SureSelect^{XT} Automated RNA Target Enrichment

Strand-Specific RNA Library Prep and Target Enrichment for Illumina Paired-End Multiplexed Sequencing

Protocol

Version C.0, December 2014

SureSelect platform manufactured with Agilent SurePrint Technology

Research Use Only. Not for use in Diagnostic Procedures.

Agilent Technologies

Notices

Manual Part Number

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In this Guide...

This guide describes an optimized protocol to prepare target-enriched mRNA sequencing libraries from total RNA samples using the SureSelect Automated Strand-Specific RNA Library Prep and Target Enrichment system.

This protocol is specifically developed for RNA library preparation for Illumina paired-end multiplexed sequencing. Sample processing steps are automated using the NGS Workstation.

1 Before You Begin

This chapter contains information (such as procedural notes, safety information, required reagents and equipment) that you should read and understand before you start an experiment.

2 Using the Agilent NGS Workstation for SureSelect RNA Library Preparation

This chapter contains an orientation to the Agilent NGS Workstation, an overview of the SureSelect RNA protocol, and considerations for designing SureSelect experiments for automated processing using the Agilent NGS Workstation.

3 Sample Preparation

This chapter describes the steps to prepare strand-specific mRNA libraries from total RNA samples for sequencing on the Illumina platform.

4 Hybridization

This chapter describes the steps to hybridize the prepped library with the SureSelect RNA capture library and to capture the targeted sequences for enrichment.

5 Indexing and Sample Prep for Multiplexed Sequencing

This chapter describes the steps to index by amplification, purify, and assess the quality and quantity of the target-enriched samples. Indexed samples are pooled by mass prior to sequencing.

6 Reference

This chapter contains reference information.

What's New in Version C.0

- Support for kits supplied with either of two indexing primer configurations.

  Kits with revised index configuration (typically received December, 2014 or later) include indexing primers A01 through H12 provided in a blue plate. For kit content details see page 130. For nucleotide sequences of the 8-bp indexes in this revised configuration, see Table 75 on page 134.

  Kits with original index configuration (typically received before December, 2014), include indexing primers 1–96 provided in a clear plate. For kit content details see page 135. For nucleotide sequences of the 8-bp indexes in this original configuration, see Table 82 on page 140 through Table 87 on page 145.

What's New in Version B.0

- Support for revised kit configuration, now including RNA Seq Second Strand + End Repair Enzyme Mix and RNA Seq Second Strand + End Repair Oligo Mix (both replacing RNA Seq Second Strand + End Repair Master Mix). Protocol modifications to support the revised kit configuration begin on page 58 and end on page 61. See Table 70 on page 131 for updated kit contents.
- Updated DMSO supplier information (Table 1 on page 12)
- Updated ordering information for Agilent 2200 TapeStation ScreenTapes and reagents (Table 3 on page 15)
- Updated total RNA preparation considerations (Note on page 34)
- Updated sequence analysis information, including library strandedness (page 126 to page 127)
- Footnote removed from Table 1 on page 12 and *Note* removed from page 130.

Content

1 Before You Begin

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 Workstation. For non-automated sample processing procedures for Agilent's SureSelect Strand-Specific RNA Target Enrichment Kit for sequencing on the Illumina platform, see publication G9691-90000.

Procedural Notes

- 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 Workstation to allow rapid and efficient plate transfer.
- Use of Agilent's SureCycler 8800 thermal cycler and associated plasticware is recommended for optimal performance. The workflow is compatible with additional thermal cyclers, but performance should be validated before running a large number of samples. See page 32 for a list of supported PCR plate types and ensure that the thermal cycler to be used is compatible with one of the supported PCR plate types.
- Prepare and load the Agilent NGS Workstation as detailed in each of the protocol steps before initiating each automated protocol run. When loading plates in the workstation's Labware MiniHub, always place plates in the orientation shown in Figure 4 on page 38.
- 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.
- Avoid repeated freeze-thaw cycles of stock and diluted RNA and cDNA solutions. 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.
- When preparing master mix reagent stock solutions for use:
  1. Thaw the reagent vial as rapidly as possible without heating above room temperature.
  2. Mix on a vortex mixer, then spin in a centrifuge for 5 to 10 seconds to drive the contents off of walls and lid.
  3. Store vials used during an experiment on ice or in a cold block.
  4. Library Preparation Master Mixes should not be frozen and thawed more than five times. If you plan to use the reagents in more than five experiments, aliquot to multiple vials to minimize freeze/thaw cycles for each vial.
- In general, follow Biosafety Level 1 (BL1) safety rules.

Safety Notes

CAUTION

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

Required Reagents

Table 1 Required Reagents for SureSelect^{XT} RNA Target Enrichment Automation

Description	Vendor and part number
SureSelect RNA Capture Library	Select one library from Table 2
SureSelect^{XT} RNA Reagent Kit*, Illumina platforms (ILM), 96 Samples*	Agilent p/n G9692B
Actinomycin D†	Sigma p/n A1410
DMSO	Sigma p/n D8418
Dynabeads M-270 Streptavidin Beads	Life Technologies p/n 65306
Agencourt AMPure XP Kit 5 mL 60 mL 450 mL	Beckman Coulter Genomics p/n A63880 p/n A63881 p/n A63882
1X Low TE Buffer (10 mM Tris-HCl, pH 8.0, 0.1 mM EDTA)	Life Technologies p/n 12090-015, or equivalent
100% Ethanol, molecular biology grade	Sigma-Aldrich p/n E7023

* Each 96-reaction kit contains sufficient reagents for 96 reactions used in runs that include at least 3 columns of samples per run.

† Actinomycin D should be obtained as a solid and prepared at 4 µg/µl concentration in DMSO no more than one month before use. See page 35 for more information.

CAUTION Use only the recommended Dynabeads M-270 Streptavidin Beads for this automated protocol. Use of other streptavidin bead preparations may adversely affect performance and is not supported by Agilent.

Table 2 SureSelect RNA Capture Libraries

Capture Library	96 Samples
Custom RNA Capture 1 kb up to 499 kb	5190-7281
(reorder)	(5190-7282)
Custom RNA Capture 0.5 Mb up to 2.9 Mb	5190-7283
(reorder)	(5190-7284)
Custom RNA Capture 3 Mb up to 5.9 Mb	5190-7285
(reorder)	(5190-7286)
SureSelect RNA Kinome	5190-7287

Required Equipment

Table 3 Required Equipment

Description	Vendor and part number
Agilent NGS Workstation Option B, with VWorks software version 11.3.0.1195.	Contact Agilent Automation Solutions for ordering information: Customerservice.automation@agilent.com
Bravo 96-well PCR plate insert (red)	Agilent p/n G5498B#13
Robotic Pipetting Tips (Sterile, Filtered, 250 µL)	Agilent p/n 19477-022
Thermal cycler and accessories	SureCycler 8800 Thermal Cycler (Agilent p/n G8810A), 96 well plate module (Agilent p/n G8810A) and compression mats (Agilent p/n 410187) or equivalent
PCR plates compatible with selected Thermal Cycler, e.g. Agilent semi-skirted PCR plate for the SureCycler 8800 Thermal Cycler See page 32 for a list of supported PCR plates for automation protocols	Agilent p/n 401334
Eppendorf twin.tec full-skirted 96-well PCR plates	Eppendorf p/n 951020401 or 951020619
Thermo Scientific Reservoirs	Thermo Scientific p/n 1064156
Nunc DeepWell Plates, sterile, 1.3-mL well volume	Thermo Scientific p/n 260251
Axygen 96 Deep Well Plate, 2.2 mL, Square Well (waste reservoirs)	Axygen p/n P-2ML-SQ-C E & K Scientific p/n EK-2440
NucleoClean Decontamination Wipes	Millipore p/n 3097
Vacuum concentrator	Savant SpeedVac, model DNA120, with 96-well plate rotor, model RD2MP, or equivalent
Magnetic separator	DynaMag-50 magnet, Life Technologies p/n 123-02D or equivalent

Table 3 Required Equipment (continued)

Description	Vendor and part number
DNA Analysis Platform and Consumables	
Agilent 2100 Bioanalyzer Laptop Bundle	Agilent p/n G2943CA
Agilent 2100 Bioanalyzer Electrophoresis Set	Agilent p/n G2947CA
Agilent DNA 1000 Kit	Agilent p/n 5067-1504
Agilent High Sensitivity DNA Kit	Agilent p/n 5067-4626
OR	
Agilent 2200 TapeStation	Agilent p/n G2964AA or G2965AA
Agilent D1000 ScreenTape	Agilent p/n 5067-5582
Agilent D1000 Reagents	Agilent p/n 5067-5583
Agilent High Sensitivity D1000 ScreenTape	Agilent p/n 5067-5584
Agilent D1000 Reagents	Agilent p/n 5067-5585
DNA LoBind Tubes, 1.5-mL PCR clean, 250 pieces	Eppendorf p/n 022431021 or equivalent
P10, P20, P200 and P1000 pipettes	Pipetman P10, P20, P200, P1000 or equivalent
Ice bucket	
Powder-free gloves	
Vortex mixer	
Timer	

2 Using the Agilent NGS Workstation for SureSelect RNA Library Preparation

This chapter contains an orientation to the Agilent NGS Workstation, an overview of the SureSelect single-stranded RNA library preparation and target enrichment protocol, and considerations for designing SureSelect RNA experiments for automated processing using the Agilent NGS Workstation.

About the Agilent NGS Workstation

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 seven interchangeable fixed-tip or disposable-tip pipette heads, it accurately dispenses fluids from 0.1 µL to 250 µL.

CAUTION Before you begin, make sure that you have read and understand operating, maintenance and safety instructions for using your Bravo platform. Refer to the *Bravo Platform User Guide* (G5409-90006) and the *VWorks Software User Guide* (G5415-90063).

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.

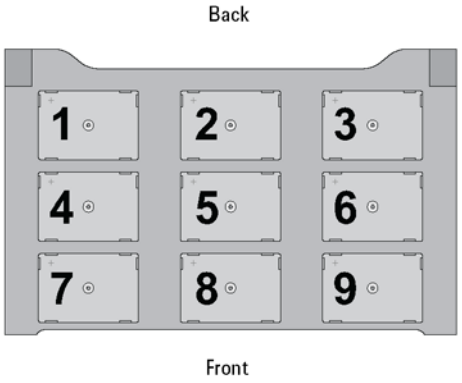


Figure 1 Bravo platform deck

Setting the Temperature of Bravo Deck Heat Blocks

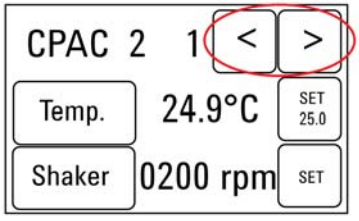
Bravo deck positions 4 and 6 are equipped with Inheco heat blocks, used to incubate sample plates at defined temperatures during the run. Runs that include high- (85°C) or low- (4°C) temperature incubation steps may be expedited by pre-setting the temperature of the affected block before starting the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

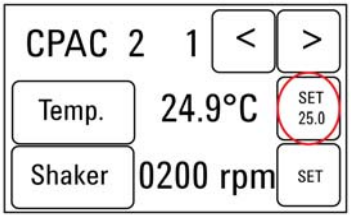
Table 4 Inheco Multi TEC Control touchscreen designations

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

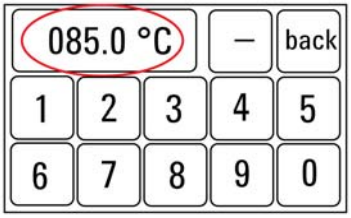
1 Using the arrow buttons, select the appropriate block (CPAC 2 block 1 or CPAC 2 block 2).



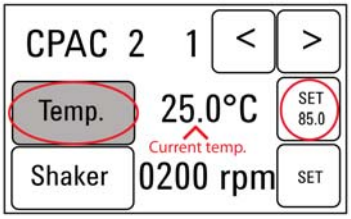
2 To set the temperature of the selected block, press the SET button.



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 will then initates temperature control of Bravo deck position 9 at the displayed set point.

VWorks Automation Control Software

VWorks software, included with your Agilent NGS Workstation, allows you to control the robot and integrated devices using a PC. The Agilent NGS Workstation 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 is 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 11.3.0.1195.

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

Logging in to the VWorks software

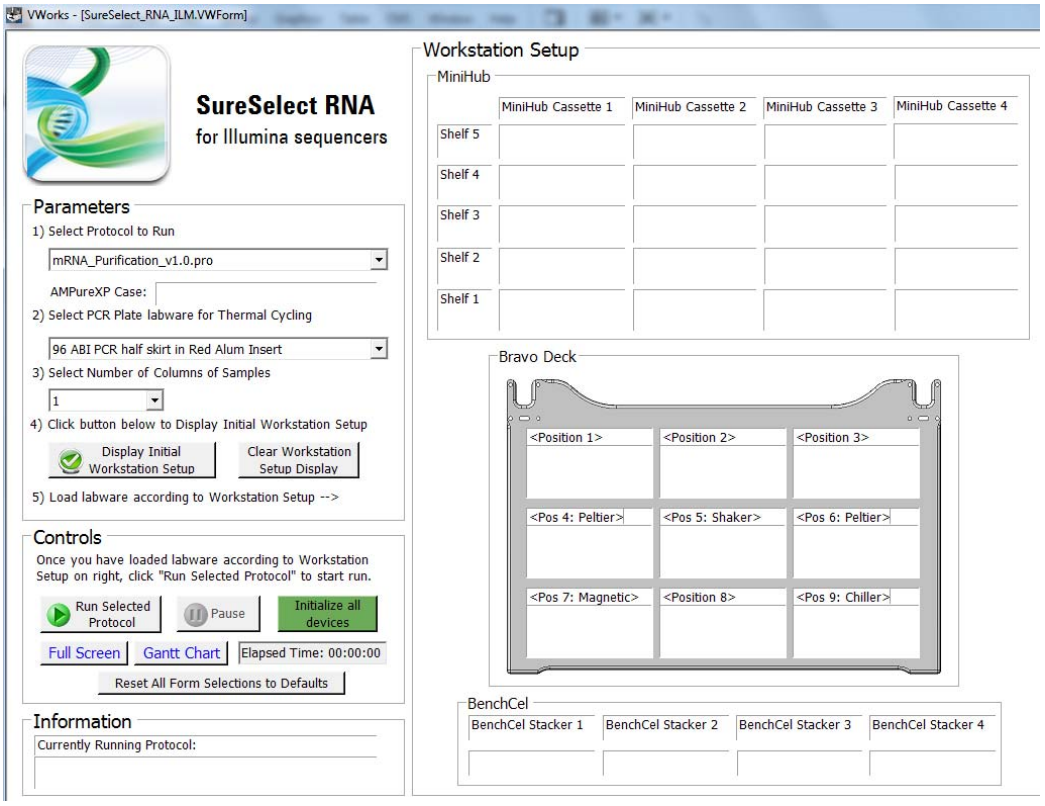
1. Double-click the VWorks icon or the SureSelect_RNA_ILM.VWForm shortcut on the Windows desktop to start the VWorks software.
2. If User Authentication dialog is not visible, click **Log in** on the VWorks window toolbar.
3. In the User Authentication dialog, type your VWorks user name and password,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

VWorks protocol and runset files

VWorks software uses two file types for automation runs, .pro (protocol) files and .rst (runset) files. Runset files are used for automated procedures in which the workstation uses more than one automation protocol during the run.

Using the SureSelect_RNA_ILM.VWForm to setup and start a run

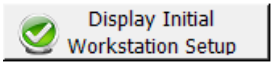
Use the VWorks form SureSelect_RNA_ILM.VWForm, shown below, to set up and start each SureSelect automation protocol or runset.



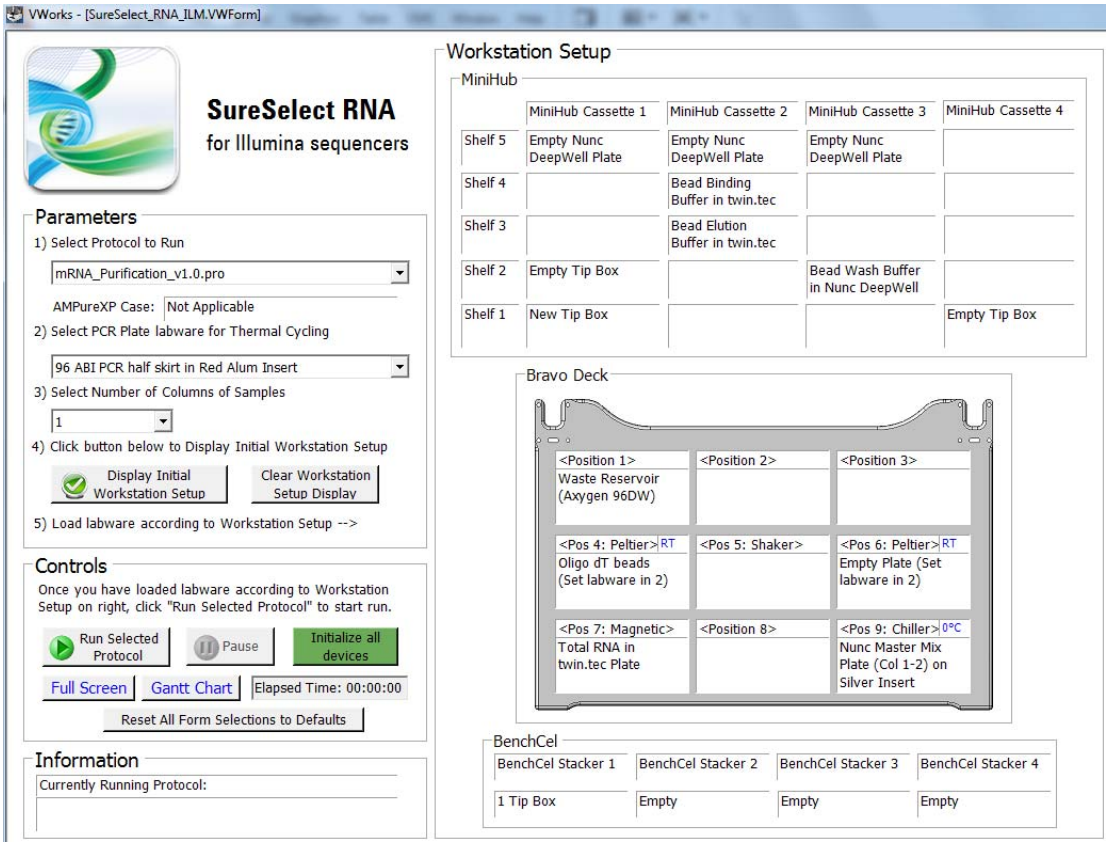
1 Open the form using the SureSelect_RNA_ILM.VWForm shortcut on your desktop.

2 Use the drop-down menus on the form to select the appropriate SureSelect workflow step and number of columns of samples for the run.

3 Once all run parameters have been specified on the form, click **Display Initial Workstation Setup.**



4 The Workstation Setup region of the form will then display the required placement of reaction components and labware in the NGS Workstation for the specified run parameters.

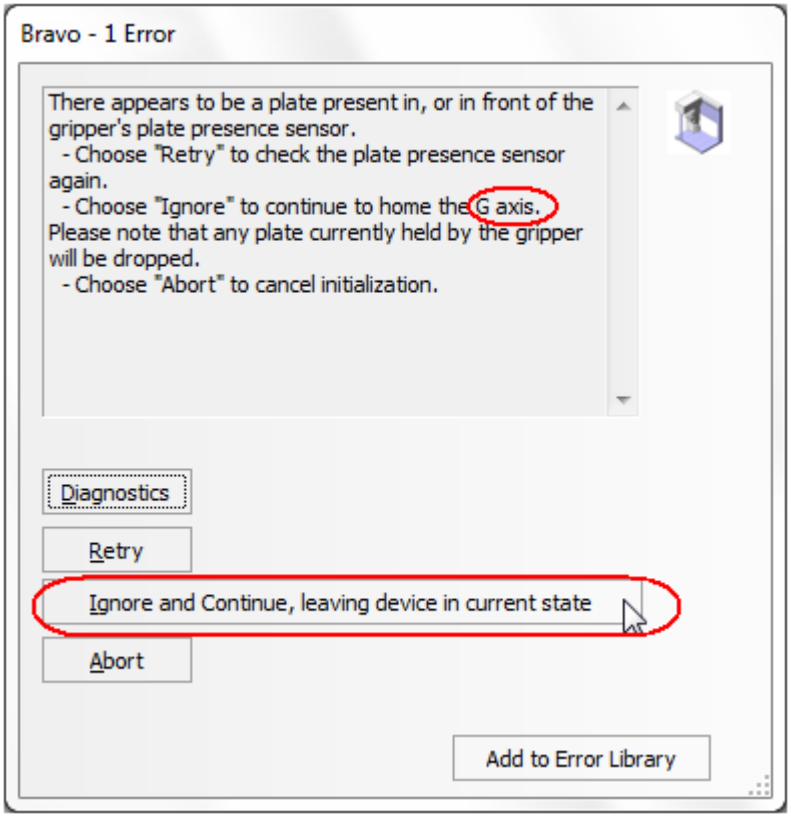


5 After verifying that the NGS Workstation has been set up correctly, click **Run Selected Protocol**.

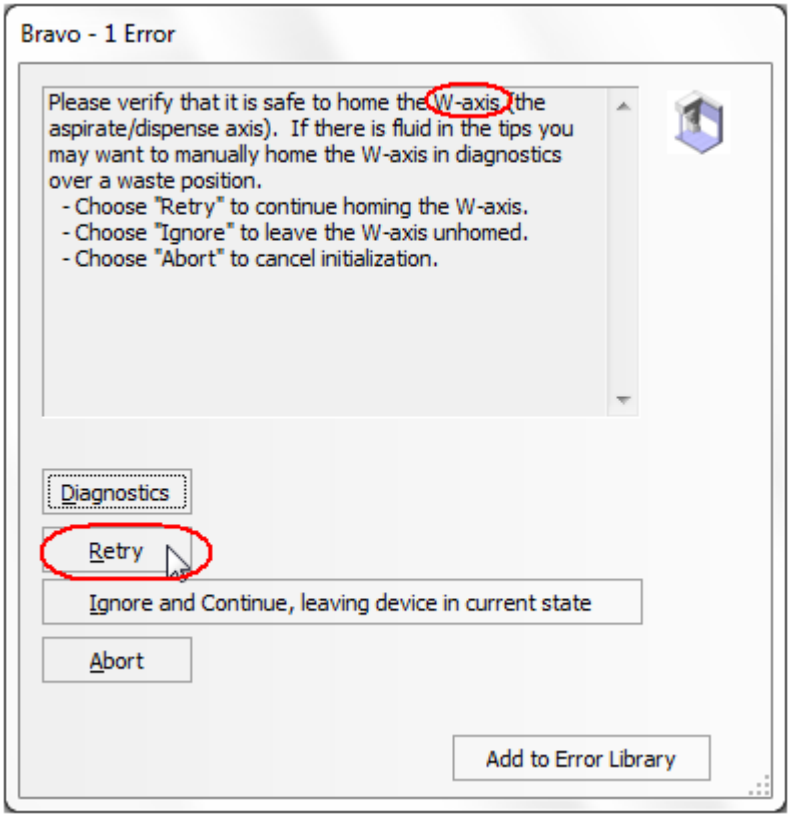
Error messages encountered at start of run

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 workstation 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 workstation. If workstation devices do not respond when you start a run, verify the simulation mode status in VWorks using the following steps.

