BD Rhapsody™ System

mRNA Whole Transcriptome Analysis (WTA), AbSeq, and Sample Tag Library Preparation Protocol

For Research Use Only

23-24120(01)
2021-12

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Regulatory Information

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History

Revision	Date	Change made
23-24120(01)	2021-12	Initial release

Contents

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Introduction

This protocol provides instructions on creating single-cell whole transcriptome mRNA, AbSeq, and Sample Tag libraries after cell capture on 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* (Doc ID 214062) or the *BD Rhapsody™ Express Single-Cell Analysis System Instrument User Guide* (Doc ID 214063).

The cDNA of mRNA and AbSeq targets is first encoded on BD Rhapsody™ Enhanced Cell Capture Beads (PN 700027881), as described in the instrument user guides. At the same time, the barcode information from BD Rhapsody™ Enhanced Cell Capture Beads is also added to AbOligos during reverse transcription, which enables amplification of the AbOligos and Sample Tags in solution. To generate the AbSeq and Sample Tag sequencing libraries, the extended AbOligos and Sample Tags are first denatured from the BD Rhapsody™ Enhanced Cell Capture Beads, which are later amplified separately through a series of PCR steps. Meanwhile, the whole transcriptome amplification library is generated directly from the BD Rhapsody™ Enhanced Cell Capture Beads using a random priming approach, followed by an index PCR step. The whole transcriptome mRNA, AbSeq, and Sample Tag libraries can be combined together for sequencing on various Illumina sequencers.

This protocol is intended to provide a method to screen RNA expression of single cells using a 3' whole transcriptome analysis (WTA) approach through the BD Rhapsody™ WTA Amplification Kit for samples that have been labeled using BD® AbSeq AbOligo reagents, as well as Sample Tags from the BD® Single Cell Multiplexing Kit. The data set generated from this protocol can be used to generate a custom panel for subsequent 3' targeted mRNA sequencing. Specifically, the protocol outlines how to generate whole transcriptome libraries for BD Rhapsody™ Enhanced Cell Capture Beads inputs between 1,000 to 20,000 resting PBMCs per sample for library generation. For BD Rhapsody™ Enhanced Cell Capture Beads inputs between 1,000 to <5,000 cells per sample, there are additional sections in the protocol, **Purifying RPE product on page 13** and **Purification of the WTA index PCR product (dual-sided cleanup) on page 29**. For cell types other than resting PBMCs, protocol optimization might be required by the user.

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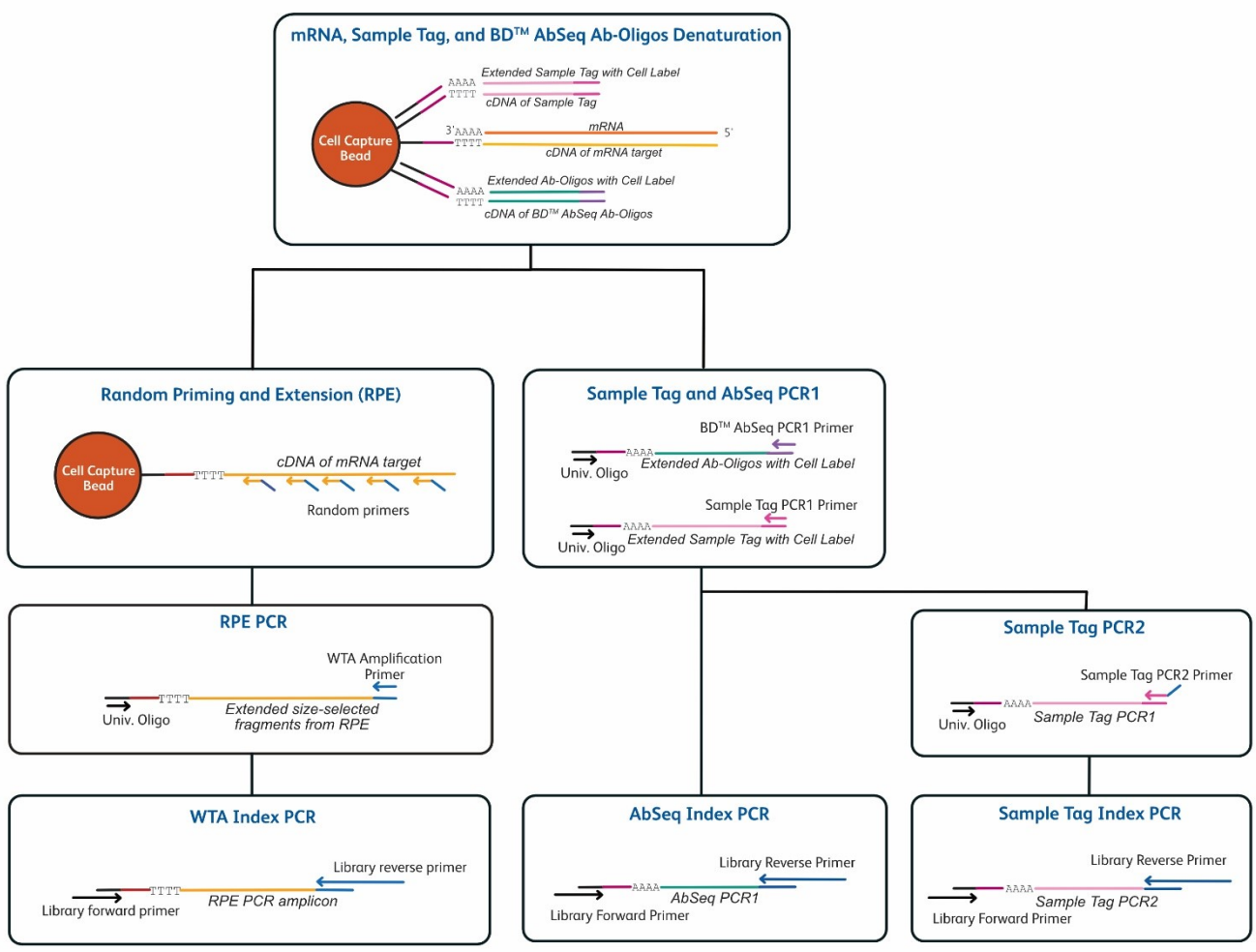
Workflow



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Required materials

- Exonuclease I-treated BD Rhapsody™ Enhanced Cell Capture Beads containing sample
- BD Rhapsody™ WTA Amplification Kit (Cat. no. 633801)

Kit component	Part number	Cap color
Nuclease-free water	650000076	Clear
WTA Extension Buffer	91-1114	Blue
WTA Extension Primers	91-1115	Blue
10 mM dNTP	650000077	Orange
Bead RT/PCR Enhancer	91-1082	Black
WTA Extension Enzyme	91-1117	Blue
PCR MasterMix	91-1118	White
Universal Oligo	650000074	White
BD® AbSeq Primer	91-1086	Green
WTA Amplification Primer	91-1116	White
Elution Buffer	91-1084	Pink
Bead Resuspension Buffer	650000066	Black
Library Forward Primer	91-1085	Red
Library Reverse Primer 1	650000080	Red
Library Reverse Primer 2	650000091	Red
Library Reverse Primer 3	650000092	Red
Library Reverse Primer 4	650000093	Red
Sample Tag PCR1 Primer	91-1088	Purple
Sample Tag PCR2 Primer	91-1089	Purple

- BD® Human Sample Multiplexing Kit (Cat. no. 633781)
- BD® AbSeq AbOligo reagents
- Agencourt® AMPure® XP magnetic beads (Beckman Coulter Life Sciences, Cat. no. A63880)
- Absolute ethyl alcohol, molecular biology grade (major supplier)
- Nuclease-free water (major supplier)

NOTE The kit provides enough to prepare the PCR MasterMix. You will need to purchase additional nuclease-free water for the AMPure purification steps.

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- 6-Tube Magnetic Separation Rack for 1.5-mL tubes (New England Biolabs, Cat. no. S1506S)
- 0.2-mL PCR strip tube magnet
- Qubit™ dsDNA HS Assay Kit (Thermo Fisher Scientific, Cat. no. Q32851)
- Agilent® DNA High Sensitivity Kit (Agilent Technologies, Cat. no. 5067-4626)

  OR

  - Agilent® High Sensitivity D5000 ScreenTape (Agilent Technologies, Cat. no. 5067-5592)
  - Agilent® High Sensitivity D5000 Reagents (Agilent Technologies, Cat. no. 5067-5593)

  OR

  - Agilent® High Sensitivity D1000 ScreenTape (Agilent Technologies, Cat. no. 5067-5584)
  - Agilent® High Sensitivity D1000 Reagents (Agilent Technologies, Cat. no. 5067-5585)

Before you begin

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

Best practices

- Use low-retention filtered pipette tips.
- When working with Enhanced Cell Capture Beads, use low-retention filtered tips and LoBind® tubes. **Never vortex the beads. Pipet-mix only.**
- Bring Agencourt AMPure XP magnetic beads to room temperature and mix thoroughly before use. See the *AMPure XP User's Guide* for information.
- Remove supernatants without disturbing the AMPure XP magnetic beads.

