



SureSelect^{QXT} Automated Target Enrichment for the Illumina Platform

Featuring Transposase-Based Library Prep Technology

Automated using Agilent NGS Bravo Option A

Protocol

Version E0, November 2021

SureSelect platform manufactured with Agilent SurePrint technology.

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Notices

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Manual Part Number

G9681-90020

Edition

Version E0, November 2021

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Acknowledgment

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In this Guide...

This guide describes an optimized protocol for Illumina paired-end multiplexed library preparation using the SureSelect^{QXT} Automated Target Enrichment system.

This protocol is specifically developed and optimized to enrich targeted regions of the genome from repetitive sequences and sequences unrelated to the research focus prior to sample sequencing. Sample processing steps are automated using Agilent's NGS Bravo Option A.

1 Before You Begin

This chapter contains information that you should read and understand before you start an experiment.

2 Using the Agilent NGS Bravo Option A for SureSelect Target Enrichment

This chapter contains an orientation to the Agilent NGS Bravo, an overview of the SureSelect target enrichment protocol, and considerations for designing SureSelect experiments for automated processing.

3 Sample Preparation

This chapter describes the steps to prepare gDNA sequencing libraries for target enrichment.

4 Hybridization

This chapter describes the steps to hybridize and capture the prepared DNA library using a SureSelect or ClearSeq Probe Capture Library.

5 Indexing

This chapter describes the steps for post-capture amplification and guidelines for sequencing sample preparation.

6 Reference

This chapter contains reference information, including component kit contents and index sequences.

What's New in Version E0

- Support for SureSelect XT HS Human All Exon V8 Probe, SureSelect XT HS Human All Exon V8+UTR Probe, and SureSelect XT HS Human All Exon V8+NCV Probe (see **Table 2** on page 11).
- Updates to the Agilent NGS Bravo components user guide part numbers (see **Table 6** on page 16).
- Updated information on the pipette head options and fluid transfer capabilities of the Bravo platform (see **page 16**).
- Updates to downstream sequencing guidelines (see **Table 59** on page 79).
- Updated document look and feel.

What's New in Version D1

- Updates to thermal cycler and plasticware recommendations (see **Table 5** on page 13 and see *Caution* on **page 27**)
- Updates to downstream sequencing support information including sequencing kit selection and seeding concentration updates (see **Table 59** on page 79) and support for the NovaSeq platform (see **page 79** through **page 84** and see **page 88**)
- Updates to instructions for adaptor trimming using SureCall (see **page 83**) or AGeNT (see **page 84**)

What's New in Version D0

- Support for revised SureSelect custom probe products, produced using an updated manufacturing process beginning August, 2020 (see **Table 3** on page 12). Custom probes produced using the legacy manufacturing process are also fully supported by the protocols in this document. Probe information was reorganized (see **Table 2** on page 11 and **Table 3** on page 12), and probe nomenclature throughout document updated.
- Support for Agilent 4150 TapeStation system and Agilent 5200 Fragment Analyzer system (see **page 14**).
- Minor updates to 2100 Bioanalyzer and 4200/4150 TapeStation use instructions and reference document links (see **page 43**, **page 45**, **page 76**, and **page 76**).
- Updates to ordering information for AMPure XP Kits and 1X Low TE Buffer (see **Table 1** on page 11) and for Qubit Fluorometer (see **Table 5** on page 13).
- Removal reference information for expired SureSelect^{QXT} Reagent Kits p/n G9681A/G9681B, replaced by G9683A/G9683B in 2018 (see **Table 1** on page 11, **Table 71** on page 86, and **Table 72** on page 86 for current Reagent Kit information).
- Updates to Technical Support contact information (see **page 2**)

Content

1 Before You Begin

Procedural Notes 10

Safety Notes 10

Required Reagents 11

Optional Reagents 12

Required Equipment 13

2 Using the Agilent NGS Bravo Option A for SureSelect Target Enrichment

About the NGS Bravo Option A 16

About the Bravo Platform 16

VWorks Automation Control Software 19

Overview of the SureSelect^{QXT} Target Enrichment Procedure 24

Experimental Setup Considerations for Automated Runs 26

Considerations for Placement of gDNA Samples in 96-well Plates for Automated Processing 26

Considerations for Equipment Setup 27

PCR Plate Type Considerations 27

3 Sample Preparation

Step 1. Prepare the genomic DNA samples and Library Prep reagents 30

Step 2. Fragment and adaptor-tag the genomic DNA samples 31

Step 3. Purify adaptor-tagged DNA using AMPure XP beads 35

Step 4. Amplify adaptor-ligated libraries 37

Step 5. Purify amplified DNA using AMPure XP beads 41

Step 6. Assess Library DNA quantity and quality 43

4 Hybridization

Step 1. Aliquot prepped DNA samples for hybridization 48

Step 2. Hybridize the gDNA library and probe 51

Step 3. Capture the hybridized DNA 60

Step 4. Wash the captured DNA 64

5 Indexing

Step 1. Amplify the captured DNA libraries to add index tags 68

Step 2. Purify the amplified indexed libraries using AMPure XP beads	74
Step 3. Assess indexed DNA quality	76
Step 4. Quantify each index-tagged library by QPCR (optional)	77
Step 5. Pool samples for Multiplexed Sequencing	78
Step 6. Prepare sequencing samples	79
Step 7. Set up the sequencing run and trim adaptors from the reads	83

6 Reference

Kit Contents	86
Nucleotide Sequences of SureSelect ^{QXT} Dual Indexes	88
Guidelines for Multiplexing with Dual-Indexed Samples	90

1 Before You Begin

Procedural Notes	10
Safety Notes	10
Required Reagents	11
Optional Reagents	12
Required Equipment	13

Make sure you read and understand the information in this chapter and have the necessary equipment and reagents listed before you start an experiment.

NOTE

This protocol describes automated sample processing using the Agilent NGS Bravo Option A. For automated sample processing using the Agilent NGS Workstation Option B, see publication G9681-90010. For non-automated sample processing procedures see publication G9681-90000.

NOTE

Agilent guarantees performance and provides technical support for the SureSelect reagents required for this workflow only when used as directed in this Protocol.

Procedural Notes

- The SureSelect^{QXT} system requires high-quality DNA samples for optimal performance. Use best practices for verifying DNA sample quality before initiating the workflow. For best practice, store diluted DNA solutions at 4°C to avoid repeated freeze-thaw cycles, which may compromise DNA quality.
- Performance of the SureSelect^{QXT} library preparation protocol is very sensitive to variations in amounts of DNA sample and other reaction components. It is important to quantify and dilute DNA samples as described on [page 30](#). Carefully measure volumes for all reaction components, and combine components as described in this instruction manual. Use best-practices for liquid handling, including regular pipette calibration, to ensure precise volume measurement.
- Use care in handling the SureSelect QXT Enzyme Mix. After removing the vial from storage at –20°C, keep on ice or in a cold block while in use. Return the vial to storage at –20°C promptly after use.
- Certain protocol steps require the rapid transfer of sample plates between the Bravo deck and a thermal cycler. Locate your thermal cycler in close proximity to the Agilent NGS Bravo to allow rapid and efficient plate transfer.
- Use best-practices to prevent PCR product contamination of samples throughout the workflow:
 - 1 Assign separate pre-PCR and post-PCR pipettors, supplies, and reagents. In particular, never use materials designated to post-PCR segments for the pre-PCR segments of the workflow. For the pre-PCR workflow steps, always use dedicated pre-PCR pipettors with nuclease-free aerosol-resistant tips to pipette dedicated pre-PCR solutions.
 - 2 Maintain clean work areas. Clean pre-PCR surfaces that pose the highest risk of contamination daily using a 10% bleach solution.
 - 3 Wear powder-free gloves. Use good laboratory hygiene, including changing gloves after contact with any potentially-contaminated surfaces.
- Possible stopping points, where samples may be stored at –20°C, are marked in the protocol. Do not subject the samples to multiple freeze/thaw cycles.
- To prevent contamination of reagents by nucleases, always wear powder-free laboratory gloves and use dedicated solutions and pipettors with nuclease-free aerosol-resistant tips.
- In general, follow Biosafety Level 1 (BSL1) safety rules.

Safety Notes

CAUTION

- Wear appropriate personal protective equipment (PPE) when working in the laboratory.

Required Reagents

Table 1 Required Reagents for SureSelect^{QXT} Target Enrichment

Description	Vendor and part number
SureSelect or ClearSeq Probe Capture Library	Select the appropriate probe from Table 2 or Table 3
SureSelect ^{QXT} Reagent Kit, 96 Samples (for Illumina HiSeq, MiSeq, and NextSeq platforms)	Agilent p/n G9683B
AMPure XP Kit	Beckman Coulter Genomics
5 mL	p/n A63880
60 mL	p/n A63881
450 mL	p/n A63882
Dynabeads MyOne Streptavidin T1	Thermo Fisher Scientific
2 mL	p/n 65601
10 mL	p/n 65602
50 mL	p/n 65604D
1X Low TE Buffer (10 mM Tris-HCl, pH 7.5-8.0, 0.1 mM EDTA)	Thermo Fisher Scientific p/n 12090-015, or equivalent
100% Ethanol, molecular biology grade	Sigma-Aldrich p/n E7023
Qubit dsDNA HS Assay Kit or	Thermo Fisher Scientific p/n Q32851
Qubit dsDNA BR Assay Kit	Thermo Fisher Scientific
100 assays	p/n Q32850
500 assays	p/n Q32853
Nuclease-free Water (not DEPC-treated)	Thermo Fisher Scientific p/n AM9930

Table 2 Compatible Pre-Designed Probes for Automation

Probe Capture Library	96 Reactions
SureSelect XT HS Human All Exon V8	5191-6875
SureSelect XT HS Human All Exon V8+UTR	5191-7403
SureSelect XT HS Human All Exon V8+NCV	5191-7409
SureSelect XT Human All Exon V7	5191-4006
SureSelect XT Human All Exon V6	5190-8865
SureSelect XT Human All Exon V6 + UTRs	5190-8883
SureSelect XT Human All Exon V6 + COSMIC	5190-9309
SureSelect XT Clinical Research Exome V2	5190-9493
SureSelect XT Focused Exome	5190-7789
SureSelect XT Mouse All Exon	5190-4643
ClearSeq Comprehensive Cancer XT	5190-8013
ClearSeq Inherited Disease XT	5190-7520

Table 2 Compatible Pre-Designed Probes for Automation (continued)

Probe Capture Library	96 Reactions
Pre-designed Probes customized with additional <i>Plus</i> custom content	
SureSelect XT Human All Exon V7 Plus 1	Please visit the SureDesign website to design the customized <i>Plus</i> content and obtain ordering information. Contact the SureSelect support team (see page 2) or your local representative if you need assistance.
SureSelect XT Human All Exon V7 Plus 2	
SureSelect XT Human All Exon V6 Plus 1	
SureSelect XT Human All Exon V6 Plus 2	
SureSelect XT Clinical Research Exome V2 Plus 1	
SureSelect XT Clinical Research Exome V2 Plus 2	
SureSelect XT Focused Exome Plus 1	
SureSelect XT Focused Exome Plus 2	
ClearSeq Comprehensive Cancer Plus XT	
ClearSeq Inherited Disease Plus XT	

Table 3 Compatible Custom Probes for Automation*

Probe Capture Library	96 Reactions	480 Reactions
SureSelect Custom Tier1 1–499 kb	Please visit the SureDesign website to design Custom SureSelect probes and obtain ordering information. Contact the SureSelect support team (see page 2) or your local representative if you need assistance.	
SureSelect Custom Tier2 0.5 –2.9 Mb		
SureSelect Custom Tier3 3 –5.9 Mb		
SureSelect Custom Tier4 6 –11.9 Mb		
SureSelect Custom Tier5 12–24 Mb		

* Custom Probes designed August 2020 or later are produced using an updated manufacturing process; design size Tier is shown on labeling for these products. Custom Probes designed and ordered prior to August 2020 may be reordered, with these probes produced using the legacy manufacturing process; design-size Tier is not shown on labeling for the legacy-process products. Custom Probes of both categories use the same optimized target enrichment protocols detailed in this publication.

Optional Reagents

Table 4 Optional Reagents for SureSelect^{QXT} Target Enrichment

Description	Vendor and part number
Agilent QPCR NGS Library Quantification Kit (Illumina GA)	Agilent p/n G4880A

Required Equipment

Table 5 Required Equipment for SureSelect^{QXT} Target Enrichment

Description	Vendor and part number
Agilent NGS Bravo Option A Contact Agilent Automation Solutions for more information: Customerservice.automation@agilent.com	Agilent p/n G5522A (VWorks software version 13.1.0.1366, 13.0.0.1360, or 11.3.0.1195) OR Agilent p/n G5573AA (VWorks software version 13.1.0.1366)
Robotic Pipetting Tips (Sterile, Filtered, 250 µL)	Agilent p/n 19477-022
PlateLoc Thermal Microplate Sealer with Small Hotplate	Agilent p/n G5402G#226
Clear Peelable Seal plate seals (for use with the PlateLoc Thermal Plate Sealer)	Agilent p/n 16985-001
Thermal cycler and accessories	Various suppliers <i>Important:</i> Not all PCR plate types are supported for use in the VWorks automation protocols for the Agilent NGS Workstation. Select a thermal cycler that is compatible with one of the supported PCR plate types. See supported plate types in the listing below.
PCR plates compatible with the Agilent NGS Bravo and associated VWorks automation protocols	Only the following PCR plates are supported: <ul style="list-style-type: none"> • 96 ABI PCR half-skirted plates (MicroAmp Optical plates), Thermo Fisher Scientific p/n N8010560 • 96 Agilent semi-skirted PCR plate, Agilent p/n 401334 • 96 Eppendorf Twin.tec half-skirted PCR plates, Eppendorf p/n 951020303 • 96 Eppendorf Twin.tec PCR plates (full-skirted), Eppendorf p/n 951020401
Eppendorf twin.tec full-skirted 96-well PCR plates	Eppendorf p/n 951020401 or 951020619
Thermo Scientific Reservoirs	Thermo Fisher Scientific p/n 1064-15-6
Nunc DeepWell Plates, sterile, 1.3-mL well volume	Thermo Fisher Scientific p/n 260251
Axygen 96 Deep Well Plate, 2 mL, Square Well (waste reservoirs; working volume 2.2 mL)	Axygen p/n P-2ML-SQ-C E & K Scientific p/n EK-2440
DNA LoBind Tubes, 1.5-mL PCR clean, 250 pieces	Eppendorf p/n 022431021 or equivalent
Nucleic acid surface decontamination wipes	DNA Away Surface Decontaminant Wipes, Thermo Fisher Scientific p/n 7008, or equivalent
Qubit Fluorometer	Thermo Fisher Scientific p/n Q33238
Qubit Assay Tubes	Thermo Fisher Scientific p/n Q32856
Magnetic separator	DynaMag-50 magnet, Thermo Fisher Scientific p/n 123-02D or equivalent
Vacuum concentrator	Savant SpeedVac, model DNA120, with 96-well plate rotor, model RD2MP, or equivalent

Table 5 Required Equipment for SureSelect^{QXT} Target Enrichment (continued)

Description	Vendor and part number
DNA Analysis Platform and Consumables*	
Agilent 2100 Bioanalyzer Instrument	Agilent p/n G2939BA
Agilent 2100 Expert SW Laptop Bundle (optional)	Agilent p/n G2953CA
DNA 1000 Kit	Agilent p/n 5067-1504
High Sensitivity DNA Kit	Agilent p/n 5067-4626
OR	
Agilent 4200/4150 TapeStation	Agilent p/n G2991AA/G2992AA
96-well sample plates	Agilent p/n 5042-8502
96-well plate foil seals	Agilent p/n 5067-5154
8-well tube strips	Agilent p/n 401428
8-well tube strip caps	Agilent p/n 401425
D1000 ScreenTape	Agilent p/n 5067-5582
D1000 Reagents	Agilent p/n 5067-5583
High Sensitivity D1000 ScreenTape	Agilent p/n 5067-5584
High Sensitivity D1000 Reagents	Agilent p/n 5067-5585
Centrifuge	Eppendorf Centrifuge model 5804 or equivalent
Plate or strip tube centrifuge	Labnet International MPS1000 Mini Plate Spinner p/n C1000 (requires adapter, p/n C1000-ADAPT, for use with strip tubes) or equivalent
Pipettes (multichannel pipette and P10, P20, P200 and P1000 pipettes)	Pipetman or equivalent
Vortex mixer	
Ice bucket	
Powder-free gloves	
Sterile, nuclease-free aerosol barrier pipette tips	

* DNA samples may also be analyzed using the Agilent 5200 Fragment Analyzer, p/n M5310AA, and associated NGS Fragment Kits (DNF-473-0500 and DNF-474-0500). Implement any sample dilution instructions provided in protocols in this document, and then follow the assay instructions provided for each NGS Fragment Kit.

2 Using the Agilent NGS Bravo Option A for SureSelect Target Enrichment

About the NGS Bravo Option A **16**

Overview of the SureSelect^{QXT} Target Enrichment Procedure **24**

Experimental Setup Considerations for Automated Runs **26**

This chapter contains an orientation to the Agilent NGS Bravo Option A, an overview of the SureSelect^{QXT} target enrichment protocol, and considerations for designing SureSelect^{QXT} experiments for automated processing using the Agilent NGS Bravo Option A.

About the NGS Bravo Option A

CAUTION

Before you begin, make sure that you have read and understand operating, maintenance and safety instructions for using the Bravo platform and additional devices and software. Refer to the user guides listed in [Table 6](#).

Review the user guides listed in [Table 6](#) (available at Agilent.com) to become familiar with the general features and operation of the automation components. Instructions for using the Bravo platform and other automation components in the SureSelect^{QXT} Target Enrichment workflow are detailed in this user guide.

Table 6 Agilent NGS Workstation components User Guide reference information

Device	User Guide part number
Bravo Platform	SD-V1000376 (previously G5562-90000)
VWorks Software	G5415-90068 (VWorks versions 13.1.0.1366 and 13.0.0.1360), or G5415-90063 (VWorks version 11.3.0.1195)
PlateLoc Thermal Microplate Sealer	G5402-90001

About the Bravo Platform

The Bravo platform is a versatile liquid handler with a nine plate-location platform deck, suitable for handling 96-well, 384-well, and 1536-well plates. The Bravo platform is controlled by the VWorks Automation Control software. Fitted with a choice of three interchangeable disposable-tip pipette heads, it accurately dispenses fluids from 0.3 µL to 250 µL.

Bravo Platform Deck

The protocols in the following sections include instructions for placing plates and reagent reservoirs on specific Bravo deck locations. Use [Figure 1](#) to familiarize yourself with the location numbering convention on the Bravo platform deck.

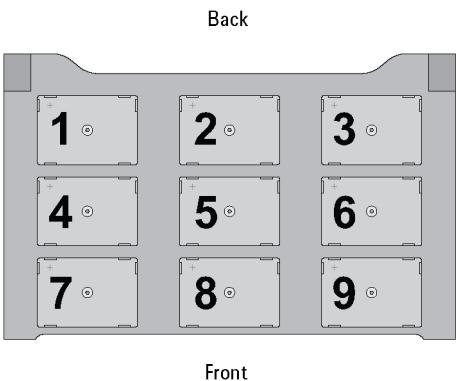


Figure 1 Bravo platform deck

Setting the Temperature of Bravo Deck Heat Blocks

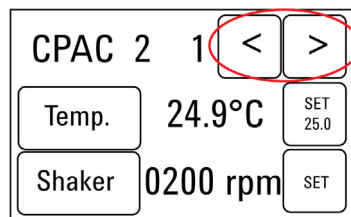
Bravo deck positions 4 and 6 are equipped with Inheco heat blocks, used to incubate sample plates at defined temperatures during the run. Runs that include high- (85°C) or low- (4°C) temperature incubation steps may be expedited by pre-setting the temperature of the affected block before starting the run.

Bravo deck heat block temperatures may be changed using the Inheco Multi TEC Control device touchscreen as described in the steps below. See [Table 7](#) for designations of the heat block-containing Bravo deck positions on the Multi TEC control device.

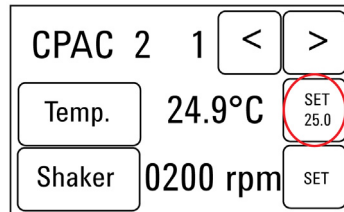
Table 7 Inheco Multi TEC Control touchscreen designations

Bravo Deck Position	Designation on Inheco Multi TEC Control Screen
4	CPAC 2 1
6	CPAC 2 2

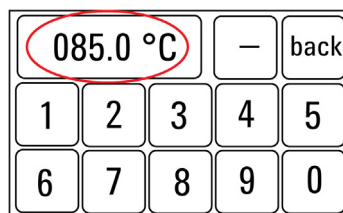
- 1 Using the arrow buttons, select the appropriate block (CPAC 2 block 1 or CPAC 2 block 2).



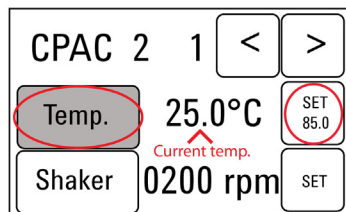
- 2 To set the temperature of the selected block, press the SET button.



- 3 Using the numeral pad, enter the desired temperature. The entered temperature appears in the top, left rectangle. Once the correct temperature is displayed, press the rectangle to enter the temperature.



- 4 Press the Temp button until the new temperature is displayed on the SET button and until the Temp button is darkened, indicating that the selected heat block is heating or cooling to the new temperature setting. The current temperature of the block is indicated in the center of the display.



Setting the Temperature of Bravo Deck Position 9 Using the ThermoCube Device

Bravo deck position 9 is equipped with a ThermoCube thermoelectric temperature control system, used to incubate components at a defined temperature during the run. During protocols that require temperature control at position 9, you will be instructed to start and set the temperature of the ThermoCube device before starting the run.