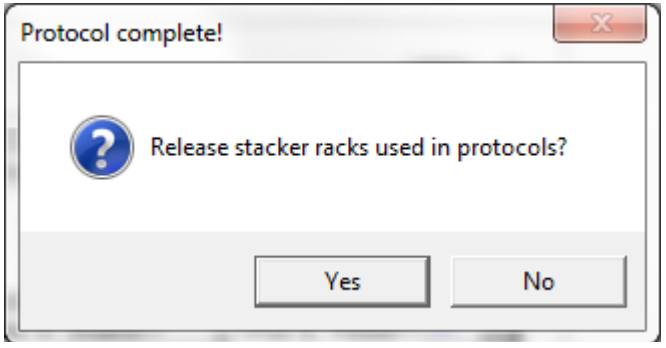
1 Verify that **Simulation is off** is displayed on the status indicator (accessible by clicking **View** > **Control Toolbar**).

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 SureSelect 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.

Finishing a protocol or runset

The window below appears when each run is complete. Click **Yes** to release the BenchCel racks to allow removal of components used in the current run in preparation for the next .pro or .rst run.



Overview of the SureSelect RNA Library Prep Procedure

Figure 2 summarizes the SureSelect workflow for RNA samples to be sequenced using the Illumina sequencing platform. For each sample to be sequenced, an individual cDNA library is prepared. The libraries are then target enriched and tagged by PCR with an index sequence. Depending on the capacity of the sequencing platform, up to 96 samples can be pooled and sequenced in a single lane using the multiplex index tags that are provided with the SureSelect Strand-Specific RNA Library Prep kit.

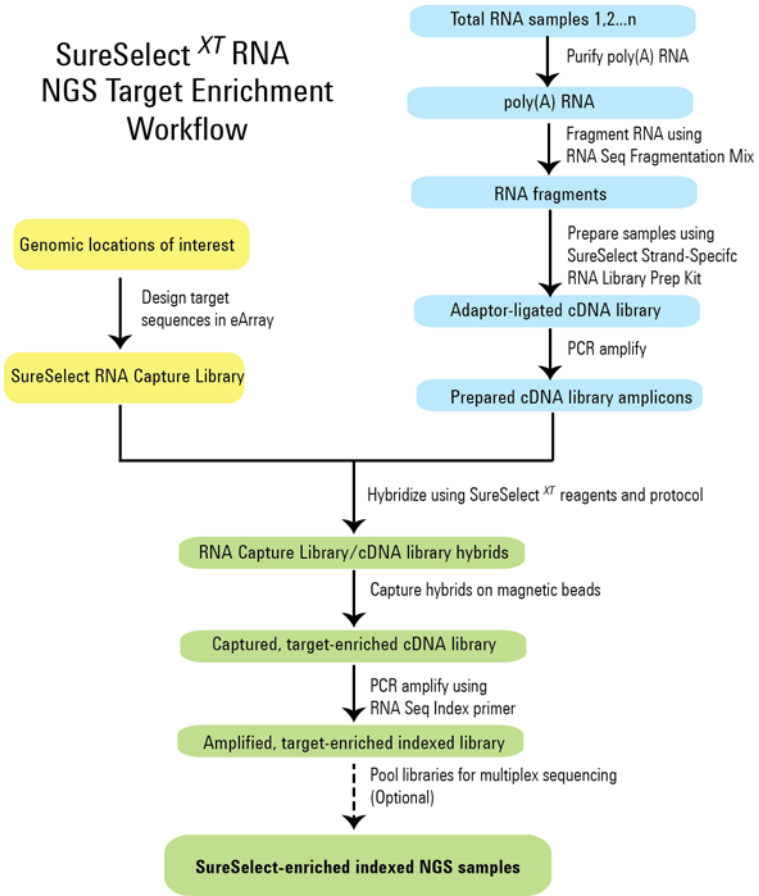


Figure 2 Overall sequencing sample preparation workflow

Table 5 summarizes how the VWorks protocols are integrated into the Strand-Specific RNA Library Prep and Target Enrichment workflow. See the Sample Preparation chapter for complete instructions for use of the VWorks protocols for sample processing.

Table 5 Overview of VWorks protocols and runsets used during the workflow

Workflow Step	VWorks Protocols Used for Agilent NGS Workstation automation
• Purify poly(A) RNA using oligo(dT) beads • Chemically fragment the poly(A) RNA • Synthesize first-strand cDNA	mRNA_Purification_v1.0.pro
Purify first-strand cDNA using AMPure XP beads	AMPureXP_v1.1.pro:First Strand
• Synthesize second-strand cDNA • Repair DNA ends • Purify end-repaired DNA • Adenylate DNA 3'-ends • Ligate adaptors • Purify adaptor-ligated DNA	LibraryPrep_RNASeq_ILM_v1.1.rst
Amplify adaptor-ligated cDNA library	Pre-CapturePCR_RNASeq_ILM_v1.0.pro
Purify library amplicons using AMPure XP beads	AMPureXP_v1.1.pro:Pre-Capture PCR
Aliquot 100 ng of prepped libraries for hybridization	Aliquot_Libraries_v1.0.pro
Hybridize prepped DNA to Capture Library	SureSelectHybridization_v1.0.pro
Capture and wash DNA hybrids	SureSelectCapture&Wash_v1.0.rst
Add index tags by PCR	Post-CapturePCR_RNASeq_ILM_v1.0.pro
Purify indexed amplicons using AMPure XP beads	AMPureXP_v1.1.pro:Post-Capture PCR

Experimental Setup Considerations for Automated Runs

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

Table 6 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 RNA Samples in 96-well Plates for Automated Processing

- The Agilent NGS Workstation processes samples column-wise beginning at column 1. RNA 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.
- For sample indexing by PCR (see Figure 2), you will need to prepare a separate plate containing the indexing primers. Assign the wells to be indexed with their respective indexing primers during experimental design.

CAUTION

This guide includes information for kits containing two different sets of indexing primers. **Verify that you are referencing the information appropriate for your kit version before you proceed.**

Kits with indexing primers supplied in a blue plate include 8-bp indexes A01 through H12. See page 133 through page 134 for indexing primer A01–H12 plate map and nucleotide sequence information.

Kits with indexing primers supplied in a clear plate include 8-bp indexes 1 through 96. See page 139 through page 145 for indexing primer 1–96 plate map and nucleotide sequence information.

Protocol steps for indexing using primers provided in either configuration are identical.

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 Workstation to allow rapid and efficient plate transfer.
- Several workflow steps require that the sample plate be sealed using the PlateLoc thermal microplate sealer on the Agilent NGS Workstation, and then centrifuged to collect any dispersed liquid. To maximize efficiency, locate the centrifuge in close proximity to the Agilent NGS Workstation.

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 SureSelect_RNA_ILM.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 7.

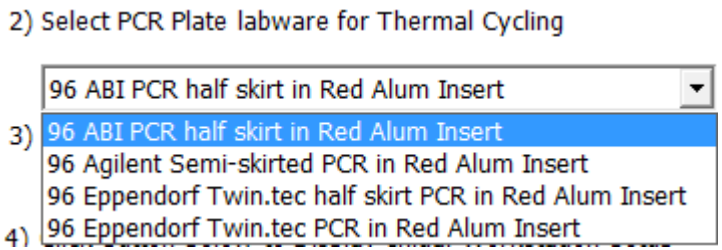


Table 7 Ordering information for supported PCR plates

Description in VWorks menu	Vendor and part number
96 ABI PCR half-skirted plates (MicroAmp Optical plates)	Life Technologies 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

This section contains instructions for RNA library preparation specific to the Illumina paired-read sequencing platform and to automated processing using the Agilent NGS Workstation.

For each sample to be sequenced, individual library preparations are performed in separate wells of a 96-well plate. The samples are then target-enriched and indexed by PCR amplification allowing multiplexing of up to 96 samples for sequencing on Illumina platforms.

Refer to Illumina's protocol *Preparing Samples for Paired-End Sequencing* (p/n 1005361), or the appropriate Illumina protocol for more information.

Step 1. Purify poly(A) RNA/fragment RNA/synthesize first strand cDNA

In this step, automation protocol mRNA_Purification_v1.0.pro is used to complete multiple steps of the RNA Library Preparation workflow. First, poly(A) RNA is purified from total RNA using two serial rounds of binding to oligo(dT) magnetic particles. After purification, the poly(A) RNA is chemically-fragmented to the appropriate size and then is converted to first-strand cDNA.

Total RNA samples containing 200 ng to 4 µg RNA are suitable for the mRNA library preparation automation protocol. Each total RNA sample must be prepared for the run in 25 µL of nuclease-free water.

NOTE For optimal performance, total RNA samples should have an RNA Integrity Number (RIN) of 8 or more, based on analysis using Agilent's 2100 Bioanalyzer.

A workstation operator must be present during this automation protocol to transfer plates between the workstation, which completes most liquid handling steps, and the thermal cycler, which is used for several incubation steps. In addition, the operator must prepare and dispense a master mix immediately before it is used in the automation protocol (see step 30 on page 49).

Prepare the workstation

1. Open the SureSelect setup form using the SureSelect_RNA_ILM.VWForm shortcut on your desktop.
2. Log in to the VWorks software.
3. Turn on the ThermoCube, set to 0°C, at position 9 of the Bravo deck. Be sure that the chiller reservoir contains at least 300 mL of 25% ethanol.
4. Clear the Labware MiniHub and BenchCel of all plates and tip boxes.

Prepare reagents for the run

5 Bring the reagents listed in Table 8 to room temperature.

Table 8 Reagents for poly(A) RNA purification and RNA fragmentation

Kit Component	Storage Location	Where Used in Protocol
Oligo(dT) Microparticles	RNA Library Prep Kit Box 2, 4°C	page 36
RNA Seq Bead Washing Buffer	RNA Library Prep Kit Box 2, 4°C	page 36
RNA Seq Bead Elution Buffer	RNA Library Prep Kit Box 2, 4°C	page 36
RNA Seq Bead Binding Buffer	RNA Library Prep Kit Box 2, 4°C	page 36
RNA Seq Fragmentation Mix	RNA Library Prep Kit Box 1, –20°C	page 37

6 Locate or prepare a stock solution of 4 µg/µL Actinomycin D in DMSO. A 3-µL aliquot of this DMSO stock solution will be used on page 49 to prepare a fresh dilution of 120 ng/µL Actinomycin D in water for the run.

CAUTION

The 4 µg/µL Actinomycin D in DMSO stock solution must be prepared less than one month prior to use and stored in aliquots at –20°C, protected from light. To ensure strand-specificity, you must prepare the 120 ng/µL Actinomycin D dilution immediately before use on page 49.

Prepare the RNA samples source plate

7 Place 25 µL of each RNA sample (0.2–4 µg RNA in nuclease-free water) into the wells of a 96-well Eppendorf twin.tec plate. Load samples into the plate column-wise, in well order A1 to H1, then A2 to H2, ending with A12 to H12 for processing on the Agilent NGS Workstation.

NOTE

SureSelect Strand-Specific RNA Library Prep runs may include 1, 2, 3, 4, 6, or 12 columns of the plate. See Using the Agilent NGS Workstation for SureSelect RNA Library Preparation for additional sample placement considerations.

Prepare the oligo(dT) beads and mRNA purification source plates

When preparing each of the source plates below, add the indicated amount of reagent to wells of the source plate corresponding to the total RNA sample wells in step 7 above. For example, for 3-column runs, fill source well plate wells A1 to H3, but leave wells A4 to H12 empty.

8 Prepare the oligo(dT) beads source plate.

- **a** Vortex the Oligo(dT) Microparticles until the suspension appears homogeneous and consistent in color. If bead aggregates are still present after vortexing, mix thoroughly by pipetting up and down until the suspension appears homogeneous.
- **b** In a PCR plate that is compatible with the thermal cycler to be used in the run, place 25 µL of the homogeneous Oligo(dT) bead suspension into each well to be used for sample purification.

9 Prepare the Bead Binding Buffer source plate. Place 30 µL of RNA Seq Bead Binding Buffer into wells of a 96-well Eppendorf twin.tec plate. Fill each well that corresponds to an RNA sample well.

10 Prepare the Bead Elution Buffer source plate. Place 30 µL of RNA Seq Bead Elution Buffer into wells of a 96-well Eppendorf twin.tec plate. Fill each well that corresponds to an RNA sample well.

11 Prepare the Bead Wash Buffer source plate. Place 410 µL of RNA Seq Bead Washing Buffer into wells of a Nunc DeepWell plate. Fill each well that corresponds to an RNA sample well.

Prepare the master mix source plate

12 Prepare the master mix source plate by adding the appropriate volume of RNA Seq Fragmentation Mix (see Table 9) to all wells of Column 1 of a Nunc DeepWell plate. The configuration of the source plate is shown in Figure 3.

Table 9 Preparation of the Master Mix Source Plate for mRNA_Purification_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
RNA Seq Fragmentation Mix	Column 1 (A1-H1)	28.5 µL	47.5 µL	66.5 µL	85.5 µL	123.5 µL	247.0 µL

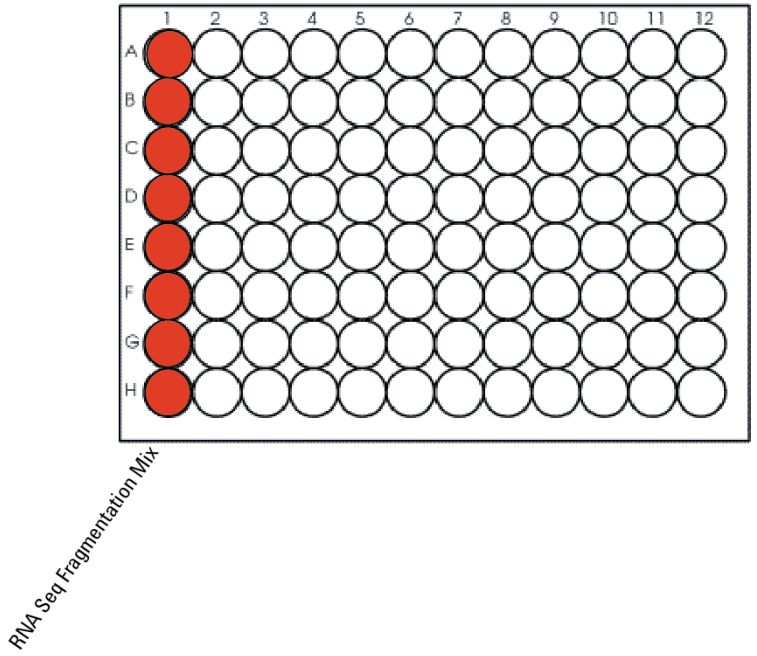


Figure 3 Initial configuration of master mix source plate for mRNA_Purification_v1.0.pro

Load the Agilent NGS Workstation

13 Load the Labware MiniHub according to Table 10, using the plate orientations shown in Figure 4.

Table 10 Initial MiniHub configuration for mRNA_Purification_v1.0.pro

Vertical Shelf Position	Cassette 1	Cassette 2	Cassette 3	Cassette 4
Shelf 5 (Top)	Empty Nunc DeepWell plate	Empty Nunc DeepWell plate	Empty Nunc DeepWell plate	Empty
Shelf 4	Empty	Bead Binding Buffer in twin.tec plate	Empty	Empty
Shelf 3	Empty	Bead Elution Buffer in twin.tec plate	Empty	Empty
Shelf 2	Empty tip box	Empty	Bead Wash Buffer in Nunc DeepWell plate	Empty
Shelf 1 (Bottom)	New tip box	Empty	Empty	Empty tip box

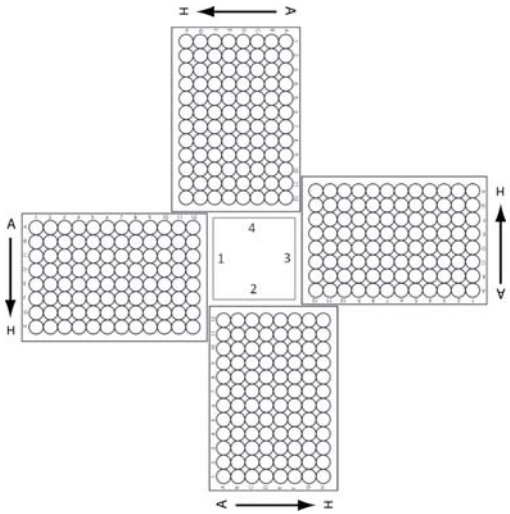


Figure 4 Agilent Labware MiniHub plate orientation. For Thermo Scientific reservoirs, place the notched corner facing the center of the hub.

14 Load the Bravo deck according to Table 11.

Table 11 Initial Bravo deck configuration for mRNA_Purification_v1.0.pro

Location	Content
1	Empty waste reservoir (Axygen 96 Deep Well Plate, square wells)
4	Oligo(dT) beads in PCR plate seated on red insert (PCR plate type must be specified on setup form under step 2)
6	Empty PCR plate seated on red insert (PCR plate type must be specified on setup form under step 2)
7	Total RNA samples in twin.tec plate
9	Master Mix Source Plate seated on silver insert (Nunc DeepWell; see Figure 3 on page 37 for column content)

15 Load the BenchCel Microplate Handling Workstation according to Table 12.

Table 12 Initial BenchCel configuration for mRNA_Purification_v1.0.pro

No. of Columns Processed	Rack 1	Rack 2	Rack 3	Rack 4
1	1 Tip box	Empty	Empty	Empty
2	2 Tip boxes	Empty	Empty	Empty
3	3 Tip boxes	Empty	Empty	Empty
4	3 Tip boxes	Empty	Empty	Empty
6	5 Tip boxes	Empty	Empty	Empty
12	9 Tip boxes	Empty	Empty	Empty

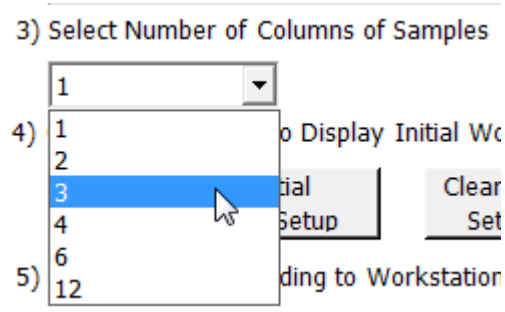
Run VWorks protocol mRNA_Purification_v1.0.pro

16 On the SureSelect setup form, under **Select Protocol to Run**, select **mRNA_Purification_v1.0.pro.**

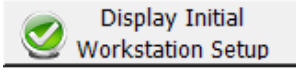
17 Under **Select PCR plate labware for Thermal Cycling**, select the specific type of PCR plate that was loaded on Bravo deck positions 4 and 6. The plate type selected must be compatible with the thermal cycler to be used for incubation steps during the protocol.

NOTE During run setup, be sure to use the plate type selected from this menu at positions 4 and 6 of the Bravo deck. In addition, when the workstation issues prompts to add plates to postion 4 or 6 during the run, use only the same PCR plate type specified here.

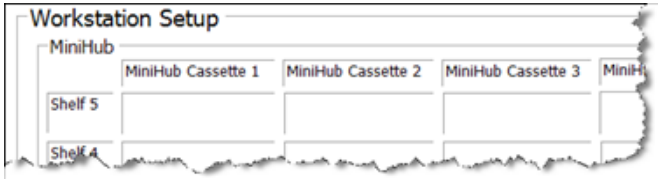
18 Select the number of columns of samples to be processed. Runs must include 1, 2, 3, 4, 6, or 12 columns.



19 Click **Display Initial Workstation Setup**.



20 Verify that the NGS workstation has been set up as displayed in the Workstation Setup region of the form.



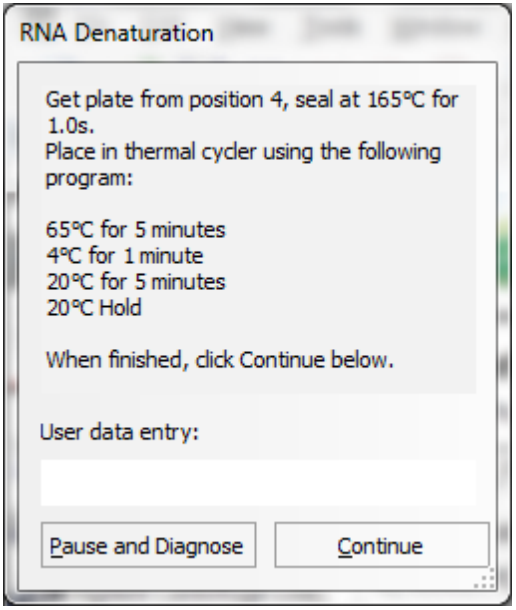
21 When verification is complete, click **Run Selected Protocol**.

