

BD Rhapsody™ System

TCR/BCR Next, BD OMICS-One™ WTA Next, BD® AbSeq, and Sample Tag

Library Preparation Protocol

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Regulatory information

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

History

Revision	Date	Change made
23-24998(01)	2025-10	Initial release.

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Introduction

This protocol enables high throughput single-cell transcriptome and protein analysis alongside TCR and BCR profiling of individual cells captured on the BD Rhapsody™ system, providing instructions for amplifying Illumina-compatible single-cell barcoded mRNA, TCR, BCR, BD® AbSeq, and Sample Tag libraries. The addition of a Sample Tag library enables demultiplexing of samples that were pooled before capture on the BD Rhapsody™ system.

After staining cells with BD[®] AbSeq and Sample Tag antibodies and partitioning and lysis of cells, cDNA is encoded on BD Rhapsody™ Enhanced Cell Capture beads using both the 3' and 5' ends of transcripts as templates. Whole transcriptome library is generated directly from the beads using a random priming approach, followed by an index polymerase chain reaction (PCR) step. TCR and BCR libraries are amplified from cDNA on bead using a two-step nested PCR, followed by additional random priming to capture complementarity determining regions (CDR) 1–3 and framework regions (FR) 1–4. BD® AbSeq and Sample Tag libraries are amplified from the supernatant that was denatured from the beads.

Symbols

The following symbols are used in this guide:

Symbol	Description
<u>^</u>	Important information for maintaining measurement accuracy or data integrity.
	Noteworthy information.
STOP	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 15) section.

	BD Rhαpsody™ cDNA Kit	
Cap Color	Name	Quantity
	RT buffer	1
	RT 0.1M DTT	1
	Reverse transcriptase	1
	dNTP	1
	RNase inhibitor	1
•	Bead RT/PCR enhancer	1
	10X Exonuclease I buffer	1
	Exonuclease I	1
	Nuclease-free water	2
	Bead resuspension buffer	1

Cap Color	Name	Quantity
	BD Rhapsody™ HT Enhanced Cell Capture Beads v3	4
\bigcirc	Sample buffer	1
\bigcirc	Cartridge wash buffer 1	1
\bigcirc	Cartridge wash buffer 2	1
\bigcirc	Lysis buffer	4
\bigcirc	Bead wash buffer	1
\bigcirc	Waste collection container	4
\bigcirc	1M DTT	1

	1	2	3	4	5	6	7	8	9	10
Α										
В										
С	1	2	3	4	5	6	7	8		
D	1	2	3	4	5	6	7	8		
Ε	1	2	3	4	5	6	7	8	Em	ipty

BD OMICS-One™ WTA Next Amplificαtion Kit					
Cap Color	Name	Part Number	Vial Placement		
	BD OMICS-One™ Nuclease-Free Water	51-9025552	A1–A4		
	BD OMICS-One™ WTA Extension Buffer	51-9025488	A5		
	BD OMICS-One™ WTA Extension Primer	51-9025467	A6		
	BD OMICS-One™ dNTP Mixture	51-9025491	A7		
	BD OMICS-One™ Bead RT/PCR Enhancer	51-9025495	A8		
	BD OMICS-One™ WTA Extension Enzyme	51-9025499	A9		
	BD OMICS-One™ AbSeq Primer	51-9025468	A10		
	BD OMICS-One™ PCR Master Mix	51-9025466	B1		
	BD OMICS-One™ Universal Oligo	51-9025553	В2		
	BD OMICS-One™ WTA Amplification Primer	51-9025469	В3		
	BD OMICS-One™ Elution Buffer	51-9025554	B4-B8		
	BD OMICS-One™ Sample Tag PCR1 Primer	51-9025470	В9		
	BD OMICS-One™ Sample Tag PCR2 Primer	51-9025471	B10		
	BD OMICS-One™ Bead Resuspension Buffer	51-9025555	C9, C10, D9, D10		
	BD OMICS-One™ Library Forward Primer 1–8	See Part numbers	C1–C8		
	BD OMICS-One™ WTA Library Reverse Primer 1–8	for primers in rows	D1-D8		
\bigcirc	BD OMICS-One™ Multiomic Library Reverse Primer 1–8	C–E (page 8)	E1–E8		

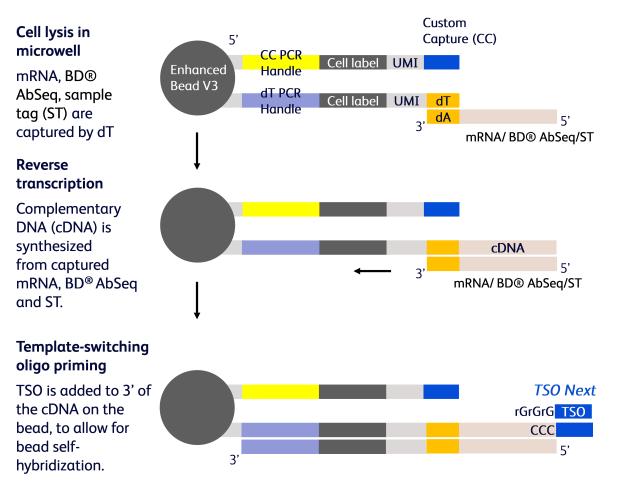
Part numbers for primers in rows C–E

Name	Part Number
BD OMICS-One™ Library Forward Primer 1	51-9025472
BD OMICS-One™ Library Forward Primer 2	51-9025473
BD OMICS-One™ Library Forward Primer 3	51-9025474
BD OMICS-One™ Library Forward Primer 4	51-9025475
BD OMICS-One™ Library Forward Primer 5	51-9025476
BD OMICS-One™ Library Forward Primer 6	51-9025477
BD OMICS-One™ Library Forward Primer 7	51-9025478
BD OMICS-One™ Library Forward Primer 8	51-9025479
BD OMICS-One™ WTA Library Reverse Primer 1	51-9025480
BD OMICS-One™ WTA Library Reverse Primer 2	51-9025600
BD OMICS-One™ WTA Library Reverse Primer 3	51-9025482
BD OMICS-One™ WTA Library Reverse Primer 4	51-9025483
BD OMICS-One™ WTA Library Reverse Primer 5	51-9025484
BD OMICS-One™ WTA Library Reverse Primer 6	51-9025485
BD OMICS-One™ WTA Library Reverse Primer 7	51-9025486
BD OMICS-One™ WTA Library Reverse Primer 8	51-9025487
BD OMICS-One™ Multiomic Library Reverse Primer 1	51-9025489
BD OMICS-One™ Multiomic Library Reverse Primer 2	51-9025490
BD OMICS-One™ Multiomic Library Reverse Primer 3	51-9025492
BD OMICS-One™ Multiomic Library Reverse Primer 4	51-9025493
BD OMICS-One™ Multiomic Library Reverse Primer 5	51-9025494
BD OMICS-One™ Multiomic Library Reverse Primer 6	51-9025496
BD OMICS-One™ Multiomic Library Reverse Primer 7	51-9025497
BD OMICS-One™ Multiomic Library Reverse Primer 8	51-9025498

	BD Rhαpsody™ TCR/BCR Next Amplific	Lation Kit
Cap Color	Name	Quantity
\bigcirc	TCR/BCR extension primers	1
\bigcirc	TCR/BCR extension buffer	1
\bigcirc	TCR/BCR extension enzyme	1
	10 mM dNTP	2
	Nuclease-free water	2
•	Bead RT/PCR enhancer	1
	TSO Next	1
	TCR N1 primer	1
	TCR N2 primer	1
	BCR N1 primer	1
	BCR N2 primer	1
\bigcirc	PCR master mix	1
	TCR/BCR universal oligo N1	1
	TCR/BCR universal oligo N2	1
	Elution buffer	2
	1M MgCl ₂	1
	Hybridization buffer	4

Workflows

On bead workflow



Denaturation Supernatant:

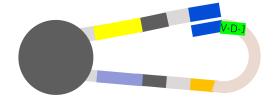
The BD® AbSeq and ST template are denatured off the bead. KEEP the supernatant.

Bead: Single-stranded DNA is generated on beads to prepare for self-hybridization.



Self-hybridization

Resuspend the beads in pre-warmed hybridization buffer, then gradually cool down to allow the cDNA self-hybridized on bead by CC.



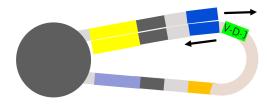
VDJ region is flipped and captured by bead CC strand

Extension

Copy cell label, UMI, TCR/BCR universal oligo

Exo I

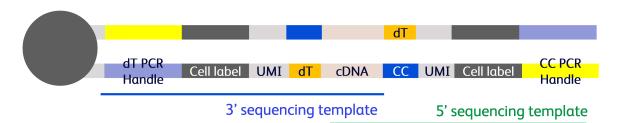
Remove unused oligo capture sequences



Final bead layout

3' sequencing template (blue): mRNA library

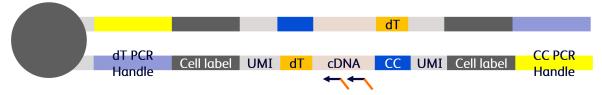
5' sequencing template (green): TCR/BCR library



WTA library amplification workflow

WTA RPE

Random priming on bead



WTA extension primer :

GGCTCGGAGATGTGTATAAGAGACAGNNNNNNNNN

Denature off the RPE product



WTA RPE PCR Amplify RPE product

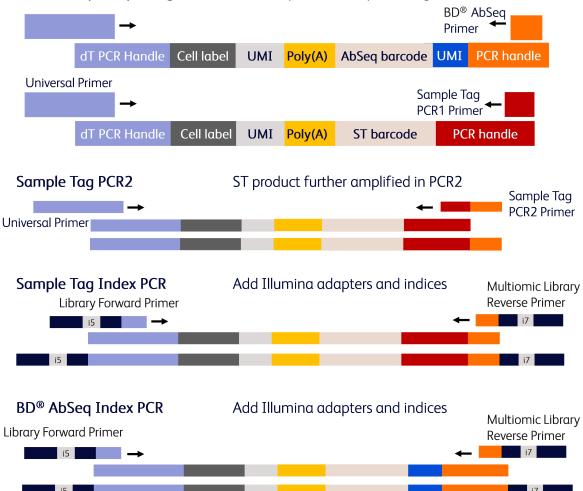


WTA Index PCR Add Illumina adapters and indices



BD® AbSeq/Sample Tag library amplification workflow

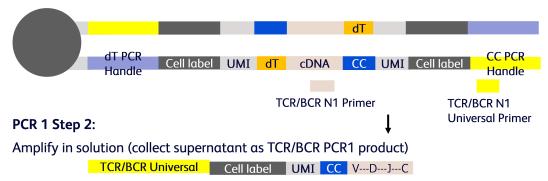
BD® AbSeq/Sample Tag PCR1 Denatured products amplified together



TCR/BCR library amplification workflow

PCR 1 Step 1:

TCR/BCR universal primer and TCR/BCR N1 primer copy target region from bead



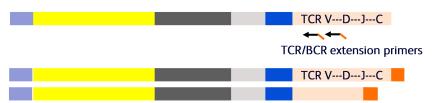
PCR 2:

TCR/BCR universal N2 primer adds sequencing handle; TCR N2 or BCR N2 primer for nested PCR enrichment



RPE for fragmentation:

Random priming is used for fragmentation for sequencing, full-length VDJ is assembled bioinformatically. TCR and BCR RPE are done separately



Index PCR:

Add Illumina adapters and indices. TCR and BCR Index are done separately



Required and recommended materials

Required reagents

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

Material	Supplier	Catalog no.
BD Rhapsody™ cDNA Kit ^a	BD Biosciences	633773
BD Rhapsody™ Enhanced Cartridge Reagent Kit V3 ^{a, b}	BD Biosciences	667052
BD OMICS-One™ WTA Next Amplification Kit	BD Biosciences	572620
BD Rhapsody™ TCR/BCR Next Amplification Kit ^a	BD Biosciences	667058
AMPure® XP magnetic beads	Beckman Coulter	A63880
100% ethyl alcohol, molecular biology grade	Major supplier	_
Nuclease-free water	Major supplier	_

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

b. The Enhanced Cartridge Reagent Kit V3 must be used before beginning this protocol.

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 ^a Or,	Corning	PCR96HSC
MicroAmp™ Optical 96–Reaction Plate ^α	Thermo Fisher Scientific	N8010560
MicroAmp™ Clear Adhesive Film ^a	Thermo Fisher Scientific	4306311
15-mL conical tube	Major supplier	-
DNA LoBind [®] Tubes, 1.5 mL	Eppendorf	0030108051
DNA LoBind [®] Tubes, 5.0 mL	Eppendorf	0030108310
Qubit™ Assay Tubes	Thermo Fisher Scientific	Q32856
Qubit™ dsDNA HS Assay Kit	Thermo Fisher Scientific	Q32851
Agilent High Sensitivity DNA Kit Or,	Agilent	5067-4626
Agilent High Sensitivity D1000 ScreenTape Agilent High Sensitivity D1000 Reagents Or,	Agilent Agilent	5067-5584 5067-5585
Agilent High Sensitivity D5000 ScreenTape Agilent High Sensitivity D5000 Reagents	Agilent Agilent	5067-5592 5067-5593

 $[\]alpha.$ Recommended for processing high throughput library preparation workflows.

Equipment

Material	Supplier	Catalog no.
Microcentrifuge for 1.5–2.0-mL tubes	Major supplier	_
Microcentrifuge for 0.2-mL tubes	Major supplier	_
Vortexer	Major supplier	_
Digital timer	Major supplier	_
Eppendorf ThermoMixer [®] C	Eppendorf	5382000023
6-tube magnetic separation rack for 1.5-mL tubes	New England Biolabs	S1506S
Or, 12-tube magnetic separation rack ^a Or,	New England Biolabs	S1509S
Invitrogen™ DynaMag™-2 magnet ^a	Thermo Fisher Scientific	12321D
Low-profile magnetic separation stand for 0.2 mL, 8-strip tubes	V&P Scientific, Inc.	VP772F4-1
Magnetic Stand-96 ^b	Thermo Fisher Scientific	AM10027
Qubit™ 3.0 Fluorometer or similar	Thermo Fisher Scientific	Q33216
Agilent [®] 2100 Bioanalyzer	Agilent Technologies	G2940CA
Or, Agilent [®] 4200 TapeStation System	Agilent Technologies	G2991AA
Heat block	Major supplier	_

a. Recommended for processing greater than six samples.

 $b.\ Recommended\ for\ processing\ high\ throughput\ library\ preparation\ workflows.$

Best practices



The BD Rhapsody™ Enhanced Cartridge Reagent Kit V3 (Catalog no. 667052) must be used for this protocol. The BD Rhapsody™ TCR/BCR Next Amplification Kit (Catalog no. 667058) is not compatible with the BD Rhapsody™ Enhanced Cartridge Reagent Kit (Catalog no. 664887).

Cell capture

- Ensure that the intended total cell load is 7,500–20,000. Cell loads outside this recommended range might require protocol optimization and might yield suboptimal results.
- 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.

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.

Denaturation and self-hybridization

- Remove supernatant promptly after 95 °C denaturation step (≤30 seconds after placing on magnet).
- Ensure that hybridization buffer is preheated at 80 °C for at least 20 minutes before resuspending beads in step 9 of 1.2 Denaturation and Self-hybridization (page 25).



Using cold or room temperature hybridization buffer might negatively impact self-hybridization efficiency.

Supernatant handling

- Read the 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 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.
- Save beads after the first amplification step (WTA Random Priming and Extension (RPE) (page 31)). They must be used again for the second bead amplification step (TCR/BCR PCR1 (page 67)).

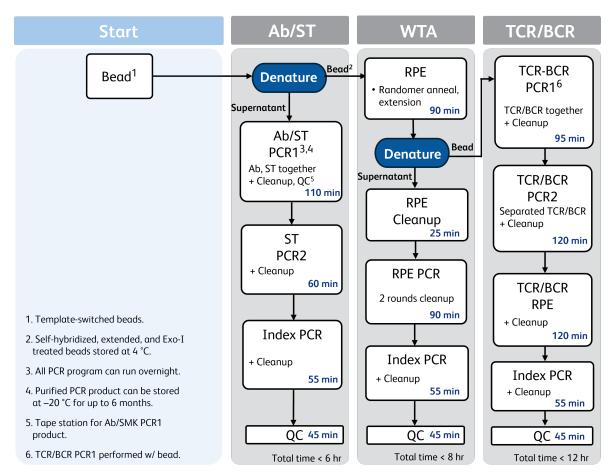
Additional documentation

- 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® AbSeq Ab-Oligos for Intracellular CITE-seq Protocol (doc ID: 23-24464)
- BD Rhapsody™ System Single-Cell Labeling with BD[®] Single-Cell Multiplexing Kits Protocol (doc ID: 23-21340)

Safety information

For safety information, see the BD Rhapsody™ HT Single-Cell Analysis System Extended-Lysis Single-Cell Capture and cDNA Synthesis Protocol (doc ID: 23-24984) or the BD Rhapsody™ HT Xpress System Extended-Lysis Single-Cell Capture and cDNA Synthesis Protocol (doc ID: 23-24983).

Time considerations



Procedure

After staining the antibodies (as described in the BD Rhapsody^M System Single-Cell Labeling with BD[®] Single-Cell Multiplexing Kits Protocol), continue with this procedure.

Perform the experiment on the BD Rhapsody™ Single-Cell Analysis system following either the:

• BD Rhapsody™ HT Single-Cell Analysis Extended-Lysis System Single-Cell Capture and cDNA Synthesis Protocol (doc ID 23-24984)



After the "Washing BD Rhapsody™ Enhanced Cell Capture Beads" section and follow this protocol from Reverse transcription, template switching, and Exonuclease I treatment (page 22) and subsequent steps.

or

 BD Rhapsody™ HT Xpress System Extended-Lysis Single-Cell Capture and cDNA Synthesis Protocol (doc ID 23-24983)



After the "Washing BD Rhapsody™ Enhanced Cell Capture Beads" section and follow this protocol from Reverse transcription, template switching, and Exonuclease I treatment (page 22) and subsequent steps.



The BD Rhapsody™ Enhanced Cartridge Reagent Kit V3 (Catalog no. 667052) must be used for this protocol.

Ensure that the intended total cell load is between 7,500-20,000 single cells for this protocol. Cell load below or above this recommended range might not be suitable for current protocol configuration. Then proceed as described in the following procedure.

1. Reverse transcription, template switching, and Exonuclease I treatment

1.1 cDNA Synthesis and Template Switching

Summary:

- Prepare cDNA mixture
- · cDNA synthesis
- Add Template Switch Oligo (TSO Next)

Preparation list:

Item BD Part Number		BD Part Number	Preparation and Handling	Storage			
Equili	brate to room temperatu	ire:					
	RT buffer	650000067					
	dNTP	650000077					
	0.1 M DTT	650000068	Equilibrate to room temperature 30 minutes before setting up cDNA synthesis. Centrifuge briefly.	−20 °C			
\bigcirc	Nuclease-free water	650000076					
•	1M MgCl ₂	91-1198					
Place	Place on ice:						
•	Bead RT/PCR enhancer	91-1082	Centrifuge briefly before adding to mix.	−20 °C			
	TSO Next	91-1295					
Leave	in freezer until ready to	use:					
	RNase inhibitor	650000078	Centrifuge briefly before adding to mix.	−20 °C			
	Reverse transcriptase	700026321					
Obtai	n:						
Wash	ed enhanced cell capture l	beads	Centrifuge briefly and keep on ice until ready.	4 °C			
Ice bu	ıcket						
1.5-m	1.5-mL tube magnetic rack						
1.5-m	1.5-mL DNA LoBind [®] tubes						
Set up	Set up:						
Therm	nomixer at 42 °C						

Procedure steps:



This section should be performed in the pre-amplification workspace.

- 1. Set a thermomixer to 42 °C.
- 2. If performing self-hybridization on the same day, set a second thermomixer to:
 - 1,200 rpm and at 80 °C for 3 minutes.
 - 1,200 rpm and at 25 °C for 1 minute.
 - 1,200 rpm and at 25 °C infinite (optional).



The thermomixer set to 80 °C will be used as a heat block to warm the hybridization buffer, and then used with programmed cooling during 1.2 Denaturation and Self-hybridization (page 25).

