

BD Rhapsody™ System

mRNA Whole Transcriptome Analysis (WTA) Library Preparation Protocol

For Research Use Only

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Becton, Dickinson and Company
BD Biosciences
2350 Qume Drive
San Jose, CA 95131 USA
Tel 1.877.232.8995

bdbiosciences.com
scomix@bdscomix.bd.com

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Regulatory Information

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

History

| Revision | Date | Change made |
|-------------|--------|-----------------|
| 23-21711-00 | 7/2019 | Initial release |

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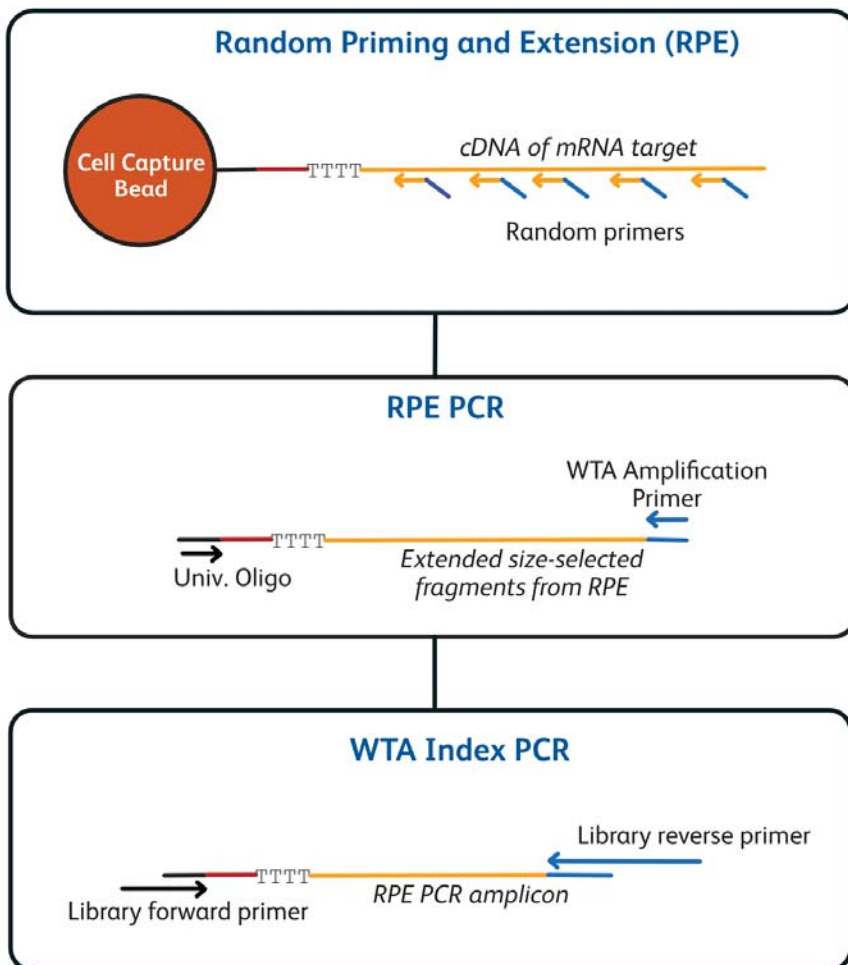
Introduction

This protocol provides instructions on creating a single cell whole transcriptome mRNA library 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 targets is first encoded on BD Rhapsody™ Cell Capture Beads as described in the instrument user guides. This protocol then continues from that point to generate a whole transcriptome amplification library by employing a random priming approach, followed by an index PCR step. The generated library can be sequenced 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. 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 Cell Capture Beads inputs between 1,000 to 10,000 resting PBMCs per sample for library generation. For BD Rhapsody 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 12](#) and [Purification of the WTA Index PCR product \(dual-sided cleanup\) on page 19](#). The procedure described herein is currently not compatible with the BD™ AbSeq assay. For a workflow showing WTA library preparation with the Sample Multiplexing Kit, see *BD Rhapsody™ mRNA Whole Transcriptome Analysis (WTA) and Sample Tag Library Preparation Protocol* (23-21647-00). For cell types other than resting PBMCs, protocol optimization might be required by the user.

Workflow



Required materials

- Exonuclease I-treated 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 |

- 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 MasterMixes. You will need to purchase additional nuclease-free water for the AMPure purification steps.