ThermoCube temperature settings are modified using the control panel (LCD display screen and four input buttons) on the front panel of the device using the following steps.

- 1 Turn on the ThermoCube and wait for the LCD screen to display **TEMP**.
- 2 Press the **UP** or **DOWN** button to change **SET TEMP 1** to the required set point.
- 3 Press the **START** button.

The ThermoCube then initiates temperature control of Bravo deck position 9 at the displayed set point.

VWorks Automation Control Software

VWorks software, included with your Agilent NGS Bravo Option A, allows you to control the integrated devices using a PC. The Agilent NGS Bravo Option A is preloaded with VWorks software containing all of the necessary SureSelect system liquid handling protocols. General instructions for starting up the VWorks software and the included protocols are provided below. Each time a specific VWorks protocol is used in the SureSelect procedure, any settings required for that protocol are included in the relevant section of this manual.

NOTE

The instructions in this manual are compatible with VWorks software version 13.1.0.1366, 13.0.0.1360, or 11.3.0.1195, including SureSelect^{QXT} automation protocols version 1.0.

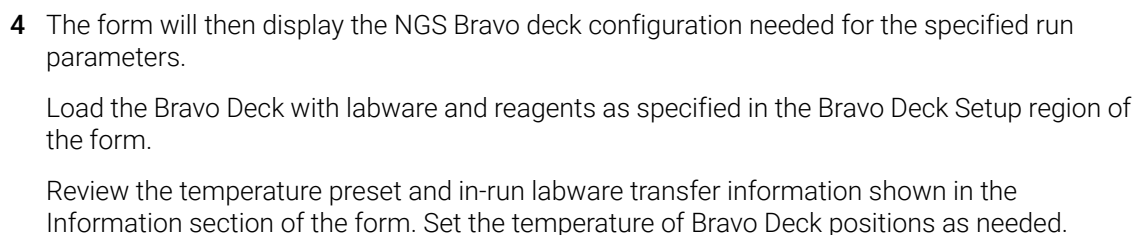
If you have questions about VWorks version compatibility, please contact service.automation@agilent.com.

Logging in to the VWorks software

- 1 Double-click the VWorks icon or the QXT_ILM_OptA_v1.0.VWForm shortcut on the Windows desktop to start the VWorks software.
- 2 If User Authentication dialog is not visible, click **Log in** on the VWorks window toolbar.
- 3 In the User Authentication dialog, type your VWorks user name and password, and click **OK**. (If no user account is set up, contact the administrator.)

Use the VWorks form QXT_ILM_OptA_v1.0.VWForm, shown below, to set up and start each SureSelect automation protocol.

- 1 Open the form using the QXT_ILM_OptA_v1.0.VWForm shortcut on your desktop.
- 2 Use the drop-down menus on the form to select the appropriate SureSelect workflow step and other Parameters for the run.
- 3 Once all run parameters have been specified on the form, click **Display Initial Bravo Deck Setup**.





SureSelect^{QXT} Transposase Library Prep for Illumina sequencers

Parameters

- 1) Select Protocol
01 Tn_QXT_ILM_v1.0.pro
- 2) Select PCR Plate Labware (Protocols 3, 4, 6, 7, 9 and 10)
96 ABI PCR half skirt in Red Alum Insert
- 3) Select Number of Columns of Samples to Process
4
- 4) ☒ Display Initial Bravo Deck Setup
- 5) Load labware according to Bravo Deck Setup
- 6) Update current tip state (omit for Protocol 05)

Current Tip State

Select columns of unused tips (Box 2)

☒ ☒ ☒ ☒ ☒ ☒ ☒ ☒ ☒ ☒ ☒ ☒

Select columns of used tips (Box 8)

☐ ☐ ☐ ☐ ☐ ☐ ☐ ☐ ☐ ☐ ☐ ☐

Reset

Clear

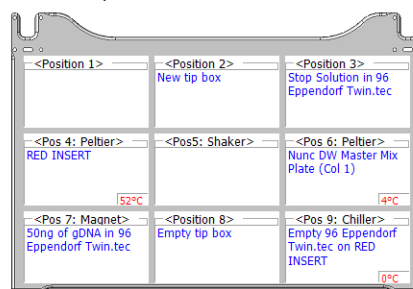
Controls

Elapsed Time: 00:00:00

Advanced Settings

- ☒ Enable audio alerts ☐ Ignore all incubation times (TESTING ONLY)

Bravo Deck Setup



Reference

Final DNA Location	Labware Needs	Protocol Duration	Temperature Presets
--------------------	---------------	-------------------	---------------------

Information

Position 4 can be pre-heated to 52°C, Position 6 can be pre-chilled to 4°C and Position 9 can be pre-chilled to 0°C.

Status

C:/VWorks Workspace/NGS Option A/QXT_ILM_v1.0/Protocol Files/01 Tn_QXT_ILM_v1.0.pro

- 5 Verify that the **Current Tip State** indicator on the form (shown below) matches the configuration of unused tips in the tip box at Bravo Deck position 2.

For a fresh tip box, containing 12 columns of tips, all positions of the **Current Tip State** unused tip indicator (top portion, Box 2) should be selected, as shown below. Clicking **Reset** selects all columns for position 2.

Current Tip State

Select columns of unused tips (Box 2)

☒ ☒ ☒ ☒ ☒ ☒ ☒ ☒ ☒ ☒ ☒ ☒

Select columns of used tips (Box 8)

☐ ☐ ☐ ☐ ☐ ☐ ☐ ☐ ☐ ☐ ☐ ☐

Also verify that the used tip indicator (bottom portion, Box 8) matches the configuration of used tips in the tip box at Bravo Deck position 8.

For an empty tip box, all positions of the **Current Tip State** used tip indicator (bottom portion, Box 8) should be cleared, as shown above. Clicking **Reset** clears all columns for position 8.

NOTE

It is important that the **Current Tip State** indicator matches the configuration of tips present at Bravo Deck positions 2 and 8 when initiating the run. Tips that are inappropriately loaded onto the Bravo platform pipette head, or tips missing from the pipette head, will interfere with automated processing steps.

You can use partial tip boxes for NGS Bravo Option A automation protocols, as long as positions of available tips are accurately indicated during run setup.

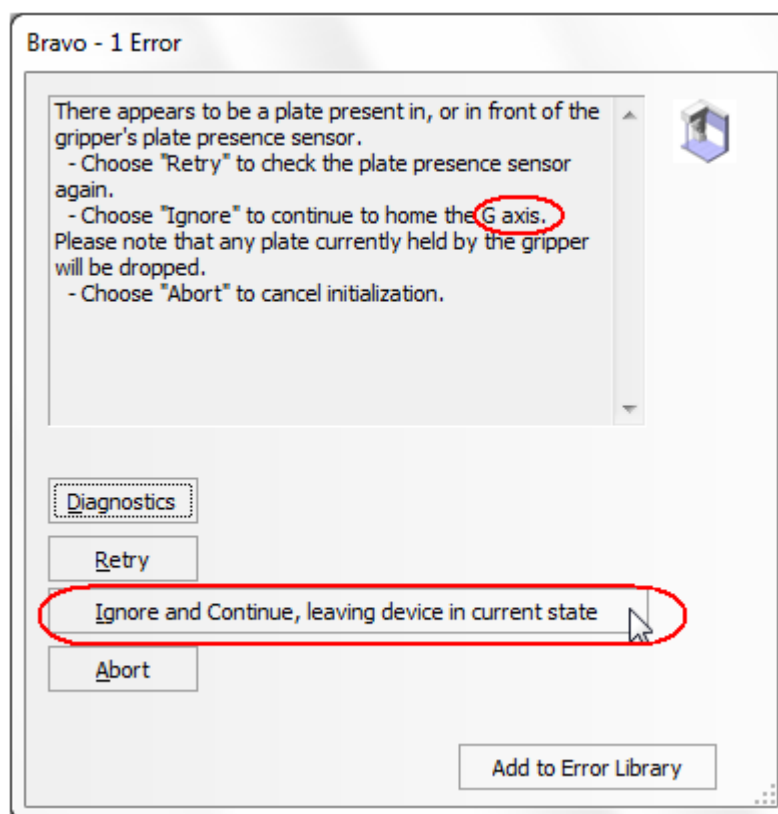
- 6 After verifying that the NGS Bravo has been set up correctly, click **Run Selected Protocol**.



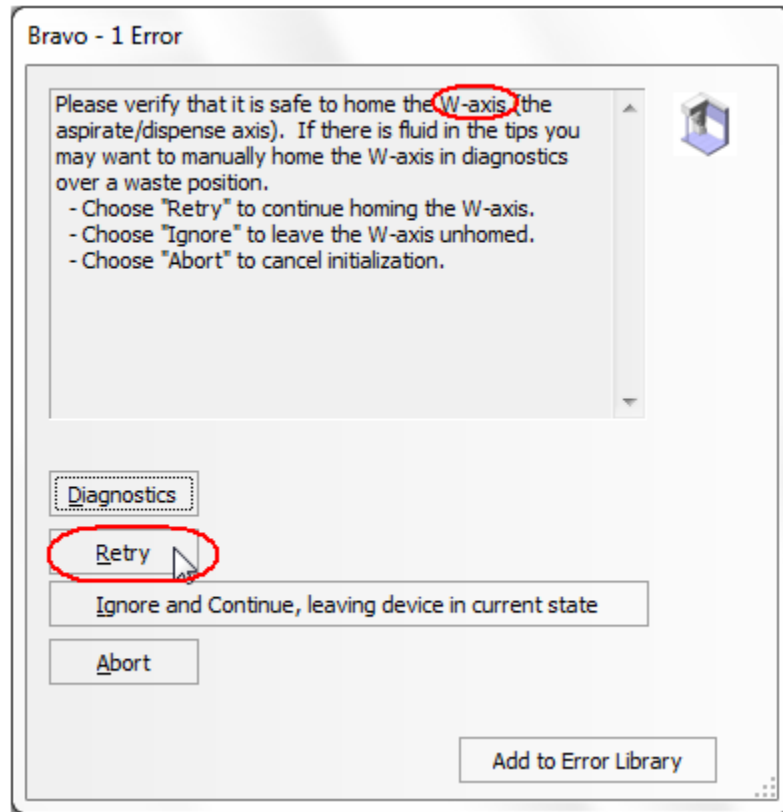
Error messages encountered at start of run

After starting the run, you may see the error messages displayed below. When encountered, make the indicated selections and proceed with the run. Encountering either or both of these error messages is not indicative of a problem with the NGS Bravo or your run setup.

- 1 If you encounter the G-axis error message shown below, select **Ignore and Continue**, leaving device in current state.



- 2 If you encounter the W-axis error message shown below, select **Retry**.



Verifying the Simulation setting

VWorks software may be run in simulation mode, during which commands entered on screen are not completed by the NGS Bravo. If NGS Bravo devices do not respond when you start a run, verify the simulation mode status in VWorks using the following steps.

- 1 Verify that Simulation is off is displayed on the status indicator (accessible by clicking **View > Control Toolbar**).



- 2 If the indicator displays **Simulation is on**, click the status indicator button to turn off the simulation mode.

NOTE

If you cannot see the toolbar above the VWorks form, click the **Full Screen** button to exit full screen mode. If the toolbar is still not visible, right-click on the form and then select **Control Toolbar** from the menu.

Overview of the SureSelect^{QXT} Target Enrichment Procedure

Figure 2 summarizes the SureSelect^{QXT} target enrichment workflow for samples to be sequenced using the Illumina paired-read sequencing platform. For each sample to be sequenced, individual library preparations, hybridizations, and captures are performed. The samples are then tagged by PCR with an index sequence. Depending on the target size of the SureSelect capture, up to 96 samples can be pooled and sequenced in a single lane using the dual index tags that are provided with SureSelect^{QXT} Library Prep kits.

Table 8 summarizes how the VWorks protocols are integrated into the SureSelect^{QXT} workflow. See **Sample Preparation**, **Hybridization**, and **Indexing** chapters for complete instructions for use of the VWorks protocols for sample processing.

SureSelect^{QXT} NGS Target Enrichment Workflow

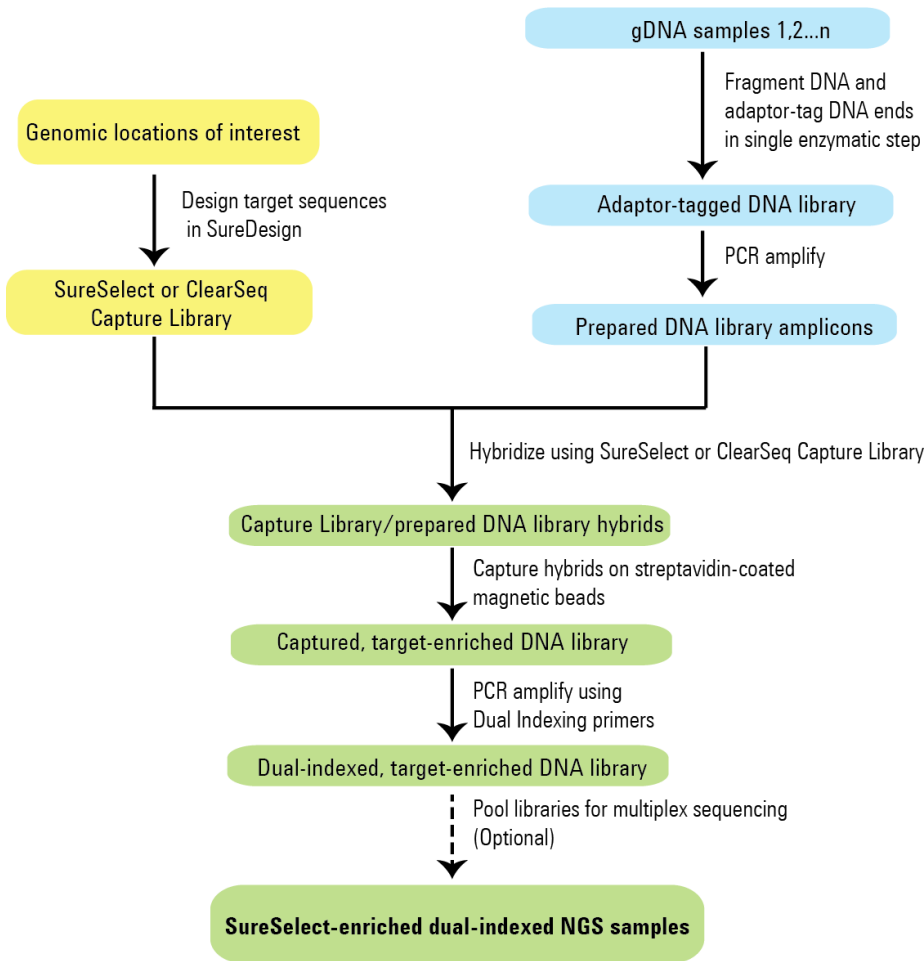


Figure 2 Overall sequencing sample preparation workflow.

Table 8 Overview of VWorks protocols used for SureSelect^{QXT} Target Enrichment using NGS Bravo Option A

Workflow Step (Protocol Chapter)	Substep	VWorks Protocols Used for Agilent NGS Bravo Option A automation
Sample Preparation	Prepare fragmented and adaptor-tagged DNA	01 Tn_QXT_ILM_v1.0.pro
	Purify DNA using AMPure XP beads	02 Cleanup_Tn_v1.0.pro
	Amplify adaptor-tagged DNA	03b Pre-CapturePCR_QXT_ILM_v1.0.pro
	Purify DNA using AMPure XP beads	04b Cleanup_Pre-CapturePCR_QXT_ILM_v1.0.pro
Hybridization	Aliquot prepped libraries for hybridization	05 Aliquot_Libraries_v1.0.pro
	Hybridize prepped DNA to Probe	06 Hybridization_QXT_v1.0.pro
	Capture DNA hybrids	07 SureSelectQXT_Capture_v1.0.pro
	Wash captured DNA hybrids	08 SureSelectQXT_Wash_v1.0.pro
Indexing	Add index tags by PCR	09 Post-CapturePCR_QXT_ILM_v1.0.pro
	Purify DNA using AMPure XP beads	10 Cleanup_Post-CapturePCR_QXT_ILM_v1.0.pro

Experimental Setup Considerations for Automated Runs

Agilent SureSelect Automated Library Prep and Capture System runs may include 1, 2, 3, 4, 6, or 12 columns (equivalent to 8, 16, 24, 32, 48, or 96 wells) of gDNA samples to be enriched for sequencing on the Illumina platform. Plan your experiments using complete columns of samples.

Table 9 Columns to Samples Equivalency

Number of Columns Processed	Total Number of Samples Processed
1	8
2	16
3	24
4	32
6	48
12	96

The number of columns or samples that may be processed using the supplied reagents will depend on the experimental design. For greatest efficiency of reagent use, plan experiments using at least 3 columns per run. Each 96-reaction kit contains sufficient reagents for 96 reactions configured as 4 runs of 3 columns of samples per run.

Considerations for Placement of gDNA Samples in 96-well Plates for Automated Processing

- The NGS Bravo processes samples column-wise beginning at column 1. gDNA samples should be loaded into 96-well plates column-wise, in well order A1 to H1, then A2 to H2, ending with A12 to H12. When processing partial runs with <12 sample columns, do not leave empty columns between sample columns; always load the plate using the left-most column that is available.
- At the hybridization step (see [Figure 2](#)), you can add a different Probe Capture Library to each row of the plate. Plan your experiment such that each prepared DNA library corresponds to the appropriate probe row in the sample plate.
- For post-capture amplification (see [Figure 2](#)), different probes can require different amplification cycle numbers, based on the probe design sizes. It is most efficient to process similar-sized probes on the same plate. See [Table 55](#) on page 73 to determine which probes may be amplified on the same plate.
- Post-capture dual index assignments for the DNA samples can affect sample placement decisions at the beginning of the workflow. For example, all samples on the same row of the DNA sample plate must be assigned to the same P5 indexing primer during sample indexing after hybridization (see [Figure 2](#)). It is important to review and understand the guidelines for assignment of dual indexing primers on [page 70](#) while planning sample placement for the run to ensure that the indexing design is compatible with the initial DNA sample placement.

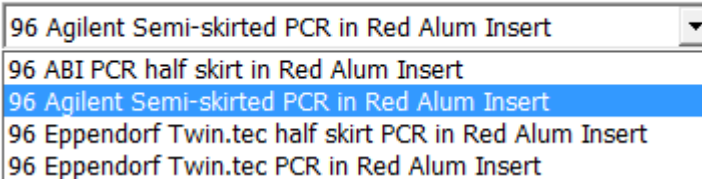
Considerations for Equipment Setup

- Some workflow steps require the rapid transfer of sample plates between the Bravo deck and a thermal cycler. Locate your thermal cycler in close proximity to the Agilent NGS Bravo to allow rapid and efficient plate transfer.
- Several workflow steps require that the sample plate be sealed using the PlateLoc thermal microplate sealer and then centrifuged to collect any dispersed liquid. To maximize efficiency, locate the centrifuge in close proximity to the Agilent NGS Bravo.

PCR Plate Type Considerations

Automation protocols include several liquid-handling steps in which reagents are dispensed to PCR plates in preparation for transfer to a thermal cycler. For these steps you must specify the PCR plate type to be used on the QXT_ILM_OptA_v1.0.VWForm to allow correct configuration of the liquid handling components for the PCR plate type. Before you begin the automation protocol, make sure that you are using a supported PCR plate type. The PCR plate type to be used in the protocol is specified using the menu below. Vendor and part number information is provided for the supported plate types in [Table 10](#).

2) Select PCR Plate Labware (Protocols 3, 4, 6, 7, 9 and 10)



96 Agilent Semi-skirted PCR in Red Alum Insert

96 ABI PCR half skirt in Red Alum Insert

3) 96 Agilent Semi-skirted PCR in Red Alum Insert

96 Eppendorf Twin.tec half skirt PCR in Red Alum Insert

96 Eppendorf Twin.tec PCR in Red Alum Insert

CAUTION

The plates listed in [Table 10](#) are compatible with the Agilent NGS Bravo and associated VWorks automation protocols, designed to support use of various thermal cyclers.

Do not use PCR plates that are not listed in [Table 10](#) even if they are compatible with your chosen thermal cycler.

Table 10 Ordering information for supported PCR plates

Description in VWorks menu	Vendor and part number
96 ABI PCR half-skirted plates (MicroAmp Optical plates)	Thermo Fisher Scientific p/n N8010560
96 Agilent semi-skirted PCR plate	Agilent p/n 401334
96 Eppendorf Twin.tec half-skirted PCR plates	Eppendorf p/n 951020303
96 Eppendorf Twin.tec PCR plates (full-skirted)	Eppendorf p/n 951020401 or 951020619

3 Sample Preparation

- Step 1. Prepare the genomic DNA samples and Library Prep reagents **30**
- Step 2. Fragment and adaptor-tag the genomic DNA samples **31**
- Step 3. Purify adaptor-tagged DNA using AMPure XP beads **35**
- Step 4. Amplify adaptor-ligated libraries **37**
- Step 5. Purify amplified DNA using AMPure XP beads **41**
- Step 6. Assess Library DNA quantity and quality **43**

This section contains instructions for gDNA library preparation specific to the Illumina paired-read sequencing platform and to automated processing using the Agilent NGS Bravo Option A.

Step 1. Prepare the genomic DNA samples and Library Prep reagents

It is important to have all materials prepared in advance of use in the SureSelect^{QXT} automated Library Prep protocol. In this step, the gDNA is carefully quantified and dispensed into the sample plate. Additional reagents that require modification or temperature equilibration before use are also prepared in this step.