3. In a new 1.5-mL LoBind $^{\circledR}$ tube, pipet the following reagents.

cDNA/template switching mix

Сар	Component	1 librαry (μL)	1 library with 20% overage (μL)	4 libraries with 20% overage (μL)	8 libraries with 20% overage (μL)
	RT buffer	40.0	48.0	192.0	384.0
	dNTP	20.0	24.0	96.0	192.0
	RT 0.1 M DTT	10.0	12.0	48.0	96.0
•	Bead RT/PCR enhancer	12.0	14.4	57.6	115.2
	RNase inhibitor	10.0	12.0	48.0	96.0
	Reverse transcriptase	10.0	12.0	48.0	96.0
	Nuclease-free water	98.0	117.6	470.4	940.8
	Total	200.0	240.0	960.0	1920.0

- 4. Gently vortex mix, briefly centrifuge, and place back on ice.
- 5. Place the tube of washed BD Rhapsody™ Enhanced Cell Capture Beads on a magnet for ≥2 minutes.
- 6. Discard the supernatant.
- 7. Remove the tube from the magnet and pipet **200** μ L of cDNA mix into the beads. Pipet-mix.



Keep the prepared cDNA mix with beads on ice until the suspension is transferred in the next step.

8. Transfer the bead suspension to a new 1.5-mL LoBind[®] tube.

9. Incubate the bead suspension on the thermomixer at 1,200 rpm and 42 °C for 30 minutes.



Shaking is critical for this incubation.

10. While the bead suspension is still incubating at 1,200 rpm and 42 °C, pipet the following reagents in a new 1.5-mL LoBind® tube.



Prepare the TSO mix approximately **within 2 minutes** before the 30 minute incubation at 42 °C is finished.



Use immediately.

TSO mix

Сар	Component	1 librαry (μL)	1 library with 20% overage (μL)	4 libraries with 20% overage (μL)	8 libraries with 20% overage (μL)
	TSO Next	6.0	7.2	28.8	57.6
	1M MgCl ₂	2.0	2.4	9.6	19.2
	Total	8.0	9.6	38.4	76.8

- 11. Gently vortex mix, briefly centrifuge, and keep on ice.
- 12. Add **8 μL** of TSO mix to the reaction, gently pipet-mix, and incubate on the thermomixer for another **30 minutes** at 1,200 rpm and **42 °C**.



If you are performing self-hybridization on the same day, complete steps 3 and 4 from 1.2 Denaturation and Self-hybridization (page 25) now.

- 13. Place the bead suspension on the 1.5-mL tube magnet until the solution is clear (≤1 minute). Discard the supernatant.
- 14. Remove the tube from the magnet and pipet **75** μ L of elution buffer into the tube. Pipet-mix. Place on ice.

OPTIONAL



BD Rhapsody™ Enhanced Cell Capture Beads can be stored up to 7 days at 2–8 °C after template switching.

15. If using the BD Rhapsody™ HT Single-Cell Analysis System Instrument User Guide, view the BD Rhapsody™ Scanner image analysis to see if the analysis metrics passed.

1.2 Denaturation and Self-hybridization

Summary:

- Denature mRNA, BD^{\circledR} AbSeq, and Sample Tag
- Add hybridization buffer to hybridize TSO onto bead

Preparation list:

Item		BD Part Number	Preparation and Handling	Storage				
Equil	Equilibrate to room temperature:							
	Hybridization buffer	91-1199	Equilibrate to room temperature 30 minutes before	20.00				
	Elution buffer	91-1084	setting up hybridization. Centrifuge briefly.	−20 °C				
Obta	in:			<u>'</u>				
Enhai	nced cell capture beads af	ter cDNA Synthesi	s and Template Switching					
Ice b	ucket							
1.5-m	L tube magnetic rack							
1.5-m	L DNA LoBind [®] tubes							
Set u	p:							
Heat block at 95 °C								
Heat block at 80 °C (Optional)								
Thermomixer with self-hybridization program								

Procedure steps:

- 1. Set a heat block to 95 °C.
- 2. Program a thermomixer with the self-hybridization program.
 - a. 1,200 rpm and at 80 °C for 3 minutes.
 - b. 1,200 rpm and at 25 °C for 1 minute.
 - c. 1,200 rpm and at 25 °C infinite (optional).



If you performed cDNA synthesis on the same day, this is the same thermomixer from step 2 of 1.1 cDNA Synthesis and Template Switching (page 22), and the thermomixer is already programmed.



Confirm "Time Mode" on the thermomixer is set to "Temperature Control" to ensure that the 25 °C temperature is reached before the 1 minute at 25 °C (step 2b) begins.

- 3. Prepare hybridization buffer for self-hybridization.
- 4. Aliquot **1.2 mL** hybridization buffer into a new 1.5-mL LoBind[®] tube and place the tube in the pre-heated 80 °C thermomixer (from step 2a) without shaking.
- 5. Keep the tube of hybridization buffer in the 80 °C thermomixer until ready to use, at least **20 minutes** before resuspending beads in step 6a of this section.
- 6. To denature, incubate the tube in the following order:
 - a. Pipet-mix to resuspend the beads.
 - b. Incubate the tube at 95 °C in a heat block for 5 minutes.
 - c. Immediately after the completion of the 95 $^{\circ}$ C incubation, slightly open the lid of the tube to release air pressure within the tube.
- 7. Immediately place the tube on the magnet for ≤30 seconds until clear.



Keep the supernatant.

8. Remove the supernatant and transfer to a new 1.5-mL LoBind® tube. This contains the BD® AbSeq and Sample Tag products.



To minimize BD[®] AbSeq and Sample Tag contamination in the TCR/BCR and WTA libraries, ensure that all liquid is removed from the tube. Keep the supernatant tube at 4 °C until ready to proceed to AbSeq/Sample Tag PCR1 (page 49).

9. Resuspend the beads in **1.0 mL** of pre-heated 80 °C hybridization buffer, and immediately place in the pre-programed thermomixer from step 2a. Start the program.



Incubation will take approximately 25 minutes.

10. After the hybridization step, place tube on **ice** for at least **1 minute** while TCR/BCR extension mix is being prepared.

1.3 TCR/BCR Extension

Summary:

- Prepare extension enzyme mix
- Extend TSO to copy cell label from bead

Preparation list:

Item BD Part Number		BD Part Number	Preparation and Handling	Storage		
Equili	Equilibrate to room temperature:					
\bigcirc	TCR/BCR extension buffer	91-1206				
	dNTP	650000077	Equilibrate to room temperature 30 minutes before setting up extension. Centrifuge briefly.	–20 °C		
	Nuclease-free water	650000076				
Leave	in freezer until ready to	use:				
\bigcirc	TCR/BCR extension enzyme	91-1207	Centrifuge briefly before adding to mix.	–20 °C		
Obtai	n:					
Enhar	nced cell capture beads aft	er self-hybridization	Centrifuge briefly and keep on ice until ready.	4 °C		
Ice bu	ıcket					
1.5-mL tube magnetic rack						
1.5-m	1.5-mL DNA LoBind [®] tubes					
Set up:						
Therm	nomixer at 37 °C					

Procedure steps:

- 1. Set a thermomixer to 37 °C.
- 2. Ensure all reagents other than the TCR/BCR extension enzyme are at room temperature.
- 3. In a new 1.5-mL LoBind $^{\circledR}$ tube, pipet the following reagents.

TCR/BCR extension mix

Сар	Component	For 1 librαry (μL)	For 1 library with 20% overage (µL)	For 4 libraries with 20% overage (µL)	For 8 libraries with 20% overage (µL)
	TCR/BCR extension buffer	20	24	96	192
	dNTP	20	24	96	192
	TCR/BCR extension enzyme	10	12	48	96
	Nuclease-free water	150	180	720	1440
	Total	200	240	960	1920

- 4. Gently vortex mix, briefly centrifuge, and keep at room temperature.
- 5. Briefly spin the tube with the bead suspension.
- 6. Place the tube of BD Rhapsody™ Enhanced Cell Capture Beads on a magnet for ≤2 minutes. Discard the supernatant.
- 7. Remove the tubes from the magnet and resuspend using 200 μ L of TCR/BCR extension mix. Pipet-mix.
- 8. Incubate the bead suspension on a thermomixer at 1,200 rpm and 37 °C for 30 minutes.



During TCR/BCR Extension incubation, begin BD[®] AbSeq/Sample Tag PCR1. See AbSeq/Sample Tag PCR1 (page 49). You can leave the BD[®] AbSeq/Sample Tag PCR1 reaction in the thermocycler when complete. TCR/BCR PCR1 can be performed after 2.4 WTA RPE PCR cleanup and quantification (page 40). All PCR1 product purification (TCR/BCR and BD[®] AbSeq/Sample Tag) can be done at the same time.

9. Briefly spin the tube with the beads suspension and place the tube on ice.

1.4 Exonuclease I Treatment

Summary:

- Prepare Exonuclease I enzyme mix
- Treat beads with Exonuclease I
- Heat inactivation

Preparation list:

Item		BD Part Number	Preparation and Handling	Storage		
Equili	Equilibrate to room temperature:					
	10X Exonuclease I buffer	650000071				
\bigcirc	Nuclease-free water	650000076	Equilibrate to room temperature 30 minutes before setting up Exo-I treatment. Centrifuge briefly.	−20 °C		
•	Bead resuspension buffer	650000066				
Leave	in freezer until ready to	use:				
	Exonuclease I	650000072	Centrifuge briefly before adding to mix.	–20 °C		
Obtai	n:					
Enhar exten	nced cell capture beads aft sion	ter TCR/BCR	Centrifuge briefly and keep on ice until ready. 4 °C			
Ice bu	icket					
1.5-m	L tube magnetic rack					
1.5-m	1.5-mL DNA LoBind [®] tubes					
Set u	Set up:					
Therm	Thermomixer at 37 °C					
Heat I	olock at 80 °C					

Procedure steps:

- 1. Set one thermomixer to 37 °C and a heat block to 80 °C.
- 2. In a new 1.5-mL LoBind[®] tube, pipet the following reagents.

Exonuclease I mix

Сар	Component	For 1 librαry (μL)	For 1 library with 20% overage (µL)	For 4 libraries with 20% overage (µL)	For 8 libraries with 20% overage (µL)
	10X Exonuclease I buffer	20	24	96	192
	Exonuclease I	10	12	48	96
	Nuclease-free water	170	204	816	1632
	Total	200	240	960	1920

- 3. Gently vortex-mix, briefly centrifuge, and keep at room temperature.
- 4. Place the tube of BD Rhapsody™ Enhanced Cell Capture Beads with TCR/BCR extension mix on a 1.5-mL tube magnet for ≤1 minute.
- 5. Discard the supernatant.
- 6. Remove the tube from the magnet and pipet 200 μ L Exonuclease I mix into the tube. Pipet-mix.
- 7. Incubate the bead suspension on thermomixer at 1,200 rpm and 37 °C for 30 minutes.
- 8. Incubate the bead suspension in the heat block at 80 °C for 20 minutes.
- 9. Place the tube on ice for ~1 minute.
- 10. Briefly spin the tube with the bead suspension.
- 11. Place the tube on the magnet for ≤1 minute until clear. Discard the supernatant.
- 12. Remove the tube from the magnet and pipet **200** μ L of cold bead resuspension buffer into the tube. Pipet-mix.



Exonuclease I-treated beads can be stored in bead resuspension buffer at 4 °C for up to 1 year.

13. Proceed to library preparation.

2. WTA library amplification

2.1 WTA Random Priming and Extension (RPE)

Summary:

- Prepare random priming mix and extension enzyme mix
- Anneal random primers
- Extend random primers
- Denature RPE products

Preparation list:

Item		BD Part Number	Preparation and Handling	Storage		
			Joe and the state of the state			
Equili	brate to room temperatu	ire:		T		
	WTA extension buffer	51-9025488				
	WTA extension primer	51-9025467	Equilibrate to room temperature 30 minutes before			
	dNTP mixture	51-9025491	setting up RPE.	−20 °C		
\bigcirc	Nuclease-free water	51-9025552	Centrifuge briefly.			
	Elution buffer	51-9025554				
Place	on ice:					
	Bead RT/PCR enhancer	51-9025495	Centrifuge briefly before adding to mix.	–20 °C		
Leave	in freezer until ready to	use:				
	WTA extension enzyme	51-9025499	Centrifuge briefly before adding to mix.	−20 °C		
Obtai	n:					
Exonu	ıclease I-treated enhanced	d cell capture beads	Centrifuge briefly and keep on ice until ready.	4 °C		
Ice bu	ıcket					
1.5-m	L tube magnetic rack					
1.5-mL DNA LoBind [®] tubes						
Set up:						
Heat I	Heat block at 95 °C					
Therm	Thermomixer at 37 °C (Optional)					
Therm	nomixer at 25 °C					
Progra	ammed thermomixer with	RPE program				

Procedure steps:

This section describes how to generate random priming products. First, random primers are hybridized to the cDNA on the BD Rhapsody™ Enhanced Cell Capture Beads, followed by extension with an enzyme.



Perform this procedure in the pre-amplification workspace. We recommend using a separate heat block for the $95\,^{\circ}$ C incubations.

1. Set a heat block to 95 °C and set two thermomixers to 37 °C and 25 °C, respectively.



If you are using one thermomixer, skip the 37 °C incubation in step 10b.

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

Random primer mix

Сар	Component	1 librαry (μL)	1 library with 20% overage (μL)	4 libraries with 20% overage (μL)	8 libraries with 20% overage (μL)
	WTA extension buffer	20.0	24.0	96.0	192.0
	WTA extension primer	40.0	48.0	192.0	384.0
	Nuclease-free water	114.0	136.8	547.2	1,094.4
	Total	174.0	208.8	835.2	1670.4

- 3. Pipet-mix the random primer mix and keep at room temperature.
- 4. Briefly centrifuge the tube of Exonuclease I-treated BD Rhapsody™ Enhanced Cell Capture Beads and use the entire sample of beads.



For multiomics including Sample Tag and BD[®] AbSeq, subsampling is not compatible.

- 5. Place the tube on a magnet until the supernatant is clear (<2 minutes).
- 6. Remove and discard the supernatant.
- 7. Remove the tube from the magnet.
- 8. Add 174 μ L of random primer mix into the tube.
- 9. Pipet-mix 10 times to resuspend the beads.
- 10. 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.



Optional: If you are using one thermomixer, skip the 37 °C incubation.

- c. Thermomixer at 1,200 rpm and at 25 °C for 5 minutes.
- 11. Briefly centrifuge the tube.
- 12. Place at room temperature until ready to use.
- 13. In a new 1.5-mL LoBind[®] tube, pipet the following reagents.

Extension enzyme mix

Сар	Component	For 1 librαry (μL)	For 1 library with 20% overage (µL)	For 4 libraries with 20% overage (µL)	For 8 libraries with 20% overage (µL)
	dNTP	8.0	9.6	38.4	76.8
	Bead RT/PCR enhancer	12.0	14.4	57.6	115.2
	WTA extension enzyme	6.0	7.2	28.8	57.6
	Total	26.0	31.2	124.8	249.6

- 14. Pipet $26 \mu L$ of the extension enzyme mix into the sample tube containing the beads (for a total volume of $200 \mu L$) and keep on ice 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.



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

- 16. Place the tube of extension enzyme mix with BD Rhapsody™ Enhanced Cell Capture Beads in the programmed thermomixer. The program takes 45 minutes.
- 17. Remove the tube after the program is complete.
- 18. Place the tube on a magnet until the supernatant is clear (<2 minutes).
- 19. Remove and discard the supernatant.
- 20. Remove the tube from the magnet.
- 21. Pipet **200** μ L of elution buffer into the tube.
- 22. Pipet-mix 10 times until the beads are fully resuspended.
- 23. Place the tube on a magnet until the supernatant is clear (<2 minutes).
- 24. Remove and discard the supernatant.
- 25. Remove the tube from the magnet.
- 26. Pipet **80** μ L of elution buffer into the tube.

- 27. To denature the random priming products off the beads.
 - a. Pipet-mix 10 times to resuspend the beads.
 - b. Incubate the tube at 95 °C in a heat block for 5 minutes (no shaking).
 - c. Slightly open the lid of the tube to release air pressure within the tube.
 - d. Place the tube on ice for 1 minute.
 - e. Briefly centrifuge the tube.
 - f. Place the tube on a magnet until the supernatant is clear (<2 minutes).



SAVE SUPERNATANT AT THIS STEP. Do not discard!

- g. Transfer **80 \muL** of the supernatant (RPE product) to a new 1.5-mL LoBind $^{\circledR}$ tube.
- 28. Place the tube containing the RPE product on ice. The total volume of RPE product will be 80 μ L. Proceed to WTA RPE cleanup (page 35).
- 29. 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.
- 30. Store the beads on ice or at 4 °C in the pre-amplification workspace until needed.



These beads will be used for TCR/BCR library amplification (page 67). DO NOT THROW AWAY!

2.2 WTA RPE cleanup

Summary:

• RPE cleanup

Preparation list:

Item	BD Part Number	Preparation and Handling	Storage
Equilibrate to room temperature:			
Elution buffer	51-9025554	Centrifuge briefly.	–20 °C
AMPure [®] XP magnetic beads		Manufacturer's recommendations	
Qubit dsDNA HS Assay Kit			
Obtain:			
WTA RPE product			4 °C
1.5-mL tube magnetic rack			
1.5-mL DNA LoBind [®] tubes			
Set up:			
Prepare fresh 80% ethyl alcohol			

Procedure steps:

This section describes how to perform a single-sided AMPure[®] XP beads cleanup, which removes primer dimers and other small molecular weight byproducts. The final product is purified single-stranded DNA.



Perform the RPE purification in the pre-amplification workspace.

1. Make fresh 80% ethyl alcohol for use within 24 hours.



Adjust the volume depending on the number of samples. One sample requires 0.5 mL of 80% ethyl alcohol.

- 2. Bring AMPure[®] XP beads to room temperature. Vortex the AMPure[®] XP beads at high speed for **1 minute** until the beads are fully resuspended.
- 3. Pipet 128 μ L of AMPure[®] XP beads into the tube containing the 80 μ L of RPE product supernatant (1.6x). Pipet-mix at least 10 times, then briefly centrifuge.
- 4. Incubate at room temperature for 5 minutes.
- 5. Place the tube on the magnet for **3 minutes**. Discard the supernatant.
- Keeping the tube on the magnet, gently add 250 μL of fresh 80% ethyl alcohol into the tube and incubate for 30 seconds. Discard the supernatant.
- 7. Repeat step 6 for a total of two ethyl alcohol washes.
- 8. Keeping the tube on the magnet, use a P20 pipette to remove and discard any residual supernatant from the tube.
- 9. Air-dry the beads at room temperature for 5 minutes or until the beads no longer look glossy.
- 10. Remove the tube from the magnet and resuspend the bead pellet in 80 μ L of elution buffer.
- 11. Incubate the sample at room temperature for **2 minutes**. Briefly centrifuge the tube to collect the contents at the bottom.
- 12. Place the tube on the magnet until the solution is clear, usually ~30 seconds.
- 13. Pipet the eluate (\sim 80 μ L) to a new PCR tube. This is the purified RPE product.
- 14. Keep on ice until ready to proceed with WTA RPE PCR (page 37).

2.3 WTA RPE PCR

Summary:

- Prepare RPE PCR mix
- Amplify using RPE PCR program

Item		BD Part Number	Preparation and Handling	Storage	
Equili	brate to room temperatu	ire:			
	Universal oligo	51-9025553	Equilibrate to room tomporature 20 minutes hefere		
	WTA amplification primer	51-9025469	Equilibrate to room temperature 30 minutes before setting up RPE PCR. Centrifuge briefly.	−20 °C	
Leave	e in freezer until ready to	use:			
	PCR master mix	51-9025466	Centrifuge briefly before adding to mix.	−20 °C	
Obtai	n:				
RPE p	roduct				
Ice bu	ucket				
0.2-m	0.2-mL PCR tubes				
Set up:					
Thern	nocycler with RPE PCR pro	gram			

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



Perform this section in the pre-amplification workspace.

