®] AbSeq in final sequencing pool as it may impact sequencing quality of Targeted mRNA libraries.



To determine the ratio of BD Rhapsody™ Targeted mRNA library to BD[®] AbSeq library to Sample Tag library to pool for sequencing, use the sequencing calculator available by contacting your local Field Application Specialist (FAS) or scomix@bdscomix.bd.com.

Sequencing analysis pipeline


Contact customer support at scomix@bdscomix.bd.com for access to the latest whole transcriptome sequencing analysis pipeline.

Troubleshooting

Library preparation

Observation	Possible causes	Recommended solutions
PCR2 product yield too low.	PCR1 and PCR2 primers might have been swapped by mistake.	Ensure 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 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 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.	<ol style="list-style-type: none"> 1. Determine the product size range: <ol style="list-style-type: none"> a. Load 1 μL of purified PCR2 product at 1 ng/μL in a High Sensitivity DNA Chip on the Agilent Bioanalyzer. b. Follow the manufacturer's instructions. 2. Confirm that the mRNA tTargeted PCR2 products should show an average size range of 350–600 bp. <ul style="list-style-type: none"> • If the products pass quality control, see Step 6: Targeted mRNA, BD[®] AbSeq, and Sample Tag index PCR (page 21) to prepare final libraries. 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 or input amount of PCR2 products too high.	Repeat the index PCR with a lower input of PCR2 products.
	Upper and lower markers on the Agilent Bioanalyzer or TapeStation 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.
BD [®] AbSeq PCR1 product size too low.	BD [®] AbSeq primer not added to PCR1 or too few PCR1 cycles. Incorrect volumes of AMPure [®] XP beads used during double-sided selection.	Contact your local Field Application Specialist (FAS) or 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.

Observation	Possible causes	Recommended solutions
Yield of BD® AbSeq library too low after index PCR, but yield of BD® AbSeq/Sample Tag 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.
Expected size of Sample Tag products is too short (<276 bp).	Upper and lower markers on the Agilent Bioanalyzer or Agilent TapeStation 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 Step 4: Targeted mRNA and Sample Tag PCR2 (page 19) . Analyze products using the Agilent Bioanalyzer or the Agilent TapeStation and look for a ~182 bp peak that corresponds to Sample Tag PCR2 products.  ~160 bp peak might be present that corresponds to BD® AbSeq products. If the ~182 bp peak is observed, proceed to index PCR. If the ~182 bp peak is not observed, contact your local Field Application Specialist (FAS) or scomix@bdscmix.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 protocol.
Low sequencing quality.	Insufficient PhiX.	Use the recommended concentration of PhiX with the library to be sequenced.
	Suboptimal cluster density, or library denaturation, or both.	See troubleshooting in Illumina documentation.

Observation	Possible causes	Recommended solutions
<p>High proportion of undetermined Sample Tag calls in sequencing results.</p>	<p>Insufficient sequencing of the Sample Tag Library.</p>	<ol style="list-style-type: none"> 1. Set pooled samples of the same cell type to 120 reads/cell. 2. Set pooled samples of different cell types to 600 reads/cell. 3. Repeat sequencing of Sample Tag library. If issue persists, contact your local Field Application Specialist (FAS) or scomix@bdscomix.bd.com.
	<p>Insufficient washes after labeling cells with Sample Tags.</p>	<p>Follow the washing steps in this protocol.</p>
	<p>BD Rhapsody™ Cartridge overloaded with cells.</p>	<p>Follow the cell loading steps in the <i>BD Rhapsody™ Single-Cell Analysis System Instrument User Guide</i>.</p>

Appendix

Oligonucleotides in BD Rhapsody™ Targeted mRNA and BD® AbSeq Amplification Kit

The following table lists the sequences of all oligonucleotides included in the BD Rhapsody™ Targeted mRNA and AbSeq Amplification Kit (Cat No. 633774).