- 1 Remove the DMSO vial from the SureSelect QXT Library Prep Kit Box 2 in -20°C storage. Leave the DMSO vial at room temperature in preparation for use on [page 38](#).
- 2 Prepare reagents for the purification protocols on [page 35](#) and [page 41](#).
 - a Transfer the AMPure XP beads to room temperature. The beads should be held at room temperature for at least 30 minutes before use. *Do not freeze the beads at any time.*
 - b Prepare 150 mL of fresh 70% ethanol for use in the purification steps. The 70% ethanol may be used for multiple steps done on the same day, when stored in a sealed container.
- 3 Obtain the bottle of SureSelect QXT Stop Solution from SureSelect QXT Hyb Module Box 1 (stored at room temperature). Verify that the SureSelect QXT Stop Solution contains 25% ethanol, by referring to the container label and the instructions below.

Before the first use of a fresh container, add 1.5 mL of ethanol to the provided bottle containing 4.5 mL of stop solution, for a final ethanol concentration of 25%. Seal the bottle then vortex well to mix. After adding the ethanol, be sure to mark the label for reference by later users.

Keep the prepared 1X SureSelect QXT Stop Solution at room temperature, tightly sealed, until it is used on [page 32](#).

- 4 Quantify and dilute gDNA samples using two serial fluorometric assays:
 - a Use the Qubit dsDNA BR Assay or Qubit dsDNA HS Assay to determine the initial concentration of each gDNA sample. Follow the manufacturer's instructions for the specific assay kit and the Qubit instrument. This step is critical for successful preparation of input DNA at the required concentration to ensure optimal fragmentation.
 - b Dilute each gDNA sample with nuclease-free water to a final concentration of 100 ng/ μL in a LoBind tube.
 - c Carefully measure the DNA concentration of each of the 100 ng/ μL dilutions using a second Qubit dsDNA BR or HS Assay.
 - d Adjust each gDNA sample with nuclease-free water to a final concentration of 10 ng/ μL in a LoBind tube.
- 5 Transfer 5 μL of the 10 ng/ μL -DNA samples into the wells of a 96-well Eppendorf plate, column-wise, for processing on the NGS Bravo, in well order A1 to H1, then A2 to H2, ending with A12 to H12.

NOTE

SureSelect Automated Library Prep and Capture System runs may include 1, 2, 3, 4, 6, or 12 columns of the plate. See [Experimental Setup Considerations for Automated Runs](#) on [page 26](#) for additional sample placement considerations.

- 6 Seal the plate using the PlateLoc Thermal Microplate Sealer, with sealing settings of 165°C and 1.0 sec.
- 7 Centrifuge the plate for 30 seconds to drive the well contents off the walls and plate seal and to remove air bubbles.

Store the sample plate on ice until it is used on [page 34](#).

Step 2. Fragment and adaptor-tag the genomic DNA samples

In this step, automation protocol 01 Tn_QXT_ILM_v1.0.pro is used to enzymatically fragment the gDNA and to add adaptors to ends of the fragments in a single reaction. This step uses the SureSelect^{QXT} Reagent Kit components listed in [Table 11](#) in addition to reagents prepared for use on [page 30](#) to [page 30](#).

Table 11 Reagents for DNA fragmentation and adaptor-tagging

Kit Component	Storage Location	Where Used
SureSelect QXT Buffer	SureSelect QXT Library Prep Kit Box 2, -20°C	page 31
SureSelect QXT Enzyme Mix ILM	SureSelect QXT Library Prep Kit Box 2, -20°C	page 31

Prepare the NGS Bravo

- 1 Clear the Bravo deck of all plates and tip boxes, then wipe it down with a DNA Away decontamination wipe.
- 2 Pre-set the temperature of Bravo deck positions 4, 6, and 9 as indicated in [Table 12](#). See [page 17](#) to [page 18](#) for more information on how to do this step.

Table 12 Bravo Deck Temperature Presets

Bravo Deck Position	Temperature Preset	Preset Method
4	52°C	Inheco Multi TEC control touchscreen (CPAC 2-1)
6	4°C	Inheco Multi TEC control touchscreen (CPAC 2-2)
9	0°C	ThermoCube control panel

- 3 Place red PCR plate inserts at Bravo deck positions 4 and 9.

Prepare the Library Prep Master Mix and Stop Solution source plates

- 4 Prepare the Stop Solution source plate using an Eppendorf twin.tec full-skirted PCR plate. Add 35 µL of 1X SureSelect QXT Stop Solution per well, for each well to be processed. Place the source plate on Bravo deck position 3.
- 5 Before use, vortex the SureSelect QXT Buffer and SureSelect QXT Enzyme Mix ILM tubes vigorously at high speed.

These components are in liquid form when removed from –20°C storage and should be returned to –20°C storage promptly after use.

CAUTION

Minor variations in volumes of the solutions combined in **step 6** below may result in DNA fragment size variation.

The SureSelect QXT Buffer and Enzyme Mix solutions are highly viscous. Thorough mixing of the reagents is critical for optimal performance.

- 6 Prepare the appropriate volume of Library Prep Master Mix, according to **Table 13**. Mix well by vortexing for 20 seconds and then keep on ice.

Table 13 Preparation of Library Prep Master Mix

SureSelect ^{QXT} Reagent	Volume for 1 Library	Volume for 1 Column	Volume for 2 Columns	Volume for 3 Columns	Volume for 4 Columns	Volume for 6 Columns	Volume for 12 Columns
SureSelect QXT Buffer	17.0 µL	216.8 µL	361.3 µL	505.8 µL	650.3 µL	939.3 µL	1878.5 µL
SureSelect QXT Enzyme Mix ILM	2.0 µL	25.5 µL	42.5 µL	59.5 µL	76.5 µL	110.5 µL	221.0 µL
Total Volume	19 µL	242.3 µL	403.8 µL	565.3 µL	726.8 µL	1049.8 µL	2099.5 µL

- 7 Prepare the Library Prep master mix source plate using a Nunc DeepWell plate, containing the mixture from **step 6**. Add the volume indicated in **Table 14** to all wells of column 1 of the Nunc DeepWell plate. Keep the master mix on ice during the aliquoting steps. The final configuration of the master mix source plate is shown in **Figure 3**.

Table 14 Preparation of the Master Mix Source Plate for 01 Tn_QXT_ILM_v1.0.pro

Master Mix Solution	Position on Source Plate	Volume of Master Mix added per Well of Nunc Deep Well Source Plate					
		1-Column Runs	2-Column Runs	3-Column Runs	4-Column Runs	6-Column Runs	12-Column Runs
Library Prep Master Mix	Column 1 (A1-H1)	27.9 µL	48.1 µL	68.3 µL	88.5 µL	128.8 µL	260.1 µL

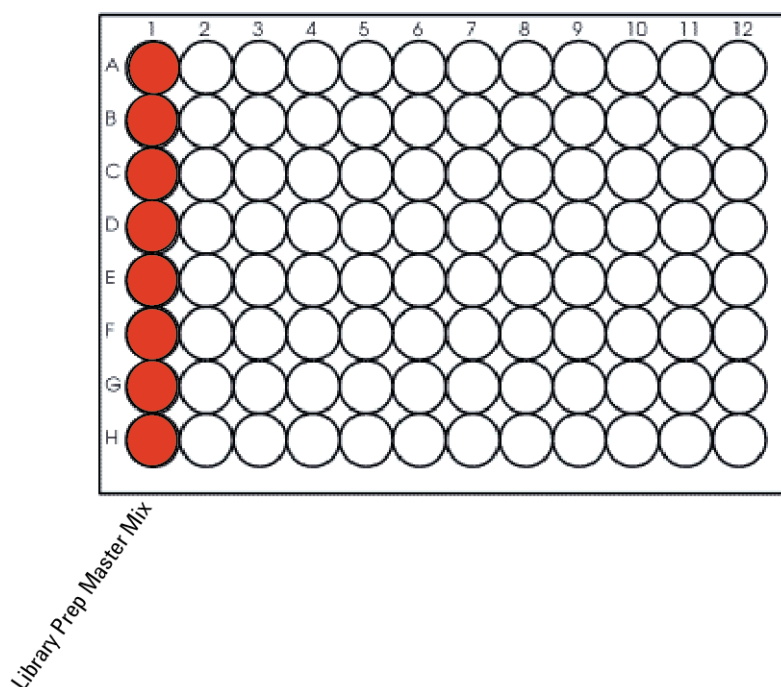


Figure 3 Configuration of the master mix source plate for 01 Tn_QXT_ILM_v1.0.pro

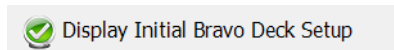
- 8 Seal the master mix source plate using the PlateLoc Thermal Microplate Sealer, with sealing settings of 165°C and 1.0 sec.
- 9 Centrifuge the plate for 30 seconds to drive the well contents off the walls and plate seal and to eliminate any bubbles. Keep the master mix source plate on ice.

NOTE

The presence of bubbles in source plate solutions may cause inaccurate volume transfer by the Bravo liquid handling platform. Ensure that the source plate is sealed and centrifuged prior to use in a run.

Setup and run VWorks protocol 01 Tn_QXT_ILM_v1.0.pro

- 10 On the SureSelect setup form, under **Select Protocol to Run**, select **01 Tn_QXT_ILM_v1.0.pro**.
- 11 Select the number of columns of samples to be processed. Runs must include 1, 2, 3, 4, 6, or 12 columns.
- 12 Click **Display Initial Bravo Deck Setup**.



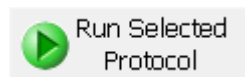
- 13 Load the Bravo deck according to the Bravo Deck Setup region of the form and as shown in **Table 15**

Table 15 Initial Bravo deck configuration for 01 Tn_QXT_ILM_v1.0.pro

Location	Content
1	–(empty)–
2	New tip box
3	Stop Solution in Eppendorf plate
4	Empty red insert
5	–(empty)–
6	Library Prep Master Mix source plate (unsealed)
7	gDNA samples (5 µl of 10 ng/µL DNA per well) in Eppendorf plate (unsealed)
8	Empty tip box
9	Empty Eppendorf plate on red insert

14 Verify that the Current Tip State indicator on the form matches the configuration of unused and used tips in the tip boxes at Bravo Deck positions 2 and 8, respectively. See [page 21](#) for more information on using this segment of the form during the run.

15 When setup and verification is complete, click **Run Selected Protocol**.



Running the 01 Tn_QXT_ILM_v1.0.pro protocol takes approximately 20 minutes. Once complete, the adaptor-tagged DNA samples are located in the Eppendorf plate at position 6 of the Bravo deck.

Step 3. Purify adaptor-tagged DNA using AMPure XP beads

This step uses automation protocol 02 Cleanup_Tn_v1.0.pro.

In this step the NGS Bravo combines the adaptor-tagged samples with AMPure XP beads and then collects and washes the bead-bound DNA. The purified eluted DNA is transferred to an Eppendorf twin.tec plate for further processing.

Prepare the NGS Bravo and reagents

- 1 Clear the Bravo deck of all plates and tip boxes, then wipe it down with a DNA Away decontamination wipe.
- 2 Pre-set the temperature of Bravo deck positions 4 and 6 as indicated in [Table 16](#). See [page 17](#) for more information on how to do this step.

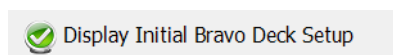
Table 16 Bravo Deck Temperature Presets

Bravo Deck Position	Temperature Preset	Preset Method
4	45°C	Inheco Multi TEC control touchscreen (CPAC 2-1)
6	20°C	Inheco Multi TEC control touchscreen (CPAC 2-2)

- 3 Mix the AMPure XP bead suspension well so that the reagent appears homogeneous and consistent in color.
- 4 Prepare a Nunc DeepWell source plate for the beads by adding 52 µL of homogeneous AMPure XP beads per well, for each well to be processed.
- 5 Prepare a Thermo Scientific Matrix reservoir containing 15 mL of nuclease-free water.
- 6 Prepare a separate Thermo Scientific Matrix reservoir containing 45 mL of freshly-prepared 70% ethanol.

Setup and Run VWorks protocol 02 Cleanup_Tn_v1.0.pro

- 7 On the SureSelect setup form, under **Select Protocol**, select **02 Cleanup_Tn_v1.0.pro**.
- 8 Select the number of columns of samples to be processed. Runs must include 1, 2, 3, 4, 6, or 12 columns.
- 9 Click **Display Initial Bravo Deck Setup**.



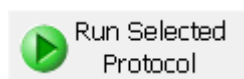
- 10** Load the Bravo deck according to the Bravo Deck Setup region of the form and as shown in **Table 17**.

Table 17 Initial Bravo deck configuration for 02 Cleanup_Tn_v1.0.pro

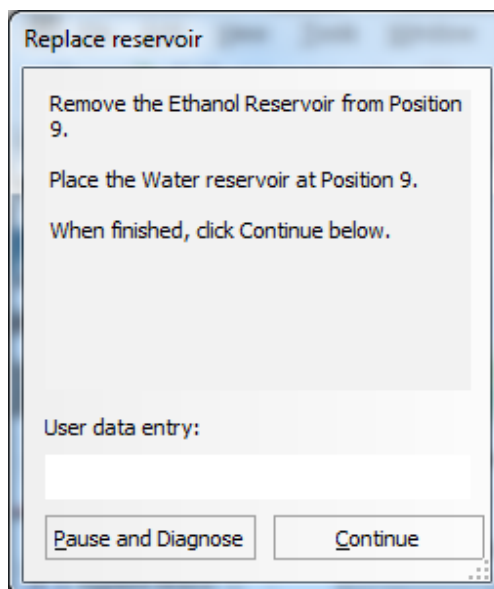
Location	Content
1	Empty waste reservoir (Axygen 96 Deep Well Plate, square wells)
2	New tip box
3	–(empty)–
4	–(empty)–
5	AMPure XP beads in Nunc DeepWell plate (52 µl beads per processing well)
6	Adaptor-tagged DNA samples in Eppendorf twin.tec plate
7	–(empty)–
8	Empty tip box
9	70% ethanol in Matrix reservoir

- 11** Verify that the Current Tip State indicator on the form matches the configuration of unused and used tips in the tip boxes at Bravo Deck positions 2 and 8, respectively. See **page 21** for more information on using this segment of the form during the run.

- 12** When setup and verification is complete, click **Run Selected Protocol**.



Running the 02 Cleanup_Tn_v1.0.pro protocol takes approximately 45 minutes. An operator must be present during the run to complete tip box replacement and to transfer the water reservoir to the Bravo deck, when directed by the VWorks prompt shown below.



Once the protocol is complete, the purified DNA samples are located in the Nunc DeepWell plate at position 7 of the Bravo deck.

Step 4. Amplify adaptor-ligated libraries

In this step, the Agilent NGS Bravo completes the liquid handling steps for amplification of the adaptor-ligated DNA samples using automation protocol 03b Pre-CapturePCR_QXT_ILM_v1.0.pro. Afterward, you transfer the PCR plate to a thermal cycler for amplification.

This step uses the SureSelect^{QXT} Reagent Kit components listed in [Table 18](#).

Table 18 Reagents for precapture amplification

Kit Component	Storage Location	Where Used
Herculase II Fusion DNA Polymerase	SureSelect QXT Library Prep Kit Box 2, -20°C	page 38
Herculase II 5× Reaction Buffer	SureSelect QXT Library Prep Kit Box 2, -20°C	page 38
100 mM dNTP Mix (25 mM each dNTP)	SureSelect QXT Library Prep Kit Box 2, -20°C	page 38
SureSelect QXT Primer Mix	SureSelect QXT Hyb Module Box 2, -20°C	page 38
DMSO	Transferred to Room Temperature storage on page 30	page 38

CAUTION

To avoid cross-contaminating libraries, set up PCR master mixes in a dedicated clean area or PCR hood with UV sterilization and positive air flow.

- 1 Clear the Bravo deck of all plates and tip boxes, then wipe it down with a DNA Away decontamination wipe.
- 2 Pre-set the temperature of Bravo deck positions 6 and 9 as indicated in [Table 19](#). See [page 17](#) to [page 18](#) for more information on how to do this step.

Table 19 Bravo Deck Temperature Presets

Bravo Deck Position	Temperature Preset	Preset Method
6	4°C	Inheco Multi TEC control touchscreen (CPAC 2-2)
9	0°C	ThermoCube control panel

- 3 Place a red PCR plate insert at Bravo deck position 6 and a silver deep well plate insert at Bravo deck position 9.

Prepare the pre-capture PCR master mix and master mix source plate

- 4 Prepare the appropriate volume of pre-capture PCR Master Mix, according to [Table 20](#). Mix well using a vortex mixer and keep on ice.

Table 20 Preparation of Pre-Capture PCR Master Mix

SureSelect ^{QXT} Reagent	Volume for 1 Library	Volume for 1 Column	Volume for 2 Columns	Volume for 3 Columns	Volume for 4 Columns	Volume for 6 Columns	Volume for 12 Columns
Nuclease-free water	13.5 µL	172.1 µL	286.9 µL	401.6 µL	516.4 µL	745.9 µL	1491.8 µL
Herculase II 5X Reaction Buffer	10.0 µL	127.5 µL	212.5 µL	297.5 µL	382.5 µL	552.5 µL	1105 µL
DMSO	2.5 µL	31.9 µL	53.1 µL	74.4 µL	95.6 µL	138.1 µL	276.3 µL
dNTP mix	0.5 µL	6.4 µL	10.6 µL	14.9 µL	19.1 µL	27.6 µL	55.3 µL
SureSelect QXT Primer Mix	1.0 µL	12.8 µL	21.3 µL	29.8 µL	38.3 µL	55.3 µL	110.5 µL
Herculase II Fusion DNA Polymerase	1.0 µL	12.8 µL	21.3 µL	29.8 µL	38.3 µL	55.3 µL	110.5 µL
Total Volume	28.5 µL	363.4 µL	605.6 µL	847.9 µL	1090.1 µL	1574.6 µL	3149.3 µL

- 5 Using the same Nunc DeepWell master mix source plate that was used for the 01 Tn_QXT_ILM_v1.0.pro run, add the volume of PCR Master Mix indicated in [Table 21](#) to all wells of column 2 of the master mix source plate. The final configuration of the master mix source plate is shown in [Figure 4](#).

Table 21 Preparation of the Master Mix Source Plate for 03b Pre-CapturePCR_QXT_ILM_v1.0.pro

Master Mix Solution	Position on Source Plate	Volume of Master Mix added per Well of Nunc Deep Well Source Plate					
		1-Column Runs	2-Column Runs	3-Column Runs	4-Column Runs	6-Column Runs	12-Column Runs
Pre-Capture PCR Master Mix	Column 2 (A2-H2)	41.9 µL	72.1 µL	102.4 µL	132.7 µL	193.3 µL	390.1 µL

NOTE

If you are using a new DeepWell plate for the pre-capture PCR source plate, leave column 1 empty and add the PCR Master Mix to column 2 of the new plate.

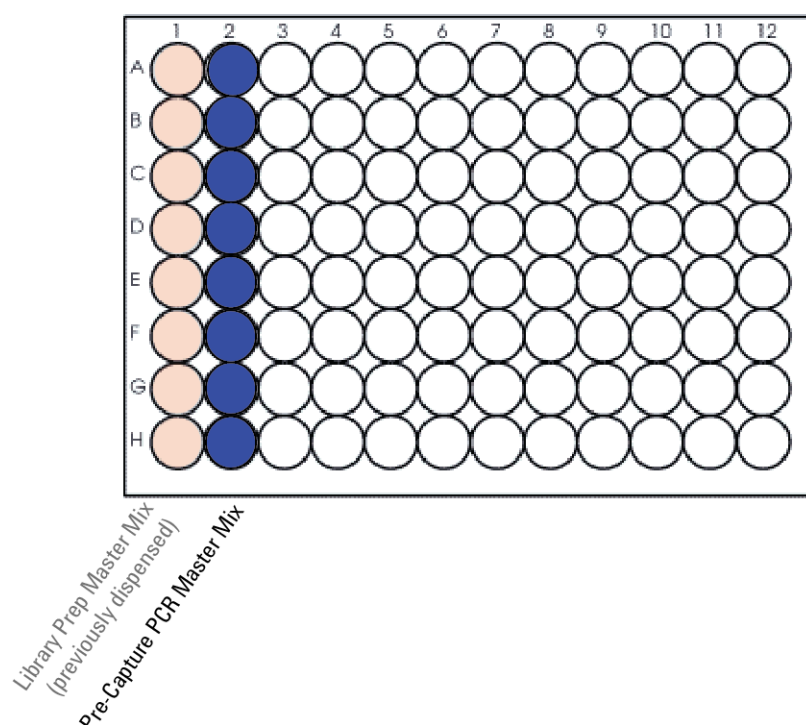


Figure 4 Configuration of the master mix source plate for 03b Pre-CapturePCR_QXT_ILM_v1.0.pro. Column 1 was used to dispense master mix during the previous protocol.

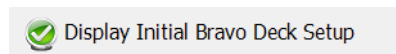
- 6 Seal the master mix source plate using the PlateLoc Thermal Microplate Sealer, with sealing settings of 165°C and 1.0 sec.
- 7 Centrifuge the plate for 30 seconds to drive the well contents off the walls and plate seal and to eliminate any bubbles.

NOTE

The presence of bubbles in source plate solutions may cause inaccurate volume transfer by the Bravo liquid handling platform. Ensure that the source plate is sealed and centrifuged prior to use in a run.

Setup and run VWorks protocol 03b Pre-CapturePCR_QXT_ILM_v1.0.pro

- 8 On the SureSelect setup form, under **Select Protocol to Run**, select **03b Pre-CapturePCR_QXT_ILM_v1.0.pro**.
- 9 Under **Select PCR plate Labware**, select the specific type of PCR plate to be used for thermal cycling (placed at position 6 of the Bravo deck).
- 10 Select the number of columns of samples to be processed. Runs must include 1, 2, 3, 4, 6, or 12 columns.
- 11 Click **Display Initial Bravo Deck Setup**.