Additional documentation

- *BD Rhapsody™ Single-Cell Analysis System Instrument User Guide* (Doc ID 214062).
- *BD Rhapsody™ Express Single-Cell Analysis System Instrument User Guide* (Doc ID 214063).
- *BD® Single-Cell Multiomics Bioinformatics Handbook* (Doc ID 54169)

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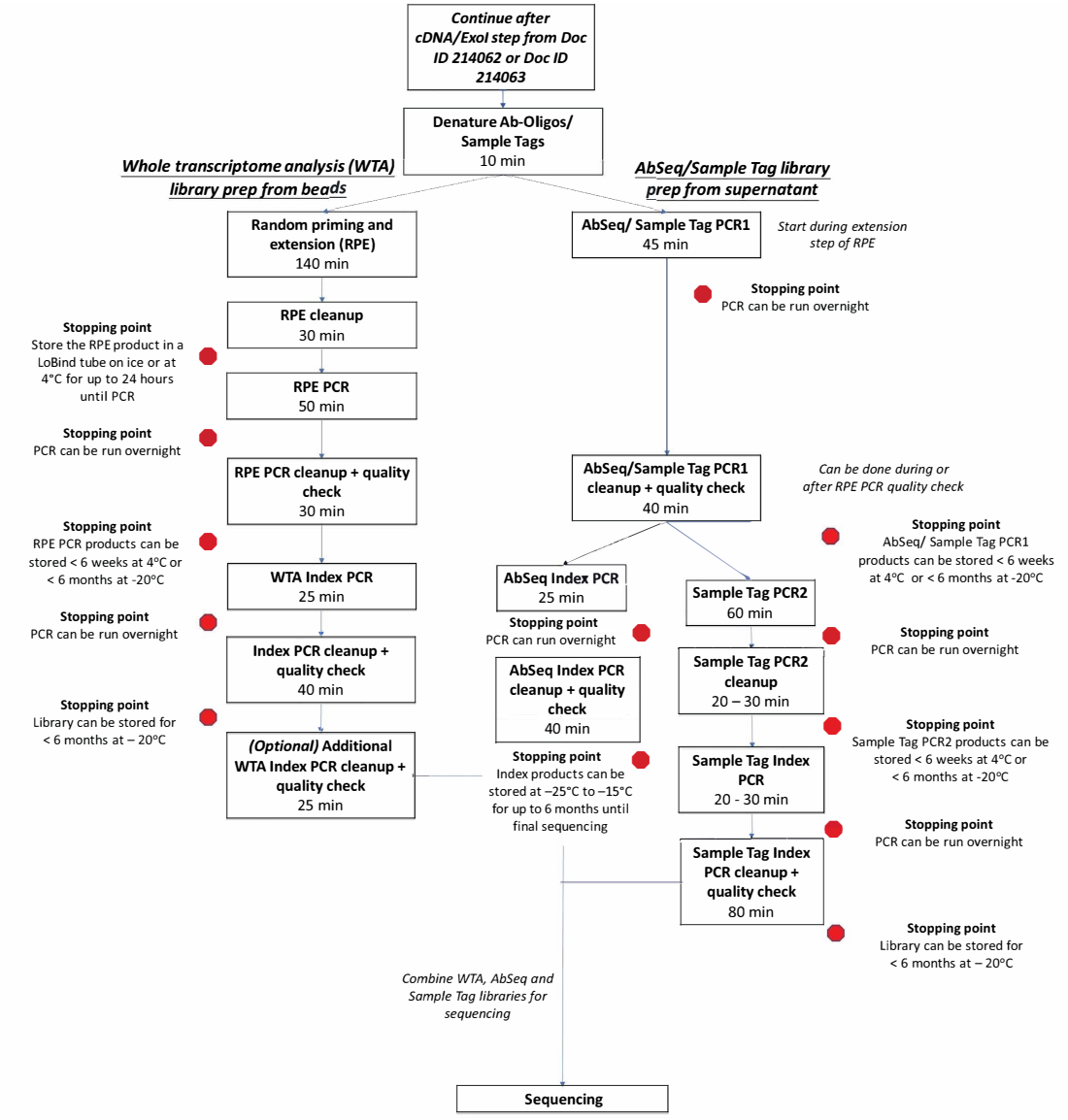
Safety information

For safety information, see the *BD Rhapsody™ Single-Cell Analysis Instrument User Guide* (Doc ID 214062) or the *BD Rhapsody™ Express Single-Cell Analysis System Instrument User Guide* (Doc ID 214063).

Time considerations



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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.

This protocol is intended for the whole transcriptome amplification library generation of cell inputs between 1,000 to 20,000 single cells, specifically resting PBMCs. There are additional sections within the protocol for cell inputs between 1,000 to 5,000 single cells. For this cell input range, follow the additional steps outlined in both **Purifying RPE product on page 13** and **Purification of the WTA index PCR product (dual-sided cleanup) on page 29**.

Please ensure that the intended total cell load is between 1,000 to 20,000 single cells for this protocol. Cell load below or above this recommendation might not be suitable for the current protocol configuration. Then proceed as described in the following procedure.

Performing random priming and extension (RPE) on BD Rhapsody™ Enhanced Cell Capture Beads with cDNA

This section describes how to generate random priming products. First, AbOligos with cell barcode and UMI information from BD Rhapsody™ Enhanced Cell Capture Beads are denatured off of the beads and saved for AbSeq/Sample Tag amplification. Then, random primers are hybridized to the cDNA on the BD Rhapsody™ Enhanced Cell Capture Beads, followed by extension with an enzyme. This random primers hybridization and extension is repeat for a second time to increase assay sensitivity.

NOTE Perform this procedure in the pre-amplification workspace.

1 Set a heat block to 95 °C, one thermomixer to 37 °C, and one thermomixer to 25 °C.

2 In a new 1.5-mL LoBind® tube, pipet the following reagents.

Random primer mix

Kit component	For 1 library (µL)	For 1 library with 20% overage (µL)	For 2 libraries with 10% overage (µL)
WTA Extension Buffer (Cat. no. 91-1114)	20	24	44
WTA Extension Primers (Cat. no. 91-1115)	20	24	44
Nuclease-free water (Cat. no. 650000076)	134	160.8	294.8
Total	**174**	**208.8**	**382.8**

3 Pipet-mix the Random Primer Mix and keep at room temperature.

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4 Choose between using the entire sample or a sub-sample of the Exonuclease I-treated BD Rhapsody™ Enhanced Cell Capture Beads. If using the entire sample of beads, skip to **step 6**. If using a sub-sample, proceed to **step 5**.

5 (Optional) Sub-sample the Exonuclease I-treated BD Rhapsody™ Enhanced Cell Capture Beads:

   a Based on the expected number of viable cells captured on the beads in the final bead resuspension volume, determine the volume of beads to sub-sample for sequencing.

   b Completely resuspend the beads by pipet-mixing, then pipet the calculated volume of the bead suspension into a new 1.5-mL LoBind® tube. If needed, bring the total volume up to 200 µL with Bead Resuspension Buffer.

   NOTE The remaining beads can be stored in Bead Resuspension Buffer at 4 °C for up to 3 months.

6 Resuspend the Exonuclease I-treated BD Rhapsody™ Enhanced Cell Capture Beads with a pipette.

7 Place the tube of Exonuclease I-treated beads in Bead Resuspension Buffer on the 1.5-mL magnet for 2 minutes. Remove the supernatant.

8 Remove the tube from the magnet and resuspend the beads in 75 µL of Elution Buffer. Pipet-mix 10 times to resuspend the beads.

9 Place the tube with the beads in a 95 °C heat block for 5 minutes (no shaking).

10 Label a new 1.5-mL tube as *AbSeq/Sample Tag products*.

11 Briefly centrifuge the tube, then place the tube on a 1.5-mL magnet for <2 minutes. Immediately remove the supernatant and transfer to the *AbSeq/Sample Tag products* tube. To minimize AbSeq/Sample Tag contamination in the WTA library, ensure that all liquid is removed from the tube. Keep the supernatant tube at 4 °C for up to 24 hours until ready to proceed to **Performing AbSeq/Sample Tag PCR1 on page 18**.

12 Remove the tube with the BD Rhapsody™ Enhanced Cell Capture Beads from the magnet, and use a low-retention tip to pipet 200 µL of Elution Buffer into the tube. Pipet-mix 10 times to resuspend the beads.

13 Briefly centrifuge the tube, then place the tube on a 1.5-mL magnet for 2 minutes. Remove and dispose of the supernatant.

14 Remove the tube with the BD Rhapsody™ Enhanced Cell Capture Beads from the magnet, and use a low-retention tip to pipet 87 µL of Random Primer Mix into the tube. Pipet-mix 10 times to resuspend the beads. Save the remaining volume of Random Primer Mix for a second RPE. Keep Random Primer Mix at room temperature.

15 Incubate the tube in the following order:

   a 95 °C in a heat block (no shaking) for 5 minutes

   b Thermomixer at 1,200 rpm and at 37 °C for 5 minutes

   c Thermomixer at 1,200 rpm and at 25 °C for 5 minutes

16 Briefly centrifuge the tube and keep it at room temperature.

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17 In a new 1.5-mL LoBind® tube, pipet the following reagents.

Primer extension enzyme mix

Kit component	For 1 library (µL)	For 1 library with 20% overage (µL)	For 2 libraries with 20% overage (µL)
10 mM dNTP (Cat. no. 650000077)	8	9.6	19.2
Bead RT/PCR Enhancer (Cat. no. 91-1082)	12	14.4	28.8
WTA Extension Enzyme (Cat. no. 91-1117)	6	7.2	14.4
Total	**26**	**31.2**	**62.4**

18 Pipet-mix the Extension Enzyme Mix.

19 Pipet 13 µL of the Extension Enzyme Mix into the sample tube containing the beads (for a total volume of 100 µL) and keep at room temperature until ready. Save the remaining volume of Primer Extension Enzyme Mix for a second RPE. Keep Primer Extension Enzyme Mix on ice.

20 Program the thermomixer.

a 1,200 rpm and at 25 °C for 10 minutes

b 1,200 rpm and at 37 °C for 15 minutes

c 1,200 rpm and at 45 °C for 10 minutes

d 1,200 rpm and at 55 °C for 10 minutes

IMPORTANT Confirm "Time Mode" is set to "Time Control" before the program begins.

21 Place the tube from **step 19** in the thermomixer. Remove the tube after the program is finished.

NOTE While the thermomixer program is running, begin AbSeq/Sample Tag PCR1. See **Performing AbSeq/ Sample Tag PCR1 on page 18**.

