# SureSelect XT HS2 DNA Target Enrichment using the Magnis NGS Prep System

## Protocol

***For Research Use Only. Not for use in diagnostic procedures.***

**Version C0, August 2025**

# Notices



## Manual Part Number

G9751-90000

## Edition

Version C0, August 2025

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## Technical Support

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# In This Guide…

This guide provides instructions for automated preparation of SureSelect XT HS2 DNA target-enriched Illumina paired-end multiplexed sequencing libraries using the Magnis NGS Prep System.

The SureSelect XT HS2 system is used to prepare dual-indexed library samples with molecular barcodes prior to target enrichment to allow high-sensitivity sequencing on the Illumina platform.

## What's New in Version C0

- Support for Magnis SureSelect XT HS2 Clinical Research Exome V4 kits (see Table 1 on page 10 and Table 23 on page 61)
- Updates to Table 3 on page 11 to show current availability of Agilent's automated electrophoresis platforms
- Support for run setup using various Magnis firmware versions. For instruments running firmware v1.4 or earlier, see page 25. For instruments running firmware v1.5 or later, see page 27. Firmware v1.5 includes a new *Application* menu on the *Enter Run Info* screens
- Labware positioning precaution added to page 29
- Final library sample volume added to page 41, with *Troubleshooting* information on page 74
- Updates to downstream sequencing support information on page 56 to page 59 and page 64. Tween 20 removed from Table 6 on page 12.
- Link to the SureSelect XT HS2 Index Sequence Resource spreadsheet added to page 58, page 64 and page 67
- Removal of inapplicable notices from page 2

## What's New in Version B0

- Support for Magnis protocol *SSEL-DNA-XTHS2-EPIS-ILM,* run using Magnis SureSelect XT HS2 Reagent Kit PN G9750B, which is supplied with empty probe input strips (EPIS). See page 50 to page 52 for detailed probe input strip filling and run setup instructions for this protocol. See page 23, page 26 and page 36 for related run setup updates, and see page 73 for related troubleshooting. For information on kit PN G9750B, see page 10 and page 61.
- Support for Magnis SureSelect Cancer CGP kits (see page 10 and page 61)
- Updates to Magnis NGS Prep System ordering information in Table 2 on page 10
- Updates to kit reagent and plasticware preparation instructions on page 20 to page 23
- Recommendation for use of adhesive seal applicator (see page 12 and *Note* on page 22)
- New *Note* on page 23 with index pair assignment considerations for multiplex sequencing
- Updates to information on instrument LED light color indicators on page 24
- Updates to deck setup summary on page 29 including new chiller strip tube color map
- Minor updates to chiller strip tube loading instructions on page 34 to clarify requirement to leave foil covers intact for all strips loaded for the run
- Minor updates to page 41 including addition of final library solvent composition
- New *Disposal* section on page 42
- Minor updates to DNA sample dilution instructions to clarify use of 1x Low TE Buffer solvent for all workflows (see page 44 and page 47)
- Updates to Covaris instrument setup instructions on page 45 and page 48
- Updates to downstream sequencing support information (see page 57 to page 59)
- Support for use of Agilent's Alissa Reporter software for SureSelect XT HS2 DNA library sequence pre-processing and human germline DNA variant analysis
- Updates to page 64 through page 70 to clarify P5 index sequence orientation usage
- Updates to troubleshooting information on touchscreen response issues on page 72
- Removal of *Notice to Purchaser* from page 2

# Content

# 1 Before You Begin



This chapter contains information for you to read and understand before you start.

# Overview of the Workflow

The workflow for SureSelect XT HS2 DNA target enrichment using the Magnis NGS Prep System is summarized in Figure 1. DNA samples, pre-plated reagents and labware are loaded on the instrument. Once loaded, the Magnis NGS Prep System performs all SureSelect XT HS2 DNA library preparation and target enrichment liquid handling and incubation steps. After the Magnis NGS Prep System run is complete, the target-enriched libraries are ready to be pooled for multiplexed NGS sample preparation and sequence analysis using Illumina sequencers.

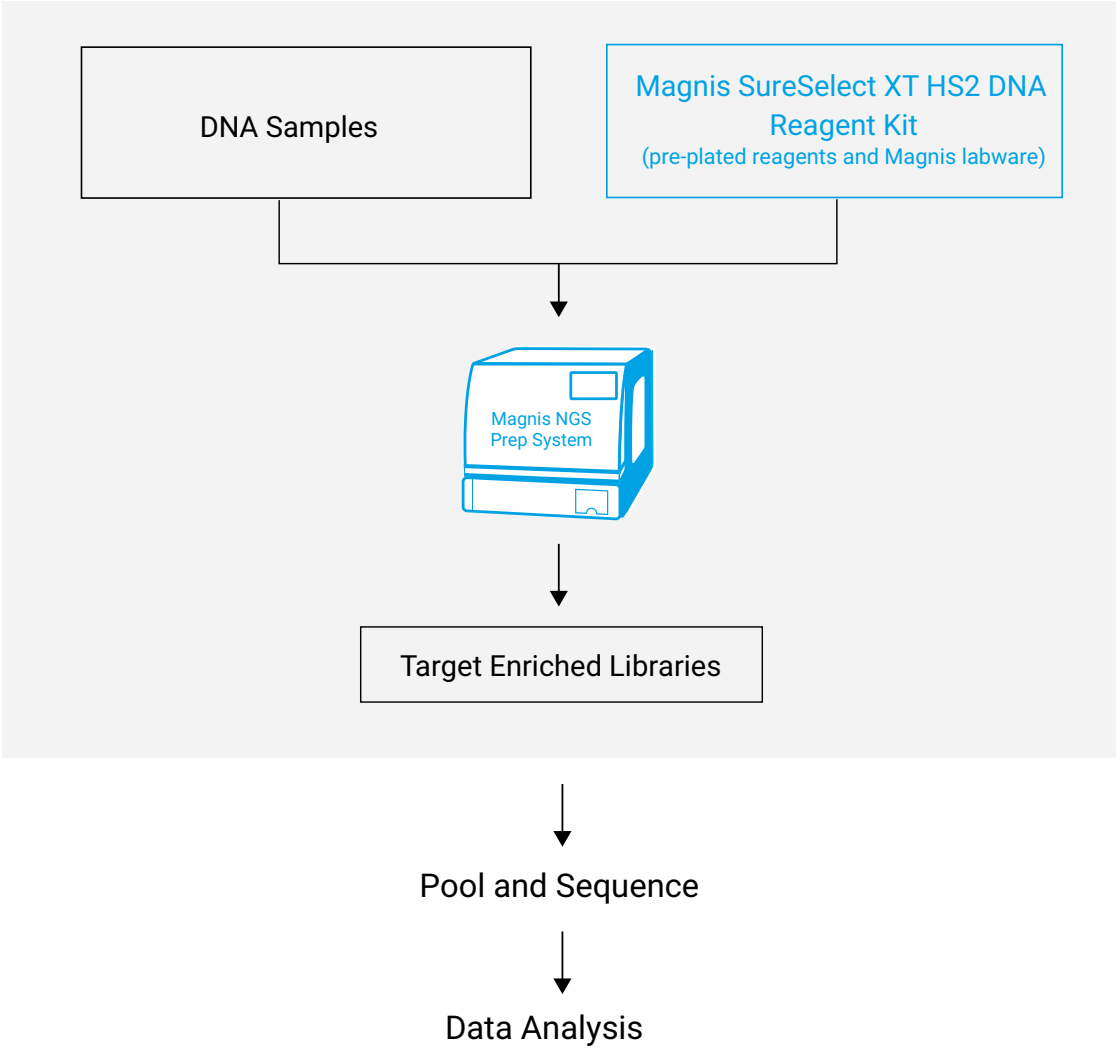



**Figure 1** Overall Magnis NGS Prep System NGS sample preparation workflow.

# Safety Notes

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

### Danger of Ultraviolet (UV) Light Exposure

The Magnis instrument door and side panels are not UV-transparent, therefore exposure to UV light is minimal. However, the following precautions are still needed.

- During decontamination of the instrument deck with UV light, do not look directly or indirectly at the UV light source.
- Always perform decontamination with the instrument door closed and locked. The instrument door is programmed to remain locked while the UV light is on.
- Replacement UV tubes must be provided by Agilent and must be installed by an Agilent engineer or Agilent authorized service provider.

### Danger of Burns

- During protocol runs, the thermal block and other components of the thermal cycler module quickly attain temperatures of greater than 50°C. To ensure safe operation, the instrument door must remain closed during runs. The instrument is programmed to keep the door locked while protocol runs are in progress.
- Use only Agilent materials (plates, adhesive seals, foils, mats) intended for use on the Magnis NGS Prep System. These materials are sufficiently temperature-stable (up to 120°C).

# Materials Required

## Required Materials for SureSelect XT HS2 DNA Magnis Runs

**Table 1** Supported Reagent Kits (select one)

| Description | 96 Reactions* | 32 Reactions† |
|---|---|---|
| Magnis SureSelect XT HS2 DNA Reagent Kit: | Agilent | Agilent |
| with Tier 1 (1–499 kb) Probe | p/n G9751B | p/n G9751A |
| with Tier 2 (0.5–2.9 Mb) Probe | p/n G9752B | p/n G9752A |
| with Tier 3 (3–5.9 Mb) Probe | p/n G9753B | p/n G9753A |
| with Tier 4 (6–11.9 Mb) Probe | p/n G9754B | p/n G9754A |
| with Tier 5 (12–24 Mb) Probe | p/n G9755B | p/n G9755A |
| with 24–50 Mb Probe | p/n G9756B | p/n G9756A |
| with Human All Exon V7 Probe | p/n G9773B | p/n G9773A |
| with Human All Exon V8 Probe | p/n G9774B | p/n G9774A |
| with SureSelect Clinical Research Exome V4 (CRE V4) Probe | p/n G9775B | p/n G9775A |
| with SureSelect Cancer CGP DNA Probe | p/n G9777B | p/n G9777A |
| with empty Magnis Probe Input Strips‡ | p/n G9750B | Not offered |

For a list of kit contents, see page 61 to page 63.

* 96-reaction kits are formatted for 12 runs containing 8 samples per run.

† 32-reaction kits are formatted for 4 runs containing 8 samples per run.

‡ Probe must be purchased separately. See page 51 for information on filling the empty Magnis Probe Input Strip for the run.

**Table 2** Required Equipment

| Description | Vendor and part number |
|---|---|
| Magnis NGS Prep System* | Agilent p/n G9710A |
| Robotic Pipetting Tips (Sterile, Filtered, 250 µL) | Agilent p/n G9477G |
| Hygrometer | Traceable Temperature/Humidity Data Logger, Cole-Parmer p/n 18004-13 or equivalent |
| Vortex mixer | Vortex Genie-2, VWR p/n 58815-234 or equivalent |
| Microcentrifuge | Eppendorf microcentrifuge model 5417C or equivalent† |
| Swinging bucket centrifuge | Eppendorf centrifuge model 5804 with A-2-DWP rotor or equivalent‡ |
| Pipettes (10-, 20-, and 200-µL capacity) | Rainin Pipet-Lite Pipettes or equivalent |
| Sterile, nuclease-free aerosol barrier pipette tips | General laboratory supplies vendor |
| Freezers (2) set to –20°C and –80°C | General laboratory supplies vendor |
| Refrigerator set to +4°C | General laboratory supplies vendor |
| Ice bucket | General laboratory supplies vendor |
| Powder-free gloves | General laboratory supplies vendor |

* The Magnis SureSelect XT HS2 Reagent Kits and the protocols detailed in this publication are also compatible with the MagnisDx NGS Prep System (p/n K1007A).

† Centrifuge rotor must accommodate the strip tubes supplied with Magnis SureSelect XT HS2 Reagent Kits.

‡ Centrifuge rotor must accommodate the deep-well plates supplied with Magnis SureSelect XT HS2 Reagent Kits. Refrigeration system is not required.

# Required Materials for DNA Sample Preparation and Analysis

**Table 3** Required Materials for DNA Sample Preparation and Analysis--All Sample Types

| Description | Vendor and part number |
|---|---|
| 1X Low TE Buffer (10 mM Tris-HCl, pH 7.5-8.0, 0.1 mM EDTA) | Thermo Fisher Scientific p/n 12090-015, or equivalent |
| Qubit BR dsDNA Assay Kit<br>100 assays<br>500 assays | Thermo Fisher Scientific<br>p/n Q32850<br>p/n Q32853 |
| Qubit Fluorometer | Thermo Fisher Scientific p/n Q33238 |
| Qubit Assay Tubes | Thermo Fisher Scientific p/n Q32856 |
| DNA Analysis System and Consumables:*<br>Agilent 4150/4200 TapeStation<br>TapeStation-compatible 8-well tube strips<br>8-well tube strip caps<br>High Sensitivity D1000 ScreenTape<br>High Sensitivity D1000 Reagents<br>**OR**<br>Agilent 5200/5300/5400 Fragment Analyzer Instrument<br>HS NGS Fragment Kit | <br>Agilent p/n G2992AA/Agilent p/n G2991AA<br>Agilent p/n 401428<br>Agilent p/n 401425<br>Agilent p/n 5067-5584<br>Agilent p/n 5067-5585<br><br>Agilent p/n M5310AA/M5311AA/M5312AA<br>p/n DNF-474-0500 |

* If available in your laboratory, the Agilent 2100 Bioanalyzer and High Sensitivity DNA Kit (p/n 5067-2646) may also be used for library DNA analysis.

**Table 4** Required Materials--High-Quality DNA Samples Only

| Description | Vendor and part number |
|---|---|
| High-quality gDNA purification system, for example:<br>QIAamp DNA Mini Kit<br>50 Samples<br>250 Samples | <br>Qiagen<br>p/n 51304<br>p/n 51306 |

**Table 5** Required Materials--FFPE DNA Samples Only

| Description | Vendor and part number |
|---|---|
| FFPE gDNA purification system, for example:<br>QIAamp DNA FFPE Tissue Kit, 50 Samples<br>Deparaffinization Solution | Qiagen<br>p/n 56404<br>p/n 19093 |
| FFPE DNA integrity assessment system:<br>Agilent NGS FFPE QC Kit (recommended method)<br>16 reactions<br>96 reactions<br>**OR**<br>TapeStation Genomic DNA analysis assay:*<br>Genomic DNA ScreenTape<br>Genomic DNA Reagents | <br>Agilent<br>p/n G9700A<br>p/n G9700B<br><br>Agilent<br>p/n 5067-5365<br>p/n 5067-5366 |

* Agilent's 4150 TapeStation or 4200 TapeStation, and compatible plasticware, are also required. See Table 3 above for ordering information.

## Optional Materials

**Table 6** Supplier Information for optional materials in protocols

| Description | Purpose | Vendor and part number |
|---|---|---|
| Covaris Sample Preparation System | Mechanical DNA shearing (non-automated alternative to enzymatic fragmentation) | Covaris model E220 |
| Covaris microTUBE sample holders | Mechanical DNA shearing (non-automated alternative to enzymatic fragmentation) | Covaris p/n 520045 |
| Dilute bleach (10%) wipes | Surface-cleaning of instrument deck (see page 18)* | Hype-Wipe Bleach Towelettes (VWR p/n 16200-218), or equivalent |
| Alcohol (70%) wipes | Surface-cleaning of instrument deck (see page 18)* | VWR Pre-Moistened Clean Wipes (VWR p/n 21910-110), or equivalent |
| Dry, lint-free, scratch-free wipers | Surface-cleaning of the barcode scanner window | Kimwipes wipers (VWR p/n 21905-026), or equivalent |
| Adhesive seal applicator | Application of foil seals to filled Magnis Sample Input Strips with reduced contamination risk (see page 22) | Thermo Fisher Scientific p/n AB1391, or equivalent |
| D1000 ScreenTape and D1000 Reagents | Analysis of optional pre-capture library QC samples using Agilent 4200/4150 TapeStation system (see page 41) | Agilent p/n 5067-5582 and p/n 5067-5583 |

* Agilent recommends use of the Magnis instrument UV-mediated decontamination programs for routine instrument decontamination. If solvent-based cleaning is required, see the instrument User Guide for complete surface cleaning instructions. Allowed solvents must be applied to a solid cloth support before use. Do not spray water, bleach, alcohol or other liquids inside the instrument. Remove any excess liquid from wipes or towelettes before use to prevent introduction of liquids into instrument components.

# 2 Sequencing Library Preparation using the Magnis NGS Prep System



This chapter contains instructions for SureSelect XT HS2 target-enriched DNA sequencing library preparation using the Magnis NGS Prep System. For an overview of the workflow, see Figure 1 on page 8.

Detailed instructions are provided here for setting up the Magnis NGS Prep System instrument and assay components for a run, then running a Magnis instrument protocol for automated NGS library sample preparation.

For each sample to be sequenced, an individual dual-indexed and molecular-barcoded library is prepared. Libraries prepared using the protocols described here are ready for sequencing using the Illumina paired-read system.

# Critical Sample Tracking Information

Accurate sample tracking is critical to the interpretation of your sequencing results. Before beginning a run, make sure you read and understand the sample tracking information in this section, including 1) sample number orientation in the Magnis Sample Input Strip wells and 2) how to enter sample identities in the Magnis software during run setup.

## Sample orientation in the Magnis Sample Input Strip wells

Magnis NGS Prep System runs use the sample orientation shown in Figure 2, below, with Sample 1 loaded in the well farthest from the barcode in the provided Magnis Sample Input Strips. Samples must be loaded in the Magnis Sample Input Strip wells in this orientation during run setup on page 21.

Before setting up the run, assign each sample to a specific sample number 1 through 8 and record the sample number assignments. Methods for entering sample assignments for a run into the Magnis software are described on page 15 to page 16.

**CAUTION** Do not add any writing or labels that may obscure the barcode on the Magnis Sample Input Strip.

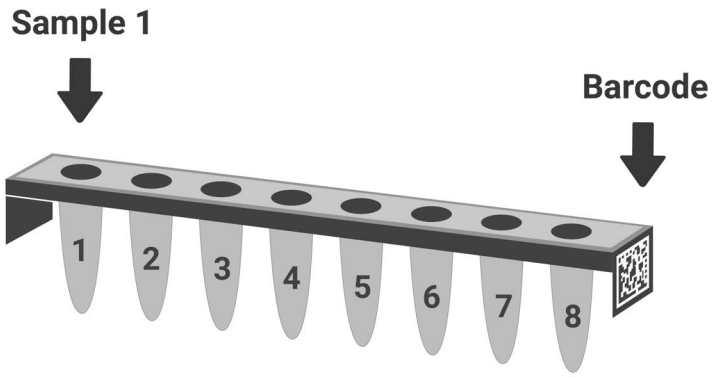



**Figure 2** Required orientation of sample numbers 1 through 8 in the Magnis Sample Input Strip.

## Assignment of samples to well positions in the Magnis software

The identity of each sample in the run must be specified in the Magnis instrument software using one of the two methods described below. The specific sample IDs to be included in a run are entered in the Magnis system during run setup as detailed in section "Step 4. Enter Sample Info" on page 37. Make sure you understand the sample positioning and tracking information below before you begin run setup.

Each Sample ID must contain 1–30 characters and must be unique within the run. Sample IDs may be reused in different runs.

### Sample assignment Method 1: Import of sample assignments using a .csv file

1 Create a .csv (comma separated value) file containing the ordered sample names. The sample name data may be entered in table format using a spreadsheet application, such as Microsoft Excel software, and then saved in .csv format.

**a** Enter the header text **sample_id** in cell A1, as shown in Figure 3.

**b** Enter the name of each sample in cells A2 through A9 (see Figure 3, left panel). The sample input file must contain 8 unique sample IDs. If any sample wells are left empty for the run, you must enter placeholder text in the corresponding positions (see Figure 3, right panel).

8 samples in run

| | A | B |
|---|---|---|
| 1 | sample_id | |
| 2 | HD18060701 | |
| 3 | HD18060702 | |
| 4 | HD18060703 | |
| 5 | HD18060704 | |
| 6 | HD18060705 | |
| 7 | HD18060706 | |
| 8 | HD18060707 | |
| 9 | HD18060708 | |
| 10 | | |

6 samples in run with 2 placeholder Sample IDs

| | A | B |
|---|---|---|
| 1 | sample_id | |
| 2 | HD18060701 | |
| 3 | HD18060702 | |
| 4 | HD18060703 | |
| 5 | HD18060704 | |
| 6 | HD18060705 | |
| 7 | HD18060706 | |
| 8 | empty1 | |
| 9 | empty2 | |
| 10 | | |

**Figure 3** Example .csv file content (shown in spreadsheet format) for uploading sample assignments

2 Save the file in .csv format.

3 Download the .csv file onto a unencrypted USB drive.

4 When setting up the run, on the *Enter Sample Info* screen, press the sample upload button shown below, then follow the protocol setup wizard prompts to transfer the Sample IDs from the USB drive.

### Sample assignment Method 2: Manual sample assignment using the Magnis instrument touchscreen

1 Record the identity of each sample number for the run using appropriate hardcopy or softcopy record keeping procedures before dispensing samples into the Magnis Sample Input Strip wells.

2 When setting up the run, follow the Magnis touchscreen prompts to enter the Sample ID for each sample well position using the *Enter Sample Info* screen shown below. The Magnis system automatically assigns a default Sample ID for each sample position. To change the Sample ID, first select a specific sample position on the touchscreen, then use the **Edit Sample ID** tool on the right to enter the desired Sample ID text. Press **Change** to save the entered Sample ID text for the sample.