- 6-Tube Magnetic Separation Rack for 1.5- mL tubes (New England Biolabs, Cat. No. S1506S)

- 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 RhapsodyCell 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 BD Rhapsody Cell Capture Beads, use low-retention filtered tips and LoBind Tubes. **Never vortex the beads. Pipet-mix only.**
- Bring AMPure XP magnetic beads to room temperature before use.
- Remove supernatants without disturbing AMPure XP magnetic beads.

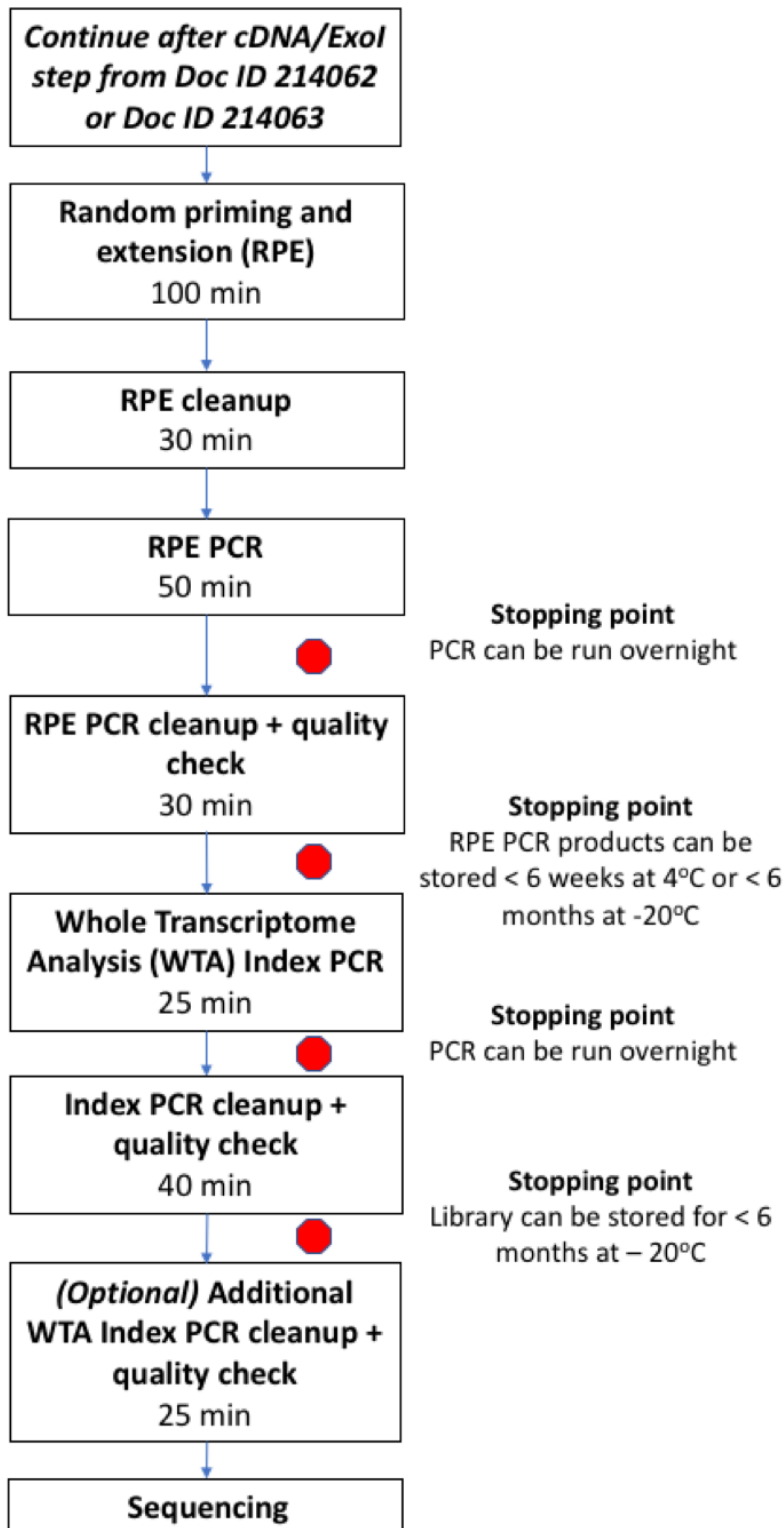
Additional documentation

- *BD Rhapsody™ Single-Cell Analysis System Instrument User Guide* (Doc ID 214062)
- *BD Rhapsody™ Express Single-Cell Analysis System Instrument User Guide* (Doc ID 214063)

Safety information

For 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).