22 Place the tube in a 1.5-mL tube magnet and remove the supernatant.

23 Remove the tube from the magnet and resuspend the beads in 205 µL of Elution Buffer using a P200 pipette.

24 To denature the random priming products off the beads, pipet to resuspend the beads. Then:

a Incubate the sample at 95 °C in a heat block for 5 minutes (no shaking).

b Place the tube in a thermomixer at any temperature for 10 seconds at 1,200 rpm to resuspend the beads.

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25 Place the tube in a 1.5-mL tube magnet. Immediately transfer 200 µL of the supernatant containing the Random Primer Extension Product (RPE Product) to a new 1.5-mL LoBind® tube.

26 Go to **step 14 on page 11** and repeat steps 14 to 25 for a second RPE. Store supernatant containing RPE product on ice.

27 Pipet 200 µL of cold Bead Resuspension Buffer to the tube with leftover beads. Gently resuspend the beads by pipet-mixing only. Do not vortex. Store the beads at 4 °C in the pre-amplification workspace for up to 3 months.

28 Proceed immediately to **Purifying RPE product on page 13**.

Purifying RPE product

This section describes how to perform a single-sided AMPure cleanup, which removes primer dimers and other small molecular weight by-products. The final product is purified single-stranded DNA. An additional cleanup is recommended for low cell input (<5,000 cells) to ensure maximum removal of the unwanted small molecular weight products before the next PCR.

NOTE Perform the purification in the pre-amplification workspace.

1 In a new 15-mL conical tube, prepare 10 mL of fresh 80% (v/v) ethyl alcohol by pipetting 8.0 mL of absolute ethyl alcohol to 2.0 mL of nuclease-free water (from major supplier). Vortex the tube for 10 seconds.

NOTE Make fresh 80% ethyl alcohol and use within 24 hours.

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

3 Pipet 720 µL of AMPure XP magnetic beads into the tube containing the 400 µL of RPE product supernatant. Pipet-mix at least 10 times, then briefly centrifuge. If RPE sample volume is <400 µL, bring volume to 400 µL with elution buffer.

4 Incubate the suspension at room temperature for 10 minutes.

5 Place the suspension on the 1.5-mL tube magnet for 5 minutes. Remove the supernatant.

6 Keeping the tube on the magnet, gently add 1 mL of fresh 80% ethyl alcohol to the tube.

7 Incubate the sample on the magnet for 30 seconds. Remove the supernatant.

8 Repeat the 80% ethyl alcohol wash for a total of two washes.

9 Keeping the tube on the magnet, use a P20 pipette to remove and discard any residual supernatant from the tube.

10 For best results, briefly centrifuge the AMPure beads while still wet and place the tube back on the magnet. Remove any excess ethanol that may collect at the bottom. Air dry the beads at room temperature until no longer glossy (~15-20 minutes).

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11 Remove the tube from the magnet and resuspend the bead pellet in 40 µL of Elution Buffer. Pipet-mix the suspension at least 10 times until the beads are fully suspended.

12 Incubate the sample at room temperature for 2 minutes. Briefly centrifuge the tube to collect the contents at the bottom.

13 Place the tube on the magnet until the solution is clear, usually ~30 seconds.

14 Pipet the eluate (~40 µL) to a new PCR tube. This is the purified RPE product.

NOTE For samples with low cell input (eg, starting with fewer than 5,000 PBMCs), proceed to **step 15** for an additional round of AMPure XP magnetic purification.

Additional RPE purification steps for cell input <5,000 PBMC cells

15 To the tube from **step 14**, bring the purified RPE product volume up to 100 µL with nuclease-free water and transfer to a 1.5-mL LoBind® tube.

IMPORTANT It is critical for the final volume to be exactly 100 µL to achieve the appropriate size selection of the purified RPE product.

16 Pipet-mix 10 times, then briefly centrifuge.

17 Pipet 180 µL of AMPure XP magnetic beads into the tube containing 100 µL of eluted RPE product from the first round of purification.

18 Pipet-mix 10 times, then briefly centrifuge.

19 Repeat **step 4** through **step 14** once more, resulting in a total of two rounds of purification.

20 Elute into a new PCR tube (~40 µL).

STOPPING POINT: Store the RPE product in a LoBind® tube on ice or at 4 °C for up to 24 hours until PCR.

Performing RPE PCR

This section describes how to generate more RPE product through PCR amplification, so that there are multiple copies of each random-primed molecule.

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

RPE PCR mix

Kit component	For 1 library (µL)	For 1 library with 20% overage (µL)	For 2 libraries with 10% overage (µL)
PCR MasterMix (Cat. no. 91-1118)	60	72	132
Universal Oligo (Cat. no. 650000074)	10	12	22
WTA Amplification Primer (Cat. no. 91-1116)	10	12	22
Total	**80**	**96**	**176**

2 Add 80 µL of the RPE PCR Mix to the tube with the 40 µL of purified RPE product. Pipet-mix 10 times.

3 Split the RPE PCR reaction mix into two PCR tubes with 60 µL of reaction mix per tube.

4 Bring the reaction to the post-amplification workspace and run the following PCR program.

Step	Cycles	Temperature	Time
Hot start	1	95 °C	3 min
Denaturation	Refer to the following table, **Recommended number of PCR cycles**.*	95 °C	30 s
Annealing		60 °C	1 min
Extension		72 °C	1 min
Final extension	1	72 °C	2 min
Hold	1	4 °C	∞
* Suggested PCR cycles might need to be optimized for different cell types and cell number.			

Recommended number of PCR cycles

Number of cells in RPE PCR	Recommended PCR cycles for resting PBMCs
1,000–9,999	13
10,000	12
20,000	11

STOPPING POINT: PCR can run overnight.

5 When the RPE PCR reaction is complete, briefly centrifuge to collect the contents at the bottom of the tubes.

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Purification of the RPE PCR amplification product (single-sided cleanup)

This section describes how to perform a single-sided AMPure cleanup to remove unwanted small molecular weight products from the RPE products. The final product is purified double-stranded DNA (~200–2,000 bp). Note that the cleanup for WTA with AbSeq and Sample Tag is different from the cleanup for WTA performed alone, in order to minimize the AbSeq and Sample Tag signal carried over into the WTA product. If performing WTA alone, follow the cleanup outlined in *BD Rhapsody™ System mRNA Whole Transcriptome Analysis (WTA) Library Preparation Protocol* (23-21711-00).

NOTE Perform the purification in the post-amplification workspace.

1 Combine the two 60-µL RPE PCR reactions into a new 1.5-mL tube.

2 Briefly centrifuge the tube with the RPE PCR product.

IMPORTANT It is critical for the final volume to be exactly 120 µL to achieve the appropriate size selection of the purified RPE PCR product. If the volume is <120 µL, bring the volume to 120 µL with elution buffer.

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

4 Pipet 96 µL of AMPure XP magnetic beads into the tube containing 120 µL of RPE PCR product. Pipet-mix at least 10 times, then briefly centrifuge the samples. Use care to avoid getting AMPure on the lid of the tube, as residual AMPure and PCR mix buffer can negatively impact downstream results.

5 Incubate the suspension at room temperature for 5 minutes.

6 Place the suspension on the tube magnet for 3 minutes. Discard the supernatant.

7 Keeping the tube on the magnet, gently pipet 500 µL of fresh 80% ethyl alcohol to the tube.

8 Incubate the sample for 30 seconds on the magnet. Remove the supernatant.

9 Repeat the 80% ethyl alcohol wash for a total of two washes.

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

11 Air-dry the beads at room temperature for 5 minutes or until the beads no longer look glossy.

12 Remove the tube from the magnet and pipet 40 µL of Elution Buffer into the tube. Pipet-mix the suspension at least 10 times until the beads are fully suspended.

13 Incubate the sample at room temperature for 2 minutes. Briefly centrifuge the tube to collect the contents at the bottom.

14 Place the tube on the magnet until the solution is clear, usually ~30 seconds.

15 Pipet the eluate (~40 µL) into a new 1.5-mL LoBind® tube. The RPE PCR product is ready for WTA Index PCR.

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STOPPING POINT: The RPE PCR libraries can be stored at –20 °C for up to 6 months or 4 °C for up to 6 weeks.

16 Quantify and perform quality control of the RPE PCR products with a Qubit Fluorometer using the Qubit dsDNA HS Assay and either of the following systems:

- Agilent 2100 Bioanalyzer using the Agilent High Sensitivity DNA Kit

- Agilent 4200 TapeStation system using the Agilent High Sensitivity D1000 or D5000 ScreenTape assay

a The expected concentration from the Qubit Fluorometer is ~0.5 to 10 ng/µL.

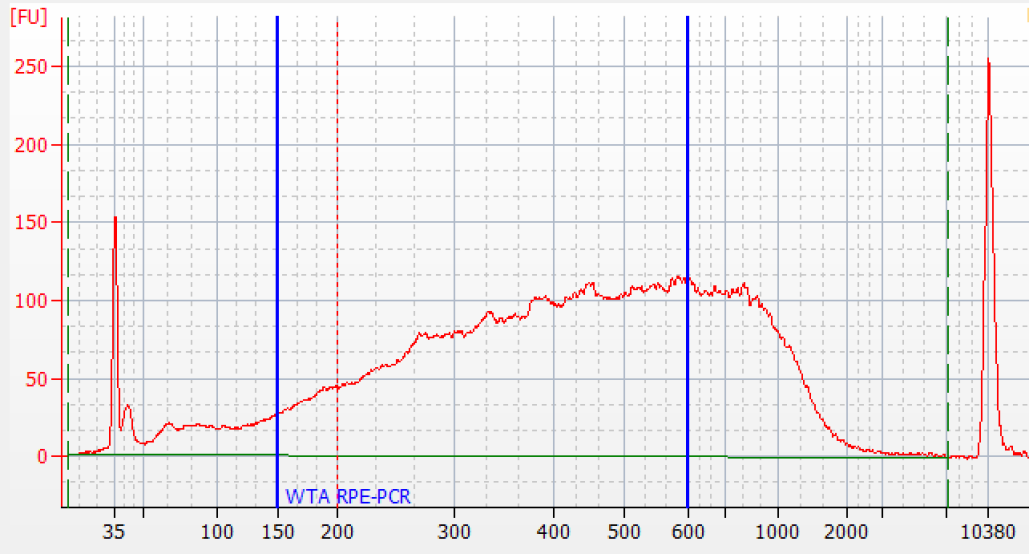
b The Bioanalyzer/TapeStation trace should show a broad peak from ~150 to 2,000 bp. Use the concentration from 200 to 600 bp to calculate how much template to add into Index PCR. Refer to the blue-boxed regions in the sample trace images on **page 17**.