NOTE If workstation devices do not respond when you start the run, but activity is recorded in the Log, verify that VWorks is not running in Simulation mode. See page 27 for more information.

Running the mRNA_Purification_v1.0.pro protocol takes approximately 90 minutes, including four incubation periods on the thermal cycler.

During the automation protocol run, a workstation operator must be present to transfer plates between the workstation and thermal cycler when prompted, as detailed on the following pages.

22 When the workstation has finished combining the RNA samples with the oligo(dT) beads, you will be prompted by VWorks as shown below.



a Remove the plate from position 4 of the Bravo deck and seal the plate using the PlateLoc Thermal Microplate Sealer, with sealing settings of 165°C and 1.0 seconds.

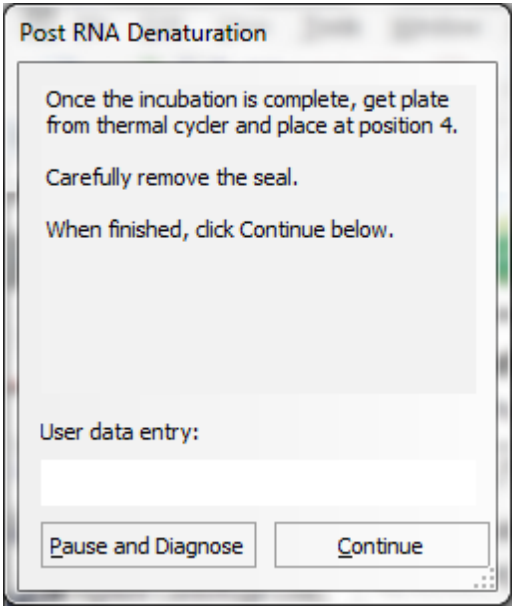
b Briefly spin the plate in a centrifuge or mini-plate spinner to collect the liquid without pelleting the beads.

c Transfer the PCR plate to a thermal cycler (with the heated lid ON) and run the RNA denaturation + bead binding program shown in Table 13. After transferring the plate, click **Continue** on the VWorks screen.

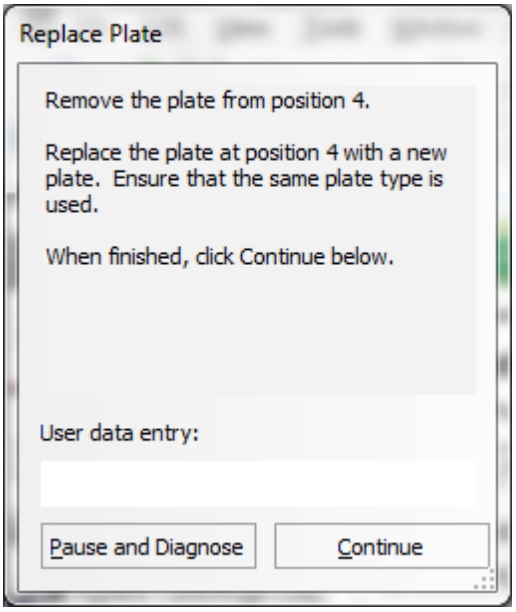
Table 13 Thermal cycler program for RNA denaturation and RNA-bead binding

Step	Temperature	Time
Step 1	65°C	5 minutes
Step 2	4°C	1 minute
Step 3	20°C	5 minutes
Step 4	20°C	Hold

23 After the thermal cycler reaches the 20°C Hold step, and when prompted by the dialog below, transfer the RNA sample plate to position 4 of the Bravo deck, seated in the red insert. Carefully unseal the plate, then click **Continue**.



24 When the workstation has finished collecting and washing the bead-bound RNA samples, you will be prompted by VWorks as shown below.

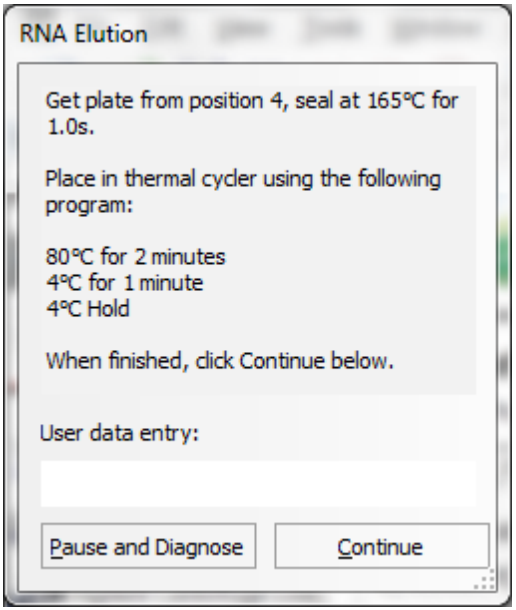


a Remove and discard the PCR plate from position 4 of the Bravo deck.

b Place a fresh PCR plate at position 4, seated in the red insert. The PCR plate type added here must be the same plate type as the one removed and as was specified during the run setup.

c After positioning the plate, click **Continue** on the VWorks screen.

25 When the workstation has finished collecting and washing the bead-bound RNA samples, you will be prompted to transfer the plate to the thermal cycler for the RNA Elution step as shown below.



a Remove the plate from position 4 of the Bravo deck and seal the plate using the PlateLoc Thermal Microplate Sealer, with sealing settings of 165°C and 1.0 seconds.

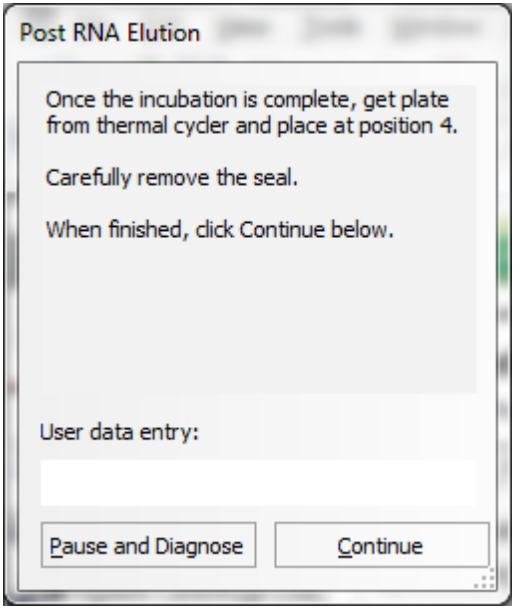
b Briefly spin the plate in a centrifuge or mini-plate spinner to collect the liquid without pelleting the beads.

c Transfer the PCR plate to a thermal cycler (with the heated lid ON) and run the RNA elution program shown in Table 14. After transferring the plate, click **Continue** on the VWorks screen.

Table 14 Thermal cycler program for RNA elution

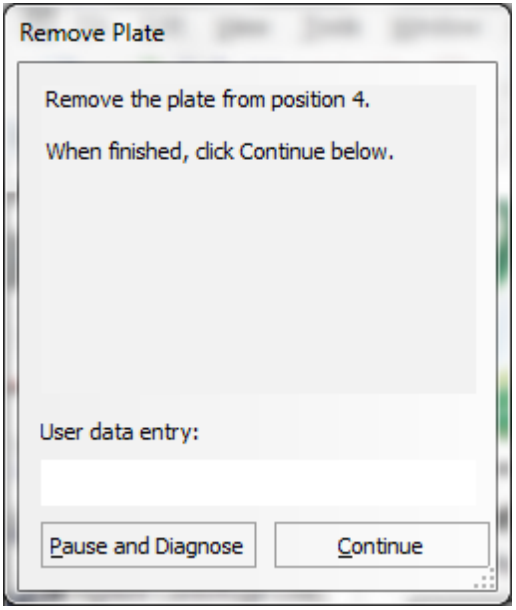
Step	Temperature	Time
Step 1	80°C	2 minutes
Step 2	4°C	1 minute
Step 3	4°C	Hold

26 After the thermal cycler reaches the 4°C Hold step and when prompted by the dialog below, transfer the RNA sample plate to position 4 of the Bravo deck, seated in the red insert. Carefully unseal the plate, then click **Continue**.

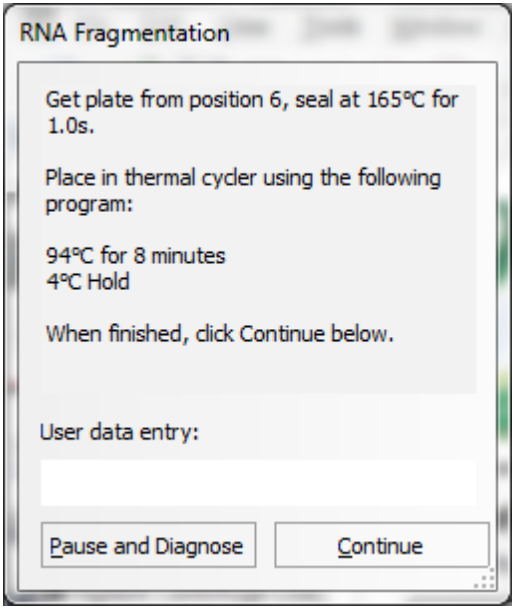


27 The workstation adds RNA Seq Bead Binding Buffer to the eluted RNA samples and then holds the samples at room temperature for 5 minutes to allow the poly(A) RNA to re-bind the beads.

28 When the workstation has finished the collecting and washing the bound RNA samples in this second round of purification, you will be prompted by VWorks as shown below. Remove and discard the PCR plate from position 4, then click **Continue**.



29 The workstation adds RNA Seq Fragmentation Mix to the bead-bound RNA samples in preparation for the RNA fragmentation step. When the workstation has finished, you will be prompted by VWorks as shown below.



a Remove the 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 1.0 seconds.

b Briefly spin the plate in a centrifuge or mini-plate spinner to collect the liquid.

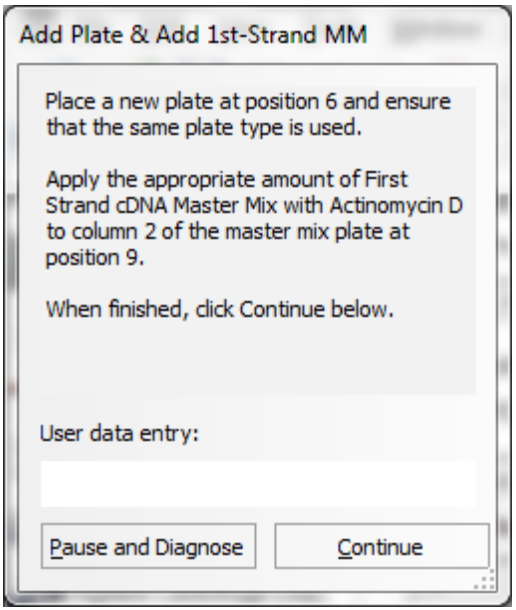
c Transfer the PCR plate to a thermal cycler (with the heated lid ON) and run the RNA fragmentation program shown in Table 15. After transferring the plate, click **Continue** on the VWorks screen.

Table 15 Thermal cycler program for RNA fragmentation

Step	Temperature	Time
Step 1	94°C	8 minutes
Step 2	4°C	Hold

30 During the 8-minute incubation step, prepare the reagents and workstation for first-strand cDNA synthesis:

a When prompted by the dialog below, place a fresh PCR plate (use the plate type specified during the run setup) at position 6, seated in the red insert. Proceed immediately to step b, below.



b Prepare a fresh 120 ng/µL Actinomycin D dilution in water from a stock solution of 4 µg/µL Actinomycin D in DMSO, according to Table 16.

Table 16 Preparation of 120 ng/µl Actinomycin D

Reagent	Volume for up to 12-column run (includes excess)
Actinomycin D (4 µg/µl in DMSO)	3 µL
Nuclease-free water	97 µL
Total	**100 µL**

c Prepare the appropriate amount of RNA Seq First Strand Master Mix + Actinomycin D mixture, on ice, according to the table below.

CAUTION SureSelect Strand Specific RNA Library Prep master mixes are viscous. Mix thoroughly by vortexing before removing an aliquot for use and after combining the master mixes with other solutions.

Table 17 Preparation of First Strand Master Mix/Actinomycin D 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
RNA Seq First Strand Master Mix	8.0 µL	98.4 µL	196.8 µL	262.4 µL	360.8 µL	492.0 µL	918.4 µL
Actinomycin D (120 ng/µl in H_2O)	0.5 µL	6.2 µL	12.3 µL	16.4 µL	22.6 µL	30.8 µL	57.4 µL
Total Volume	**8.5 µL**	**104.6 µL**	**209.1 µL**	**278.8 µL**	**383.4 µL**	**522.8 µL**	**975.8 µL**

d Add the volume listed in Table 18 of the First Strand Master Mix + Actinomycin D mixture to column 2 of the Master Mix source plate at position 9 of the Bravo deck. The final configuration of the source plate is shown in Figure 6. After adding the master mix to the source plate, click **Continue** on the VWorks screen.

Table 18 Preparation of the Master Mix Source Plate for mRNA_Purification_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
RNA Seq First Strand Master Mix + Actinomycin D mixture	Column 2 (A2-H2)	12.0 µL	25.1 µL	33.8 µL	46.9 µL	64.3 µL	120.9 µL

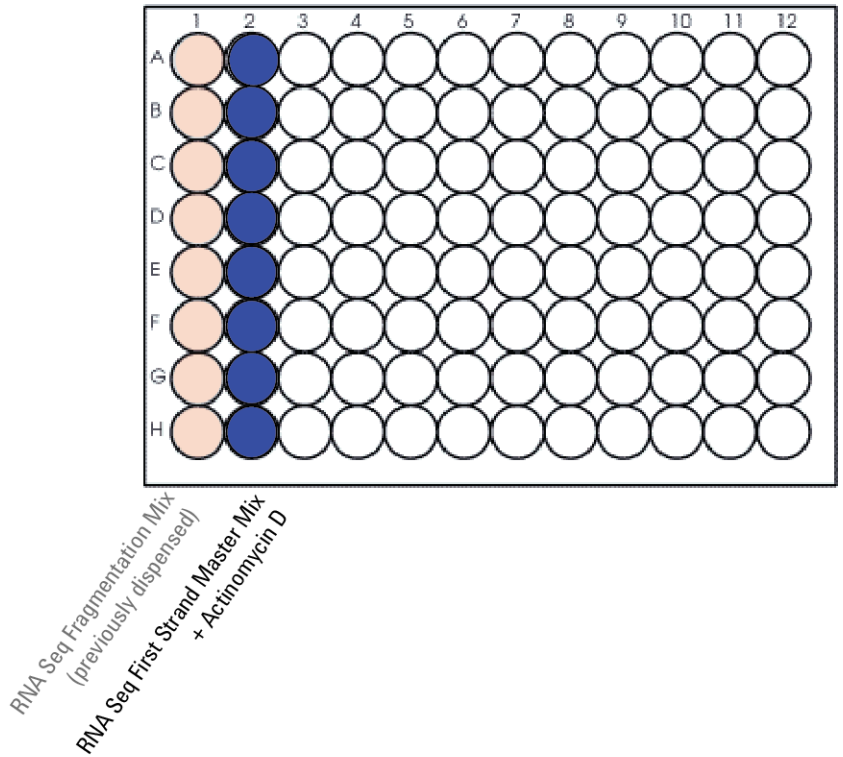
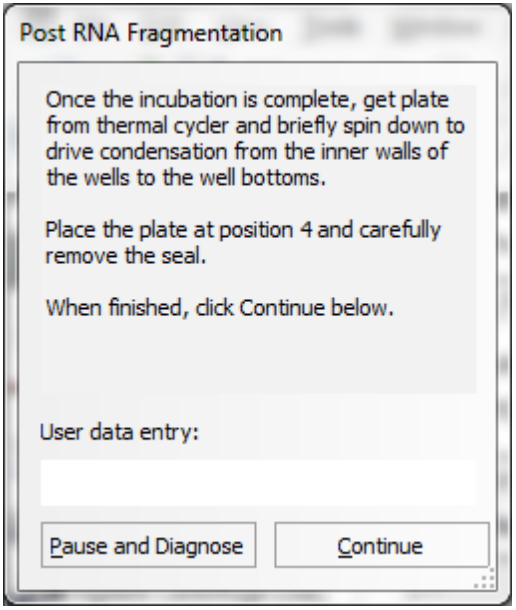


Figure 5 Final configuration of master mix source plate for mRNA_Purification_v1.0.pro

31 With the RNA sample plate still on the thermal cycler, the workstation prepares the remaining components for first-strand cDNA synthesis. When the workstation has finished, you will be prompted by VWorks as shown below.

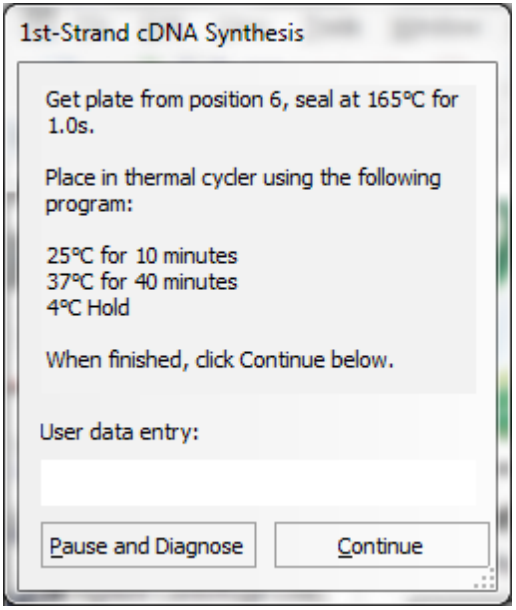


a After the thermal cycler reaches the 4°C Hold step for the RNA fragmentation program (Table 15), remove the plate from the thermal cycler and briefly spin in a centrifuge or mini-plate spinner to collect the liquid.

b Place the RNA sample plate on position 4 of the Bravo deck, seated in the red insert.

c Carefully unseal the plate, then click **Continue.**

32 The workstation removes the fragmented RNA samples from the bead-containing wells and combines the samples with RNA Seq First Strand Master Mix + Actinomycin D. When the workstation has finished, you will be prompted by VWorks as shown below.



a Remove the 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 1.0 seconds.

b Briefly spin the plate in a centrifuge or mini-plate spinner to collect the liquid.

c Transfer the PCR plate to a thermal cycler (with the heated lid ON) and run the first-strand cDNA synthesis program shown in Table 19. After transferring the plate, click **Continue** on the VWorks screen.

Table 19 Thermal cycler program for first-strand cDNA synthesis

Step	Temperature	Time
Step 1	25°C	10 minutes
Step 2	37°C	40 minutes
Step 3	4°C	Hold

Step 2. Purify first-strand cDNA using AMPure XP beads

In this step, the Agilent NGS Workstation transfers AMPure XP beads and first-strand cDNA samples to a Nunc DeepWell plate and then collects and washes the bead-bound DNA.

Prepare the workstation and reagents

1. Leave tip boxes on shelves 1 and 2 in casette 1 of the Labware MiniHub from the previous mRNA_Purification_v1.0.pro run. Otherwise, clear the remaining positions of the MiniHub and BenchCel of plates and tip boxes.
2. Gently wipe down the Labware MiniHub, Bravo deck, and BenchCel with a NucleoClean decontamination wipe.
3. Turn on the ThermoCube, set to 0°C, at position 9 of the Bravo deck. Be sure that the chiller reservoir contains at least 300 mL of 25% ethanol.
4. Let the AMPure XP beads come to room temperature for at least 30 minutes. *Do not freeze the beads at any time.*
5. Mix the bead suspension well so that the reagent appears homogeneous and consistent in color.
6. Prepare a Nunc DeepWell source plate for the beads by adding 51 µL of homogeneous AMPure XP beads per well, for each well to be processed.
7. Prepare a Thermo Scientific reservoir containing 15 mL of nuclease-free water.
8. Prepare a separate Thermo Scientific reservoir containing 45 mL of freshly-prepared 70% ethanol.

9 Load the Labware MiniHub according to Table 20, using the plate orientations shown in Figure 4.

Table 20 Initial MiniHub configuration for AMPureXP_v1.1.pro:First Strand

Vertical Shelf Position	Cassette 1	Cassette 2	Cassette 3	Cassette 4
Shelf 5 (Top)	Empty Nunc DeepWell plate	Empty	Empty	Empty
Shelf 4	Empty	Empty	Empty	Empty
Shelf 3	Empty	Empty Eppendorf twin.tec Plate	Empty	Empty
Shelf 2	Waste tip box (retained from mRNA_Purification protocol)*	Nuclease-free water reservoir from step 7	AMPure XP beads in Nunc DeepWell plate from step 6	Empty
Shelf 1 (Bottom)	Clean tip box (retained from mRNA_Purification protocol)*	70% ethanol reservoir from step 8	Empty	Empty tip box

* The tip boxes retained in Cassette 1 are not shown on the VWorks Workstation Setup table. These tip boxes are not used in AMPureXP_v1.1.pro:First Strand but are used in a later protocol. This labware should be retained in the MiniHub to ensure that empty and full tip positions are properly defined for the subsequent protocol.