Time Considerations



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 10,000 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 12](#) and [Purification of the WTA Index PCR product \(dual-sided cleanup\) on page 19](#).

Please ensure that the intended total cell load is between 1,000 to 10,000 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 Cell Capture Beads with cDNA

This section describes how to generate random priming products. First, random primers are hybridized to the cDNA on the Cell Capture beads, then extended with an enzyme.

NOTE This section should be performed 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.
- 4 Choose between using the entire sample or a subsample of the Exonuclease I-treated BD Rhapsody Cell Capture Beads. If using the entire sample of Exonuclease I-treated beads, skip to [step 6](#). If using a subsample, proceed to [step 5](#).

- 5** (Optional) Subsample the Exonuclease I-treated BD Rhapsody Cell Capture Beads:
- Based on the expected number of viable cells captured on beads in the final bead-resuspension volume, determine the volume of beads to subsample for sequencing.
 - Completely resuspend the beads by pipet-mixing, then pipet the calculated volume of bead suspension into a new 1.5-mL LoBind tube. If needed, bring the total volume up to 200 μ L 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 beads with a pipette.
- 7** Place the tube with beads in a 95°C heat block for 5 minutes (no shaking).
- 8** Afterwards, briefly centrifuge the tube, then immediately place the tube in the 1.5-mL magnetic separation rack. Remove and discard the supernatant. Avoid drying out the BD Rhapsody Cell Capture Beads.
- 9** Remove the tube from the magnet, and use a low-retention tip to pipet 174 μ L of Random Primer Mix into the tube. Pipet-mix 10 times to resuspend the beads.
- 10** Incubate the tube in the following order:
- a 95° 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 15 minutes
- 11** Briefly centrifuge the tube and keep it at room temperature.
- 12** In a new 1.5-mL LoBind tube, pipet the following reagents:

Primer Extension Enzyme Mix

| Kit component | For 1 library (μ L) | For 1 library with 50% overage (μ L) | For 2 libraries with 30% overage (μ L) |
|---|--------------------------|---|---|
| 10 mM dNTP (Cat. No. 650000077) | 8 | 12 | 20 |
| Bead RT/PCR Enhancer (Cat. No. 91-1082) | 12 | 18 | 31 |
| WTA Extension Enzyme (Cat. No. 91-1117) | 6 | 9 | 16 |
| Total | 26 | 39 | 67 |

- 13** Pipet-mix the Primer Extension Enzyme Mix.
- 14** Pipet 26 μ L of the Primer Extension Enzyme Mix into the sample tube containing the beads (for a total volume of 200 μ L) and keep at room temperature until ready.

- 15 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 Set the ramp rates at maximal and set “Time Mode” to “Temp Control” before the program begins.

- 16 Place the tube from [step 14](#) in the thermomixer. Start the program set in [step 15](#).
- 17 Place the tube in a 1.5-mL tube magnet and remove the supernatant.
- 18 Remove the tube from the magnet and resuspend the beads in 205 µL of Elution Buffer using a P200 pipette.
- 19 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.
- 20 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.
- 21 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 for up to 3 months in the pre-amplification workspace. Immediately proceed to [Purifying RPE product](#) in the following section.

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 (<5000 cells) to ensure maximum removal of the unwanted small molecular weight products before the next PCR.

NOTE This section should be performed 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 (15°C to 25°C). Vortex the AMPure XP magnetic beads at high speed for 1 minute until the beads are fully resuspended.

- 3 Pipet 360 μL of AMPure XP magnetic beads into the tube containing the 200 μL of RPE Product supernatant. Pipet-mix at least 10 times, then briefly centrifuge.
- 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 Air-dry the beads at room temperature for 5 minutes or until the beads no longer look glossy.
- 11 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.
- 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 \sim 30 seconds.
- 14 Pipet the eluate (\sim 40 μL) to a new PCR tube. This is the purified RPE product.

NOTE For samples with low cell input, e.g. 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.

NOTE It is critical for the final volume to be exactly 100 μL to achieve the desired 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 (\sim 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.