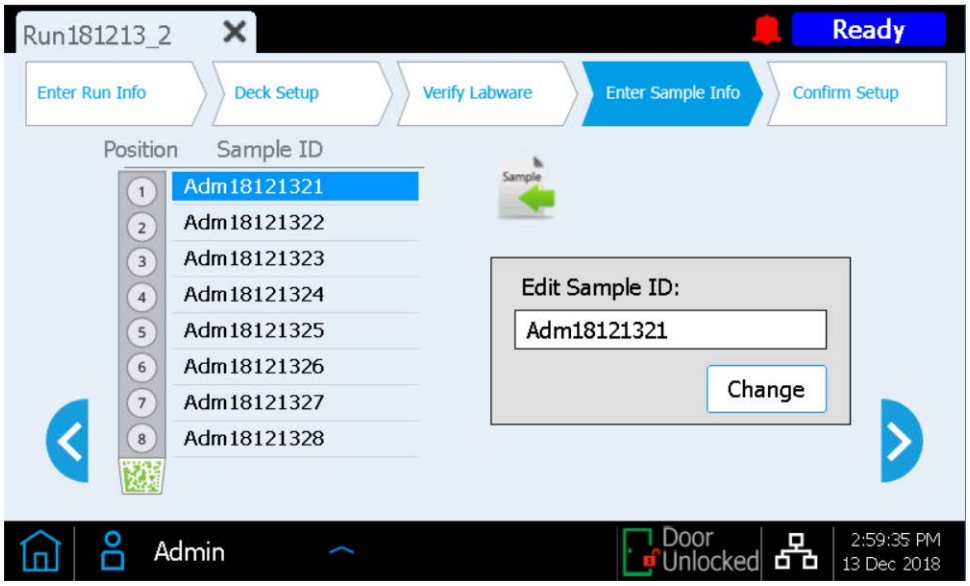



**Figure 4** Magnis touchscreen interface used for manual sample assignment during a run.

# Preparing Your DNA Samples for the Run

The library preparation protocol is compatible both with high-quality gDNA prepared from fresh or fresh-frozen samples and with lower-quality DNA prepared from FFPE samples. Runs to process either high-quality or FFPE-derived DNA can include 10 ng, 50 ng, 100 ng or 200 ng of input DNA. For optimal sequencing results, use the maximum amount of input DNA available within this range. All samples in the same run must be provided in the same quantity.

Before setting up the Magnis run, DNA samples must be prepared, quantified and qualified as described in "Appendix 1: DNA Sample Preparation Guidelines" on page 43. Some DNA sample preparation steps, especially qualification of FFPE-derived samples, may need to be completed up to a day prior to initiating the Magnis run steps.

Prior to NGS library preparation, all DNA samples must be fragmented either by enzymatic fragmentation or by mechanical shearing. Enzymatic DNA fragmentation is completed using Magnis automation when this step is included in the run setup (see page 25). Alternatively, DNA samples may be mechanically sheared immediately before use in the run using the non-automated protocols provided in "Appendix 1: DNA Sample Preparation Guidelines".

**NOTE**

Preparing the Covaris E220 instrument for DNA shearing requires approximately 30–60 minutes for chilling and degassing the water bath (see page 45 or page 48). For runs that include Covaris-sheared DNA, initiate these conditioning steps before you start any of the Magnis NGS Prep System and reagent setup steps on the following pages.

# Preparing the Magnis Instrument and the Reagents for the Run

## Step 1. Prepare the instrument for running a protocol

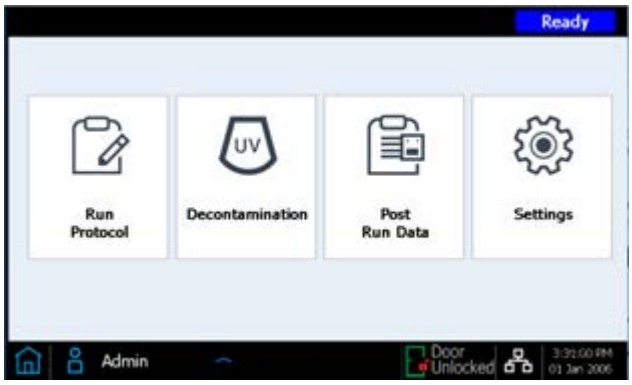
**NOTE** Instructions below include an instrument-mediated decontamination procedure that uses ultra-violet (UV) light to decontaminate the instrument deck. Other decontamination procedures (for example, using a 10% bleach solution) may be employed in addition to or as alternative to the automated UV decontamination procedure. See the Magnis instrument User Guide for complete surface decontamination and cleaning instructions.

1. Before you begin, use a hygrometer to measure the ambient humidity near the Magnis instrument. Verify that the non-condensing humidity is in the acceptable range of 30% to 70%.
2. Verify that the instrument deck is cleared of all labware from previous runs and of any other stray materials. Any materials present on the instrument deck during run setup can interfere with the instrument start-up and run setup processes.
3. Turn on the instrument by pressing the power button on the front of the device. Close the instrument door.

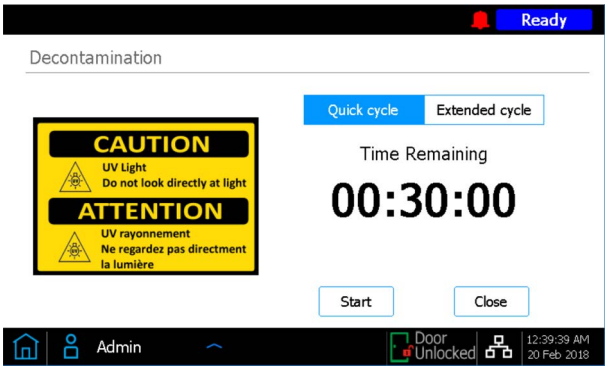
   The instrument turns on, the LED indicator lights inside the instrument illuminate, and the software launches on the touchscreen.

   Stand by as the system performs a series of start up activities, which may require several minutes.
4. Agilent recommends running the UV decontamination *Quick cycle* procedure (requires 30 minutes) prior to every run, using the steps below.

   **a** From the Home screen, press **Decontamination**.



**b** From the Decontamination screen, press **Quick cycle**, then press **Start**. The duration of the *Quick cycle* decontamination procedure is 30 minutes. The LED indicator lights are off during the UV decontamination procedure, with the instrument's UV light tube emitting UV light during this interval.




**WARNING** **Do not look directly at the UV light while decontamination is in progress.**

**NOTE** During the 30-minute decontamination process, begin the reagent preparation steps detailed on page 20.

**5** Once the decontamination cycle is complete, the instrument's LED indicator lights will emit blue light. Return to the Home screen using the touchscreen display for access to run setup steps.

# Step 2. Prepare the SureSelect XT HS2 DNA reagents and plasticware

The reagent and plasticware components used in each Magnis SureSelect XT HS2 DNA run are listed in Table 7. Review the "Plate and Strip Tube Handling Instructions" section below before starting the preparative steps listed in the table.

**Table 7** Magnis SureSelect XT HS2 DNA run consumables (RT=Room Temperature)

| Quantity | Component | Storage condition | Preparative steps |
|---|---|---|---|
| 1 | Magnis SureSelect XT HS Beads/Buffers Plate ILM* | +4°C | See step 1 on page 21.<br>Held at RT for 30 min prior to run. |
| 1 | Magnis SureSelect XT HS2 Reagent Plate ILM | –20°C | See step 2 on page 21.<br>Thawed at RT for 15–30 min prior to further processing. |
| 1 | Empty Magnis Sample Input Strip (red) and replacement foil seal from same package | RT | Ready to fill.<br>See step 3 on page 22 for filling instructions. |
| 1 | Index strip (black) from the Magnis SureSelect XT HS2 Index Primer Pairs ILM plate | –20°C | See step 4 on page 23.<br>Thawed on ice briefly prior to further processing. |
| 1 | Probe strip (white) from the Magnis SureSelect Probe Plate, Pre-filled Single Well Format† | –80°C | See step 5 on page 23.<br>Thawed on ice briefly prior to further processing. |
| 1 | Magnis Empty Consumables box containing: Magnis Tip Waste Bin, Magnis Deep-Well HSM Plate, Magnis Thermal Cycler Seal, Magnis 96-Well PCR Plate, Magnis Library Output Strip (green), Magnis QC Strip (blue), Magnis Foil Seals | RT | Ready to use. |
| 3 | Boxes Robotic Pipetting Tips (purchased separately from the Magnis Reagent Kit) | RT | Ready to use. |

* The supplied *Magnis SureSelect XT HS Beads/Buffers Plates ILM* are used in both Magnis SureSelect XT HS2 and Magnis SureSelect XT HS runs.

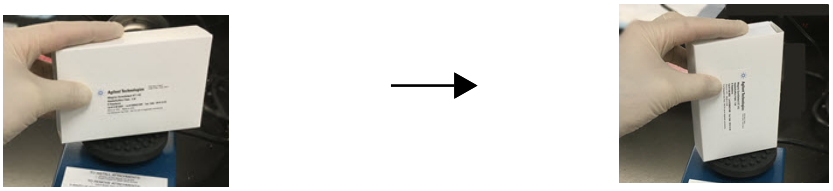
† Runs using protocol *SSEL-DNA-XTHS2-EPIS-ILM* require one (1) empty Magnis Probe Input Strip (white), stored at RT. The empty probe strip must be filled before use in the run using the instructions provided on page 51.

### Plate and Strip Tube Handling Instructions

Familiarize yourself with the important labware handling instructions below before you start the component preparation steps on page 21 to page 23.

- Magnis Sample Input Strips (red strips provided in plate format, p/n 5190-9882 or 5191-5676), along with all input DNA sample preparation and dilution reagents, should be stored and used only in pre-PCR areas of the laboratory.
- The adhesive seals and foils covering the kit plates and strip tubes must be left in place during run setup and execution. Avoid touching or damaging the foil and adhesive covers during run setup. The sample input strip foil cover is pierced during run setup, and the wells must be re-sealed with a fresh foil seal strip provided in the same package. Take care to avoid contamination or other damage to the replacement foil seals.
- Filled reagent plates (both Magnis SureSelect XT HS Beads/Buffers Plates and Magnis SureSelect XT HS2 Reagent Plates) are provided in white cardboard sleeves. Leave the filled plates in the sleeves during all of the preparation steps described below. To visually inspect the plate wells, carefully slide the reagent plate **only partially** out of the sleeve to avoid bending or damaging the foil or adhesive cover. Improper re-insertion of the plate into the sleeve may compromise the plate integrity.

- Vortex the filled reagent plates after thawing using the following procedure, illustrated in the pictures below. Use a vortex equipped with a broad, rubber-coated platform (as shown), and use a high-speed setting throughout the procedure. Hold the sleeved plate in a vertical position (on its side) instead of horizontally while vortexing. Begin by pressing one long side of the plate on the vortex head and mix for 10 seconds.Then rotate the plate 90° and press short side of the plate on the vortex head for an additional 10 seconds. Continue the rotation/10 second mixing sequence until completed on all four sides of the plate.



- If a kit component appears damaged during unpacking or run setup (e.g. foil or adhesive cover is pierced or plasticware is broken), do not use the component; contact Agilent Technical Support for assistance.

### Sample and Reagent Setup Steps

1 Prepare the **Magnis SureSelect XT HS Beads/Buffers Plate** for the run using the steps below:

   **a** Transfer one Magnis SureSelect XT HS Beads/Buffers Plate from storage at +4°C to room temperature (RT), keeping the plate in the white cardboard sleeve. Allow the sleeved plate to equilibrate to RT for at least 30 minutes before use in the run.

   **b** Vortex the sleeved plate, with the plate positioned vertically as detailed in the handling instructions section above.

   **c** Spin the sleeved plate in a centrifuge set at 250 × *g* for 3 seconds to collect the liquid without pelleting the beads (begin timing once centrifuge achieves full speed). Do not exceed the recommended spin speed and duration to prevent pelleting the beads.

   **d** Keep the sleeved plate at RT for use in same-day run.

2 Prepare the **Magnis SureSelect XT HS2 Reagent Plate** using the steps below:

   **a** Transfer one Reagent Plate from storage at –20°C to RT, keeping the plate in the white cardboard sleeve. Allow the reagents to thaw at RT for 15 to 30 minutes. Slide the plate partially out of the sleeve and visually confirm that the reagents are completely thawed.

   **b** Once the well contents are thawed, vortex the sleeved plate with the plate positioned vertically as detailed in the handling instructions section above.

   **c** Spin the sleeved plate in a centrifuge set at 250 × *g* for 1 minute (begin timing once centrifuge achieves full speed). Check bottoms of the plate wells for any bubbles, and if bubbles are present, repeat the spin step until all bubbles are released.

   **d** Keep the sleeved plate on ice for use in same-day run.

3 Prepare the **Magnis Sample Input Strip** using the steps below. Ensure that all DNA samples for the run were prepared using methods appropriate for the sample type and fragmentation method, as detailed on page 43 to page 49.

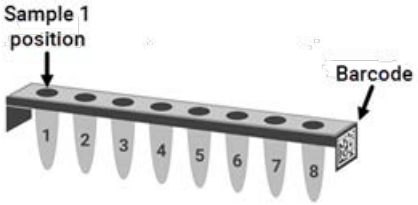
**CAUTION** Make sure to load the correct sample volume for your application in this step.

- For Magnis-automated enzymatic fragmentation of input DNA, **load 14 µL of unsheared DNA.**
- For Covaris pre-sheared input DNA, **load 50 µL of sheared DNA.**

**a** Obtain the Magnis Sample Input Strips kit from storage at RT. Remove one empty red Sample Input Strip (with "S" inscribed on end of strip) from the plate support, leaving the foil cover in place. Set aside one fresh foil seal strip and attached backing for re-sealing in step c.

**b** Place 14 µL of unsheared DNA or 50 µL of sheared DNA in each sample well, piercing the foil seal with the pipette tip just before dispensing the liquid. All wells of the strip must contain the same input amount of DNA (10 ng, 50 ng, 100 ng or 200 ng).

**Make sure to load samples in the correct sample well position, with Sample 1 in the well farthest from the barcode, as shown in the figure below.**




**c** Once all samples have been placed in the Magnis Sample Input Strip wells, re-seal the strip tube with a fresh foil seal, taking care to avoid obscuring the strip tube barcode with the foil seal. Ensure that the seal is applied firmly and evenly, without excessive overhangs or creases that could obstruct strip tube seating when loading in the instrument.

**NOTE** Take care to avoid contamination with nucleases and foreign nucleic acids during application of the foil seal. Consider using a seal applicator (cleaned before each use) for this step. See Table 6 on page 12 for applicator recommendation.

**d** Visually check the sealed sample wells to verify that no bubbles are present. Remove any bubbles by spinning the prepared sample strip in a centrifuge set at 250 × *g* for 5 seconds or until all bubbles are released from the DNA solution.

**e** Keep the sealed sample strip tube on ice until use on page 34.

4 Prepare the **index strip tube** using the steps below:

**a** Determine the appropriate set of indexes to use for the run. The provided index strips are inscribed with *D1* through *D24* on the strip tube end opposite the barcode to indicate the specific set of dual-index pairs contained in the wells (see page 65 for index maps).

**NOTE**

Ensure that each sample to be multiplexed is indexed using a unique index pair.

- If samples from different Magnis NGS library preparation runs will be multiplexed for NGS, each run must use a different-numbered index strip.
- Agilent's SureSelect XT HS2 index pairs use a uniform numbering system across all formats. For example, index pairs 1-96 provided in Magnis XT HS2 index strips *D1* to *D12* (black strip tubes) are equivalent to index pairs 1-96 provided in orange plates in the SureSelect XT HS2 Reagent Kits formatted for manual processing. Do not combine samples indexed with the same-numbered index pair from different kit formats for multiplex sequencing.

**b** Obtain the Magnis SureSelect XT HS2 Index Plate from storage at –20°C. Remove the appropriate black index strip (labeled *D1* through *D24*) from the plate support, leaving the foil cover in place. Place the removed strip on ice to thaw and return the plate with remaining index strips to storage at –20°C.

**c** Once the index strip well contents are thawed, vortex the strip at high speed for 5 seconds.

**d** Spin the index strip in a centrifuge set at 250 × *g* for 5 seconds. Check the strip wells to verify that the liquid is collected in the bottom of the wells and that no bubbles are present. Remove any bubbles by repeating the spin step until all bubbles are released.

**e** Keep the index strip tube on ice until use on page 34.

5 Prepare the **probe strip tube** using the steps below for kits supplied with a pre-filled probe plate (*Magnis SureSelect Probe Plate, Pre-filled Single Well Format*). Note that the full volume of probe solution is provided in well A, with wells B through H provided empty.

If your kit instead includes empty probe strips (kit p/n G9750B) for run-time probe filling, skip the instructions below and prepare the probe strip using the instructions on page 51.

**a** Obtain the Probe Plate from storage at –80°C. Remove one white probe strip (with "P" inscribed on strip end) from the plate support, leaving the foil cover in place. Thaw the probe strip on ice and return the plate with remaining probe strips to storage at –80°C.

**CAUTION**

The probe strips do not include human-readable labels showing the specific probe design identity. Use appropriate care to track and maintain probe strip identity once a probe strip is removed from the plate packaging. Do not open multiple boxes and remove probe strip tubes for different probe designs at the same time.

**b** Once the probe is thawed in the strip well, vortex the strip at high speed for 5 seconds.

**c** Spin the probe strip in a centrifuge set at 250 × *g* for 5 seconds. Visually inspect well A to verify that the liquid is collected in the bottom of the well and that no bubbles are present. Remove any bubbles by repeating the spin step until all bubbles are released.

**d** Keep the probe strip on ice until use on page 34.

6 Obtain one **Magnis Empty Consumables** box from storage at RT for use during deck setup.

Proceed to "Running the Library Preparation Protocol" on page 24.

# Running the Library Preparation Protocol

When the Magnis instrument and all reagents have been prepared for the SureSelect XT HS2 DNA run, follow the prompts provided on the instrument touchscreen to load the labware on the instrument and run the library preparation protocol. The steps are summarized in Figure 5.

The Magnis instrument touchscreen provides prompts for entering the run information, loading the deck, verifying that all labware is present and has the required properties, entering sample information, and confirming the protocol setup. During these setup steps, the instrument's on-deck LED indicator lights emit white light. Additional information about each of these prompted steps is provided for new users on page 25 to page 38.

During the protocol run, the system performs library preparation and target enrichment on your DNA samples to generate target-enriched DNA libraries that are ready for sequencing. During the run, the LED indicator emits green light.

When the run is complete the system touchscreen guides you through the steps for removing the final sequencing library samples and QC samples (if included) from the instrument. After the LED indicator emits blue light, the instrument door can be opened and samples removed for further processing. Guidelines for processing the final target-enriched libraries for DNA sequencing are provided in "Appendix 3: Guidelines for Post-run DNA Sample Processing for NGS" on page 53.

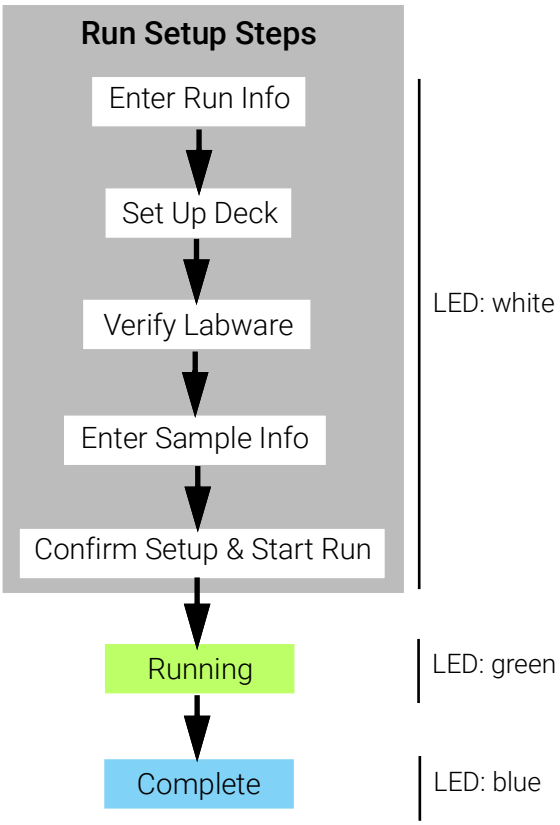



**Figure 5** Overview of steps for Magnis NGS Prep System run setup and completion. The color of the light emitted by the instrument's LED indicator lights during these steps is shown at right.

# Step 1. Initiate the protocol and Enter Run Info

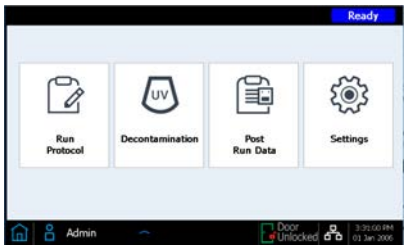
The run setup steps in this section include selection of the specific Magnis protocol to run. Table 8 describes the Magnis protocols supported by this publication. A different set of protocols may be available for use on your instrument and visible on your touchscreen. See page 73 for more information on Magnis protocol availability.

**Table 8** Usage information for Magnis protocols supported in this publication

| Protocol Name | Reagent Kit Format Supported |
|---|---|
| ***SSEL-DNA-XTHS2-ILM*** | Use to process Magnis SureSelect XT HS2 DNA Reagent Kits supplied with **pre-filled probe input strips** (kits with probe plate labeled *Magnis SureSelect Probe Plate, Pre-filled Single Well Format*) |
| ***SSEL-DNA-XTHS2-EPIS-ILM*** | Use to process Magnis SureSelect XT HS2 DNA Reagent Kits supplied with **empty probe input strips (EPIS)**. The probe input strip must be filled prior to the run as detailed on page 51. |

1 From the touchscreen Home screen, press **Run Protocol**.

The system locks the instrument door and performs an Instrument Health Check (IHC), which may require several minutes. If the display reports an IHC issue, see page 72 and page 73 for remediation guidelines.