The Bioanalyzer or TapeStation are used to calculate molarity for the WTA library because of the distribution in fragment sizes for this library type.

NOTE Although there are products ~170 bp (AbSeq contamination product) and >600 bp, these products should be removed in the double-sided cleanup after the next PCR.

Figure 1 RPE PCR product traces

A. Sample Bioanalyzer high-sensitivity DNA trace



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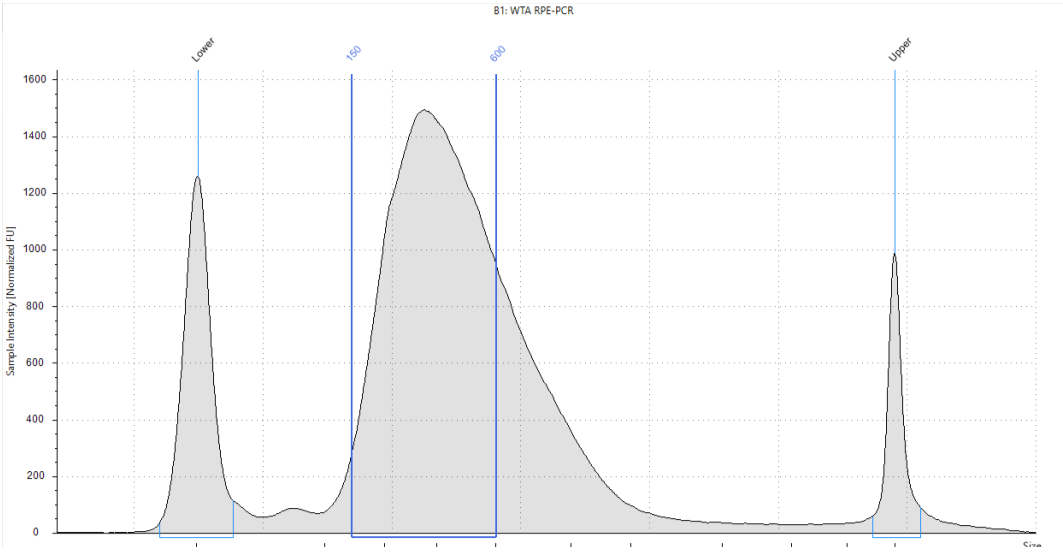
B. Sample TapeStation high-sensitivity D5000 trace



Performing AbSeq/Sample Tag PCR1

This section describes how to amplify AbSeq/Sample Tag products through PCR.

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

AbSeq/Sample Tag PCR1 reaction mix

Component	For 1 library (µL)	For 1 library with 20% overage (µL)	For 2 libraries with 10% overage (µL)
PCR MasterMix (Cat. no. 91-1118)	100	120	220
Universal Oligo (Cat. no. 650000074)	10	12	22
Sample Tag PCR1 Primer (Cat. no. 91-1088)	1	1.2	2.2
BD® AbSeq Primer (Cat. no. 91-1086)	10	12	22
Nuclease-free water (Cat. no. 650000076)	12	14.4	26.4
Total	**133**	**159.6**	**292.6**

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

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3 In a new 1.5-mL tube, pipet 133 µL of the AbSeq/Sample Tag PCR1 reaction mix. Add 67 µL of the AbSeq/Sample Tag product from **step 11** in **Performing random priming and extension (RPE) on BD Rhapsody™ Enhanced Cell Capture Beads with cDNA on page 10**. Pipet-mix 10 times. Do not vortex.

4 Pipet 50 µL AbSeq/Sample Tag reaction mix into each of four 0.2-mL PCR tubes. Transfer any residual mix to one of the tubes.

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

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

Step	Cycles	Temperature	Time
Hot start	1	95 °C	3 min
Denaturation	11–15*	95 °C	30 s
Annealing		60 °C	30 s
Extension		72 °C	1 min
Final extension	1	72 °C	5 min
Hold	1	4 °C	∞
* Suggested PCR cycles might need to be optimized for different cell types and cell number.			

Recommended number of PCR cycles

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

STOPPING POINT: The PCR can run overnight.

7 After PCR has started, proceed to **step 21** in **Performing random priming and extension (RPE) on BD Rhapsody™ Enhanced Cell Capture Beads with cDNA on page 10**.

8 After PCR, briefly centrifuge the tubes.

9 Pipet-mix and combine the four reactions into a new 1.5-mL LoBind® tube, labeled *AbSeq/Sample Tag PCR1*. Keep the tube on ice and proceed to **Purifying AbSeq/Sample Tag PCR1 products** in the following section.

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Purifying AbSeq/Sample Tag PCR1 products

This section describes how to perform a single-sided AMPure cleanup to remove primer dimers from the AbSeq/ Sample Tag PCR1 products. The final product is purified double-stranded DNA.

NOTE Perform the purification in the post-amplification workspace.

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

   NOTE Make fresh 80% ethyl alcohol, and use it within 24 hours.

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

3. Pipet 280 µL AMPure XP beads into a tube with 200 µL AbSeq PCR1 from **Performing AbSeq/Sample Tag PCR1 on page 18**. 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. Remove the supernatant.

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

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

8. Keeping the tube 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 5 minutes.

10. Remove the tube from the magnet and resuspend the bead pellet in 30 µL of Elution Buffer. Vigorously pipet-mix until the beads are uniformly dispersed. Small clumps do not affect the performance.

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

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

13. Pipet the eluate (~30 µL) into a new 1.5-mL LoBind® tube (purified AbSeq/Sample Tag PCR1 product).

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

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Quantifying BD® AbSeq/Sample Tag PCR1 products

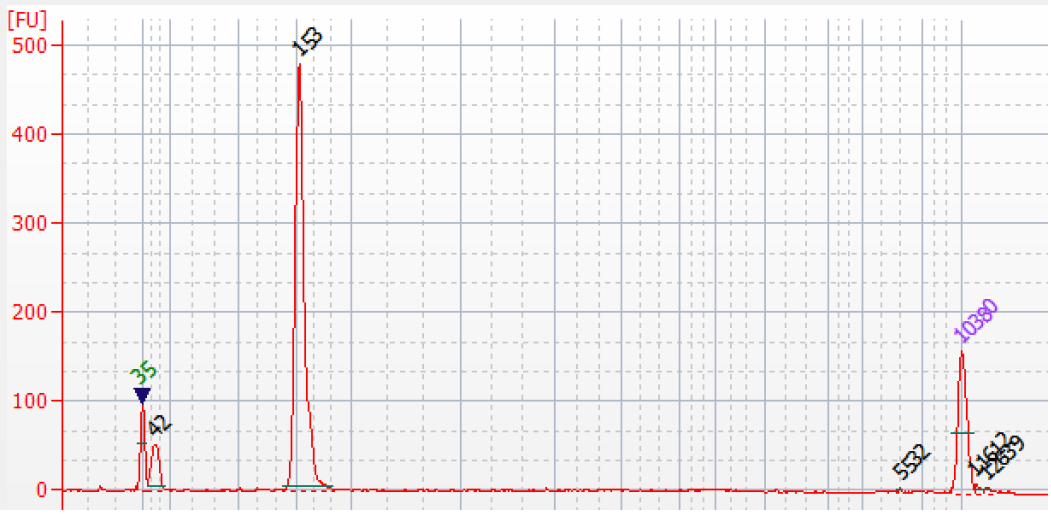
1 Measure the yield of the largest peak of the BD® AbSeq/Sample Tag PCR1 product (~153 bp) by using either the Agilent 2100 Bioanalyzer with the High Sensitivity Kit or the Agilent 4200 TapeStation system using the Agilient High Sensitivity D1000 or D5000 ScreenTape assay. Follow the manufacturer's instructions.

2 Dilute an aliquot of BD® AbSeq/Sample Tag PCR1 product to 0.1–1.1 ng/µL with Elution Buffer (Cat. no. 91-1084) before index PCR of BD® AbSeq PCR1 products. See .

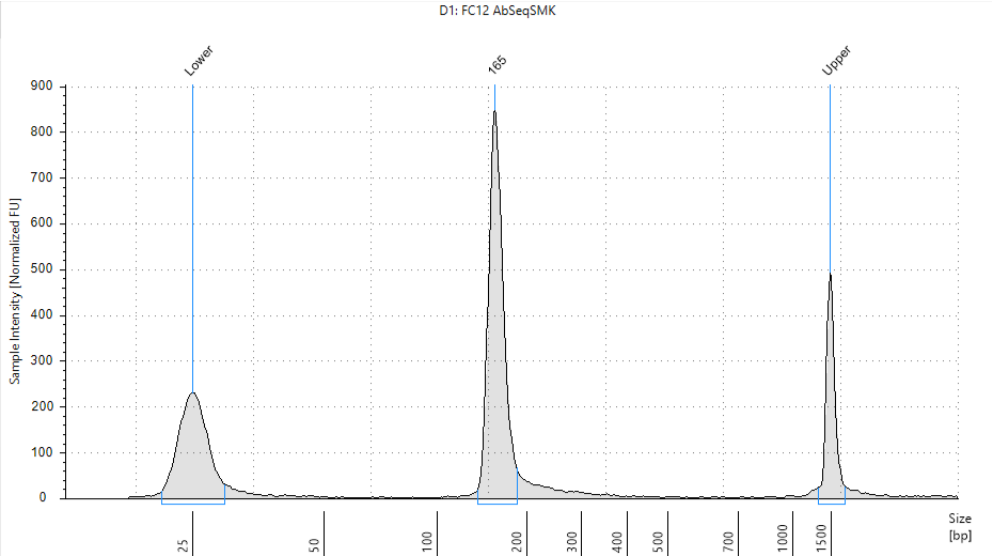
3 Use undiluted PCR1 product for Sample Tag PCR2 amplification. Refer to **Performing Sample Tag PCR2 on the AbSeq/Sample Tag PCR1 products on page 22**

Figure 2 AbSeq/Sample Tag PCR1

A. Sample Bioanalyzer high-sensitivity DNA trace



B. Sample TapeStation high-sensitivity D1000 trace



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Performing Sample Tag PCR2 on the AbSeq/Sample Tag PCR1 products

This section describes how to amplify Sample Tag products through PCR. The PCR primers include partial Illumina sequencing adapters that enable the additions of full-length Illumina sequencing indices in the next PCR.