- 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 is based on resting PBMCs only.

Recommended number of PCR cycles

| Number of cells in RPE PCR | Suggested PCR cycles for resting PBMCs |
|----------------------------|--|
| 1,000–9,999 | 13 |
| 10,000 | 12 |

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

STOPPING POINT: The PCR can run overnight.

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. The final product is purified double-stranded DNA.

NOTE Perform the purification in the post-amplification workspace.

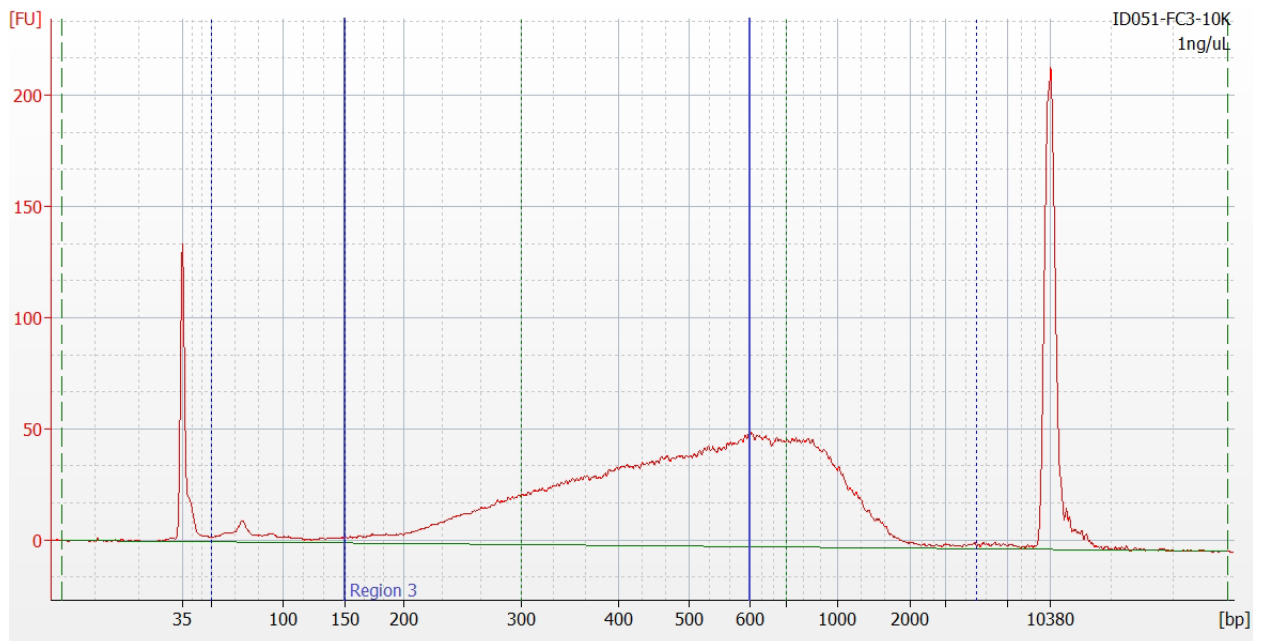
- 1 Combine the two RPE PCR reactions into a new 0.2-mL PCR tube.
- 2 Briefly centrifuge the tubes with the RPE PCR product.
- 3 Bring AMPure XP magnetic beads to room temperature (15°C to 25°C). Vortex the AMPure XP magnetic beads at high speed for 1 minute until the beads are fully resuspended.
- 4 Pipet 120 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.
- 5 Incubate the suspension at room temperature for 5 minutes.
- 6 Place the suspension on the strip tube magnet for 3 minutes. Discard the supernatant.
- 7 Keeping the tubes on the magnet, gently pipet 200 µL of fresh 80% ethyl alcohol to the tube.
- 8 Incubate the samples 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 tubes 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 beads are fully suspended.
- 13 Incubate the samples at room temperature for 2 minutes. Briefly centrifuge the tubes to collect the contents at the bottom.

- 14** Place the tubes on the magnet until the solution is clear, usually ~30 seconds.
- 15** Pipet the eluate (~40 μL) into new 1.5-mL LoBind tubes. The RPE PCR product is ready for Index PCR.
- 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 D5000 ScreenTape Assay
- a** The expected concentration from the Qubit Fluorometer is ~0.5 to 10 $\text{ng}/\mu\text{L}$.
- b** The Bioanalyzer/TapeStation trace should show a broad peak from ~200 to 2,000 bp. Use the concentration from 150 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 16](#).