1. In the pre-amplification workspace, in a new 1.5-mL LoBind $^{\textcircled{R}}$ tube, pipet the following components.

RPE PCR mix

Сар	Component	For 1 librαry (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	30.0	36.0	144.0	288.0
	Universal oligo	6.0	7.2	28.8	57.6
	WTA amplification primer	6.0	7.2	28.8	57.6
	Total	42.0	50.4	201.6	403.2

- 2. Pipet-mix the RPE PCR mix.
- 3. Place on ice until ready to use.
- 4. Add $42~\mu L$ of the RPE PCR mix to the tube with the $80~\mu L$ of RPE product.
- 5. Pipet-mix 10 times to create the RPE PCR reaction mix.
- 6. Split the RPE PCR reaction mix into two 0.2-mL PCR tubes with $61~\mu L$ mix per tube.
- 7. Transfer any residual mix to one of the tubes.



Bring the tubes to the post-amplification workspace.

8. Run the following PCR program.

RPE PCR program

Step	Cycles	Temperature	Time
Hot start	1	98 °C	45 seconds
Denaturation		98 ℃	15 seconds
Annealing	Recommended PCR cycles for resting peripheral blood mononuclear cells (PBMCs)*	60 ℃	30 seconds
Extension	7,500 – 20,000 cells: 10 cycles	72 ℃	1 minute
Final extension	1	72 ℃	2 minutes
Hold	1	4 °C	∞

^{*}Recommended number of PCR cycles might require optimization for different cell types.



The PCR can run overnight.

9. When the RPE PCR program is complete, briefly centrifuge the tubes.

2.4 WTA RPE PCR cleanup and quantification

Summary:

- RPE PCR cleanup (2 rounds)
- Quantify using Qubit Fluorometer

Item		BD Part Number	Preparation and Handling	Storage	
Equil	ibrate to room temperatu	ire:			
	Elution buffer	51-9025554	Centrifuge briefly.	−20 °C	
AMPı	ıre [®] XP magnetic beads		Manufacturer's recommendations		
Qubit	dsDNA HS Assay Kit				
Obta	in:				
RPE P	CR product				
1.5-m	L DNA LoBind [®] tubes				
0.2-m	L PCR tubes				
1.5-mL tube magnetic rack					
Set u	Set up:				
Prepo	Prepare fresh 80% ethyl alcohol				



Perform the purification in the post-amplification workspace.

- 1. Bring AMPure[®] XP beads to room temperature.
- 2. Make fresh 80% ethyl alcohol and use within 24 hours.



Adjust the volume of 80% ethyl alcohol depending on the number of samples. One sample requires 1 mL 80% ethyl alcohol.

- 3. Vortex the AMPure® XP beads until the beads are fully resuspended.
- 4. Briefly centrifuge the tubes with the RPE PCR product.
- Combine the **two** tubes of **61 \muL** RPE PCR into a new 1.5-mL LoBind[®] tube.
- Pipet-mix 10 times.
- 7. Transfer exactly **110 \muL** RPE PCR product to a new 1.5-mL LoBind[®] tube.
- Pipet 88 μ L of AMPure (0.8x) into the tube.
- 9. Pipet-mix 10 times.
- 10. Briefly centrifuge the tube.



Avoid getting AMPure® XP beads on the lid of the tube. Residual AMPure® XP beads and PCR mix buffer can negatively impact downstream results.

- 11. Incubate at room temperature for **5 minutes**.
- Place the tube on a magnet until the supernatant is clear (<5 minutes).
- Remove and discard the supernatant.
- Keeping the tube on the magnet, gently pipet 200 µL of fresh 80% ethyl alcohol into the tube.
- 15. Incubate for 30 seconds.
- 16. Remove and discard the supernatant without disturbing the beads.
- Repeat steps 14–17 once for a total of two ethyl alcohol washes.
- 18. Keeping the tube on the magnet, use a P20 pipette to remove and discard any residual supernatant from the tube.
- 19. Air-dry the beads at room temperature until the beads no longer look glossy (~ 3 minutes)



Do not overdry the AMPure® XP beads after the ethyl alcohol washes. Overdried beads appear cracked.

- 20. Remove the tube from the magnet.
- 21. Pipet 40 μ L of elution buffer into the tube.
- 22. Pipet-mix 10 times until the beads are fully resuspended.

- 23. Incubate at room temperature for 2 minutes.
- 24. Briefly centrifuge the tube.
- 25. Place the tube on a magnet until the supernatant is clear (~30 seconds).
- 26. Pipet the eluate (40 μ L) into a new 0.2-mL PCR strip tube.
- 27. Add **60 \muL** of water to the eluate for a final volume of **100 \muL**.



The volume must be exactly $100 \mu L$. Adjust the water volume if needed.

- 28. Pipet **80** μ L of AMPure[®] XP beads (**0.8**x) into the tube.
- 29. Pipet-mix 10 times.
- 30. Briefly centrifuge the tube.
- 31. Incubate at room temperature for 5 minutes.
- 32. Place the tube on a magnet until the supernatant is clear (<5 minutes).
- 33. Remove and discard the supernatant.
- 34. Keeping the tube on the magnet, gently pipet 200 µL of fresh 80% ethyl alcohol into the tube.
- 35. Incubate for 30 seconds.
- 36. Remove and discard the supernatant without disturbing the beads.
- 37. Repeat steps 34–36 for a total of two ethyl alcohol washes.
- 38. Keeping the tube on the magnet, use a P20 pipette to remove and discard any residual supernatant from the tube.
- 39. Air-dry the beads at room temperature until the beads no longer look glossy (~3 minutes).
- 40. Remove the tube from the magnet.
- 41. Pipet 30 μ L of elution buffer into the tube.
- 42. Pipet-mix 10 times until the beads are fully resuspended.
- 43. Incubate at room temperature for 2 minutes.
- 44. Briefly centrifuge the tube.
- 45. Place the tube on a magnet until the supernatant is clear (~30 seconds).
- 46. Pipet the eluate (30 μ L) into a new PCR strip tube.

The purified RPE PCR product is ready for Section 2.5: WTA index PCR (page 43).

47. Quantify the RPE PCR products with a Qubit™ Fluorometer using the Qubit™ dsDNA HS Assay.

STOP

Purified PCR product can be stored at -20 °C for up to 6 months.

2.5 WTA index PCR

Summary:

- Prepare WTA index PCR mix
- Amplify using WTA index PCR program

Item		BD Part Number	Preparation and Handling	Storage			
Equili	Equilibrate to room temperature:						
	Forward primer 1–8	Various	Equilibrate to room temperature 30 minutes				
	WTA reverse primer 1–8	Various	before setting up WTA Index PCR.	–20 °C			
\bigcirc	Nuclease-free water	51-9025552	Centrifuge briefly. Keep on ice until ready.				
Leave	e in freezer until ready to use						
	PCR master mix	51-9025466	Centrifuge briefly before adding to mix.	−20 °C			
Obtai	n:						
Purifie	ed RPE PCR product			4 ℃			
Ice bu	ucket						
1.5-m	L DNA LoBind [®] tubes						
0.2-m	0.2-mL PCR tubes						
Set u	Set up:						
Thern	nocycler with WTA index PCR p	orogram					

This section describes how to generate mRNA libraries compatible with various sequencing platforms, by adding full-length sequencing adapters and indices through PCR. We provide reagents for unique dual-indexing, with different library forward primers and reverse primers for up to 8 samples.

The same indices can be used for all library types for each lane (WTA, TCR, and BCR, for example). The libraries will be demultiplexed using the BD Rhapsody™ Sequence Analysis Pipeline. If you prefer to index each library separately, you can use combinatorial dual indexing for more index combinations.



Consult sequencing platform guidelines for low-plex pooling, to ensure the indices chosen meet the color balancing guidelines for the sequencing instrument that will be used.

1. In a new 1.5-mL LoBind $^{\textcircled{8}}$ tube, pipet the following components.

WTA index PCR mix

Сар	Component	For 1 librαry (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	12.5	15.0	60.0	120.0
	Forward primer 1–8	2.5	3.0	N/A	N/A
	WTA reverse primer 1–8	2.5	3.0	N/A	N/A
\bigcirc	Nuclease-free water	22.5	27.0	108.0	216.0
	Total	40.0	48.0	168.0	336.0

- 2. Pipet-mix the WTA index PCR mix.
- 3. Pipet 35 μ L into separate 0.2-mL PCR tubes for each sample.
- 4. Add **2.5 \muL** of Forward Primer and **2.5 \muL** of reverse primer to each sample.
- 5. Place on ice until ready to use.
- 6. Dilute an aliquot of the purified RPE PCR product from step 46 of WTA RPE PCR cleanup and quantification (page 40) with water to **0.5 ng/µL**.



If RPE PCR product concentration is <0.5 $\,$ ng/ μ L, adjust the number of index PCR cycles as outlined in the table.

- 7. Add 10 μ L of RPE PCR product to 40 μ L index PCR mix.
- 8. Pipet-mix 10 times.

9. Run the following PCR program.

WTA index PCR program

Step	Cycles	Temperature	Time
Hot start	1	98 °C	45 seconds
Denaturation	RPE PCR concentration*	98 ℃	15 seconds
Annealing	< 0.2 ng/μL: 11 cycles 0.2 ng/μL: 10 cycles	60 ℃	30 seconds
Extension	0.5 ng/μL: 8 cycles	72 °C	1 minute
Final extension	1	72 °C	2 minutes
Hold	1	4 °C	∞

^{*}Recommended number of PCR cycles might require optimization for different cell types.



The PCR can run overnight.

10. When the WTA index PCR program is complete, briefly centrifuge the tubes.

2.6 WTA index PCR cleanup and quality check

Summary:

- WTA index PCR cleanup
- Quality check using Qubit Fluorometer and BioAnalyzer/TapeStation

Item Bi		BD Part Number	Preparation and Handling	Storage		
Equili	brate to room temperat	ure:				
	Elution buffer	51-9025554		22.5		
	Nuclease-free water	51-9025552	Centrifuge briefly.	–20 °C		
AMPu	ure [®] XP magnetic beads					
Qubit	dsDNA HS Assay Kit					
OR	Agilent BioAnalyzer High Sensitivity Kit OR Agilent TapeStation ScreenTape and Reagents		Manufacturer's recommendations			
Obtai	in:					
WTA	index PCR product			4 °C		
1.5-m	L DNA LoBind® tubes					
0.2-m	L PCR tubes					
0.2-m	0.2-mL PCR tube magnetic rack					
Set u	Set up:					
Prepa	ıre fresh 80% ethyl αlcoho					

This section describes how to perform a single-sided AMPure® XP beads cleanup for sequencing. The final product is purified double-stranded DNA with full-length adapter sequences.



Perform the purification in the post-amplification workspace.

- 1. Bring AMPure[®] XP beads to room temperature.
- 2. Make fresh 80% ethyl alcohol and use within 24 hours.



Adjust the volume of 80% ethyl alcohol depending on the number of samples. One sample requires 0.5 mL 80% ethyl alcohol.

- 3. Vortex the AMPure® XP beads until the beads are fully resuspended.
- 4. Add **60** μ L of water to **50** μ L of the WTA index PCR product.
- 5. Transfer 100 μ L of WTA index PCR product into a new 0.2-mL PCR tube.



The volume must be exactly 100 μ L.

- 6. Pipet **65** μ L of AMPure[®] XP beads (**0.65**x) into the tube.
- 7. Pipet-mix 10 times.
- 8. Briefly centrifuge the tube.
- 9. Incubate at room temperature for 5 minutes.
- Place the tube on a magnet until the supernatant is clear (<5 minutes).
- Remove and discard the supernatant.
- Keeping the tube on the magnet, gently pipet 200 µL of fresh 80% ethyl alcohol into the tube. 12.
- 13. Incubate for 30 seconds.
- 14. Remove and discard the supernatant without disturbing the beads.
- Repeat steps 12–14 once for a total of two ethyl alcohol washes.
- Keeping the tube on the magnet, use a P20 pipette to remove and discard any residual supernatant from the tube.
- 17. Air-dry the beads at room temperature until the beads no longer look glossy (~2 minutes).
- 18. Remove the tube from the magnet.
- Pipet **30 μL** of elution buffer into the tube.
- Pipet-mix 10 times until the beads are fully resuspended.
- 21. Incubate at room temperature for 2 minutes.
- 22. Briefly centrifuge the tube.

- 23. Place the tube on the magnet until the solution is clear (~30 seconds).
- 24. Pipet the eluate (30 μ L) into a new 1.5-mL LoBind[®] tube. The purified eluate is the final sequencing library.



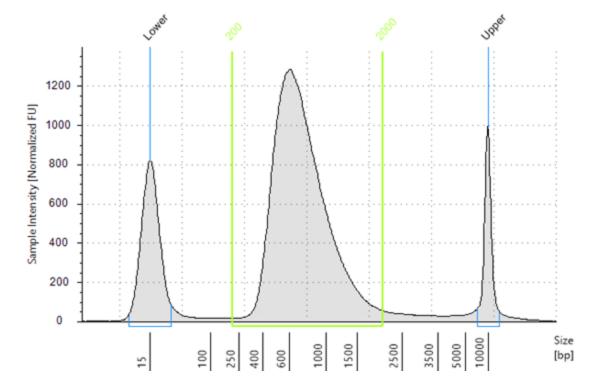
Purified PCR product can be stored at -20 °C for up to 6 months.

- 25. Quantify and perform quality control of the WTA index PCR product with a Qubit™ Fluorometer using the Qubit™ dsDNA HS Assay and one 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

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

The TapeStation trace should show a peak from \sim 200 to 2,000 bp. Refer to the representative traces in the following figures.

Figure 1 Representative TapeStation High Sensitivity D5000 trace – WTA index PCR product



3. BD® AbSeq/Sample Tag library amplification

3.1 AbSeq/Sample Tag PCR1

Summary:

- Prepare BD^{\circledR} AbSeq/Sample Tag PCR1 mix
- Amplify using BD^{\circledR} AbSeq/Sample Tag PCR1 program

Item		BD Part Number	Preparation and Handling	Storage			
Equili	Equilibrate to room temperature:						
	Universal oligo	51-9025553					
	Sample Tag PCR1 primer	51-9025470	Equilibrate to room temperature 30 minutes before setting up BD [®] AbSeq/Sample Tag PCR1. Centrifuge	−20 °C			
	BD® AbSeq primer	51-9025468	briefly.				
\bigcirc	Nuclease-free water	51-9025552					
Leave	in freezer until ready to	use:					
	PCR master mix	51-9025466	Centrifuge briefly before adding to mix.	−20 °C			
Obtai	n:						
Denat	tured BD [®] AbSeq/Sample	Tag product		4°C			
Ice bu	ıcket						
0.2-m	0.2-mL PCR tubes						
1.5-mL tube magnetic rack							
Set up:							
Therm	nocycler with BD [®] AbSeq/	Sample Tag PCR1	program				

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

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

BD® AbSeq/Sample Tag PCR1 mix

Сар	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	50.0	60.0	240.0	480.0
	Universal oligo	2.5	3.0	12.0	24.0
	BD® AbSeq primer	10.0	12.0	48.0	96.0
	Sample Tag PCR1 primer	1.0	1.2	4.8	9.6
	Nuclease-free water	68.5	82.2	328.8	657.6
	Total	132.0	158.4	633.6	1267.2

- 2. Pipet-mix the BD[®] AbSeq /Sample Tag PCR1 mix.
- 3. Place on ice until ready to use.
- 4. In a new 1.5-mL tube, add **132 \muL** of the mix with **68 \muL** of BD[®] AbSeq/Sample Tag product from step 8 in 1.2 Denaturation and Self-hybridization (page 25).
- 5. Pipet-mix to create the BD^{\circledR} AbSeq/Sample Tag PCR1 reaction mix.
- 6. Split the reaction mix into four 0.2-mL PCR tubes with 50 μ L mix per tube.
- 7. Transfer any residual mix to one of the tubes.



Bring the tubes to the post-amplification workspace.

8. Run the following PCR program.

BD® AbSeq/Sample Tag PCR1 program

Step	Cycles	Temperature	Time
Hot start	1	98 °C	45 seconds
Denaturation		98 ℃	15 seconds
Annealing	7,500–10,000 cells: 11 cycles 20,000 cells: 10 cycles ^a	60 °C	30 seconds
Extension		72 °C	1 minute
Final extension	1	72 ℃	2 minutes
Hold	1	4 °C	∞

a. Recommended number of PCR cycles might require optimization for different cell types.



The PCR can run overnight.

9. When the BD[®] AbSeq/Sample Tag PCR1 reaction is complete, briefly centrifuge the tubes.

3.2 BD® AbSeq/Sample Tag PCR1 cleanup

Summary:

- BD® AbSeq/Sample Tag PCR1 cleanup
- Quality check using BioAnalyzer/TapeStation

Item		BD Part Number	Preparation and Handling	Storage	
Equili	brate to room temperatu	ire:			
	Elution buffer	51-9025554	Centrifuge briefly.	−20 °C	
AMPu	re® XP magnetic beads				
Agilent BioAnalyzer High Sensitivity Kit OR Agilent TapeStation ScreenTape & Reagents		•	Manufacturer's recommendations		
Obtai	n:				
BD® A	AbSeq/Sample Tag PCR1 p	roduct		4 ℃	
1.5-m	L DNA LoBind [®] tubes				
0.2-m	nL PCR tubes				
1.5-m	1.5-mL tube magnetic rack				
Set up	Set up:				
Prepa	re fresh 80% ethyl alcohol				



Perform the purification in the post-amplification space.

- 1. Bring AMPure[®] XP beads to room temperature.
- 2. Make fresh 80% ethyl alcohol and use within 24 hours.



Adjust the volume of 80% ethyl alcohol depending on the number of samples. One sample requires 1 mL 80% ethyl alcohol.

- 3. Vortex the AMPure[®] XP beads until the beads are fully resuspended.
- 4. Briefly centrifuge the tubes with the ${\rm BD}^{\rm @}$ AbSeq/Sample Tag PCR1 product.
- 5. Combine the **four** tubes of **50** μ L PCR1 product into a new 1.5-mL tube.
- 6. Pipet-mix 10 times.



The volume must be exactly 200 μ L. If the volume is less than 200 μ L, use water to achieve the final volume.

- 7. Pipet **280** μ L of AMPure[®] XP beads (**1.4x**) into the tube.
- 8. Pipet-mix 10 times.
- 9. Briefly centrifuge the tube.



Avoid getting AMPure[®] XP beads on the lid of the tube. Residual AMPure[®] XP beads and PCR mix buffer can negatively impact downstream results.

- 10. Incubate at room temperature for 5 minutes.
- Place the tube on a magnet until the supernatant is clear (<5 minutes).
- 12. Remove and discard the supernatant.
- 13. Keeping the tube on the magnet, gently pipet 500 µL of fresh 80% ethyl alcohol into the tube.
- 14. Incubate for 30 seconds.
- 15. Remove and discard the supernatant without disturbing the beads.
- Repeat steps 12–14 once for a total of two ethyl alcohol washes.
- 17. Keeping the tube on the magnet, use a P20 pipette to remove and discard any residual supernatant from the tube.
- 18. Air-dry the beads at room temperature until the beads no longer look glossy (~3 minutes).



Do not overdry AMPure[®] XP beads after ethyl alcohol washes. Overdried beads appear cracked.

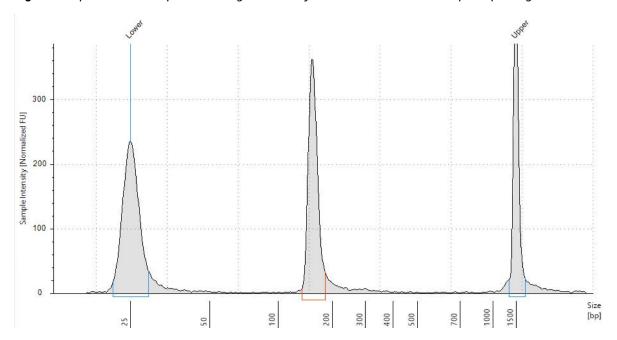
- 19. Remove the tube from the magnet.
- 20. Pipet **30 μL** of elution buffer into the tube.

- 21. Pipet-mix 10 times until the beads are fully resuspended.
- 22. Incubate at room temperature for 2 minutes.
- 23. Briefly centrifuge the tube.
- 24. Place the tube on a magnet until the supernatant is clear (~30 seconds).
- 25. Pipet the eluate (30 μ L) into a new 1.5-mL tube.