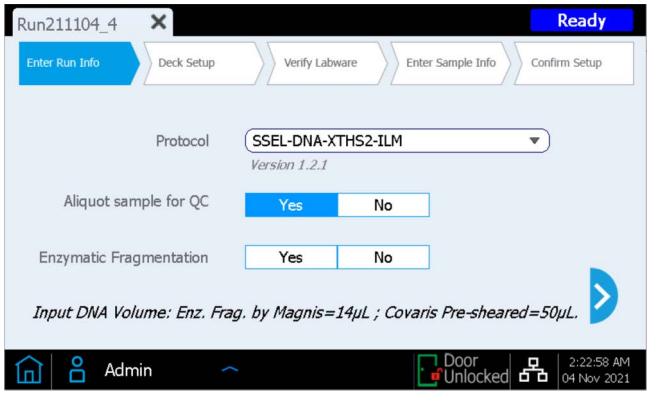



2 Follow the prompts provided on the *Enter Run Info* screens.

If you need more information about using the *Enter Run Info* screens, see the appropriate section below for the Magnis firmware version running on your instrument. For instruments running firmware version 1.5 or later, go to page 27.

### *Enter Run Info* instructions for Magnis firmware v1.4 and earlier:

1 On the first screen, specify the protocol name and whether to include optional QC sample collection and enzymatic fragmentation steps in the run.



**a** Expand the **Protocol** menu by pressing the drop-down arrow, and scroll to then select the protocol appropriate for your reagent kit format (see Table 8 on page 25).

**b** If you want the instrument to take an aliquot (3 µL) of each pre-capture library sample for optional post-run QC analysis press **Yes** next to **Aliquot sample for QC**. (The pre-capture QC samples are only available for analysis when the full run is complete.) If you are making this selection, be sure to load the blue QC Strip during deck setup on page 34.

Or, press **No** to skip the optional QC aliquot collection step.

**c** Use the **Enzymatic Fragmentation** setting buttons to include or exclude automated enzymatic DNA fragmentation in the run.

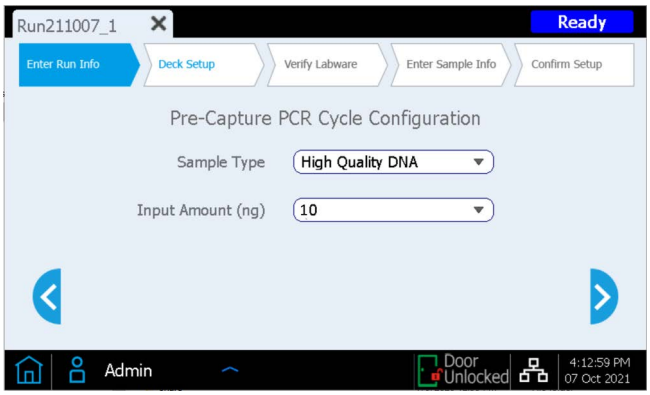
If the samples are unsheared DNA (14 µL volume), press **Yes** to include automated enzymatic fragmentation by the Magnis system in the run.

Or, if the samples are Covaris-sheared DNA (50 µL volume), press **No** to skip the enzymatic fragmentation step.

You must indicate whether to include enzymatic fragmentation in the automated protocol by selecting either **Yes** or **No** before you can proceed to the next screen.

**d** Press the forward arrow to advance to the next *Enter Run Info* screen.

2 On the second screen, select the appropriate **Sample Type** (either *High Quality DNA* or *FFPE DNA*) and the DNA **Input Amount** (*10 ng, 50 ng, 100 ng*, or *200 ng*) for the samples being processed in the run. These settings are used to determine the correct PCR cycling conditions for the run. PCR cycle number and other conditions to be used during the run are reported during *Confirm Setup* steps (see page 38).

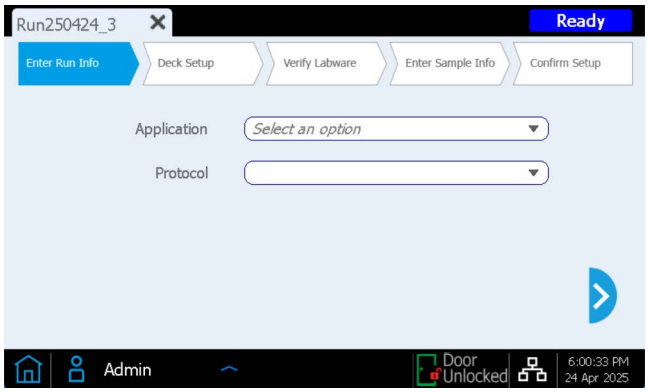



3 Press the forward arrow to advance to the *Deck Setup* screens and proceed to page 29 for deck setup instructions.

***Enter Run Info* instructions for Magnis firmware v1.5 and later:**

1 On the first screen, expand the **Application** menu by pressing the drop-down arrow and select *DNA Seq*.

Expand the **Protocol** menu and scroll to then select the protocol appropriate for your reagent kit format (see Table 8 on page 25). Press the forward arrow to advance to the next *Enter Run Info* screen.




2 Specify whether to include optional QC sample collection and enzymatic fragmentation steps in the run using the **Yes/No** buttons shown below.


**a** If you want the instrument to take an aliquot (3 µL) of each pre-capture library sample for optional post-run QC analysis press **Yes** next to **Aliquot sample for QC**. (The pre-capture QC samples are only available for analysis when the full run is complete.) If you are making this selection, be sure to load the blue QC Strip during deck setup on page 34.

Or, press **No** to skip the optional QC aliquot collection step.

**b** Use the **Enzymatic Fragmentation** setting buttons to include or exclude automated enzymatic DNA fragmentation in the run.

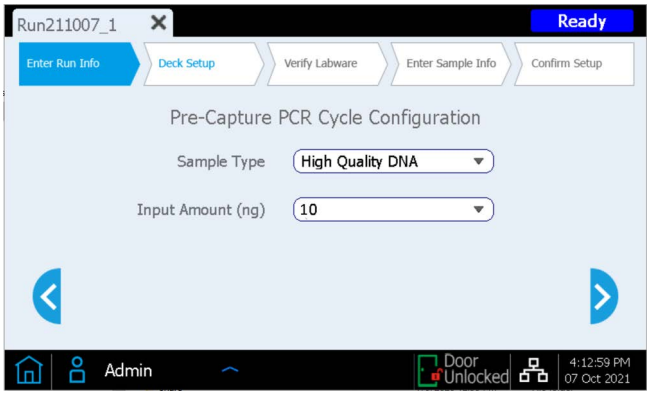
If the samples are unsheared DNA (14 µL volume), press **Yes** to include automated enzymatic fragmentation by the Magnis system in the run.

Or, if the samples are Covaris-sheared DNA (50 µL volume), press **No** to skip the enzymatic fragmentation step.

You must indicate whether to include enzymatic fragmentation in the automated protocol by selecting either **Yes** or **No** before you can proceed to the next screen.

**c** Press the forward arrow to advance to the next *Enter Run Info* screen.

3 Select the appropriate **Sample Type** (either *High Quality DNA* or *FFPE DNA*) and the DNA **Input Amount** (*10 ng, 50 ng, 100 ng*, or *200 ng*) for the samples being processed in the run. These settings are used to determine the correct PCR cycling conditions for the run. PCR cycle number and other conditions to be used during the run are reported during *Confirm Setup* steps (see page 38).




4 Press the forward arrow to advance to the *Deck Setup* screens and proceed to page 29 for deck setup instructions.

## Step 2. Set up the deck

The Magnis touchscreen interface guides you through the deck setup steps. Additional information is provided for new users on page 30 to page 34. The image below shows a fully set-up deck for orientation to the Magnis deck positions and the run labware.

While completing the deck setup steps specified on the touchscreen display, pay special attention to the critical details below to ensure an error-free run:

- Make sure that all labware is positioned flat on the designated deck platform or fully seated in the appropriate labware holder. Refer to the detailed labware loading instructions and positioning precautions provided for each labware component on page 30 to page 34. Improperly positioned labware can cause low or no final library yield for some or all samples.
- Make sure tip boxes are completely full and are seated flat on the platforms. Verify that each tip box is placed within the raised-tab frame of its platform position and that the boxes do not become unseated during lid removal.
- Load strip tubes in the chiller module in left-to-right order to facilitate proper seating of the strip tubes.
- Make sure all labware is positioned with barcode facing you (front of instrument).

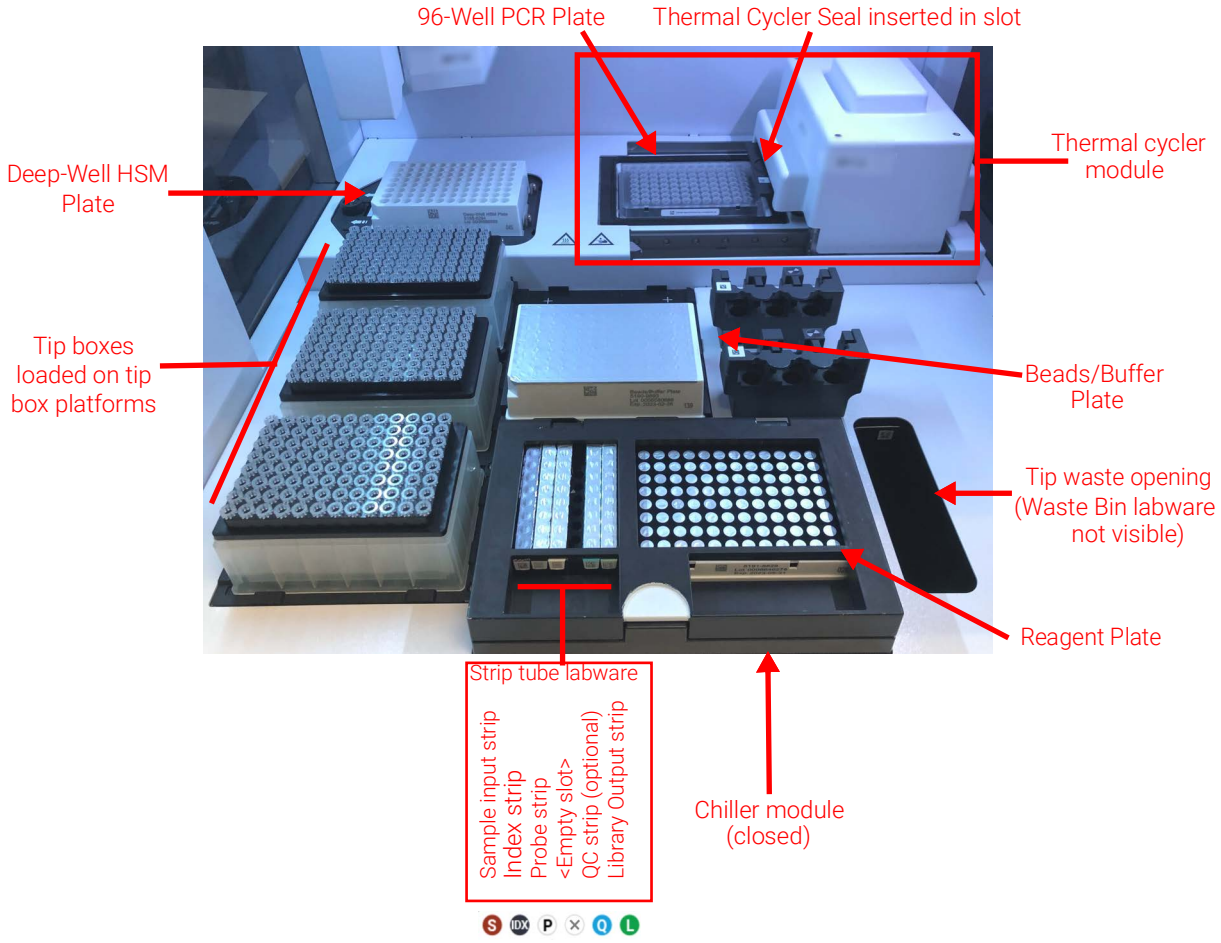
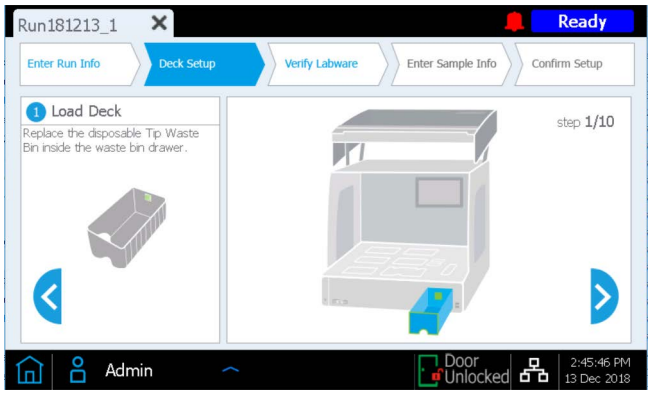


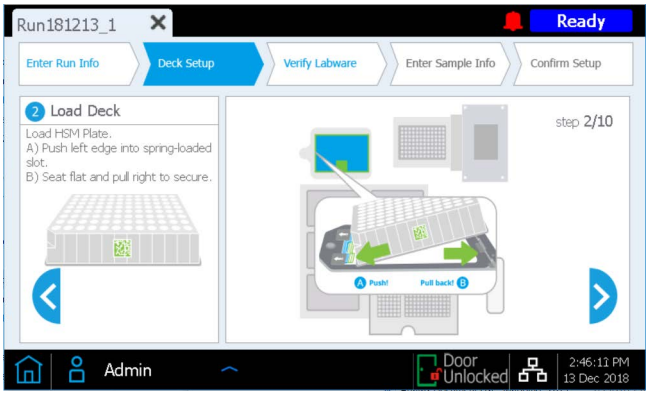

**Figure 6** Instrument deck loaded for run. Colors of the strip tube labware are shown in circles below the strip legend.

The *Deck Setup* steps prompted by the Magnis touchscreen interface are detailed below. For each deck loading step, the deck position to be loaded is shaded in blue on the touchscreen display. Once each step is completed, press the forward arrow to advance to the next screen.

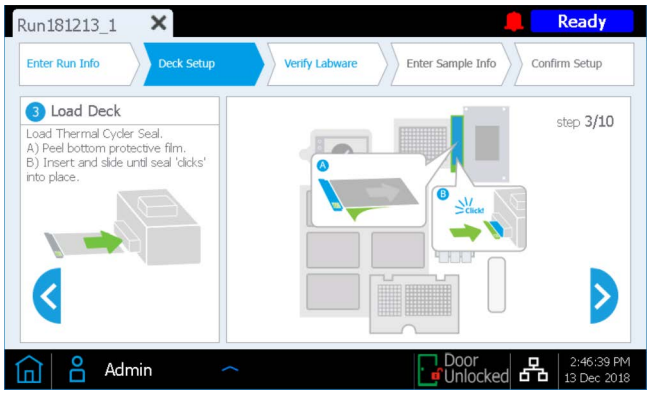
1 Remove the disposable Magnis Tip Waste Bin from the Magnis Empty Consumables package. Place the disposable bin in the waste bin drawer, with the barcode facing you, as shown on the touchscreen. Close the waste drawer.



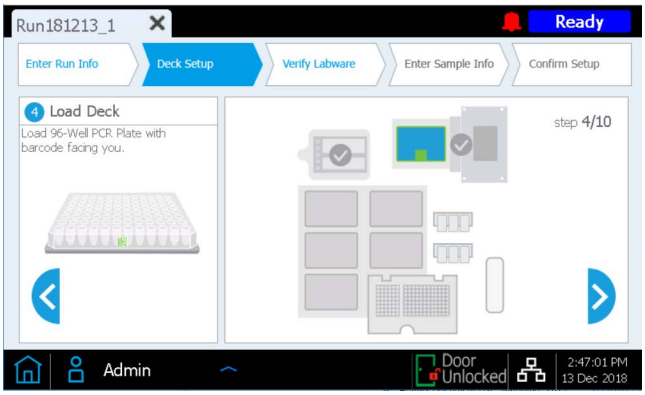

2 Remove the Magnis Deep-Well HSM Plate from the Magnis Empty Consumables package. Install the plate in the deck position shown on the touchscreen, with the barcode facing you. To load the plate, first insert the left edge of the plate into the spring-loaded slot, then lower the right edge of the plate down until the plate is flat on the platform. Once flat, shift the plate slightly to the right (as aided by the spring mechanism) and ensure that the plate is fully seated and secured inside the holder on the platform.



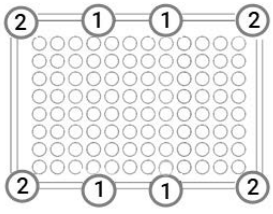
3 Remove the Magnis Thermal Cycler Seal from the Magnis Empty Consumables package. Peel the protective film from the foam pad below the metal plate, starting with the yellow tab. After the full sheet of film has been removed, insert the Thermal Cycler Seal into the slot at the position shown on the touchscreen, with the barcode facing up. Continue sliding the Thermal Cycler Seal into the slot until it clicks into place.



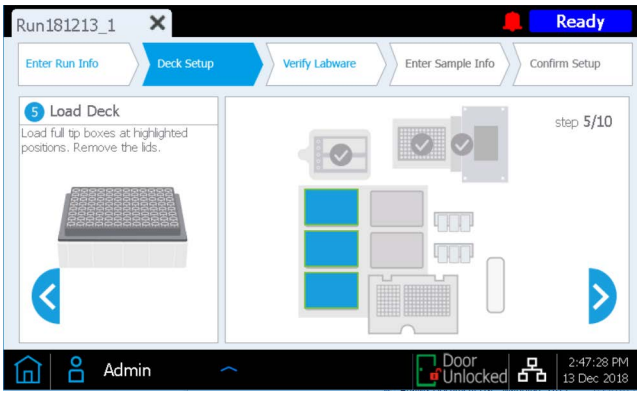

4 Remove the Magnis 96-Well PCR Plate from the Magnis Empty Consumables package. Load the plate in the deck position shown on the touchscreen by inserting the plate wells into the thermal cycler block wells, with the plate barcode facing you.



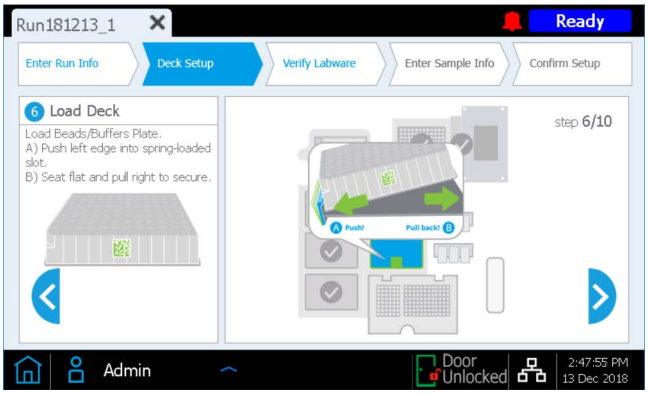

To ensure that the plate is fully seated in the block, first secure the center of the plate in the block wells by pressing evenly at plate positions marked **1** in figure below. Then press evenly on all four corners of the plate (positions marked **2** in figure below).



5 Load a fresh, full tip box at each of the deck positions indicated on the touchscreen. **Remove lids** from the boxes. After lid removal, verify that each tip box remains sitting flat and within the raised-tab frame of its platform position.

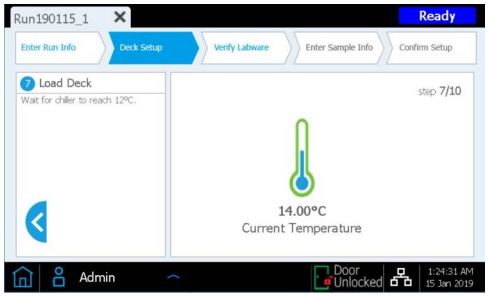



6 Obtain the Magnis SureSelect XT HS Beads/Buffers Plate that was prepared on page 21. Remove the white cardboard sleeve, then load the plate in the deck position shown on the touchscreen, with the barcode facing you. To load the plate, first insert the left edge of the plate into the spring-loaded slot, then lower the right edge of the plate down until the plate is flat on the platform. Once flat, shift the plate slightly to the right (as aided by the spring mechanism) and ensure that the plate is fully seated and secured inside the holder on the platform.



7 The instrument's chiller module must reach the correct temperature (typically 12°C) before it can be loaded for the run in step 8 below. Until the chiller reaches loading temperature, the touchscreen display appears as below, allowing you to check the status of the chiller.

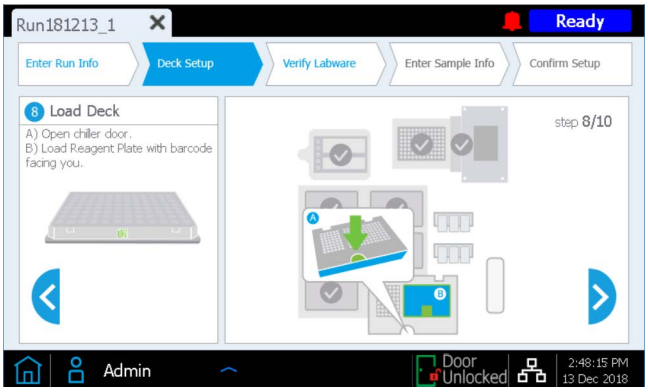
This screen may not appear during your run, if the chiller has already reached the required temperature.




8 Load the chiller module as described below.

**a** Open the chiller door by pressing on the half-circle button indicated with a green arrow on the touchscreen.

**b** Obtain the Reagent Plate that was prepared on page 21. Remove the white cardboard sleeve and check bottoms of wells for any bubbles. If bubbles are present, remove by spinning the plate as directed on page 21. Load the plate in the chiller module in position shown on the touchscreen, with the barcode facing you. Press down firmly, applying pressure evenly across the plate. Make sure the reagent plate is securely seated in the chilled plate holder.