10 Load the Bravo deck according to Table 21.

Table 21 Initial Bravo deck configuration for AMPureXP_v1.1.pro:First Strand

Location	Content
1	Empty waste reservoir (Axygen 96 Deep Well Plate, square wells)
9	First-strand cDNA samples in PCR plate seated on red insert (PCR plate type must be specified on setup form under step 2)

11 Load the BenchCel Microplate Handling Workstation according to Table 22.

Table 22 Initial BenchCel configuration for AMPureXP_v1.1.pro:First Strand

No. of Columns Processed	Rack 1	Rack 2	Rack 3	Rack 4
1	1 Tip box	Empty	Empty	Empty
2	1 Tip box	Empty	Empty	Empty
3	2 Tip boxes	Empty	Empty	Empty
4	2 Tip boxes	Empty	Empty	Empty
6	3 Tip boxes	Empty	Empty	Empty
12	6 Tip boxes	Empty	Empty	Empty

Run VWorks protocol AMPureXP_v1.1.pro:First Strand

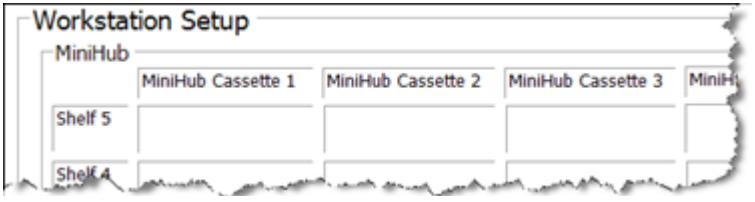
12 On the SureSelect setup form, under **Select Protocol to Run**, select **AMPureXP_v1.1.pro:First Strand.**

13 Under **Select PCR plate labware for Thermal Cycling**, select the specific type of PCR plate containing the cDNA samples at position 9.

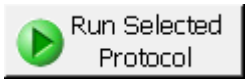
14 Select the number of columns of samples to be processed. Runs must include 1, 2, 3, 4, 6, or 12 columns.

15 Click **Display Initial Workstation Setup**.

16 Verify that the NGS workstation has been set up as displayed in the Workstation Setup region of the form.



17 When verification is complete, click **Run Selected Protocol**.



Running the AMPureXP_v1.1.pro:First Strand protocol takes approximately 45 minutes. During this time, you can prepare the purification reagents for the Library Prep automation protocol, as described on page 59.

Once the AMPureXP_v1.1.pro:First Strand protocol is complete, the purified cDNA samples are located in the Eppendorf plate at position 7 of the Bravo deck. Proceed immediately to "Step 3. Prepare cDNA libraries for Hybridization" on page 58.

Step 3. Prepare cDNA libraries for Hybridization

This step is automated using the LibraryPrep_RNASeq_ILM_v1.1.rst runset. During the runset, the Agilent NGS Workstation completes second-strand cDNA library synthesis and end modification steps, including end-repair, A-tailing, and adaptor ligation. After certain modification steps, the Agilent NGS Workstation purifies the prepared cDNA using AMPure XP beads.

This step uses the SureSelect^{XT} RNA Reagent Kit components listed in Table 23 in addition to the purification reagents prepared for use on page 59. Thaw each reagent vial and keep on ice. Vortex each vial for 5 seconds to mix before use.

Table 23 Reagents for automation runset LibraryPrep_RNASeq_ILM_v1.1.rst

Kit Component	Storage Location	Where Used
RNA Seq Second Strand + End Repair Enzyme Mix	SureSelect Strand-Specific RNA Library Prep Kit, ILM, Box 1, –20°C	page 60
RNA Seq Second Strand + End Repair Oligo Mix	SureSelect Strand-Specific RNA Library Prep Kit, ILM, Box 1, –20°C	page 60
SureSelect Ligation Master Mix	SureSelect Strand-Specific RNA Library Prep Kit, ILM, Box 1, –20°C	page 60
SureSelect Oligo Adaptor Mix	SureSelect Strand-Specific RNA Library Prep Kit, ILM, Box 1, –20°C	page 60
RNA Seq dA Tailing Master Mix	SureSelect Strand-Specific RNA Library Prep Kit, ILM, Box 1, –20°C	page 61

CAUTION SureSelect Strand Specific RNA Library Prep master mixes are viscous. Mix thoroughly by vortexing before removing an aliquot for use and after combining the master mixes with other solutions.

Prepare the workstation

1. Turn on the ThermoCube, set to 0°C, at position 9 of the Bravo deck. Be sure that the chiller reservoir contains at least 300 mL of 25% ethanol.
2. Leave tip boxes on shelves 1 and 2 in casette 1 of the Labware MiniHub from the previous mRNA_Purification_v1.0.pro run. Otherwise, clear the remaining MiniHub and BenchCel positions of plates and tip boxes.
3. Pre-set the temperature of Bravo deck position 4 to 14°C and of position 6 to 4°C using the Inheco Multi TEC control touchscreen, as described in Setting the Temperature of Bravo Deck Heat Blocks. On the control touchscreen, Bravo deck positions 4 corresponds to CPAC 2, position 1, while deck position 6 corresponds to CPAC 2, position 2.

Prepare the purification reagents

4. Verify that the AMPure XP bead suspension is at room temperature. *Do not freeze the beads at any time.*
5. Mix the bead suspension well so that the reagent appears homogeneous and consistent in color.
6. Prepare a Nunc DeepWell source plate for the beads by adding 160 µL of homogeneous AMPure XP beads per well, for each well to be processed.
7. Prepare a Thermo Scientific reservoir containing 20 mL of nuclease-free water.
8. Prepare a separate Thermo Scientific reservoir containing 150 mL of freshly-prepared 70% ethanol.

Prepare the master mix source plate

9 Prepare the appropriate amount of RNA Seq Second Strand + End Repair Master Mix according to Table 24 below.

Table 24 Preparation of RNA Seq Second Strand + End Repair Master Mix for LibraryPrep_RNASeq_ILM_v1.1.rst

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
RNA Seq Second Strand + End Repair Enzyme Mix	25.0 µL	307.5 µL	615 µL	820 µL	1127.5 µL	1640 µL	3075 µL
RNA Seq Second Strand + End Repair Oligo Mix	5.0 µL	61.5 µL	123 µL	164 µL	225.5 µL	328 µL	615 µL
Total Volume	**30 µL**	**369 µL**	**738 µL**	**984 µL**	**1353 µL**	**1968 µL**	**3690 µL**

10 Prepare the appropriate amount of Adaptor Ligation Master Mix, containing the SureSelect Ligation Master Mix and the adaptors, according to Table 25 below.

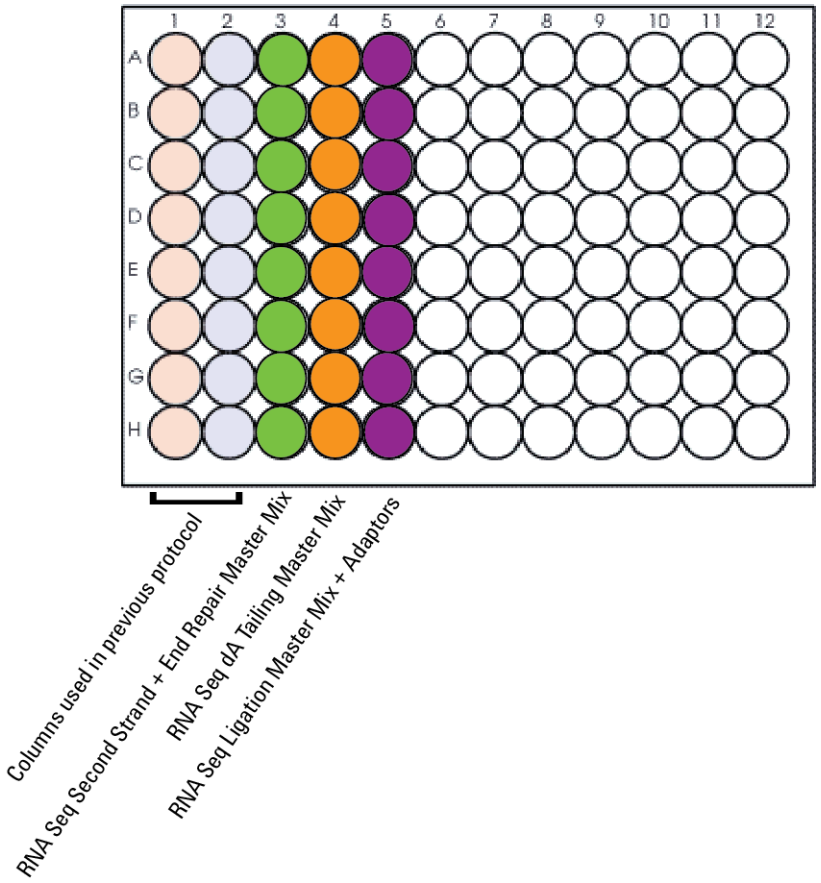
Table 25 Preparation of Adaptor Ligation Master Mix for LibraryPrep_RNASeq_ILM_v1.1.rst

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	30.8 µL	61.5 µL	82.0 µL	112.8 µL	164.0 µL	307.5 µL
SureSelect Ligation Master Mix	5.0 µL	61.5 µL	123.0 µL	164.0 µL	225.5 µL	328.0 µL	615.0 µL
SureSelect Oligo Adaptor Mix	5.0 µL	61.5 µL	123.0 µL	164.0 µL	225.5 µL	328.0 µL	615.0 µL
Total Volume	**12.5 µL**	**153.8 µL**	**307.5 µL**	**410.0 µL**	**563.8 µL**	**820.0 µL**	**1537.5 µL**

11 Using the same Nunc DeepWell master mix source plate that was used for the mRNA_Purification_v1.0.pro run, prepare the Library Prep master mix source plate. Add the volumes indicated in Table 26 of each master mix to all wells of the indicated column of the plate. Keep the master mixes on ice during the aliquoting steps. The final configuration of the master mix source plate is shown in Figure 6.

Table 26 Preparation of the Master Mix Source Plate for LibraryPrep_RNASeq_ILM_v1.1.rst

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
RNA Seq Second Strand + End Repair Master Mix (from Table 24)	Column 3 (A3-H3)	42.4 µL	88.5 µL	119.3 µL	165.4 µL	242.3 µL	457.5 µL
RNA Seq dA Tailing Master Mix	Column 4 (A4-H4)	30.0 µL	50.0 µL	70.0 µL	90.0 µL	130.0 µL	260.0 µL
Adaptor Ligation Master Mix (from Table 25)	Column 5 (A5-H5)	17.7 µL	36.9 µL	49.7 µL	68.9 µL	100.9 µL	190.6 µL



NOTE If you are using a new DeepWell plate for the Library Prep Master Mix source plate, leave columns 1 and 2 empty and add the PCR Master Mix to columns 3 to 5 of the new plate.

Figure 6 Configuration of the master mix source plate for LibraryPrep_RNASeq_ILM_v1.1.rst

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

13 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.

Load the Agilent NGS Workstation

14 Load the Labware MiniHub according to Table 27, using the plate orientations shown in Figure 4.

Table 27 Initial MiniHub configuration for LibraryPrep_RNASeq_ILM_v1.1.rst

Vertical Shelf Position	Cassette 1	Cassette 2	Cassette 3	Cassette 4
Shelf 5 (Top)	Empty	Empty Nunc DeepWell plate	Empty Nunc DeepWell plate	Empty
Shelf 4	Empty	Empty Eppendorf twin.tec plate	Empty Eppendorf twin.tec plate	Empty
Shelf 3	Empty	Empty	Empty Eppendorf twin.tec plate	Empty
Shelf 2	Waste tip box (retained from mRNA_Purification protocol)	Nuclease-free water reservoir from step 7	AMPure XP beads in Nunc DeepWell plate from step 6	Empty
Shelf 1 (Bottom)	Clean tip box (retained from mRNA_Purification protocol)	70% ethanol reservoir from step 8	Empty	Empty tip box

15 Load the Bravo deck according to Table 28.

Table 28 Initial Bravo deck configuration for LibraryPrep_RNASeq_ILM_v1.1.rst

Location	Content
1	Empty waste reservoir (Axygen 96 Deep Well Plate, square wells)
6	Empty Eppendorf twin.tec plate, oriented with well A1 in the upper-left
7	Purified first-strand cDNA samples in Eppendorf twin.tec plate, oriented with well A1 in the upper-left
9	Library Prep Master Mix Source Plate (Nunc DeepWell), unsealed and seated on silver insert

16 Load the BenchCel Microplate Handling Workstation according to Table 29.

Table 29 Initial BenchCel configuration for LibraryPrep_RNASeq_ILM_v1.1.rst

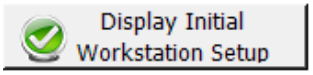
No. of Columns Processed	Rack 1	Rack 2	Rack 3	Rack 4
1	2 Tip boxes	Empty	Empty	Empty
2	3 Tip boxes	Empty	Empty	Empty
3	4 Tip boxes	Empty	Empty	Empty
4	5 Tip boxes	Empty	Empty	Empty
6	7 Tip boxes	Empty	Empty	Empty
12	11 Tip boxes	3 Tip boxes	Empty	Empty

Run VWorks runset LibraryPrep_RNASeq_ILM_v1.1.rst

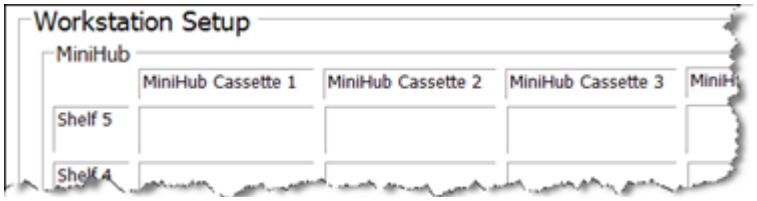
17 On the SureSelect setup form, under **Select Protocol to Run**, select **LibraryPrep_RNASeq_ILM_v1.1.rst.**

18 Select the number of columns of samples to be processed. Runs must include 1, 2, 3, 4, 6, or 12 columns.

19 Click **Display Initial Workstation Setup**.

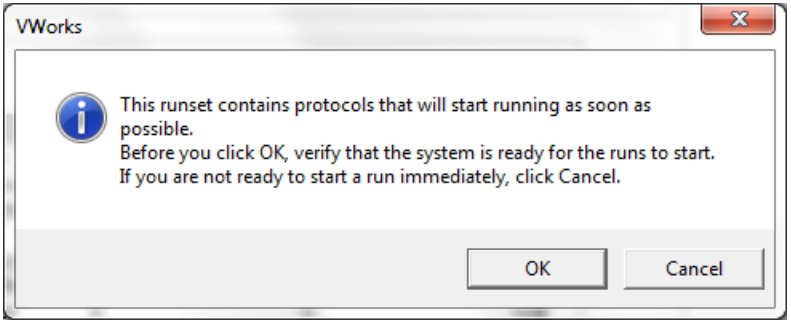


20 Verify that the NGS workstation has been set up as displayed in the Workstation Setup region of the form.



21 When verification is complete, click **Run Selected Protocol**.

22 When ready to begin the run, click **OK** in the following window.



Running the LibraryPrep_RNASeq_ILM_v1.1.rst runset takes approximately 3 hours. Once complete, the purified, adaptor-ligated cDNA samples are located in the Eppendorf plate at position 7 of the Bravo deck.

Stopping Point If you do not continue to the next step, seal the plate and store at –20°C.

Step 4. Amplify cDNA libraries by PCR

In this step, the Agilent NGS Workstation completes the liquid handling steps for PCR amplification of the adaptor-ligated cDNA samples. After the reactions are set up by the workstation, you transfer the PCR plate to a thermal cycler for amplification. The amplification cycle number is based on the initial amount of total RNA sample used for library preparation.

Use the SureSelect Strand Specific RNA Library Prep Kit, Box 1 for this step. Thaw and mix the reagents listed in Table 30 below and keep on ice.

CAUTION SureSelect Strand Specific RNA Library Prep master mixes are viscous. Mix thoroughly by vortexing before removing an aliquot for use and after combining the master mixes with other solutions.

Prepare the workstation

1. Turn on the ThermoCube, set to 0°C, at position 9 of the Bravo deck. Be sure that the chiller reservoir contains at least 300 mL of 25% ethanol.
2. Leave tip boxes on shelves 1 and 2 in casette 1 of the Labware MiniHub from the previous LibraryPrep_RNASeq_v1.0.rst run. Otherwise, clear the remaining positions of the MiniHub and BenchCel of plates and tip boxes.
3. Pre-set the temperature of Bravo deck position 6 to 4°C using the Inheco Multi TEC control touchscreen, as described in Setting the Temperature of Bravo Deck Heat Blocks. Bravo deck position 6 corresponds to CPAC 2, position 2 on the Multi TEC control touchscreen.

Prepare the PCR reaction mix and the master mix source plate

4 Prepare the appropriate volume of PCR Reaction Mix, according to Table 30. Mix well using a vortex mixer and keep on ice.

Table 30 Preparation of PCR Reaction Mix

SureSelect 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	5.0 µL	61.5 µL	102.5 µL	143.5 µL	184.5 µL	266.5 µL	533.0 µL
RNA Seq PCR Master Mix	25.0 µL	307.5 µL	512.5 µL	717.5 µL	922.5 µL	1332.5 µL	2665 µL
Uracil DNA Glycosylase (UDG)	1.0 µL	12.3 µL	20.5 µL	28.7 µL	36.9 µL	53.3 µL	106.6 µL
SureSelect Primer (Forward primer)	1.0 µL	12.3 µL	20.5 µL	28.7 µL	36.9 µL	53.3 µL	106.6 µL
RNA Seq ILM Reverse PCR Primer	1.0 µL	12.3 µL	20.5 µL	28.7 µL	36.9 µL	53.3 µL	106.6 µL
Total Volume	**33 µL**	**405.9 µL**	**676.5 µL**	**947.1 µL**	**1217.7 µL**	**1758.9 µL**	**3517.8 µL**

5 Using the same Nunc DeepWell master mix source plate that was used for the LibraryPrep_RNASeq_ILM_v1.1.rst run, add the volume of PCR Master Mix indicated in Table 31 to all wells of column 6 of the master mix source plate. The final configuration of the master mix source plate is shown in Figure 7.

Table 31 Preparation of the Master Mix Source Plate for Pre-CapturePCR_RNASeq_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 Reaction Mix	Column 6 (A6-H6)	48.6 µL	80.4 µL	114.3 µL	148.1 µL	215.7 µL	435.6 µL

NOTE If you are using a new DeepWell plate for the pre-capture PCR source plate, leave columns 1 to 5 empty and add the PCR Master Mix to column 6 of the new plate.

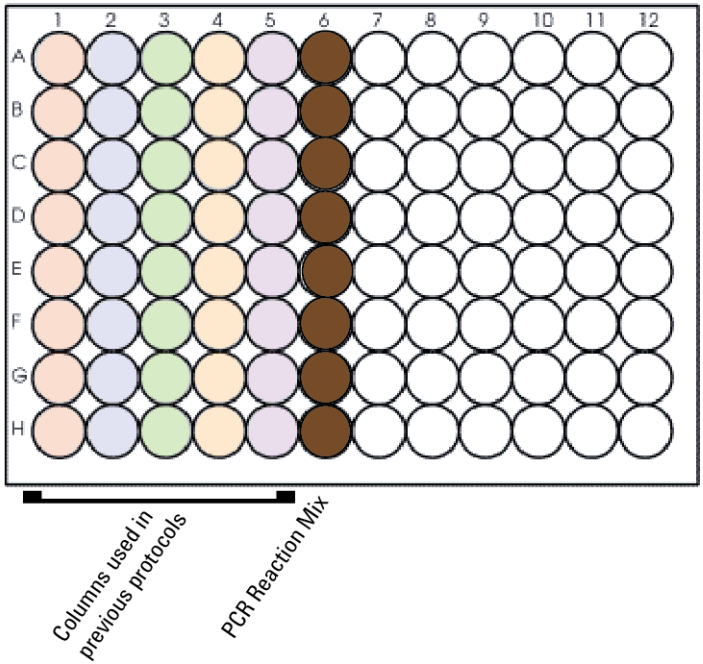


Figure 7 Configuration of the master mix source plate for Pre-CapturePCR_RNASeq_ILM_v1.0.pro. Columns 1-5 were used to dispense master mixes during previous protocols.

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.

Load the Agilent NGS Workstation

8 Load the Labware MiniHub according to Table 32, using the plate orientations shown in Figure 4.

Table 32 Initial MiniHub configuration for Pre-CapturePCR_RNASeq_ILM_v1.0.pro

Vertical Shelf Position	Cassette 1	Cassette 2	Cassette 3	Cassette 4
Shelf 5 (Top)	Empty	Empty	Empty	Empty
Shelf 4	Empty	Empty	Empty	Empty
Shelf 3	Empty	Empty	Empty	Empty
Shelf 2	Waste tip box (retained from Library Prep protocol)	Empty	Empty	Empty
Shelf 1 (Bottom)	Clean tip box (retained from Library Prep protocol)	Empty	Empty	Empty tip box

9 Load the Bravo deck according to Table 33.

Table 33 Initial Bravo deck configuration for Pre-CapturePCR_RNASeq_ILM_v1.0.pro

Location	Content
6	Empty PCR plate seated on red insert (PCR plate type must be specified on setup form under step 2)
7	Prepped cDNA samples in Eppendorf twin.tec plate, oriented with well A1 in the upper-left
9	Master mix source plate (Nunc DeepWell), unsealed and seated on silver insert

10 Load the BenchCel Microplate Handling Workstation according to Table 34.

Table 34 Initial BenchCel configuration for Pre-CapturePCR_RNASeq_ILM_v1.0.pro

No. of Columns Processed	Rack 1	Rack 2	Rack 3	Rack 4
1	1 Tip box	Empty	Empty	Empty
2	1 Tip box	Empty	Empty	Empty
3	1 Tip box	Empty	Empty	Empty
4	1 Tip box	Empty	Empty	Empty
6	1 Tip box	Empty	Empty	Empty
12	1 Tip box	Empty	Empty	Empty

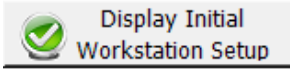
Run VWorks protocol Pre-CapturePCR_RNASeq_ILM_v1.0.pro

11 On the SureSelect setup form, under **Select Protocol to Run**, select **Pre-CapturePCR_RNASeq_ILM_v1.0.pro.**

12 Under **Select PCR plate labware for Thermal Cycling**, select the specific type of PCR plate that was loaded on Bravo deck position 6. The plate type selected must be compatible with the thermal cycler to be used for amplification.