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

Sample Tag PCR2 reaction mix

Component	For 1 library (µL)	For 1 library with 20% overage (µL)	For 2 libraries with 10% overage (µL)
PCR MasterMix (Cat. no. 91-1118)	25	30	55
Universal Oligo (Cat. no. 650000074)	2	2.4	4.4
Sample Tag PCR2 Primer (Cat. no. 91-1089)	3	3.6	6.6
Nuclease-free water (Cat. no. 650000076)	15	18	33
Total	**45**	**54**	**99**

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

3 Bring the PCR2 reaction mix to the post-amplification workspace.

4 Pipet 5.0 µL of PCR1 products into 45 µL of Sample Tag PCR2 reaction mix.

5 Gently vortex and briefly centrifuge.

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

Step	Cycles	Temperature	Time
Hot start	1	95 °C	3 min
Denaturation	10*	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	∞
* Suggested PCR cycles might need to be optimized for different cell types and cell number.			

STOPPING POINT: The PCR can run overnight.

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Purifying Sample Tag PCR2 products

This section describes how to perform a single-sided AMPure cleanup to remove primer dimers from the Sample Tag PCR2 products. The final product is purified double-stranded DNA.

NOTE Perform Sample Tag PCR2 purification in the post-amplification workspace.

1. Bring Agencourt AMPure XP beads to room temperature and vortex at high speed for 1 minute until the beads are fully resuspended.
2. To 50.0 µL of PCR2 products, pipet 90 µL of AMPure beads.
3. Pipet-mix 10 times and incubate at room temperature for 5 minutes.
4. Place the tube on the strip tube magnet for 3 minutes. Remove the supernatant.
5. Keeping the tube on the magnet, gently add 200 µL of fresh 80% ethyl alcohol to the tube and incubate for 30 seconds. Remove the supernatant.
6. Repeat **step 5** 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 the beads at room temperature for 3 minutes.
9. Remove the tube from the magnet and resuspend each bead pellet in 30 µL of Elution Buffer. Pipet-mix until the beads are fully resuspended.
10. Incubate at room temperature for 2 minutes and briefly centrifuge.
11. Place the tube on the magnet until the solution is clear, usually ~30 seconds.
12. Pipet the entire eluate (~30 µL) to a new 1.5-mL LoBind® tube (purified Sample Tag PCR2 product).

    STOPPING POINT: Store at 2 °C to 8 °C before proceeding on the same day or at –25 °C to –15 °C for up to 6 months.
13. Estimate the concentration with a Qubit Fluorometer using the Qubit dsDNA HS Assay Kit. Follow the manufacturer's instructions.
14. Dilute an aliquot of the products with Elution Buffer to 0.1–1.1 ng/µL.

Performing Sample Tag index PCR

This section describes how to generate Sample Tag libraries compatible with the Illumina sequencing platform, by adding full-length Illumina sequencing adapters and indices through PCR. For cell capture samples from multiple cartridges, the same reverse primer can be used to label all the library types from one cartridge (for example, WTA, AbSeq, and SMK from cartridge 1 can all be given reverse primer 1, while WTA, AbSeq, and SMK from cartridge

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2 can be labeled with reverse primer 2, and so on). The kit provides 4 indexing primers, and can label all sample combinations from up to 4 cartridges for the same sequencing run.

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

Sample Tag index PCR mix

Component	For 1 library (µL)	For 1 library with 20% overage (µL)	For 2 libraries with 10% overage (µL)
PCR MasterMix (Cat. no. 91-1118)	25	30	55
Library Forward Primer (Cat. no. 91-1085)	2	2.4	4.4
Library Reverse Primer 1-4* (Cat. no. 650000080, 650000091–93)	2	2.4	-
Nuclease-free water (Cat. no. 650000076)	18	21.6	39.6
Total	**47**	**56.4**	**99**
*For more than one library, use different Library Reverse Primers for each Sample Tag library.			

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

3 Bring the Sample Tag Index PCR mix to the post-amplification workspace.

4 In a new 0.2-mL PCR tube, combine Sample Tag Index PCR Mix with diluted Sample Tag PCR products as follows:

a For 1 sample, combine 47 µL of Sample Tag Index PCR Mix with 3 µL of diluted Sample Tag PCR 2 products.

b If working with multiple samples, combine 45 µL of Sample Tag Index PCR Mix with 2 µL of corresponding Library Reverse Primer and 3 µL of diluted Sample Tag PCR 2 products.

5 Pipet 3.0 µL of 0.1–1.1 ng/µL Sample Tag PCR2 product into 47.0 µL Sample Tag Index PCR mix.

6 Gently vortex, and briefly centrifuge.

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

Step	Cycles	Temperature	Time
Hot start	1	95 °C	3 min
Denaturation	Refer to the following table, **Recommended number of PCR cycles.***	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	∞
* Cycle number varies based on the concentration of the Sample Tag PCR2 product.			

Recommended number of PCR cycles

Conc. Index PCR input for Sample Tag libraries (ng/µL)	Recommended number of PCR cycles
0.5–1.1	6
0.25–0.5	7
0.1–0.25	8

STOPPING POINT: The PCR can run overnight.

Purifying Sample Tag index PCR products

This section describes how to perform a single-sided AMPure cleanup to remove primer dimers from the Sample Tag Index PCR products. The final product is purified double-stranded DNA with full-length Illumina adapter sequences.

NOTE Perform Sample Tag Index PCR purification in the post-amplification workspace.

1 Bring Agencourt AMPure XP beads to room temperature, and vortex at high speed for 1 minute until the beads are fully resuspended.

2 Briefly centrifuge the Sample Tag Index PCR product.

3 To 50.0 µL of the Sample Tag Index PCR product, add 50 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 the supernatant.

6 Keeping the tube on the magnet, gently add 200 µL of fresh 80% ethyl alcohol into the tube and incubate for 30 seconds. Remove the supernatant.

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7 Repeat **step 6** for a total of two washes.

8 Keeping the tube 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 tube from the magnet and resuspend the 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 tube on the magnet until the solution is clear, usually ~30 seconds.

13 Pipet the entire eluate (~30 µL) into a new 1.5-mL LoBind® tube (final Sample Tag sequencing library).

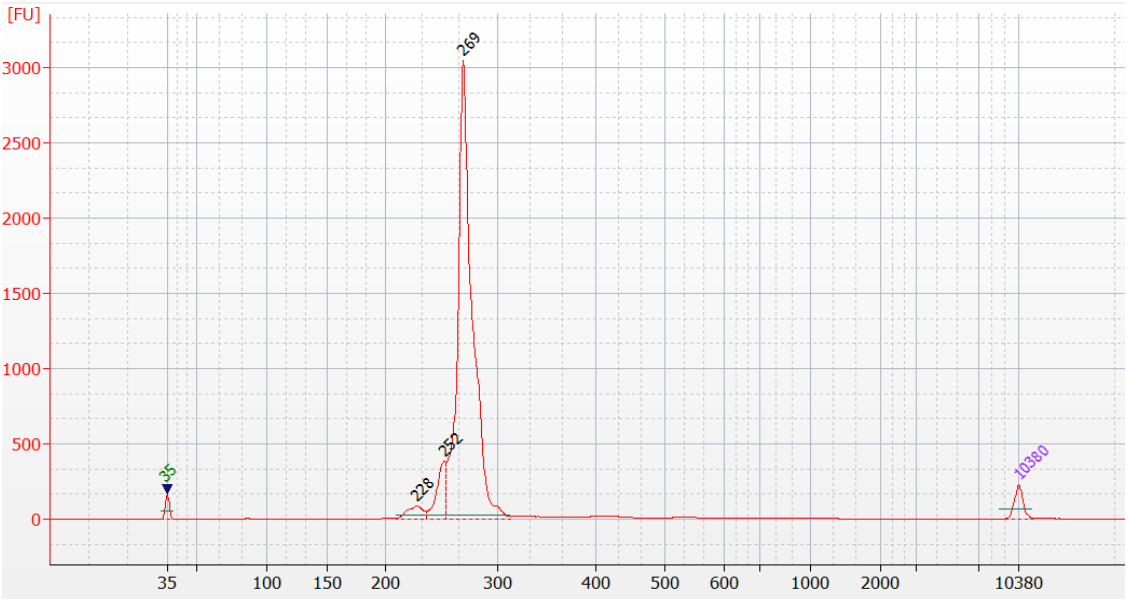
STOPPING POINT: Store at –25 °C to –15 °C for up to 6 months until sequencing.

14 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 an Agilent 4200 TapeStation system using the Agilent High Sensitivity D1000 or D5000 ScreenTape Assay. Follow the manufacturer's instructions. The expected concentration of the libraries is >1.5 ng/µL.

The Sample Tag library should show a peak of ~270 bp.