 The purified BD[®] AbSeq/Sample Tag PCR1 product is ready for Sample Tag PCR2.
- 26. Quantify the PCR1 products using one 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
- 27. Based on the yield of the largest peak (~160 bp), proceed as follows:
 - Dilute BD[®] AbSeq/Sample Tag PCR1 product to 0.1 1.1 ng/ μL for BD® AbSeq/Sample Tag index PCR (page 60)
 - Use 5 μL undiluted BD[®] AbSeq/Sample Tag PCR1 product for Sample Tag PCR2 (page 55)
 - STOP

Purified PCR product can be stored at -20 °C for up to 6 months.

Figure 2 Representative TapeStation High Sensitivity D1000 Trace - BD® AbSeq/Sample Tag PCR1



3.3 Sample Tag PCR2

Summary:

- Prepare Sample Tag PCR2 mix
- Amplify using Sample Tag PCR2 program

Item		BD Part Number	Preparation and Handling	Storage		
Equili	Equilibrate to room temperature:					
	Universal oligo	51-9025553				
	Sample Tag PCR2 primer	51-9025471	Equilibrate to room temperature 30 minutes before setting up Sample Tag PCR2. Centrifuge briefly.	−20 °C		
Nuclease-free water		51-9025552				
Leave	in freezer until ready to	use:				
	PCR master mix	51-9025466	Centrifuge briefly before adding to mix.	−20 °C		
Obtai	n:					
Purifie	ed Sample Tag PCR1 produ	uct.		4 °C		
Ice bu	Ice bucket					
0.2-mL PCR tubes						
Set up:						
Thern	nocycler with Sample Tag	PCR2 program				

This section describes how to amplify Sample Tag PCR1 products through PCR. The PCR primers include partial sequencing adapters that enable the additions of full-length sequencing indices during Index PCR.

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

Sample Tag PCR2 mix

Сар	Component	For 1 librαry (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	12.5	15.0	60.0	120.0
	1:10 dilution* of universal oligo	5.0	6.0	-	-
	Universal oligo	_	-	2.4	4.8
	Sample Tag PCR2 primer	3.0	3.6	14.4	28.8
	Nuclease-free water	24.5	29.4	139.2	278.4
	Total	45.0	54.0	216.0	432.0

^{*}If preparing Sample Tag PCR2 mix for 1 sample, dilute Universal Oligo 1:10 for pipetting accuracy.

- 2. Pipet-mix the Sample Tag PCR2 mix.
- 3. Place on ice until ready to use.
- 4. Pipet $45 \mu L$ of Sample Tag PCR2 mix into a 0.2-mL PCR tube for each sample.
- 5. Bring the tubes to the post-amplification workspace.
- 6. Add $5 \mu L$ undiluted Sample Tag PCR1 product. Total volume of reaction will be $50 \mu L$ for PCR2.
- 7. Pipet-mix 10 times.
- 8. Run the following PCR program.

Sample Tag PCR2 program

Step	Cycles	Temperature	Time
Hot start	1	98 °C	45 seconds
Denaturation		98 °C	15 seconds
Annealing	10 ^a	66 ℃	30 seconds
Extension		72 °C	1 minute
Final extension	1	72 °C	2 minutes
Hold	1	4°C	8

a. Recommended number of PCR cycles might require optimization for different cell types.



The PCR can run overnight.

3.4 Sample Tag PCR2 cleanup and quantification

Summary:

- Sample Tag PCR2 cleanup
- Quantify using Qubit Fluorometer

Item		BD Part Number	Preparation and Handling	Storage		
Equili	brate to room temperatu	ire:				
	Elution buffer	51-9025554	Centrifuge briefly.	−20 °C		
AMPu	re [®] XP magnetic beads		Manufacture's resource and etions			
Qubit	dsDNA HS Assay Kit		- Manufacturer's recommendations			
Obtai	n:					
Samp	le Tag PCR2 product			4 °C		
1.5-m	L DNA LoBind [®] tubes					
0.2-m	L PCR tubes					
0.2-m	0.2-mL tube magnetic rack					
Set u	Set up:					
Prepa	Prepare fresh 80% ethyl alcohol					

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



Perform PCR2 purification in the post-amplification workspace.

- 1. Bring AMPure® XP beads to room temperature.
- 2. Make fresh 80% ethyl alcohol and use within 24 hours.



Adjust the volume of 80% ethyl alcohol depending on the number of samples. One sample requires 0.5 mL 80% ethyl alcohol.

- 3. Vortex the AMPure® XP beads until the beads are fully resuspended.
- 4. Briefly centrifuge the tubes with the Sample Tag PCR2 product.



The volume must be exactly **50 \muL**. If the volume is less than 50 μ L, use water to achieve the final volume.

- 5. Pipet **60 μL** of AMPure[®] XP beads (**1.2x**) into the tube.
- 6. Pipet-mix 10 times.
- 7. Briefly centrifuge the tube.



Avoid getting AMPure[®] XP beads on the lid of the tube. Residual AMPure[®] XP beads and PCR mix buffer can negatively impact downstream results.

- 8. Incubate at room temperature for 5 minutes.
- 9. Place the tube on a magnet until the supernatant is clear (<5 minutes).
- 10. Remove and discard the supernatant.
- 11. Keeping the tube on the magnet, gently pipet $200 \mu L$ of fresh 80% ethyl alcohol into the tube.
- 12. Incubate for 30 seconds.
- 13. Remove and discard the supernatant without disturbing the beads.
- 14. Repeat steps 11–13 once for a total of two ethyl alcohol washes.
- 15. Keeping the tube on the magnet, use a P20 pipette to remove and discard any residual supernatant from the tube.
- 16. Air-dry the beads at room temperature until the beads no longer look glossy (~2 minutes).



Do not overdry AMPure $^{\circledR}$ XP beads after ethyl alcohol washes. Overdried beads appear cracked.

- 17. Remove the tube from the magnet.
- 18. Pipet 30 μ L of elution buffer into the tube.

- 19. Pipet-mix 10 times until the beads are fully resuspended.
- 20. Incubate at room temperature for 2 minutes.
- 21. Briefly centrifuge the tube.
- 22. Place the tube on a magnet until the supernatant is clear (~30 seconds).
- 23. Pipet the eluate (30 μ L) into a new 1.5-mL tube. The purified Sample Tag PCR2 product is ready for BD® AbSeq/Sample Tag index PCR (page 60)
- 24. Quantify the PCR2 products with a Qubit™ Fluorometer using the Qubit™ dsDNA HS Assay.
- 25. Dilute an aliquot of the PCR2 products with nuclease-free water to 0.1–1.1 $ng/\mu L$.



Purified PCR product can be stored at $-20\,^{\circ}\text{C}$ for up to 6 months.

3.5 BD® AbSeq/Sample Tag index PCR

Summary:

- Amplify using BD[®] AbSeq/Sample Tag index PCR program

Item B		BD Part Number	Preparation and Handling	Storage			
Equili	Equilibrate to room temperature:						
	Forward primer 1–8	Various					
	Multiomic reverse primer 1–8	Various	Equilibrate to room temperature 30 minutes before setting up Sample Tag Index PCR. Centrifuge briefly. Keep on ice until ready.	–20 °C			
	Nuclease-free water	51-9025552					
Leave	in freezer until reαdy to use						
	PCR master mix	51-9025466	Centrifuge briefly before adding to mix.	–20 °C			
Obtai	n:			,			
Purifie	ed BD® AbSeq PCR1/Sample T	ag PCR2 product		4 °C			
Ice bu	icket						
1.5-m	L DNA LoBind [®] tubes						
0.2-m	0.2-mL PCR tubes						
Set up	Set up:						
Therm	Thermocycler with Sample Tag index PCR program						
BD® A	AbSeq/Sample Tag index PCR	program					

This section describes how to generate Sample Tag libraries compatible with various sequencing platforms, by adding full-length sequencing adapters and indices through PCR.

1. In a new 1.5-mL tube, pipet the following components to create the BD[®] AbSeq/Sample Tag index PCR mix.

BD® AbSeq/Sample Tag index PCR Mix

Сар	Component	For 1 librαry (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	12.5	15.0	60.0	120.0
	Forward primer 1–8	2.0	2.4	-	-
0	Multiomic reverse primer 1–8	2.0	2.4	-	-
\bigcirc	Nuclease-free water	30.5	36.6	146.4	292.8
	Total	47.0	56.4	206.4	412.8

- 2. Pipet-mix the BD[®] AbSeq/Sample Tag index PCR mix.
- 3. For multiple samples, pipette 43 μ L of index PCR mix into a separate 0.2-mL PCR tube for each sample.
- 4. Add **2** μ L of forward primer and **2** μ L of multiomic reverse primer to each sample.
- 5. Place on ice until ready to use.
- 6. Dilute an aliquot of BD® AbSeq PCR1/Sample Tag PCR2 product (from BD® AbSeq/Sample Tag PCR1 cleanup (page 52) and Sample Tag PCR2 cleanup and quantification (page 57)) with water to 0.1-1.1 ng/µL.



Bring the BD® AbSeg/Sample Tag index PCR mix to the post-amplification workspace.

- 7. Add 3 μ L of theappropriate template. Total volume of reaction will be 50 μ L for index PCR.
 - BD[®] AbSeg/Sample Tag PCR1 product for BD[®]AbSeg index PCR
 - Sample Tag PCR2 product for Sample Tag index PCR



When performing dual indexing with multiple samples, ensure that the appropriate combinations of Forward Primer and Multiomic Reverse Primer are used.



Accurate primer assignment is essential to maintain sample identity during multiplexed sequencing.

8. Pipet-mix 10 times.

9. Run the following PCR program.

BD® AbSeq/Sample Tag index PCR program

Step	Cycles	Temperature	Time
Hot start	1	98 °C	45 seconds
Denaturation	Index PCR concentration ^a	98 ℃	15 seconds
Annealing	0.5–1.1 ng/μL: 6 cycles 0.25-0.5 ng/μL: 7 cycles	60 °C	30 seconds
Extension	0.1-0.25 ng/μL: 8 cycles	72 °C	1 minute
Final extension	1	72 ℃	2 minutes
Hold	1	4 °C	∞

a. Recommended PCR cycles might require optimization for different cell types.



The PCR can run overnight.

10. When the BD[®] AbSeq/Sample Tag index PCR program is complete, briefly centrifuge the tubes.

3.6 BD^{\circledR} AbSeq/Sample Tag index PCR cleanup and quality check

Summary:

- BD® AbSeq/Sample Tag index PCR cleanup
- Quality check using Qubit Fluorometer and Bioanalyzer/TapeStation

Item		BD Part Number	Preparation and Handling	Storage		
Equili	brate to room temperat	ure:				
	Elution buffer	51-9025554		20.00		
\bigcirc	Nuclease-free water	51-9025552	Centrifuge briefly.	−20 °C		
AMPu	re [®] XP magnetic beads					
Qubit	dsDNA HS Assay Kit					
OR	nt BioAnalyzer High Sensi nt TapeStation ScreenTap	-	Manufacturer's recommendations			
Obtai	n:					
BD® A	AbSeq/Sample Tag index	PCR product		4 ℃		
1.5-m	L DNA LoBind [®] tubes			,		
0.2-m	L PCR tubes					
0.2-m	0.2-mL PCR tube magnetic rack					
Set u	Set up:					
Prepa	re fresh 80% ethyl alcoho	ol				

This section describes how to perform single-sided AMPure[®] XP beads cleanup to remove primer dimers from the BD[®] AbSeq/Sample Tag index PCR products. The final product is purified double-stranded DNA with full-length adapter sequences.



Perform purification in the post-amplification workspace.

- 1. Bring AMPure® XP beads to room temperature.
- 2. Make fresh 80% ethyl alcohol and use within 24 hours.



Adjust the volume of 80% ethyl alcohol depending on the number of samples. One sample requires 0.5 mL 80% ethyl alcohol.

- 3. Vortex the AMPure® XP beads beads until the beads are fully resuspended.
- 4. Briefly centrifuge the tubes with BD® AbSeq/Sample Tag index PCR product.



The volume must be exactly **50 \muL**. If the volume is less than 50 μ L, use water to achieve the final volume.

- 5. Pipet 40 µL of AMPure® XP beads beads (0.8x) into the tube.
- 6. Pipet-mix 10 times.
- 7. Briefly centrifuge the tube.
- 8. Incubate at room temperature for 5 minutes.
- 9. Place the tube on a magnet until the supernatant is clear (<5 minutes).
- 10. Remove and discard the supernatant.
- 11. Keeping the tube on the magnet, gently pipet 200 μ L of fresh 80% ethyl alcohol into the tube.
- 12. Incubate for 30 seconds.
- 13. Remove and discard the supernatant without disturbing the beads.
- 14. Repeat steps 11–13 once for a total of two ethyl alcohol washes.
- 15. Keeping the tube on the magnet, use a P20 pipette to remove and discard any residual supernatant from the tube.
- 16. Air-dry the beads at room temperature until the beads no longer look glossy (~2 minutes).
- 17. Remove the tube from the magnet.
- 18. Pipet 30 μ L of elution buffer into the tube.
- 19. Pipet-mix 10 times until the beads are fully resuspended.
- 20. Incubate at room temperature for 2 minutes.
- 21. Briefly centrifuge the tube.
- 22. Place the tube on the magnet until the supernatant is clear (~30 seconds).

23. Pipet the eluate (30 μ L) into a new 1.5-mL LoBind[®] tube.

The purified eluate is the final sequencing library.



Purified PCR product can be stored at -20 °C for up to 6 months.

- 24. Quantify and perform quality control of the BD® AbSeq/Sample Tag index PCR product with a Qubit™ Fluorometer using the Qubit™ dsDNA HS Assay and one 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
 - The BD® AbSeq library should show a peak of ~264 bp.*
 - The Sample Tag library should show a peak of ~276 bp.*
 - * Exact size might vary due to instrument or sample purification efficiency. Select the region size between 200 and 500 bp.

Figure 3 Representative TapeStation High Sensitivity D5000 trace - BD® AbSeq index PCR product

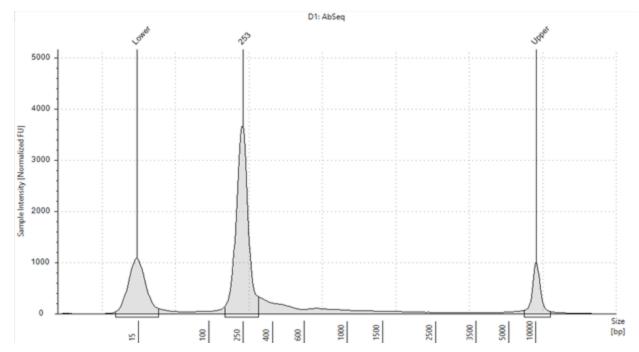
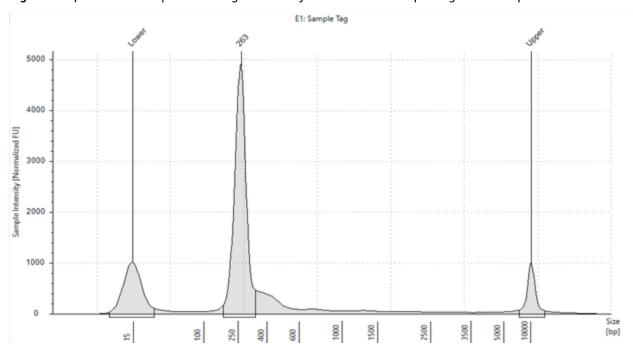


Figure 4 Representative TapeStation High Sensitivity D5000 trace - Sample Tag index PCR product



4. TCR/BCR library amplification

4.1 TCR/BCR PCR1

Summary:

- Prepare TCR/BCR PCR1 mix
- Amplify using TCR/BCR PCR1 program

Item BD Part Nu		BD Part Number	Preparation and Handling	Storage				
Equili	Equilibrate to room temperature:							
0	PCR master mix	91-1083						
	TCR/BCR universal oligo N1	91-1204						
	TCR N1 primer	91-1200	Equilibrate to room temperature 30 minutes before setting up TCR/BCR PCR1. Centrifuge briefly. Keep on ice	−20 °C				
	BCR N1 primer	91-1202	until ready.					
•	Bead RT/PCR enhancer	91-1082						
\bigcirc	Nuclease-free water	650000076						
Obtai	n:							
Enhar	nced cell capture beads aft	er WTA RPE denatu	ration	4 °C				
Ice bu	Ice bucket							
0.2-mL PCR tubes								
Set up:								
Therm	nocycler with TCR/BCR PCF	R1 program						

- 1. Obtain beads from step 30 of 2.1 WTA Random Priming and Extension (RPE) (page 31).
- 2. In the pre-amplification workspace, pipet the following reagents into a new 1.5-mL LoBind $^{\circledR}$ tube.

TCR/BCR PCR1 mix

Сар	Component	For 1 librαry (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
	TCR/BCR universal oligo N1	10.0	12.0	48.0	96.0
•	Bead RT/PCR enhancer	12.0	14.4	57.6	115.2
	TCR N1 primer ^a	2.4	2.9	11.5	23.0
	BCR N1 primer ^a	2.4	2.9	11.5	23.0
	Nuclease-free water	73.2	87.8	351.4	702.8
	Total	200.0	240.0	960.0	1920.0

a. If only doing TCR or BCR amplification, replace N1 primer volume with water. For example, if only doing TCR amplification, replace BCR N1 primer with water.

- 3. Gently vortex mix, briefly centrifuge, and place back on ice.
- 4. Briefly spin the tube with the bead suspension.
- 5. Place the tube of beads on a magnet for ≤1 minute.
- 6. Discard the supernatant.
- 7. Remove the tube from the magnet and resuspend the beads in **200 \muL** of TCR/BCR PCR1 mix to create the TCR/BCR PCR1 reaction mix.
- 8. Do not vortex.
- 9. Ensuring that the beads are fully resuspended, pipet **50** μ L of TCR/BCR PCR1 reaction mix with beads into each of four 0.2-mL PCR tubes.
- 10. Transfer any residual mix to one of the tubes.



Bring the TCR/BCR PCR1 reaction mix to the post-amplification workspace.

11. Run the following PCR program on the thermal cycler.

TCR/BCR PCR1 program

Step	Cycles	Temperature	Time
Hot start	1	95 °C ^a	3 minutes
Denaturation	Recommended PCR cycles for resting PBMCs ^b	95 °C	30 seconds
Annealing	7,500 – 10,000 cells: 11 cycles	60 °C	1 minute
Extension	20,000 cells: 10 cycles	72 °C	1 minute
Final extension	1	72 °C	5 minutes
Hold	1	4 °C	∞

a. To avoid beads settling due to prolonged incubation time on the thermal cycler before the denaturation step, it is critical to pause the instrument at 95 °C before loading the samples. Different thermal cyclers might have different pause time settings. In certain brands of thermal cyclers, however, we have observed a step-skipping error with the pause/unpause functions. To ensure that the full 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. b. Recommended PCR cycles might need to be optimized for different cell types and cell number.

12. 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.

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



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

- 14. After PCR, briefly centrifuge the tubes.
- 15. Put the tubes on a magnet for >30 seconds.
- 16. For each sample, collect and combine the supernatant from the four 0.2-mL PCR tubes into one new 1.5-mL LoBind[®] tube without disturbing the beads.
- 17. Discard the beads.

4.2 TCR/BCR PCR1 cleanup

Summary:

• TCR/BCR PCR1 cleanup

Item		BD Part Number	Preparation and Handling	Storage			
Equili	Equilibrate to room temperature:						
	Elution buffer	91-1084	Contribute				
\bigcirc	Nuclease-free water	65000076	Centrifuge briefly.	–20 °C			
AMPu	re [®] XP magnetic beads		Manufacturer's recommendations				
Obtai	n:						
TCR/E	SCR PCR1 product			4 °C			
1.5-m	L DNA LoBind [®] tubes						
0.2-m	L PCR tubes						
1.5-m	1.5-mL tube magnetic rack						
Set up	Set up:						
Prepa	Prepare fresh 80% ethyl alcohol						

This section describes how to perform a single-sided AMPure® XP beads cleanup to remove primer dimers from the TCR/BCR PCR1 products. The final product is purified double-stranded DNA.



Perform the purification in the post-amplification workspace.

1. Make fresh 80% ethyl alcohol for use within 24 hours.



Adjust the volume depending on the number of samples. One sample requires 1 mL of 80% ethyl alcohol.