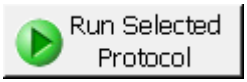
13 Select the number of columns of samples to be processed. Runs must include 1, 2, 3, 4, 6, or 12 columns.

14 Click **Display Initial Workstation Setup**.

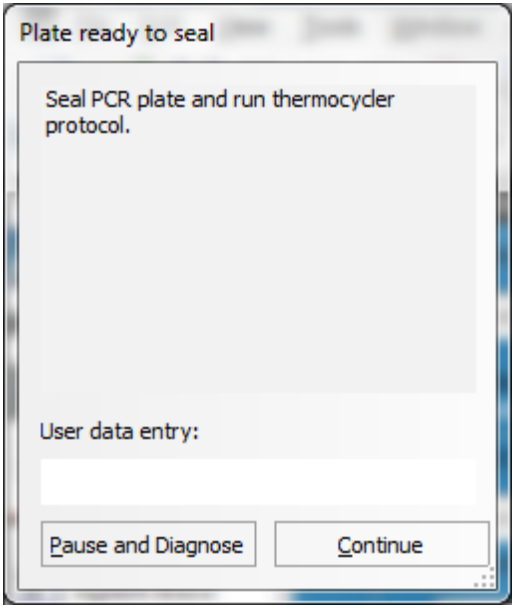


15 Verify that the NGS workstation has been set up as displayed in the Workstation Setup region of the form.

16 When verification is complete, click **Run Selected Protocol**.



17 Running the Pre-CapturePCR_RNASeq_ILM_v1.0.pro protocol takes approximately 15 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 and you will see the following prompt:



a 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.

b Centrifuge the plate for 30 seconds to drive the well contents off the walls and plate seal and to eliminate air bubbles.

c Transfer the plate to the thermal cycler (with the heated lid ON) and run the program in Table 35.

.

Table 35 Thermal cycler program for mRNA Library PCR indexing

Segment	Number of Cycles	Temperature	Time
1	1	37°C	15 minutes
2	1	95°C	2 minutes
3	9–13 cycles (see Table 36)	95°C	30 seconds
		65°C	30 seconds
		72°C	1 minute
4	1	72°C	5 minutes
5	1	4°C	Hold

Table 36 mRNA Library PCR indexing cycle number recommendations

Amount of total RNA used for library prep	Cycle Number
200 ng–2 µg	11–13
2.1 µg–4 µg	9–11

Step 5. Purify amplified DNA using AMPure XP beads

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

Prepare the workstation and reagents

1. Clear the Labware MiniHub and BenchCel of all plates and tip boxes.
2. Gently wipe down the Labware MiniHub, Bravo deck, and BenchCel with a NucleoClean decontamination wipe.
3. Turn on the ThermoCube, set to 0°C, at position 9 of the Bravo deck. Be sure that the chiller reservoir contains at least 300 mL of 25% ethanol.
4. Let the AMPure XP beads come to room temperature for at least 30 minutes. *Do not freeze the beads at any time.*
5. Mix the bead suspension well so that the reagent appears homogeneous and consistent in color.
6. Prepare a Nunc DeepWell source plate for the beads by adding 65 µL of homogeneous AMPure XP beads per well, for each well to be processed.
7. Prepare a Thermo Scientific reservoir containing 15 mL of nuclease-free water.
8. Prepare a separate Thermo Scientific reservoir containing 45 mL of freshly-prepared 70% ethanol.

9 Load the Labware MiniHub according to Table 37, using the plate orientations shown in Figure 4.

Table 37 Initial MiniHub configuration for AMPureXP_v1.1.pro:Pre-Capture PCR

Vertical Shelf Position	Cassette 1	Cassette 2	Cassette 3	Cassette 4
Shelf 5 (Top)	Empty Nunc DeepWell plate	Empty	Empty	Empty
Shelf 4	Empty	Empty	Empty	Empty
Shelf 3	Empty	Empty Eppendorf twin.tec Plate	Empty	Empty
Shelf 2	Empty	Nuclease-free water reservoir from step 7	AMPure XP beads in Nunc DeepWell plate from step 6	Empty
Shelf 1 (Bottom)	Empty	70% ethanol reservoir from step 8	Empty	Empty tip box

10 Load the Bravo deck according to Table 38.

Table 38 Initial Bravo deck configuration for AMPureXP_v1.1.pro:Pre-Capture PCR

Location	Content
1	Empty waste reservoir (Axygen 96 Deep Well Plate, square wells)
9	Amplified cDNA samples in PCR plate, unsealed and seated on red insert (PCR plate type must be specified on setup form under step 2)

11 Load the BenchCel Microplate Handling Workstation according to Table 39.

Table 39 Initial BenchCel configuration for AMPureXP_v1.1.pro:Pre-Capture PCR

No. of Columns Processed	Rack 1	Rack 2	Rack 3	Rack 4
1	1 Tip box	Empty	Empty	Empty
2	1 Tip box	Empty	Empty	Empty
3	2 Tip boxes	Empty	Empty	Empty
4	2 Tip boxes	Empty	Empty	Empty
6	3 Tip boxes	Empty	Empty	Empty
12	6 Tip boxes	Empty	Empty	Empty

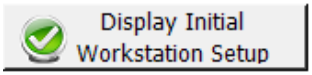
Run VWorks protocol AMPureXP_v1.1.pro:Pre-Capture PCR

12 On the SureSelect setup form, under **Select Protocol to Run**, select **AMPureXP_v1.1.pro:Pre-Capture PCR.**

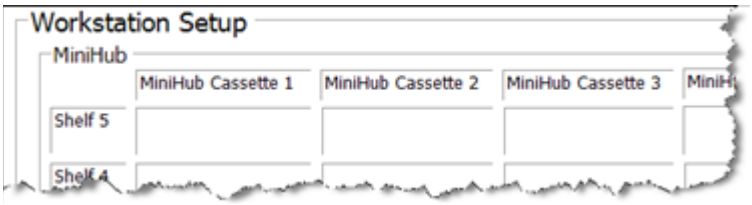
13 Under **Select PCR plate labware for Thermal Cycling**, select the specific type of PCR plate that was loaded on Bravo deck position 9.

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 Workstation Setup**.



16 Verify that the NGS workstation has been set up as displayed in the Workstation Setup region of the form.



17 When verification is complete, click **Run Selected Protocol**.

The purification protocol takes approximately 45 minutes. When complete, the purified DNA samples are in the Eppendorf plate located on Bravo deck position 7.

Stopping Point If you do not continue to the next step, seal the plate and store at –20°C.

Step 6. Assess library DNA quantity and quality

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

Use a Bioanalyzer DNA 1000 chip and reagent kit. For more information to do this step, see the *Agilent DNA 1000 Kit Guide*.

1. Set up the 2100 Bioanalyzer as instructed in the reagent kit guide.
2. Seal the sample plate using the PlateLoc Thermal Microplate Sealer, with sealing settings of 165°C and 1.0 sec.
3. Vortex the plate to mix samples in each well, then centrifuge the plate for 30 seconds to drive the well contents off the walls and plate seal.
4. Prepare the chip, samples and ladder as instructed in the reagent kit guide, using 1 µL of each sample for the analysis.
5. Load the prepared chip into the 2100 Bioanalyzer and start the run within five minutes after preparation.
6. Measure the concentration of the library (ng/µL) by integrating under the peak at approximately 180 to 550 bp. For accurate quantification, make sure that the concentration falls within the linear range of the assay.

   A sample electropherogram is shown in Figure 8.

Stopping Point If you do not continue to the next step, seal the plate and store at –20°C.

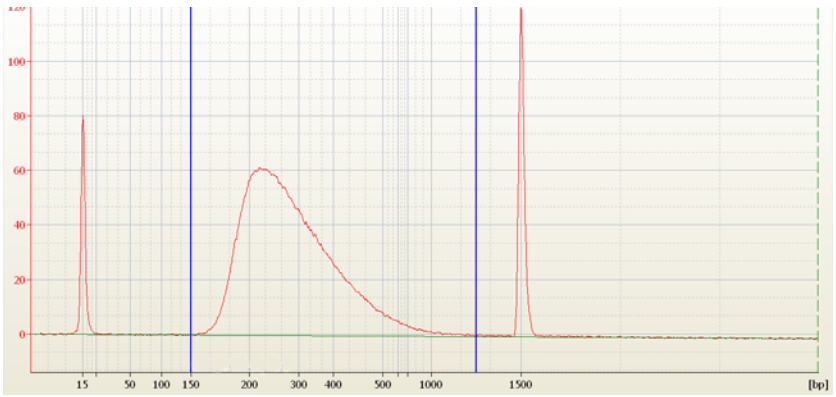


Figure 8 Analysis of amplified library DNA using a DNA 1000 assay.

Option 2: Analysis using the Agilent 2200 TapeStation and D1000 ScreenTape

Use a D1000 ScreenTape and associated reagent kit to analyze the amplified libraries. For more information to do this step, see the *Agilent 2200 TapeStation User Manual*.

1 Seal the DNA sample plate using the PlateLoc Thermal Microplate Sealer, with sealing settings of 165°C and 1.0 sec.

2 Vortex the plate to mix samples in each well, then centrifuge the plate for 30 seconds to drive the well contents off the walls and plate seal.

3 Prepare the TapeStation samples as instructed in the *Agilent 2200 TapeStation User Manual*. Use 1 µL of each amplified library DNA sample diluted with 3 µL of D1000 sample buffer for the analysis.

CAUTION Make sure that you thoroughly mix the combined DNA and D1000 sample buffer on a vortex mixer for 5 seconds for accurate quantitation.

4 Load the sample plate or tube strips from step 3, the D1000 ScreenTape, and loading tips into the 2200 TapeStation as instructed in the *Agilent 2200 TapeStation User Manual*. Start the run.

5 For each sample, measure the concentration of the library (ng/µL) by integrating under the peak at approximately 180 to 550 bp. A sample electropherogram is shown in Figure 9.

Stopping Point If you do not continue to the next step, seal the plate and store at –20°C.

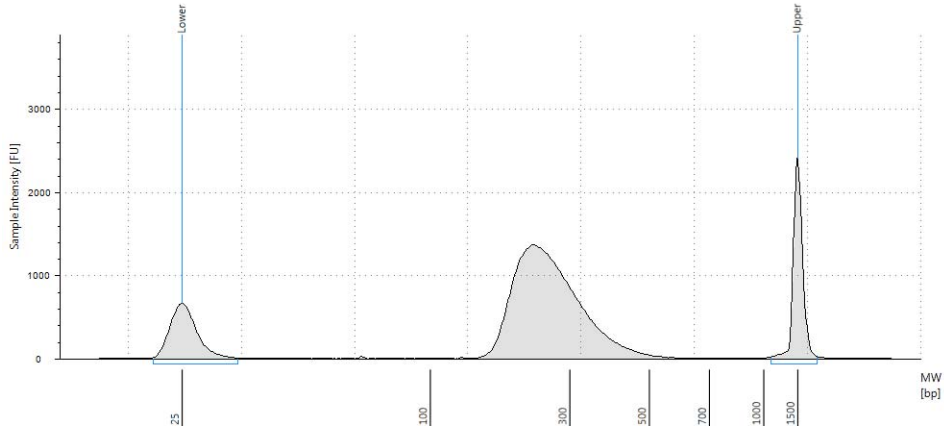


Figure 9 Analysis of amplified library DNA using the Agilent 2200 TapeStation.

4 Hybridization

This chapter describes the steps to combine the prepped library with the blocking agents and the SureSelect RNA capture library. Each cDNA library sample must be hybridized and captured individually prior to addition of the indexing tag by PCR.

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

CAUTION You must avoid evaporation from the small volumes of the capture during the 24 hour incubation.

If you want to use a duration of hybridization >24 hours, first test the conditions. Incubate 35 µL of SureSelect Hybridization Buffer (without DNA) at 65°C for 24 hours (or longer, if applicable) as a test. Include buffer in each well that you might use, including those in the center and those on the edges. Check that you do not get extensive evaporation. Evaporation should not exceed 3 to 4 µL.

Step 1. Aliquot prepped DNA libraries for hybridization

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

Each hybridization reaction will contain 100 ng of the appropriate prepped cDNA sample. Before starting the hybridization step, you must create a table containing instructions for the Agilent NGS Workstation indicating the volume of each sample required for a 100-ng aliquot.

1 Create a .csv (comma separated value) file with the headers shown in Figure 10. 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) equivalent to 100 ng DNA for each sample. These values are determined from the concentration values obtained from Bioanalyzer or TapeStation traces in the previous section. For all empty wells on the plate, enter the value 0, as shown in Figure 10; **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 10 Sample spreadsheet for 100-ng sample aliquot for 1-column run.

NOTE

You can find a sample spreadsheet in the directory **C: > VWorks Workspace > NGS Option B > XT_RNA_ILM> Aliquot Library Input Files > 100ng_transfer_full_plate_template_xlsx.**

The 100ng_transfer_full_plate_template.xlsx file may be copied and used as a template for creating the .csv files for each 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.

3 Load the .csv file onto the PC containing the VWorks software into a suitable folder, such as **C: > VWorks Workspace > NGS Option B > XT RNA_ILM > Aliquot Library Input Files.**

4 Turn on the chiller, set to 0°C, at position 9 of the Bravo deck. Be sure that the chiller reservoir contains at least 300 mL of 25% ethanol.

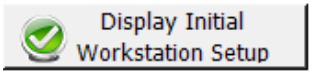
5 Load the Bravo deck according to Table 40.

Table 40 Initial Bravo deck configuration for Aliquot_Libraries_v1.0.pro

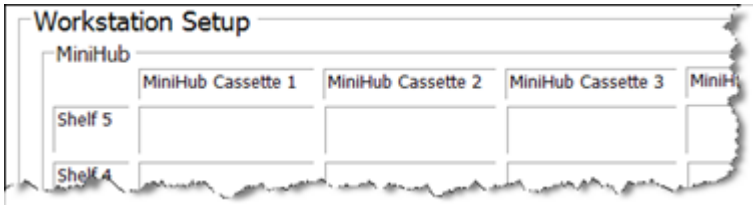
Location	Content
5	Empty PCR plate seated on red insert (PCR plate type must be specified on setup form under step 2)
6	Empty tip box
8	New tip box
9	Prepped library DNA in Eppendorf plate (oriented with well A1 in the upper-left)

6 On the SureSelect setup form, under **Select Protocol to Run**, select **Aliquot_Libraries_v1.0.pro.**

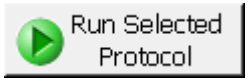
7 Click **Display Initial Workstation Setup**.



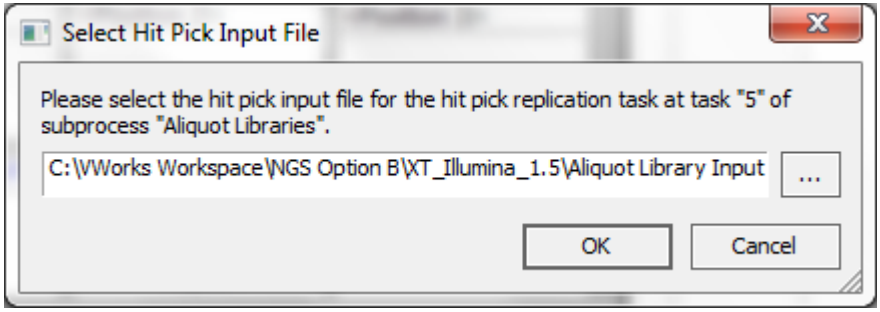
8 Verify that the NGS workstation has been set up as displayed in the Workstation Setup region of the form.



9 When verification is complete, click **Run Selected Protocol**.



10 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 100-ng samples are in the PCR plate located on Bravo deck position 5.

11 Remove the 100-ng sample plate from the Bravo deck and use a vacuum concentrator to dry the sample at ≤ 45°C.

12 Reconstitute each dried sample with 3.4 µL of nuclease-free water to bring the final concentration to 29.4 ng/µL. Pipette up and down along the sides of each well for optimal recovery.

13 Seal the plate using the PlateLoc Thermal Microplate Sealer, with sealing settings of 165°C and 1.0 sec.

14 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 DNA library and SureSelect RNA Capture Library

In this step, the Agilent NGS Workstation completes the liquid handling steps in preparation for hybridization of the prepared cDNA samples to one or more SureSelect capture libraries. Afterward, you transfer the sample plate to a thermal cycler, held at 65°C, to allow hybridization of the DNA sample to the SureSelect capture library.

Prepare the workstation

1. Clear the Labware MiniHub and BenchCel of all plates and tip boxes.
2. Gently wipe down the Labware MiniHub, Bravo decks, and BenchCel with a NucleoClean decontamination wipe.
3. Turn on the ThermoCube and set to 25°C for position 9 of the Bravo deck.
4. Place the silver Nunc DeepWell plate insert on position 9 of the Bravo deck. This insert is required to facilitate heat transfer to DeepWell source plate wells during the Hybridization protocol.

Prepare the SureSelect Block master mix

5 Prepare the appropriate volume of SureSelect Block master mix, on ice, as indicated in Table 41.

Table 41 Preparation of SureSelect Block Master Mix

SureSelect^{XT} 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	6.0 µL	76.5 µL	127.5 µL	178.5 µL	229.5 µL	331.5 µL	663.0 µL
SureSelect Indexing Block #1 (green cap)	2.5 µL	31.9 µL	53.1 µL	74.4 µL	95.6 µL	138.1 µL	276.3 µL
SureSelect Block #2 (blue cap)	2.5 µL	31.9 µL	53.1 µL	74.4 µL	95.6 µL	138.1 µL	276.3 µL
SureSelect Indexing Block #3 (brown cap)	0.6 µL	7.7 µL	12.8 µL	17.9 µL	23.0 µL	33.2 µL	66.3 µL
Total Volume	**11.6 µL**	**147.9 µL**	**246.5 µL**	**345.1 µL**	**443.7 µL**	**640.9 µL**	**1281.9 µL**

Prepare one or more SureSelect Capture Library master mixes

6 Prepare the appropriate volume of SureSelect capture library master mix for each of the capture libraries that will be used for hybridization as indicated in Table 42 to Table 45. Mix the components by pipetting. Keep the master mixes on ice during preparation and aliquoting.

NOTE

Each row of the prepped cDNA sample plate may be hybridized to a different SureSelect Capture Library.

For runs that use a single capture library for all rows of the plate, prepare the master mix as described in Step a (Table 42 or Table 43) below.

For runs that use different capture libraries for individual rows, prepare each master mix as described in Step b (Table 44 or Table 45) below.

a **For runs that use a single capture library for all rows**, prepare the SureSelect Capture Library Master Mix as listed in Table 42 or Table 43, based on the Mb target size of your design.

Table 42 Preparation of Capture Library Master Mix for target sizes <3.0 Mb, 8 rows of wells

Target size <3.0 Mb							
SureSelect^{XT} 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	612.0 µL
RNase Block (purple cap)	0.5 µL	8.5 µL	12.8 µL	17.0 µL	21.3 µL	34.0 µL	68.0 µL
SureSelect Capture Library	2.0 µL	34.0 µL	51.0 µL	68.0 µL	85.0 µL	136.0 µL	272.0 µL
Total Volume	**7.0 µL**	**119.0 µL**	**178.6 µL**	**238.0 µL**	**297.6 µL**	**476.0 µL**	**852.0 µL**

Table 43 Preparation of Capture Library Master Mix for target sizes >3.0 Mb, 8 rows of wells

Target size >3.0 Mb							
SureSelect^{XT} 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	204.0 µL
RNase Block (purple cap)	0.5 µL	8.5 µL	12.8 µL	17.0 µL	21.3 µL	34.0 µL	68.0 µL
SureSelect Capture Library	5.0 µL	85.0 µL	127.5 µL	170.0 µL	212.5 µL	340.0 µL	680.0 µL
Total Volume	**7.0 µL**	**119.0 µL**	**178.6 µL**	**238.0 µL**	**297.6 µL**	**476.0 µL**	**852.0 µL**

b **For runs that use different capture libraries in individual rows**, prepare a SureSelect Capture Library Master Mix for each capture library as listed in Table 44 or Table 45, based on the Mb target size of your design. The volumes listed in Table 44 and Table 45 are for a single row of sample wells. If a given capture library will be hybridized in multiple rows, multiply each of the values below by the number of rows assigned to that capture library.

Table 44 Preparation of Capture Library Master Mix for target sizes <3.0 Mb, single row of wells

Target size <3.0 Mb							
SureSelect^{XT} 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	75.9 µL
RNase Block (purple cap)	0.5 µL	1.0 µL	1.5 µL	2.1 µL	2.6 µL	4.2 µL	8.4 µL
SureSelect Capture Library	2.0 µL	4.0 µL	6.1 µL	8.3 µL	10.4 µL	16.8 µL	33.8 µL
Total Volume	**7.0 µL**	**14.0 µL**	**21.4 µL**	**28.9 µL**	**36.3 µL**	**58.6 µL**	**118.1 µL**

Table 45 Preparation of Capture Library Master Mix for target sizes >3.0 Mb, single row of wells

Target size >3.0 Mb							
SureSelect^{XT} 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	25.3 µL
RNase Block (purple cap)	0.5 µL	1.0 µL	1.5 µL	2.1 µL	2.6 µL	4.2 µL	8.4 µL
SureSelect Capture Library	5.0 µL	10.0 µL	15.3 µL	20.6 µL	25.9 µL	41.9 µL	84.4 µL
Total Volume	**7.0 µL**	**14.0 µL**	**21.4 µL**	**28.9 µL**	**36.3 µL**	**58.6 µL**	**118.1 µL**

Prepare the Hybridization Buffer master mix

7 Prepare the appropriate volume of Hybridization Buffer Master Mix, at room temperature, as indicated in Table 46.

Table 46 Preparation of Hybridization Buffer Master Mix

SureSelect^{XT} Reagent	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 Hyb # 1	140.9 µL	197.3 µL	250.0 µL	310.1 µL	422.8 µL	789.3 µL
SureSelect Hyb # 2 (red cap)	5.6 µL	7.9 µL	10.0 µL	12.4 µL	16.9 µL	31.6 µL
SureSelect Hyb # 3 (yellow cap)	56.4 µL	78.9 µL	100.0 µL	124.0 µL	169.1 µL	315.7 µL
SureSelect Hyb # 4	73.3 µL	102.6 µL	130.0 µL	161.2 µL	219.9 µL	410.4 µL
Total Volume	**276.2 µL**	**386.7 µL**	**490.0 µL**	**607.7 µL**	**828.7 µL**	**1547 µL**

8 If precipitate forms, warm the hybridization buffer at 65°C for 5 minutes.

Prepare the master mix source plate

9 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 47 of each master mix to each well of the indicated column of the Nunc DeepWell plate. When using multiple capture libraries 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 11.