9 Load the strip tubes for the run in the indicated positions of the chiller as detailed below, in the order listed. Before loading each strip, check bottoms of wells for any bubbles. If bubbles are present, remove by spinning the strip as directed on page 22. Ensure that each strip is properly seated by pressing firmly and evenly on the strip tube edges during loading. Avoid touching or damaging the foil covers. **Make sure to orient each strip tube with the barcode facing you.**

**a** Load the **red sample strip tube containing input DNA samples** (prepared on page 22 and held on ice) into the strip tube holder position labeled with **S**. Leave the foil cover intact.

**b** Load the **black strip tube containing indexed primers** (prepared on page 23 and held on ice) into the strip tube holder position labeled with **IDX**. Leave the foil cover intact.

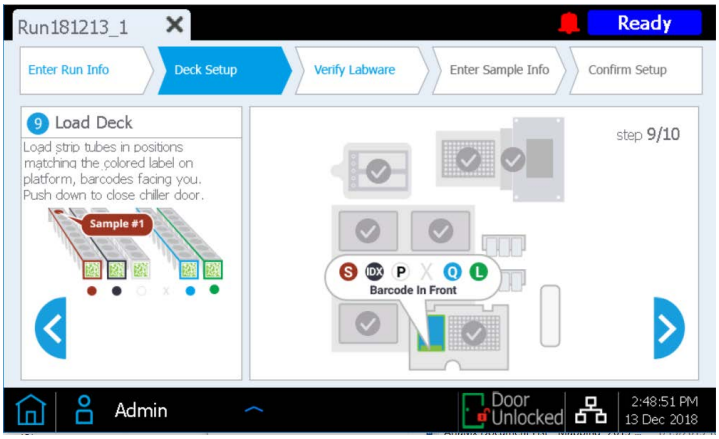
**c** Load the **white strip tube containing probe solution** (prepared on page 23 or page 51 and held on ice) into the strip tube holder position labeled with **P**. Leave the foil cover intact.

**d** Obtain the Magnis Library Output Strip, QC Strip, and Foil Seals pack from the Magnis Empty Consumables package. Load the **empty green library output strip** (with "L" inscribed on end of strip) into the strip tube holder position labeled with **L**. Leave the foil cover intact.

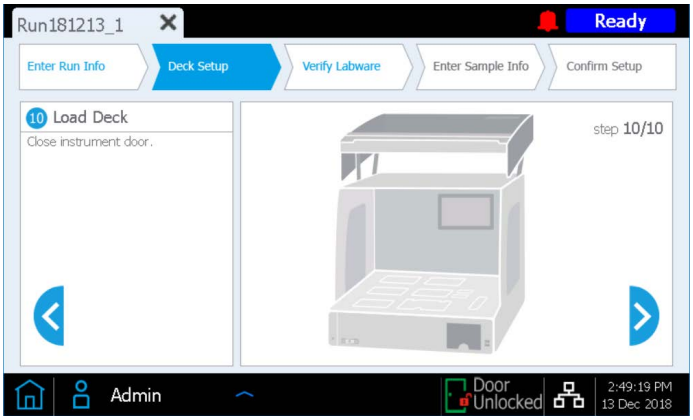
If the run will include collection of aliquots of the pre-capture library samples for QC, load the **empty blue QC strip** (with "Q" inscribed on end of strip) into the strip tube holder position labeled with **Q**. Leave the foil cover intact.

Keep the fresh Foil Seals supplied in the package ready for use at the end of the run.

**e** Once strip tubes are loaded at the **S, IDX, P, L,** and **Q** (when included) positions, close the chiller door. (Make sure door is fully closed, as indicated by an audible clicking sound).



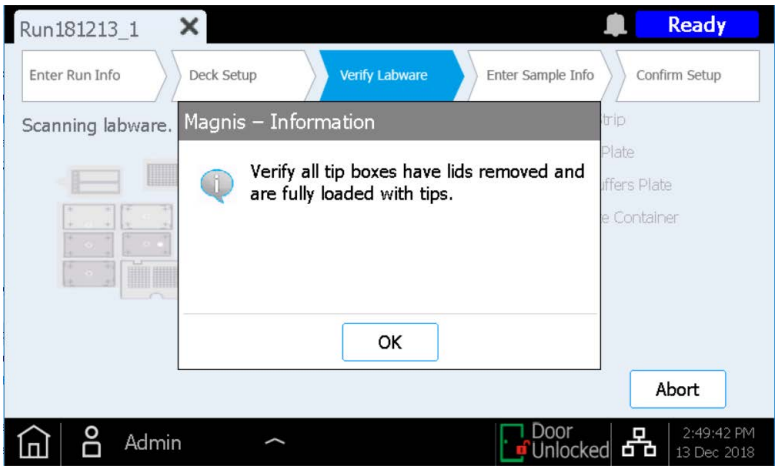

**10** Close the instrument door.



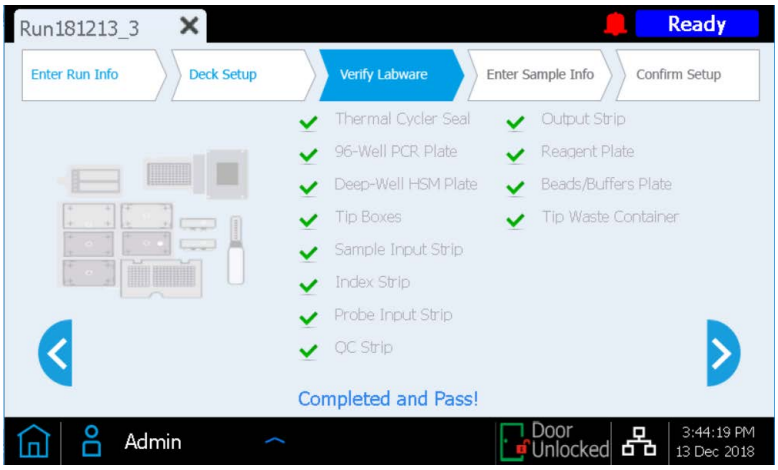
## Step 3. Verify Labware

Once all *Deck Setup* steps are complete, the instrument performs the *Verify Labware* phase of the run, in which the instrument scans the barcode on each of the labware components present on the deck.

Before starting the automated labware verification, you need to verify that lids have been removed from all tip boxes and that all tip boxes are full, as indicated in the prompt below. Once the tip box status has been verified, press **OK** to begin the instrument's automated labware verification routine.



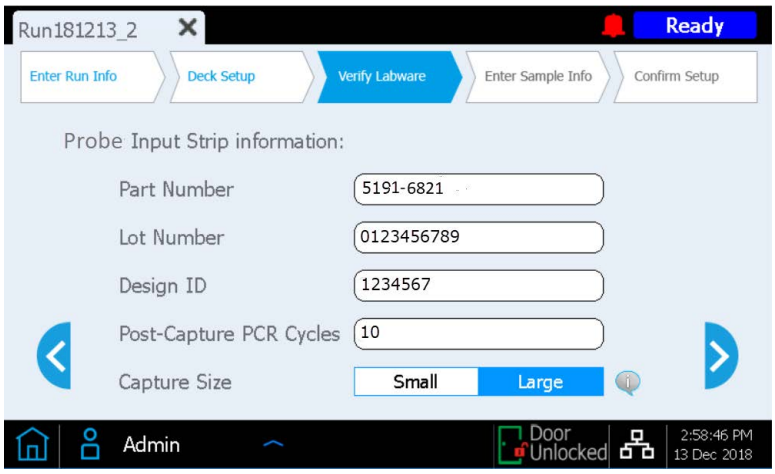

During the barcode scan, the instrument verifies that all components required for the run type are present, in the correct position and orientation, and are not expired. Results of the verification are displayed on the Magnis touchscreen. Press the forward arrow to proceed.




If the *Verify Labware* screen reports an issue with one or more run components, see troubleshooting information on page 73 for remediation guidelines.

The final *Verify Labware* screen allows you to review details for the Probe Input Strip.

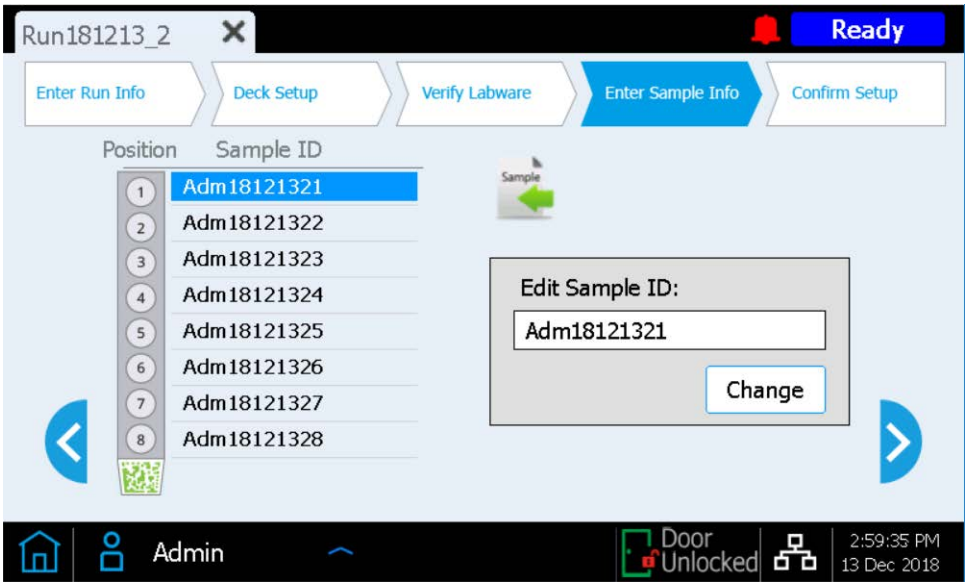
**For runs that include pre-dispensed probes** the identity of the probe solution is automatically conveyed to the Magnis software by the strip barcode, and the probe properties are reported for your review as shown below. Press the forward arrow to proceed.




**For *SSEL-DNA-XTHS2-EPIS-ILM* runs using run-time filled probe strips**, you must enter the probe-related properties on this screen manually. See the instructions on page 52. Once all fields are populated, press the forward arrow to proceed.

## Step 4. Enter Sample Info

Use this screen to assign each well position to a specific sample in the Magnis software. The Magnis software automatically assigns a default Sample ID for each sample position. The default Sample IDs can be replaced with a chosen sample name/Sample ID using either of the two methods below.




### Method 1: Import of sample assignments using a .csv file

1. Create a .csv (comma separated value) file containing the desired Sample IDs for the run in the correct order and download the .csv file onto an unencrypted USB drive, as detailed on page 15.
2. On the *Enter Sample Info* screen shown above, press the sample upload button, then follow the protocol setup wizard prompts to transfer the Sample IDs from the USB drive.


### Method 2: Manual run-time sample assignment

1. Select a specific sample position on the touchscreen.
2. Use the **Edit Sample ID** tool on the right to enter the desired Sample ID text. Press **Change** to save the entered Sample ID text for the sample position.

## Step 5. Confirm Setup and start the run

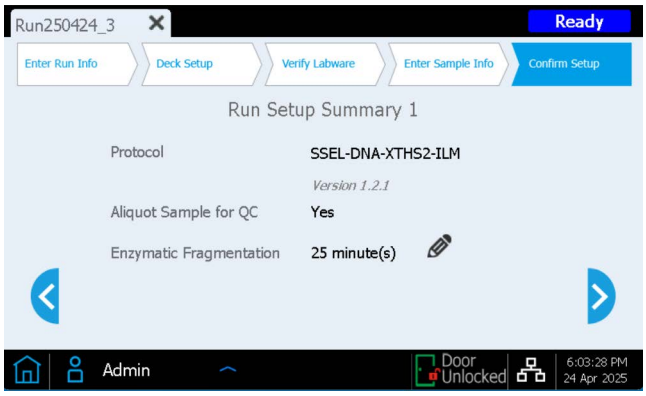
Use this set of screens to confirm the run setup details before initiating a run. Certain run parameters can be changed by pressing the pencil button adjacent to the parameter value.

**NOTE** Some parameters can only be changed when an *Advanced* access level user is logged in, and the pencil icon may not appear as shown in the screens below when a *Standard* access level user is logged in.

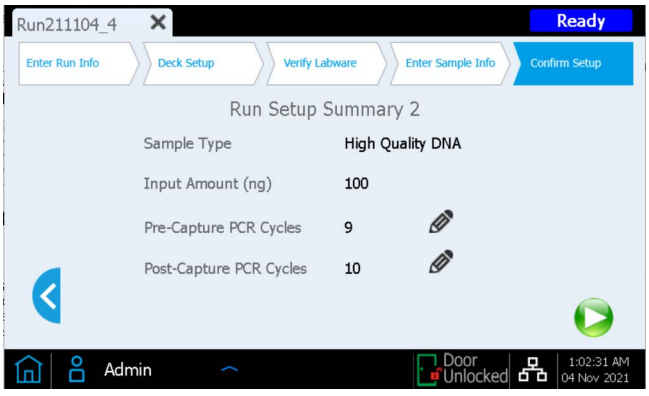
1 Verify the run settings displayed on the first *Run Setup Summary* screen. If the run includes Enzymatic Fragmentation, verify that the fragmentation duration setting is suitable for the DNA sample type and read length as summarized in the table below.

| NGS read length | High-quality DNA samples | FFPE DNA samples |
|---|---|---|
| 2 ×100 reads | 25 minutes | 25 minutes |
| 2 ×150 reads | 15 minutes | 25 minutes |

Once entries are confirmed or corrected, press the forward arrow to proceed to the final setup screen.




2 The second screen displays run details related to the characteristics of the DNA samples and probe used for the run. The pre-capture and post-capture PCR cycle numbers that will be used in the run (based on typical optimal conditions for the input DNA and probe used in the run) are displayed.

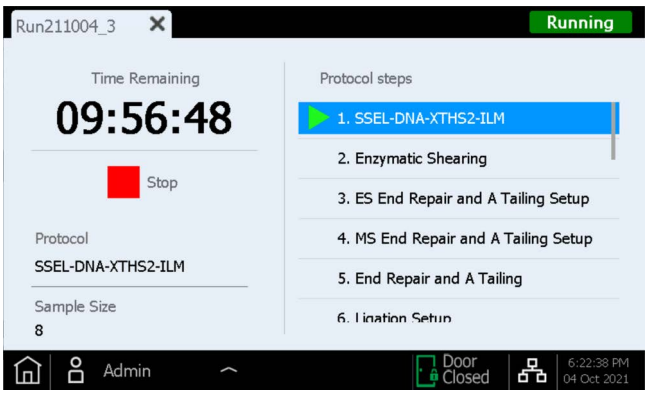



3 After confirming the run setup details, press the Start button to begin the run.

Once the run starts, the LED indicator lights are green, and the touchscreen displays the status of the run, including an estimate of the time remaining prior to run completion. Runs that include enzymatic fragmentation on Magnis take approximately 10 hours, while runs using pre-sheared DNA take approximately 9 hours.

Runs may be done overnight for convenience. Once the protocol is complete, the prepared libraries are automatically held at 12°C. Collect the libraries from the instrument within 72 hours.

If needed, press the red square **Stop** button to abort the run. A warning message opens asking you to confirm that you want to abort the run. Once you stop a run, the run cannot be resumed, and the labware used in that run cannot be reloaded for a future run.

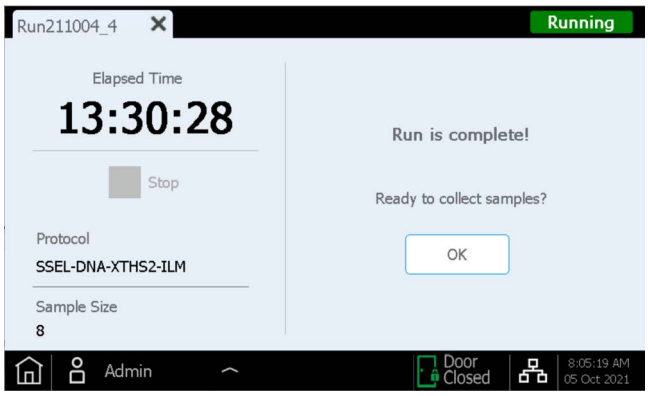



**NOTE**

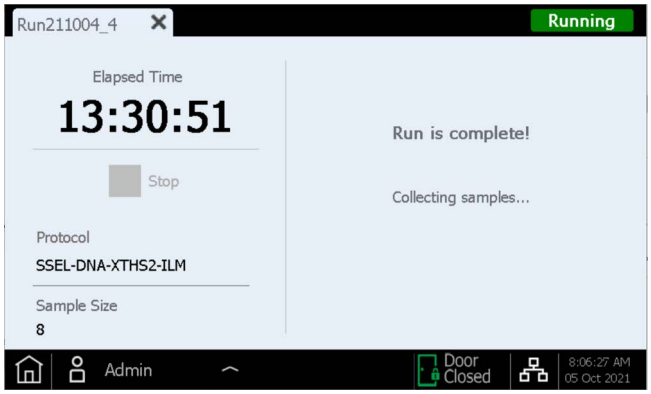
The *Running* screen must remain open through the duration of the run, and the screen close (**×**) button and other navigation buttons are inactive while the run is in progress. You cannot use the touchscreen to perform other functions during a run.

## Step 6. Collect final library samples from the instrument

When the run is complete, the touchscreen displays the prompt below. Press **OK** when you are ready to collect the library samples from the instrument.

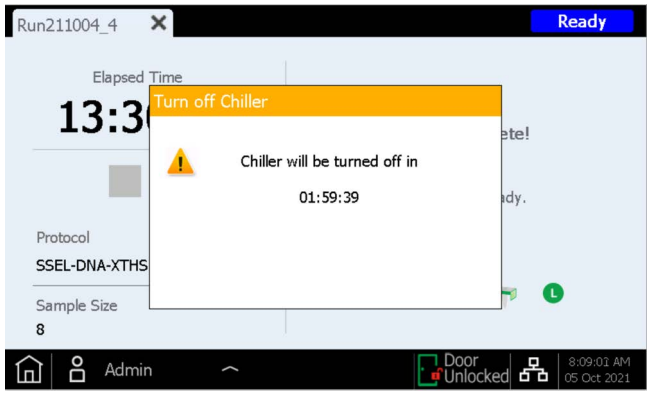



The instrument transfers the prepared library solutions from the PCR plate in the thermal cycler to the green Library Output Strip in the chiller at this time.




Wait for the LED indicator lights to turn blue, indicating that all instrument-mediated sample processing steps are complete, before opening the instrument door.

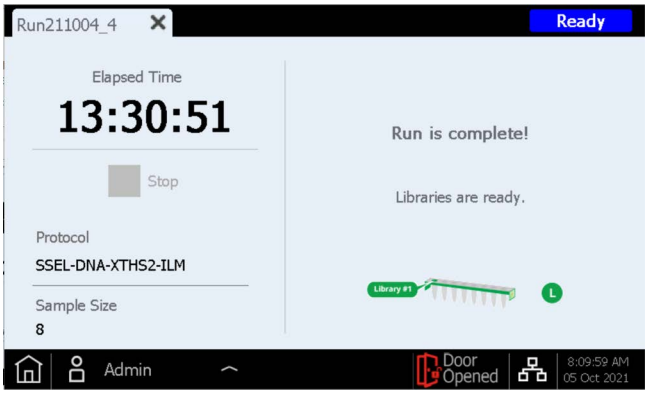
Once samples are placed in the green Library Output Strip in the chiller, the touchscreen display appears as below. The chiller, containing the library samples, is held at 12°C for up to 2 hours, with the remaining cold storage period indicated on the touchscreen dialog as shown below. The chiller is turned off once the instrument door is opened.



Fully open the instrument door (until the LED indicator lights turn white) and collect the final library samples in the green Library Output Strip from the L-position of the chiller module. Re-seal the wells using a fresh foil seal strip (provided in the Library Output and QC strip tube package). The final target-enriched libraries are in ~20–23 µL of Low TE Buffer (10 mM Tris-HCl, pH 7.5-8.0, 0.1 mM EDTA). Place the libraries under suitable storage conditions, according to your research design (see page 55 for storage recommendations).

Guidelines for processing the libraries for DNA sequencing are provided in "Appendix 3: Guidelines for Post-run DNA Sample Processing for NGS" on page 53.

Once the door is opened for library sample collection, the touchscreen appears as shown below.




Close the run screen by pressing the X on the tab to return to the Home screen.

**NOTE** Closing the screen may take several seconds. Do not repeatedly press the X button.

### Processing of the Optional Pre-Capture Library QC Samples

If the optional pre-capture library QC samples were collected for the run, remove the blue QC Strip from the chiller module. Dry the DNA in the wells by leaving the unsealed QC Strip at RT until the samples are dried. QC samples may be stored in dried condition until the sequencing libraries are analyzed.

**NOTE** QC samples may appear dried or partially dried at the end of the run, since the QC strips remain unsealed after the 3-µL aliquots are collected during the run. Samples should be completely dried before storage or reconstitution to ensure accurate QC results.

If analysis of the QC samples is required, resuspend the dried samples in 6 µL of nuclease-free water to achieve a concentration suitable for analysis using Agilent's TapeStation system and a D1000 ScreenTape assay, or similar analytical tool. After adding 6 µL of water to each well, incubate at RT for 5–10 minutes then mix well by vortexing to ensure complete resuspension.

**Expected Results:** Typical pre-capture libraries have a peak of DNA fragment size between 300 and 400 bp for high-quality input DNA or between 200 and 400 bp for FFPE-derived input DNA.