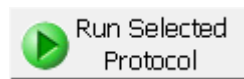
- 12** Load the Bravo deck according to the Bravo Deck Setup region of the form and as shown in **Table 22**.

Table 22 Initial Bravo deck configuration for 01 Tn_QXT_ILM_v1.0.pro

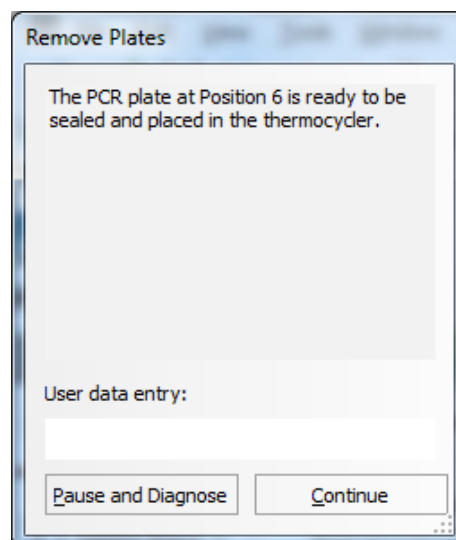
Location	Content
1	Empty waste reservoir (Axygen 96 Deep Well Plate, square wells)
2	New tip box
3	–(empty)–
4	–(empty)–
5	–(empty)–
6	Empty PCR plate seated in red insert (PCR plate type must be specified on setup form under step 2)
7	Purified adaptor-tagged DNA samples in Nunc DeepWell plate
8	Empty tip box
9	Master mix plate containing PCR Master Mix in Column 2 (unsealed), seated in silver insert

- 13** Verify that the Current Tip State indicator on the form matches the configuration of unused and used tips in the tip boxes at Bravo Deck positions 2 and 8, respectively. See **page 21** for more information on using this segment of the form during the run.

- 14** When setup and verification is complete, click **Run Selected Protocol**.



- 15** Running the 03b Pre-CapturePCR_QXT_ILM_v1.0.pro protocol takes approximately 10 minutes. Once complete, the PCR-ready samples, containing prepped DNA and PCR master mix, are located in the PCR plate at position 6 of the Bravo deck.
- 16** When you see the following prompt, remove the PCR plate from position 6 of the Bravo deck and seal the plate using the PlateLoc Thermal Microplate Sealer, with sealing settings of 165°C and 3.0 seconds.



- 17 Centrifuge the plate for 30 seconds to drive the well contents off the walls and plate seal and to eliminate air bubbles.
- 18 Transfer the PCR plate to a thermal cycler and run the PCR amplification program shown in [Table 23](#).

Table 23 Pre-Capture PCR cycling program

Segment Number	Number of Cycles	Temperature	Time
1	1	68°C	2 minutes
2	1	98°C	2 minutes
3	8	98°C	30 seconds
		57°C	30 seconds
		72°C	1 minute
4	1	72°C	5 minutes
5	1	4°C	Hold

Step 5. Purify amplified DNA using AMPure XP beads

In this step, the Agilent NGS Bravo transfers AMPure XP beads and amplified adaptor-tagged DNA to a Nunc DeepWell plate and then collects and washes the bead-bound DNA.

This step uses protocol 04b Cleanup_Pre-CapturePCR_QXT_ILM_v1.0.pro.

Prepare the NGS Bravo and reagents

- 1 Clear the Bravo deck of all plates and tip boxes, then wipe it down with a DNA Away decontamination wipe.
- 2 Pre-set the temperature of Bravo deck positions 4 and 6 as indicated in [Table 16](#). See [page 17](#) for more information on how to do this step.

Table 24 Bravo Deck Temperature Presets

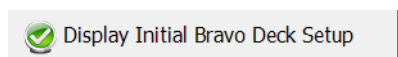
Bravo Deck Position	Temperature Preset	Preset Method
4	45°C	Inheco Multi TEC control touchscreen (CPAC 2-1)
6	4°C	Inheco Multi TEC control touchscreen (CPAC 2-2)

- 3 Verify that the AMPure XP bead suspension is at room temperature. (If necessary, allow the bead solution to come to room temperature for at least 30 minutes.) *Do not freeze the beads at any time.*
- 4 Mix the AMPure XP bead suspension well so that the reagent appears homogeneous and consistent in color.
- 5 Prepare a Nunc DeepWell source plate for the beads by adding 50 µL of homogeneous AMPure XP beads per well, for each well to be processed.
- 6 Prepare a Thermo Scientific Matrix reservoir containing 15 mL of nuclease-free water.

- 7 Prepare a separate Thermo Scientific Matrix reservoir containing 45 mL of freshly-prepared 70% ethanol.
- 8 Centrifuge the amplified DNA sample plate for 30 seconds to drive the well contents off the walls and plate seal.

Setup and run VWorks 04b Cleanup_Pre-CapturePCR_QXT_ILM_v1.0.pro

- 9 On the SureSelect setup form, under **Select Protocol**, select **04b Cleanup_Pre-CapturePCR_QXT_ILM_v1.0.pro**.
- 10 Under **Select PCR plate Labware**, select the specific type of PCR plate used for pre-capture amplification.
- 11 Select the number of columns of samples to be processed. Runs must include 1, 2, 3, 4, 6, or 12 columns.
- 12 Click **Display Initial Bravo Deck Setup**.



- 13 Load the Bravo deck according to the Bravo Deck Setup region of the form and as shown in [Table 17](#).

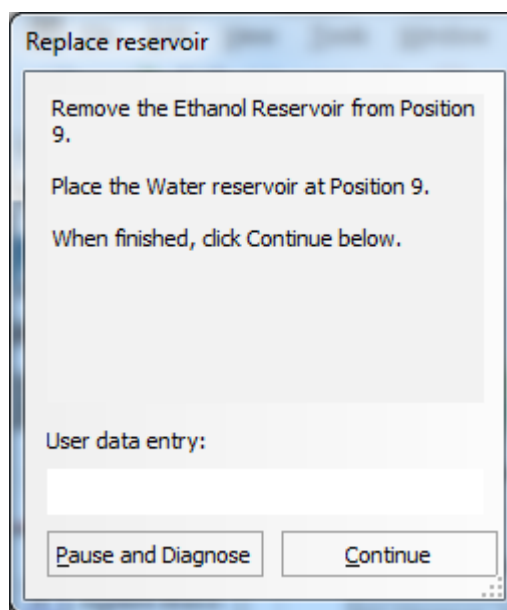
Table 25 Initial Bravo deck configuration for 04b Cleanup_Pre-CapturePCR_QXT_ILM_v1.0.pro

Location	Content
1	Empty waste reservoir (Axygen 96 Deep Well Plate, square wells)
2	New tip box
3	Empty Eppendorf plate
4	–(empty)–
5	AMPure XP beads in Nunc DeepWell plate (50 µl beads per processing well)
6	Amplified DNA libraries in unsealed PCR plate seated in red insert (PCR plate type must be specified on setup form under step 2)
7	–(empty)–
8	Empty tip box
9	70% ethanol in Matrix reservoir

- 14 Verify that the Current Tip State indicator on the form matches the configuration of unused and used tips in the tip boxes at Bravo Deck positions 2 and 8, respectively. See [page 21](#) for more information on using this segment of the form during the run.
- 15 When setup and verification is complete, click **Run Selected Protocol**.



Running the 04b Cleanup_Pre-CapturePCR_QXT_ILM_v1.0.pro protocol takes approximately 45 minutes. An operator must be present during the run to complete tip box replacement and to transfer the water reservoir to the Bravo deck, when directed by the VWorks prompt shown below.



Once the protocol is complete, the purified DNA samples are located in the Eppendorf plate at position 3 of the Bravo deck.

Step 6. Assess Library DNA quantity and quality

Measure the concentration of each library using one of the methods detailed below.

Option 1: Analysis using the Agilent 2100 Bioanalyzer and DNA 1000 Assay

Use a Bioanalyzer DNA 1000 chip and reagent kit. Perform the assay according to the [Agilent DNA 1000 Kit Guide](#).

NOTE

The presence of magnetic beads in the samples may adversely impact the Bioanalyzer results. If you suspect bead contamination in the samples, place the plate or strip tube on the magnetic rack before withdrawing samples for analysis.

- 1 Set up the 2100 Bioanalyzer instrument as instructed in the reagent kit guide.
- 2 Prepare the chip, samples and ladder as instructed in the reagent kit guide, using 1 μ L of each sample for the analysis. Load the prepared chip into the instrument and start the run within five minutes after preparation.
- 3 Verify that the electropherogram shows the peak of DNA fragment size positioned between 245 to 325 bp. Sample electropherograms are shown in [Figure 5](#). Variability of fragmentation profiles may be observed.

NOTE

A peak DNA fragment size significantly less than 245 bp may indicate too little gDNA in the fragmentation reaction and may be associated with increased duplicates in the sequencing data. In contrast, a peak DNA fragment size significantly greater than 325 bp may indicate too much gDNA in the fragmentation reaction and may be associated with decreased percent-on-target performance in sequencing results.

- 4 Measure the concentration of each library by integrating under the entire peak. For accurate quantification, make sure that the concentration falls within the linear range of the assay.

Stopping Point If you do not continue to the next step, seal the plate and store at 4°C overnight or at -20°C for prolonged storage.

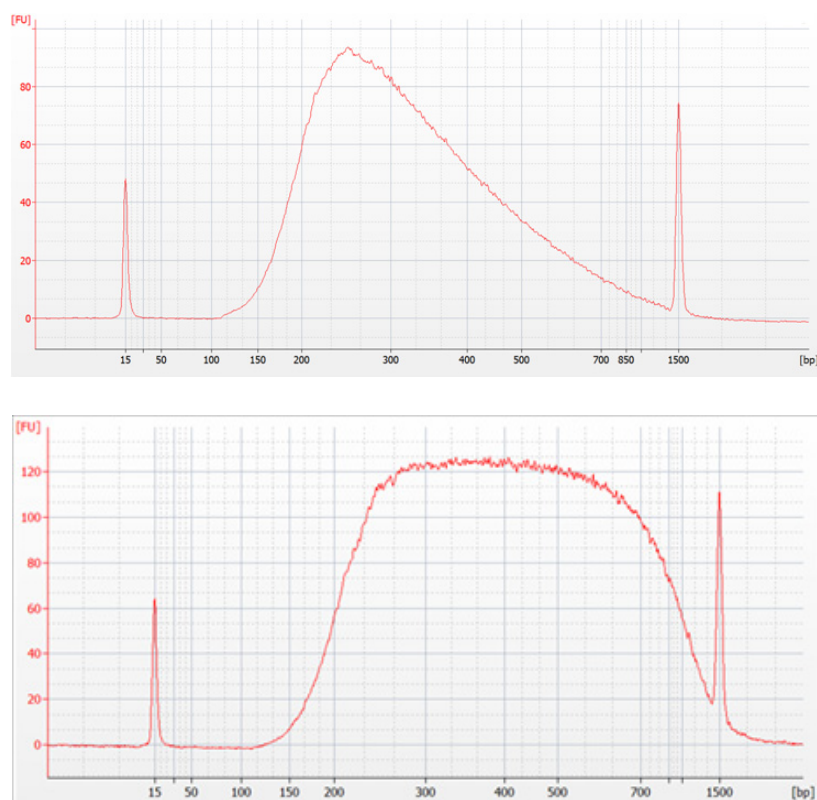


Figure 5 Representative sample electropherograms showing pre-capture analysis of amplified library DNA using the Agilent 2100 Bioanalyzer and a DNA 1000 Assay.

Option 2: Analysis using an Agilent TapeStation and D1000 ScreenTape

Use a D1000 ScreenTape and associated reagent kit. Perform the assay according to the [Agilent D1000 Assay Quick Guide](#).

- 1 Prepare the TapeStation samples as instructed in the reagent kit guide. Use 1 µL of each DNA sample diluted with 3 µL of D1000 sample buffer for the analysis.

CAUTION

For accurate quantitation, make sure to thoroughly mix the combined DNA and sample buffer by vortexing the assay plate or tube strip for 1 minute on the IKA MS3 vortex mixer provided with the 4200/4150 TapeStation system before loading the samples.

- 2 Load the sample plate or tube strips from **step 1**, the D1000 ScreenTape, and loading tips into the TapeStation as instructed in the reagent kit guide. Start the run.
- 3 Verify that the electropherogram shows the peak of DNA fragment size positioned between 245 to 325 bp. Sample electropherograms are shown in **Figure 6**. Variability of fragmentation profiles may be observed.

NOTE

A peak DNA fragment size significantly less than 245 bp may indicate too little gDNA in the fragmentation reaction and may be associated with increased duplicates in the sequencing data. In contrast, a peak DNA fragment size significantly greater than 325 bp may indicate too much gDNA in the fragmentation reaction and may be associated with decreased percent-on-target performance in sequencing results.

- 4 Measure the concentration of each library by integrating under the entire peak.

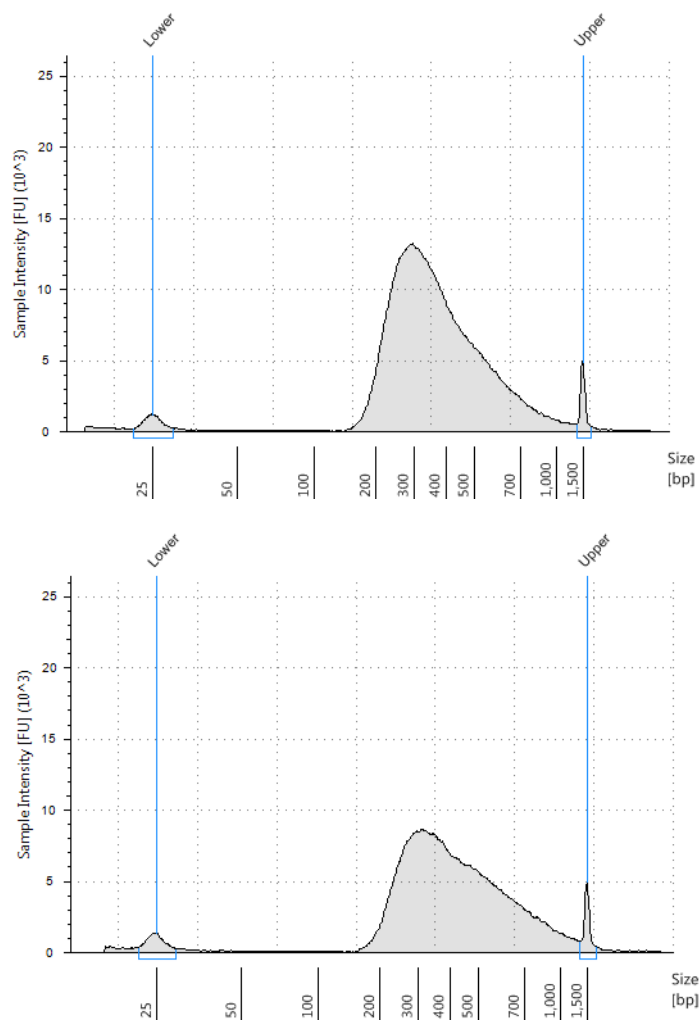


Figure 6 Representative sample electropherograms showing pre-capture analysis of amplified library DNA using a D1000 ScreenTape.

Stopping Point If you do not continue to the next step, seal the library DNA sample plate and store at 4°C overnight or at –20°C for prolonged storage.

4 Hybridization

Step 1. Aliquot prepped DNA samples for hybridization **48**

Step 2. Hybridize the gDNA library and probe **51**

Step 3. Capture the hybridized DNA **60**

This chapter describes the steps to combine the prepped library with the blocking agents and the Probe Capture Library. Each DNA library sample must be hybridized and captured individually prior to addition of the indexing tag by PCR.

CAUTION

The ratio of probe to prepped library is critical for successful capture.

Step 1. Aliquot prepped DNA samples for hybridization

For each sample library prepared, do one hybridization and capture. Do not pool samples at this stage.

The amount of prepared gDNA library used in the hybridization reaction varies according to the design size of the probe used for hybridization as outlined in [Table 26](#) below. Use the maximum possible amount of each prepped DNA, within the range listed in [Table 26](#).

Table 26 Amount of adaptor-tagged DNA libraries used for hybridization

Probe Capture Library Size	Amount of prepared gDNA library used in hybridization
Probes >3.0 Mb	750 to 1500 ng DNA
Probes ≤3.0 Mb	500 to 750 ng DNA

Using the DNA concentration for each sample determined on [page 43](#) to [page 45](#), calculate the volume of each sample to be used for hybridization using the appropriate formula below:

$$\text{Volume } (\mu\text{L}) = 750 \text{ ng/concentration (ng/}\mu\text{L)}$$

OR

$$\text{Volume } (\mu\text{L}) = 1500 \text{ ng/concentration (ng/}\mu\text{L)}$$

If the concentration of any sample is not sufficient to allow use of the recommended amount of DNA (750 ng for probes ≤3.0 Mb or 1500 ng for probes >3.0 Mb), then use the full remaining volume of DNA sample (approximately 12 μL) for the hybridization step.

The automation protocol 05 Aliquot_Libraries_v1.0.pro is used to prepare a new sample plate containing the appropriate amount of each DNA sample for hybridization. Before running the automation protocol, you must create a table containing instructions for the NGS Bravo indicating the volume of each sample to aliquot, as described in the steps below.

- 1 Create a .csv (comma separated value) file with the headers shown in [Figure 7](#). The header text must not contain spaces. The table may be created using a spreadsheet application, such as Microsoft Excel software, and then saved in .csv format. The file must include rows for all 96 wells of the plate.
- 2 Enter the information requested in the header for each DNA sample.
 - In the SourceBC field, enter the sample plate description or barcode. The SourceBC field contents must be identical for all rows.
 - In the SourceWell and DestinationWell fields, enter each well position for the plate. SourceWell and DestinationWell field contents must be identical for a given sample.
 - In the Volume field, enter the volume (in μL) of each DNA sample to be used in the hybridization step (see [page 48](#) for guidelines). For all empty wells on the plate, enter the value 0, as shown in [Figure 7](#); do not delete rows for empty wells.

	A	B	C	D
1	SourceBC	SourceWell	DestinationWell	Volume
2	SamplePlateXYZ	A1	A1	5.35
3	SamplePlateXYZ	B1	B1	4.28
4	SamplePlateXYZ	C1	C1	4.76
5	SamplePlateXYZ	D1	D1	5.19
6	SamplePlateXYZ	E1	E1	5.49
7	SamplePlateXYZ	F1	F1	4.86
8	SamplePlateXYZ	G1	G1	5.05
9	SamplePlateXYZ	H1	H1	4.37
10	SamplePlateXYZ	A2	A2	0
11	SamplePlateXYZ	B2	B2	0
12	SamplePlateXYZ	C2	C2	0
13	SamplePlateXYZ	D2	D2	0

Figure 7 Sample spreadsheet for 1-column run.

NOTE

You can find a sample spreadsheet in the directory **C: > VWorks Workspace > NGS Option A> QXT_ILM_v1.0 > Aliquot Library Input Files > Aliquot_Libraries_full_plate_template.csv**.

The Aliquot_Libraries_full_plate_template.csv file may be copied and used as a template for creating the .csv files for each 05 Aliquot_Libraries_v1.0.pro run. If you are using the sample file as a template for runs with fewer than 12 columns, be sure to retain rows for all 96 wells, and populate the Volume column with 0 for unused wells.

- Load the .csv file onto the PC containing the VWorks software into a suitable folder, such as **C: > VWorks Workspace > NGS Option A> QXT_ILM_v1.0 > Aliquot Library Input Files**.

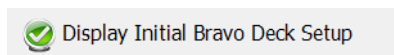
Setup and Run VWorks protocol 05 Aliquot_Libraries_v1.0.pro

- Clear the Bravo deck of all plates and tip boxes, then wipe it down with a DNA Away decontamination wipe.
- Pre-set the temperature of Bravo deck position 9 as indicated in [Table 27](#). See [page 18](#) for more information on how to do this step.

Table 27 Bravo Deck Temperature Presets

Bravo Deck Position	Temperature Preset	Preset Method
9	0°C	ThermoCube control panel

- On the SureSelect setup form, under **Select Protocol**, select **05 Aliquot_Libraries_v1.0.pro**.
- Select the number of columns of samples to be processed. Runs must include 1, 2, 3, 4, 6, or 12 columns.
- Click **Display Initial Bravo Deck Setup**.



- 6 Load the Bravo deck according to the Bravo Deck Setup region of the form and as shown in **Table 28**.

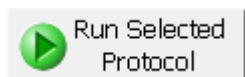
Table 28 Initial Bravo deck configuration for 05 Aliquot_Libraries_v1.0.pro

Location	Content
1	–(empty)–
2	–(empty)–
3	–(empty)–
4	–(empty)–
5	Empty Eppendorf plate
6	Empty tip box
7	–(empty)–
8	New tip box
9	Prepped library DNA in Eppendorf plate

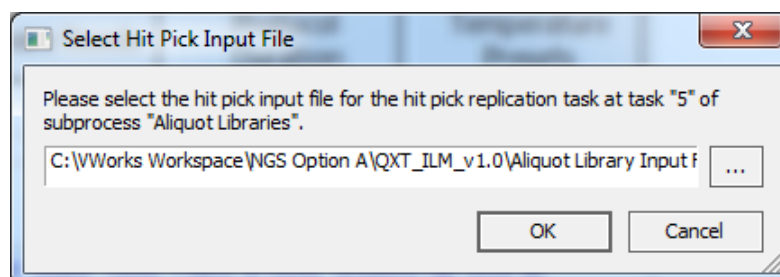
CAUTION

This protocol does not use the Current Tip State indicator function. Be sure to place a completely full box of tips at position 8 and a completely empty tip box at position 6.