Table 47 Preparation of the Master Mix Source Plate for SureSelectHybridization_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)	17.0 µL	29.4 µL	41.7 µL	54.0 µL	78.7 µL	158.8 µL
Capture Library Master Mix	Column 2 (A2-H2)	14.0 µL	21.4 µL	28.9 µL	36.3 µL	51.2 µL	99.5 µL
Hybridization Buffer Master Mix	Column 3 (A3-H3)	30.5 µL	44.3 µL	57.2 µL	71.9 µL	99.5 µL	189.3 µL

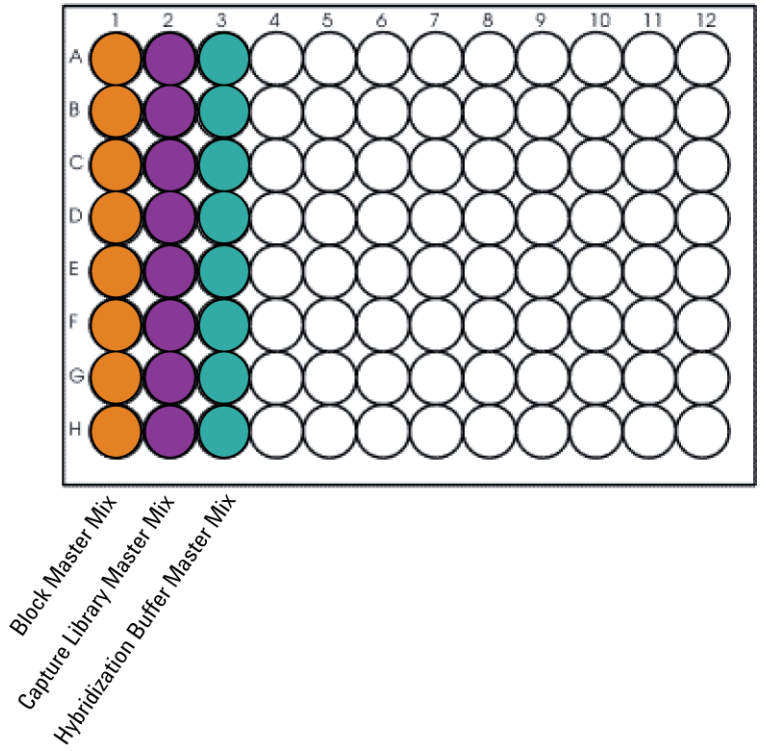


Figure 11 Configuration of the master mix source plate for SureSelectHybridization_v1.0.pro.

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

11 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.

Load the Agilent NGS Workstation

12 Load the Bravo deck according to Table 48.

Table 48 Initial Bravo deck configuration for SureSelectHybridization_v1.0.pro

Location	Content
5	Empty Eppendorf twin.tec plate
6	100-ng aliquots of prepped DNA libraries in PCR plate seated on red insert (PCR plate type must be specified on setup form under step 2)
8	Empty tip box
9	Hybridization Master Mix source plate seated on silver insert

13 Load the BenchCel Microplate Handling Workstation according to Table 49.

Table 49 Initial BenchCel configuration for SureSelectHybridization_v1.0.pro

No. of Columns Processed	Rack 1	Rack 2	Rack 3	Rack 4
1	1 Tip box	Empty	Empty	Empty
2	1 Tip box	Empty	Empty	Empty
3	2 Tip boxes	Empty	Empty	Empty
4	2 Tip boxes	Empty	Empty	Empty
6	3 Tip boxes	Empty	Empty	Empty
12	5 Tip boxes	Empty	Empty	Empty

Run VWorks protocol SureSelectHybridization_v1.0.pro

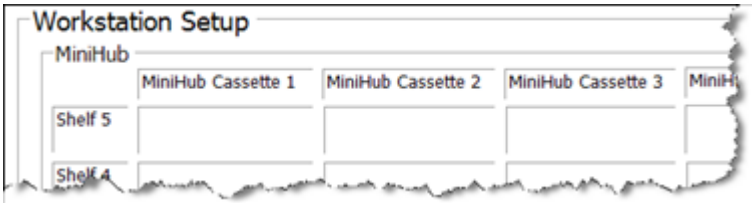
14 On the SureSelect setup form, under **Select Protocol to Run**, select **SureSelectHybridization_v1.0.pro.**

15 Under **Select PCR plate labware for Thermal Cycling**, select the specific type of PCR plate containing the DNA samples at position 6.

16 Select the number of columns of samples to be processed. Runs must include 1, 2, 3, 4, 6, or 12 columns.

17 Click **Display Initial Workstation Setup**.

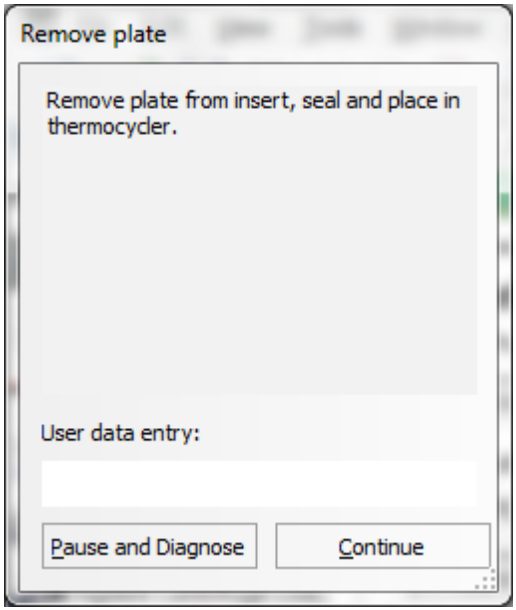
18 Verify that the NGS workstation has been set up as displayed in the Workstation Setup region of the form.



19 When verification is complete, click **Run Selected Protocol**.

The Agilent NGS Workstation transfers SureSelect Block Master Mix to the prepped DNA-containing wells of the PCR plate. When this process is complete, you will be prompted to transfer the plate to the thermal cycler for sample denaturation prior to hybridization.

20 When prompted by VWorks as shown below, remove the PCR plate from position 6 of the Bravo deck, leaving the red insert in place.



21 Seal the sample plate using the PlateLoc Thermal Microplate Sealer, with sealing settings of 165°C and 3.0 sec.

22 Transfer the sealed plate to a thermal cycler and run the following program shown in Table 50. After transferring the plate, click **Continue** on the VWorks screen.

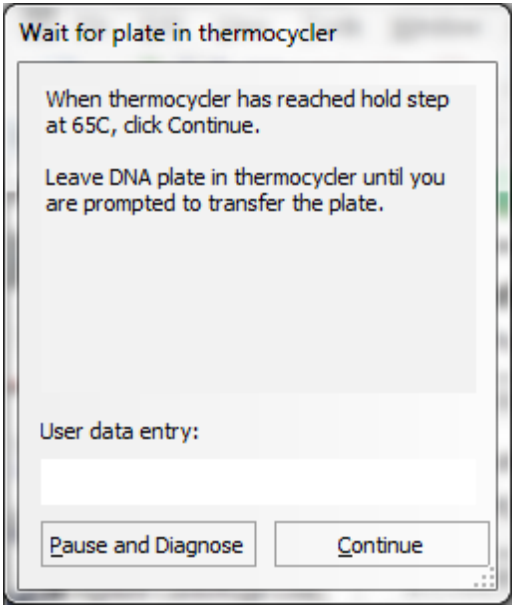
Table 50 Thermal cycler program used for sample denaturation prior to hybridization

Step	Temperature	Time
Step 1	95°C	5 minutes
Step 2	65°C	Hold

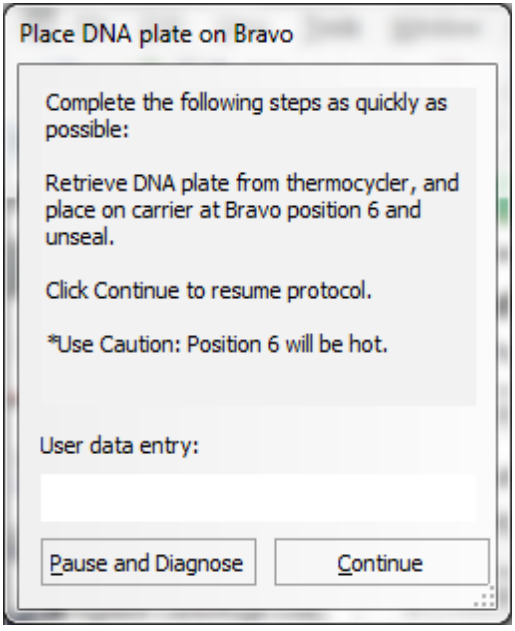
While the sample plate incubates on the thermal cycler, the Agilent NGS Workstation combines aliquots of the SureSelect Capture Library master mix and Hybridization Buffer master mix.

CAUTION You must complete step 23 to step 27 quickly, and immediately after being prompted by the VWorks software. It is important that sample temperature remains approximately 65°C during transfers between the Agilent NGS Workstation and thermal cycler.

23 When the workstation 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.



24 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 6 of the Bravo deck, seated in the red insert. Click **Continue**.



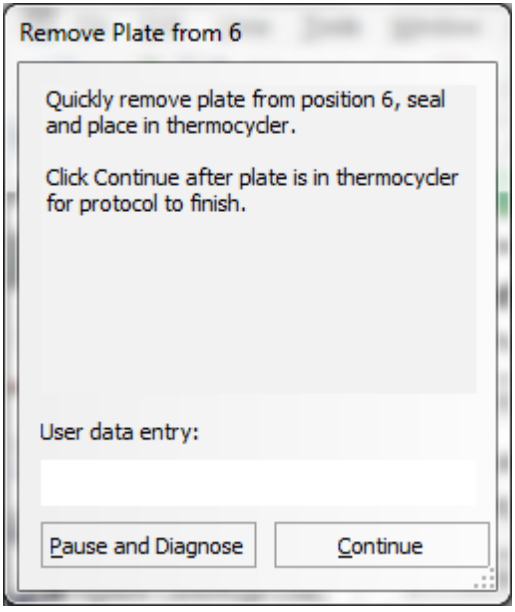
WARNING

Bravo deck position 6 will be hot.

Use caution when handling components that contact heated deck positions.

The Agilent NGS Workstation transfers the capture library-hybridization buffer mixture to the wells of the PCR plate, containing the mixture of prepped DNA samples and blocking agents.

25 When prompted by VWorks as shown below, quickly remove the PCR plate from Bravo deck position 6, leaving the insert in place.



26 Seal the sample plate using the PlateLoc Thermal Microplate Sealer, with sealing settings of 165°C and 3.0 sec.

27 Quickly transfer the plate back to the thermal cycler, held at 65°C. After transferring the plate, click **Continue** on the VWorks screen.

28 To finish the VWorks protocol, click **Continue** in the **Unused Tips** and **Empty Tip box** dialogs, and click **Yes** in the **Protocol Complete** dialog.

CAUTION The temperature of the plate in the thermal cycler should be 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.

29 Incubate the hybridization mixture in the thermal cycler for 24 hours at 65°C with a heated lid at 105°C. If you are using the SureCycler thermal cycler, place a compression mat over the PCR plate before closing the thermal cycler lid for the 24-hour incubation period.

Step 3. Capture the hybridized DNA

In this step, the cDNA-capture library hybrids are captured using streptavidin-coated magnetic beads. This step is run immediately after the 24-hour hybridization period.

This step is automated by the NGS workstation using the SureSelectCapture&Wash_v1.0.rst runset, with a total duration of approximately 3 hours. A workstation operator must be present to complete two actions during the runset, at the time points in the table below. The times provided are approximate; each action is completed in response to a VWorks prompt at the appropriate time in the runset.

Table 51

Operator action	Approximate time after run start
Transfer hybridization reactions from thermal cycler to NGS workstation	<5 minutes
Remove PCR plate from red aluminum insert	5-10 minutes

Prepare the workstation

1. Clear the Labware MiniHub and BenchCel of all plates and tip boxes.
2. Gently wipe down the Labware MiniHub, Bravo decks, and BenchCel with a NucleoClean decontamination wipe.
3. Pre-set the temperature of Bravo deck position 4 to 66°C using the Inheco Multi TEC control touchscreen, as described in Setting the Temperature of Bravo Deck Heat Blocks. Bravo deck position 4 corresponds to CPAC 2, position 1 on the Multi TEC control touchscreen.

Prepare the Dynabeads M-270 streptavidin beads

CAUTION Use only the recommended Dynabeads M-270 Streptavidin Beads for this automated protocol. Use of other streptavidin bead preparations may adversely affect performance and is not supported by Agilent.

4 Vigorously resuspend the Dynabeads M-270 Streptavidin magnetic beads on a vortex mixer. The beads settle during storage.

5 Wash the magnetic beads.

a In a conical vial, combine the components listed in Table 52. The volumes below include the required overage.

Table 52 Components required for magnetic bead washing procedure

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
M-270 Streptavidin 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 device, such as the Dynal magnetic separator.

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.)

6 Resuspend the beads in SureSelect Binding buffer, according to Table 53 below.

Table 53 Preparation of magnetic beads for SureSelectCapture&Wash_v1.0.rst

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

7 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.

8 Place the streptavidin bead source plate at position 5 of the Bravo deck.

Prepare capture and wash solution source plates

9 Prepare a Thermo Scientific reservoir containing 15 mL of nuclease-free water.

10 Prepare an Eppendorf twin.tec source plate labeled *Wash #1*. For each well to be processed, add 160 µL of SureSelect Wash Buffer #1.

11 Prepare a Nunc DeepWell source plate labeled *Wash #2*. For each well to be processed, add 800 µL of SureSelect Wash Buffer #2.

12 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 Capture&Wash runset.

13 Place the *Wash #2* source plate on the silver insert at position 6 of the Bravo deck. Make sure the plate is seated properly on the silver DeepWell insert.

Load the Agilent NGS Workstation

14 Load the Labware MiniHub according to Table 54, using the plate orientations shown in Figure 4.

Table 54 Initial MiniHub configuration for SureSelectCapture&Wash_v1.0.rst

Vertical Shelf Position	Cassette 1	Cassette 2	Cassette 3	Cassette 4
Shelf 5 (Top)	Empty	Empty	Empty	Empty
Shelf 4	Empty	Empty	Empty	Empty
Shelf 3	Empty Eppendorf plate	Empty	*Wash #1* Eppendorf source plate	Empty
Shelf 2	Empty	Nuclease-free water reservoir	Empty	Empty
Shelf 1 (Bottom)	Empty	Empty	Empty	Empty tip box

15 Load the Bravo deck according to Table 55 (positions 5 and 6 should already be loaded).

Table 55 Initial Bravo deck configuration for SureSelectCapture&Wash_v1.0.rst

Location	Content
1	Empty waste reservoir (Axygen 96 Deep Well Plate, square wells)
4	Empty red aluminum insert
5	Dynabeads M-270 streptavidin bead DeepWell source plate
6	*Wash #2* DeepWell source plate seated on silver insert

16 Load the BenchCel Microplate Handling Workstation according to Table 56.

Table 56 Initial BenchCel configuration for SureSelectCapture&Wash_v1.0.rst

No. of Columns Processed	Rack 1	Rack 2	Rack 3	Rack 4
1	1 Tip box	Empty	Empty	Empty
2	2 Tip boxes	Empty	Empty	Empty
3	3 Tip boxes	Empty	Empty	Empty
4	4 Tip boxes	Empty	Empty	Empty
6	6 Tip boxes	Empty	Empty	Empty
12	11 Tip boxes	Empty	Empty	Empty

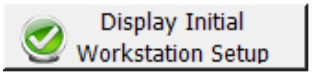
Run VWorks runset SureSelectCapture&Wash_v1.0.rst

17 On the SureSelect setup form, under **Select Protocol to Run**, select **SureSelectCapture&Wash_v1.0.rst.**

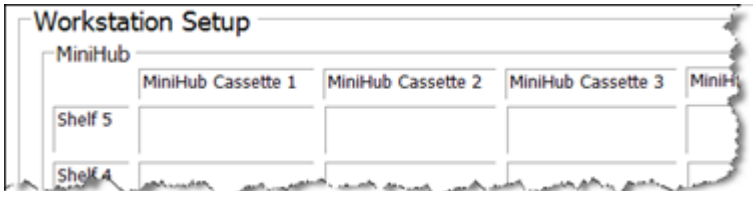
18 Under **Select PCR plate labware for Thermal Cycling**, select the specific type of PCR plate containing the DNA samples at position 6.

19 Select the number of columns of samples to be processed. Runs must include 1, 2, 3, 4, 6, or 12 columns.

20 Click **Display Initial Workstation Setup**.

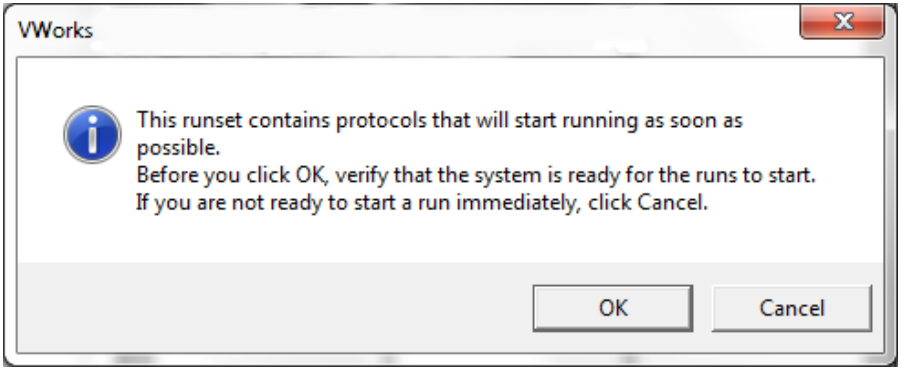


21 Verify that the NGS workstation has been set up as displayed in the Workstation Setup region of the form.



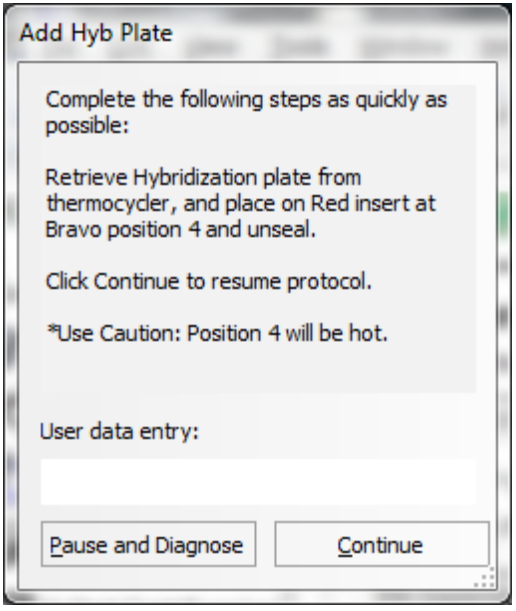
22 When verification is complete, click **Run Selected Protocol**.

23 When ready to begin the run, click **OK** in the following window. If the temperature of Bravo deck position 4 was not pre-set to 66°C, the runset will pause while position 4 reaches temperature.



CAUTION It is important to complete step 24 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 Agilent NGS Workstation is completely prepared, with deck platforms at temperature and all components in place, before you transfer the sample plate to the Bravo deck.

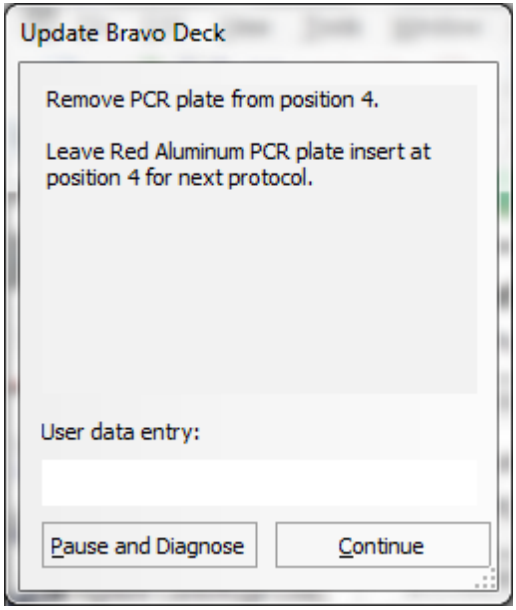
24 When prompted by VWorks as shown below, quickly remove the PCR plate, containing the hybridization reactions held at 65°C, from the thermal cycler. Unseal the plate carefully to avoid splashing, and quickly transfer the plate to position 4 of the Bravo deck, seated in red insert. Click **Continue**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



WARNING **Bravo deck position 4 will be hot.**

Use caution when handling components that contact heated deck positions.

25 When the hybridization samples have been transferred from the PCR plate to the capture plate wells, you will be prompted by VWorks as shown below. Remove the PCR plate from position 4 of the Bravo deck, leaving the red insert in place. When finished, click **Continue** to resume the runset.