Figure 3 Sample Tag index PCR product

A. Sample Bioanalyzer high-sensitivity DNA trace



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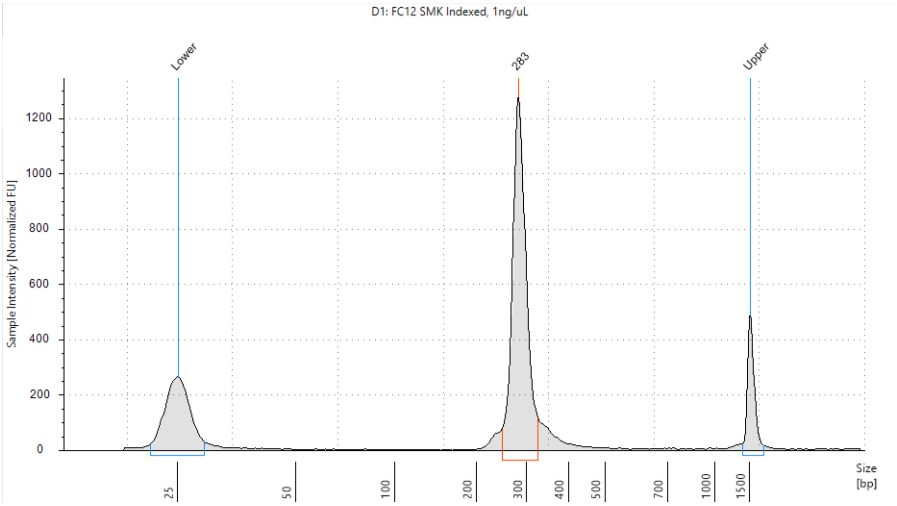
B. Sample TapeStation high-sensitivity D1000 trace



Performing WTA index PCR

This section describes how to generate mRNA libraries compatible with the Illumina sequencing platform, by adding full-length Illumina sequencing adapters and indices through PCR. For cell capture samples from multiple cartridges, the same reverse primer can be used to label all the library types from one cartridge (for example, WTA, AbSeq, and SMK from cartridge 1 can both be given reverse primer 1, while WTA, AbSeq, and SMK from cartridge 2 can be labeled with reverse primer 2, and so on). The kit provides 4 indexing primers, and can label all sample combinations from up to 4 cartridges for the same sequencing run.

NOTE Perform this procedure in the post-amplification workspace.

1 Dilute the RPE PCR products from **Purification of the RPE PCR amplification product (single-sided cleanup) on page 16** with Elution Buffer such that the concentration of the 200–600 bp peak is 2 nM. If the product concentration is <2 nM, do not dilute and continue.

For example, if the Bioanalyzer measurement of the 200–600 bp peak is 6 nM, then dilute the sample three-fold with Elution Buffer to 2 nM.

2 In a new 1.5-mL tube, pipet the following components.

WTA index PCR mix

Kit component	For 1 library (µL)	For 1 library with 20% overage (µL)	For 2 libraries with 10% overage (µL)
PCR MasterMix (Cat. no. 91-1118)	25	30	55
Library Forward Primer (Cat. no. 91-1085)	5	6	11

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WTA index PCR mix

Kit component	For 1 library (µL)	For 1 library with 20% overage (µL)	For 2 libraries with 10% overage (µL)
Library Reverse Primer (1-4)* (Cat. no. 650000080, 650000091-93)	5	6	–
Nuclease-free water (Cat. no. 650000076)	5	6	11
Total	**40**	**48**	**77**
* For more than one library, use different Library Reverse Primers for each library.			

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

4 In a new 0.2-mL PCR tube, combine WTA Index PCR Mix with diluted RPE PCR products as follows:

a For one sample, combine 40 µL of WTA Index PCR Mix with 10 µL of 2 nM of RPE PCR product.

b If working with multiple samples, in separate tubes for each sample combine 35 µL of WTA Index PCR Mix with 5 µL of corresponding Library Reverse Primer and 10 µL of 2 nM of RPE PCR products.

5 Pipet-mix 10 times.

6 Run the following PCR program.

Step	Cycles	Temperature	Time
Hot start	1	95 °C	3 min
Denaturation	Refer to the following table, **Recommended number of PCR cycles**.	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	∞
*Cycle number varies based on the concentration of the RPE PCR product.			

Recommended number of PCR cycles

Concentration of diluted RPE PCR products	Recommended number of PCR cycles
1 to <2 nM	9
2 nM	8

If the concentrations of diluted RPE PCR products are <1 nM, additional PCR cycles might be needed.

STOPPING POINT: The PCR can run overnight.

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7 When the WTA Index PCR is complete, briefly centrifuge to collect the contents at the bottom of the tubes.

Purification of the WTA index PCR product (dual-sided cleanup)

This section describes how to perform a double-sided AMPure cleanup to ensure that the library is at a proper size (~250–1,000 bp) for Illumina sequencing. The final product is purified double-stranded DNA with full-length Illumina adapter sequences.

NOTE Perform the purification in the post-amplification workspace.

1 Add 60 µL of nuclease-free water to the WTA Index PCR product for a final volume of 110 µL.

2 Transfer 100 µL of WTA Index PCR product into a new 0.2-mL PCR tube.

3 Bring AMPure XP magnetic beads to room temperature Vortex the AMPure XP magnetic beads at high speed for 1 minute. The beads should appear homogeneous and uniform in color.

4 Add 60 µL of AMPure XP magnetic beads to the 0.2-mL PCR tube from **step 2**.

5 Pipet-mix at least 10 times, then briefly centrifuge.

6 Incubate the suspensions at room temperature for 5 minutes, then place on the 0.2-mL strip tube magnet for 2 minutes.

7 Pipet 15 µL of AMPure XP magnetic beads into a different strip tube.

8 While the strip tube in **step 6** is still on the magnet, carefully, without disturbing the beads, remove and transfer the 160 µL of supernatant into the 0.2-mL strip tube with AMPure XP magnetic beads (from **step 7**) and pipet-mix 10 times.

9 Incubate the suspension at room temperature for 5 minutes, then place the new tube on a 0.2-mL tube magnet for 1 minute.

10 While on the magnet, carefully remove and appropriately discard only the supernatant without disturbing the AMPure XP magnetic beads.

11 Keeping the tubes on the magnet, gently pipet 200 µL of fresh 80% ethyl alcohol into the tube.

12 Incubate the sample for 30 seconds on the magnet.

13 While on the magnet, carefully remove and appropriately discard only the supernatant without disturbing the AMPure XP magnetic beads.

14 Repeat the 200 µL of fresh 80% ethyl alcohol wash for a total of two washes.

15 Keeping the tubes on the magnet, use a small-volume pipette to remove any residual supernatant from the tube.

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16 Leave the tube open on the magnet to dry the AMPure XP magnetic beads at room temperature for ~1 minute. Do not over-dry the AMPure XP magnetic beads.

17 Remove tube from magnet and pipet 30 µL of Elution Buffer into the tube and pipet-mix to completely resuspend the AMPure XP magnetic beads.

18 Incubate the sample at room temperature for 2 minutes.

19 Briefly centrifuge the tube to collect the contents at the bottom.

20 Place the tube on the magnet until the solution is clear, usually ~30 seconds.

21 Pipet the eluate (~30 µL) into a new 1.5-mL LoBind® tube. The WTA Index PCR eluate is the final sequencing libraries.

STOPPING POINT: The Index PCR libraries can be stored at –20 °C for up to 6 months until sequencing.

22 Quantify and perform quality control of the Index PCR libraries with a Qubit Fluorometer using the Qubit dsDNA HS Assay and either of the following systems:

- Agilent 2100 Bioanalyzer using the Agilent High Sensitivity DNA Kit

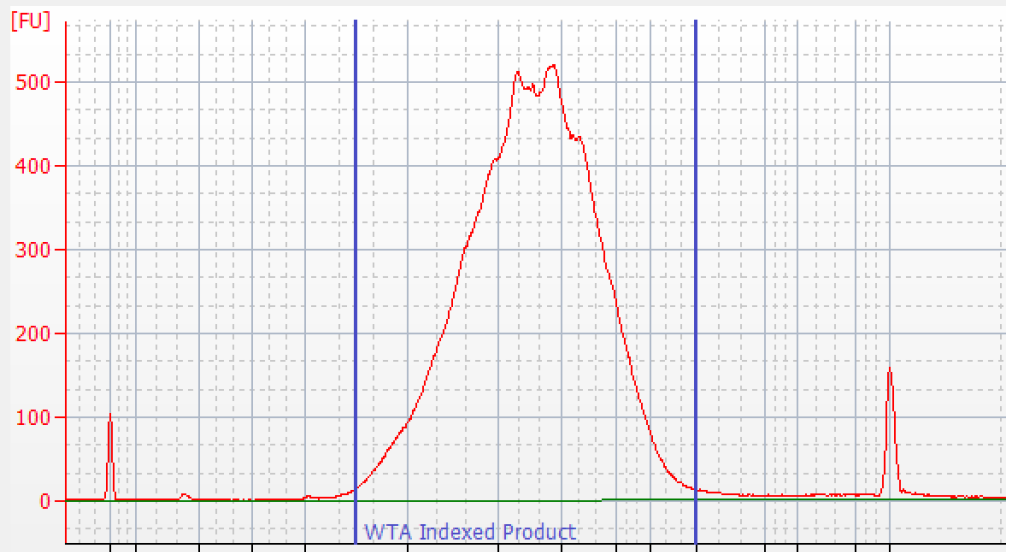
- Agilent 4200 TapeStation system using the Agilent High Sensitivity D1000 or D5000 ScreenTape assay.

a The expected concentration from the Qubit Fluorometer is >1 ng/µL.

b The Bioanalyzer/TapeStation trace should show a peak from ~250–1,000 bp. Refer to the sample trace images in the following **Figure 4**.