QC samples that were dried and resuspended in 6 µL should have a concentration of approximately 30–100 ng/µL depending on input DNA quality and the pre-capture PCR cycle number. The overall pre-capture library yield may be calculated as the amount of DNA in 1 µL of the reconstituted QC sample x 36 (includes both dilution and sampling adjustments).

## Step 7. Clear the instrument after the run

Remove and dispose of all used consumables remaining on the instrument deck:

- Remove the filled tip waste bin from waste bin drawer, then return drawer to closed position
- Remove the used Deep-Well HSM plate from the HSM module
- Remove the used 96-Well PCR Plate and the thermal cycler seal from the PCR module
- Remove all tip boxes, including any partially filled boxes
- Remove the used deep-well Beads/Buffers Plate from the central deck plateholder
- Open the chiller module and remove the used Reagent Plate and the used red, black, and white strip tubes. Make sure that any green Library Output (L) strip tubes and blue QC sample (Q) strip tubes were removed from the chiller and retained for further processing.

**NOTE** It is critical to remove all labware components and any other stray materials from the instrument deck before initiating a new run. The presence of any materials on the deck when a new run is initiated can cause Instrument Health Check failure for the new run.

If any spilled or leaked materials are observed on the instrument deck, Agilent recommends running the UV decontamination Extended Cycle procedure (see page 18 for more information on UV decontamination). Clean the spill using an alcohol or dilute bleach wipe (see Table 6 on page 12; for complete cleaning instructions see the instrument User Guide).

### Disposal

Dispose of unused reagents, waste, and specimens in accordance with country, federal, state and local regulations.

# 3 Appendix 1: DNA Sample Preparation Guidelines



Before setting up the Magnis SureSelect XT HS2 DNA sequencing library preparation run, DNA samples must be prepared, quantified and qualified using the guidelines in this Appendix.

Magnis library preparation protocols are compatible both with high-quality gDNA prepared from fresh or fresh frozen samples and with lower-quality DNA prepared from FFPE samples. For high-quality gDNA samples, see page 44. For FFPE-derived DNA samples, see page 46.

Magnis runs can include 10 ng, 50 ng, 100 ng or 200 ng of input DNA. For optimal sequencing results, use the maximum amount of input DNA available within this range. All samples in the same run must be provided in the same quantity. Magnis Sample Input Strips (red strip tubes provided in plate format, p/n 5190-9882 or 5191-5676), along with all input DNA sample preparation and dilution reagents, should be stored and used only in pre-PCR areas of the laboratory.

Prior to NGS library preparation, all DNA samples must be fragmented either by Magnis-automated enzymatic fragmentation or by non-automated mechanical shearing. Protocols for non-automated Covaris shearing of both high-quality and FFPE-derived DNA samples are provided in this Appendix.

When using Magnis-automated enzymatic fragmentation, the default duration used in the automated protocols (25 minutes) is optimal for most workflows. Reducing the duration of enzymatic fragmentation is recommended for workflows using high-quality DNA samples and longer NGS read lengths (≥150 bp reads) in order to increase the DNA fragment size distribution. Guidelines are summarized in Table 9. The duration of automated enzymatic fragmentation can be adjusted during run setup as described on page 38.

**Table 9** Magnis-automated enzymatic fragmentation duration guidelines

| NGS read length | Recommended automated enzymatic fragmentation duration | |
|---|---|---|
| | High-quality DNA samples | FFPE DNA samples |
| 2 ×100 reads | 25 minutes | 25 minutes |
| 2 ×150 reads | 15 minutes | 25 minutes |

# I. Preparation of High-Quality DNA Samples for Magnis Runs

## Step 1. Prepare, quantify, and qualify the genomic DNA samples

1 Prepare high-quality gDNA from fresh or frozen biological samples using a suitable purification system, such as Qiagen's QIAamp DNA Mini Kit, following the manufacturer's protocol.

NOTE

Make sure genomic DNA samples are of high quality with an OD 260/280 ratio ranging from 1.8 to 2.0.

2 Use the Qubit BR dsDNA Assay Kit to determine the concentration of each gDNA sample. Follow the manufacturer's instructions for the instrument and assay kit.

## Step 2. Dilute the DNA samples for the run

1 Prepare each DNA sample for library preparation using the chosen shearing method by diluting the appropriate amount (10 ng, 50 ng, 100 ng or 200 ng) of each gDNA sample in 1X Low TE Buffer using the volume shown in Table 10. Keep the samples on ice.

**Table 10** DNA sample dilution parameters

| Fragmentation Method | Solvent | Final Sample Volume |
|---|---|---|
| Enzymatic fragmentation (Magnis-automated) | 1X Low TE Buffer | 14 µL |
| Mechanical shearing using Covaris (non-automated) | 1X Low TE Buffer | 50 µL |

NOTE

**Do not dilute samples to be sheared using water.** Shearing samples in water reduces the overall library preparation yield and complexity.

2 For runs that include Magnis-automated DNA fragmentation, proceed to page 22 and follow the instructions for filling the sample input strips with the unsheared DNA samples.

For runs using non-automated Covaris shearing, proceed to the DNA shearing instructions below.

## Step 3. Shear the DNA (runs without enzymatic fragmentation only)

In this step the 50-µL gDNA samples are sheared using conditions optimized for high-quality DNA, summarized in Table 11.

**Table 11** High-quality DNA shearing guidelines

| Planned NGS read length | Target fragment size | Optimal shearing duration |
|---|---|---|
| 2 ×100 reads | 150 to 200 bp | 2 × 120 seconds |
| 2 ×150 reads | 180 to 250 bp | 2 × 60 seconds |

NOTE

This protocol has been optimized using a Covaris model E220 instrument and the 130-µL Covaris microTUBE. Consult the manufacturer's recommendations for use of other Covaris instruments or sample holders to achieve the same target DNA fragment size.

1 Set up the Covaris instrument according to the manufacturer's instructions. Allow enough time (typically 30–60 minutes) for instrument degassing and water bath chilling before starting the shearing protocol.

2 Complete the DNA shearing steps below for each of the gDNA samples.

   **a** Transfer the 50-µL DNA sample into a Covaris microTUBE, using a tapered pipette tip to slowly transfer the sample through the pre-split septum of the cap.

   **b** Spin the microTUBE for 30 seconds to collect the liquid and to remove any bubbles from the bottom of the tube.

   **c** Secure the microTUBE in the tube holder and shear the DNA with the settings in Table 12. After shearing, proceed directly to the next step, do not leave the sheared DNA in the Covaris microTUBE for longer than required.

**Table 12** High-quality DNA shear settings for Covaris E-series instrument (SonoLab software v7 or later)

| Setting | Value | Method Details |
|---|---|---|
| Duty Factor | 10% | — |
| Peak Incident Power (PIP) | 175 | — |
| Cycles per Burst | 200 | — |
| Bath Temperature | 2° to 8° C | — |
| Treatment Time | 2 × 120 seconds for 2x100 bp NGS<br>**OR**<br>2 × 60 seconds for 2x150 bp NGS | • Shear for 120 **OR** 60 seconds<br>• Spin the microTUBE for 10 seconds, then vortex at high speed for 5 seconds and spin for 10 seconds to collect the liquid<br>• Repeat full sequence once more, retaining the sample in the microTUBE throughout process |

3 Put the Covaris microTUBE containing sheared DNA back into the loading and unloading station. Keeping the microTUBE snap-cap on, insert a pipette tip through the pre-split septum, then slowly remove the sheared DNA.

4 Proceed to page 22 and follow the instructions for filling the sample input strip with each sheared DNA sample.

NOTE

To avoid loss of low-abundance DNA samples at this step, spin the microTUBE briefly after transferring the DNA to the Magnis Sample Input Strip and transfer any residual liquid to the same well. Visually inspect the microTUBE to ensure that all of the sample has been transferred. If droplets remain in the microTUBE, repeat the spinning and transfer steps.

# II. Preparation of FFPE-Derived DNA Samples for Magnis Runs

## Step 1. Prepare genomic DNA from FFPE samples

Prepare gDNA from FFPE tissue sections using Qiagen's QIAamp DNA FFPE Tissue Kit and Qiagen's Deparaffinization Solution, following the manufacturer's protocol. Elute the final gDNA samples from the MinElute column in two rounds, using 30 µL Buffer ATE in each round, for a final elution volume of approximately 60 µL.

**NOTE** If tissue lysis appears incomplete after one hour of digestion with Proteinase K, add an additional 10 µL of Proteinase K and continue incubating at 56°C, with periodic mixing, for up to three hours.

Store the gDNA samples on ice for same-day library preparation, or at –20°C for later processing.

## Step 2. Qualify and quantify the FFPE DNA samples

Assess the quality (DNA integrity) for each FFPE-derived DNA sample using one of the two methods below. The DNA integrity measured at this step determines the appropriate means of sample quantification needed to include 10 ng, 50 ng, 100 ng or 200 ng of amplifiable gDNA samples in the run.

**Method Option 1: Qualification using the Agilent NGS FFPE QC Kit (Recommended Method)**

The Agilent NGS FFPE QC Kit provides a qPCR-based assay for DNA sample integrity determination. Results include a ΔΔCq DNA integrity score and the precise quantity of amplifiable DNA in the sample, allowing direct normalization of DNA input for each sample. DNA input recommendations based on ΔΔCq scores for individual samples are summarized in Table 13.

1. Use the Qubit BR dsDNA Assay Kit to determine the concentration of each gDNA sample. Follow the manufacturer's instructions for the instrument and assay kit.
2. Remove a 1 µL aliquot of the FFPE gDNA sample for analysis using the Agilent NGS FFPE QC Kit to determine the ΔΔCq DNA integrity score. See the kit user manual at www.agilent.com for more information.
3. For all samples with ΔΔCq DNA integrity score ≤1, use the Qubit-based gDNA concentration determined in step 1, above, to determine volume of input DNA needed for the protocol.
4. For all samples with ΔΔCq DNA integrity score >1, use the qPCR-based concentration of amplifiable gDNA, reported by the Agilent NGS FFPE QC Kit results, to determine amounts of input DNA for the protocol.

**Table 13** SureSelect XT HS2 DNA input modifications based on ΔΔCq DNA integrity score

| Protocol Parameter | ΔΔCq≤1* | ΔΔCq >1 |
|---|---|---|
| DNA input for Library Preparation | 10 ng, 50 ng, 100 ng or 200 ng DNA, based on Qubit Assay | 10 ng, 50 ng, 100 ng or 200 ng of amplifiable DNA, based on qPCR quantification |

* FFPE samples with ΔΔCq scores ≤1 should be treated like non-FFPE samples for DNA input amount determinations. For samples of this type, make sure to use the DNA concentration determined by the Qubit Assay, instead of the concentration determined by qPCR, to calculate the volume required for 10–200 ng DNA.

### Method Option 2: Qualification using Agilent's Genomic DNA ScreenTape assay DIN score

Agilent's Genomic DNA ScreenTape assay, used in conjunction with Agilent's 4200 TapeStation, provides a quantitative electrophoretic assay for DNA sample integrity determination. This assay reports a DNA Integrity Number (DIN) score for each sample which is used to estimate the appropriate normalization of DNA input required for low-integrity DNA samples.

1 Use the Qubit BR dsDNA Assay Kit to determine the concentration of each gDNA sample. Follow the manufacturer's instructions for the instrument and assay kit.

2 Remove a 1 µL aliquot of the FFPE gDNA sample and analyze using the Genomic DNA ScreenTape assay. See the user manual at www.agilent.com for more information.

3 Using the DIN score reported for each sample in the Genomic DNA ScreenTape assay, consult Table 14 to determine the recommended amount of input DNA for the sample.

**Table 14** SureSelect XT HS2 DNA input modifications based on DNA Integrity Number (DIN) score

| Protocol Parameter | non-FFPE Samples | FFPE Samples | | |
|---|---|---|---|---|
| | | DIN > 8* | DIN 3–8 | DIN<3 |
| DNA input for Library Preparation | 10 ng, 50 ng, 100 ng or 200 ng DNA, quantified by Qubit Assay | 10 ng, 50 ng, 100 ng or 200 ng DNA, quantified by Qubit Assay | Use 50 ng, 100 ng or 200 ng DNA (use the maximum amount of DNA available, up to 200 ng). Quantify by Qubit Assay to determine volume required for 50 ng, 100 ng or 200 ng input. | Use 100 ng or 200 ng DNA (use the maximum amount of DNA available, up to 200 ng). Quantify by Qubit Assay to determine volume required for 100 ng or 200 ng input. |

* FFPE samples with DIN>8 should be treated like non-FFPE samples for DNA input amount determinations.

## Step 3. Dilute the qualified FFPE DNA samples for the run

1 Prepare each DNA sample for library preparation using the chosen shearing method by diluting the appropriate amount (10 ng, 50 ng, 100 ng or 200 ng) of each gDNA sample in 1X Low TE Buffer using the volume shown in Table 15. Keep the samples on ice.

**Table 15** DNA sample dilution parameters

| Fragmentation Method | Solvent | Final Sample Volume |
|---|---|---|
| Enzymatic fragmentation (Magnis-automated) | 1X Low TE Buffer | 14 µL |
| Mechanical shearing using Covaris (non-automated) | 1X Low TE Buffer | 50 µL |

NOTE **Do not dilute samples to be sheared using water.** Shearing samples in water reduces the overall library preparation yield and complexity.

2 For runs that include Magnis-automated DNA fragmentation, proceed to page 22 and follow the instructions for filling the sample input strips with the unsheared DNA samples.

For runs using non-automated Covaris shearing, proceed to the DNA shearing instructions below.

## Step 4. Shear the FFPE DNA (runs without enzymatic fragmentation only)

In this step the 50-µL gDNA samples are sheared using conditions optimized for FFPE-derived DNA, summarized in Table 16.

**Table 16** FFPE-derived DNA shearing guidelines

| Planned NGS read length | Target fragment size* | Optimal shearing duration† |
|---|---|---|
| 2 ×100 reads | 150 to 200 bp | 240 seconds |
| 2 ×150 reads | 180 to 250 bp | 240 seconds |

* This table shows the ideal target fragment size for each read length. The initial DNA fragment size of FFPE-derived samples may impact the post-shear fragment size distribution, resulting in fragment sizes shorter than the target ranges listed in this table. Libraries prepared from FFPE samples should be analyzed using an NGS read length suitable for the final library fragment size distribution.

† All FFPE samples are sheared for 240 seconds to generate fragment ends suitable for library construction.

**NOTE** This protocol has been optimized using a Covaris model E220 instrument and the 130-µL Covaris microTUBE. Consult the manufacturer's recommendations for use of other Covaris instruments or sample holders to achieve similar target fragment sizes.

1. Set up the Covaris instrument according to the manufacturer's instructions. Allow enough time (typically 30–60 minutes) for instrument degassing and water bath chilling before starting the shearing protocol.
2. Complete the DNA shearing steps below for each of the gDNA samples.
   a. Transfer the 50-µL DNA sample into a Covaris microTUBE, using a tapered pipette tip to slowly transfer the sample through the pre-split septum of the cap.
   b. Spin the microTUBE for 30 seconds to collect the liquid and to remove any bubbles from the bottom of the tube.
   c. Secure the microTUBE in the tube holder and shear the DNA with the settings in Table 17. After shearing, proceed directly to the next step, do not leave the sheared DNA in the Covaris microTUBE for longer than required.

**Table 17** FFPE DNA shear settings for Covaris E-series instrument (SonoLab software v7 or later)

| Setting | Value |
|---|---|
| Duty Factor | 10% |
| Peak Incident Power (PIP) | 175 |
| Cycles per Burst | 200 |
| Bath Temperature | 2° to 8° C |
| Treatment Time | 240 seconds |

3. Put the Covaris microTUBE containing sheared DNA back into the loading and unloading station. Keeping the microTUBE snap-cap on, insert a pipette tip through the pre-split septum, then slowly remove the sheared DNA.

4 Proceed to page 22 and follow the instructions for filling the sample input strip with each sheared FFPE DNA sample.

**NOTE** To avoid loss of low-abundance DNA samples at this step, spin the microTUBE briefly after transferring the DNA to the Magnis Sample Input Strip and transfer any residual liquid to the same well. Visually inspect the microTUBE to ensure that all of the sample has been transferred. If droplets remain in the microTUBE, repeat the spinning and transfer steps.

# 4 Appendix 2: Use of Run-time Prepared Probe Strips



The instructions in this section are specifically for self-filled probe strip preparation and use in *SSEL-DNA-XTHS2-EPIS-ILM* Magnis protocol runs, set up using Reagent Kit part number G9750B (Magnis SureSelect XT HS2 DNA Reagent Kit provided with empty Probe Input Strips). The *SSEL-DNA-XTHS2-EPIS-ILM* Magnis protocol requires run-time filling of the provided empty probe strips and requires additional probe data entry steps, as described in this section.

Instructions in this section do not apply to kits that include pre-filled probe strips; see page 23 for pre-filled probe strip set up information.

# Run-Time Preparation of the Empty Probe Input Strip (EPIS)

The empty Magnis Probe Input Strips (p/n 5190-9883, white strips provided in a plate format) should be stored and filled in a pre-PCR area of the laboratory. Prepare the probe input strip just before use in the *SSEL-DNA-XTHS2-EPIS-ILM* run; do not pre-fill and freeze-thaw the probe input strips used in this protocol.

The 8 wells of the empty Magnis Probe Input Strip may be filled with the same or different probe solutions. All probes used in the same run must, however, have a similar design size to allow use of the same run conditions by the Magnis (see Table 19 on page 52 for compatible probe design size ranges).

1 Obtain one empty white Magnis Probe Input Strip and one fresh foil seal strip (with backing) from kit p/n 5190-9883, stored at RT.

2 Thaw and mix the vial(s) of SureSelect Probe to be used for the run and keep on ice.

3 Refer to Table 18 below to determine the volume of SureSelect Probe solution required for your probe design size.

**Table 18** Probe volume requirements

| Probe Capture Size | Volume to Pipette per Well | Volume Required for 8-Sample Run | Protocol Selected on *Enter Run Info* Screen |
|---|---|---|---|
| ≥3 Mb (**Large** *Capture Size*)* | 5 µL | 40 µL | *SSEL-DNA-XTHS2-EPIS-ILM* |
| <3 Mb (**Small** *Capture Size*)* | 2 µL | 16 µL | |

* The **Large** vs. **Small** *Capture Size* designation for the probe(s) used in the run is entered in the Magnis software as described on page 52. All probes used in a run must have the same *Capture Size* designation and must use the same post-capture PCR cycling conditions (see Table 19 on page 52).

4 Fill the wells of the empty Magnis Probe Input Strip with the appropriate volume of SureSelect Probe solution using the steps below:

**a** Use an empty 200-µL pipette tip to pre-pierce the foil seal of each well of the probe input strip to be filled for the run.

**b** Using a micropipette qualified to accurately dispense the probe volume listed in Table 18, dispense the indicated amount of SureSelect Probe solution into each well.

Use a 2-µL capacity micropipette and pipette tip when dispensing 2 µL of probe.

Use a 10-µL capacity micropipette and pipette tip when dispensing 5 µL of probe.

**NOTE** It is important to fill the probe input strip wells using precisely the volumes indicated in Table 18. Use a calibrated pipette qualified to dispense the indicated volume with high accuracy and precision.

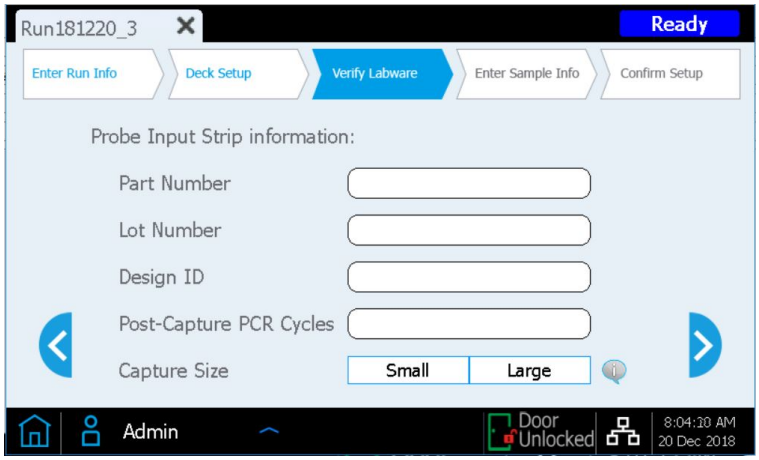
5 After dispensing the probe solution into all wells, re-seal the wells with the fresh foil seal provided in the kit, taking care to avoid obscuring the probe strip barcode with the foil seal. Ensure that the seal is applied firmly and evenly, without excessive overhangs or creases that could obstruct strip tube seating when loading in the instrument.

6 Visually check the probe strip wells to verify that no bubbles are present. Remove any bubbles by spinning the prepared probe strip in a centrifuge set at 250 × *g* for 5 seconds or until all bubbles are released from the probe solution.

7 Keep the probe strip on ice until use in the *SSEL-DNA-XTHS2-EPIS-ILM* run. Load the filled probe strip during the deck setup steps described on page 34. When loading the probe strip, make sure to verify that the strip is properly seated in the chiller module.

# Entering Probe Information during Run Setup

**For *SSEL-DNA-XTHS2-EPIS-ILM* runs** you must enter the probe-related properties in the fields shown below during the *Verify Labware* phase of run setup (see page 36).




Enter information in the *Part Number*, *Lot Number* and *Design ID* fields according to the record keeping requirements of your facility. The Design ID and Lot Number for Agilent-supplied SureSelect or ClearSeq probes is provided on the product vial and on the Certificate of Analysis.