- 7 When verification is complete, click **Run Selected Protocol**.



- 8 When prompted by the dialog below, browse to the .csv file created for the source plate of the current run, and then click **OK** to start the run.



The library aliquoting protocol takes approximately 1 hour for 96 samples. When complete, the DNA sample plate is on Bravo deck position 5.

- 9 Remove the sample plate from the Bravo deck and use a vacuum concentrator to dry the samples at $\leq 45^{\circ}\text{C}$.
- 10 Reconstitute each dried sample with 12 μL of nuclease-free water. Pipette up and down along the sides of each well for optimal recovery.
- 11 Seal the plate using the PlateLoc Thermal Microplate Sealer, with sealing settings of 165°C and 1.0 sec.
- 12 Vortex the plate for 30 seconds to ensure complete reconstitution, then centrifuge the plate for 1 minute to drive the well contents off the walls and plate seal.

Step 2. Hybridize the gDNA library and probe

In this step, automation protocol 06 Hybridization_QXT_v1.0.pro is used to complete the liquid handling steps to set up the hybridization reactions. Afterward, you transfer the sample plate to a thermal cycler, held at 65°C, to allow hybridization of the DNA samples to the Probe Capture Library.

This step uses the SureSelect^{QXT} Reagent Kit components listed in [Table 29](#). Thaw each component under the conditions indicated in the table. Vortex each reagent to mix, then spin briefly to collect the liquid.

Table 29 Reagents for Hybridization and Capture

Kit Component	Storage Location	Thawing Conditions	Where Used
SureSelect Fast Hybridization Buffer	SureSelect QXT Hyb Module Box 2, –20°C	Warm to Room Temperature (RT), then keep at RT	page 54
SureSelect QXT Fast Blocker Mix	SureSelect QXT Hyb Module Box 2, –20°C	Thaw on ice	page 52
SureSelect RNase Block	SureSelect QXT Hyb Module Box 2, –20°C	Thaw on ice	page 53 or page 54
Probe Capture Library	–80°C	Thaw on ice	page 53 or page 54

Program the thermal cycler

- 1 Pre-program the thermal cycler for the Hybridization workflow by entering the thermal cycling program shown in [Table 30](#) below.

It is critical to pre-program the thermal cycler before starting the automation protocol for Hybridization, in order to maintain the required sample and reagent temperatures during the workflow.

Table 30 Thermal cycler program for Hybridization*

Segment Number	Purpose	Number of Cycles	Temperature	Time
1	Denaturation	1	95°C	5 minutes
2	Blocking	1	65°C	10 minutes
3	Hold for NGS Bravo steps [†]	1	65°C	Hold
4	Hybridization	60	65°C	1 minute
			37°C	3 seconds
5	Hold until start of Capture [‡]	1	65°C	Hold

* When setting up the thermal cycling program, use a reaction volume setting of 35 µl (final volume of hybridization reactions during cycling in Segment 4).

[†] Samples are transferred to the NGS Bravo during this Hold step when prompted by the VWorks software.

[‡] Samples are held at 65°C until they are processed in the Capture & Wash automation protocol that begins on [page 60](#).

CAUTION

The lid of the thermal cycler is hot and can cause burns. Use caution when working near the lid.

Prepare the NGS Bravo

- 1 Clear the Bravo deck of all plates and tip boxes, then wipe it down with a DNA Away decontamination wipe.
- 2 Pre-set the temperature of Bravo deck positions 4 and 6 as indicated in [Table 31](#). See [page 17](#) for more information on how to do this step.

Table 31 Bravo Deck Temperature Presets

Bravo Deck Position	Temperature Preset	Preset Method
4	23°C	Inheco Multi TEC control touchscreen (CPAC 2-1)
6	23°C	Inheco Multi TEC control touchscreen (CPAC 2-2)

- 3 Place a red PCR plate insert at Bravo deck position 4.
- 4 Place the silver Nunc DeepWell plate insert on position 6 of the Bravo deck. This insert is required to facilitate heat transfer to DeepWell source plate wells during the Hybridization protocol. When loading a source plate on the silver insert, make sure the plate is seated properly to ensure proper heat transfer.

Prepare the Block Master Mix

- 5 Prepare the appropriate volume of Block Master Mix, on ice, as indicated in [Table 32](#).

Table 32 Preparation of Block Master Mix

SureSelect ^{QXT} Reagent	Volume for 1 Library	Volume for 1 Column	Volume for 2 Columns	Volume for 3 Columns	Volume for 4 Columns	Volume for 6 Columns	Volume for 12 Columns
Nuclease-free water	2.5 µL	31.9 µL	53.1 µL	74.4 µL	95.6 µL	138.1 µL	276.3 µL
SureSelect QXT Fast Blocker Mix (blue cap)	5.0 µL	63.8 µL	106.3 µL	148.8 µL	191.3 µL	276.3 µL	552.5 µL
Total Volume	7.5 µL	95.6 µL	159.4 µL	223.1 µL	286.9 µL	414.4 µL	828.8 µL

Prepare one or more Capture Library Master Mixes

- 6 Prepare the appropriate volume of Capture Library Master Mix for each of the Probes that will be used for hybridization as indicated in [Table 33](#) to [Table 36](#). Mix thoroughly by vortexing at high speed then spin down briefly. Keep the Capture Library Master Mix(es) on ice.

NOTE

Each row of the prepped gDNA sample plate may be hybridized to a different Probe. However, Probes of different sizes require different post-capture amplification cycles. Plan experiments such that similar-sized Probes are hybridized on the same plate.

For runs that use a single Probe for all rows of the plate, prepare the master mix as described in Step a ([Table 33](#) or [Table 34](#)) on [page 53](#).

For runs that use different Probes for individual rows, prepare each master mix as described in Step b ([Table 35](#) or [Table 36](#)) on [page 54](#).

- a For runs that use a single Probe for all rows, prepare a Master Mix as described in [Table 33](#) or [Table 34](#), based on the Mb target size of your design.

Table 33 Preparation of Capture Library Master Mix for Probes <3 Mb, 8 rows of well

Target size <3.0 Mb							
Reagent	Volume for 1 Library	Volume for 1 Column	Volume for 2 Columns	Volume for 3 Columns	Volume for 4 Columns	Volume for 6 Columns	Volume for 12 Columns
Nuclease-free water	4.5 µL	76.5 µL	114.8 µL	153.0 µL	191.3 µL	306.0 µL	592.9 µL
RNase Block (purple cap)	0.5 µL	8.5 µL	12.8 µL	17.0 µL	21.3 µL	34.0 µL	65.9 µL
Probe (with design <3 Mb)	2.0 µL	34.0 µL	51.0 µL	68.0 µL	85.0 µL	136.0 µL	263.5 µL
Total Volume	7.0 µL	119.0 µL	178.6 µL	238.0 µL	297.6 µL	476.0 µL	922.3 µL

Table 34 Preparation of Capture Library Master Mix for Probes ≥3 Mb, 8 rows of wells

Target size >3.0 Mb							
Reagent	Volume for 1 Library	Volume for 1 Column	Volume for 2 Columns	Volume for 3 Columns	Volume for 4 Columns	Volume for 6 Columns	Volume for 12 Columns
Nuclease-free water	1.5 µL	25.5 µL	38.3 µL	51.0 µL	63.8 µL	102.0 µL	197.6 µL
RNase Block (purple cap)	0.5 µL	8.5 µL	12.8 µL	17.0 µL	21.3 µL	34.0 µL	65.9 µL
Probe (with design ≥3 Mb)	5.0 µL	85.0 µL	127.5 µL	170.0 µL	212.5 µL	340.0 µL	658.8 µL
Total Volume	7.0 µL	119.0 µL	178.6 µL	238.0 µL	297.6 µL	476.0 µL	922.3 µL

- b For runs that use different Probes in individual rows, prepare a Master Mix for each Probe as listed in [Table 35](#) or [Table 36](#), based on the Mb target size of each design. The volumes listed in [Table 35](#) and [Table 36](#) are for a single row of sample wells. If a given Probe will be hybridized in multiple rows, multiply each of the values below by the number of rows assigned to that Probe.

Table 35 Preparation of Capture Library Master Mix for Probes <3 Mb, single row of wells

Target size <3.0 Mb							
Reagent	Volume for 1 Library	Volume for 1 Column	Volume for 2 Columns	Volume for 3 Columns	Volume for 4 Columns	Volume for 6 Columns	Volume for 12 Columns
Nuclease-free water	4.5 µL	9.0 µL	13.8 µL	18.6 µL	23.3 µL	37.7 µL	73.5 µL
RNase Block (purple cap)	0.5 µL	1.0 µL	1.5 µL	2.1 µL	2.6 µL	4.2 µL	8.2 µL
Probe (with design <3 Mb)	2.0 µL	4.0 µL	6.1 µL	8.3 µL	10.4 µL	16.8 µL	32.7 µL
Total Volume	7.0 µL	14.0 µL	21.4 µL	28.9 µL	36.3 µL	58.6 µL	114.4 µL

Table 36 Preparation of Capture Library Master Mix for Probes ≥3 Mb, single row of wells

Target size >3.0 Mb							
Reagent	Volume for 1 Library	Volume for 1 Column	Volume for 2 Columns	Volume for 3 Columns	Volume for 4 Columns	Volume for 6 Columns	Volume for 12 Columns
Nuclease-free water	1.5 µL	3.0 µL	4.6 µL	6.2 µL	7.8 µL	12.6 µL	24.5 µL
RNase Block (purple cap)	0.5 µL	1.0 µL	1.5 µL	2.1 µL	2.6 µL	4.2 µL	8.2 µL
Probe (with design ≥3 Mb)	5.0 µL	10.0 µL	15.3 µL	20.6 µL	25.9 µL	41.9 µL	81.7 µL
Total Volume	7.0 µL	14.0 µL	21.4 µL	28.9 µL	36.3 µL	58.6 µL	114.4 µL

Prepare the Hybridization Buffer master mix

- 7 Prepare the appropriate volume of Hybridization Buffer Master Mix, at room temperature, as indicated in [Table 37](#).

Table 37 Preparation of Hybridization Buffer Master Mix

SureSelect ^{QXT} Reagent	Volume for 1 Library	Volume for 1 Column	Volume for 2 Columns	Volume for 3 Columns	Volume for 4 Columns	Volume for 6 Columns	Volume for 12 Columns
Nuclease-free water	2.5 µL	53.1 µL	74.4 µL	95.6 µL	116.9 µL	159.4 µL	297.5 µL
SureSelect Fast Hybridization Buffer (bottle)	6.0 µL	127.5 µL	178.5 µL	229.5 µL	280.5 µL	382.5 µL	714.0 µL
Total Volume	8.5 µL	180.6 µL	252.9 µL	325.1 µL	397.4 µL	541.9 µL	1011.5 µL

Prepare the master mix source plate

- 8 In a Nunc DeepWell plate, prepare the master mix source plate containing the master mixes prepared in [step 5](#) to [step 7](#) at room temperature. Add the volumes indicated in [Table 38](#) of each master mix to each well of the indicated column of the Nunc DeepWell plate. When using multiple Probes in a run, add each Capture Library Master Mix to the appropriate row(s) of the Nunc DeepWell plate. The final configuration of the master mix source plate is shown in [Figure 8](#).

Table 38 Preparation of the Master Mix Source Plate for 06 Hybridization_QXT_v1.0.pro

Master Mix Solution	Position on Source Plate	Volume of Master Mix added per Well of Nunc Deep Well Source Plate					
		1-Column Runs	2-Column Runs	3-Column Runs	4-Column Runs	6-Column Runs	12-Column Runs
Block Master Mix	Column 1 (A1-H1)	11.0 µL	19.0 µL	27.0 µL	34.9 µL	50.9 µL	102.7 µL
Capture Library Master Mix	Column 2 (A2-H2)	14.0 µL	21.4 µL	28.9 µL	36.3 µL	58.6 µL	114.4 µL
Hybridization Buffer Master Mix	Column 3 (A3-H3)	19.9 µL	29.0 µL	38.0 µL	47.0 µL	65.1 µL	123.8 µL

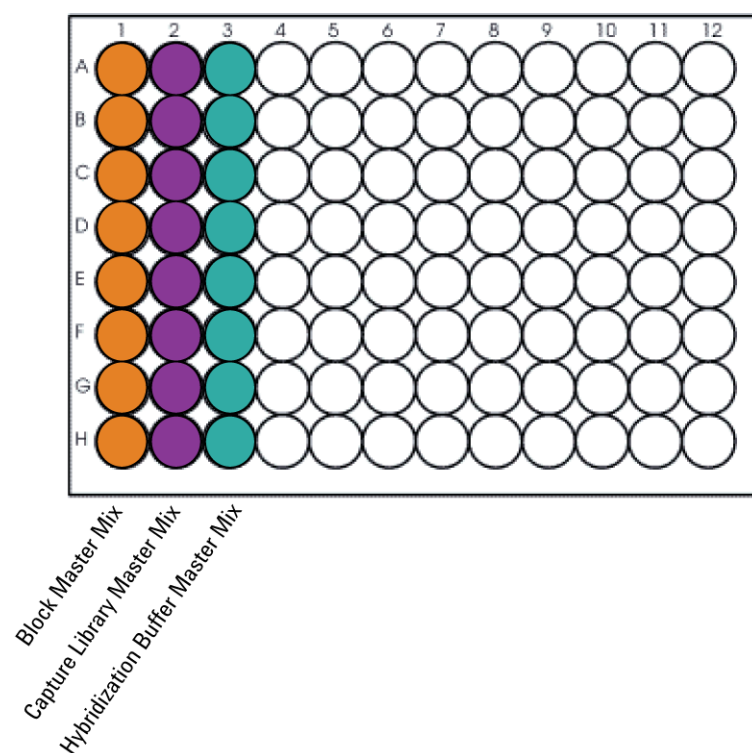


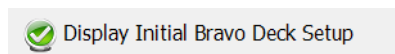
Figure 8 Configuration of the master mix source plate for 06 Hybridization_QXT_v1.0.pro.

- 9 Seal the master mix source plate using the PlateLoc Thermal Microplate Sealer, with sealing settings of 165°C and 1.0 sec.

10 Centrifuge the plate for 30 seconds to drive the well contents off the walls and plate seal and to eliminate any bubbles. Keep the master mix plate at room temperature.

Setup and run VWorks protocol 06 Hybridization_QXT_v1.0.pro

- 11 On the SureSelect setup form, under **Select Protocol**, select **06 Hybridization_QXT_v1.0.pro**.
- 12 Under **Select PCR Plate Labware**, select the plate type to be used for the hybridization step (to be loaded at Bravo deck position 4).
- 13 Select the number of columns of samples to be processed. Runs must include 1, 2, 3, 4, 6, or 12 columns.
- 14 Click **Display Initial Bravo Deck Setup**.



- 15 Load the Bravo deck according to the Bravo Deck Setup region of the form and as shown in **Table 39**.

Table 39 Initial Bravo deck configuration for 06 Hybridization_QXT_v1.0.pro

Location	Content
1	–(empty)–
2	New tip box
3	–(empty)–
4	Empty PCR plate, seated in red insert (PCR plate type must be specified on setup form under step 2)
5	Empty Eppendorf twin.tec plate
6	Master Mixes in Columns 1-3 of Nunc DeepWell, seated in silver Nunc DeepWell insert
7	–(empty)–
8	Empty tip box
9	Prepped library aliquots in Eppendorf twin.tec plate

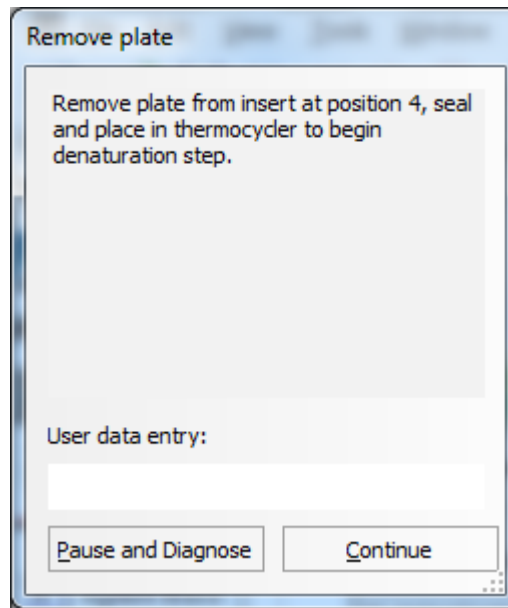
- 16 Verify that the Current Tip State indicator on the form matches the configuration of unused and used tips in the tip boxes at Bravo Deck positions 2 and 8, respectively. See **page 21** for more information on using this segment of the form during the run.
- 17 When setup and verification is complete, click **Run Selected Protocol**.



Running the 06 Hybridization_QXT_v1.0.pro protocol takes approximately 30 minutes. An operator must be present during the run to complete tip box replacement and other labware transfer steps, as directed by the VWorks prompts detailed below.

The NGS Bravo combines the prepped gDNA in the wells of the sample plate with the aliquotted SureSelect Block Master Mix. When this process is complete, you will be prompted to transfer the plate to the thermal cycler for sample denaturation and blocking prior to hybridization.

- 18 When prompted by VWorks as shown below, remove the PCR plate from position 4 of the Bravo deck, leaving the red insert in place. After removing the sample plate, click **Continue**.



- 19 Seal the sample plate using the PlateLoc Thermal Microplate Sealer, with sealing settings of 165°C and 3.0 sec.
- 20 Transfer the sealed plate to a thermal cycler and initiate the preprogrammed thermal cycling program described in **Table 30** on page 51. The denaturation and blocking segments of the preprogrammed thermal cycler program are shown in **Figure 9** below for reference.

Table 28 Thermal cycler program for Hybridization*

Segment Number	Purpose	Number of Cycles	Temperature	Time
1	Denaturation	1	95°C	5 minutes
2	Blocking	1	65°C	10 minutes
3	Hold for NGS workstation steps†	1	65°C	Hold

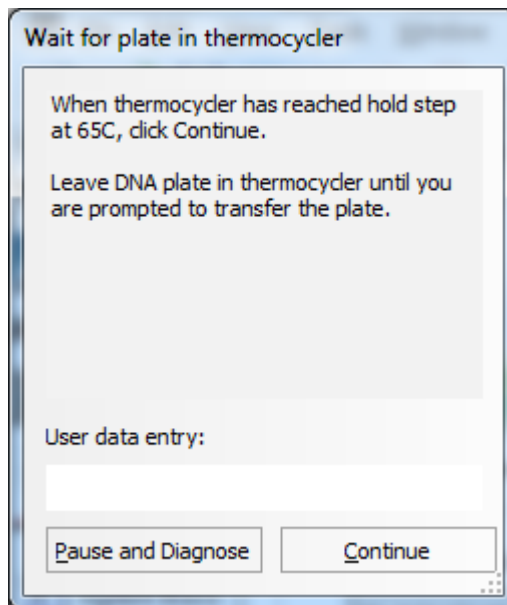
Figure 9 Preprogrammed thermal cycler segments used for sample denaturation and blocking prior to hybridization.

While the sample plate incubates on the thermal cycler, the NGS Bravo combines aliquots of the Capture Library Master Mix and Hybridization Buffer Master Mix.

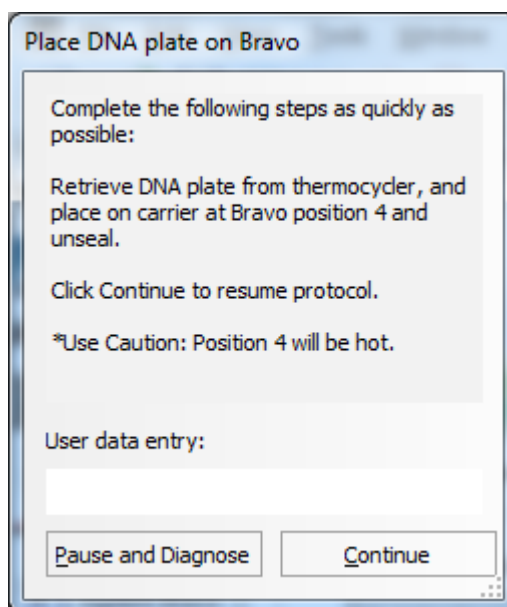
CAUTION

You must complete **step 21** to **step 25** quickly, and immediately after being prompted by the VWorks software. It is important that sample temperature remains approximately 65°C during transfers between the NGS Bravo and thermal cycler.

- 21 When the NGS Bravo has finished aliquoting the Capture Library and Hybridization Buffer Master Mixes, you will be prompted by VWorks as shown below. When the thermal cycler reaches the 65°C hold step, click **Continue**. Leave the sample plate in the thermal cycler until you are notified to move it.



- 22 When prompted by VWorks as shown below, quickly remove the sample plate from the thermal cycler, unseal the plate carefully to avoid splashing, and transfer the plate to position 4 of the Bravo deck, seated in the red insert. Click **Continue**.



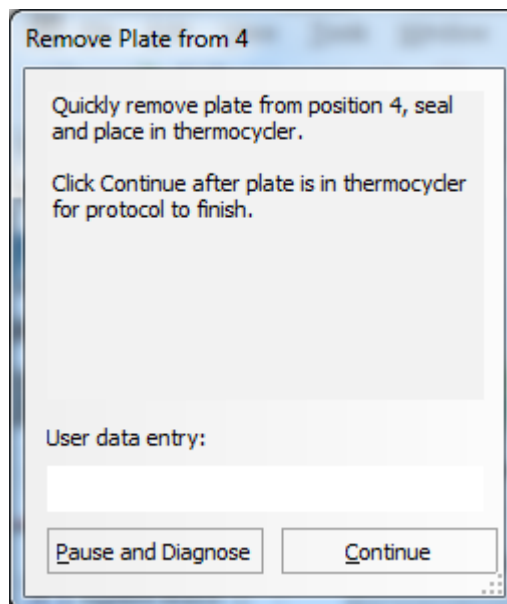
WARNING

Bravo deck position 4 will be hot.