Oligonucleotide	Use	Part/ catalog no.	Sequence (5'–3')
BD Rhapsody™ Universal Oligo	Forward primer for WTA RPE PCR, Sample Tag PCR1 and PCR2, and BD® AbSeq PCR1	650000074	ACACGACGCTCTCCGATCT
BD® AbSeq Primer	Reverse primer for BD® AbSeq PCR1	91-1086	CAGACGTGTGCTCTCCGATCT
BD Rhapsody™ Sample Tag PCR1 Primer	Reverse primer for Sample Tag PCR1	91-1088	GTTGTCAAGATGCTACCGTT
BD Rhapsody™ Sample Tag PCR2 Primer	Reverse primer for Sample Tag PCR2	91-1089	CAGACGTGTGCTCTCCGATCTGTTGTCAAGATGCTACCGTT
BD Rhapsody™ Library Forward Primer	Forward primer for WTA, Sample Tag, and BD® AbSeq Index PCR	91-1085	AATGATACGGCGACCACCGAGATCTACACTATAGCCT ACACTCTTCCCTACACGACGCTCTTCCGATC*T
BD Rhapsody™ Library Reverse Primer 1	WTA, Sample Tag, and BD® AbSeq Index PCR	650000080	CAAGCAGAAGACGGCATAACGAGATAGCGTAGCGTGA CTGGAGTTCAGACGTGTGCTCTTCCGATC*T
BD Rhapsody™ Library Reverse Primer 2		650000091	CAAGCAGAAGACGGCATAACGAGATCAGCCTCGGTGA CTGGAGTTCAGACGTGTGCTCTTCCGATC*T
BD Rhapsody™ Library Reverse Primer 3		650000092	CAAGCAGAAGACGGCATAACGAGATTGCCTCTTGTGA CTGGAGTTCAGACGTGTGCTCTTCCGATC*T
BD Rhapsody™ Library Reverse Primer 4		650000093	CAAGCAGAAGACGGCATAACGAGATTCCTCTACGTGA CTGGAGTTCAGACGTGTGCTCTTCCGATC*T

Forward index name	i5 bases for sample sheet NovaSeq, MiSeq, HiSeq 2000/2500	i5 bases for sample sheet iSeq, MiniSeq, NexSeq, HiSeq 3000/4000
BD Rhapsody™ Library Forward Primer	TATAGCCT	AGGCTATA

Reverse index name	i7 bases for sample sheet
BD Rhapsody™ Library Reverse Primer 1 (N709)	GCTACGCT
BD Rhapsody™ Library Reverse Primer 2 (N710)	CGAGGCTG
BD Rhapsody™ Library Reverse Primer 3 (N711)	AAGAGGCA
BD Rhapsody™ Library Reverse Primer 4 (N712)	GTAGAGGA

BD® OMICS-One Dual Index Kit sequences

Forward index name	i5 bases for sample sheet NovaSeq, MiSeq, HiSeq 2000/2500	i5 bases for sample sheet iSeq, MiniSeq, NexSeq, HiSeq 3000/4000
Dual index forward primer 1	TATAGCCT	AGGCTATA
Dual index forward primer 2	ATAGAGGC	GCCTCTAT
Dual index forward primer 3	CCTATCCT	AGGATAGG
Dual index forward primer 4	GGCTCTGA	TCAGAGCC
Dual index forward primer 5	AGGCGAAG	CTTCGCCT
Dual index forward primer 6	TAATCTTA	TAAGATTA
Dual Index Forward Primer 7	CAGGACGT	ACGTCCTG
Dual Index Forward Primer 8	GTACTGAC	GTCAGTAC

Reverse index name	i7 bases for sample sheet
Dual index reverse primer 1	ATTACTCG
Dual index reverse primer 2	TCCGGAGA
Dual index reverse primer 3	CGCTCATT
Dual index reverse primer 4	GAGATTCC
Dual index reverse primer 5	ATTCAGAA
Dual index reverse primer 6	GAATTCGT
Dual index reverse primer 7	CTGAAGCT
Dual index reverse primer 8	TAATGCGC

Sample Tag sequences

Human Sample Tag sequences

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, with the Sample Tag sequence between them:

- GTTGTCAAGATGCTACCGTTCAGAG(**Sample Tag sequence**)AAAAAAAAAAAAAAAAAAAAAAAAAAAA

Sample Tag	Sample Tag sequence
Sample Tag 1–Human	ATTCAAGGGCAGCCGCGTCACGATTGGATACGACTGTTGGACCGG
Sample Tag 2–Human	TGGATGGGATAAGTGCCTGATGGACCGAAGGGACCTCGTGGCCGG
Sample Tag 3–Human	CGGCTCGTGCTGCGTCGTCTCAAGTCCAGAACTCCGTGTATCCT
Sample Tag 4–Human	ATTGGGAGGCTTTCGTACCGCTGCCGCCACCAGGTGATACCCGCT
Sample Tag 5–Human	CTCCCTGGTGTTC AATACCCGATGTGGTGGGCAGAATGTGGCTGG
Sample Tag 6–Human	TTACCCGCAGGAAGACGTATACCCCTCGTGCCAGGCGACCAATGC
Sample Tag 7–Human	TGTCTACGTGCGACCGCAAGAAGTGAGTCAGAGGCTGCACGCTGT
Sample Tag 8–Human	CCCCACCAGGTTGCTTTGTCGGACGAGCCCGCACAGCGCTAGGAT
Sample Tag 9–Human	GTGATCCGCGCAGGCACACATACCGACTCAGATGGGTTGTCCAGG
Sample Tag 10–Human	GCAGCCGGCGTCGTACGAGGCACAGCGGAGACTAGATGAGGCCCC
Sample Tag 11–Human	CGCGTCCAATTTCCGAAGCCCCGCCCTAGGAGTCCCCTGCGTGC
Sample Tag 12–Human	GCCCATTCATTGCACCCGCCAGTGATCGACCCTAGTGGAGCTAAG