- 2. Bring the AMPure® XP beads to room temperature. Vortex at a high speed for 1 minute until the beads are fully resuspended.
- 3. To **200 µL** of TCR/BCR PCR1 products, pipet **140 µL** AMPure[®] XP beads (**0.7x**) (from step 17 in TCR/BCR PCR1 (page 67)).
- 4. Pipet-mix 10 times. Incubate at room temperature for 5 minutes.
- 5. Place the 1.5-mL LoBind[®] tube on the magnet for **5 minutes**.
- 6. Discard the supernatant.
- 7. Keeping the tube on the magnet, gently add 500 μ L of fresh 80% ethyl alcohol into the tube and incubate for 30 seconds.
- 8. Discard the supernatant.
- 9. Repeat step 7–8 once for a total of two ethyl alcohol washes.
- 10. Keeping the tube on the magnet, use a P20 pipette to remove and discard any residual supernatant from the tube.
- 11. Air-dry the beads at room temperature for **5 minutes**.
- 12. Remove the tube from the magnet and resuspend the bead pellet in 50 μ L of elution buffer.
- 13. Vigorously pipet-mix until the beads are uniformly dispersed. Small clumps do not affect performance.
- 14. Incubate at room temperature for **2 minutes** and briefly centrifuge.
- 15. Place the tube on the magnet until the solution is clear, usually ~30 seconds.
- 16. Pipet the eluate (~50 μL) into a new 1.5-mL LoBind[®] tube (purified TCR/BCR PCR1 products).



Purified PCR product can be stored at -20 °C for up to 6 months.

4.3 TCR/BCR PCR2

Summary:

- Prepare TCR/BCR PCR2 mix
- Amplify using TCR/BCR PCR2 program

Item		BD Part Number	Preparation and Handling	Storage
Equilibrate to room temperature:				
\bigcirc	PCR master mix	91-1083	Equilibrate to room temperature 30 minutes before setting up PCR2. Centrifuge briefly. Keep on ice until ready.	−20 °C
	TCR/BCR universal oligo N2	91-1205		
	TCR N2 primer OR BCR N2 primer	91-1201 OR 91-1203		
\bigcirc	Nuclease-free water	650000076		
Obtain:				
Purified TCR/BCR PCR1 product				
Ice bucket				
0.2-mL PCR tubes				
Set up:				
Thermocycler with TCR/BCR PCR2 program				

Procedure steps:

This section describes how to amplify TCR/BCR products through PCR.

1. In the pre-amplification workspace, pipet reagents into a new 1.5-mL LoBind $^{\circledR}$ tube on ice.

TCR and BCR PCR2 mixes

Сар	Component	For 1 librαry (μL)	For 1 library with 20% overage (µL)	For 4 libraries with 20% overage (µL)	For 8 libraries with 20% overage (µL)
\bigcirc	PCR master mix	25.0	30.0	120.0	240.0
	TCR/BCR universal oligo N2	2.0	2.4	9.6	19.2
	TCR N2 primer OR BCR N2 primer ^a	6.0	7.2	28.8	57.6
	Nuclease-free water	12.0	14.4	57.6	115.2
	Total	45.0	54.0	216.0	432.0

a. PCR2 mixes for TCR and BCR are made separately.

- 2. Gently vortex mix, briefly centrifuge, and place back on ice.
- 3. Pipet $45 \mu L$ of PCR2 mix into one 0.2-mL PCR tube for each library.



Bring the TCR PCR2 mix and the BCR PCR2 mix to the post-amplification workspace.

- 4. Pipet 5.0 μL of PCR1 products into 45 μL of PCR2 mix for each library to create the TCR PCR2 reaction mix and BCR PCR2 reaction mix, respectively. Total volume of reaction will be $50~\mu L$ for PCR2.
- 5. Gently vortex and briefly centrifuge.
- 6. Run the following PCR program on the thermal cycler.

TCR/BCR PCR2 program

Step	Cycles	Temperature	Time	
Phase I:	1	95 ℃	3 minutes	
	15	95 ℃	30 seconds	
		75–61 °C	1 minute	Press Option > Auto
		72 °C	1 minute	Delta Starting cycle >
Phase II:	8	95 ℃	30 seconds	Delta > "1 degree" > Done
		60 ℃	1 minute	The temperature decreases by 1 °C each
		72 °C	1 minute	cycle, from 75–61 °C.
	1	72 °C	5 minutes	
	1	4 °C	∞	1



The PCR can run overnight.

4.4 TCR/BCR PCR2 cleanup

Summary:

- TCR/BCR PCR2 cleanup
- Quality check using Qubit Fluorometer

Preparation list:

Item		BD Part Number	Preparation and Handling	Storage	
Equili	brate to room temperatu	ire:			
	Elution buffer	91-1084	Combridge and building	−20 °C	
\bigcirc	Nuclease-free water	65000076	Centrifuge briefly.	-20 C	
AMPu	re [®] XP magnetic beads		M 6 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1		
Qubit	dsDNA HS Assay Kit		- Manufacturer's recommendations		
Obtai	n:				
TCR/E	SCR PCR2 product			4 °C	
1.5-m	L DNA LoBind [®] tubes				
0.2-m	0.2-mL PCR tubes				
0.2-mL PCR tube magnetic rack					
Set up	Set up:				
Prepa	Prepare fresh 80% ethyl alcohol				

Procedure steps:

This section describes how to perform a single-sided AMPure[®] XP beads cleanup to remove primer dimers from the TCR and BCR PCR2 products. The final product is purified double-stranded DNA.



Perform PCR2 purification in the post-amplification workspace.

1. Make fresh 80% ethyl alcohol for use within 24 hours.



Adjust the volume depending on the number of samples. One sample requires 0.5 mL of 80% ethyl alcohol.

- 2. Bring AMPure[®] XP beads to room temperature and vortex at high speed for **1 minute** until beads are fully resuspended.
- 3. To **50** μ L PCR2 products, pipet **35** μ L of AMPure[®] XP beads (**0.7**x).
- 4. Pipet-mix 10 times and incubate at room temperature for 5 minutes.
- 5. Place the tube on the magnet for 3 minutes. Discard the supernatant.
- 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**.
- 7. Discard the supernatant.
- 8. Repeat step 6–7 once for a total of two ethyl alcohol 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 3 minutes.
- 11. Remove the tube from the magnet and resuspend the bead pellet in $50 \mu L$ of elution buffer. Pipet-mix until the beads are fully resuspended.
- 12. Incubate at room temperature for **2 minutes** and briefly centrifuge.
- 13. Place the tube on the magnet until the solution is clear, usually ~30 seconds.
- 14. Pipet the eluate (~50 μ L) into a new 1.5-mL LoBind[®] tube.



Purified PCR product can be stored at -20 °C for up to 6 months.

15. Estimate the concentration by quantifying 2 µL of the TCR/BCR PCR2 library with a Qubit™ Fluorometer using the Qubit™ dsDNA HS Assay Kit. Follow the manufacturer's instructions.

4.5 TCR/BCR RPE

Summary:

- Prepare random priming mix and extension enzyme mix
- Anneal random primers
- Extend random primers

Preparation list:

Item	Item BD Part Numb		Preparation and Handling	Storage		
Equili	brate to room temperature:					
\bigcirc	TCR/BCR extension buffer	91-1206				
\circ	TCR/BCR extension primers	91-1208				
	dNTP	650000077	Equilibrate to room temperature 30 minutes before setting up RPE. Centrifuge briefly.	−20 °C		
\bigcirc	Nuclease-free water	650000076				
	Elution buffer	91-1084				
Leave	Leave in freezer until ready to use:					
\bigcirc	TCR/BCR extension enzyme	91-1207	Centrifuge briefly before adding to mix.	–20 °C		
Obtai	n:					
Purifie	ed TCR/BCR PCR2 product					
Ice bu	icket					
1.5-m	1.5-mL DNA LoBind [®] tubes					
0.2-m	0.2-mL PCR tubes					
Set up:						
Therm	Thermocycler with TCR/BCR denaturation and random priming program					
Therm	nocycler with TCR/BCR random	n primer extension p	orogram			

Procedure steps:

1. Dilute an aliquot of the TCR and BCR PCR2 products with water to 1.0 ng/µL.



If PCR2 concentration is <1 $\,\mathrm{ng}/\mu\mathrm{L}$, increase the volume of PCR2 product needed to ensure 5 $\,\mathrm{ng}$ total concentration and decrease the volume of water in the random primer mix accordingly.

2. In pre-amplification workspace, pipet the following reagents into a new 1.5 mL LoBind $^{\circledR}$ tube:

Random primer mix

Сар	Component	For 1 librαry (μL)	For 1 library with 20% overage (µL)	For 4 libraries with 20% overage (µL)	For 8 libraries with 20% overage (µL)
	TCR/BCR extension buffer	5.0	6.0	24.0	48.0
0	TCR/BCR extension primers	2.5	3.0	12.0	24.0
	Nuclease-free water	Up to 34.0	Up to 40.8	Up to 163.2	Up to 326.4
	Total	41.5	49.8	199.2	398.4

- 3. Pipet-mix the random primer mix and keep at room temperature.
- 4. Pipet 41.5 μ L of random primer mix into one 0.2-mL PCR tube for each library.



Bring the TCR RPE mix and the BCR RPE mix to the post-amplification workspace.

- 5. Add **5** μ L of 1.0 ng/ μ L purified TCR or BCR PCR2 products into each 0.2-mL PCR tube containing random primer mix.
- 6. Total volume of reaction will be $46.5 \mu L$ for random priming.
- 7. Perform denaturation and random priming on thermocycler using the following program:

Program

Temperature	Time	Cycles
95 °C	5 minutes	
37 ℃	5 minutes	1
25 ℃	15 minutes	

- 8. Briefly centrifuge the tube and keep at room temperature.
- 9. In pre-amplification workspace, pipet the following reagents into a new 1.5 mL LoBind[®] tube:

Primer extension enzyme mix

Сар	Component	For 1 librαry (μL)	For 1 library with 20% overage (µL)	For 4 libraries with 20% overage (µL)	For 8 libraries with 20% overage (µL)
	dNTP	2.0	2.4	9.6	19.2
\bigcirc	TCR/BCR extension enzyme	1.5	1.8	7.2	14.4
	Total	3.5	4.2	16.8	33.6

- 10. Gently vortex mix, centrifuge, and place on ice.
- 11. Add $3.5~\mu L$ primer extension enzyme mix to the random priming reaction tube to bring total volume up to **50 \mu L**. Run the following protocol on a thermocycler for extension:

Program

Temperature	Time	Cycles
25 ℃	10 minutes	
37 ℃	15 minutes	1
45 °C	10 minutes	
55 ℃	10 minutes	

12. When the PCR program is complete, briefly centrifuge the tubes.

4.6 TCR/BCR RPE cleanup

Summary:

• TCR/BCR RPE cleanup

Preparation list:

Item		BD Part Number	Preparation and Handling	Storage			
Equili	Equilibrate to room temperature:						
	Elution buffer	91-1084	Contribute by office	−20 °C			
\bigcirc	Nuclease-free water	65000076	Centrifuge briefly.	-20 C			
AMPu	re [®] XP magnetic beads		Manufacturer's recommendations				
Obtai	n:						
TCR/E	SCR RPE product			4 °C			
1.5-m	L DNA LoBind [®] tubes						
0.2-m	L PCR tubes						
0.2-m	0.2-mL PCR tube magnetic rack						
Set u	Set up:						
Prepa	Prepare fresh 80% ethyl alcohol						

Procedure steps:



Perform purification in the post-amplification workspace.

1. Make fresh 80% ethyl alcohol for use within 24 hours.



Adjust the volume depending on the number of samples. One sample requires 0.5 mL of 80% ethyl alcohol.

- 2. Bring AMPure® XP beads to room temperature and vortex at high speed for 1 minute until beads are fully resuspended.
- 3. To the **50 \muL** of TCR and BCR RPE products, add **90 \muL** AMPure[®] XP beads (**1.8x**).
- 4. Pipet-mix 10 times and incubate at room temperature for 5 minutes.
- 5. Place the tube on the magnet for 3 minutes.
- 6. Discard the supernatant.
- 7. Keeping the tube on the magnet, gently add $200 \mu L$ of fresh 80% ethyl alcohol into the tube and incubate for 30 seconds.
- 8. Discard the supernatant.
- 9. Repeat step 7–8 once for a total of two ethyl alcohol washes.
- 10. Keeping the tube on the magnet, use a P20 pipette to remove and discard any residual supernatant from the tube.
- 11. Air-dry the beads at room temperature for 3 minutes.
- 12. Remove tubes from the magnet and add $50 \mu L$ of elution buffer.
- 13. Incubate at room temperature for 2 minutes and briefly centrifuge.
- 14. Place the tube on the magnet until the solution is clear, usually ≤ 30 seconds.
- 15. Pipet the entire eluate (\sim 50 μ L) into a new 1.5-mL LoBind[®] tube separately (purified TCR and BCR RPE products).

4.7 TCR/BCR index PCR

Summary:

- Prepare TCR/BCR index mix
- Amplify using TCR/BCR index program

Preparation list:

Item BD Pa		BD Part Number	Preparation and Handling	Storage		
Equili	Equilibrate to room temperature:					
	Forward primer 1–8	Various				
\bigcirc	Multiomic reverse primer 1–8	Various	Equilibrate to room temperature 30 minutes before setting up TCR/BCR Index PCR.	−20 °C		
0	Nuclease-free water	650000076	Centrifuge briefly. Keep on ice until ready.			
\bigcirc	PCR master mix	91-1083				
Obtai	n:					
Purifie	ed TCR/BCR RPE product					
Ice bu	icket					
1.5-m	1.5-mL DNA LoBind [®] tubes					
0.2-m	0.2-mL PCR tubes					
Set up:						
Therm	nocycler with TCR/BCR index P	CR program				

Procedure steps:

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

1. In the pre-amplification workspace, pipet reagents into a new 1.5-mL LoBind $^{(8)}$ tube on ice.

TCR/BCR index PCR mix

Сар	Component	For 1 librαry (μL)	For 1 library with 20% overage (µL)	For 4 libraries with 20% overage (µL)	For 8 libraries with 20% overage (μL)
\bigcirc	PCR master mix	25.0	30.0	120.0	240.0
	Forward primer 1–8	2.0	2.4	N/A	N/A
	Multiomic reverse primer 1–8	2.0	2.4	N/A	N/A
	Total	29.0	34.8	120.0	240.0

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



Bring the TCR/BCR index PCR mix to post-amplification workspace.

- 3. For multiple samples, pipet 25 μ L of index PCR mix into separate 0.2-mL PCR tubes to each sample.
- 4. Add $2 \mu L$ of forward primer and $2 \mu L$ of multiomic reverse primer to each sample.
- 5. Add 21 μ L of TCR/BCR RPE purified products into 29 μ L of TCR/BCR index PCR mix. Total volume of reaction will be $50 \mu L$ for index PCR.
- 6. Gently vortex, and briefly centrifuge.
- 7. Run the following PCR program on the thermal cycler.

TCR/BCR index PCR program

Step	Cycles	Temperαture	Time
Hot start	1	95 ℃	3 minutes
Denaturation		95 ℃	30 seconds
Annealing	10	60 °C	30 seconds
Extension		72 °C	30 seconds
Final extension	1	72 °C	1 minute
Hold	1	4 °C	∞



The PCR can run overnight.

4.8 TCR/BCR index PCR cleanup and quality check

Summary:

- TCR/BCR index PCR cleanup
- Quality check using Qubit Fluorometer and BioAnalyzer/TapeStation

Preparation list:

Item		BD Part Number	Preparation and Handling	Storage			
Equili	Equilibrate to room temperature:						
	Elution buffer	91-1084	Combridge on bright	20 °C			
\bigcirc	Nuclease-free water	650000076	Centrifuge briefly.	–20 °C			
AMPu	re [®] XP magnetic beads						
Qubit	dsDNA HS Assay Kit		Manufacturer's recommendations				
OR	nt BioAnalyzer High Sensit nt TapeStation ScreenTap	-	— Manufacturer's recommendations				
Obtai	n:						
TCR/E	CR index PCR product		4 °C				
0.2-m	0.2-mL PCR tubes						
0.2-m	0.2-mL PCR tube magnetic rack						
Set up	Set up:						
Prepa	re fresh 80% ethyl alcohol			_			

Procedure steps:

This section describes how to perform a single-sided AMPure® XP beads cleanup to remove primer dimers from the TCR/BCR index PCR products. The final product is purified double-stranded DNA with full-length Illumina adapter sequences.



Perform index PCR purification in the post-amplification workspace.

1. Make fresh 80% ethyl alcohol for use within 24 hours.

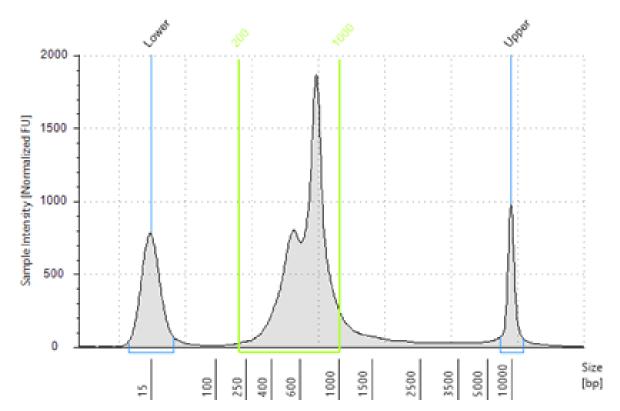


Adjust the volume depending on the number of samples. One sample requires 0.5 mL of 80% ethyl alcohol.

- 2. Bring AMPure® XP beads to room temperature and vortex at high speed for 1 minute until the beads are fully resuspended.
- 3. Briefly centrifuge all the index PCR products.
- 4. Transfer 40 μ L of the TCR and/or BCR index PCR products to a new 0.2 mL PCR tubes.
- 5. Pipet **26 μL** of AMPure[®] XP beads (**0.65x**).
- 6. Pipet-mix 10 times and incubate at room temperature for 5 minutes.
- 7. Place the tube on the strip tube magnet for 3 minutes.
- 8. Discard the supernatant.
- 9. Keeping the tube on the magnet, gently add $200 \mu L$ of fresh 80% ethyl alcohol into the tube and incubate for 30 seconds.
- 10. Discard the supernatant.
- 11. Repeat step 9–10 for a total of two ethyl alcohol washes.
- 12. Keeping the tube on the magnet, use a P20 pipette to remove and discard the residual supernatant from the tube.
- 13. Air-dry the beads at room temperature for 1 minute.
- 14. Remove the tube from the magnet and resuspend the bead pellet in 50 μ L of elution buffer. Pipet-mix until the beads are fully resuspended.
- 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 entire eluate (\sim 50 μ L) into a new 1.5-mL LoBind[®] tube (final sequencing libraries).
- 18. Perform quality control before freezing samples.
 - a. 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. Follow the manufacturer's instructions. The expected concentration of the libraries is >1.5 ng/ μ L.

b. Measure the average fragment size of the TCR/BCR library 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/ μ L. Follow the manufacturer's instructions.

Figure 5 Sample TapeStation high-sensitivity D5000 trace - TCR index PCR product



Sample Intensity [Normalized FU] Size [bp]

Figure 6 Sample TapeStation high-sensitivity D5000 trace - BCR index PCR product

Purified PCR product can be stored at $-20\,^{\circ}\text{C}$ for up to 6 months.

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 WTA mRNA, BD[®] AbSeq, Sample Tag, TCR, and BCR libraries.

Read requirements for libraries

Library	Read requirement for data analysis
WTA mRNA	10,000–100,000 reads/cell
Sample Tag: Samples from the same type of cell (combining different donor PBMCs)	120 reads/cell
Sample Tag: Samples from different types of cells (combining cell lines with PBMCs)	600 reads/cell
BD® AbSeq	300 reads/cell/AbSeq ^a
TCR	~5,000 reads/T cell
BCR	~5,000 reads/B cell

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

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 highly saturated deep sequencing to identify the majority of UMIs in the library.