Use caution when handling components that contact heated deck positions.

The NGS Bravo transfers the Capture Library-Hybridization Buffer mixture to the wells of the PCR plate that contain the mixture of prepped gDNA samples and blocking agents.

- 23** When prompted by VWorks as shown below, quickly remove the PCR sample plate from Bravo deck position 4, leaving the red insert in place.



- 24** Seal the sample plate using the PlateLoc Thermal Microplate Sealer, with sealing settings of 165°C and 3.0 sec.
- 25** Quickly transfer the plate back to the thermal cycler, held at 65°C. Press the *Play* button to initiate the hybridization segment of the pre-programmed thermal cycling program (segment 4 from **Table 30** on page 51). During this step, the prepared DNA samples are hybridized to the Probe.

CAUTION

The thermal cycler is held at 65°C using a heated lid at 105°C. The lid of the thermal cycler is hot and can cause burns. Use caution when working near the lid.

- 26** After initiating hybridization on the thermal cycler, click **Continue** on the VWorks screen to finish the NGS Bravo protocol.

During the thermal cycler incubation for hybridization (approximately 1.5-hour duration), complete the reagent and NGS Bravo setup steps for the capture automation protocol as described on [page 60](#) to [page 61](#).

Step 3. Capture the hybridized DNA

This step uses automation protocol 07 SureSelectQXT_Capture_v1.0.pro to automate capture of the gDNA-probe hybrids using streptavidin-coated magnetic beads. Setup tasks for the Capture protocol ([step 1](#), below, through [step 16](#) on [page 62](#)) should be completed during the thermal cycler incubation for hybridization (approximately 1.5-hour duration) started on [page 59](#).

This step uses the SureSelect^{QXT} Reagent Kit components in [Table 40](#) in addition to streptavidin-coated magnetic beads obtained from another supplier (see [Table 1](#) on page 11).

Table 40 Reagents for hybrid capture

Kit Component	Storage Location	Where Used
SureSelect Binding Buffer	SureSelect QXT Hyb Module Box 1, RT	page 61
SureSelect Wash Buffer 2	SureSelect QXT Hyb Module Box 1, RT	page 61

Prepare the NGS Bravo

- 1 Clear the Bravo deck of all plates and tip boxes, then wipe it down with a DNA Away decontamination wipe.
- 2 Pre-set the temperature of Bravo deck position 4 as indicated in [Table 41](#). See [page 17](#) for more information on how to do this step.

Table 41 Bravo Deck Temperature Presets

Bravo Deck Position	Temperature Preset	Preset Method
4	66°C	Inheco Multi TEC control touchscreen (CPAC 2-1)

- 3 Place a red PCR plate insert at Bravo deck position 4.
- 4 Place the silver Nunc DeepWell plate insert at Bravo deck position 6. This insert is required to facilitate heat transfer to DeepWell source plate wells.

Prepare the Dynabeads streptavidin beads and Wash Buffer 2 source plates

- 5 Vigorously resuspend the Dynabeads MyOne Streptavidin T1 magnetic beads on a vortex mixer. The beads settle during storage.

- 6 Wash the magnetic beads.
 - a In a conical vial, combine the components listed in [Table 42](#). The volumes below include the required overage.

Table 42 Magnetic bead washing mixture

Reagent	Volume for 1 Library	Volume for 1 Column	Volume for 2 Columns	Volume for 3 Columns	Volume for 4 Columns	Volume for 6 Columns	Volume for 12 Columns
Dynabeads MyOne Streptavidin T1 bead suspension	50 µL	425 µL	825 µL	1225 µL	1.65 mL	2.5 mL	5.0 mL
SureSelect Binding Buffer	0.2 mL	1.7 mL	3.3 mL	4.9 mL	6.6 mL	10 mL	20 mL
Total Volume	0.25 mL	2.125 mL	4.125 mL	6.125 mL	8.25 mL	12.5 mL	25 mL

- b Mix the beads on a vortex mixer for 5 seconds.
 - c Put the vial into a magnetic separator device.
 - d Remove and discard the supernatant.
 - e Repeat **step a** through **step d** for a total of 3 washes. (Retain the beads after each wash and combine with a fresh aliquot of the indicated volume of SureSelect Binding Buffer.)
- 7 Resuspend the beads in SureSelect Binding buffer, according to [Table 43](#) below.

Table 43 Preparation of magnetic beads for 07 SureSelectQXT_Capture_v1.0.pro

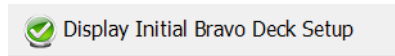
Reagent	Volume for 1 Library	Volume for 1 Column	Volume for 2 Columns	Volume for 3 Columns	Volume for 4 Columns	Volume for 6 Columns	Volume for 12 Columns
SureSelect Binding Buffer	0.2 mL	1.7 mL	3.3 mL	4.9 mL	6.6 mL	10 mL	20 mL

- 8 Prepare a Nunc DeepWell source plate for the washed streptavidin bead suspension. For each well to be processed, add 200 µL of the homogeneous bead suspension to the Nunc DeepWell plate.
- 9 Place the streptavidin bead source plate at position 5 of the Bravo deck.
- 10 Prepare a Nunc DeepWell source plate labeled *Wash #2*. For each well to be processed, add 1150 µL of SureSelect Wash Buffer 2. Place the Wash #2 source plate at position 6 of the Bravo deck.

Setup VWorks protocol 07 SureSelectQXT_Capture_v1.0.pro

- 11 On the SureSelect setup form, under **Select Protocol**, select **07 SureSelectQXT_Capture_v1.0.pro**.
- 12 Under **Select PCR Plate Labware**, select the specific type of PCR plate used for hybridization. This plate will be transferred from the thermal cycler to Bravo deck position 4 when prompted by VWorks.
- 13 Select the number of columns of samples to be processed. Runs must include 1, 2, 3, 4, 6, or 12 columns.

14 Click **Display Initial Bravo Deck Setup**.



15 Load the Bravo deck according to the Bravo Deck Setup region of the form and as shown in [Table 44](#).

Table 44 Initial Bravo deck configuration for 07 SureSelectQXT_Capture_v1.0.pro

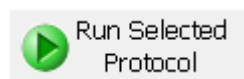
Location	Content
1	–(empty)–
2	New tip box
3	–(empty)–
4	Empty red insert
5	Prepared Dynabeads streptavidin bead DeepWell source plate
6	Wash #2 DeepWell source plate seated on silver Nunc DeepWell insert
7	–(empty)–
8	Empty tip box
9	–(empty)–

16 Verify that the Current Tip State indicator on the form matches the configuration of unused and used tips in the tip boxes at Bravo Deck positions 2 and 8, respectively. See [page 21](#) for more information on using this segment of the form during the run.

Run VWorks protocol 07 SureSelectQXT_Capture_v1.0.pro

Start the 07 SureSelectQXT_Capture_v1.0.pro protocol upon completion of the hybridization incubation that was started on [page 59](#), when the thermal cycler program reaches the 65°C Hold step in Segment 5.

After verifying that the hybridization step is complete and that all NGS Bravo setup steps for capture are complete, click **Run Selected Protocol**. Leave the hybridization plate in the thermal cycler until you are prompted to transfer the plate to the NGS Bravo.



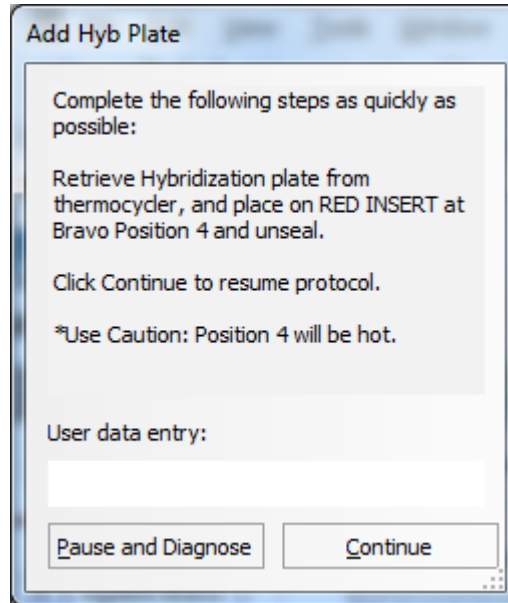
The total duration of the 07 SureSelectQXT_Capture_v1.0.pro protocol is approximately 35 minutes. An operator must be present to transfer the hybridization plate from the thermal cycler when prompted by VWorks as shown in [step 17](#) below (<5 minutes after starting the protocol).

If the temperature of Bravo deck position 4 was not pre-set to 66°C, the protocol will pause while position 4 reaches temperature.

CAUTION

It is important to complete [step 17](#) quickly and carefully. Transfer the sample plate to the Bravo platform quickly to retain the 65°C sample temperature. Unseal the plate without tilting or jerking the plate to avoid sample splashing. Make sure that the NGS Bravo is completely prepared, with deck platforms at temperature and all components in place, before you transfer the sample plate to the Bravo deck.

- 17 When prompted by VWorks as shown below, quickly remove the PCR plate, containing the hybridization reactions held at 65°C, from the thermal cycler. Unseal the plate carefully to avoid splashing, and quickly transfer the plate to position 4 of the Bravo deck, seated in the red insert. Click **Continue** to resume the protocol.

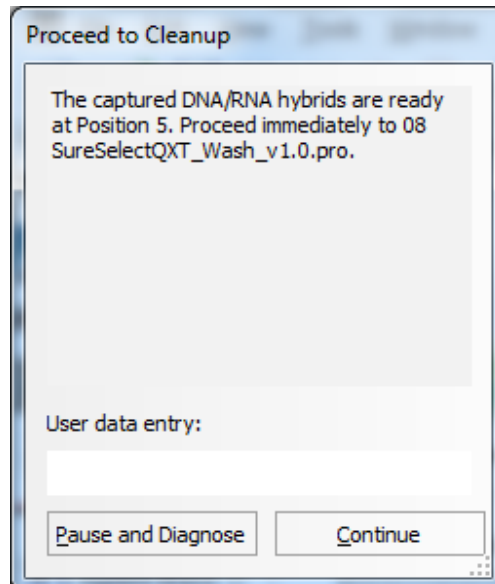


WARNING

Bravo deck position 4 will be hot.

Use caution when handling components that contact heated deck positions.

- 18 When the capture incubation period is complete you will be prompted by VWorks as shown below. Retain the hybrid-capture bead suspension plate at position 5 and proceed immediately to automation protocol 08 SureSelectQXT_Wash_v1.0.pro.



Step 4. Wash the captured DNA

This step uses automation protocol 08 SureSelectQXT_Wash_v1.0.pro to automate washing of the captured DNA-RNA hybrids.

This step uses the SureSelect^{QXT} Reagent Kit component in [Table 40](#) in addition to components retained from the previous automation protocol.

Table 45 Reagents for capture wash protocol

Kit Component	Storage Location	Where Used
SureSelect Wash Buffer 1	SureSelect QXT Hyb Module Box 1, RT	page 64

Prepare the NGS Bravo

- 1 Retain all plates, inserts, and tip boxes used in the previous automation protocol on the Bravo deck, including the hybrid-capture bead suspension plate at position 5 and the pre-warmed Wash Buffer 2 source plate at position 6.
- 2 Pre-set the temperature of Bravo deck positions 4 and 6 as indicated in [Table 31](#). See [page 17](#) for more information on how to do this step.

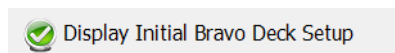
Table 46 Bravo Deck Temperature Presets

Bravo Deck Position	Temperature Preset	Preset Method
4	69°C	Inheco Multi TEC control touchscreen (CPAC 2-1)
6	74°C	Inheco Multi TEC control touchscreen (CPAC 2-2)

- 3 Place an empty square-well plate waste reservoir at position 1 of the Bravo deck.
- 4 Prepare an Eppendorf source plate labeled *Wash #1*. For each well to be processed, add 160 µL of SureSelect Wash Buffer 1. Place the Wash #1 source plate at position 3 of the Bravo deck.
- 5 Prepare a Thermo Scientific reservoir containing 15 mL of nuclease-free water and place the reservoir at position 9 of the Bravo deck.

Setup and Run VWorks protocol 08 SureSelectQXT_Wash_v1.0.pro

- 6 On the SureSelect setup form, under **Select Protocol**, select **08 SureSelectQXT_Wash_v1.0.pro**.
- 7 Select the number of columns of samples to be processed. Runs must include 1, 2, 3, 4, 6, or 12 columns.
- 8 Click **Display Initial Bravo Deck Setup**.



- 9 Verify that the Bravo deck has been set up according to the Bravo Deck Setup region of the form and as shown in [Table 47](#).

Table 47 Initial Bravo deck configuration for 08 SureSelectQXT_Wash_v1.0.pro

Location	Content
1	Empty waste reservoir (Axygen 96 Deep Well Plate, square wells)
2	New tip box
3	Wash #1 Eppendorf source plate
4	Empty red insert
5	DNA-RNA hybrids captured on streptavidin beads in DeepWell plate
6	Wash #2 DeepWell source plate seated on silver Nunc DeepWell insert (pre-heated during Capture protocol)
7	–(empty)–
8	Empty tip box
9	Nuclease-free water reservoir

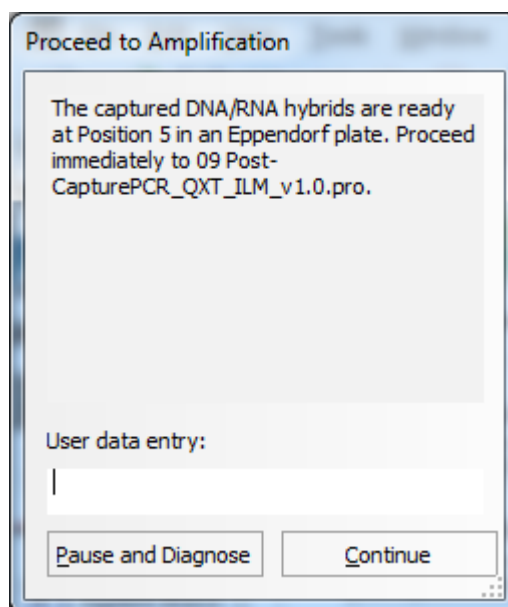
- 10 Verify that the Current Tip State indicator on the form matches the configuration of unused and used tips in the tip boxes at Bravo Deck positions 2 and 8, respectively. See [page 21](#) for more information on using this segment of the form during the run.
- 11 When setup and verification is complete, click **Run Selected Protocol**.



Running the 08 SureSelectQXT_Wash_v1.0.pro protocol takes approximately 60 minutes. An operator must be present during the run to complete tip box replacement as directed by VWorks prompts. Once complete, you will be prompted as shown below.

- 12 When the wash protocol is complete, the captured, bead-bound DNA samples are located in the Eppendorf plate at position 5 of the Bravo deck, and you will be prompted by VWorks as shown below. Click Continue on the VWorks screen to finish the protocol.

Remove the DNA sample plate from position 5 and seal the wells using the PlateLoc Thermal Microplate Sealer, with sealing settings of 165°C and 1.0 sec. Store the plate on ice until it is used on [page 73](#). Proceed immediately to the 09 Post-CapturePCR_QXT_ILM_v1.0.pro protocol, starting on [page 68](#).



NOTE

Captured DNA is retained on the streptavidin beads during the post-capture amplification step.

5 Indexing

- Step 1. Amplify the captured DNA libraries to add index tags **68**
- Step 2. Purify the amplified indexed libraries using AMPure XP beads **74**
- Step 3. Assess indexed DNA quality **76**
- Step 4. Quantify each index-tagged library by QPCR (optional) **77**
- Step 5. Pool samples for Multiplexed Sequencing **78**
- Step 6. Prepare sequencing samples **79**
- Step 7. Set up the sequencing run and trim adaptors from the reads **83**

This chapter describes the steps to add index tags by amplification, purify, assess quality and quantity of the libraries, and pool indexed samples for multiplexed sequencing.

Step 1. Amplify the captured DNA libraries to add index tags

In this step, the Agilent NGS Bravo completes the liquid handling steps for PCR-based addition of dual indexing tags to the captured DNA samples using automation protocol

09 Post-CapturePCR_QXT_ILM_v1.0.pro. After the PCR plate is prepared by the NGS Bravo, you transfer the plate to a thermal cycler for amplification.

This step uses the components listed in **Table 48**. Thaw then vortex to mix the reagents listed below and keep on ice.

Table 48 Reagents for post-capture indexing by PCR amplification

Kit Component	Storage Location	Where Used
Herculase II Fusion DNA Polymerase	SureSelect QXT Library Prep Kit Box 2, –20°C	page 69
Herculase II 5× Reaction Buffer	SureSelect QXT Library Prep Kit Box 2, –20°C	page 69
100 mM dNTP Mix (25 mM each dNTP)	SureSelect QXT Library Prep Kit Box 2, –20°C	page 69
SureSelect QXT P7 and P5 dual indexing primers	SureSelect QXT Library Prep Kit Box 2, –20°C	page 70

Prepare the NGS Bravo

- 1 Clear the Bravo deck of all plates and tip boxes, then wipe it down with a DNA Away decontamination wipe.
- 2 Pre-set the temperature of Bravo deck positions 6 and 9 as indicated in **Table 49**. See [page 17](#) to [page 18](#) for more information on how to do this step.

Table 49 Bravo Deck Temperature Presets

Bravo Deck Position	Temperature Preset	Preset Method
6	4°C	Inheco Multi TEC control touchscreen (CPAC 2-2)
9	0°C	ThermoCube control panel

- 3 Place a red PCR plate insert at Bravo deck position 6 and a silver deep well plate insert at Bravo deck position 9.

Prepare the PCR master mix

CAUTION

To avoid cross-contaminating libraries, set up PCR master mixes in a dedicated clean area or PCR hood with UV sterilization and positive air flow.

- 4 Prepare the appropriate volume of PCR master mix, according to [Table 50](#). Mix well using a vortex mixer and keep on ice.

Table 50 Preparation of PCR Master Mix for 09 Post-CapturePCR_QXT_ILM_v1.0.pro,

SureSelect ^{QXT} Reagent	Volume for 1 Library	Volume for 1 Column	Volume for 2 Columns	Volume for 3 Columns	Volume for 4 Columns	Volume for 6 Columns	Volume for 12 Columns
Nuclease-free water	9.5 µL	121.1 µL	201.9 µL	282.6 µL	363.4 µL	524.9 µL	1049.8 µL
Herculase II 5× Reaction Buffer	10.0 µL	127.5 µL	212.5 µL	297.5 µL	382.5 µL	552.5 µL	1105.0 µL
100 mM dNTP Mix	0.5 µL	6.4 µL	10.6 µL	14.9 µL	19.1 µL	27.6 µL	55.3 µL
Herculase II Fusion DNA Polymerase	1.0 µL	12.8 µL	21.3 µL	29.8 µL	38.3 µL	55.3 µL	110.5 µL
Total Volume	21.0 µL	267.8 µL	446.3 µL	624.8 µL	803.3 µL	1160.3 µL	2320.6 µL

- 5 Using the same Nunc DeepWell master mix source plate that was used for the 06 Hybridization_QXT_v1.0.pro protocol, add the volume of PCR master mix indicated in [Table 51](#) to all wells of column 4 of the plate. Keep the source plate on ice until it is used on [page 70](#).

Table 51 Preparation of the Master Mix Source Plate for 09 Post-CapturePCR_QXT_ILM_v1.0.pro,

Master Mix Solution	Position on Source Plate	Volume of Master Mix added per Well of Nunc Deep Well Source Plate					
		1-Column Runs	2-Column Runs	3-Column Runs	4-Column Runs	6-Column Runs	12-Column Runs
PCR Master Mix	Column 4 (A4-H4)	30.8 µL	53.2 µL	75.5 µL	97.8 µL	142.4 µL	287.4 µL

NOTE

If you are using a new DeepWell plate for the post-capture PCR source plate, leave columns 1 to 3 empty and add the PCR Master Mix to column 4 of the new plate.

Assign and aliquot indexing primers

- Determine the appropriate index assignments for each sample. See the **Reference** section for sequences of the index portion of the P7 (page 88) and P5 (page 88) indexing primers used to amplify the DNA libraries in this step.

Use the following guidelines for dual index assignments:

- Use a different indexing primer combination for each sample to be sequenced in the same lane.
 - All samples on the same row of the target-enriched DNA library plate must be assigned to the same P5 indexing primer (P5 i13 through P5 i20). This design results from the automation protocol configuration in which the P5 indexing primer is dispensed from a single source plate column to all columns of the indexing PCR plate. Each row of samples may be assigned to the same or different P5 primers, depending on run size and multiplexing requirements. (See **step 9**, below, for details of P5 primer addition to the master mix source plate.)
 - The automation protocol configuration allows for any of the provided P7 indexing primers (P7 i1 through P7 i12) to be assigned to any sample position of the target-enriched DNA library plate. (See **step 7** and **step 8** below, for P7 primer source plate setup details.)
 - For sample multiplexing, Agilent recommends maximizing index diversity on both P7 and P5 primers as required for color balance. For example, when 8-plexing, use eight different P7 index primers with two P5 index primers. See **Table 78** on page 90 for additional details.
- Dilute each P7 indexing primer (P7 i1 through P7 i12) to be used in the run according to **Table 52**. The volumes below include the required excess.