Figure 4 WTA Index PCR product

A. Sample Bioanalyzer high-sensitivity DNA trace



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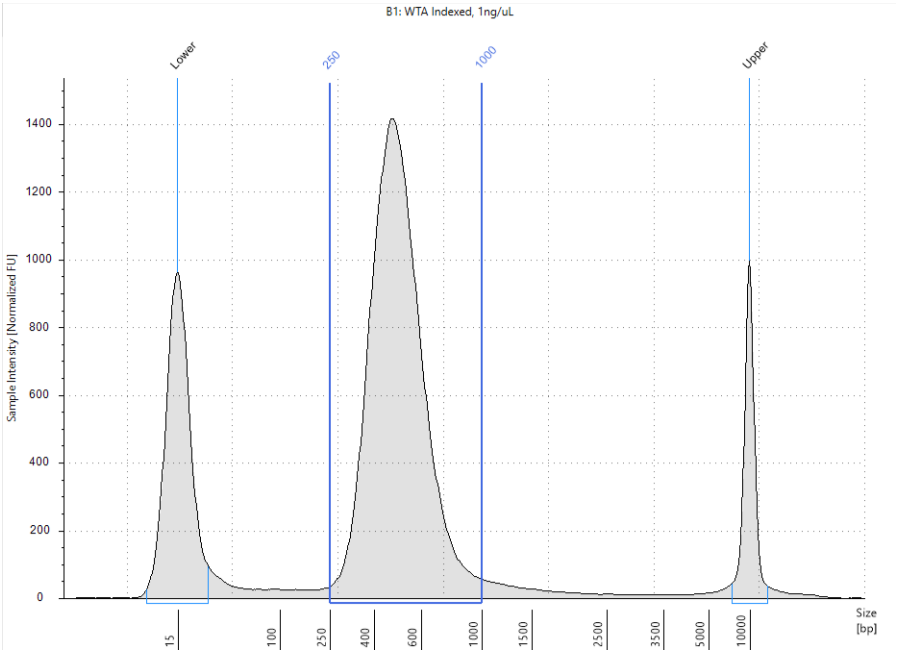
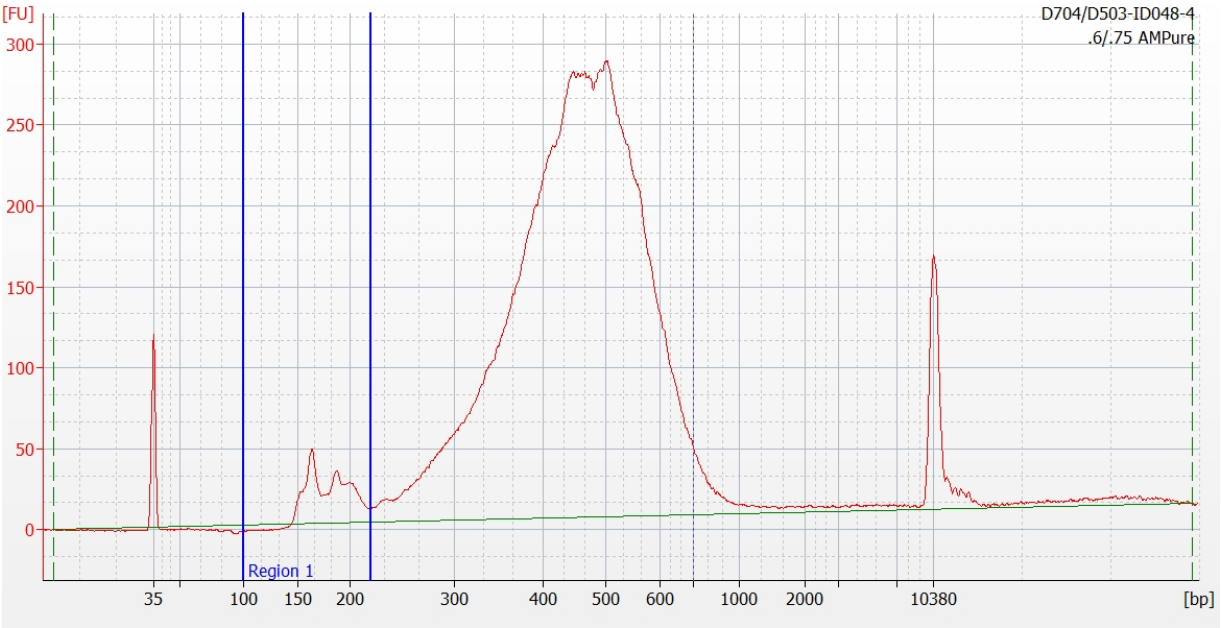
B. Sample TapeStation high-sensitivity D5000 trace



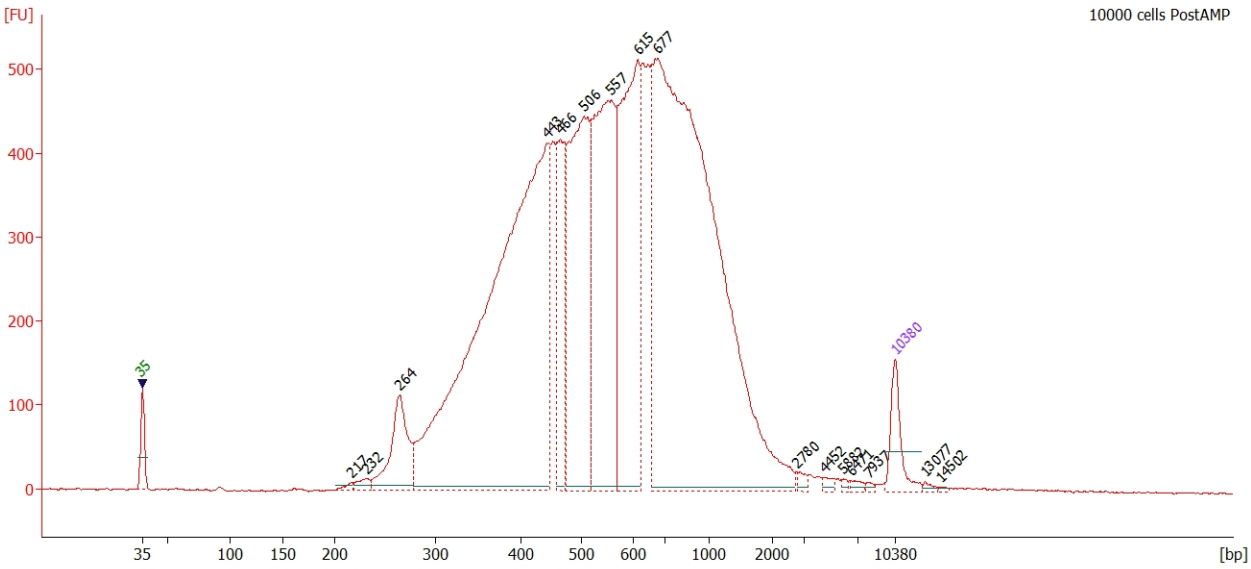
NOTE If smaller products (~165 bp or ~270 bp) are observed in **Figure 4**, such as the peaks shown in **Figure 5**, a second round of AMPure XP magnetic purification is recommended. See **Additional WTA index PCR purification steps on page 33**.

Figure 5 Sample traces of noise peaks in WTA index PCR product

A. Sample Bioanalyzer high-sensitivity DNA trace for an index PCR product with an observable peak at ~165 bp



B. Sample Bioanalyzer high-sensitivity DNA trace for an index PCR product with an observable peak at ~270 bp



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Additional WTA index PCR purification steps

If peaks at ~160–170 bp are observed from **Figure 4**, Bioanalyzer /TapeStation traces, a second round of AMPure XP magnetic purification is recommended.

1. To the tube from **step 21**, bring the total purified WTA Index PCR elute volume up to 100 µL with nuclease-free water.

   NOTE It is critical for the final volume to be exactly 100 µL to achieve the appropriate size selection of the purified WTA Index PCR library.

2. Pipet-mix 10 times, then briefly centrifuge.

3. Pipet 75 µL of AMPure XP magnetic beads into the tube containing 100 µL of eluted WTA Index product from the first round of purification.

4. Pipet-mix 10 times, then briefly centrifuge.

5. Repeat **step 9** through **step 20** beginning on **page 29** once more, resulting in a total of two rounds of purification.

6. Collect the elute (~30 µL) to a new PCR tube.

7. Repeat the quality control step ().

   STOPPING POINT: The Index PCR libraries can be stored at –20 °C for up to 6 months until sequencing.

Performing AbSeq index PCR

This section describes how to generate AbSeq libraries compatible with the Illumina sequencing platform, by adding full-length Illumina sequencing adapters and indices through PCR. For cell capture samples from multiple cartridges, the same reverse primer can be used to label all the library types from one cartridge (for example, WTA, AbSeq, and SMK from cartridge 1 can both be given reverse primer 1, while WTA, AbSeq, and SMK from cartridge 2 can be labeled with reverse primer 2, and so on). The kit provides 4 indexing primers, and can label all sample combinations from up to 4 cartridges for the same sequencing run.

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

AbSeq Index PCR mix

Kit component	For 1 library (µL)	For 1 library with 20% overage (µL)	For 1 library with 10% overage (µL)
PCR MasterMix (Cat. no. 91-1118)	25	30	55
Library Forward Primer (Cat. no. 91-1085)	2	2.4	4.4
Library Reverse Primer (1-4)* (Cat. no. 650000080, 650000091-93)	2	2.4	-
Nuclease-free water (Cat. no. 650000076)	18	21.6	39.6
Total	**47**	**56.4**	**99**
* For more than one library, use different Library Reverse Primers for each AbSeq library.			

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

3 In a new 0.2-mL PCR tube, combine AbSeq Index PCR Mix with diluted AbSeq PCR products as follows:

- **a** For 1 sample, combine 47 µL of AbSeq Index PCR Mix with 3 µL of diluted Sample Tag PCR 2 products.
- **b** If working with multiple samples, combine 45 µL of AbSeq Index PCR Mix with 2 µL of corresponding Library Reverse Primer and 3 µL of diluted AbSeq products.