The remainder of the SureSelectCapture&Wash_v1.0.rst runset takes approximately 1.5 hours. Once the runset is complete, the captured, bead-bound DNA samples are located in the Eppendorf plate at position 9 of the Bravo deck.

When the runset is complete, seal the plate using the PlateLoc Thermal Microplate Sealer, with sealing settings of 165°C and 1.0 sec and store the plate on ice while setting up the next automation protocol.

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

5 Indexing and Sample Prep for Multiplexed Sequencing

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

Step 1. Amplify the captured libraries to add index tags

In this step, the Agilent NGS Workstation completes the liquid handling steps for PCR-based addition of indexing tags to the SureSelect-enriched DNA samples. After the PCR plate is prepared by the Agilent NGS Workstation, you transfer the plate to a thermal cycler for amplification.

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.

Assign indexes to DNA samples

Select the appropriate indexing primer for each sample.

CAUTION This guide contains two sets of index sequence information. **Verify that you are referencing the information appropriate for your kit version before you proceed.**

Kits with indexing primers supplied in a blue plate include 8-bp indexes A01 through H12. See page 133 through page 134 for indexing primer A01–H12 plate map and nucleotide sequence information.

Kits with indexing primers supplied in a clear plate include 8-bp indexes 1 through 96. See page 139 through page 145 for indexing primer 1–96 plate map and nucleotide sequence information.

Use a different index primer for each sample to be sequenced in the same lane. The number of samples that may be combined per lane depends on the sequencing platform performance and the Capture Library size. See Table 57 for sequence data requirement guidelines. Calculate the number of indexes that can be combined per lane based on these guidelines.

Table 57 Sequencing data requirement guidelines

Capture Library Size	Recommended Amount of Sequencing Data per Sample
1 kb up to 499 kb	0.1 to 50 Mb*
0.5 Mb up to 2.9 Mb	50 to 290 Mb*
3 Mb up to 5.9 Mb	300 to 590 Mb*
Human RNA Kinome	320 Mb

* For custom libraries, Agilent recommends analyzing 100X amount of sequencing data compared to the Capture Library size for each sample. Pool samples according to your expected sequencing output.

Prepare the workstation

1 Clear the Labware MiniHub and BenchCel of plates and tip boxes.

2 Gently wipe down the Labware MiniHub, Bravo decks, and BenchCel with a Nucleoclean decontamination wipe.

3 Turn on the ThermoCube, set to 0°C, at position 9 of the Bravo deck. Be sure that the chiller reservoir contains at least 300 mL of 25% ethanol. Place the silver insert at position 9.

4 Pre-set the temperature of Bravo deck positions 4 and 6 to 4°C using the Inheco Multi TEC control touchscreen, as described in Setting the Temperature of Bravo Deck Heat Blocks. On the control touchscreen, Bravo deck positions 4 corresponds to CPAC 2, position 1, while deck position 6 corresponds to CPAC 2, position 2.

Prepare the index and PCR Master Mix source plates

5 Add 5 µL of the appropriate indexing primer to the appropriate wells of a PCR plate.

The well position for each index should correspond to the position of the RNA sample assigned to that index in the original total RNA sample plate. Keep the plate on ice.

6 Prepare the appropriate volume of PCR master mix, according to Table 58. Mix well using a vortex mixer and keep on ice.

Table 58 Preparation of PCR Master Mix for Post-CapturePCR_RNASeq_ILM_v1.0.pro

SureSelect^{XT} 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
RNA Seq PCR Master Mix	25.0 µL	307.5 µL	512.5 µL	717.5 µL	922.5 µL	1332.5 µL	2665 µL
RNA Seq ILM Post-Capture PCR Primer	1.0 µL	12.3 µL	20.5 µL	28.7 µL	36.9 µL	53.3 µL	106.6 µL
Total Volume	**26.0 µL**	**319.8 µL**	**533.0 µL**	**746.2 µL**	**959.4 µL**	**1385.8 µL**	**2771.6 µL**

7 Using the same Nunc DeepWell master mix source plate that was used for the SureSelectHybridization_v1.0.pro protocol, add the volume of PCR master mix indicated in Table 59 to all wells of column 4 of the master mix source plate. The final configuration of the master mix source plate is shown in Figure 12.

Table 59 Preparation of the Master Mix Source Plate for Post-CapturePCR_RNASeq_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)	36.7 µL	63.4 µL	90.0 µL	116.7 µL	170.0 µL	343.2 µL

NOTE If you are using a new DeepWell plate for the post-capture PCR source plate (for example, when amplifying the second half of the captured DNA sample), leave columns 1 to 3 empty and add the PCR Master Mix to column 4 of the new plate.

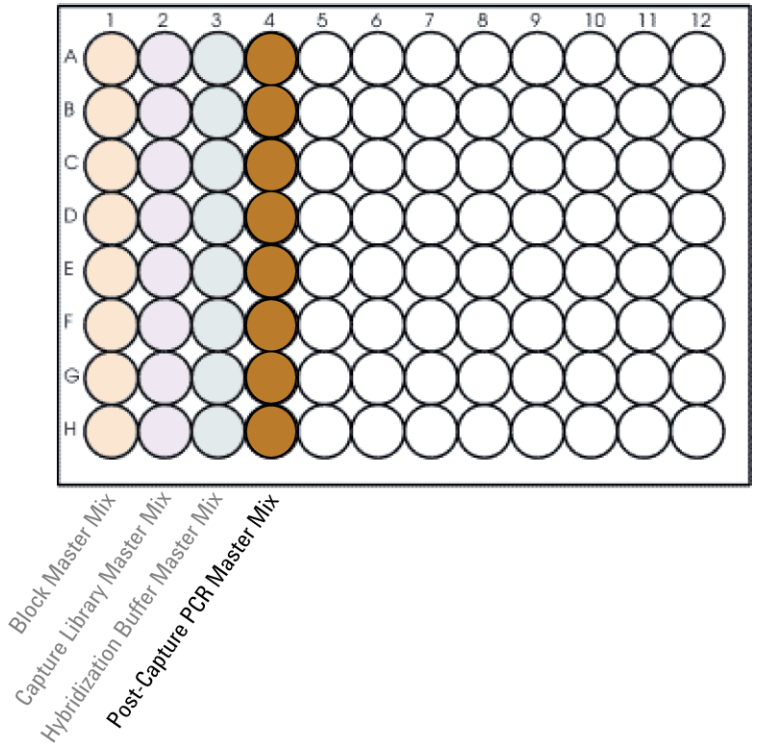


Figure 12 Configuration of the master mix source plate for Post-CapturePCR_RNASeq_ILM_v1.0.pro. Columns 1-3 were used to dispense master mixes for the SureSelectHybridization_v1.0.pro protocol.

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.

Load the Agilent NGS Workstation

10 Load the Labware MiniHub according to Table 60, using the plate orientations shown in Figure 4.

Table 60 Initial MiniHub configuration for Post-CapturePCR_RNASeq_ILM_v1.0.pro

Vertical Shelf Position	Cassette 1	Cassette 2	Cassette 3	Cassette 4
Shelf 5 (Top)	Empty	Empty	Empty	Empty
Shelf 4	Empty	Empty	Empty	Empty
Shelf 3	Empty	Empty	Empty	Empty
Shelf 2	Empty tip box	Empty	Empty	Empty
Shelf 1 (Bottom)	New tip box	Empty	Empty	Empty tip box

11 Load the Bravo deck according to Table 61.

Table 61 Initial Bravo deck configuration for Post-CapturePCR_RNASeq_ILM_v1.0.pro

Location	Content
4	Captured DNA bead suspensions in Eppendorf twin.tec plate
6	Indexing primers in PCR plate seated on red insert (PCR plate type must be specified on setup form under step 2)
9	Master mix plate containing PCR Master Mix in Column 4 (Nunc DeepWell plate seated on silver insert)

12 Load the BenchCel Microplate Handling Workstation according to Table 62.

Table 62 Initial BenchCel configuration for Post-CapturePCR_RNASeq_ILM_v1.0.pro

No. of Columns Processed	Rack 1	Rack 2	Rack 3	Rack 4
1	1 Tip box	Empty	Empty	Empty
2	1 Tip box	Empty	Empty	Empty
3	1 Tip box	Empty	Empty	Empty
4	1 Tip box	Empty	Empty	Empty
6	1 Tip box	Empty	Empty	Empty
12	1 Tip box	Empty	Empty	Empty

Run VWorks protocol Post-CapturePCR_RNASeq_ILM_v1.0.pro

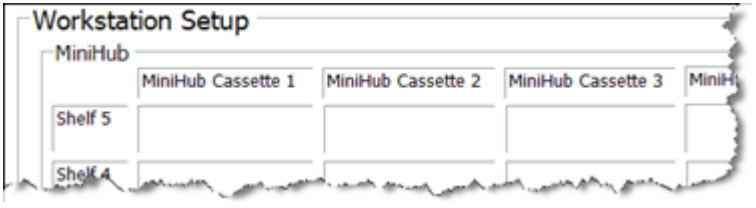
13 On the SureSelect setup form, under **Select Protocol to Run**, select **Post-CapturePCR_RNASeq_ILM_v1.0.pro.**

14 Under **Select PCR plate labware for Thermal Cycling**, select the specific type of PCR plate containing the indexing primers at position 6.

15 Select the number of columns of samples to be processed. Runs must include 1, 2, 3, 4, 6, or 12 columns.

16 Click **Display Initial Workstation Setup**.

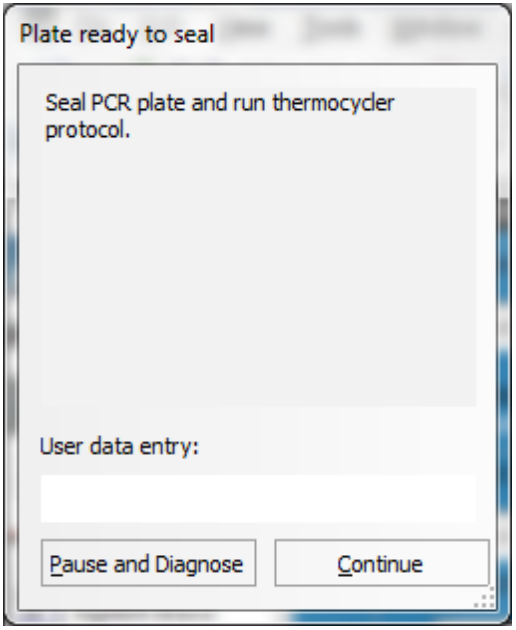
17 Verify that the NGS workstation has been set up as displayed in the Workstation Setup region of the form.



18 When verification is complete, click **Run Selected Protocol**.

Running the Post-CapturePCR_RNASeq_ILM_v1.0.pro protocol takes approximately 15 minutes. Once complete, the PCR-ready samples, containing captured DNA, indexing primer, and PCR master mix are located in the PCR plate at position 6 of the Bravo deck. The Eppendorf plate containing the remaining bead-bound captured DNA samples, which may be stored for future use at 4°C overnight, or at –20°C for longer-term storage, is located at position 4 of the Bravo deck.

19 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.



20 Centrifuge the plate for 30 seconds to drive the well contents off the walls and plate seal and to eliminate air bubbles.

21 Transfer the PCR plate to a thermal cycler and run the PCR amplification program shown in Table 63.

Table 63 Post-Capture PCR cycling program

Segment	Number of Cycles	Temperature	Time
1	1	95°C	2 minutes
2	12	95°C	30 seconds
		57°C	30 seconds
		72°C	1 minute
3	1	72°C	5 minutes
4	1	4°C	Hold

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

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

Prepare the workstation and reagents

1. Clear the Labware MiniHub and BenchCel of all plates and tip boxes.
2. Gently wipe down the Labware MiniHub, Bravo decks, and BenchCel with a Nucleoclean decontamination wipe.
3. Let the AMPure XP beads come to room temperature for at least 30 minutes. *Do not freeze the beads at any time*.
4. Mix the bead suspension well so that the reagent appears homogeneous and consistent in color.
5. Prepare a Nunc DeepWell source plate containing AMPure XP beads. For each well to be processed, add 95 µL of homogeneous AMPure XP beads per well to the Nunc DeepWell plate.
6. Prepare a Thermo Scientific reservoir containing 15 mL of nuclease-free water.
7. Prepare a separate Thermo Scientific reservoir containing 45 mL of freshly-prepared 70% ethanol.

8 Load the Labware MiniHub according to Table 64, using the plate orientations shown in Figure 4.

Table 64 Initial MiniHub configuration for AMPureXP_v1.1.pro:Post-Capture PCR

Vertical Shelf Position	Cassette 1	Cassette 2	Cassette 3	Cassette 4
Shelf 5 (Top)	Empty Nunc DeepWell plate	Empty	Empty	Empty
Shelf 4	Empty	Empty	Empty	Empty
Shelf 3	Empty	Empty Eppendorf twin.tec plate	Empty	Empty
Shelf 2	Empty	Nuclease-free water reservoir from step 6	AMPure XP beads in Nunc DeepWell plate from step 5	Empty
Shelf 1 (Bottom)	Empty	70% ethanol reservoir from step 7	Empty	Empty tip box

9 Load the Bravo deck according to Table 65.

Table 65 Initial Bravo deck configuration for AMPureXP_v1.1.pro:Post-Capture PCR

Location	Content
1	Empty waste reservoir (Axygen 96 Deep Well Plate, square wells)
9	Indexed library samples in PCR plate seated on red insert (PCR plate type must be specified on setup form under step 2)

10 Load the BenchCel Microplate Handling Workstation according to Table 66.

Table 66 Initial BenchCel configuration for AMPureXP_v1.1.pro:Post-Capture PCR

No. of Columns Processed	Rack 1	Rack 2	Rack 3	Rack 4
1	1 Tip box	Empty	Empty	Empty
2	1 Tip box	Empty	Empty	Empty
3	2 Tip boxes	Empty	Empty	Empty
4	2 Tip boxes	Empty	Empty	Empty
6	3 Tip boxes	Empty	Empty	Empty
12	6 Tip boxes	Empty	Empty	Empty

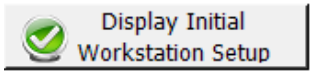
Run VWorks protocol AMPureXP_v1.1.pro:Post-Capture PCR

11 On the SureSelect setup form, under **Select Protocol to Run**, select **AMPureXP_v1.1.pro:Post-Capture PCR.**

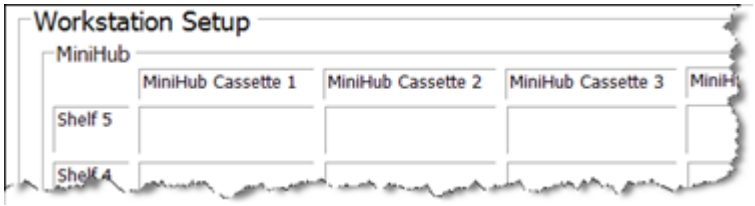
12 Under **Select PCR plate labware for Thermal Cycling**, select the specific type of PCR plate containing the DNA samples at position 9.

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 Workstation Setup**.



15 Verify that the NGS workstation has been set up as displayed in the Workstation Setup region of the form.



16 When verification is complete, click **Run Selected Protocol**.

The purification protocol takes approximately 45 minutes. When complete, the purified DNA samples are in the Eppendorf plate located on Bravo deck position 7.

Step 3. Assess DNA quality and quantity

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

1 Set up the 2100 Bioanalyzer as instructed in the High Sensitivity DNA Assay kit guide.

NOTE Version B.02.07 or higher of the Agilent 2100 Expert Software is required for High Sensitivity DNA Assay Kit runs.

2 Seal the sample plate using the PlateLoc Thermal Microplate Sealer, with sealing settings of 165°C and 1.0 sec.

3 Vortex the plate to mix samples in each well, then centrifuge the plate for 30 seconds to drive the well contents off the walls and plate seal.

4 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.

5 Load the prepared chip into the 2100 Bioanalyzer and start the run within five minutes after preparation.

Verify that the electropherogram shows an average DNA fragment size of approximately 200 to 700 bp. A sample electropherogram is shown in Figure 13.

Stopping Point If you do not continue to the next step, seal the plate and store at –20°C.

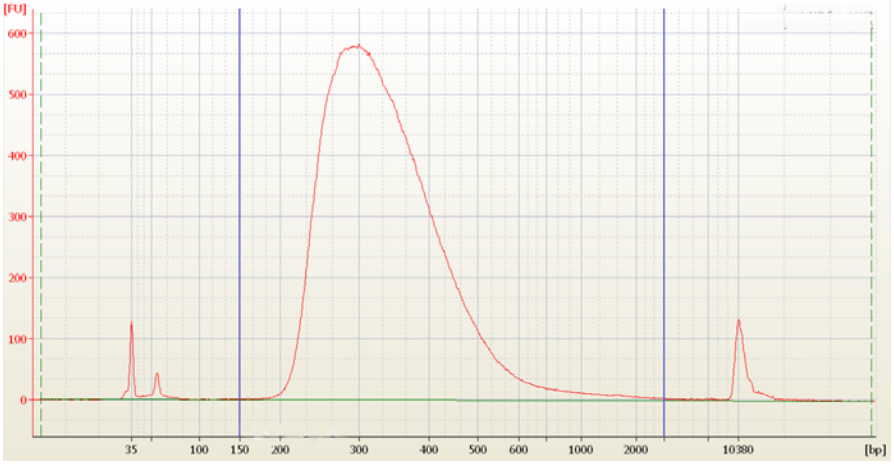


Figure 13 Analysis of indexed DNA using the High Sensitivity DNA Assay.

Option 2: Analysis using the Agilent 2200 TapeStation and High Sensitivity D1000 ScreenTape

Use a High Sensitivity D1000 ScreenTape and reagent kit to analyze the indexed DNA. For more information to do this step, see the *Agilent 2200 TapeStation User Manual*.

1. Seal the DNA sample plate using the PlateLoc Thermal Microplate Sealer, with sealing settings of 165°C and 1.0 sec.
2. Vortex the plate to mix samples in each well, then centrifuge the plate for 30 seconds to drive the well contents off the walls and plate seal.
3. Prepare the TapeStation samples as instructed in the *Agilent 2200 TapeStation User Manual*. Use 2 µL of each indexed DNA sample diluted with 2 µL of High Sensitivity D1000 sample buffer for the analysis.

CAUTION Make sure that you thoroughly mix the combined DNA and High Sensitivity D1000 sample buffer on a vortex mixer for 5 seconds for accurate quantitation.

4. Load the sample plate or tube strips from step 3, the High Sensitivity D1000 ScreenTape, and loading tips into the 2200 TapeStation as instructed in the *Agilent 2200 TapeStation User Manual*. Start the run.
5. For each sample, measure the concentration of the library (ng/µL) by integrating under the peak at approximately 200 to 700 bp. A sample electropherogram is shown in Figure 14.

Stopping Point If you do not continue to the next step, seal the plate and store at –20°C.

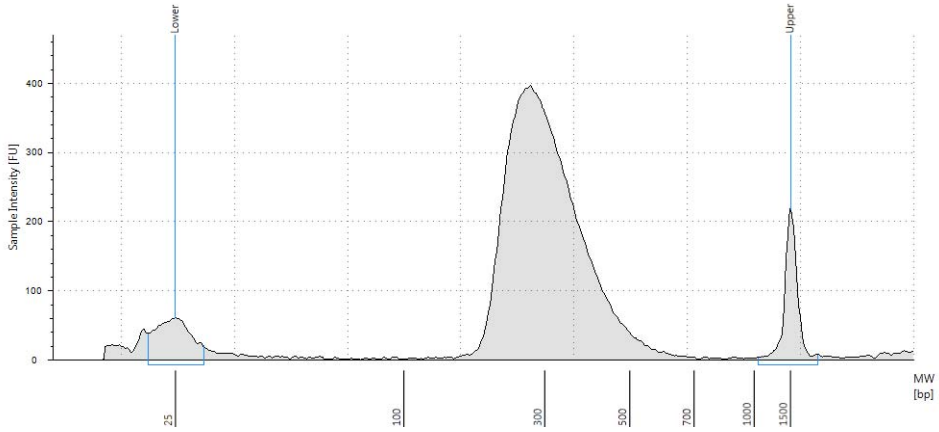


Figure 14 Analysis of purified indexed DNA amplicons using the 2200 TapeStation.

Step 4. Pool samples for multiplexed sequencing

The number of indexed libraries that may be multiplexed in a single sequencing lane is determined by the output specifications of the platform used, together with the amount of sequencing data required for your research design. Calculate the number of indexes that can be combined per lane, according to the capacity of your platform and the amount of sequencing data required per sample.

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 67 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 67 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.

Exact library pool dilution and processing can vary based on the flow cell capacity and analysis pipeline versions being used. Refer to the appropriate Illumina user guide for instructions.

Step 5. Prepare and analyze sequencing samples

Proceed to cluster amplification using the Illumina Paired-End Cluster Generation Kit; refer to the manufacturer's instructions for this step. The optimal seeding concentration for cluster amplification from SureSelect RNA target-enriched libraries is approximately 8-10 pM.

NOTE The optimal seeding concentration may vary, depending on the method used for library quantification and fragment size distribution.

This protocol has been validated with 2 x 100-base paired-end reads. However, read length can be adjusted to achieve the desired research goals.

Sequencing run setup guidelines for 8-bp indexes

Sequencing runs must be set up to perform an 8-nt index read. For the HiSeq platform, use the *Cycles* settings shown in Table 68. Cycle number settings can be specified on the *Run Configuration* screen of the instrument control software interface after choosing *Custom* from the index type selection buttons.

For complete index sequence information, see the Reference section starting on page 129.

Table 68 HiSeq platform Run Configuration screen Cycle Number settings*

Run Segment	Cycle Number
Read 1	100
Index 1 (i7)	9
Index 2 (i5)	0
Read 2	100

* Settings apply to v3.0 SBS chemistry.