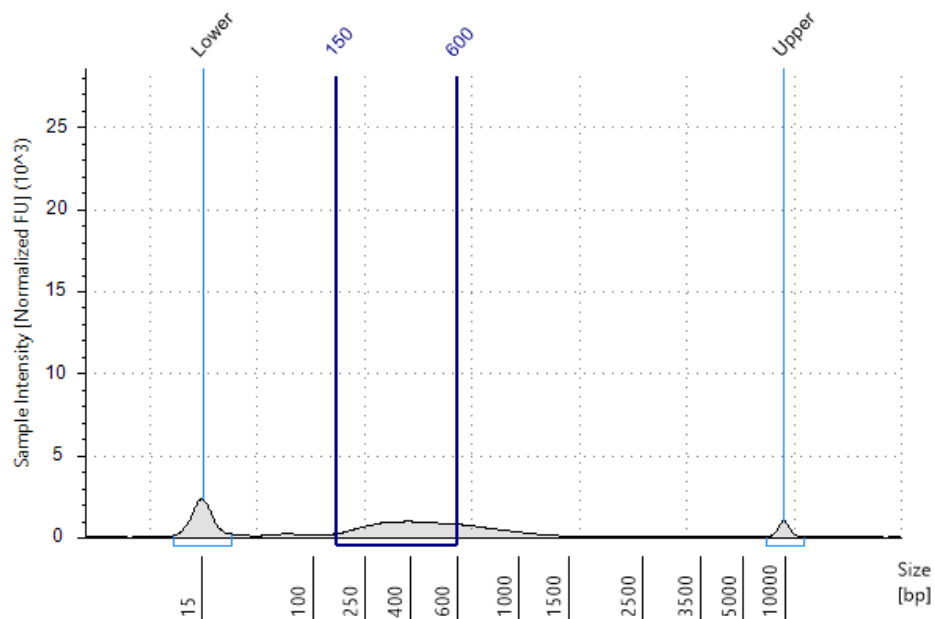
NOTE Although there are products >600 bp, these products should be removed in the double-sided cleanup after the next PCR.

Figure 1 RPE PCR product traces

A. Sample Bioanalyzer High Sensitivity DNA trace



B. Sample TapeStation High Sensitivity D5000 trace



Performing WTA Index PCR

This section describes how to generate libraries compatible with the Illumina sequencing platform, by adding full-length Illumina sequencing adapters and indices through PCR.

NOTE This section should be performed in the post-amplification workspace.

- 1 Dilute the RPE PCR products with Elution Buffer such that the concentration of the 150–600 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 150–600 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 |
| *Library Reverse Primer (1-4) (Cat. Nos. 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 1 sample, combine 40 µL of WTA Index PCR Mix with 10 µL of 2 nM of RPE PCR products.
 - b** For multiple samples, combine 35 µL of WTA Index PCR Mix with 5 µL of Library Reverse Primer and 10 µL of 2 nM 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 | ∞ |

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.

- 1 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 μ L of nuclease-free water to the WTA Index PCR product for a final volume of 110 μ L.
- 2 Transfer 100 μ L of WTA Index PCR product into a new 0.2-mL PCR tube.
- 3 Bring AMPure XP magnetic beads to room temperature (15°C to 25°C). Vortex the AMPure XP magnetic beads at high speed for 1 minute. The beads should appear homogeneous and uniform in color.
- 4 Add 60 μ L 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 the samples.
- 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 μ L 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 μ L 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 μ L of fresh 80% ethyl alcohol into the tubes.