Pooling libraries for sequencing

The efficiency of sequencing on Illumina instruments is influenced by many conditions, library size being one of them. The TCR and BCR libraries are \sim 200–300 bp larger than the WTA mRNA library and \sim 600 bp larger than the BD[®] AbSeq and Sample Tag libraries which will cause them to produce less sequencing data if pooled in a 1:1 ratio with the other libraries. To overcome the difference in sequencing efficiency, more DNA of the TCR and BCR libraries needs to be included in the pool than would be expected when calculating ratios based on read depth. The following tables show examples of different pooling strategies and the expected sequencing outcome, with and without correction for the size of the TCR and BCR libraries. Validation data indicates a 5X

volume correction factor is needed for sequencing TCR and BCR libraries with WTA mRNA, BD^{\circledR} AbSeq, and Sample Tag libraries.



BD[®] AbSeq and Sample Tag libraries can be sequenced together or separately from WTA and TCR/BCR libraries. For optimal clustering of TCR/BCR libraries on Illumina platforms, however, we recommend sequencing BD[®] AbSeq and Sample Tag libraries separately. Recommendations for sequencing BD[®] AbSeq and Sample Tag libraries alone or in a pool with other libraries are in the next section.

Example of pooling with correction

In this example, a total of 5,000 enriched T cells were processed. These calculations are using a correction factor of 5 for the TCR library to overcome the differences in sequencing efficiency. The amount of data needing to be generated (Column D) is based on the cell number (Column B) and expected number of reads per cell (Column C). Based on this example, 165.6 million reads are needed to achieve the appropriate read depths. Changing the pooling ratios by correcting for the lower TCR sequencing efficiency will help ensure the correct amount of data is generated for each library. This modified pooling scheme, however, does not change the total amount of data needing to be generated, which is 165.6 million reads.

Pooling for WTA mRNA, TCR, Ab® Seq, and Sample Tag libraries

А	В	С	D	E	F	G	Н	I	J
Library type	Number of cells	Expected reads/cell	Reads needed	Pooling ratio before correction	Correction	Reads needed for pooling	Pooling ratio with correction	Sequencing results	Sequencing results (reads/cell)
WTA mRNA	5,000	25,000	125,000,000	75.5%	N/A	125,000,000	47.1%	125,000,000	25,000
TCR	5,000	5,000	25,000,000	15.1%	5 ^a	125,000,000	47.1%	25,000,000	5,000
BD [®] AbSeq	5,000	3,000	15,000,000	9.1%	N/A	15,000,000	5.6%	15,000,000	3,000
Sample Tag	5,000	120	600,000	0.4%	N/A	600,000	0.2%	600,000	120
Total		•	165,600,000 ^b	100%	-	265,600,000 ^c	100%	165,600,000	-

- a. The 5X correction factor is a recommended starting point and some fine tuning might be required to achieve the optimal library balance.
- b. Total amount of data to be requested from the sequencing facility plus 3% PhiX.
- c. Read total only for pooling purposes.

After sequencing, the total amount of data generated (Column I) as well as the reads/cell for each library (Column J) are as expected (Columns D and C, respectively). The correction for library pooling did not change the amount of data generated (165.6 million reads) but helped ensure the data was spread out appropriately to each library.

Example of pooling with a mixed population

The following table shows the pooling logic for two samples of purified B and T cells, each stained with a different sample tag and 10-plex BD[®] AbSeq panel.

Pooling for WTA mRNA, TCR, BCR, BD® AbSeq, and Sample Tag libraries

А	В	С	D	E	F	G	Н	I	J
Library type	Number of cells	Expected reads/cell	Reads needed	Pooling ratio before correction	Correction	Reads needed for pooling	Pooling ratio with correction	Sequencing results	Sequencing results (reads/cell)
WTA mRNA	10,000	25,000	250,000,000	74.4%	N/A	250,000,000	46.6%	250,000,000	25,000
TCR	7,000	5,000	35,000,000	10.4%	5 ^a	175,000,000	32.6%	35,000,000	5,000
BCR	3,000	5,000	15,000,000	4.5%	5 ^a	75,000,000	14%	15,000,000	5,000
BD [®] AbSeq	10,000	3,000	30,000,000	8.9%	N/A	30,000,000	5.6%	30,000,000	3,000
Sample Tag	10,000	600	6,000,000	1.8%	N/A	6,000,000	1.1%	6,000,000	600
Total			336,000,000 ^b	100%	-	536,000,000 ^c	100%	336,000,000	_

a. The 5X correction factor is a recommended starting point and some fine tuning may be required to achieve the optimal library balance.

Example of pooling with correction while sequencing the BD[®] AbSeq and Sample Tag libraries separately

The following table shows the pooling logic for the previous example of a mixed population where the BD^{\otimes} AbSeq and Sample Tag libraries are sequenced together and the WTA mRNA, TCR, and BCR libraries are sequenced together.

Pooling for BD® AbSeq and Sample Tag libraries

Α	В	С	D	Е	F	G
Library type	Number of cells	Expected reads/cell	Reads needed	Pooling ratio	Sequencing results	Sequencing results (reads/cell)
BD [®] AbSeq	10,000	3,000	30,000,000	83.3%	30,000,000	3,000
Sample Tag	10,000	600	6,000,000	16.7%	6,000,000	600
Total			360,000,000 ^α	100%	360,000,000	-

a. Total amount of data to be requested from the sequencing facility plus 1% PhiX.

b. Total amount of data to be requested from the sequencing facility plus 3% PhiX.

c. Read total only for pooling purposes.

Pooling for WTA mRNA	, TCR, and BCR libraries
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Α	В	С	D	Е	F	G	Н	I	J
Library type	Number of cells	Expected reads/cell	Reads needed	Pooling ratio before correction	Correction	Reads needed for pooling	Pooling ratio with correction	Sequencing results	Sequencing results (reads/cell)
WTA mRNA	10,000	25,000	250,000,000	83%	N/A	250,000,000	50%	250,000,000	25,000
TCR	7,000	5,000	35,000,000	12%	5 ^a	175,000,000	35%	35,000,000	5,000
BCR	3,000	5,000	15,000,000	5%	5 ^a	75,000,000	15%	15,000,000	5,000
Total	•	•	300,000,0000	100%	-	500,000,000	100%	300,000,000	-

a. The 5X correction factor is a recommended starting point and some fine tuning may be required to achieve the optimal library balance.

Additional considerations

- The 5X volume correction factor for TCR/BCR libraries is a recommended starting place for pooling these libraries. This might need to be adjusted to accommodate different types of flow cells (for example, patterned vs non-patterned).
- It can be easier to achieve the desired sequencing depth when sequencing multiple TCR or BCR libraries alone since all the libraries are the same size. Pooling will not require a correction and will only be dependent on the number of cells and the reads/cell. This scheme, however, would require 10–15% PhiX, rather than the 3% PhiX when sequencing with the WTA mRNA library.
- Sequencing BD[®] AbSeq and Sample Tag libraries separately can help ensure each library receives enough data during sequencing due to size discrepancies. However, these libraries can be successfully sequenced in combination with WTA mRNA, TCR, and BCR libraries.
- All libraries derived from the same cartridge can be indexed with the same Illumina indices or reverse index
 primer from the BD Rhapsody™ reagents. The primary analysis pipeline can differentiate the library types
 (for example, WTA mRNA vs TCR) based on their structure and sequences. Demultiplexing statistics are
 reported from the pipeline, but should these statistics be desired prior to running the pipeline, then unique
 indices will be required for each library.

For additional support with pooling and sequencing, reach out to your local Field Application Specialist (FAS) or scomix@bd.com.

b. Total amount of data to be requested from the sequencing facility plus 3% PhiX.

c. Read total only for pooling purposes.

Sequencing recommendations

BD® AbSeq/Sample Tag libraries

For a NextSeq High or Mid Output and MiniSeq High or Mid Output runs, load the flow cell at a concentration between 1.8–2.2 pM with 1% PhiX for a sequencing run.

Required parameters

Parameter	Requirement
Platform	Illumina and Element*
Paired-end reads	Recommended: Read 1: 52 cycles; Read 2: 72 cycles Index 1 (i7): 8 cycles; Index 2 (i5): 8 cycles
PhiX	Required (1%)
Analysis	See the BD [®] Single-Cell Multiomics Bioinformatics Handbook

^{*} To review Index sequences, see the Appendix (page 96).

WTA and TCR/BCR libraries (with or without BD® AbSeq/Sample Tag).

For a NextSeq High or Mid Output run and MiniSeq High or Mid Output run, load the flow cell at a concentration between 1.4–1.8 pM with 3% PhiX for a sequencing run.



If using less than 10,000 reads/cell for the WTA library, increase PhiX percentage to 5–10% to account for lower library diversity.

Set up sequencing run on Illumina[®] BaseSpace. Enter the pooled libraries as one sample if libraries were made with the same Library Forward primer but with different i7 indices.

Required parameters

Parameter	Requirement
Platform	Illumina and Element*
Paired-end reads	Minimum: Read 1: 65 cycles; Read 2: 150 cycles Recommended: Read 1: 150 cycles; Read 2: 150 cycles Index 1 (i7): 8 cycles; Index 2 (i5): 8 cycles
PhiX	Required (3%)
Analysis	See the BD [®] Single-Cell Multiomics Bioinformatics Handbook

^{*} To review Index sequences, see the Appendix (page 96).

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)		
NovαSeq 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)		
NovαSeq 6000 S1 (Single Flow Cell)	2×50, 2×100, 2×150*	350–650 pM (standard workflow)		
NovαSeq 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)		
NovαSeq 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. Loading concentration may need to be titrated to optimize yield.

Sequencing analysis pipeline

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

Troubleshooting

Library preparation

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.
Lower number of reads/cell than expected from mRNA.	264 bp or ~160 bp products taking reads from mRNA library.	If noise peak is seen in the 264 bp or ~160 bp range, perform a second round of AMPure purification according to WTA index PCR cleanup and quality check (page 46).

TCR/BCR metrics

Observation	Possible causes	Recommended solutions
Low yield of TCR/BCR PCR2, unexpected profile of TCR/BCR	Incorrect components were used.	Ensure BD Rhapsody™ Enhanced Cartridge Reagent Kit V3 (PN 667052) and TSO Next (PN 91-1295) are used for all TCR/BCR Next assays.
Index products, or low TCR/BCR pairing efficiency.	Incorrect handling during earlier protocol steps (cDNA synthesis, template switching, denaturation, self-hybridization, and TCR/BCR extension).	Carefully follow all protocol steps in Section 1, especially noting warnings for thermomixer settings, reagent storage temperatures, and incubation timing.
	Low viability cells or other challenging samples.	Optimization might be required. Contact your local Field Application Specialist (FAS) or scomix@bd.com.

Sequencing

Observation	Possible causes	Recommended solutions
Over-clustering on the flow cell due to under-estimation of the library.	Inaccurate measurement of the library concentration.	Quantify 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 sequencing platform documentation.
One or more libraries are not correctly demultiplexed.	Failure to correctly detect one or more index sequences during sequencing.	Try demultiplexing with a single index. For Illumina sequencers, adjust the mismatch threshold from the default of 1 to allow 2 mismatches.
Failed cluster generation or other sequencing challenges with low-plex pooling.	Sequencing instrument-specific color balance guidelines were not met. For example, the NovaSeq X platform requires signal in the green channel for every cycle. Low % reads in the green channel in a given cycle might not be sufficient.	Consult indexing and pooling guidelines for your sequencing platform. Be sure to consider the final pooling ratio—some libraries might make up a small fraction of the final pool.

Appendix

Oligonucleotides in BD OMICS-One™ WTA Next Amplification Kit

The following table lists the sequences of all oligonucleotides included in the BD OMICS-One $^{\text{\tiny M}}$ WTA Next Amplification Kit (Catalog No. 572620).

Oligonucleotide	Use	Part/Catalog No.	Sequence (5' – 3')
BD OMICS-One™ Universal Oligo	Forward primer for WTA RPE PCR, Sample Tag PCR1 and PCR2, and BD® AbSeq PCR1	51-9025553	ACA CGA CGC TCT TCC GAT CT
BD OMICS-One™ AbSeq Primer	Reverse primer for BD® AbSeq PCR1	51-9025468	CAG ACG TGT GCT CTT CCG ATC T
BD OMICS-One™ WTA Extension Primer	Random primer for WTA RPE	51-9025467	GGC TCG GAG ATG TGT ATA AGA GAC AG NNNNNNNN
BD OMICS-One™ WTA Amplification Primer	Reverse primer for WTA RPE PCR	51-9025469	GGC TCG GAG ATG TGT ATA AGA GAC AG

Oligonucleotide	Use	Part/Catalog No.	Sequence (5' – 3')
BD OMICS-One™ Library Forward Primer 1	Forward primer for WTA, Sample Tag, and BD [®] AbSeq	51-9025472	AAT GAT ACG GCG ACC ACC GAG ATC TAC AC TATAGCCT ACACTCTTTCCCTACACGACGCTCTTCCGAT*C*T
BD OMICS-One™ Library Forward Primer 2	index PCR	51-9025473	AAT GAT ACG GCG ACC ACC GAG ATC TAC AC ATAGAGGC ACACTCTTTCCCTACACGACGCTCTTCCGAT*C*T
BD OMICS-One™ Library Forward Primer 3		51-9025474	AAT GAT ACG GCG ACC ACC GAG ATC TAC AC CCTATCCT ACACTCTTTCCCTACACGACGCTCTTCCGAT*C*T
BD OMICS-One™ Library Forward Primer 4		51-9025475	AAT GAT ACG GCG ACC ACC GAG ATC TAC AC GGCTCTGA ACACTCTTTCCCTACACGACGCTCTTCCGAT*C*T
BD OMICS-One™ Library Forward Primer 5		51-9025476	AAT GAT ACG GCG ACC ACC GAG ATC TAC AC AGGCGAAG ACACTCTTTCCCTACACGACGCTCTTCCGAT*C*T
BD OMICS-One™ Library Forward Primer 6		51-9025477	AAT GAT ACG GCG ACC ACC GAG ATC TAC AC TAATCTTA ACACTCTTTCCCTACACGACGCTCTTCCGAT*C*T
BD OMICS-One™ Library Forward Primer 7		51-9025478	AAT GAT ACG GCG ACC ACC GAG ATC TAC AC CAGGACGT ACACTCTTTCCCTACACGACGCTCTTCCGAT*C*T
BD OMICS-One™ Library Forward Primer 8		51-9025479	AAT GAT ACG GCG ACC ACC GAG ATC TAC AC GTACTGAC ACACTCTTTCCCTACACGACGCTCTTCCGAT*C*T

Oligonucleotide	Use	Part/Catalog No.	Sequence (5' – 3')
BD OMICS-One™ WTA Library Reverse Primer 1	Reverse primer for WTA index PCR	51-9025480	CAA GCA GAA GAC GGC ATA CGA GAT TACTACGC GTCTCGTGGGCTCGGAGATGTGTATAAGA*G
BD OMICS-One™ WTA Library Reverse Primer 2		51-9025600	CAA GCA GAA GAC GGC ATA CGA GAT AGGCTCCG GTCTCGTGGGCTCGGAGATGTGTATAAGA*G
BD OMICS-One™ WTA Library Reverse Primer 3		51-9025482	CAA GCA GAA GAC GGC ATA CGA GAT GCAGCGTA GTCTCGTGGGCTCGGAGATGTGTATAAGA*G
BD OMICS-One™ WTA Library Reverse Primer 4		51-9025483	CAA GCA GAA GAC GGC ATA CGA GAT CTGCGCAT GTCTCGTGGGCTCGGAGATGTGTATAAGA*G
BD OMICS-One™ WTA Library Reverse Primer 5		51-9025484	CAA GCA GAA GAC GGC ATA CGA GAT GAGCGCTA GTCTCGTGGGCTCGGAGATGTGTATAAGA*G
BD OMICS-One™ WTA Library Reverse Primer 6		51-9025485	CAA GCA GAA GAC GGC ATA CGA GAT CGCTCAGT GTCTCGTGGGCTCGGAGATGTGTATAAGA*G
BD OMICS-One™ WTA Library Reverse Primer 7		51-9025486	CAA GCA GAA GAC GGC ATA CGA GAT GTCTTAGG GTCTCGTGGGCTCGGAGATGTGTATAAGA*G
BD OMICS-One™ WTA Library Reverse Primer 8		51-9025487	CAA GCA GAA GAC GGC ATA CGA GAT ACTGATCG GTCTCGTGGGCTCGGAGATGTGTATAAGA*G

Oligonucleotide	Use	Part/Catalog No.	Sequence (5' – 3')
BD OMICS-One™ Multiomic Library Reverse Primer 1	Reverse primer for Sample Tag and BD [®] AbSeq index	51-9025489	CAA GCA GAA GAC GGC ATA CGA GAT TACTACGC GTGACTGGAGTTCAGACGTGTGCTCTTCCGATC*T
BD OMICS-One™ Multiomic Library Reverse Primer 2	PCR	51-9025490	CAA GCA GAA GAC GGC ATA CGA GAT AGGCTCCG GTGACTGGAGTTCAGACGTGTGCTCTTCCGATC*T
BD OMICS-One™ Multiomic Library Reverse Primer 3		51-9025492	CAA GCA GAA GAC GGC ATA CGA GAT GCAGCGTA GTGACTGGAGTTCAGACGTGTGCTCTTCCGATC*T
BD OMICS-One™ Multiomic Library Reverse Primer 4		51-9025493	CAA GCA GAA GAC GGC ATA CGA GAT CTGCGCAT GTGACTGGAGTTCAGACGTGTGCTCTTCCGATC*T
BD OMICS-One™ Multiomic Library Reverse Primer 5		51-9025494	CAA GCA GAA GAC GGC ATA CGA GAT GAGCGCTA GTGACTGGAGTTCAGACGTGTGCTCTTCCGATC*T
BD OMICS-One™ Multiomic Library Reverse Primer 6		51-9025496	CAA GCA GAA GAC GGC ATA CGA GAT CGCTCAGT GTGACTGGAGTTCAGACGTGTGCTCTTCCGATC*T
BD OMICS-One™ Multiomic Library Reverse Primer 7		51-9025497	CAA GCA GAA GAC GGC ATA CGA GAT GTCTTAGG GTGACTGGAGTTCAGACGTGTGCTCTTCCGATC*T
BD OMICS-One™ Multiomic Library Reverse Primer 8		51-9025498	CAA GCA GAA GAC GGC ATA CGA GAT ACTGATCG GTGACTGGAGTTCAGACGTGTGCTCTTCCGATC*T

Forward Index Name	i5 bases for sample sheet	i5 bases for sample sheet
	NovαSeq, MiSeq, HiSeq 2000/2500	iSeq, MiniSeq, NextSeq, HiSeq 3000/4000
BD OMICS-One™ Library Forward Primer 1	TATAGCCT	AGGCTATA
BD OMICS-One™ Library Forward Primer 2	ATAGAGGC	GCCTCTAT
BD OMICS-One™ Library Forward Primer 3	ССТАТССТ	AGGATAGG
BD OMICS-One™ Library Forward Primer 4	GGCTCTGA	TCAGAGCC
BD OMICS-One™ Library Forward Primer 5	AGGCGAAG	СТТССССТ
BD OMICS-One™ Library Forward Primer 6	ТААТСТТА	TAAGATTA
BD OMICS-One™ Library Forward Primer 7	CAGGACGT	ACGTCCTG
BD OMICS-One™ Library Forward Primer 8	GTACTGAC	GTCAGTAC

Reverse Index Name	Bases in adapter	i7 bases for sample sheet
BD OMICS-One™ WTA Library Reverse Primer 1 BD OMICS-One™ Multiomic Library Reverse Primer 1	TACTACGC	GCGTAGTA
BD OMICS-One™ WTA Library Reverse Primer 2 BD OMICS-One™ Multiomic Library Reverse Primer 2	AGGCTCCG	CGGAGCCT
BD OMICS-One™ WTA Library Reverse Primer 3 BD OMICS-One™ Multiomic Library Reverse Primer 3	GCAGCGTA	TACGCTGC
BD OMICS-One™ WTA Library Reverse Primer 4 BD OMICS-One™ Multiomic Library Reverse Primer 4	CTGCGCAT	ATGCGCAG
BD OMICS-One™ WTA Library Reverse Primer 5 BD OMICS-One™ Multiomic Library Reverse Primer 5	GAGCGCTA	TAGCGCTC
BD OMICS-One™ WTA Library Reverse Primer 6 BD OMICS-One™ Multiomic Library Reverse Primer 6	CGCTCAGT	ACTGAGCG
BD OMICS-One™ WTA Library Reverse Primer 7 BD OMICS-One™ Multiomic Library Reverse Primer 7	GTCTTAGG	CCTAAGAC
BD OMICS-One™ WTA Library Reverse Primer 8 BD OMICS-One™ Multiomic Library Reverse Primer 8	ACTGATCG	CGATCAGT

Human T cell PCR1 primers

Primer name	Primer sequence (5'–3')
TRAC_N1	CTGGAATAATGCTGTTGTTGAAGG
TRBC_N1	AGCCCGTAGAACTGGACTT
TRDC_N1	CTTCAAAGTCAGTGGAGTGCA
TRGC_N1	CACCGTTAACCAGCTAAATTTCATG

Human T cell PCR2 primers

Primer name	Primer sequence (5'-3')
TRAC_N2	ATCAAAATCGGTGAATAGGCAGAC
TRBC_N2	GATCTCTGCTTCTGATGGCTCA
TRDC_N2	ATATCCTTGGGGTAGAATTCCTTC
TRGC_N2	GGGAAACATCTGCATCAAGTTG

Human B cell PCR1 primers

Primer name	Primer sequence (5'–3')
IGHA_N1	CACAGTCACATCCTGGCT

Primer name	Primer sequence (5'–3')
IGHD_N1	GATCTCCTTCTTACTCTTGCTGG
IGHE_N1	CGCTGAAGGTTTTGTTGTCG
IGHG_N1	TGTTGCTGGGCTTGTGAT
IGHM_N1	CGTTCTTTTCTTTGTTGCCGT
IGKC_N1	TTTGTGTTTCTCGTAGTCTGCT
IGLC_N1	TGTAGCTTCTGTGGGACTTC

Human B cell PCR2 primers

Primer name	Primer sequence (5'–3')
IGHA_N2	CTTTCGCTCCAGGTCACACT
IGHD_N2	TGTCTGCACCCTGATATGATGG
IGHE_N2	GTCAAGGGAAGACGGATG
IGHG_N2	AAGTAGTCCTTGACCAGGCA
IGHM_N2	ACAGGAGACGAGGGGAAAA
IGKC_N2	TCAGATGGCGGGAAGATGAA
IGLC_N2	ACCAGTGTGGCCTTGTTG

BD Rhapsody™ System TCR/BCR Next, BD OMICS-One™ WTA Next, BD® AbSeq, and Sample Tag Library Preparation Quick Reference Guide

This guide is designed as a quick reference for users who are already familiar with the long-form BD RhapsodyTM System TCR/BCR Next, BD OMICS-OneTM WTA Next, BD AbSeq, and Sample Tag Library Preparation Protocol, but do not need detailed instructions.