Sequence analysis guidelines

The SureSelect^{XT} RNA sequencing library preparation method preserves RNA strandedness as described here. The first strand of cDNA is the reverse complement of the poly(A) RNA transcript strand. Since the second strand of cDNA is eliminated before PCR, the sequence of read 1, which starts at the P5 end, matches only the first strand of cDNA. Read 2, which starts at the P7 end, matches the second strand of cDNA (the poly(A) RNA transcript strand). When running analysis of this data to determine strandedness, it is important to include this information. For example, when using the Picard tools (http://picard.sourceforge.net/) to calculate RNA sequencing metrics, it is important to include the parameter *STRAND_SPECIFICITY= SECOND_READ_TRANSCRIPTION_STRAND* to correctly calculate the strand specificity metrics.

6 Reference

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

CAUTION This chapter contains two sets of index sequence and kit content information. The first section covers kits with indexing primers supplied in Library Prep Kit p/n 5500-0135 (typically received December, 2014 or later). The second section covers kits with indexing primers supplied in Library Prep Kit 5500-0117 (typically received before December, 2014). **Verify that you are referencing the information appropriate for your kit version before you proceed.**

Reference Information for Kits with Revised Index Configuration (indexing primers in blue plate)

Use the reference information in this section if your kit includes Library Prep Kit p/n 5500-0135. If your kit does not include this component kit, see page 135 for kit content and indexing primer information.

Kit Contents

The SureSelect^{XT} RNA Reagent Kits contain the following component kits:

Table 69 SureSelect RNA-Seq Kit Content-Revised Index Configuration

Component Kits	Storage Condition	Part Number
SureSelect Strand Specific RNA Library Prep, ILM, Box 1	–20°C	5500-0135
SureSelect Strand Specific RNA Library Prep, ILM, Box 2	4°C	5190-6411
SureSelect Target Enrichment Box 1	Room Temperature	5190-4394
SureSelect Target Enrichment Box 2	–20°C	5190-6262

NOTE SureSelect capture libraries and reagents must be used within one year of receipt.

The contents of each of the component kits listed in Table 69 are described in the tables below.

Table 70 SureSelect Strand Specific RNA Library Prep, ILM, Box 1 Content-Revised Index Configuration

Kit Component	Details
RNA Seq Fragmentation Mix	bottle
RNA Seq First Strand Master Mix	tube with orange cap
RNA Seq Second-Strand + End-Repair Enzyme Mix	bottle
RNA Seq Second-Strand + End-Repair Oligo Mix	tube with yellow cap
RNA Seq dA Tailing Master Mix	bottle
SureSelect Ligation Master Mix	tube with purple cap
SureSelect Oligo Adaptor Mix	tube with blue cap
RNA Seq PCR Master Mix	bottle
Uracil DNA Glycosylase (UDG)	tube with yellow cap
SureSelect Primer	tube with brown cap
RNA Seq ILM Reverse PCR Primer	tube with black cap
RNA Seq ILM Post-capture PCR Primer	tube with green cap
SureSelect^{XT} Indexes, 8 bp*	SureSelect 8 bp Indexes A01 through H12, provided in blue 96-well plate†

* See Table 75 on page 134 for index sequences.

† See Table 74 on page 133 for a plate map.

Table 71 SureSelect Strand Specific RNA Library Prep, ILM, Box 2 Content

Kit Component	Details
Oligo(dT) Microparticles	bottle
RNA Seq Bead Binding Buffer	bottle
RNA Seq Bead Washing Buffer	bottle
RNA Seq Bead Elution Buffer	bottle
Nuclease Free Water	bottle

Table 72 SureSelect Target Enrichment Box 1 Content

Kit Component	Details
SureSelect Hyb 1	tube with orange cap
SureSelect Hyb 2	tube with red cap
SureSelect Hyb 4	tube with black cap
SureSelect Binding Buffer	bottle
SureSelect Wash Buffer 1	bottle
SureSelect Wash Buffer 2	bottle
SureSelect Elution Buffer*	bottle
SureSelect Neutralization Buffer*	bottle

* The provided SureSelect Elution Buffer and Neutralization Buffer are not used in the automated RNA Target Enrichment workflow described in this manual.

Table 73 SureSelect Target Enrichment-Box 2 Content

Kit Component	Details
SureSelect Hyb 3	tube with yellow cap
SureSelect Indexing Block 1	tube with green cap
SureSelect Block 2	tube with blue cap
SureSelect ILM Indexing Block 3	tube with brown cap
SureSelect RNase Block	tube with purple cap

Table 74 Plate map for SSEL 8bp Indexes A01 through H12 provided in blue plate in Library Prep kit p/n 5500-0135

	1	2	3	4	5	6	7	8	9	10	11	12
A	A01	A02	A03	A04	A05	A06	A07	A08	A09	A10	A11	A12
B	B01	B02	B03	B04	B05	B06	B07	B08	B09	B10	B11	B12
C	C01	C02	C03	C04	C05	C06	C07	C08	C09	C10	C11	C12
D	D01	D02	D03	D04	D05	D06	D07	D08	D09	D10	D11	D12
E	E01	E02	E03	E04	E05	E06	E07	E08	E09	E10	E11	E12
F	F01	F02	F03	F04	F05	F06	F07	F08	F09	F10	F11	F12
G	G01	G02	G03	G04	G05	G06	G07	G08	G09	G10	G11	G12
H	H01	H02	H03	H04	H05	H06	H07	H08	H09	H10	H11	H12

Nucleotide Sequences of SureSelect^{XT} Indexes A01 to H12

Each index is 8 nt in length. See page 56 for sequencing run setup requirements for sequencing libraries using 8-bp indexes.

Table 75 SureSelect RNA Seq Indexes, for indexing primers in blue 96-well plate

Index	Sequence	Index	Sequence	Index	Sequence	Index	Sequence
A01	ATGCCTAA	A04	AACTCACC	A07	ACGTATCA	A10	AATGTTGC
B01	GAATCTGA	B04	GCTAACGA	B07	GTCTGTCA	B10	TGAAGAGA
C01	AACGTGAT	C04	CAGATCTG	C07	CTAAGGTC	C10	AGATCGCA
D01	CACTTCGA	D04	ATCCTGTA	D07	CGACACAC	D10	AAGAGATC
E01	GCCAAGAC	E04	CTGTAGCC	E07	CCGTGAGA	E10	CAACCACA
F01	GACTAGTA	F04	GCTCGGTA	F07	GTGTTCTA	F10	TGGAACAA
G01	ATTGGCTC	G04	ACACGACC	G07	CAATGGAA	G10	CCTCTATC
H01	GATGAATC	H04	AGTCACTA	H07	AGCACCTC	H10	ACAGATTC
A02	AGCAGGAA	A05	AACGCTTA	A08	CAGCGTTA	A11	CCAGTTCA
B02	GAGCTGAA	B05	GGAGAACA	B08	TAGGATGA	B11	TGGCTTCA
C02	AAACATCG	C05	CATCAAGT	C08	AGTGGTCA	C11	CGACTGGA
D02	GAGTTAGC	D05	AAGGTACA	D08	ACAGCAGA	D11	CAAGACTA
E02	CGAACTTA	E05	CGCTGATC	E08	CATACCAA	E11	CCTCCTGA
F02	GATAGACA	F05	GGTGCGAA	F08	TATCAGCA	F11	TGGTGGTA
G02	AAGGACAC	G05	CCTAATCC	G08	ATAGCGAC	G11	AACAACCA
H02	GACAGTGC	H05	CTGAGCCA	H08	ACGCTCGA	H11	AATCCGTC
A03	ATCATTCC	A06	AGCCATGC	A09	CTCAATGA	A12	CAAGGAGC
B03	GCCACATA	B06	GTACGCAA	B09	TCCGTCTA	B12	TTCACGCA
C03	ACCACTGT	C06	AGTACAAG	C09	AGGCTAAC	C12	CACCTTAC
D03	CTGGCATA	D06	ACATTGGC	D09	CCATCCTC	D12	AAGACGGA
E03	ACCTCCAA	E06	ATTGAGGA	E09	AGATGTAC	E12	ACACAGAA
F03	GCGAGTAA	F06	GTCGTAGA	F09	TCTTCACA	F12	GAACAGGC
G03	ACTATGCA	G06	AGAGTCAA	G09	CCGAAGTA	G12	AACCGAGA
H03	CGGATTGC	H06	CCGACAAC	H09	CGCATACA	H12	ACAAGCTA

Reference Information for Kits with Original Index Configuration (indexing primers in clear plate)

Use the reference information in this section if your kit includes Library Prep Kit p/n 5500-0117. If your kit does not include this component kit, see page 130 for kit content and indexing primer information.

Kit Contents

The SureSelect^{XT} RNA Reagent Kits contain the following component kits:

Table 76 SureSelect RNA-Seq Kit Content-Original Index Configuration

Component Kits	Storage Condition	Part Number
SureSelect Strand Specific RNA Library Prep, ILM, Box 1	–20°C	5500-0117
SureSelect Strand Specific RNA Library Prep, ILM, Box 2	4°C	5190-6411
SureSelect Target Enrichment Box 1	Room Temperature	5190-4394
SureSelect Target Enrichment Box 2	–20°C	5190-6262

NOTE SureSelect capture libraries and reagents must be used within one year of receipt.

The contents of each of the component kits listed in Table 76 are described in the tables below.

Table 77 SureSelect Strand Specific RNA Library Prep, ILM, Box 1 Content-Original Index Configuration

Kit Component	Details
RNA Seq Fragmentation Mix	bottle
RNA Seq First Strand Master Mix	tube with orange cap
RNA Seq Second-Strand + End-Repair Enzyme Mix	bottle
RNA Seq Second-Strand + End-Repair Oligo Mix	tube with yellow cap
RNA Seq dA Tailing Master Mix	bottle
SureSelect Ligation Master Mix	tube with purple cap
SureSelect Oligo Adaptor Mix	tube with blue cap
RNA Seq PCR Master Mix	bottle
Uracil DNA Glycosylase (UDG)	tube with yellow cap
SureSelect Primer	tube with brown cap
RNA Seq ILM Reverse PCR Primer	tube with black cap
RNA Seq ILM Post-capture PCR Primer	tube with green cap
RNA Seq Indexes, 8 bp*	RNA Seq Indexes 1-96, 8 bp provided in clear 96-well plate†

* See Table 82 on page 140 through Table 87 on page 145 for index sequence information.

† See Table 81 on page 139 for a plate map.

Table 78 SureSelect Strand Specific RNA Library Prep, ILM, Box 2 Content

Kit Component	Details
Oligo(dT) Microparticles	bottle
RNA Seq Bead Binding Buffer	bottle
RNA Seq Bead Washing Buffer	bottle
RNA Seq Bead Elution Buffer	bottle
Nuclease Free Water	bottle

Table 79 SureSelect Target Enrichment Box 1 Content

Kit Component	Details
SureSelect Hyb 1	tube with orange cap
SureSelect Hyb 2	tube with red cap
SureSelect Hyb 4	tube with black cap
SureSelect Binding Buffer	bottle
SureSelect Wash Buffer 1	bottle
SureSelect Wash Buffer 2	bottle
SureSelect Elution Buffer*	bottle
SureSelect Neutralization Buffer*	bottle

* The provided SureSelect Elution Buffer and Neutralization Buffer are not used in the automated RNA Target Enrichment workflow described in this manual.

Table 80 SureSelect Target Enrichment-Box 2 Content

Kit Component	Details
SureSelect Hyb 3	tube with yellow cap
SureSelect Indexing Block 1	tube with green cap
SureSelect Block 2	tube with blue cap
SureSelect ILM Indexing Block 3	tube with brown cap
SureSelect RNase Block	tube with purple cap

Table 81 Plate map for RNA Seq Indexes 1-96, 8 bp, provided in clear plate in Library Prep kit p/n 5500-0117

	1	2	3	4	5	6	7	8	9	10	11	12
A	Index 1	Index 9	Index 17	Index 25	Index 33	Index 41	Index 49	Index 57	Index 65	Index 73	Index 81	Index 89
B	Index 2	Index 10	Index 18	Index 26	Index 34	Index 42	Index 50	Index 58	Index 66	Index 74	Index 82	Index 90
C	Index 3	Index 11	Index 19	Index 27	Index 35	Index 43	Index 51	Index 59	Index 67	Index 75	Index 83	Index 91
D	Index 4	Index 12	Index 20	Index 28	Index 36	Index 44	Index 52	Index 60	Index 68	Index 76	Index 84	Index 92
E	Index 5	Index 13	Index 21	Index 29	Index 37	Index 45	Index 53	Index 61	Index 69	Index 77	Index 85	Index 93
F	Index 6	Index 14	Index 22	Index 30	Index 38	Index 46	Index 54	Index 62	Index 70	Index 78	Index 86	Index 94
G	Index 7	Index 15	Index 23	Index 31	Index 39	Index 47	Index 55	Index 63	Index 71	Index 79	Index 87	Index 95
H	Index 8	Index 16	Index 24	Index 32	Index 40	Index 48	Index 56	Index 64	Index 72	Index 80	Index 88	Index 96

Nucleotide Sequences of SureSelect RNA Seq Indexes-Original Kit Configuration

The nucleotide sequence of each SureSelect RNA Seq Index provided in the original kit configuration is provided in the tables below.

Refer to the sequence information below only if your kit includes Library Prep kit p/n 5500-0117, with indexing primers provided in a clear 96-well plate.

Each index is 8 nt in length. See page 126 for sequencing run setup requirements for sequencing libraries using 8-bp indexes.

Table 82 SureSelect RNA Seq Indexes 1-16

Index Number	Sequence
1	AACGTGAT
2	AAACATCG
3	ATGCCTAA
4	AGTGGTCA
5	ACCACTGT
6	ACATTGGC
7	CAGATCTG
8	CATCAAGT
9	CGCTGATC
10	ACAAGCTA
11	CTGTAGCC
12	AGTACAAG
13	AACAACCA
14	AACCGAGA
15	AACGCTTA
16	AAGACGGA

Table 83 SureSelect RNA Seq Indexes 17-32

Index Number	Sequence
17	AAGGTACA
18	ACACAGAA
19	ACAGCAGA
20	ACCTCCAA
21	ACGCTCGA
22	ACGTATCA
23	ACTATGCA
24	AGAGTCAA
25	AGATCGCA
26	AGCAGGAA
27	AGTCACTA
28	ATCCTGTA
29	ATTGAGGA
30	CAACCACA
31	CAAGACTA
32	CAATGGAA

Table 84 SureSelect RNA Seq Indexes 33-48

Index Number	Sequence
33	CACTTCGA
34	CAGCGTTA
35	CATACCAA
36	CCAGTTCA
37	CCGAAGTA
38	CCGTGAGA
39	CCTCCTGA
40	CGAACTTA
41	CGACTGGA
42	CGCATACA
43	CTCAATGA
44	CTGAGCCA
45	CTGGCATA
46	GAATCTGA
47	GACTAGTA
48	GAGCTGAA

Table 85 SureSelect RNA Seq Indexes 49-64

Index Number	Sequence
49	GATAGACA
50	GCCACATA
51	GCGAGTAA
52	GCTAACGA
53	GCTCGGTA
54	GGAGAACA
55	GGTGCGAA
56	GTACGCAA
57	GTCGTAGA
58	GTCTGTCA
59	GTGTTCTA
60	TAGGATGA
61	TATCAGCA
62	TCCGTCTA
63	TCTTCACA
64	TGAAGAGA

Table 86 SureSelect RNA Seq Indexes 65-80

Index Number	Sequence
65	TGGAACAA
66	TGGCTTCA
67	TGGTGGTA
68	TTCACGCA
69	AACTCACC
70	AAGAGATC
71	AAGGACAC
72	AATCCGTC
73	AATGTTGC
74	ACACGACC
75	ACAGATTC
76	AGATGTAC
77	AGCACCTC
78	AGCCATGC
79	AGGCTAAC
80	ATAGCGAC

Table 87 SureSelect RNA Seq Indexes 81-96

Index Number	Sequence
81	ATCATTCC
82	ATTGGCTC
83	CAAGGAGC
84	CACCTTAC
85	CCATCCTC
86	CCGACAAC
87	CCTAATCC
88	CCTCTATC
89	CGACACAC
90	CGGATTGC
91	CTAAGGTC
92	GAACAGGC
93	GACAGTGC
94	GAGTTAGC
95	GATGAATC
96	GCCAAGAC

Plasticware quantities for automation protocols

The tables below show the quantity of each plasticware type used in each automation protocol in the workflow. Quantities listed in the tables only include unique labware that was not used in other protocols or runsets. For example, Nunc DeepWell master mix plates may be reused in multiple protocols but are counted below only where first used.

mRNA_Purification_v1.0.pro

Labware	1-Column Runs	2-Column Runs	3-Column Runs	4-Column Runs	6-Column Runs	12-Column Runs
Tip boxes (filled)	2	3	4	4	6	10
Empty tip boxes (for waste tips)	2	2	2	2	2	2
Nunc DeepWell Plates	5	5	5	5	5	5
96 Eppendorf twin.tec full-skirt plates	3	3	3	3	3	3
PCR plates (compatible with thermal cycler)	4	4	4	4	4	4
Axygen square-well plate (waste)	1	1	1	1	1	1

AMPureXP_v1.1.pro:First Strand

Labware	1-Column Runs	2-Column Runs	3-Column Runs	4-Column Runs	6-Column Runs	12-Column Runs
Tip boxes (filled)	1	1	2	2	3	6
Empty tip boxes (for waste tips)	1	1	1	1	1	1
Nunc DeepWell Plates	2	2	2	2	2	2
96 Eppendorf twin.tec full-skirt plates	1	1	1	1	1	1
Thermo Scientific Reservoirs	2	2	2	2	2	2
Axygen square-well plate (waste)	1	1	1	1	1	1

LibraryPrep_RNASeq_ILM_v1.1.rst

Labware	1-Column Runs	2-Column Runs	3-Column Runs	4-Column Runs	6-Column Runs	12-Column Runs
Tip boxes (filled)	2	3	4	5	7	14
Empty tip boxes (for waste tips)	1	1	1	1	1	1
Nunc DeepWell Plates	3	3	3	3	3	3
96 Eppendorf twin.tec full-skirt plates	4	4	4	4	4	4
Thermo Scientific Reservoirs	2	2	2	2	2	2
Axygen square-well plate (waste)	1	1	1	1	1	1

Pre-CapturePCR_RNASeq_ILM_v1.0.pro

Labware	1-Column Runs	2-Column Runs	3-Column Runs	4-Column Runs	6-Column Runs	12-Column Runs
Tip boxes (filled)	1	1	1	1	1	1
Empty tip boxes (for waste tips)	1	1	1	1	1	1
PCR plates (compatible with thermal cycler)	1	1	1	1	1	1

AMPureXP_v1.1.pro:Pre-Capture PCR

Labware	1-Column Runs	2-Column Runs	3-Column Runs	4-Column Runs	6-Column Runs	12-Column Runs
Tip boxes (filled)	1	1	2	2	3	6
Empty tip boxes (for waste tips)	1	1	1	1	1	1
Nunc DeepWell Plates	2	2	2	2	2	2
96 Eppendorf twin.tec full-skirt plates	1	1	1	1	1	1
Thermo Scientific Reservoirs	2	2	2	2	2	2
Axygen square-well plate (waste)	1	1	1	1	1	1

Aliquot_Libraries_v1.0.pro

Labware	1-Column Runs	2-Column Runs	3-Column Runs	4-Column Runs	6-Column Runs	12-Column Runs
Tip boxes (filled)	1	1	1	1	1	1
Empty tip boxes (for waste tips)	1	1	1	1	1	1
PCR plates (compatible with thermal cycler)	1	1	1	1	1	1

SureSelectHybridization_v1.0.pro

Labware	1-Column Runs	2-Column Runs	3-Column Runs	4-Column Runs	6-Column Runs	12-Column Runs
Tip boxes (filled)	1	1	2	2	3	5
Empty tip boxes (for waste tips)	1	1	1	1	1	1
Nunc DeepWell Plates	1	1	1	1	1	1
96 Eppendorf twin.tec full-skirt plates	1	1	1	1	1	1

SureSelectCapture&Wash_v1.0.rst

Labware	1-Column Runs	2-Column Runs	3-Column Runs	4-Column Runs	6-Column Runs	12-Column Runs
Tip boxes (filled)	1	2	3	4	6	11
Empty tip boxes (for waste tips)	1	1	1	1	1	1
Nunc DeepWell Plates	2	2	2	2	2	2
96 Eppendorf twin.tec full-skirt plates	2	2	2	2	2	2
Thermo Scientific Reservoir	1	1	1	1	1	1
Axygen square-well plate (waste)	1	1	1	1	1	1

Post-CapturePCR_RNASeq_ILM_v1.0.pro

Labware	1-Column Runs	2-Column Runs	3-Column Runs	4-Column Runs	6-Column Runs	12-Column Runs
Tip boxes (filled)	2	2	2	2	2	2
Empty tip boxes (for waste tips)	2	2	2	2	2	2
PCR plates (compatible with thermal cycler)	1	1	1	1	1	1

AMPureXP_v1.1.pro:Post-Capture PCR

Labware	1-Column Runs	2-Column Runs	3-Column Runs	4-Column Runs	6-Column Runs	12-Column Runs
Tip boxes (filled)	1	1	2	2	3	6
Empty tip boxes (for waste tips)	1	1	1	1	1	1
Nunc DeepWell Plates	2	2	2	2	2	2
96 Eppendorf twin.tec full-skirt plates	1	1	1	1	1	1
Thermo Scientific Reservoirs	2	2	2	2	2	2
Axygen square-well plate (waste)	1	1	1	1	1	1

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In This Book

This guide contains information to run the SureSelect^{XT} Automated RNA Target Enrichment protocol using the Agilent NGS Workstation.

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