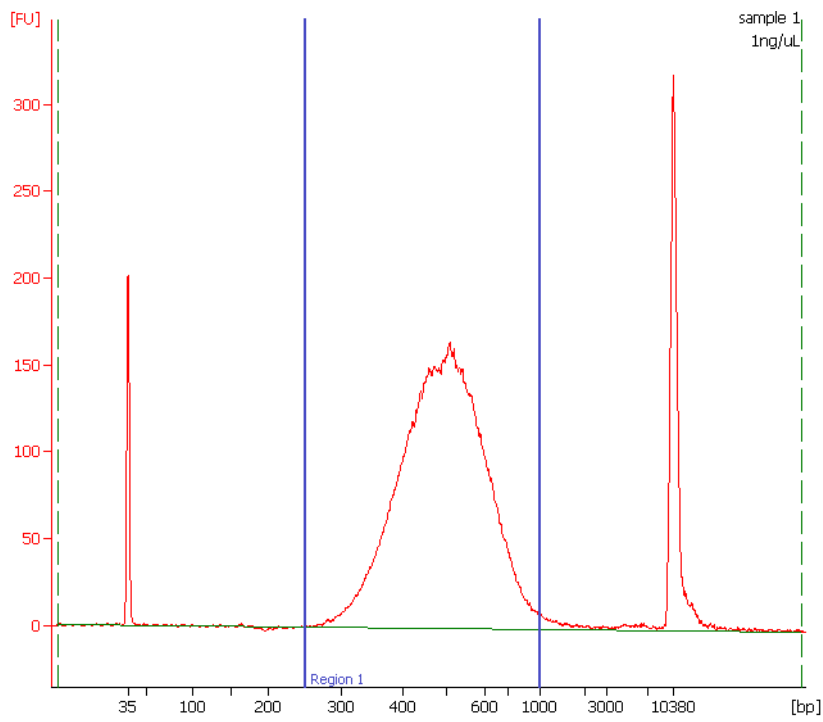
- 12 Incubate the samples for 30 seconds on the magnet.
- 13 While on the magnet, carefully remove and appropriately discard only the supernatant without disturbing the AMPure XP magnetic beads.
- 14 Repeat the 200 μ L of fresh 80% ethyl alcohol wash for a total of two washes.
- 15 Keeping the tubes on the magnet, use a small-volume pipette to remove any residual supernatant from the tube.
- 16 Leave the tubes 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 Pipet 30 μ L of Elution Buffer into the tubes and pipet-mix to completely resuspend the AMPure XP magnetic beads.
- 18 Incubate the samples at room temperature for 2 minutes.
- 19 Briefly centrifuge the tubes to collect the contents at the bottom.
- 20 Place the tubes on the magnet until the solution is clear, usually ~30 seconds.
- 21 Pipet the eluate (~30 μ L) into new 1.5-mL LoBind tubes. 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.

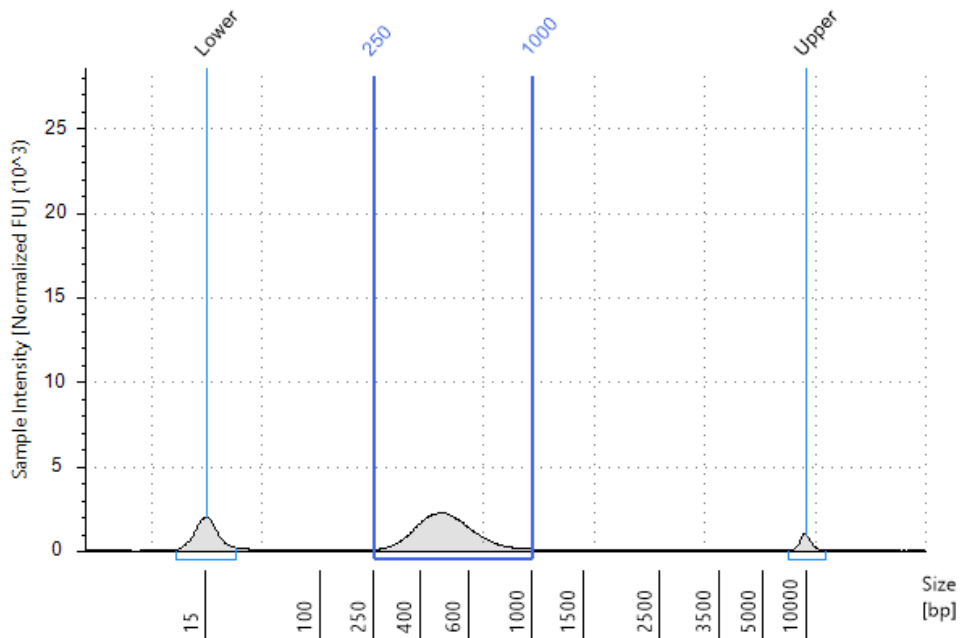
- 22 Quantify and perform quality control of the Index PCR libraries with a Qubit Fluorometer using the Qubit dsDNA HS Assay and either of the following systems:
 - Agilent 2100 Bioanalyzer using the Agilent High Sensitivity DNA Kit
 - Agilent 4200 TapeStation system using the Agilent High Sensitivity D100 or D5000 ScreenTape Assay
 - a The expected concentration from the Qubit Fluorometer is >1 ng/ μ L.
 - b The Bioanalyzer/TapeStation trace should show a peak from ~250 to 1,000 bp. Refer to the sample trace images on [page 21](#).