Table 52 Preparation of P7 indexing primer dilutions

Reagent	Volume to Index 1 Sample	Volume to Index 8 Samples
Nuclease-free water	4.0 µL	34 µL
SureSelect QXT P7 dual indexing primer (P7 i1 to P7 i12)	1.0 µL	8.5 µL
Total Volume	5.0 µL	42.5 µL

- In a fresh PCR plate, aliquot 5 µL of the appropriate P7 indexing primer dilution from **Table 52** to the intended sample indexing well position(s).

Keep the plate on ice.

- Obtain the Nunc DeepWell master mix source plate containing the PCR Master Mix in column 4 (prepared in **step 5**, above). Add each P5 indexing primer (P5 i13 through P5 i20) to be used in the run to the master mix in the appropriate well of column 4. Add the volume listed in **Table 53** to each well of column 4, according to the number of sample columns in the run. Each well of column 4 can contain the same or different P5 indexing primers. The final configuration of the master mix source plate is shown in **Figure 10** on page 71.

Keep the source plate on ice.

Table 53 Addition of P5 indexing primers to the post-capture PCR master mix source plate

Solution added to Source Plate	Position on Source Plate	Volume of Primer added per Well of Nunc Deep Well Source Plate					
		1-Column Runs	2-Column Runs	3-Column Runs	4-Column Runs	6-Column Runs	12-Column Runs
SureSelect QXT P5 dual indexing primer(s)*	Column 4 (A4-H4)	1.5 µL	2.5 µL	3.6 µL	4.7 µL	6.8 µL	13.7 µL

* Each well of column 4 may contain the same or different P5 indexing primer. Typical 12-column runs include all eight of the provided SureSelect QXT P5 dual indexing primers (P5 i13 through P5 i20), resulting in a different P5 primer assignment to each row of the PCR indexing plate.

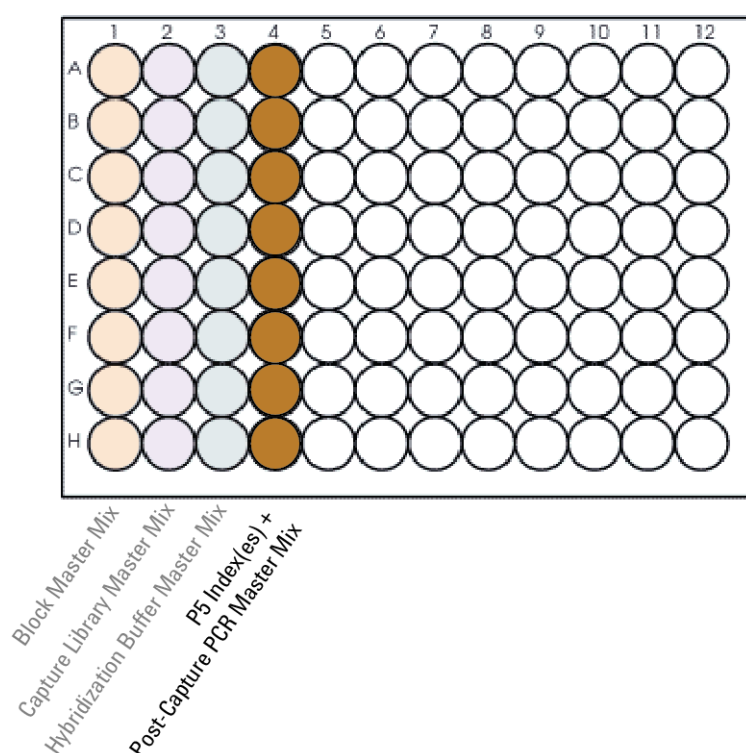
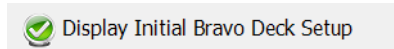


Figure 10 Configuration of the master mix source plate for 09 Post-CapturePCR_QXT_ILM_v1.0.pro.

- 10** Seal the master mix source plate using the PlateLoc Thermal Microplate Sealer, with sealing settings of 165°C and 1.0 sec.
- 11** Vortex the plate to ensure complete mixing, then centrifuge the plate for 30 seconds to drive the well contents off the walls and plate seal and to eliminate any bubbles.

Setup and run VWorks protocol 09 Post-CapturePCR_QXT_ILM_v1.0.pro

- 12 On the SureSelect setup form, under **Select Protocol to Run**, select **09 Post-CapturePCR_QXT_ILM_v1.0.pro**.
- 13 Under **Select PCR plate Labware**, select the specific type of PCR plate used at position 6 of the Bravo deck.
- 14 Select the number of columns of samples to be processed. Runs must include 1, 2, 3, 4, 6, or 12 columns.
- 15 Click **Display Initial Bravo Deck Setup**.



- 16 Load the Bravo deck according to the Bravo Deck Setup region of the form and as shown in **Table 54**.

Table 54 Initial Bravo deck configuration for 09 Post-CapturePCR_QXT_ILM_v1.0.pro

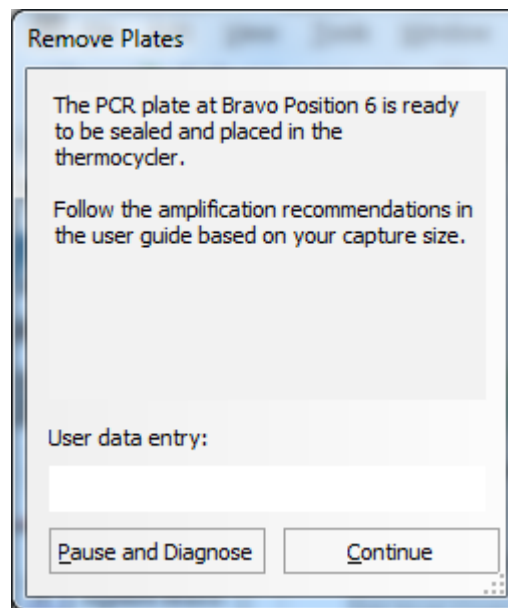
Location	Content
1	–(empty)–
2	New tip box
3	–(empty)–
4	–(empty)–
5	Captured DNA bead suspensions in Eppendorf twin.tec plate
6	Diluted P7 indexing primers in PCR plate seated in red insert (PCR plate type must be specified on setup form under step 2)
7	–(empty)–
8	Empty tip box
9	Master mix plate containing P5 indexing primers and PCR Master Mix in Column 4 (unsealed), seated in silver insert

- 17 Verify that the Current Tip State indicator on the form matches the configuration of unused and used tips in the tip boxes at Bravo Deck positions 2 and 8, respectively. See **page 21** for more information on using this segment of the form during the run.
- 18 When setup and verification is complete, click **Run Selected Protocol**.



- 19 Running the 09 Post-CapturePCR_QXT_ILM_v1.0.pro, protocol takes approximately 15 minutes. Once complete, the PCR-ready samples, containing captured DNA, PCR master mix, and indexing primers are located in the PCR plate at position 6 of the Bravo deck.

- 20 When you see the following prompt, remove the PCR plate from position 6 of the Bravo deck and seal the plate using the PlateLoc Thermal Microplate Sealer, with sealing settings of 165°C and 3.0 seconds.



- 21 Transfer the PCR plate to a thermal cycler and run the PCR amplification program shown in [Table 55](#).

Table 55 Post-Capture PCR cycling program

Segment	Number of Cycles	Temperature	Time
1	1	98°C	2 minutes
2	Probes >3 Mb: 10 Cycles	98°C	30 seconds
	Probes 1 to 3 Mb: 12 Cycles	58°C	30 seconds
	Probes <1 Mb: 14 Cycles	72°C	1 minute
3	1	72°C	5 minutes
4	1	4°C	Hold

Step 2. Purify the amplified indexed libraries using AMPure XP beads

In this step, the Agilent NGS Bravo transfers AMPure XP beads to the indexed DNA sample plate and then collects and washes the bead-bound DNA.

This step uses protocol 10 Cleanup_Post-CapturePCR_QXT_ILM_v1.0.pro.

Prepare the NGS Bravo and reagents

- 1 Clear the Bravo deck of all plates and tip boxes, then wipe it down with a DNA Away decontamination wipe.
- 2 Pre-set the temperature of Bravo deck positions 4 and 6 as indicated in [Table 56](#). See [page 17](#) for more information on how to do this step.

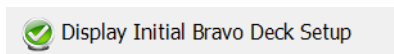
Table 56 Bravo Deck Temperature Presets

Bravo Deck Position	Temperature Preset	Preset Method
4	45°C	Inheco Multi TEC control touchscreen (CPAC 2-1)
6	4°C	Inheco Multi TEC control touchscreen (CPAC 2-2)

- 3 Verify that the AMPure XP bead suspension is at room temperature. (If necessary, allow the bead solution to come to room temperature for at least 30 minutes.) *Do not freeze the beads at any time.*
- 4 Mix the AMPure XP bead suspension well so that the reagent appears homogeneous and consistent in color.
- 5 Prepare a Nunc DeepWell source plate for the beads by adding 60 µL of homogeneous AMPure XP beads per well, for each well to be processed.
- 6 Prepare a Thermo Scientific Matrix reservoir containing 20 mL of nuclease-free water.
- 7 Prepare a separate Thermo Scientific Matrix reservoir containing 45 mL of freshly-prepared 70% ethanol.
- 8 Centrifuge the amplified DNA sample plate for 30 seconds to drive the well contents off the walls and plate seal.

Setup and run VWorks 10 Cleanup_Post-CapturePCR_QXT_ILM_v1.0.pro

- 9 On the SureSelect setup form, under **Select Protocol**, select **10 Cleanup_Post-CapturePCR_QXT_ILM_v1.0.pro**.
- 10 Under **Select PCR plate Labware**, select the specific type of PCR plate used for post-capture amplification.
- 11 Select the number of columns of samples to be processed. Runs must include 1, 2, 3, 4, 6, or 12 columns.
- 12 Click **Display Initial Bravo Deck Setup**.



13 Load the Bravo deck according to the Bravo Deck Setup region of the form and as shown in **Table 57**.

Table 57 Initial Bravo deck setup for 10 Cleanup_Post-CapturePCR_QXT_ILM_v1.0.pro

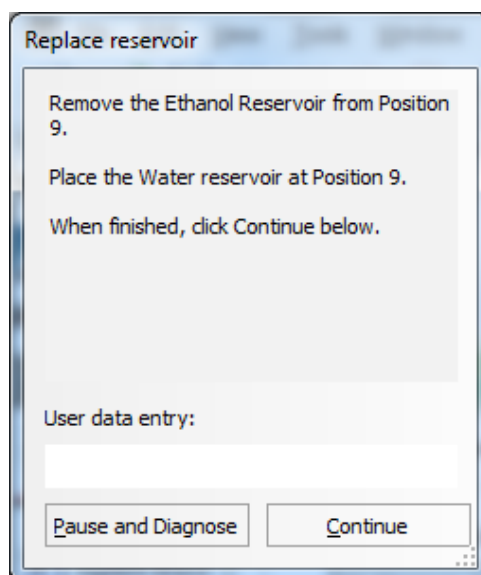
Location	Content
1	Empty waste reservoir (Axygen 96 Deep Well Plate, square wells)
2	New tip box
3	Empty Eppendorf plate
4	–(empty)–
5	AMPure XP beads in Nunc DeepWell plate (60 µl beads per processing well)
6	Amplified DNA libraries in unsealed PCR plate seated in red insert (PCR plate type must be specified on setup form under step 2)
7	–(empty)–
8	Empty tip box
9	70% ethanol in Matrix reservoir

14 Verify that the Current Tip State indicator on the form matches the configuration of unused and used tips in the tip boxes at Bravo Deck positions 2 and 8, respectively. See **page 21** for more information on using this segment of the form during the run.

15 When setup and verification is complete, click **Run Selected Protocol**.



Running the 10 Cleanup_Post-CapturePCR_QXT_ILM_v1.0.pro protocol takes approximately 45 minutes. An operator must be present during the run to complete tip box replacement and to transfer the water reservoir to the Bravo deck, when directed by the VWorks prompt shown below.



Once the protocol is complete, the purified DNA samples are located in the Eppendorf plate at position 3 of the Bravo deck.

Step 3. Assess indexed DNA quality

Option 1: Analysis using the 2100 Bioanalyzer and High Sensitivity DNA Assay

Use the Bioanalyzer High Sensitivity DNA Assay to analyze the amplified indexed DNA. Perform the assay according to the [High Sensitivity DNA Kit Guide](#).

- 1 Set up the 2100 Bioanalyzer instrument as instructed in the reagent kit guide.
- 2 Prepare the chip, samples and ladder as instructed in the reagent kit guide, using 1 μL of each sample for the analysis.
- 3 Prepare the chip, samples and ladder as instructed in the reagent kit guide, using 1 μL of each sample for the analysis.

NOTE

For some samples, Bioanalyzer results are improved by diluting 1 μL of the sample in 9 μL of 10 mM Tris, 1 mM EDTA prior to analysis. Be sure to mix well by vortexing at 2000 rpm on the IKA vortex supplied with the Bioanalyzer before analyzing the diluted samples.

- 4 Load the prepared chip into the 2100 Bioanalyzer and start the run within five minutes after preparation.
- 5 Verify that the electropherogram shows the peak of DNA fragment size positioned between 325 and 450 bp. A sample electropherogram is shown in [Figure 11](#).

Stopping Point If you do not continue to the next step, seal the plate and store at 4°C overnight or at –20°C for prolonged storage.

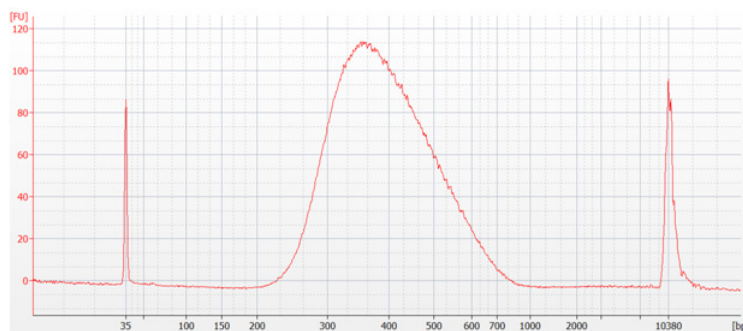


Figure 11 Post-capture analysis of library DNA using the High Sensitivity DNA Assay.

Use a High Sensitivity D1000 ScreenTape and associated reagent kit. Perform the assay according to the [Agilent High Sensitivity D1000 Assay Quick Guide](#).

- 1 Prepare the TapeStation samples as instructed in the reagent kit guide. Use 2 μL of each indexed DNA sample diluted with 2 μL of High Sensitivity D1000 sample buffer for the analysis.

CAUTION

For accurate quantitation, make sure to thoroughly mix the combined DNA and sample buffer by vortexing the assay plate or tube strip for 1 minute on the IKA MS3 vortex mixer provided with the 4200/4150 TapeStation system before loading the samples.

- 2 Load the sample plate or tube strips from [step 1](#), the High Sensitivity D1000 ScreenTape, and loading tips into the TapeStation as instructed in the reagent kit guide. Start the run.

- 3 Verify that the electropherogram shows the peak of DNA fragment size positioned between 325 and 450 bp. A sample electropherogram is shown in **Figure 12**.

Stopping Point If you do not continue to the next step, seal the indexed DNA sample plate and store at 4°C overnight or at –20°C for prolonged storage.

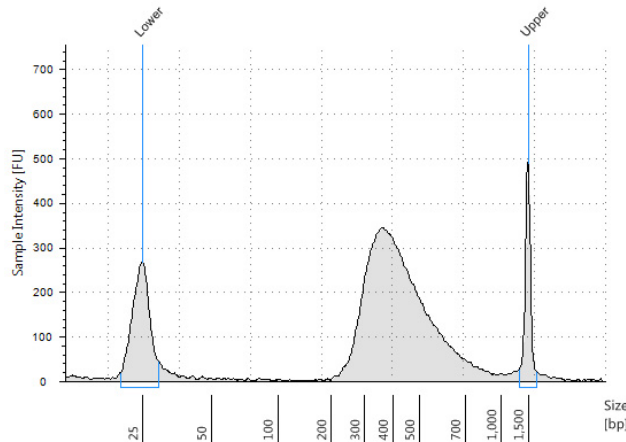


Figure 12 Post-capture library DNA analyzed using a High Sensitivity D1000 ScreenTape.

Step 4. Quantify each index-tagged library by QPCR (optional)

Refer to the protocol that is included with the Agilent QPCR NGS Library Quantification Kit (p/n G4880A) for more details to do this step.

- 1 Use the Agilent QPCR NGS Library Quantification Kit (for Illumina) to determine the concentration of each index-tagged captured library.
- 2 Prepare a standard curve using the quantification standard included in the kit, according to the instructions provided in the user guide.
- 3 Dilute each index-tagged captured library such that it falls within the range of the standard curve.

Typically this corresponds to approximately a 1:1000 to 1:10,000 dilution of the captured DNA.

- 4 Prepare the QPCR master mix with Illumina adaptor-specific PCR primers according to instructions provided in the kit.
- 5 Add an aliquot of the master mix to PCR tubes and add template.
- 6 On a QPCR system, such as the Mx3005p, run the thermal profile outlined in the QPCR NGS Library Quantification kit user guide. Use the SYBR Green instrument setting.
- 7 Use the standard curve to determine the concentration of each unknown index-tagged library, in nM.

The concentration will be used to accurately pool samples for multiplexed sequencing.

Step 5. Pool samples for Multiplexed Sequencing

- 1 Combine the libraries such that each index-tagged sample is present in equimolar amounts in the pool. For each library, use the formula below to determine the amount of indexed sample to use.

$$\text{Volume of Index} = \frac{V(f) \times C(f)}{\# \times C(i)}$$

where $V(f)$ is the final desired volume of the pool,

$C(f)$ is the desired final concentration of all the DNA in the pool

$\#$ is the number of indexes, and

$C(i)$ is the initial concentration of each indexed sample.

Table 58 shows an example of the amount of 4 index-tagged samples (of different concentrations) and Low TE needed for a final volume of 20 μL at 10 nM.

Table 58 Example of indexed sample volume calculation for total volume of 20 μL

Component	V(f)	C(i)	C(f)	#	Volume to use (μL)
Sample 1	20 μL	20 nM	10 nM	4	2.5
Sample 2	20 μL	10 nM	10 nM	4	5
Sample 3	20 μL	17 nM	10 nM	4	2.9
Sample 4	20 μL	25 nM	10 nM	4	2
Low TE					7.6

- 2 Adjust the final volume of the pooled library to the desired final concentration.
 - If the final volume of the combined index-tagged samples is less than the desired final volume, $V(f)$, add Low TE to bring the volume to the desired level.
 - If the final volume of the combined index-tagged samples is greater than the final desired volume, $V(f)$, lyophilize and reconstitute to the desired volume.
- 3 If you store the library before sequencing, add Tween 20 to 0.1% v/v and store at -20°C short term.

Step 6. Prepare sequencing samples

Proceed to cluster amplification using the appropriate Illumina Paired-End Cluster Generation Kit. See [Table 59](#) for kit configurations compatible with the recommended read length plus reads for the SureSelect^{QXT} 8-bp dual indexes.

The optimal seeding concentration for SureSelect^{QXT} target-enriched libraries varies according to sequencing platform, run type and Illumina kit version. See [Table 59](#) for guidelines. Seeding concentration and cluster density may also need to be optimized based on the DNA fragment size range for the library and on the desired output and data quality.

To do this step, refer to the manufacturer's instructions, using the modifications described on [page 79](#) for use of the SureSelect^{QXT} Read Primers with the Illumina Paired-End Cluster Generation Kits. Follow Illumina's recommendation for a PhiX control in a low-concentration spike-in for improved sequencing quality control.

Table 59 Illumina Kit Configuration Selection Guidelines

Platform	Run Type	Read Length*	SBS Kit Configuration	Chemistry	Seeding Concentration
HiSeq 2500	Rapid Run	2 × 100 bp	200 Cycle Kit	v2	10–13 pM
HiSeq 2500	High Output	2 × 100 bp	250 Cycle Kit	v4	13–16 pM
MiSeq	All Runs	2 × 100 bp or 2 × 150 bp	300 Cycle Kit	v2	10–13 pM
MiSeq	All Runs	2 × 75 bp	150 Cycle Kit	v3	14–19 pM
NextSeq 500/550	All Runs	2 × 100 bp or 2 × 150 bp	300 Cycle Kit	v2.5	1.3–1.8 pM
HiSeq 3000/4000	All Runs	2 × 100 bp or 2 × 150 bp	300 Cycle Kit	v1	300–400 pM
NovaSeq 6000	Standard Workflow Runs	2 × 100 bp or 2 × 150 bp	300 Cycle Kit	v1.0 or v1.5	300–600 pM
NovaSeq 6000	Xp Workflow Runs	2 × 100 bp or 2 × 150 bp	300 Cycle Kit	v1.0 or v1.5	200–400 pM

* If your application requires a different read length, verify that you have sufficient sequencing reagents to complete Reads 1 and 2 in addition to the dual 8-bp index reads.

Using the SureSelect^{QXT} Read Primers with Illumina's Paired-End Cluster Generation Kits

To sequence the SureSelect^{QXT} libraries on Illumina's sequencing platforms, you need to use the following custom sequencing primers, provided in SureSelect QXT Library Prep Kit Box 2:

- SureSelect QXT Read Primer 1
- SureSelect QXT Read Primer 2
- SureSelect QXT Index 1 Read Primer
- SureSelect QXT Index 2 Read Primer (this primer is used only for HiSeq 3000, HiSeq 4000, and NextSeq platforms and for NovaSeq platform runs using v1.5 chemistry)

These SureSelect^{QXT} custom sequencing primers are provided at 100 μM and must be diluted in the corresponding Illumina primer solution, using the platform-specific instructions below:

For the HiSeq 2500 platform, combine the primers as shown in [Table 60](#) or [Table 61](#) on [page 80](#).

For the HiSeq 3000 or HiSeq 4000 platform, combine the primers as shown in [Table 62](#) on [page 80](#).