Enter the PCR cycle number to be used in the run in the *Post-Capture PCR Cycles* field, according to the size of your probe design(s) and press the appropriate *Capture Size* description for the probe(s) used in the run. See Table 19 below for guidelines. The suggested PCR cycle number is typically optimal for the listed probe design size, but the PCR cycle number may be adjusted to meet the needs of your experimental design. The 8 wells of the Magnis Probe Input Strip may contain different probe solutions, but all probes used in the same run must use the same *Post-Capture PCR Cycles* and *Capture Size* settings.

**Table 19 Recommended settings for run-time dispensed probes**

| SureSelect XT HS Probe Size | Post-Capture PCR Cycles | Capture Size |
|---|---|---|
| <200 kb | 14 | Small |
| 200–749 kb | 13 | Small |
| 750–2999 kb | 12 | Small |
| 3–5 Mb | 10 | Large |
| >5 Mb | 9 | Large |

Once all fields are populated, press the forward arrow to proceed to the *Enter Sample Info* screen and follow the remaining run setup steps starting on page 37.

# 5 Appendix 3: Guidelines for Post-run DNA Sample Processing for NGS



After completing the Magnis SureSelect XT HS2 DNA library preparation run, the DNA samples are quantified and qualified, then analyzed by NGS. Guidelines for typical post-run sample processing for NGS are provided in this section; your post-run NGS processing and analysis workflow may vary.

# Step 1. Analyze quantity and quality of library DNA samples

Prior to sample pooling for multiplexed sequencing, analyze the quantity and quality of DNA in the individual prepared library samples using an Agilent TapeStation instrument with the High Sensitivity D1000 ScreenTape and associated reagent kit. See Table 3 on page 11 for ordering information. Refer to the Agilent High Sensitivity D1000 Assay Quick Guide for detailed instructions.

**NOTE** Alternatively, library DNA samples may be analyzed using the Agilent 5200 Fragment Analyzer and HS NGS Fragment Kit or using the Agilent 2100 Bioanalyzer and the Bioanalyzer High Sensitivity DNA Assay. Refer to the linked assay user guides for complete instructions.

1 Prepare the TapeStation assay samples in a fresh tube strip as instructed in the assay Quick Guide. Use 2 µL of each library 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 sample buffer on the IKA vortex mixer, as instructed in the assay Quick Guide, for accurate quantitation.

2 Load the High Sensitivity D1000 assay tube strips from step 1, the High Sensitivity D1000 ScreenTape, and loading tips into the TapeStation as instructed in the assay Quick Guide. Start the run.

3 Verify that the electropherogram shows the peak of DNA fragment size positioned between 200 and 400 bp. Sample electropherograms are shown in Figure 7 (library prepared from high-quality DNA), Figure 8 (library prepared from medium-quality FFPE DNA), and Figure 9 (library prepared from low-quality FFPE DNA).

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

.

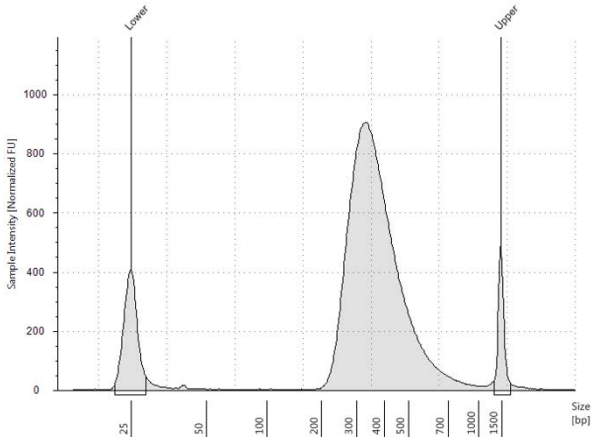



**Figure 7** Post-capture library prepared from a high-quality gDNA sample analyzed using a High Sensitivity D1000 ScreenTape assay.

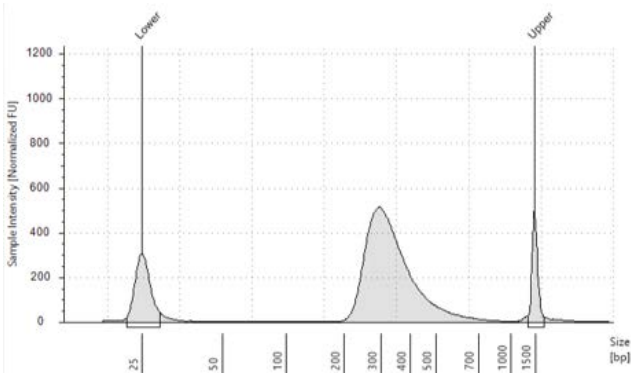



**Figure 8** Post-capture library prepared from a typical FFPE gDNA sample analyzed using a High Sensitivity D1000 ScreenTape assay.

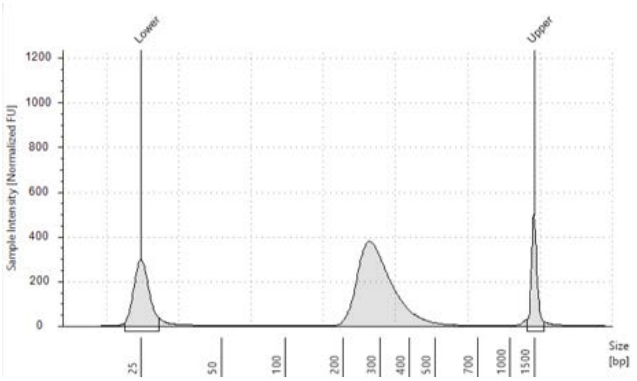



**Figure 9** Post-capture library prepared from a low-quality FFPE gDNA sample analyzed using a High Sensitivity D1000 ScreenTape assay.

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

# Step 2. Pool samples for multiplexed sequencing (optional)

The number of indexed libraries that may be multiplexed in a single sequencing lane is determined by the output specifications of the sequencer 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 the sequencer and the amount of sequencing data required per sample.

Combine the libraries such that each index-tagged library is present in equimolar amounts in the pool using one of the following methods. Use the diluent specified by your sequencing provider, such as Low TE, for the dilution steps.

**Method 1:** Dilute each library sample to be pooled to the same final concentration (typically 4–15 nM, or the concentration of the most dilute sample) then combine equal volumes of all samples to create the final pool.

**Method 2:** Starting with library samples at different concentrations, add the appropriate volume of each sample to achieve equimolar concentration in the pool, then adjust the pool to the desired final volume using Low TE. The formula below is provided for determination of the amount of each indexed sample to add to the pool.

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

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 (typically 4 nM–15 nM or the concentration of the most dilute sample)

*#* is the number of indexes, and

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

Table 20 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 DNA.

**Table 20** Example of volume calculation for total volume of 20 µL at 10 nM concentration

| 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 |

Store the library pool under the conditions specified by your sequencing provider. Typically, libraries should be stored at –20°C for short-term storage.

# Step 3. Prepare the sequencing samples

The final SureSelect XT HS2 library pool is ready for direct sequencing using standard Illumina paired-end primers and chemistry. Each fragment in the prepared library contains one target insert surrounded by sequence motifs required for multiplexed sequencing using Illumina sequencers, as shown in Figure 10.


**Figure 10** Content of SureSelect XT HS2 sequencing library. Each fragment contains one target insert (blue) surrounded by the Illumina paired-end sequencing elements (black), unique dual sample indexes (red and green), molecular barcodes (MBCs; brown) and the library PCR primers (yellow).

Proceed to cluster amplification using the appropriate Illumina Paired-End Cluster Generation Kit. Table 21 provides guidelines for use of several instrument and chemistry combinations suitable for this application. For other Illumina NGS platforms, consult Illumina's documentation for kit configuration and seeding concentration guidelines.

**Table 21** Illumina Kit Configuration Selection Guidelines

| Instrument | Run Type | Read Length | SBS Kit Configuration | Chemistry | Seeding Concentration |
|---|---|---|---|---|---|
| MiSeq | All Runs | 2 × 100 bp or 2 × 150 bp | 300 Cycle Kit | v2 | 9–10 pM |
| | | | 600 Cycle Kit | v3 | 12–16 pM |
| iSeq 100 | All Runs | 2 × 100 bp or 2 × 150 bp | 300 Cycle Kit | v2 | 50–150 pM |
| NextSeq 500/550 | All Runs | 2 × 100 bp or 2 × 150 bp | 300 Cycle Kit | v2.5 | 1.2–1.5 pM |
| NextSeq 1000/2000 | All Runs | 2 × 100 bp or 2 × 150 bp | 200 or 300 Cycle Kit | Standard SBS | 650–1000 pM |
| | | | | XLEAP-SBS | 650–1000 pM |
| NovaSeq 6000 | Standard Workflow Runs | 2 × 100 bp or 2 × 150 bp | 200 or 300 Cycle Kit | v1.5 | 300–600 pM |
| NovaSeq 6000 | Xp Workflow Runs | 2 × 100 bp or 2 × 150 bp | 200 or 300 Cycle Kit | v1.5 | 200–400 pM |
| NovaSeq X | All runs | 2 × 100 bp or 2 × 150 bp | 200 or 300 Cycle Kit | v1 | 90–180 pM |

Seeding concentration and cluster density may also need to be optimized based on the DNA fragment size range for the library and on the desired output and data quality. Begin optimization using a seeding concentration in the middle of the range listed in Table 21 or provided by Illumina. Follow Illumina's recommendation for a PhiX control in a low-concentration spike-in for improved sequencing quality control.

# Step 4. Sequence the libraries

Set up the sequencing run to generate Read 1 and Read 2 FASTQ files for each sample using the instrument's software in standalone mode or using an Illumina run management tool such as Local Run Manager (LRM), Illumina Experiment Manager (IEM) or BaseSpace. Enter the appropriate **Cycles** or **Read Length** value for your library read length and using 8-bp dual index reads. See Table 22 showing example settings for 2x150 bp sequencing.

**Table 22** Run settings for 2x150 bp sequencing

| Run Segment | Cycles/Read Length |
|---|---|
| Read 1 | 151* |
| Index 1 (i7) | 8 |
| Index 2 (i5) | 8 |
| Read 2 | 151* |

* Follow Illumina's recommendation to add one (1) extra cycle to the desired read length.

Follow Illumina's instructions for each platform and setup software option, incorporating the additional setup guidelines below:

- Each of the sample-level indexes (i7 and i5) requires an 8-bp index read. For complete index sequence information, see page 64.
- No custom primers are used for SureSelect XT HS2 library sequencing. Leave all *Custom Primers* options for *Read 1*, *Read 2*, *Index 1* and *Index 2* primers cleared/deselected during run setup.
- Turn off any adaptor trimming tools included in Illumina's run setup and read processing software applications. Adaptors are trimmed in later processing steps to ensure proper processing of the adaptors, including the degenerate molecular barcodes (MBCs) in the adaptor sequences.
- For runs set up using Illumina's LRM, IEM, or BaseSpace applications, refer to Illumina's instructions and support resources for setting up runs with custom library prep kits and index kits in the selected software. For use in these applications, the SureSelect XT HS2 index sequences can be obtained by downloading the SureSelect XT HS2 Index Sequence Resource Excel spreadsheet from Agilent.com. The provided sequences should be converted to .tsv/.csv file format or copied to a Sample Sheet according to Illumina's specifications for each application. If you need assistance with SureSelect XT HS2 run setup in your selected application, contact the SureSelect support team (see page 2) or your local representative.

# Step 5. Process the reads

Guidelines are provided below for typical NGS read processing pipeline steps appropriate for SureSelect XT HS2 DNA libraries. Your NGS pipeline may vary.

- Demultiplex using Illumina's bcl2fastq, BCL Convert or DRAGEN software to generate paired end reads based on the dual indexes and remove sequences with incorrectly paired P5 and P7 indexes. Turn off the MBC/UMI trimming options in Illumina's demultiplexing software to allow proper adaptor and MBC processing by downstream software tools.
- The demultiplexed FASTQ data needs to be pre-processed to trim the sequencing adaptors and to extract and use MBC sequences for de-duplication. Agilent's Genomics NextGen Toolkit (AGeNT) software modules, described below, can be used for these pre-processing steps.

**NOTE**

Read pre-processing steps can also be completed using suitable open-source software tools, such as fgbio. Performance of open-source tools should be verified for appropriate adaptor and MBC sequence processing on both strands. Some non-Agilent adaptor trimmers may fail to remove the MBC sequences from the opposite adaptor, which may affect alignment quality.

- If your sequence analysis pipeline excludes MBCs, you can remove MBCs during the demultiplexing step by trimming or masking the first five bases from each read using the guidelines below.

  If demultiplexing using bcl2fastq, MBCs may be masked by including the base mask **N5Y*,I8,I8,N5Y*** (where * is replaced with the remaining read length after subtracting the 5 masked bases, e.g., use **N5Y146,I8,I8,N5Y146** for 2x150 NGS set up as shown in Table 22 on page 58). The sum of the values following N and Y must match the read length value in the RunInfo.xml file.

  If demultiplexing using BCL Convert, MBCs may be trimmed by including the following string in the sample sheet header: **OverrideCycles,N5Y*;I8;I8;N5Y*** (where * is replaced with read length after trimming, e.g., use **N5Y146;I8;I8;N5Y146** for 2x150 NGS set up as shown in Table 22 on page 58). The sum of the values following N and Y must match the read length value in the RunInfo.xml file.

## AGeNT software read processing guidelines

Agilent's AGeNT is a Java-based toolkit for library read processing steps, designed for users with bioinformatics expertise to enable building internal analysis pipelines. To download this toolkit, visit the AGeNT page at www.agilent.com. Use of the AGeNT read processing tools is outlined briefly below. See the AGeNT Best Practices document for more information.

- Prior to variant discovery, demultiplexed SureSelect XT HS2 library FASTQ data are pre-processed to remove sequencing adaptors and extract the MBC sequences using the AGeNT Trimmer module.
- The trimmed reads should be aligned, and MBC tags added to the aligned BAM file using a suitable tool such as BWA-MEM.
- Once alignment and tagging are complete, the AGeNT CReaK (Consensus Read Kit) tool is used to generate consensus reads and mark or remove duplicates. The resulting BAM files are ready for downstream analysis including variant discovery.

# 6 Reference



This chapter contains reference information, including reagent kit contents, index sequences, and troubleshooting information for the SureSelect XT HS2 DNA library preparation runs.

# Reagent Kit Contents

Agilent part numbers for the Magnis SureSelect XT HS2 DNA Reagent Kits are summarized in Table 23.

**Table 23** Reagent Kit Part Numbers

| Included Probe | Magnis SureSelect XT HS2 DNA Reagent Kits | |
|---|---|---|
| | 96 Reactions | 32 Reactions |
| Custom 1–499 kb | G9751B | G9751A |
| Custom 0.5–2.9 Mb | G9752B | G9752A |
| Custom 3–5.9 Mb | G9753B | G9753A |
| Custom 6–11.9 Mb | G9754B | G9754A |
| Custom 12–24 Mb | G9755B | G9755A |
| Custom 24–50 Mb | G9756B | G9756A |
| Human All Exon V7 | G9773B | G9773A |
| Human All Exon V8 | G9774B | G9774A |
| SureSelect Clinical Research Exome V4 (CRE V4) | G9775B | G9775A |
| SureSelect Cancer CGP DNA | G9777B | G9777A |
| None (kit includes empty Probe Input Strips for run-time probe setup) | G9750B | Not offered |

Magnis SureSelect XT HS2 DNA Reagent Kits include the component kits listed in Table 24, with the contents of each component kit detailed in Table 25 through Table 30.

**Table 24** Component kits provided with Magnis SureSelect XT HS2 DNA Reagent Kits

| Component kit name | Storage condition | Component kit p/n | |
|---|---|---|---|
| | | 96 Reactions | 32 Reactions |
| Magnis SureSelect Probe Plate, Pre-filled Single Well Format | –80°C | p/n varies; see Table 25* | p/n varies; see Table 25 |
| Magnis SureSelect XT HS2 Reagent Plates ILM | –20°C | 5191-6831 | 5191-6830 |
| Magnis SureSelect XT HS2 Index Primer Pairs ILM | –20°C | 5191-6833 (Index Pairs 1-96) **OR** 5191-6835 (Index Pairs 97-192) | 5191-6837 (Index Pairs 1-32) |
| Magnis SureSelect XT HS Beads/Buffers Plates ILM† | +4°C | 5190-9692 | 5191-5674 |
| Magnis Empty Consumables | Room Temperature | 5190-9712 | 5191-5675 |
| Magnis Sample Input Strips | Room Temperature | 5190-9882 | 5191-5676 |

* Kit part number G9750B does not include a Magnis Probe Plate. Instead the G9750B kit, configured for run-time probe setup, includes empty Magnis Probe Input Strips for 12 runs (p/n 5190-9883), stored at Room Temperature.

† The supplied *Magnis SureSelect XT HS Beads/Buffers Plates ILM* are compatible with Magnis SureSelect XT HS2 Reagent Kits and with Magnis SureSelect XT HS Reagent Kits.

**Table 25** Probe Plate part numbers

| Reagent Kit p/n | Included Probe design | Probe Plate p/n | Quantity per kit |
|---|---|---|---|
| G9751B (96 Reactions) | Custom 1–499 kb (Tier 1) | 5191-6817 | 1 plate (12 strips) |
| G9751A (32 Reactions) | Custom 1–499 kb (Tier 1) | 5191-6807 | 1 plate (4 strips) |
| G9752B (96 Reactions) | Custom 0.5 –2.9 Mb (Tier 2) | 5191-6819 | 1 plate (12 strips) |
| G9752A (32 Reactions) | Custom 0.5 –2.9 Mb (Tier 2) | 5191-6809 | 1 plate (4 strips) |
| G9753B (96 Reactions) | Custom 3–5.9 Mb (Tier 3) | 5191-6821 | 1 plate (12 strips) |
| G9753A (32 Reactions) | Custom 3–5.9 Mb (Tier 3) | 5191-6811 | 1 plate (4 strips) |
| G9754B (96 Reactions) | Custom 6–11.9 Mb (Tier 4) | 5191-6823 | 1 plate (12 strips) |
| G9754A (32 Reactions) | Custom 6–11.9 Mb (Tier 4) | 5191-6813 | 1 plate (4 strips) |
| G9755B (96 Reactions) | Custom 12–24 Mb (Tier 5) | 5191-6825 | 1 plate (12 strips) |
| G9755A (32 Reactions) | Custom 12–24 Mb (Tier 5) | 5191-6815 | 1 plate (4 strips) |
| G9756B (96 Reactions) | Custom 24–50 Mb | 5191-6846 | 1 plate (12 strips) |
| G9756A (32 Reactions) | Custom 24–50 Mb | 5191-6845 | 1 plate (4 strips) |
| G9773B (96 Reactions) | Human All Exon V7 | 5191-6827 | 1 plate (12 strips) |
| G9773A (32 Reactions) | Human All Exon V7 | 5191-6826 | 1 plate (4 strips) |
| G9774B (96 Reactions) | Human All Exon V8 | 5191-6974 | 1 plate (12 strips) |
| G9774A (32 Reactions) | Human All Exon V8 | 5191-6973 | 1 plate (4 strips) |
| G9775B (96 Reactions) | SureSelect CRE V4 | 5282-0042 | 1 plate (12 strips) |
| G9775A (32 Reactions) | SureSelect CRE V4 | 5282-0041 | 1 plate (4 strips) |
| G9777B (96 Reactions) | SureSelect Cancer CGP DNA | 5282-0037 | 1 plate (12 strips) |
| G9777A (32 Reactions) | SureSelect Cancer CGP DNA | 5282-0036 | 1 plate (4 strips) |

**Table 26** Components of Magnis SureSelect XT HS2 Reagent Plates ILM kit

| Component provided | Part Number (kit size) | Quantity and format |
|---|---|---|
| Magnis SureSelect XT HS2 Reagent Plate ILM | 5191-6831 (96 Reactions) | 12 plates (use 1 plate per run) |
| | 5191-6830 (32 Reactions) | 4 plates (use 1 plate per run) |

**Table 27** Components of Magnis SureSelect XT HS2 Index Primer Pairs ILM kit

| Component provided | Part Number (kit size) | Quantity and format |
|---|---|---|
| Magnis SureSelect HS2 Index Primer Pairs ILM | 5191-6833 (Index Pairs 1-96)<br>**OR**<br>5191-6835 (Index Pairs 97-192) | 1 plate of 12 strips (use 1 strip per run) |
| | 5191-6837 (32 Reactions) | 1 plate of 4 strips (use 1 strip per run) |

**Table 28** Components of Magnis SureSelect XT HS Beads/Buffers Plates, ILM kit

| Component provided | Part Number (kit size) | Quantity and format |
|---|---|---|
| Magnis SureSelect XT HS Beads/Buffers Plate, ILM | 5190-9692 (96 Reactions) | 12 plates (use 1 plate per run) |
| | 5191-5674 (32 Reactions) | 4 plates (use 1 plate per run) |

**Table 29** Components of Magnis Empty Consumables kit

| Components provided | Quantity and format* |
|---|---|
| Magnis Deep-Well HSM Plate | 1 plate |
| Magnis 96-Well PCR Plate | 1 plate |
| Magnis Library Output Strip | 1 green strip tube |
| Magnis QC Strip | 1 blue strip tube |
| Magnis Foil Seals | 1 sheet (6 single-strip tube foil sealing strips) |
| Magnis Thermal Cycler Seal | 1 single-use metal sealing plate |
| Magnis Tip Waste Bin | 1 single-use bin liner |

* Parts listed are per single-run box of consumables. Each 96 Reaction kit is supplied with 12 individual boxes (p/n 5190-9712) of consumables for single run, and each 32 Reaction kit is supplied with 4 individual boxes (p/n 5191-5675) of consumables for single run.