Figure 2 WTA Index PCR product

A. Sample Bioanalyzer High Sensitivity DNA trace

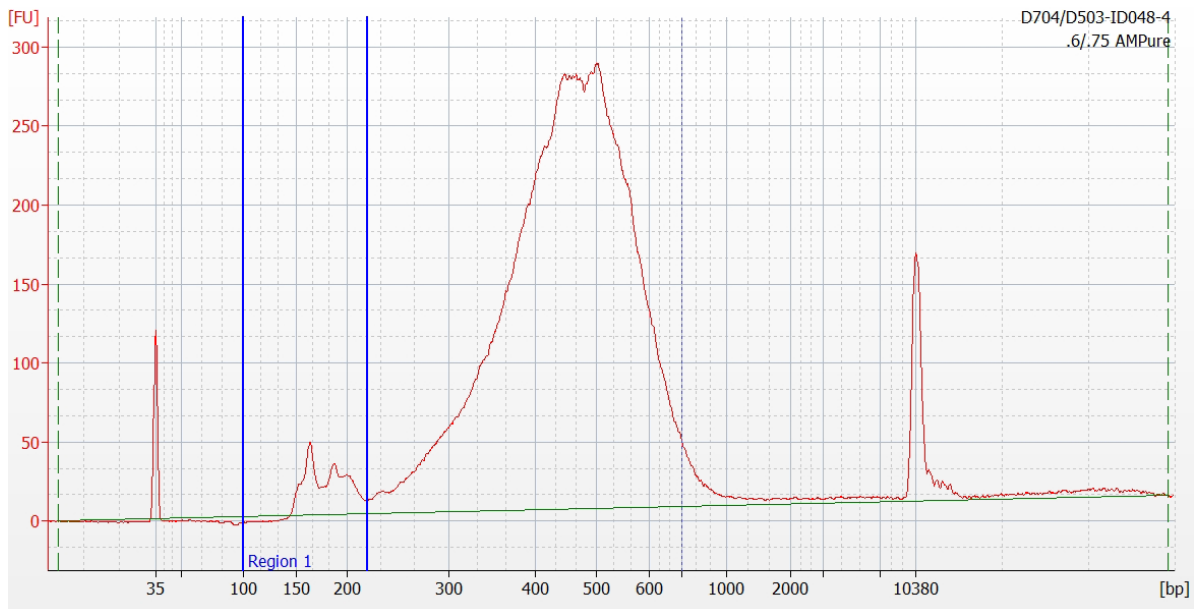


B. Sample TapeStation High Sensitivity D5000 trace



NOTE If a ~165 bp peak is observed from the [Figure 2](#), such as the peak shown in [Figure 3](#), a second round of AMPure XP magnetic purification is recommended. See [Additional WTA Index PCR purification steps](#) in the following section.

Figure 3 Sample Bioanalyzer High-Sensitivity DNA trace for an Index PCR product with observable peaks at ~165 bp



Additional WTA Index PCR purification steps

If a ~165 bp peak is observed from the [Figure 2](#) 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 μ L with nuclease-free water.

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

- 2 Pipet-mix 10 times, then briefly centrifuge.
- 3 Pipet 75 μ L of AMPure XP magnetic beads into the tube containing 100 μ L of eluted RPE product from the first round of purification.
- 4 Pipet-mix 10 times, then briefly centrifuge.
- 5 Repeat [step 9](#) through [step 21 on page 20](#) once more, resulting in a total of two rounds of purification.
- 6 Collect the elute (~30 μ L) to a new PCR tube.
- 7 Repeat the quality control step ([step 22 on page 20](#)).

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

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 1–1.2 pM with 20% PhiX for a sequencing run.
- Sequencing depth 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 Analysis Pipeline

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

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