Mouse Immune Sample Tag sequences

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, with the Sample Tag sequence between them:

- GTTGTCAAGATGCTACCGTTCAGAG(**Sample Tag sequence**)AAAAAAAAAAAAAAAAAAAAAAAAAAAA

Sample Tag	Sample Tag sequence
Sample Tag 1–Mouse Immune	AAGAGTCGACTGCCATGTCCCCTCCGCGGGTCCGTGCCCCCAAG
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	ACCGGAGGCGTGTGTACGTGCGTTTCGAATCCTGTAAGCCCACC
Sample Tag 8–Mouse Immune	TCGCTGCCGTGCTTCATTGTCGCCGTTCTAACCTCCGATGTCTCG
Sample Tag 9–Mouse Immune	GCCTACCCGCTATGCTCGTCGGCTGGTTAGAGTTTACTGCACGCC
Sample Tag 10–Mouse Immune	TCCCATTGCAATCACGAGGCCGGGTGCGTTCTCCTATGCAATCCC
Sample Tag 11–Mouse Immune	GGTTGGCTCAGAGGCCCCAGGCTGCGGACGTCGTCGGACTCGCGT
Sample Tag 12–Mouse Immune	CTGGGTGCCTGGTCGGGTTACGTCGGCCCTCGGGTCGCGAAGGTC

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, with the Sample Tag sequence between them:

- GTTGTCAAGATGCTACCGTTCAGAG(**Sample Tag sequence**)AAAAAAAAAAAAAAAAAAAAAAAAAAAA

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



Not for use together with Hu SMK Tags 1–6 (Catalog No. 633781) in the same experiment.

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	TGGATGGGATAAGTGCCTGATGGACCGAAGGGACCTCGTGGCCGG	Barcode sequence is the same as human SMK Sample Tag 2
Sample Tag 3–Flex	CGGCTCGTGCTGCGTCGTCTCAAGTCCAGAACTCCGTGTATCCT	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 (Catalog No. 633850)

Not for use together with Hu SMK Tags 7–12 (Catalog No. 633781) in the same experiment.

Sample Tag	Sample Tag sequence	Notes
Sample Tag 7–Flex	TGTCTACGTCCGACCGCAAGAAGTGAGTCAGAGGCTGCACGCTGT	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	CGCGTCCAATTTCCGAAGCCCCGCCCTAGGAGTCCCCTGCGTGC	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 (Catalog No. 633851)



Not for use together with Ms SMK Tags 1–6 (Catalog No. 633793) in the same experiment.

Sample Tag	Sample Tag sequence	Notes
Sample Tag 13–Flex	AAGAGTCGACTGCCATGTCCCCTCCGCGGGTCCGTGCCCCCAAG	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	AGGAGGCCCGCGTGAGAGTGATCAATCCAGGATACATTCCCGTC	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	GGCAAGGTGTCACATTGGGCTACCGCGGGAGGTGACCCAGATCCT	Barcode sequence is the same as mouse SMK Sample Tag 5
Sample Tag 18–Flex	GCGGGCACAGCGGCTAGGGTGTCCGGGTGGACCATGGTTCAGGC	Barcode sequence is the same as mouse SMK Sample Tag 6

BD[®] Flex Single-Cell Multiplexing Kit D (Catalog No. 633852)

Not for use together with Ms SMK Tags 7–12 (Catalog No. 633793) in the same experiment.

Sample Tag	Sample Tag sequence	Notes
Sample Tag 19–Flex	ACCGGAGGCGTGTGTACGTGCGTTTCGAATCCTGTAAGCCCACC	Barcode sequence is the same as mouse SMK Sample Tag 7
Sample Tag 20–Flex	TCGCTGCCGTGCTTCATTGTGCGCCGTCTAACCTCCGATGTCTCG	Barcode sequence is the same as mouse SMK Sample Tag 8
Sample Tag 21–Flex	GCCTACCCGCTATGCTCGTGGCTGGTTAGAGTTTACTGCACGCC	Barcode sequence is the same as mouse SMK Sample Tag 9
Sample Tag 22–Flex	TCCCATTGAATCACGAGGCCGGGTGCGTTCTCCTATGCAATCCC	Barcode sequence is the same as mouse SMK Sample Tag 10
Sample Tag 23–Flex	GGTTGGCTCAGAGGCCCCAGGCTGCGGACGTCGCGGACTCGCGT	Barcode sequence is the same as mouse SMK Sample Tag 11
Sample Tag 24–Flex	CTGGGTGCCTGGTCGGGTTACGTGCGCCCTCGGGTCGCGAAGGTC	Barcode sequence is the same as mouse SMK Sample Tag 12

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