4 Bring the AbSeq Index PCR mix to the post-amplification workspace.

5 Pipet 3.0 µL of 0.1–1.1 ng/µL AbSeq PCR1 product into 47 µL AbSeq Index PCR mix.

6 Gently vortex and briefly centrifuge.

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

Step	Cycles	Temperature	Time
Hot start	1	95 °C	3 min
Denaturation	Refer to the following table, **Recommended number of PCR cycles.**	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	∞
* Cycle number varies based on the concentration of the AbSeq PCR1 products.			

Recommended number of PCR cycles

Conc. index PCR input for AbSeq libraries (ng/µL)	Recommended number of PCR cycles
0.5–1.1	6
0.25–0.5	7
0.1–0.25	8

STOPPING POINT: The PCR can run overnight.

Purifying AbSeq index PCR products

This section describes how to perform a single-sided AMPure cleanup to remove primer dimers from the AbSeq Index PCR products. The final product is purified double-stranded DNA with full-length Illumina sequences.

NOTE Perform the purification in the post-amplification workspace.

1 Bring the AMPure XP beads to room temperature and vortex at high speed for 1 minute until the beads are fully resuspended.

2 Briefly centrifuge the AbSeq Index PCR products.

3 To 50 µL of AbSeq Index PCR products, pipet 40 µL of AMPure beads.

4 Pipet-mix 10 times and incubate at room temperature for 5 minutes.

5 Place each tube on the strip tube magnet for 3 minutes. Remove the supernatant.

6 Keeping the tubes on the magnet, gently add 200 µL of fresh 80% ethyl alcohol into each tube and incubate for 30 seconds. Remove the supernatant.

7 Repeat **step 6** for a total of two washes.

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

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

10 Remove the tube 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 tube on the magnet until the solution is clear, usually ~30 seconds.

13 Pipet the entire eluate (~30 µL) to a new 1.5-mL LoBind® tube. These are the final AbSeq sequencing libraries.

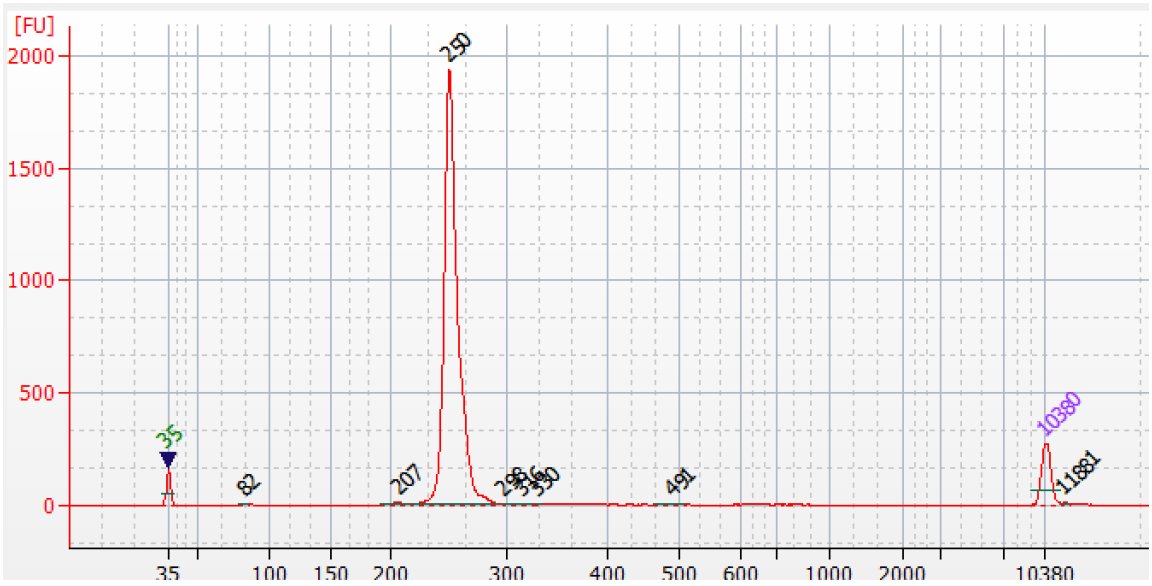
STOPPING POINT: Store at –25 °C to –15 °C for up to 6 months until final sequencing.

14 Estimate the library 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 an Agilent 4200 TapeStation system using the Agilent High Sensitivity D1000 or D5000 ScreenTape assay. Follow the manufacturer's instructions. The expected concentration of the libraries is >1.5 ng/µL.

The AbSeq library should show a peak of ~250 bp.

Figure 6 AbSeq index PCR product

A. Sample Bioanalyzer high-sensitivity DNA trace



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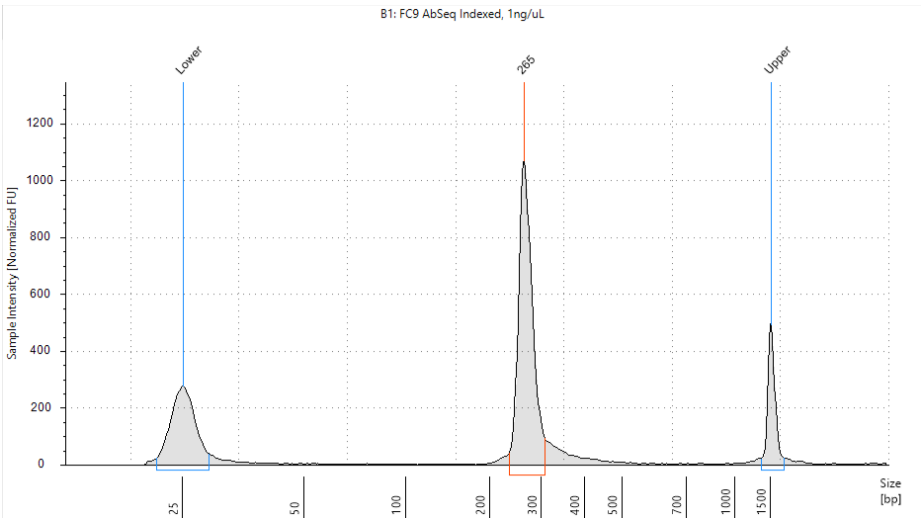
B. AbSeq TapeStation high-sensitivity D1000 trace



Sequencing

Requirements

- 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*
Paired-end reads	Recommend Read 1: 51 cycles; Read 2: 71 cycles
PhiX	1% recommended
Analysis	See the *BD® Single-Cell Multiomics Bioinformatics Handbook* (Doc ID: 54169)

a. To review Illumina index 1 (i7) sequences, see **Appendix A: Illumina index 1 (i7) sequences on page 43**.

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 1.5-1.8 pM with 1% PhiX for a sequencing run.
- Sequencing depth of the WTA mRNA libraries can vary depending on whether the sample contains high- or low-content RNA cells. For resting PBMCs, we recommend:
  - 10,000 reads per cell for shallow sequencing. Genes per cell and UMI per cell detected is generally lower but can be useful for cell type identification.
  - 50,000 reads per cell for moderate sequencing
  - 100,000 reads per cell for deep sequencing to harvest the majority of UMIs in the library
- Sequencing amount for AbSeq libraries:
  - The amount of sequencing needed for BD® AbSeq libraries will vary depending on application, BD® AbSeq panel plexy, and cell type. BD Biosciences has 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.
- Sequencing amount for Sample Tag libraries:
  - Pooling samples of the same type: 120 reads/cell; for example, combining different donor PBMCs.
  - Pooling different sample types: 600 reads/cell; for example, combining Jurkat cells with PBMCs.

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NOTE To determine the ratio of BD Rhapsody™ WTA mRNA library to AbSeq library to Sample Tag library to pool for sequencing, use the sequencing calculator available by contacting BD Biosciences technical support at 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.

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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.
	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.
No RPE-PCR product.	RPE step failed due to lack of addition of all required components.	Repeat RPE from beads again.
Low yield of RPE-PCR.	Cell number lower than expected.	Repeat RPE from beads again and increase PCR cycle number. Alternatively, repeat PCR using the RPE PCR product, for additional cycles. Alternatively, increase index cycles.
Index PCR BioAnalyzer trace of WTA library has 250 bp peak.	AbSeq library contamination in mRNA library.	If peak takes up high percentage of sequencing reads (manifests as lower reads/cell than expected for WTA library, alongside higher reads/cell than expected for AbSeq) perform a second round of AMPure purification according to **Additional WTA index PCR purification steps on page 33**.

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Observation	Possible causes	Recommended solutions
Low yield of indexing PCR.	Input DNA not high enough or cycle number too low	Repeat indexing PCR with higher cycle number. Alternatively, if RPE-PCR product was diluted before adding to indexing PCR, repeat indexing PCR with less or no dilution.
Index PCR BioAnalyzer trace of WTA library shows large amount of product larger than 600 bp.	Over-amplification during indexing PCR	Repeat indexing PCR with lower cycle number. Alternatively, repeat indexing PCR with diluted RPE-PCR product.
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 Agilent 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 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/ 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.
Lower number of reads/cell than expected from mRNA.	250 bp or ~150 bp products taking reads from mRNA library.	If noise peak is seen in the 250 bp or ~150 bp range, perform a second round of AMPure purification according to **Additional WTA index PCR purification steps on page 33**.

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Observation	Possible causes	Recommended solutions
Expected size of Sample Tag products is too short (<280 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 **Performing Sample Tag PCR2 on the AbSeq/Sample Tag PCR1 products on page 22**. Analyze products using the Agilent BioAnalyzer or the Agilent TapeStation and look for a ~165bp peak that corresponds to Sample Tag PCR2 products. Note that a ~150 bp peak might be present that corresponds to BD® AbSeq products. If the ~165 bp peak is observed, proceed to index PCR. If the ~165 bp peak is not observed, contact BD Biosciences technical support at 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 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.
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 of Sample Tag library. If issue persists, contact BD Biosciences technical support at 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 guide.

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Appendix A: Illumina index 1 (i7) sequences

Library Reverse Primer	Sequence
1	GCTACGCT
2	CGAGGCTG
3	AAGAGGCA
4	GTAGAGGA

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