Introduction

This quick reference assumes that users are experts in the use of AMPure® XP magnetic beads (AMPure), the preparation of 80% ethyl alcohol (ethanol), and knowledgeable about the proper technique for WTA library preparation and common pitfalls. Users who are not familiar with these steps should review them in the long-form protocol.

To maintain brevity in this guide, longer names and terms are shortened as indicated in the following key:

Abbreviation	Full-length description
Amp.	Amplification
Analyzer	Refers to either the Agilent® 2100 Bioanalyzer System or Agilent® 4200 TapeStation® System. Used for all quality checking steps.
Beads, Cell Capture Beads	BD Rhapsody™ Enhanced Cell Capture Beads
Fluorometer	Invitrogen™ Qubit™ Fluorometer. Used for all quantification steps.
Fwd.	Forward
Fwd. Index Primer	Library Forward Primer 1–8
Magnet	The action of putting the sample tube on a magnet, then waiting for the solution to clear. Typically takes <2 minutes.
Purification	Purification using the AMPure reagent following the standard workflow in the long-form protocol. Includes: Adding the indicated volume of AMPure and pipet-mixing the well (~10x), incubating for 5 minutes, putting the sample with AMPure on a magnet, removing and discarding the supernatant, washing twice with sufficient 80% ethanol to cover the AMPure beads, drying the AMPure beads, then eluting into room-temperature elution buffer.
Rev.	Reverse
Rev. Index Primer	Library Reverse Primer 1–8
RPE	Random Priming and Extension
RT	Reverse Transcriptase
Spin-down	Briefly centrifuge <1 minute to collect liquid at bottom of tube.
ST	Sample Tag
Wash	Includes: Putting the sample tube on the magnet, adding the indicated volume of buffer, removing the buffer while the sample is still on the magnet, and then discarding the buffer.
Water	Nuclease-free water
WTA Amp. Primer	WTA Amplification Primer

Introduction to purification with AMPure® XP magnetic beads

The BD OMICS-One™ WTA Next protocol uses AMPure® XP magnetic beads (AMPure) for size-selection and purification throughout the workflow. This page provides general instructions for using AMPure, eliminating the need to repeat instructions with every purification.

- All PCR purifications will follow the same mixing, washing, and incubating steps.
- The volumes of PCR, AMPure, and room temperature elution buffer differ for each purification.
- Specific PCR purification volumes will be provided in tables contained within the guide.

NOTE: Correct volumes are **critical** for accurate size selection.

Volumes in these instructions are color-coded to match the volumes in Table 1 Example PCR purification.

Users who need more guidance should see the long-form protocol for detailed instructions.

Getting started

- Bring AMPure to room temperature approximately
 minutes before starting.
- 2. Determine the amount of ethanol required for purification using the following table.

Ethanol required per wash (Two washes per purification)

Volume PCR + AMPure	Tube needed	Vol. Ethanol per wash (mL)
>220 µL	1.5-mL	0.5
<220 µL	0.2-mL (PCR)	0.2

3. Prepare 80% ethanol according to the following table.

Component	1 mL	2 mL	5 mL	10 mL
Water	0.2	0.4	1	2
100% ethanol	0.8	1.6	4	8

Purifying the sample with AMPure (example)

- Pipet 110 μL PCR product into a new 1.5-mL tube. See row 1 of Table 1 Example PCR purification.
- 2. Vortex AMPure until beads are completely resuspended.
- 3. Add 88 µL AMPure to the 110 µL sample.
- 4. Pipet-mix ~10 times.
 - Do NOT mix by vortexing.
 - Avoid getting AMPure buffer on the tube cap.
- 5. Incubate **5** minutes at room temperature.
- 6. Magnet for **3 minutes**.
- 7. Discard supernatant.
- 8. Wash AMPure pellet as follows:
 - a. Add 0.5 mL 80% ethanol.
 - b. Discard 0.5 mL ethanol.
 - c. Repeat steps a and b for a total of **two** ethanol washes.
- Remove the tube containing the AMPure pellet from the magnet.
- 10. Spin-down tube with pellet.
- 11. Magnet tube containing the pellet.
- 12. Remove all residual ethanol with a P20 pipet.
- Air-dry pellet.
 Do not let the pellet over-dry and crack.
- 14. Remove tube from the magnet.
- 15. Resuspend pellet in $40 \mu L$ room temperature elution buffer.
- 16. Incubate 2 minutes at room temperature.
- 17. Magnet until solution is clear (about 30 sec).
- 18. Collect supernatant into a new PCR tube.
- 19. Add 60 µL water to the purified PCR product.
- 20. Mix.
- 21. Repeat purification steps 1–19 using the corresponding volumes in row 2 of Table1 Example PCR purification.

Table 1 Example PCR purification

Purification	Water Vol. μL	PCR Vol. μL	AMPure Vol. μL	Elution Vol. μL
PCR product	0	110	88	40
1x purified PCR	60	100	80	30

Preparing the thermomixers

- 1. Preheat a 42 °C thermomixer.
- 2. Preheat a second **80 °C thermomixer.** (Optional, for *same-day* self-hybridization.)

Synthesizing the cDNA

1. Prepare the **cDNA mix** using the following table. Keep the mixture on ice.

Can	Component			Sample	count wit	h % overa	ge (volum	nes in μL)		
Сар	Component	1+0%	1+20%	2+20%	3+20%	4+20%	5+20%	6+20%	7+20%	8+20%
	RT Buffer	40.0	48.0	96.0	144.0	192.0	240.0	288.0	336.0	384.0
	dNTP	20.0	24.0	48.0	72.0	96.0	120.0	144.0	168.0	192.0
	RT 0.1 M DTT	10.0	12.0	24.0	36.0	48.0	60.0	72.0	84.0	96.0
	Bead Enhancer	12.0	14.4	28.8	43.2	57.6	72.0	86.4	100.8	115.2
	RNase Inhibitor	10.0	12.0	24.0	36.0	48.0	60.0	72.0	84.0	96.0
	Reverse Transcriptase	10.0	12.0	24.0	36.0	48.0	60.0	72.0	84.0	96.0
O	Water	98.0	117.6	235.2	352.8	470.4	588.0	705.6	823.2	940.8
	Total	200.0	240.0	480.0	720.0	960.0	1200.0	1440.0	1680.0	1920.0

- 2. Magnet cell capture beads.
- 3. Discard supernatant.
- 4. Add 200 µL cDNA mix.
- 5. Remove sample from magnet.
- 6. Transfer bead suspension to a new 1.5-mL tube.
- 7. Incubate at 42 °C at 1,200 RPM for 30 minutes.
- 3. Mix.
 - 4. Incubate at 42 °C at 1,200 RPM for 30 minutes.

2. After incubation, add 8 μL TSO mix.

- 5. After incubation, magnet tube.
- 6. Discard supernatant.
- 7. Resuspend beads in **75 \muL elution buffer.**
- 8. Place on ice.

Switching the template

 Prepare TSO mix approx. 2 minutes before cDNA incubation ends using the following table. Keep the mixture on ice.



Safe stopping point.

Beads can be stored up to 7 days at 4 °C after template switching.

Can	Component	Sample count with % overage (volumes in μL)									
Cap (Component	1+0%	1+20%	2+20%	3+20%	4+20%	5+20%	6+20%	7+20%	8+20%	
0	TSO Next	6.0	7.2	14.4	21.6	28.8	36.0	43.2	50.4	57.6	
	1 M MgCl ₂	2.0	2.4	4.8	7.2	9.6	12.0	14.4	16.8	19.2	
	Total	8.0	9.6	19.2	28.8	38.4	48.0	57.6	67.2	76.8	

Preparing the thermomixers

- 1. Program a thermomixer with the **Hybridization program** (see Table 2 Hybridization program).
- 2. Preheat the following:
 - 95 °C heat block
 - 80 °C thermomixer (programmed with the Hybridization program)
 - 37 °C thermomixer

Denaturing the BD® AbSeq/ST product

- 1. For each sample, aliquot **1.2 mL hybridization buffer** into a 1.5-mL tube.
- 2. Heat the hybridization buffer aliquots to 80 °C for a minimum of 20 minutes before using.

NOTE: Keep hybridization buffer at **80 °C** until ready to use.

- 2. Label a 1.5-mL tube as BD® AbSeq/ST product.
- 3. Denature BD® AbSeq/ST product as follows:
 - a. Resuspend beads by pipetting.
 - b. Incubate at 95 °C (no shaking) for 5 minutes.
 - c. Immediately magnet sample.
 - d. Collect supernatant into the 1.5-mL tube.
 - e. Keep on ice until BD® AbSeq/ST PCR 1. You will need the product for step 2 on page QRG-10.
- 4. Proceed immediately to the next step, "Self-hybridizing the template".

Self-hybridizing the template

- 1. Add 1.0 mL of **80 °C hybridization buffer** to beads.
- 2. Incubate using **Table 2 Hybridization program** below (approx. 25 minutes).

Table 2 Hybridization program (all steps at 1,200 rpm)

Step	Temperature	Time	Mode
1	80 °C	3 min	
2	25 ℃	1 min	TEMP Control
3	25 ℃	∞*	Control

^{*}Optional

3. After program is complete, incubate on **ice** for *at least* **1 minute**.

Extending the TCR/BCR product

1. Prepare the TCR/BCR Extension mix (see Table 3 TCR/BCR Extension mix).

NOTE: The mixture can be kept at room temperature.

- 2. Magnet sample.
- 3. Discard supernatant.
- 4. Resuspend beads in 200 μL TCR/BCR Extension mix.
- 5. Incubate sample in the 37 °C thermomixer at 1,200 rpm for 30 minutes.
- 6. After incubation, spin-down sample.

NOTE: Keep on ice.

7. Proceed to the "Exonuclease I Treatment" section on the next page.

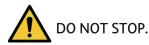


Table 3 TCR/BCR Extension mix

Can	Component	Sample count with % overage (volumes in μL)									
Сар	Component	1+0%	1+20%	2+20%	3+20%	4+20%	5+20%	6+20%	7+20%	8+20%	
0	TCR/BCR Extension Buffer	20.0	24.0	48.0	72.0	96.0	120.0	144.0	168.0	192.0	
	dNTP	20.0	24.0	48.0	72.0	96.0	120.0	144.0	168.0	192.0	
0	TCR/BCR Extension Enzyme	10.0	12.0	24.0	36.0	48.0	60.0	72.0	84.0	96.0	
0	Water	150.0	180.0	360.0	540.0	720.0	900.0	1080.0	1260.0	1440.0	
	Total	200.0	240.0	480.0	720.0	960.0	1200.0	1440.0	1680.0	1920.0	

Treating the beads with Exonuclease I

- 1. Heat a thermomixer to 80 °C.
- 2. Prepare the **Exonuclease I mix** (see Table 4 Exonuclease I mix).

NOTE: The mixture can be kept at room temperature.

- 3. Magnet the sample from step 6 on page QRG-4.
- 4. Discard supernatant.
- 5. Resuspend beads in 200 µL Exonuclease I mix.
- 6. Incubate sample in the 37 °C thermomixer at 1,200 rpm for 30 minutes.
- 7. Incubate sample in the 80 °C thermomixer for 20 minutes (no shaking).
- 8. Incubate sample on ice for at least 1 minute.
- 9. Spin-down sample.
- 10. Magnet sample.
- 11. Discard supernatant.
- 12. Resuspend beads in **200 µL bead resuspension** buffer.



Safe stopping point.

Beads can be stored in bead resuspension buffer for up to 1 year at 4 °C.

Table 4 Exonuclease I mix

) Can	Component	Sample count with % overage (volumes in µL)								
Сар		1+0%	1+20%	2+20%	3+20%	4+20%	5+20%	6+20%	7+20%	8+20%
0	10X Exonuclease I Buffer	20.0	24.0	48.0	72.0	96.0	120.0	144.0	168.0	192.0
0	Exonuclease I	10.0	12.0	24.0	36.0	48.0	60.0	72.0	84.0	96.0
0	Water	170.0	204.0	408.0	612.0	816.0	1020.0	1224.0	1428.0	1632.0
	Total	200.0	240.0	480.0	720.0	960.0	1200.0	1440.0	1680.0	1920.0

BD OMICS-One™ WTA Next, BD® AbSeq, and Sample Tag library preparation

Preparing the thermomixers

Preheat the following instruments:

- 95 °C heat block
- 37 °C thermomixer
- 25 °C thermomixer

Preparing the reagent mixes

1. Prepare the **Random Primer mix** using the following table. Keep the mixture at room temperature.

Can	Component	Sample count with % overage (volumes in μL)								
Сар		1+0%	1+20%	2+20%	3+20%	4+20%	5+20%	6+20%	7+20%	8+20%
0	WTA Extension Buffer	20.0	24.0	48.0	72.0	96.0	120.0	144.0	168.0	192.0
0	WTA Extension Primer	40.0	48.0	96.0	144.0	192.0	240.0	288.0	336.0	384.0
0	Water	114.0	136.8	273.6	410.4	547.2	684.0	820.8	957.6	1094.4
	Total	174.0	208.8	417.6	626.4	835.2	1044.0	1252.8	1461.6	1670.4

2. Prepare the Extension Enzyme mix using the following table. Keep the mixture on ice.

Сар	Component	Sample count with % overage (volumes in μL)								
Сар		1+0%	1+20%	2+20%	3+20%	4+20%	5+20%	6+20%	7+20%	8+20%
0	dNTP	8.0	9.6	19.2	28.8	38.4	48.0	57.6	67.2	76.8
0	Bead Enhancer	12.0	14.4	28.8	43.2	57.6	72.0	86.4	100.8	115.2
0	WTA Extension Enzyme	6.0	7.2	14.4	21.6	28.8	36.0	43.2	50.4	57.6
	Total	26.0	31.2	62.4	93.6	124.8	156.0	187.2	218.4	249.6

Generating the RPE product

- 1. Spin-down cell capture beads stored in bead resuspension buffer.
- 2. Magnet beads and discard supernatant
- 3. Add **174 µL of Random Primer mix** (keep at room temperature).
- 4. Pipet-mix to resuspend beads (~10 times).
- 5. Incubate the sample as follows:
 - a. 95 °C heat block (no shaking) for 5 minutes.
 - b. 37 °C thermomixer at 1,200 rpm for 5 minutes.
 - c. 25 °C thermomixer at 1,200 rpm for 5 minutes.
- 6. Add $26 \mu L$ of the Extension Enzyme mix to the tube containing beads.
- 7. Incubate the tube in the thermomixer programmed with the following **RPE program**.

RPE program (all steps at 1,200 rpm)

Temperature	Time	Mode
25 ℃	10 min	_
37 <i>°</i> ℃	15 min	- - TIMF
45 °C	10 min	IIIVIE
55 ℃	10 min	•
	25 °C 37 °C 45 °C	25 °C 10 min 37 °C 15 min 45 °C 10 min

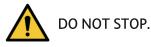
- 8. Label a new 1.5-mL tube as RPE product.
- 9. After the Enzyme Extension program completes, spin-down the sample.
- 10. Magnet beads.
- 11. Discard supernatant.
- 12. Wash beads in **200 µL room temperature** elution buffer.
- 13. Denature the product as follows:
 - a. Resuspend beads in **80 µL room** temperature elution buffer.
 - b. Incubate sample at 95 °C for 5 minutes.
 - c. Incubate sample 1 minute on ice.
 - d. Magnet sample.
 - e. Transfer **80 μL** supernatant containing denatured **RPE product** to previously labeled 1.5-mL tube.
- 14. Store used beads in **200 μL bead** resuspension buffer at 4 °C. You will need the beads for step 2 on page QRG-13.
- 15. Proceed immediately to the next step, "Purifying the RPE product".

Purifying the RPE product

- 1. Spin-down the denatured RPE product.
- 2. Purify the denatured RPE product according to the following RPE product purification table.

Purification	Product Vol. μL	AMPure Vol. μL	Elution Vol. µL
RPE product	80	128	80

3. Continue to the "WTA RPE PCR" section on the next page.



Amplifying the RPE product

1. Prepare the RPE PCR mix using the following table.

Сар	Component	Sample count with % overage (volumes in μL)								
Сар	Component	1 + 0%	1+20%	2+20%	3+20%	4+20%	5+20%	6+20%	7+20%	8+20%
	PCR Master Mix*	30.0	36.0	72.0	108.0	144.0	180.0	216.0	252.0	288.0
	Universal Oligo	6.0	7.2	14.4	21.6	28.8	36.0	43.2	50.4	57.6
	WTA Amp. Primer	6.0	7.2	14.4	21.6	28.8	36.0	43.2	50.4	57.6
	Total	42.0	50.4	100.8	151.2	201.6	252.0	302.4	352.8	403.2

^{*}Important: Use the PCR Master Mix from the BD OMICS-One™ WTA Next kit with the **green cap** (PN: 51-9025466).

- 2. Combine 42 μL RPE PCR mix with 80 μL RPE product.
- 3. Mix well.
- 4. Split all the PCR mix with product into **two PCR tubes** containing ~60 μL each.
- 5. Amplify using the RPE PCR program table.



- 6. After PCR, spin-down sample.
- 7. Combine into a PCR tube.
- 8. Purify the RPE PCR product **twice** according to the following **RPE PCR purification** table.

D	DE	PCR	nro	~	~-	~
_ [rc.	PUR	DIC	uu	uı	ш

Step	Cycles	Temp	Time
Hot start	1	98 ℃	45 sec
Denaturation		98 ℃	15 sec
Annealing	7.5k–20k cells: 10 cycles	60 ℃	30 sec
Extension		72 <i>°</i> C	1 min
Extension	1	72 °C	2 min
Hold	1	4℃	8

Purification	Water Vol. μL	PCR Vol. μL	AMPure Vol. μL	Elution Vol. μL
RPE PCR product	0	110	88	40
1x purified RPE PCR	60	100*	80	30

^{*100} μ L = 40 μ L elution + 60 μ L water



Safe stopping point.