**Table 30** Components of the Magnis Sample Input Strips kit

| Part Number (kit size) | Components provided | Quantity and format |
|---|---|---|
| 5190-9882 (96 Reactions) | Magnis Sample Input Strips | 12 empty red, foil-sealed strips |
| | Magnis Foil Seals | 2 sheets (6 single-strip tube foil sealing strips per sheet) |
| 5191-5676 (32 Reactions) | Magnis Sample Input Strips | 4 empty red, foil-sealed strips |
| | Magnis Foil Seals | 1 sheet (6 single-strip tube foil sealing strips per sheet) |

# Reference Information for SureSelect XT HS2 Indexes

Magnis SureSelect XT HS2 Reagent Kits include the appropriate set of SureSelect XT HS2 Index Primer Pairs in single-use aliquots in the individual wells of index strip tubes, supplied on a plate platform. The primer pairs are provided pre-combined. Each member of the primer pair contains a unique 8-bp P7 or P5 index, resulting in dual-indexed NGS libraries.

Index sequences are provided on page 67 through page 70. Index sequences can also be obtained by downloading the SureSelect XT HS2 Index Sequence Resource Excel spreadsheet from Agilent.com.

**NOTE**

Clicking the Excel spreadsheet link from Agilent.com automatically downloads the index spreadsheet to the default folder for downloaded files saved by your web browser. Locate the file in the folder and open it in Microsoft Excel or another compatible spreadsheet program. The first tab of the spreadsheet provides instructions for use of the spreadsheet contents.

In Table 35 on page 67 through Table 38 on page 70 and in the downloadable Excel spreadsheet, P7 indexes are shown in forward orientation, applicable to any of the Illumina platforms. P5 indexes are shown in two orientations (forward and reverse complement) for use with different platforms and sequencing run setup and management tools, e.g., Local Run Manager and Instrument Run Setup. A selection of Illumina sequencing platforms and their P5 sequencing orientations are shown in Table 31. Correct representation of the P5 index orientation in sample sheets or during sequencing run setup is crucial to successful demultiplexing. Refer to Illumina support documentation and resources to determine the correct P5 index orientation for your application.

**Table 31** P5 index sequencing orientation by Illumina platform

| P5 Index Orientation | Platform |
|---|---|
| Forward | MiSeq |
| Reverse Complement* | NovaSeq 6000 with v1.5 chemistry<br>NextSeq 500/550/1000/2000<br>iSeq 100<br>MiniSeq |

* Some run setup and management tools used with these platforms automatically create the reverse complement sequence for the P5 index sequence entered for the run. Be sure to consult Illumina's support documentation for the combination of platform and tools used in your pipeline to determine the correct index orientation to enter during run setup.

## Plate Position Information

The plate provided with 32 Reaction kits (p/n 5191-6837) contains one set of four (4) index strips labeled *D1*, *D2*, *D3*, or *D4*, with each of 32 unique dual indexing primer pairs 1-32 provided in a single well. See Table 32 for a plate map.

**Table 32** Index map for Magnis SureSelect XT HS2 Index Primer Pairs 1-32, ILM provided with **32 Reaction kits**

| Plate Column | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 | 12 |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **Strip Tube Label** | **D1** | **D2** | **D3** | **D4** | **(No index strips provided in plate columns 5–12)** | | | | | | | |
| **Index Pair Numbers** | 1 | 9 | 17 | 25 | — | — | — | — | — | — | — | — |
| | 2 | 10 | 18 | 26 | — | — | — | — | — | — | — | — |
| | 3 | 11 | 19 | 27 | — | — | — | — | — | — | — | — |
| | 4 | 12 | 20 | 28 | — | — | — | — | — | — | — | — |
| | 5 | 13 | 21 | 29 | — | — | — | — | — | — | — | — |
| | 6 | 14 | 22 | 30 | — | — | — | — | — | — | — | — |
| | 7 | 15 | 23 | 31 | — | — | — | — | — | — | — | — |
| | 8 | 16 | 24 | 32 | — | — | — | — | — | — | — | — |

The plate provided with 96 Reaction kits contains one set of 12 index strips, containing 96 unique dual indexing primer pairs, with each pair in a single well. Kits are supplied either with p/n 5191-6833, containing primer pairs 1-96 in index strips labeled *D1* through *D12*, or with p/n 5191-6835, containing primer pairs 97-192 in index strips labeled *D13* through *D24*. See Table 33 and Table 34 for plate maps.

**Table 33** Index map for Magnis SureSelect XT HS2 Index Primer Pairs 1-96, ILM provided with **96 Reaction kits**

| Plate Column | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 | 12 |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **Strip Tube Label** | **D1** | **D2** | **D3** | **D4** | **D5** | **D6** | **D7** | **D8** | **D9** | **D10** | **D11** | **D12** |
| **Index Pair Numbers** | 1 | 9 | 17 | 25 | 33 | 41 | 49 | 57 | 65 | 73 | 81 | 89 |
| | 2 | 10 | 18 | 26 | 34 | 42 | 50 | 58 | 66 | 74 | 82 | 90 |
| | 3 | 11 | 19 | 27 | 35 | 43 | 51 | 59 | 67 | 75 | 83 | 91 |
| | 4 | 12 | 20 | 28 | 36 | 44 | 52 | 60 | 68 | 76 | 84 | 92 |
| | 5 | 13 | 21 | 29 | 37 | 45 | 53 | 61 | 69 | 77 | 85 | 93 |
| | 6 | 14 | 22 | 30 | 38 | 46 | 54 | 62 | 70 | 78 | 86 | 94 |
| | 7 | 15 | 23 | 31 | 39 | 47 | 55 | 63 | 71 | 79 | 87 | 95 |
| | 8 | 16 | 24 | 32 | 40 | 48 | 56 | 64 | 72 | 80 | 88 | 96 |

**Table 34** Index map for Magnis SureSelect XT HS2 Index Primer Pairs 97-192, ILM provided with **96 Reaction kits**

| **Plate Column** | **1** | **2** | **3** | **4** | **5** | **6** | **7** | **8** | **9** | **10** | **11** | **12** |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **Strip Tube Label** | **D13** | **D14** | **D15** | **D16** | **D17** | **D18** | **D19** | **D20** | **D21** | **D22** | **D23** | **D24** |
| **Index Pair Numbers** | 97 | 105 | 113 | 121 | 129 | 137 | 145 | 153 | 161 | 169 | 177 | 185 |
| | 98 | 106 | 114 | 122 | 130 | 138 | 146 | 154 | 162 | 170 | 178 | 186 |
| | 99 | 107 | 115 | 123 | 131 | 139 | 147 | 155 | 163 | 171 | 179 | 187 |
| | 100 | 108 | 116 | 124 | 132 | 140 | 148 | 156 | 164 | 172 | 180 | 188 |
| | 101 | 109 | 117 | 125 | 133 | 141 | 149 | 157 | 165 | 173 | 181 | 189 |
| | 102 | 110 | 118 | 126 | 134 | 142 | 150 | 158 | 166 | 174 | 182 | 190 |
| | 103 | 111 | 119 | 127 | 135 | 143 | 151 | 159 | 167 | 175 | 183 | 191 |
| | 104 | 112 | 120 | 128 | 136 | 144 | 152 | 160 | 168 | 176 | 184 | 192 |

## Index Nucleotide Sequences

The nucleotide sequence of each SureSelect XT HS2 index is shown in Table 35 through Table 38. Each index is 8 nt in length, and sequencing runs should be completed using 8-bp index reads (see page 58.) Sequences can also be obtained by downloading the SureSelect XT HS2 Index Sequence Resource Excel spreadsheet from Agilent.com.

**Table 35** SureSelect XT HS2 Index Primer Pairs 1–48

| Primer Pair # | Index Strip | P7 Index Forward | P5 Index Forward | P5 Index Reverse Complement | Primer Pair # | Index Strip | P7 Index Forward | P5 Index Forward | P5 Index Reverse Complement |
|---|---|---|---|---|---|---|---|---|---|
| 1 | D1 | CAAGGTGA | ATGGTTAG | CTAACCAT | 25 | D4 | AGATGGAT | TGGCACCA | TGGTGCCA |
| 2 | D1 | TAGACCAA | CAAGGTGA | TCACCTTG | 26 | D4 | GAATTGTG | AGATGGAT | ATCCATCT |
| 3 | D1 | AGTCGCGA | TAGACCAA | TTGGTCTA | 27 | D4 | GAGCACTG | GAATTGTG | CACAATTC |
| 4 | D1 | CGGTAGAG | AGTCGCGA | TCGCGACT | 28 | D4 | GTTGCGGA | GAGCACTG | CAGTGCTC |
| 5 | D1 | TCAGCATC | AAGGAGCG | CGCTCCTT | 29 | D4 | AATGGAAC | GTTGCGGA | TCCGCAAC |
| 6 | D1 | AGAAGCAA | TCAGCATC | GATGCTGA | 30 | D4 | TCAGAGGT | AATGGAAC | GTTCCATT |
| 7 | D1 | GCAGGTTC | AGAAGCAA | TTGCTTCT | 31 | D4 | GCAACAAT | TCAGAGGT | ACCTCTGA |
| 8 | D1 | AAGTGTCT | GCAGGTTC | GAACCTGC | 32 | D4 | GTCGATCG | GCAACAAT | ATTGTTGC |
| 9 | D2 | CTACCGAA | AAGTGTCT | AGACACTT | 33 | D5 | ATGGTAGC | GTCGATCG | CGATCGAC |
| 10 | D2 | TAGAGCTC | CTACCGAA | TTCGGTAG | 34 | D5 | CGCCAATT | ATGGTAGC | GCTACCAT |
| 11 | D2 | ATGTCAAG | TAGAGCTC | GAGCTCTA | 35 | D5 | GACAATTG | CGCCAATT | AATTGGCG |
| 12 | D2 | GCATCATA | ATGTCAAG | CTTGACAT | 36 | D5 | ATATTCCG | GACAATTG | CAATTGTC |
| 13 | D2 | GACTTGAC | GCATCATA | TATGATGC | 37 | D5 | TCTACCTC | ATATTCCG | CGGAATAT |
| 14 | D2 | CTACAATG | GACTTGAC | GTCAAGTC | 38 | D5 | TCGTCGTG | TCTACCTC | GAGGTAGA |
| 15 | D2 | TCTCAGCA | CTACAATG | CATTGTAG | 39 | D5 | ATGAGAAC | TCGTCGTG | CACGACGA |
| 16 | D2 | AGACACAC | TCTCAGCA | TGCTGAGA | 40 | D5 | GTCCTATA | ATGAGAAC | GTTCTCAT |
| 17 | D3 | CAGGTCTG | AGACACAC | GTGTGTCT | 41 | D6 | AATGACCA | GTCCTATA | TATAGGAC |
| 18 | D3 | AATACGCG | CAGGTCTG | CAGACCTG | 42 | D6 | CAGACGCT | AATGACCA | TGGTCATT |
| 19 | D3 | GCACACAT | AATACGCG | CGCGTATT | 43 | D6 | TCGAACTG | CAGACGCT | AGCGTCTG |
| 20 | D3 | CTTGCATA | GCACACAT | ATGTGTGC | 44 | D6 | CGCTTCCA | TCGAACTG | CAGTTCGA |
| 21 | D3 | ATCCTCTT | CTTGCATA | TATGCAAG | 45 | D6 | TATTCCTG | CGCTTCCA | TGGAAGCG |
| 22 | D3 | GCACCTAA | ATCCTCTT | AAGAGGAT | 46 | D6 | CAAGTTAC | TATTCCTG | CAGGAATA |
| 23 | D3 | TGCTGCTC | GCACCTAA | TTAGGTGC | 47 | D6 | CAGAGCAG | CAAGTTAC | GTAACTTG |
| 24 | D3 | TGGCACCA | TGCTGCTC | GAGCAGCA | 48 | D6 | CGCGCAAT | CAGAGCAG | CTGCTCTG |

**Table 36** SureSelect XT HS2 Index Primer Pairs 49–96

| Primer Pair # | Index Strip | P7 Index Forward | P5 Index Forward | P5 Index Reverse Complement | Primer Pair # | Index Strip | P7 Index Forward | P5 Index Forward | P5 Index Reverse Complement |
|---|---|---|---|---|---|---|---|---|---|
| 49 | D7 | TGAGGAGT | CGCGCAAT | ATTGCGCG | 73 | D10 | AACGCATT | ATAGTGAC | GTCACTAT |
| 50 | D7 | ATGACGAA | TGAGGAGT | ACTCCTCA | 74 | D10 | CAGTTGCG | AACGCATT | AATGCGTT |
| 51 | D7 | TACGGCGA | ATGACGAA | TTCGTCAT | 75 | D10 | TGCCTCGA | CAGTTGCG | CGCAACTG |
| 52 | D7 | AGCGAGTT | TACGGCGA | TCGCCGTA | 76 | D10 | AAGGCTTA | TGCCTCGA | TCGAGGCA |
| 53 | D7 | TGTATCAC | AGCGAGTT | AACTCGCT | 77 | D10 | GCAATGAA | AAGGCTTA | TAAGCCTT |
| 54 | D7 | GATCGCCT | TGTATCAC | GTGATACA | 78 | D10 | AAGAACCT | GCAATGAA | TTCATTGC |
| 55 | D7 | GACTCAAT | GATCGCCT | AGGCGATC | 79 | D10 | CTGTGCCT | AAGAACCT | AGGTTCTT |
| 56 | D7 | CAGCTTGC | GACTCAAT | ATTGAGTC | 80 | D10 | TACGTAGC | CTGTGCCT | AGGCACAG |
| 57 | D8 | AGCTGAAG | CAGCTTGC | GCAAGCTG | 81 | D11 | AAGTGGAC | TACGTAGC | GCTACGTA |
| 58 | D8 | ATTCCGTG | AGCTGAAG | CTTCAGCT | 82 | D11 | CAACCGTG | AAGTGGAC | GTCCACTT |
| 59 | D8 | TATGCCGC | ATTCCGTG | CACGGAAT | 83 | D11 | CTGTTGTT | CAACCGTG | CACGGTTG |
| 60 | D8 | TCAGCTCA | TATGCCGC | GCGGCATA | 84 | D11 | GCACGATG | CTGTTGTT | AACAACAG |
| 61 | D8 | AACTGCAA | TCAGCTCA | TGAGCTGA | 85 | D11 | GTACGGAC | GCACGATG | CATCGTGC |
| 62 | D8 | ATTAGGAG | AACTGCAA | TTGCAGTT | 86 | D11 | CTCCAAGC | GTACGGAC | GTCCGTAC |
| 63 | D8 | CAGCAATA | ATTAGGAG | CTCCTAAT | 87 | D11 | TAGTCTGA | CTCCAAGC | GCTTGGAG |
| 64 | D8 | GCCAAGCT | CAGCAATA | TATTGCTG | 88 | D11 | TTCGCCGT | TAGTCTGA | TCAGACTA |
| 65 | D9 | TCCGTTAA | GCCAAGCT | AGCTTGGC | 89 | D12 | GAACTAAG | ATACGAAG | CTTCGTAT |
| 66 | D9 | GTGCAACG | TCCGTTAA | TTAACGGA | 90 | D12 | AAGCCATC | GAGATTCA | TGAATCTC |
| 67 | D9 | AGTAACGC | GTGCAACG | CGTTGCAC | 91 | D12 | AACTCTTG | AAGCCATC | GATGGCTT |
| 68 | D9 | CATAGCCA | AGTAACGC | GCGTTACT | 92 | D12 | GTAGTCAT | AACTCTTG | CAAGAGTT |
| 69 | D9 | CACTAGTA | CATAGCCA | TGGCTATG | 93 | D12 | CTCGCTAG | GTAGTCAT | ATGACTAC |
| 70 | D9 | TTAGTGCG | CACTAGTA | TACTAGTG | 94 | D12 | AGTCTTCA | CAGTATCA | TGATACTG |
| 71 | D9 | TCGATACA | TTAGTGCG | CGCACTAA | 95 | D12 | TCAAGCTA | CTTCGTAC | GTACGAAG |
| 72 | D9 | ATAGTGAC | TCGATACA | TGTATCGA | 96 | D12 | CTTATCCT | TCAAGCTA | TAGCTTGA |

**Table 37** SureSelect XT HS2 Index Primer Pairs 97–144

| Primer Pair # | Index Strip | P7 Index Forward | P5 Index Forward | P5 Index Reverse Complement | Primer Pair # | Index Strip | P7 Index Forward | P5 Index Forward | P5 Index Reverse Complement |
|---|---|---|---|---|---|---|---|---|---|
| 97 | D13 | TCATCCTT | CTTATCCT | AGGATAAG | 121 | D16 | CAGGCAGA | AGACGCCT | AGGCGTCT |
| 98 | D13 | AACACTCT | TCATCCTT | AAGGATGA | 122 | D16 | TCCGCGAT | CAGGCAGA | TCTGCCTG |
| 99 | D13 | CACCTAGA | AACACTCT | AGAGTGTT | 123 | D16 | CTCGTACG | TCCGCGAT | ATCGCGGA |
| 100 | D13 | AGTTCATG | CACCTAGA | TCTAGGTG | 124 | D16 | CACACATA | CTCGTACG | CGTACGAG |
| 101 | D13 | GTTGGTGT | AGTTCATG | CATGAACT | 125 | D16 | CGTCAAGA | CACACATA | TATGTGTG |
| 102 | D13 | GCTACGCA | GTTGGTGT | ACACCAAC | 126 | D16 | TTCGCGCA | CGTCAAGA | TCTTGACG |
| 103 | D13 | TCAACTGC | GCTACGCA | TGCGTAGC | 127 | D16 | CGACTACG | TTCGCGCA | TGCGCGAA |
| 104 | D13 | AAGCGAAT | TCAACTGC | GCAGTTGA | 128 | D16 | GAAGGTAT | CGACTACG | CGTAGTCG |
| 105 | D14 | GTGTTACA | AAGCGAAT | ATTCGCTT | 129 | D17 | TTGGCATG | GAAGGTAT | ATACCTTC |
| 106 | D14 | CAAGCCAT | GTGTTACA | TGTAACAC | 130 | D17 | CGAATTCA | TTGGCATG | CATGCCAA |
| 107 | D14 | CTCTCGTG | CAAGCCAT | ATGGCTTG | 131 | D17 | TTAGTTGC | CGAATTCA | TGAATTCG |
| 108 | D14 | TCGACAAC | CTCTCGTG | CACGAGAG | 132 | D17 | GATGCCAA | TTAGTTGC | GCAACTAA |
| 109 | D14 | TCGATGTT | TCGACAAC | GTTGTCGA | 133 | D17 | AGTTGCCG | GATGCCAA | TTGGCATC |
| 110 | D14 | CAAGGAAG | TCGATGTT | AACATCGA | 134 | D17 | GTCCACCT | AGTTGCCG | CGGCAACT |
| 111 | D14 | ATTGATGC | AGAGAATC | GATTCTCT | 135 | D17 | ATCAAGGT | GTCCACCT | AGGTGGAC |
| 112 | D14 | TCGCAGAT | TTGATGGC | GCCATCAA | 136 | D17 | GAACCAGA | ATCAAGGT | ACCTTGAT |
| 113 | D15 | GCAGAGAC | TCGCAGAT | ATCTGCGA | 137 | D18 | CATGTTCT | GAACCAGA | TCTGGTTC |
| 114 | D15 | CTGCGAGA | GCAGAGAC | GTCTCTGC | 138 | D18 | TCACTGTG | CATGTTCT | AGAACATG |
| 115 | D15 | CAACCAAC | CTGCGAGA | TCTCGCAG | 139 | D18 | ATTGAGCT | TCACTGTG | CACAGTGA |
| 116 | D15 | ATCATGCG | CAACCAAC | GTTGGTTG | 140 | D18 | GATAGAGA | ATTGAGCT | AGCTCAAT |
| 117 | D15 | TCTGAGTC | ATCATGCG | CGCATGAT | 141 | D18 | TCTAGAGC | GATAGAGA | TCTCTATC |
| 118 | D15 | TCGCCTGT | TCTGAGTC | GACTCAGA | 142 | D18 | GAATCGCA | TCTAGAGC | GCTCTAGA |
| 119 | D15 | GCGCAATT | TCGCCTGT | ACAGGCGA | 143 | D18 | CTTCACGT | GAATCGCA | TGCGATTC |
| 120 | D15 | AGACGCCT | GCGCAATT | AATTGCGC | 144 | D18 | CTCCGGTT | CTTCACGT | ACGTGAAG |