For the MiSeq platform, combine the primers as shown in [Table 63](#) on page 81.

For the NextSeq platform, combine the primers as shown in [Table 64](#) or [Table 65](#) on [page 81](#).

For the NovaSeq platform, combine the primers as shown in [Table 66](#) through [Table 69](#) on [page 81](#).

NOTE

It is important to combine the primers precisely in the indicated ratios. Carefully follow the instructions indicated in [Table 60](#) to [Table 69](#). Where specified, add the custom primer volume directly to the solution already in cBot reagent plate wells. Otherwise, combine measured volumes of each solution; do not rely on volumes reported on vial labels or in Illumina literature. Vortex each mixture vigorously to ensure homogeneity for proper detection of the indexes using the custom read primers.

Table 60 HiSeq 2500 High Output custom sequencing primer preparation

Sequencing Read	Volume of SureSelect ^{QXT} Primer	Volume of Illumina TruSeq Primer	Total Volume
Read 1	6 µL SureSelect QXT Read Primer 1 (brown cap)	1194 µL HP10	1.2 mL*
Index	15 µL SureSelect QXT Index 1 Read Primer (clear cap)	2985 µL HP12	3 mL
Read 2	15 µL SureSelect QXT Read Primer 2 (black cap)	2985 µL HP11	3 mL

* Aliquot the mixture as directed for HP6 or HP10 in Illumina's cluster generation protocol.

Table 61 HiSeq 2500 Rapid Mode custom sequencing primer preparation

Sequencing Read	Volume of SureSelect ^{QXT} Primer	Volume of Illumina TruSeq Primer	Total Volume
Read 1	8.8 µL SureSelect QXT Read Primer 1 (brown cap)	1741.2 µL HP10	1.75 mL
Index	8.8 µL SureSelect QXT Index 1 Read Primer (clear cap)	1741.2 µL HP12	1.75 mL
Read 2	8.8 µL SureSelect QXT Read Primer 2 (black cap)	1741.2 µL HP11	1.75 mL

Table 62 HiSeq 3000 and HiSeq 4000 custom sequencing primer preparation

Sequencing Read	Volume of SureSelect ^{QXT} Primer	Volume of Illumina TruSeq Primer	Total Volume	Reagent Rack Position
Read 1	1.5 µL SureSelect QXT Read Primer 1 (brown cap)	298.5 µL HP10*	0.3 mL per well	cBot Column 11
Read 2	15 µL SureSelect QXT Read Primer 2 (black cap)	2985 µL HP11	3 mL	16
Index 1 + Index 2	22.5 µL SureSelect QXT Index 1 Read Primer (clear cap) + 22.5 µL SureSelect QXT Index 2 Read Primer (purple cap)	4455 µL HP14	4.5 mL	17

* Use cBot recipe *HiSeq_3000_4000_HD_Exclusion_Amp_v1.0*. Add 1.5 µL SureSelect QXT Read Primer 1 to the 298.5 µL of HP10 in each well of column 11 in the cBot reagent plate.

Table 63 MiSeq platform custom sequencing primer preparation

Sequencing Read	Volume of SureSelect ^{QXT} Primer	Volume of Illumina TruSeq Primer	Total Volume	Final Cartridge Position
Read 1	3 µL SureSelect QXT Read Primer 1 (brown cap)	597 µL HP10 (well 12)	0.6 mL	well 18
Index	3 µL SureSelect QXT Index 1 Read Primer (clear cap)	597 µL HP12 (well 13)	0.6 mL	well 19
Read 2	3 µL SureSelect QXT Read Primer 2 (black cap)	597 µL HP11 (well 14)	0.6 mL	well 20

Table 64 NextSeq 500/550 High-Output v2 Kit custom sequencing primer preparation

Sequencing Read	Volume of SureSelect ^{QXT} Primer	Volume of Illumina Primer	Total Volume	Final Cartridge Position
Read 1	3.9 µL SureSelect QXT Read Primer 1 (brown cap)	1296.1 µL BP10 (from well 20)	1.3 mL	well 7
Read 2	4.2 µL SureSelect QXT Read Primer 2 (black cap)	1395.8 µL BP11 (from well 21)	1.4 mL	well 8
Index 1+ Index 2	6 µL SureSelect QXT Index 1 Read Primer (clear cap) + 6 µL SureSelect QXT Index 2 Read Primer (purple cap)	1988 µL BP14 (from well 22)	2 mL	well 9

Table 65 NextSeq 500/550 Mid-Output v2 Kit custom sequencing primer preparation

Sequencing Read	Volume of SureSelect ^{QXT} Primer	Volume of Illumina Primer	Total Volume	Final Cartridge Position
Read 1	2.7 µL SureSelect QXT Read Primer 1 (brown cap)	897.3 µL BP10 (from well 20)	0.9 mL	well 7
Read 2	3.3 µL SureSelect QXT Read Primer 2 (black cap)	1096.7 µL BP11 (from well 21)	1.1 mL	well 8
Index 1+ Index 2	4.8 µL SureSelect QXT Index 1 Read Primer (clear cap) + 4.8 µL SureSelect QXT Index 2 Read Primer (purple cap)	1590.4 µL BP14 (from well 22)	1.6 mL	well 9

Table 66 NovaSeq 6000 using SP/S1/S2 flowcell with v1.0 chemistry custom sequencing primer preparation

Sequencing Read	Volume of SureSelect ^{QXT} Primer	Volume of Illumina Primer	Total Volume	Final Cartridge Position
Read 1	12 µL SureSelect QXT Read Primer 1 (brown cap)	3988 µL BP10 (well 24)	4 mL	5
Index	15 µL SureSelect QXT Index 1 Read Primer (clear cap)	4985 µL BP14 (well 23)	5 mL	7
Read 2	6 µL SureSelect QXT Read Primer 2 (black cap)	1994 µL BP11 (well 13)	2 mL	6

Table 67 NovaSeq 6000 using S4 flowcell with v1.0 chemistry custom sequencing primer preparation

Sequencing Read	Volume of SureSelect ^{QXT} Primer	Volume of Illumina Primer	Total Volume	Final Cartridge Position
Read 1	21.9 µL SureSelect QXT Read Primer 1 (brown cap)	7278.1 µL BP10 (well 24)	7.3 mL	5
Index	15 µL SureSelect QXT Index 1 Read Primer (clear cap)	4985 µL BP14 (well 23)	5 mL	7
Read 2	10.5 µL SureSelect QXT Read Primer 2 (black cap)	3489.5 µL BP11 (well 13)	3.5 mL	6

Table 68 NovaSeq 6000 using SP/S1/S2 flowcell with v1.5 chemistry custom sequencing primer preparation

Sequencing Read	Volume of SureSelect ^{QXT} Primer	Volume of Illumina Primer	Total Volume	Final Cartridge Position
Read 1	12 µL SureSelect QXT Read Primer 1 (brown cap)	3988 µL BP10 (well 24)	4 mL	5
Index 1+ Index 2	15 µL SureSelect QXT Index 1 Read Primer (clear cap) + 15 µL SureSelect QXT Index 2 Read Primer (purple cap)	4970 µL VP14 (well 23)	5 mL	7
Read 2	6 µL SureSelect QXT Read Primer 2 (black cap)	1994 µL BP11 (well 13)	2 mL	6

Table 69 NovaSeq 6000 using S4 flowcell with v1.5 chemistry custom sequencing primer preparation

Sequencing Read	Volume of SureSelect ^{QXT} Primer	Volume of Illumina Primer	Total Volume	Final Cartridge Position
Read 1	21.9 µL SureSelect QXT Read Primer 1 (brown cap)	7278.1 µL BP10 (well 24)	7.3 mL	5
Index 1+ Index 2	15 µL SureSelect QXT Index 1 Read Primer (clear cap) + 15 µL SureSelect QXT Index 2 Read Primer (purple cap)	4970 µL VP14 (well 23)	5 mL	7
Read 2	10.5 µL SureSelect QXT Read Primer 2 (black cap)	3489.5 µL BP11 (well 13)	3.5 mL	6

Step 7. Set up the sequencing run and trim adaptors from the reads

Refer to Illumina protocols to set up custom sequencing primer runs, using the additional guidelines outlined below.

For SureSelect^{QXT} dual index sequence information, see [page 88](#).

Before aligning reads to the reference genome, SureSelect^{QXT} adaptor sequences must be trimmed from the reads. You can use SureCall, Agilent's NGS data analysis software, to perform adaptor trimming, alignment of reads and variant calling of FASTQ sequencing data files generated by Illumina sequencers. To download SureCall free-of-charge and for additional information, including tutorials on this software, visit the [SureCall page at www.agilent.com](http://www.agilent.com).

To use SureCall to analyze SureSelect^{QXT} library data, you first need to define an analysis workflow. This analysis workflow identifies the libraries as SureSelect^{QXT} libraries and enables automated adaptor trimming. The trimmed FASTQ files can then be used for alignment to generate BAMs for downstream analysis.

To create the analysis workflow, refer to [Figure 13 on page 83](#). Upon starting SureCall, click the Analysis Workflow tab. Choose the appropriate analysis type (single sample, paired, or trio analysis), and then click the Import Unaligned Files button. Using the menus near the top of the screen, choose the appropriate design description from the *Design* menu, select Default SureSelect Method from the *Analysis Method* menu, and select QXT from the *Library Prep* menu. Within the *Select Unaligned Sample Files* window, specify your read 1 and read 2 files using the Add buttons. Once done, refer to the SureCall guide for next steps on alignment and variant calling.

If using another pipeline for alignment and downstream analysis, refer to the platform-specific guidelines starting on [page 84](#).

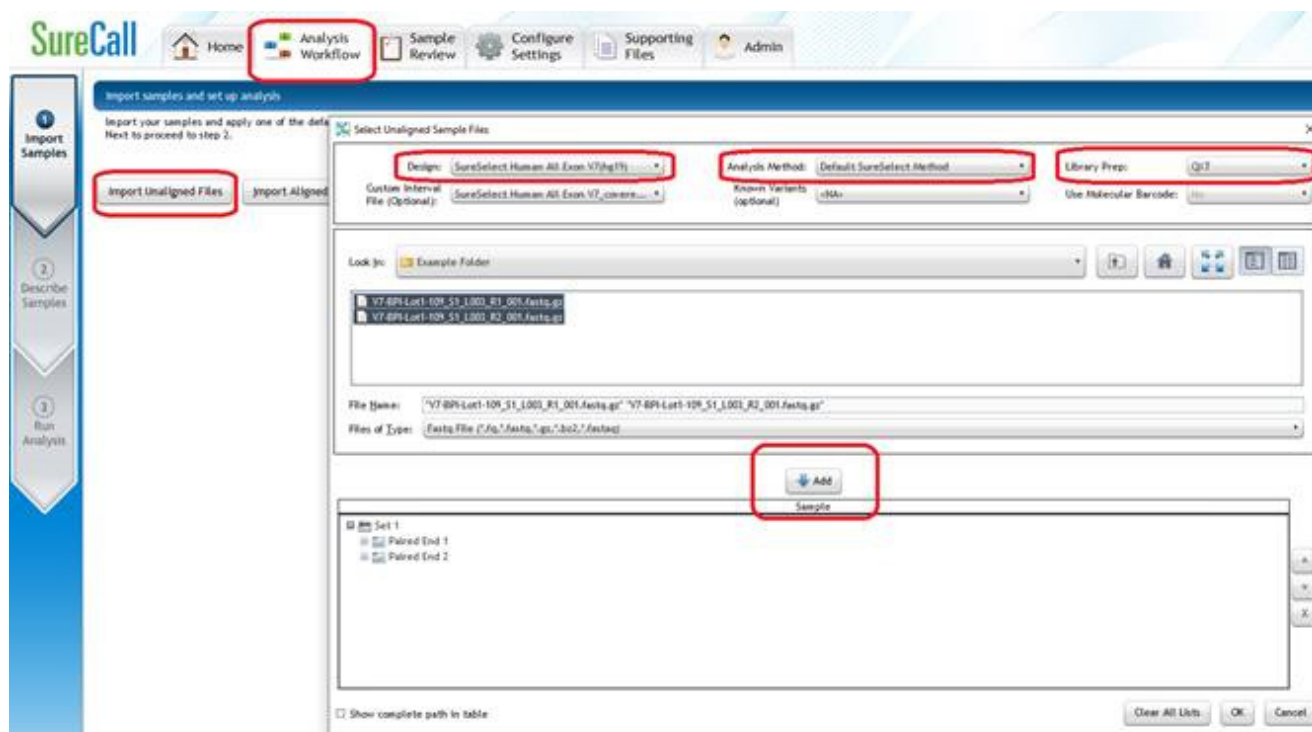


Figure 13 Analysis workflow setup in SureCall.

MiSeq platform sequencing run setup and adaptor trimming guidelines

Use the Illumina Experiment Manager (IEM) software to generate a custom primer Sample Sheet.

Set up the run to include adaptor trimming using the IEM Sample Sheet Wizard. When prompted by the wizard, select the *Use Adaptor Trimming* option, and specify **CTGTCTCTTATCACA** as the adaptor sequence. This enables the MiSeq Reporter software to identify the adaptor sequence and trim the adaptor from reads.

HiSeq/NextSeq/NovaSeq platform sequencing run setup and adaptor trimming guidelines

Set up sequencing runs using the settings shown in **Table 70**. For HiSeq runs, select *Dual Index* on the *Run Configuration* screen of the instrument control software interface. Since custom primers are spiked into the standard sequencing primer tubes, no additional specialized settings are required to accommodate the use of custom primers in the run.

For the NextSeq or NovaSeq platform, Cycle Number and custom sequencing primer settings can be specified on the *Run Configuration* screen of the instrument control software interface.

Table 70 Run Configuration screen Cycle Number settings

Run Segment	Cycle Number
Read 1	100
Index 1 (i7)	8
Index 2 (i5)	8
Read 2	100

After the sequencing run is complete, generate demultiplexed FASTQ data following Illumina's instructions and then trim adaptor sequences from the reads using the Trimmer utility of the Agilent Genomics NextGen Toolkit (AGeNT). For additional information and to download this toolkit free-of-charge, visit the [AGeNT page at www.agilent.com](http://www.agilent.com).

6 Reference

Kit Contents **86**

Nucleotide Sequences of SureSelect^{QXT} Dual Indexes **88**

Guidelines for Multiplexing with Dual-Indexed Samples **90**

This chapter contains reference information, including component kit contents and reference information for use during the downstream sample sequencing steps.

Kit Contents

SureSelect^{QXT} Reagent Kits contain the following component kits:

Table 71 SureSelect^{QXT} Reagent Kit Contents

Component Kits	Storage Condition	Part Number
SureSelect QXT Library Prep Kit, ILM, Box 2*	–20°C	5500-0127
SureSelect QXT Target Enrichment Kit, ILM Hyb Module, Box 1	Room Temperature	5190-7335
SureSelect QXT Target Enrichment Kit, ILM Hyb Module, Box 2	–20°C	5190-7334

* SureSelect QXT Library Prep Kit, ILM, Box 1 is not required for the workflow described in this manual.

The contents of each of the component kits listed in **Table 71** are described in **Table 72** to **Table 74** below.

Table 72 SureSelect QXT Library Prep Kit Box 2 Content

Kit Component	Format
SureSelect QXT Buffer	bottle
SureSelect QXT Enzyme Mix ILM	tube with orange cap
Herculase II Fusion DNA Polymerase	tube with red cap
Herculase II 5× Reaction Buffer	tube with clear cap
100 mM dNTP Mix (25 mM each dNTP)	tube with green cap
DMSO	tube with green cap
SureSelect QXT Read Primer 1	tube with amber cap
SureSelect QXT Read Primer 2	tube with black cap
SureSelect QXT Index 1 Read Primer	tube with clear cap
SureSelect QXT Index 2 Read Primer	tube with purple cap
SureSelect QXT P7 dual indexing primers	P7 i1 through P7 i12 provided in 12 tubes with yellow caps (one tube per primer)
SureSelect QXT P5 dual indexing primers	P5 i13 through P5 i20 provided in 8 tubes with blue caps (one tube per primer)

Table 73 SureSelect QXT Hyb Module Box 1 Content

Kit Component	Format
SureSelect QXT Stop Solution	bottle
SureSelect Binding Buffer	bottle
SureSelect Wash Buffer 1	bottle
SureSelect Wash Buffer 2	bottle

Table 74 SureSelect QXT Hyb Module Box 2 Content

Kit Component	Format
SureSelect Fast Hybridization Buffer	bottle
SureSelect QXT Fast Blocker Mix	tube with blue cap
SureSelect QXT Primer Mix	tube with clear cap
SureSelect RNase Block	tube with purple cap

Nucleotide Sequences of SureSelect^{QXT} Dual Indexes

The nucleotide sequence of each SureSelect^{QXT} index is provided in the tables below.

Note that some index number assignments of the SureSelect^{QXT} P5 and P7 indexes differ from the index number assignments used by Illumina for indexes of similar or identical sequence.

Each index is 8 bases in length. Refer to Illumina's sequencing run setup instructions for sequencing libraries using 8-base indexes.

Table 75 SureSelect^{QXT} P7 Indexes 1 to 12

Index Number	Sequence
P7 Index 1 (P7 i1)	TAAGGCGA
P7 Index 2 (P7 i2)	CGTACTAG
P7 Index 3 (P7 i3)	AGGCAGAA
P7 Index 4 (P7 i4)	TCCTGAGC
P7 Index 5 (P7 i5)	GTAGAGGA
P7 Index 6 (P7 i6)	TAGGCATG
P7 Index 7 (P7 i7)	CTCTCTAC
P7 Index 8 (P7 i8)	CAGAGAGG
P7 Index 9 (P7 i9)	GCTACGCT
P7 Index 10 (P7 i10)	CGAGGCTG
P7 Index 11 (P7 i11)	AAGAGGCA
P7 Index 12 (P7 i12)	GGACTCCT

Table 76 SureSelect^{QXT} P5 Indexes 13 to 20 for HiSeq 2500, MiSeq, or NovaSeq (v1.0 chemistry) platform

Index Number	Sequence
P5 Index 13 (P5 i13)	TAGATCGC
P5 Index 14 (P5 i14)	CTCTCTAT
P5 Index 15 (P5 i15)	TATCCTCT
P5 Index 16 (P5 i16)	AGAGTAGA
P5 Index 17 (P5 i17)	GTAAGGAG
P5 Index 18 (P5 i18)	ACTGCATA
P5 Index 19 (P5 i19)	AAGGAGTA
P5 Index 20 (P5 i20)	CTAAGCCT

Table 77 SureSelect^{QXT} P5 Indexes 13 to 20 for HiSeq 3000/4000, NextSeq, or NovaSeq (v1.5 chemistry) platform*

Index Number	Sequence
P5 Index 13 (P5 i13)	GCGATCTA
P5 Index 14 (P5 i14)	ATAGAGAG
P5 Index 15 (P5 i15)	AGAGGATA
P5 Index 16 (P5 i16)	TCTACTCT
P5 Index 17 (P5 i17)	CTCCTTAC
P5 Index 18 (P5 i18)	TATGCAGT
P5 Index 19 (P5 i19)	TACTCCTT
P5 Index 20 (P5 i20)	AGGCTTAG

* When doing runs on these platforms through BaseSpace, use the reverse complement sequences provided in [Table 76](#).

Guidelines for Multiplexing with Dual-Indexed Samples

Agilent recommends following the dual index sample pooling guidelines and shown in [Table 78](#). These are designed to maintain color balance at each cycle of the index reads on both ends. They also provide flexibility of demultiplexing as single or dual indexed samples in low-plexity experiments. One-base mismatches should be allowed during demultiplexing.

Table 78 Dual index sample pooling guidelines for 96 Reaction Kits

Plexity of Sample Pool	Recommended SureSelect ^{QXT} P7 Indexes	Recommended SureSelect ^{QXT} P5 Indexes
1-plex	Any P7 index i1 to i12	Any P5 index (i13 to i20)
2-plex	P7 i1 and P7 i2 OR P7 i2 and P7 i4	P5 i13 and P5 i14 OR P5 i15 and P5 i16 OR P5 i17 and P5 i18
3-plex	P7 i1, P7 i2 and P7 i4 OR P7 i3, P7 i4 and P7 i6 OR P7 i5, P7 i7 and P7 i8	P5 i13 and P5 i14 OR P5 i15 and P5 i16 OR P5 i17 and P5 i18 (as needed)
4-plex	P7 i1, P7 i2, P7 i3* and P7 i4 OR P7 i3, P7 i4, P7 i5* and P7 i6 OR P7 i5, P7 i6*, P7 i7 and P7 i8	P5 i13 and P5 i14 OR P5 i15 and P5 i16 OR P5 i17 and P5 i18 (as needed)
5-plex	P7 i1, P7 i2, P7 i3*, P7 i4 and P7 i5* OR P7 i3, P7 i4, P7 i5*, P7 i6 and p7 i7* OR P7 i5, P7 i6*, P7 i7, P7 i8 and p7 i9*	P5 i13 and P5 i14 OR P5 i15 and P5 i16 OR P5 i17 and P5 i18 (as needed)
6- to 12-plex	Any combination of P7 indexes i1 to i12 using each index only once	P5 i13 and P5 i14 OR P5 i15 and P5 i16 OR P5 i17 and P5 i18 (as needed)
13-to 96-plex	All twelve P7 indexes (i1 to i12)	P5 i13 and P5 i14 and any other P5 index OR P5 i15 and P5 i16 and any other P5 index OR P5 i17 and P5 i18 and any other P5 index (as needed)

* The indicated indexes may be substituted with another index, as long as the substitute index differs from all others used in the sample pool.

In This Book

This guide contains information to run the SureSelect^{QXT} Automated Library Prep and Target Enrichment protocol using Agilent's NGS Bravo Option A.