Purified PCR product can be stored at -20 °C for up to 6 months.

Quantifying the RPE PCR product

- 1. Quantify purified RPE PCR product with the fluorometer.
- 2. Dilute purified RPE PCR product to **0.2–0.5 ng/μL**.
- 3. Continue to the "WTA Index PCR" section.

Indexing the WTA libraries

1. Prepare the WTA Index PCR mix using the following table.

Сар	Component	Sample count with % overage (volumes in μL)								
Сар	Component	1+0%	1+20%	2+20%	3+20%	4+20%	5+20%	6+20%	7+20%	8+20%
	PCR Master Mix*	12.5	15.0	30.0	45.0	60.0	75.0	90.0	105.0	120.0
	Fwd. Index Primer	2.5	3.0	N/A						
	WTA Rev. Index Primer	2.5	3.0	N/A						
0	Water	22.5	27.0	54.0	81.0	108.0	135.0	162.0	189.0	216.0
	Total	40.0	48.0	84.0	126.0	168.0	210.0	252.0	294.0	336.0

^{*}Important: Use the PCR Master Mix from the BD OMICS-One™ WTA Next kit with the **green cap** (PN: 51-9025466).

- 2. Combine 40 μL WTA Index PCR mix with 10 μL diluted and purified RPE PCR product. See "Amplifying the RPE product" on page QRG-8.
- 3. Mix well.
- 4. Amplify using the **WTA Index PCR program** table.



- 5. After PCR, spin-down sample.
- 6. Purify according to the following **WTA Index PCR purification** table.

Step	Cycles	Temp	Time
Hot start	1	98 ℃	45 sec
Denaturation	0.05 ng/μL: 12 cycles	98 ℃	15 sec
Annealing	0.1 ng/μL: 11 cycles 0.2 ng/μL: 10 cycles	60 ℃	30 sec
Extension	0.5 ng/μL: 8 cycles	72 ℃	1 min
Extension	1	72 °C	2 min
Hold	1	4℃	8

Purification	Water Vol.	PCR Vol.	AMPure Vol.	Elution Vol.
	μL	μL	μL	μL
WTA Index PCR	60	100	65	30



Quantifying the indexed WTA libraries

- 1. Quantify purified WTA Index PCR with the fluorometer.
- 2. Quality check purified WTA Index PCR product using an analyzer.
- 3. Determine the average fragment size from 200–2000 bp.

Amplifying the BD® AbSeq and Sample Tag (ST) product

1. Prepare the BD® AbSeq/ST PCR 1 mix using the following table.

Can	Component	Sample count with % overage (volumes in μL						es in μL)		
Сар	Component	1+0%	1+20%	2+20%	3+20%	4+20%	5+20%	6+20%	7+20%	8+20%
	PCR Master Mix*	50.0	60.0	120.0	180.0	240.0	300.0	360.0	420.0	480.0
	Universal Oligo	2.5	3.0	6.0	9.0	12.0	15.0	18.0	21.0	24.0
	BD® AbSeq Primer	10.0	12.0	24.0	36.0	48.0	60.0	72.0	84.0	96.0
	ST PCR 1 Primer	1.0	1.2	2.4	3.6	4.8	6.0	7.2	8.4	9.6
0	Water	68.5	82.2	164.4	246.6	328.8	411.0	493.2	575.4	657.6
	Total	132.0	158.4	316.8	475.2	633.6	792.0	950.4	1108.8	1267.2

^{*}Important: Use the PCR Master Mix from the BD OMICS-One™ WTA Next kit with the **green cap** (PN: 51-9025466).

- Combine 68 μL BD® AbSeq/ST product (see "Denaturing the BD® AbSeq/ST product" on page QRG-4) with 132 μL BD® AbSeq/ST PCR 1 mix.
- 3. Mix well.
- 4. Split BD® AbSeq/ST PCR mix-containing product across **four PCR tubes** containing 50 µL each.
- 5. Amplify using the following table.

Step	Cycles	Temp.	Time
Hot start	1	98 ℃	45 sec
Denaturation		98 ℃	15 sec
Annealing	≤10,000 cells: 11 cycles 20,000 cells: 10 cycles	60℃	30 sec
Extension		72 <i>°</i> C	1 min
Extension	1	72 °C	2 min
Hold	1	4 ℃	∞



- 6. After PCR, spin-down sample.
- 7. Transfer sample to 1.5-mL tube.
- 8. Purify according to the following BD® AbSeq/ST PCR 1 purification table.

Purification	PCR Vol.	AMPure Vol.	Elution Vol.
	μL	μL	μL
BD® AbSeq/ ST PCR 1	200	280	30



Safe stopping point.

Purified PCR product can be stored at -20 °C for up to 6 months.

Quantifying the BD® AbSeq/ST PCR 1 product

- 1. Quality check purified BD® AbSeq/ST PCR 1 using an analyzer.
- Dilute BD® AbSeq/ST PCR 1 product to 0.1–1.1 ng/μL for BD® AbSeq Index PCR.
- 3. Use 5 μL *undiluted* BD® AbSeq/ST PCR 1 product for ST PCR 2.
- 4. Proceed to the "Sample Tag (ST) PCR 2" section on the next page.

Generating the Sample Tag PCR 2 product

1. Prepare the **ST PCR 2 mix** using the following table.

Can	Component			Sample	count with	n % overa	ge (volum	es in μL)		
Сар	Component	1+0%	1+20%	2+20%	3+20%	4+20%	5+20%	6+20%	7+20%	8+20%
	PCR Master Mix*	12.5	15.0	30.0	45.0	60.0	75.0	90.0	105.0	120.0
	1:10 Dilution† of Universal Oligo	5.0	6.0	N/A	N/A	N/A	N/A	N/A	N/A	N/A
	Universal Oligo	N/A	N/A	1.2	1.8	2.4	3.0	3.6	4.2	4.8
	ST PCR 2 Primer	3.0	3.6	7.2	10.8	14.4	18.0	21.6	25.2	28.8
0	Water	24.5	29.4	69.6	104.4	139.2	174.0	208.8	243.6	278.4
	Total	45.0	54.0	108.0	162.0	216.0	270.0	324.0	378.0	432.0

^{*}Important: Use the PCR Master Mix from the BD OMICS-One™ WTA Next kit with the **green cap** (PN: 51-9025466).

- 2. Combine 5 μL purified and undiluted BD® AbSeq/ST PCR 1 product with 45 μL ST PCR 2 mix.
- 3. Mix well.
- 4. Amplify using the following table.

Step	Cycles	Temp.	Time
Hot start	1	98 ℃	45 sec
Denaturation		98 ℃	15 sec
Annealing	10	66 °C	30 sec
Extension		72 °C	1 min
Extension	1	72 °C	2 min
Hold	1	4 ℃	∞

Safe stopping point.
PCR can run overnight.

- 5. After PCR, spin-down sample.
- 6. Purify according to the following **ST PCR 2** purification table.

Purification	PCR Vol.	AMPure Vol.	Elution Vol.
	μL	μL	µL
ST PCR 2	50	60	30



Quantifying the ST PCR 2 product

- 1. Quantify purified ST PCR 2 product with the fluorometer.
- 2. Dilute ST PCR 2 product to **0.1–1.1 ng/μL** and continue to the "BD® AbSeq/Sample Tag (ST) Index PCR" section on the next page.

[†]If preparing ST PCR 2 mix for one sample, dilute the Universal Oligo 1:10 for pipetting accuracy.

Indexing the BD® AbSeq or ST libraries

1. Prepare the BD® AbSeq/ST Index PCR mix using the following table.

Can	Component	Sample count with % overage (volumes in μL)								
Сар	cup Component	1+0%	1+20%	2+20%	3+20%	4+20%	5+20%	6+20%	7+20%	8+20%
	PCR Master Mix*	12.5	15.0	30.0	45.0	60.0	75.0	90.0	105.0	120.0
	Fwd. Index Primer	2.0	2.4	N/A						
0	Multiomic Rev. Index Primer	2.0	2.4	N/A						
0	Water	30.5	36.6	73.2	109.8	146.4	183.0	219.6	256.2	292.8
	Total	47.0	56.4	103.2	154.8	206.4	258.0	309.6	361.2	412.8

^{*}Important: Use the PCR Master Mix from the BD OMICS-One™ WTA Next kit with the **green cap** (PN: 51-9025466).

- 2. Combine 47 μL BD® AbSeq/ST Index PCR mix with 3 μL of one of the following *diluted* and *purified* products:
 - BD® AbSeq/ST PCR 1 product (see "Amplifying the BD® AbSeq and Sample Tag (ST) product" on page QRG-10).
 - ST PCR 2 product (see "Generating the Sample Tag PCR 2 product" on page QRG-11).
- 3. Mix well.
- 4. Amplify using the following table.

Step	Cycles	Temp.	Time
Hot start	1	98 ℃	45 sec
Denaturation	0.1-0.25 ng/μL: 8 cycles	98 ℃	15 sec
Annealing	0.25-0.5 ng/μL: 7 cycles	60 ℃	30 sec
Extension	0.5–1.1 ng/μL: 6 cycles	72 °C	1 min
Extension	1	72 ℃	2 min
Hold	1	4℃	8



- 5. After PCR, spin-down sample.
- 6. Purify according to the following **BD® AbSeq/ST Index PCR purification** table.

Purification	PCR Vol.	AMPure Vol.	Elution Vol.
	μL	μL	µL
BD® AbSeq/ST Index PCR	50	40	30



Safe stopping point.

Purified PCR product can be stored at -20 °C for up to 6 months.

Quantifying the indexed BD® AbSeq and ST libraries

- 1. Quantify purified BD® AbSeq and ST Index PCR product with the fluorometer.
- 2. Quality check purified BD® AbSeq and ST Index PCR product using an analyzer.
- 3. Determine average fragment size from 200–500 bp.

Amplifying the TCR/BCR product

1. Prepare the TCR/BCR PCR 1 mix using the following table.

Can	Component			Sample	count witl	n % overa	ge (volum	es in μL)		
Сар	Component	1+0%	1+20%	2+20%	3+20%	4+20%	5+20%	6+20%	7+20%	8+20%
0	PCR Master Mix*	100.0	120.0	240.0	360.0	480.0	600.0	720.0	840.0	960.0
	TCR/BCR Universal Oligo N1	10.0	12.0	24.0	36.0	48.0	60.0	72.0	84.0	96.0
	Bead Enhancer	12.0	14.4	28.8	43.2	57.6	72.0	86.4	100.8	115.2
	TCR N1 Primer	2.4	2.9	5.8	8.6	11.5	14.4	17.3	20.2	23.0
	BCR N1 Primer	2.4	2.9	5.8	8.6	11.5	14.4	17.3	20.2	23.0
0	Water	73.2	87.8	175.7	263.5	351.4	439.2	527.0	614.9	702.7
	Total	200.0	240.0	480.0	720.0	960.0	1200.0	1440.0	1680.0	1920.0

^{*}Important: Use the PCR Master Mix from the BD Rhapsody™ TCR/BCR Next kit with the white cap (PN: 91-1083).

- 2. Magnet cell capture beads stored in bead resuspension buffer from step 14 on page QRG-7.
- 3. Discard supernatant.
- 4. Resuspend beads in $200 \mu L$ TCR/BCR PCR 1 mix.
- 5. Keeping beads suspended, split beads in PCR mix across **four PCR tubes** (~50 µL each).
- 6. Amplify using the following TCR/BCR PCR 1 program, making sure to:
 - a. Preheat thermocycler to 95 °C
 - b. Resuspend the beads.

TCR/BCR PCR 1 program

Step	Cycles	Temp.	Time
Hot start	1	95 ℃	3 min
Denaturation	751 401 11 44 1	95 ℃	30 sec
Annealing	7.5k–10k cells: 11 cycles >20k cells: 10 cycles	60 °C	1 min
Extension	ZOR CCIIS. TO CYCICS	72 °C	1 min
Extension	1	72 °C	5 min
Hold	1	4 ℃	∞

- 7. After PCR, spin-down sample.
- 8. Combine into 1.5-mL tube.
- 9. Purify according to the following TCR/BCR PCR 1 product table.

Purification	PCR Vol.	AMPure Vol.	Elution Vol.
	μL	μL	μL
TCR/BCR PCR 1	200	140	50



Safe stopping point.

Purified PCR product can be stored at -20 °C for up to 6 months.

Generating the TCR or BCR PCR 2 product

1. Prepare TCR <u>OR</u> BCR PCR 2 mix using the following table.

Can	Component	Sample count with % overage (volumes in μL)								
Сар	Component	1+0%	1+20%	2+20%	3+20%	4+20%	5+20%	6+20%	7+20%	8+20%
0	PCR Master Mix*	25.0	30.0	60.0	90.0	120.0	150.0	180.0	210.0	240.0
	TCR/BCR Universal Oligo N2	2.0	2.4	4.8	7.2	9.6	12.0	14.4	16.8	19.2
	TCR <u>OR</u> BCR N2 Primer	6.0	7.2	14.4	21.6	28.8	36.0	43.2	50.4	57.6
0	Water	12.0	14.4	28.8	43.2	57.6	72.0	86.4	100.8	115.2
	Total	45.0	54.0	108.0	162.0	216.0	270.0	324.0	378.0	432.0

^{*}Important: Use the PCR Master Mix from the BD Rhapsody™ TCR/BCR Next kit with the white cap (PN: 91-1083).

- 2. Combine 45 μL TCR/BCR PCR 2 mix with 5 μL undiluted and purified TCR/BCR PCR 1 product. See "Amplifying the TCR/BCR product" on page QRG-13.
- 3. Mix well.
- 4. Amplify using the following table.

Step	Phase	Cycles	Temp.	Time
Hot start		1	95 ℃	3 min
Denaturation			95 ℃	30 sec
Annealing	I	15	75–61 °C*	1 min
Extension			72 °C	1 min
Denaturation			95 ℃	30 sec
Annealing	II	8	60 ℃	1 min
Extension			72 °C	1 min
Extension		1	72 °C	5 min
Hold		1	4 ℃	∞

^{*}Decrease temperature 1 °C per cycle.



- 5. After PCR, spin-down sample.
- 6. Purify according to the following TCR/BCR PCR 2 purification table.

Purification	PCR Vol.	AMPure Vol.	Elution Vol.
	μL	μL	μL
TCR/BCR PCR 2	50	35	50



Safe stopping point.

Purified PCR product can be stored at -20 °C for up to 6 months.

Quantifying the TCR/BCR PCR 2 product

- 1. Quantify purified TCR or BCR PCR 2 product with the fluorometer.
- 2. Dilute the TCR or BCR PCR 2 product to 1 ng/μL.
- 3. Continue to the "TCR/BCR RPE" section on the next page.

Preparing the reagent mixes

1. Prepare the **Random Primer mix** using the following table. Keep the mixture at room temperature.

Can	Component	Sample count with % overage (volumes in μL)								
Сар		1+0%	1+20%	2+20%	3+20%	4+20%	5+20%	6+20%	7+20%	8+20%
0	TCR/BCR Extension Buffer	5.0	6.0	12.0	18.0	24.0	30.0	36.0	42.0	48.0
0	TCR/BCR Extension Primers	2.5	3.0	6.0	9.0	12.0	15.0	18.0	21.0	24.0
0	Water	34.0	40.8	81.6	122.4	163.2	204.0	244.8	285.6	326.4
	Total	41.5	49.8	99.6	149.4	199.2	249.0	298.8	348.6	398.4

2. Prepare the **Extension Enzyme mix** using the following table. Keep the mixture on ice.

Con	Component	Sample count with % overage (volumes in μL)								
Сар		1+0%	1+20%	2+20%	3+20%	4+20%	5+20%	6+20%	7+20%	8+20%
	dNTP	2.0	2.4	4.8	7.2	9.6	12.0	14.4	16.8	19.2
0	TCR/BCR Extension Enzyme	1.5	1.8	3.6	5.4	7.2	9.0	10.8	12.6	14.4
	Total	3.5	4.2	8.4	12.6	16.8	21.0	25.2	29.4	33.6

- 3. Combine **41.5** µL Random Primer mix with 5 µL diluted and purified TCR <u>OR</u> BCR PCR 2 product. See "Generating the TCR or BCR PCR 2 product" on page QRG-14.
- 4. Mix well.
- 5. Denature and anneal primers using the following table.

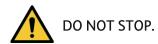
Step	Cycles	Temp.	Time
Denaturation		95 ℃	5 min
Annealing	1	37 ℃	5 min
		25 ℃	15 min

- 6. After program is complete, add **3.5** µL Extension Enzyme mix.
- 7. Mix well.

8. Incubate the sample using the following table.

Step	Cycles	Temp.	Time
1		25 ℃	10 min
2	1	37 ℃	15 min
3		45 °C	10 min
4		55 ℃	10 min

9. Continue to the "Purifying the TCR or BCR RPE product" procedure on the next page.



Purifying the TCR or BCR RPE product

Purify TCR <u>OR</u> BCR RPE product according to the following table.

Purification	PCR Vol.	AMPure Vol.	Elution Vol.
	μL	μL	μL
TCR/BCR RPE	50	90	50

Indexing the TCR or BCR libraries

1. Prepare the TCR/BCR Index PCR mix using the following table. Keep samples on ice.

Can	Component	Sample count with % overage (volumes in μL)								
Сар		1+0%	1+20%	2+20%	3+20%	4+20%	5+20%	6+20%	7+20%	8+20%
0	PCR Master Mix*	25.0	30.0	60.0	90.0	120.0	150.0	180.0	210.0	240.0
	Fwd. Index Primer	2.0	2.4	N/A						
0	Multiomic Rev. Index Primer	2.0	2.4	N/A						
	Total	29.0	34.8	60.0	90.0	120.0	150.0	180.0	210.0	240.0

^{*}Important: Use the PCR Master Mix from the BD Rhapsody™ TCR/BCR Next kit with the **white cap** (PN: 91-1083).

- 2. Combine 29 μL TCR/BCR Index PCR mix with 21 μL purified TCR <u>OR</u> BCR RPE product.
- 3. Mix well.
- 4. Amplify using the following table.

Step	Cycles	Temp.	Time
Hot start	1	95 ℃	3 min
Denaturation		95 ℃	30 sec
Annealing	10	60 °C	30 sec
Extension		72 °C	30 sec
Extension	1	72 °C	1 min
Hold	1	4 ℃	8



- 5. After PCR, spin-down sample.
- 6. Purify according to the following TCR/BCR Index PCR purification table.

Purification	PCR Vol.	AMPure Vol.	Elution Vol.		
	μL	μL	μL		
TCR/BCR Index PCR	40	26	50		



Safe stopping point.

Purified PCR product can be stored at -20 °C for up to 6 months.

Quantifying the indexed TCR/BCR libraries

- 1. Quantify purified TCR or BCR Index PCR product with the fluorometer.
- 2. Quality check purified TCR or BCR Index PCR product using an analyzer.
- 3. Determine average fragment size from 200–1000 bp.
- 4. Refer to sequencing guidelines in long-form protocol.

BD Rhapsody™ System TCR/BCR Next, BD OMICS-One™ WTA Next, BD® AbSeq, and Sample Tag Quick Reference Guide

Expiry

Kit Lot

Date

The following note sheet is provided for user convenience.

Experiment

Use the area below to record sample information:

ST
Index
PCR
Quant.
ng/µL ST Rev. Index ST Fwd. Index Expiry ST PCR
2
Quant.
ng/µL Notes BD®
AbSeq
Index
PCR
Quant.
ng/µL BCR Index PCR Quant. ng/μL Kit Lot BD[®]
AbSeq
Rev.
Index BCR Rev. Index BD[®]
AbSeq
Fwd.
Index BCR Fwd. Index **1 Quality** bp (αvg) AbSeq/ ST PCR BCR 2 Quant. ng/µL $\mathsf{BD}^{\circledcirc}$ Date WTA
Index
PCR
Quant.
ng/µL TCR Index PCR Quant. ng/µL WTA Rev. Index TCR Rev. Index User WTA Fwd. Index TCR Fwd. Index RPE PCR Quant. ng/µL TCR PCR 2 Quant. ng/µL Description Experiment Description Sample Sample 2 Ŋ 9 ∞ က 4 2 ო 4 Ŋ ဖ _ ω

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