**Table 38** SureSelect XT HS2 Index Primer Pairs 145–192

| Primer Pair # | Index Strip | P7 Index Forward | P5 Index Forward | P5 Index Reverse Complement | Primer Pair # | Index Strip | P7 Index Forward | P5 Index Forward | P5 Index Reverse Complement |
|---|---|---|---|---|---|---|---|---|---|
| 145 | D19 | TGTGACTA | CTCCGGTT | AACCGGAG | 169 | D22 | CGCTCAGA | CTAACAAG | CTTGTTAG |
| 146 | D19 | GCTTCCAG | TGTGACTA | TAGTCACA | 170 | D22 | TAACGACA | CGCTCAGA | TCTGAGCG |
| 147 | D19 | CATCCTGT | GCTTCCAG | CTGGAAGC | 171 | D22 | CATACTTG | TAACGACA | TGTCGTTA |
| 148 | D19 | GTAATACG | CATCCTGT | ACAGGATG | 172 | D22 | AGATACGA | CATACTTG | CAAGTATG |
| 149 | D19 | GCCAACAA | GTAATACG | CGTATTAC | 173 | D22 | AATCCGAC | AGATACGA | TCGTATCT |
| 150 | D19 | CATGACAC | GCCAACAA | TTGTTGGC | 174 | D22 | TGAAGTAC | AATCCGAC | GTCGGATT |
| 151 | D19 | TGCAATGC | CATGACAC | GTGTCATG | 175 | D22 | CGAATCAT | TGAAGTAC | GTACTTCA |
| 152 | D19 | CACATTCG | TGCAATGC | GCATTGCA | 176 | D22 | TGATTGGC | CGAATCAT | ATGATTCG |
| 153 | D20 | CAATCCGA | CACATTCG | CGAATGTG | 177 | D23 | TCGAAGGA | TGATTGGC | GCCAATCA |
| 154 | D20 | CATCGACG | CAATCCGA | TCGGATTG | 178 | D23 | CAGTCATT | TCGAAGGA | TCCTTCGA |
| 155 | D20 | GTGCGCTT | CATCGACG | CGTCGATG | 179 | D23 | CGCGAACA | CAGTCATT | AATGACTG |
| 156 | D20 | ATAGCGTT | GTGCGCTT | AAGCGCAC | 180 | D23 | TACGGTTG | CGCGAACA | TGTTCGCG |
| 157 | D20 | GAGTAAGA | ATAGCGTT | AACGCTAT | 181 | D23 | AGAACCGT | TACGGTTG | CAACCGTA |
| 158 | D20 | CTGACACA | GAGTAAGA | TCTTACTC | 182 | D23 | AGGTGCTT | AGAACCGT | ACGGTTCT |
| 159 | D20 | ATACGTGT | CTGACACA | TGTGTCAG | 183 | D23 | ATCGCAAC | AGGTGCTT | AAGCACCT |
| 160 | D20 | GACCGAGT | ATACGTGT | ACACGTAT | 184 | D23 | GCCTCTCA | ATCGCAAC | GTTGCGAT |
| 161 | D21 | GCAGTTAG | GACCGAGT | ACTCGGTC | 185 | D24 | TCGCGTCA | GCCTCTCA | TGAGAGGC |
| 162 | D21 | CGTTCGTC | GCAGTTAG | CTAACTGC | 186 | D24 | GAGTGCGT | TCGCGTCA | TGACGCGA |
| 163 | D21 | CGTTAACG | CGTTCGTC | GACGAACG | 187 | D24 | CGAACACT | GCATAAGT | ACTTATGC |
| 164 | D21 | TCGAGCAT | CGTTAACG | CGTTAACG | 188 | D24 | TAAGAGTG | AGAAGACG | CGTCTTCT |
| 165 | D21 | GCCGTAAC | TCGAGCAT | ATGCTCGA | 189 | D24 | TGGATTGA | TAAGAGTG | CACTCTTA |
| 166 | D21 | GAGCTGTA | GCCGTAAC | GTTACGGC | 190 | D24 | AGGACATA | TGGATTGA | TCAATCCA |
| 167 | D21 | AGGAAGAT | GAGCTGTA | TACAGCTC | 191 | D24 | GACATCCT | AGGACATA | TATGTCCT |
| 168 | D21 | CTAACAAG | AGGAAGAT | ATCTTCCT | 192 | D24 | GAAGCCTC | GACATCCT | AGGATGTC |

## Post-Run Tracking of Index Identity

The specific Index Strip used for a Magnis Prep System run is reported in the **Post-Run Data**, accessible from the touchscreen Home screen. From the **Post-Run Data** screen, open the **Labware Info** tab, and under *Labware*, locate the *Index Strip* row to view various properties of the index strip used for the run. The Index Strip number, reported as a 1–24 value, can be viewed by scrolling to the right-most part of the screen, and looking in the *Index Strip* column. The equivalent Index Strip number of 1–24 can also be found in the run log file.

The specific SureSelect XT HS2 dual indexing primer pairs associated with each Index Strip number 1–24 are shown in Table 39.

**Table 39** Use of Index Strip numbers from Post-Run Data for Index tracking

| ***Index Strip*** **Number from Post-Run Data Screen or Log** | **Index Strip Tube Label (Inscription)** | **Dual Index Primer Pair by Sample Number in Run** | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|
| | | **Sample 1** | **Sample 2** | **Sample 3** | **Sample 4** | **Sample 5** | **Sample 6** | **Sample 7** | **Sample 8** |
| **1** | D1 | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 |
| **2** | D2 | 9 | 10 | 11 | 12 | 13 | 14 | 15 | 16 |
| **3** | D3 | 17 | 18 | 19 | 20 | 21 | 22 | 23 | 24 |
| **4** | D4 | 25 | 26 | 27 | 28 | 29 | 30 | 31 | 32 |
| **5** | D5 | 33 | 34 | 35 | 36 | 37 | 38 | 39 | 40 |
| **6** | D6 | 41 | 42 | 43 | 44 | 45 | 46 | 47 | 48 |
| **7** | D7 | 49 | 50 | 51 | 52 | 53 | 54 | 55 | 56 |
| **8** | D8 | 57 | 58 | 59 | 60 | 61 | 62 | 63 | 64 |
| **9** | D9 | 65 | 66 | 67 | 68 | 69 | 70 | 71 | 72 |
| **10** | D10 | 73 | 74 | 75 | 76 | 77 | 78 | 79 | 80 |
| **11** | D11 | 81 | 82 | 83 | 84 | 85 | 86 | 87 | 88 |
| **12** | D12 | 89 | 90 | 91 | 92 | 93 | 94 | 95 | 96 |
| **13** | D13 | 97 | 98 | 99 | 100 | 101 | 102 | 103 | 104 |
| **14** | D14 | 105 | 106 | 107 | 108 | 109 | 110 | 111 | 112 |
| **15** | D15 | 113 | 114 | 115 | 116 | 117 | 118 | 119 | 120 |
| **16** | D16 | 121 | 122 | 123 | 124 | 125 | 126 | 127 | 128 |
| **17** | D17 | 129 | 130 | 131 | 132 | 133 | 134 | 135 | 136 |
| **18** | D18 | 137 | 138 | 139 | 140 | 141 | 142 | 143 | 144 |
| **19** | D19 | 145 | 146 | 147 | 148 | 149 | 150 | 151 | 152 |
| **20** | D20 | 153 | 154 | 155 | 156 | 157 | 158 | 159 | 160 |
| **21** | D21 | 161 | 162 | 163 | 164 | 165 | 166 | 167 | 168 |
| **22** | D22 | 169 | 170 | 171 | 172 | 173 | 174 | 175 | 176 |
| **23** | D23 | 177 | 178 | 179 | 180 | 181 | 182 | 183 | 184 |
| **24** | D24 | 185 | 186 | 187 | 188 | 189 | 190 | 191 | 192 |

# Troubleshooting Guide

Troubleshooting guidelines are included below for running the automated SureSelect XT HS2 DNA NGS Library Preparation protocols on the Magnis NGS Prep System and for the upstream sample preparation and downstream library analysis steps. For general Magnis instrument troubleshooting, see the instrument User Guide, publication K1007-90000.

### If touchscreen appears unresponsive

✓Reboot the system to reset touchscreen functionality.

### If the instrument LED indicator lights turn red and touchscreen displays error message "*Teach points are shifted. Please perform auto teaching from the Settings screen*."

✓This error message appears when the Instrument Health Check (IHC) does not pass the teachpoint verification, indicating that the teachpoint markers on the instrument deck may be obscured or that the instrument needs to perform a teachpoint Auto Teaching routine before setting up a run. Complete the steps below to ready the instrument for a run:

- Verify that all Magnis deck positions are cleared of kit consumables and other debris. The presence of any materials on the instrument deck can prevent the successful detection of the teach point markers.
- Clean the barcode scanner window using the cleaning instructions in the instrument User Guide. Debris or fingerprints on the scanner can obscure the teach points, causing verification failure.
- Reboot the system. After login, the instrument will perform another IHC. If this health check is successful, you can resume the setup process without performing Auto Teaching. If the IHC is unsuccessful, complete Auto Teaching using the steps below.
- From the Home screen, open the **Settings** screen and press **Auto Teaching**. Follow the instructions on the touchscreen display. The Auto Teaching process requires approximately 30 minutes, and requires that an operator be present for placement of labware on the instrument.
- Once Auto Teaching is complete, you can begin run setup by pressing **Run Protocol** from the Home screen.

### If the instrument LED indicator lights turn red and touchscreen displays an Instrument Health Check (IHC) failure message

✓Agilent recommends restarting the instrument after IHC failure using the steps below:

- From the error dialog, press **Cancel** to decline initiation of diagnostic testing.
- Press the error icon at the bottom of the screen and record the error code for potential use in troubleshooting with Agilent Support.
- Turn off the instrument by pressing the power button on the front of the instrument.
- Verify that all Magnis deck positions are cleared of kit consumables and other debris. The presence of any materials on the instrument deck can interfere with the IHC upon restart.
- Turn on the instrument by pressing the power button on the front of the instrument.
- After login, the instrument will perform another IHC. If this health check is successful, you can begin or restart run setup by pressing **Run Protocol** from the Home screen.

If the IHC fails again after the instrument is restarted, contact Agilent Worldwide Technical Support for assistance.

### If a protocol is missing from the Protocol menu on the *Enter Run Info* screen

✓The Magnis run protocols visible on the touchscreen *Enter Run Info* screen and available to run on your instrument may vary, depending on date of instrument purchase, protocol availability date, and whether any post-purchase updates have been made on your instrument. If you need a protocol that is not currently available on your instrument, visit the Magnis protocol download page at Agilent.com for more information.

### If seating of strip tubes in chiller module is difficult

✓To facilitate proper seating of strip tubes in the chiller module, load the strips in left-to-right order (filled sample strip, index strip, probe strip, empty QC strip and empty library strip).

✓Improperly-placed foil seals can obstruct strip tube positioning and seating when loading the chiller. When re-sealing the sample input strip or a self-filled probe strip with a foil seal, take care to apply the seal firmly and evenly, without excessive overhangs or creases.

### If the *Verify Labware* screen reports an issue with one or more labware components after scanning the labware barcodes

✓If all or most of the labware failed verification, then the barcode scanner window may require cleaning. See the instrument User Guide for cleaning instructions. Once cleaning is completed, repeat the *Verify Labware* step.

✓If only one or a few labware components failed verification, then press the error icon at the bottom of the screen and expand the information for the failed position to view the reason for the failure.

- **If the barcode scanner failed to scan a particular labware component**

  Verify that the labware is present at the required deck position and oriented correctly, with the barcode facing the front of the instrument. Review pages page 30 to page 34 for complete deck loading steps. Correct the omission or positioning error(s) and then repeat the *Verify Labware* step. If the failed labware components are present and correctly positioned, then visually inspect the barcode to verify integrity. For successful scanning, barcodes must be free of scratches, smudges, condensation, obstruction by foil seals, and writing or other marks on the plasticware. If barcode damage or obstruction is suspected, adjust or replace the labware component and repeat the *Verify Labware* step.

- **If the scanned labware is past its expiration date**

  Replace any expired components with unexpired components then repeat the *Verify Labware* step. The expiration date can be found on the Certificate of Analysis provided with each component kit containing pre-filled reagents. Components provided as empty plasticware do not have an expiration date.

- **If scanned labware components are identified as *wrong labware***

  When scanned labware (e.g., the Beads/Buffers Plate or the Probe Input Strip) is identified as *wrong labware*, it is important to verify that the correct protocol was selected for the format of the Reagent Kit loaded on the instrument. Check the format of the Reagent Kit loaded for the run, then use the table below to verify that the correct protocol was selected during run setup. If an incorrect protocol was selected, return to the *Enter Run Info* screen by pressing the backward arrow on the touchscreen and select the correct protocol from the menu, expanding the protocol menu if required. After selecting the correct protocol, use the forward arrow keys to advance back to the *Verify Labware* screen, then repeat the *Verify Labware* step.

| Reagent Kit | Correct Processing Protocol |
|---|---|
| Magnis SureSelect XT HS2 **DNA** Reagent Kits supplied with **pre-filled probe input strips** | *SSEL-DNA-XTHS2-ILM* |
| Magnis SureSelect HS2 **DNA** Reagent Kits supplied with **empty probe input strips** (filled at run time) | *SSEL-DNA-XTHS2-EPIS-ILM* |
| Magnis SureSelect HS2 **RNA** Reagent Kits supplied with Magnis SureSelect **RNA** Beads/Buffers Plates ILM and pre-filled or empty probe input strips | *SSEL-RNA-XTHS2-ILM* or *SSEL-RNA-XTHS2-EPIS-ILM* |

- **If labware was identified as the *wrong labware*, with correct protocol selected**

  Replace the misplaced labware with the correct labware and repeat the *Verify Labware* step.

### If an unattached micropipettor tip is sitting on the instrument deck during run

✓ Occasionally, when the instrument ejects used tips into the waste container, a tip may bounce out and land on the instrument deck. With a gloved hand, move the tip to the waste container or dispose of it as you would when emptying the waste container.

### If the touchscreen *Turn off Chiller* dialog obscures the run screen after the instrument door is opened and libraries are collected at end of run

✓ If the instrument door is opened at the end of the run before the LED indicator lights turn blue (indicating completion of all instrument run steps) or if the instrument door is only partially opened at the end of the run, the *Turn off Chiller* dialog may be retained on the run screen, obscuring the screen content. In future runs, wait for the LED indicator lights to turn blue, indicating that the instrument has reached a post-run idle state, before opening the instrument door. Open the door fully (until LED indicator lights turn white) before collecting your samples.

### If the touchscreen *Time Remaining* display does not read 0:00 immediately before proceeding to completed run/sample collection screens

✓ The **Time Remaining** value displayed on the touchscreen is only an estimate of time left in the run. The counter may adjust the remaining time estimate during the run and may display time greater than 0:00 when the system is ready to begin sample collection. This is not indicative of an issue with the run or the instrument.

### If volume of final library sample is lower than expected

✓ At the end of the run, the final library samples (20–23 µL) are transferred to wells of the green Library Output Strip and held in the chiller at 12°C until removed from the instrument. The duration and the relative humidity conditions of the post-run chiller hold can affect the volume recovered from the Library Output Strip.

## If yield of post-capture library is low

- ✓For runs performed using automated enzymatic fragmentation, verify that DNA samples were prepared containing 10 ng, 50 ng, 100 ng or 200 ng DNA in 14 µL. Loading a greater volume of lower-concentration sample is invalid; the Magnis instrument removes 14 µL of the sample loaded in the sample input strip for further processing.
- ✓Verify that enzymatic or mechanical DNA shearing was performed in Low TE Buffer, and not in water. Shearing DNA samples in water reduces overall library yield and complexity.
- ✓Verify that the input DNA sample meets the guidelines for quality and concentration range specified in "Appendix 1: DNA Sample Preparation Guidelines"
- ✓Verify that the run was set up for the appropriate input DNA concentration and quality. Settings may be checked on the **Run Setup** tab of the **Post Run Data** screen for the run.
- ✓Ensure that runs are completed in humidity conditions of 30% to 70% (non-condensing). Operating the system at humidity levels outside of this range can impact performance and result in lower or zero library yield.
- ✓Very low or zero yield for one or more samples in the run may indicate an issue with the pipette tips used in the run. While loading tips on the instrument, verify that all tip boxes are completely filled and that all tip boxes are seated flat and within the raised-tab frames of the platforms. Make sure that the tip boxes are not disturbed and unseated while removing the tip box lids.
- ✓Very low or zero yield for one or more samples in the run may also result from an issue with plasticware positioning or seating for the run. Review and adhere to the plasticware positioning details provided on page 30 to page 34. In particular, make sure that all strip tubes are properly seated in the chiller module; this is facilitated by loading strips in left-to-right order (filled sample input strip, index strip, probe strip, empty QC strip and empty library output strip).
- ✓PCR cycle number may require optimization. Repeat library preparation and target enrichment for the sample, increasing the post-capture PCR cycle number by 1 to 2 cycles. Only users with *Advanced* access level can change the post-capture PCR cycle number. See page 38 for more information.

## If pre-capture PCR optimization needed

- ✓When required the pre-capture PCR cycle number used in a run may be adjusted on the *Confirm Setup* screen. See page 38 for more information. Only users with *Advanced* access level can change the pre-capture PCR cycle number. Use the guidelines below as a starting point for cycle number self-optimization.

| Input DNA Quantity | Recommended Pre-Capture PCR Cycles | |
|---|---|---|
| | High Quality Input DNA | FFPE-derived Input DNA |
| 10 ng | 11 | 14 |
| 50 ng | 10 | 13 |
| 100 ng | 9 | 12 |
| 200 ng | 8 | 11 |

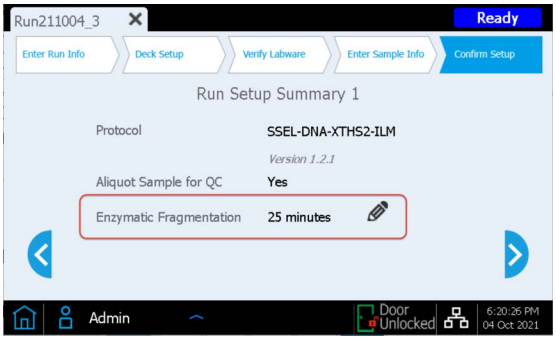
## If post-capture PCR optimization needed

✓When required the post-capture PCR cycle number used in a run may be adjusted on the *Confirm Setup* screen. See page 38 for more information. Only users with *Advanced* access level can change the post-capture PCR cycle number. Use the guidelines below as a starting point for cycle number self-optimization.

| SureSelect XT HS Probe Design Size | Recommended Post-Capture PCR Cycles |
|---|---|
| <200 kb | 14 |
| 200–749 kb | 13 |
| 750–2999 kb | 12 |
| 3–5 Mb | 10 |
| >5 Mb | 9 |

## If enzymatically-fragmented library fragment sizes are larger or smaller than expected in electropherograms

✓The duration of fragmentation may require optimization. To increase the average library fragment size, decrease the fragmentation duration, or to decrease the average library fragment size, increase the fragmentation duration. The fragmentation duration setting for the run can be adjusted on the *Confirm Setup* screen (see page 38 for more information).




Recommended settings are summarized here. The default value of 25 minutes is generally optimal for workflows using FFPE DNA samples and workflows using high-quality DNA samples with 100-bp read-length NGS. For workflows that include high-quality DNA samples and longer NGS read lengths (≥150 bp reads), decreasing the duration of fragmentation is recommended in order to increase the DNA fragment size distribution.

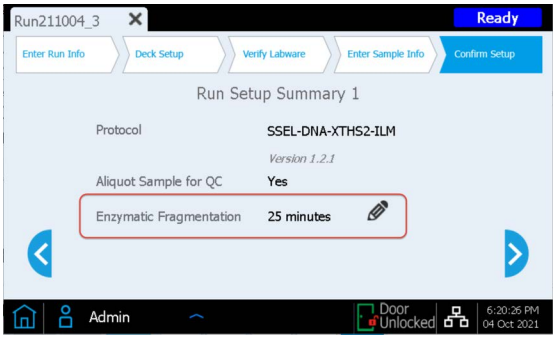
| NGS read length | Recommended automated Enzymatic Fragmentation duration | |
|---|---|---|
| | High-quality DNA samples | FFPE DNA samples |
| 2 ×100 reads | 25 minutes | 25 minutes |
| 2 ×150 reads | 15 minutes | 25 minutes |

✓The initial DNA fragment size of FFPE-derived samples may impact the final library fragment size distribution. Libraries prepared from more degraded FFPE samples may include a greater proportion of smaller library fragments and for some FFPE-derived samples final fragment size may not be increased by reducing the duration of fragmentation.

## If you need more information about the automated enzymatic fragmentation duration setting

✓The **Enzymatic Fragmentation** setting visible on the *Confirm Setup* screen controls the amount of time that the Magnis holds samples, combined with the fragmentation reagents, at 37°C to allow DNA cleavage. This setting can be adjusted during the verification process by pressing the pencil button adjacent to the setting value.

✓This duration setting has been optimized specifically for the reaction volume and other parameters used for automated fragmentation on the Magnis instrument, and the duration value may differ from values used in non-automated processing workflows. Recommended settings are summarized on page 76.




## If input DNA was enzymatically fragmented manually prior to run

✓The Magnis SureSelect XT HS2 DNA library preparation protocols include optional Magnis-automated enzymatic fragmentation and the system has not been validated using input DNA that was enzymatically-fragmented prior to the run. If you wish to self-validate a workflow using pre-fragmented input DNA generated using Agilent's SureSelect Enzymatic Fragmentation Kit, use the following guidelines:

- Starting with DNA samples containing 10 ng, 50 ng, 100 ng or 200 ng DNA, perform fragmentation according to the protocol in the kit user manual.
- Once enzymatic fragmentation is complete, dilute the fragmented DNA sample volume to 50 µL with nuclease-free water.
- Process the samples using the Magnis SureSelect XT HS2 DNA library preparation protocol **without** Enzymatic Fragmentation, as described for Covaris-sheared DNA (see page 22 and page 25).

## If Covaris-sheared library fragment sizes are larger than expected in electropherograms

✓Shearing may not be optimal. For intact, high-quality DNA samples, ensure that shearing is completed using the two-round shearing protocol provided, including all spinning and vortexing steps.

✓Any bubbles present on the microTUBE filament may disrupt complete shearing. Spin the microTUBE for 30 seconds before the first round of shearing to ensure that any bubbles are released.

## If sequencing reads do not cover the expected genomic regions

✓The wrong probe design may have been used in the protocol run for target enrichment. Review the sample and probe tracking that was recorded during the run. Repeat the protocol run with the correct probe design, if necessary.

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## In This Book

This guide provides instructions for automated preparation of SureSelect XT HS2 DNA target-enriched Illumina paired-end multiplexed sequencing libraries using the Magnis NGS Prep System.



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