

ONCO/Reveal™ Multi-Cancer Panel

Library Preparation User Guide

FOR RESEARCH USE ONLY

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INTRODUCTION

The ONCO/Reveal™ Multi-Cancer Panel targets numerous, relevant gene regions of interest for researchers looking to explore the genetic sequences of both germline and formalin-fixed paraffin-embedded (FFPE) DNA samples from solid tumor samples. The panel utilizes Pillar Biosciences' proprietary SLIMamp® (stem-loop inhibition mediated amplification) technology, allowing researchers to amplify regions of interest in a simple, multiplex reaction for subsequent sequencing on a sequencer using a paired-end read length of 150 (2x150).

The workflow of the ONCO/Reveal Multi-Cancer Panel can be performed and loaded onto the sequencing instrument by researchers within one day. The protocol also contains numerous stopping points for users who have time limitations.

How Does the ONCO/Reveal Multi-Cancer Panel Work?

A pair of DNA oligos was designed for each region of interest, or hot spot. Each region is amplified in the first round of gene-specific PCR (GS-PCR), the excess primers are digested, and the products are subsequently purified via size selection. After purification, a second round of PCR adds index adaptors and P5 and P7 sequences to each library for sample tracking and sequencing on Illumina's flow cells. Those products are further purified and sequenced (Figure 1).

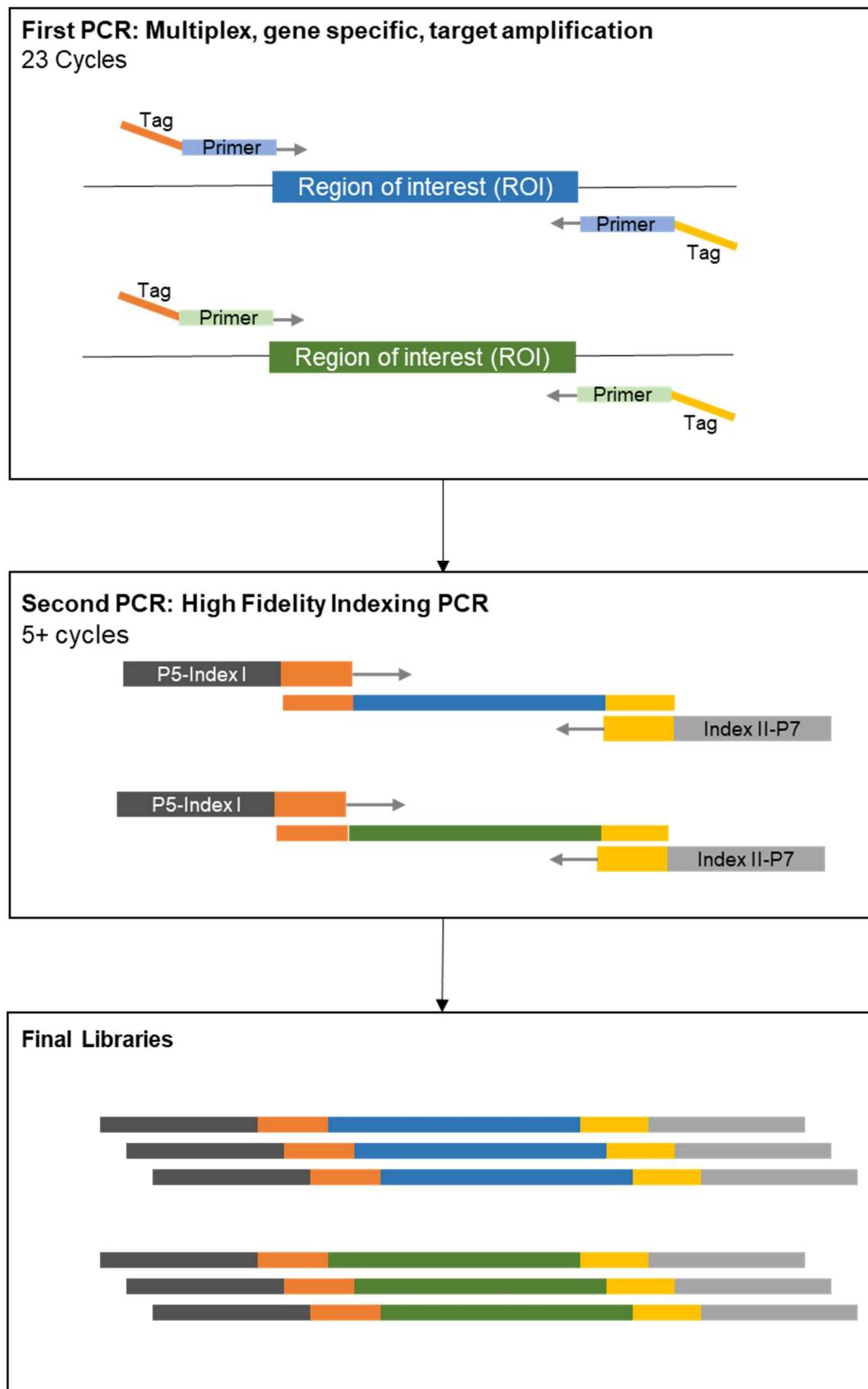


Figure 1. Overview of ONCO/Reveal Multi-Cancer Panel library preparation.

REVISION HISTORY

2017-03: User Guide created
2017-05: Exonuclease information updated
2017-08: UDG information added
2017-10: Updated indexing PCR and normalization
2018-05: Updated indexing enzyme
2019-04: Updated figure images
2019-05: Updated to product name and document format
2019-07: Index primer options and minor grammatical edits

GETTING STARTED

This section describes the necessary equipment, reagents, and consumables needed before performing the protocol.

Components of the ONCO/Reveal Multi-Cancer Panel

Reagent	Use	Area Use	Storage
<i>Gene-Specific PCR MasterMix (2x)</i>	Gene-specific PCR	Pre-PCR	-15° to -25°C
<i>Multi-Cancer Oligo Pool v1</i>	Gene-specific PCR	Pre-PCR	-15° to -25°C
<i>Exonuclease I</i>	Gene-specific PCR	Post-PCR	-15° to -25°C
<i>Indexing PCR Master Mix (2x)</i>	Indexing PCR	Pre-PCR	-15° to -25°C

ONCO/Reveal Multi-Cancer Panel Indexing Kits

Reagent and Part Number	Use	Area Use	Storage
<i>Illumina TSCA Indexing Primers Kit A, indices AI501-8, AI701-4 (32 combinations - 96 reactions) PN: IDX-AI-1001-96</i>	Indexing PCR	Pre-PCR	-15° to -25°C
<i>Illumina TSCA Indexing Primers Kit B, indices AI501-8, AI705-8 (32 combinations - 96 reactions) PN: IDX-AI-1002-96</i>	Indexing PCR	Pre-PCR	-15° to -25°C
<i>Illumina TSCA Indexing Primers Kit C, indices AI501-8, AI709-12 (32 combinations - 96 reactions) PN: IDX-AI-1003-96</i>	Indexing PCR	Pre-PCR	-15° to -25°C
<i>Illumina TSCA Indexing Primers Kit D, indices AI501-8, AI701-12 (96 combinations - 192 reactions) PN: IDX-AI-1004-192</i>	Indexing PCR	Pre-PCR	-15° to -25°C
<i>Illumina TSCA Indexing Primers Kit E, indices AI501-8, AI701-12 (96 combinations - 384 reactions) PN: IDX-AI-1005-384</i>	Indexing PCR	Pre-PCR	-15° to -25°C

Only one index kit is needed per assay. Multiple options are available to meet your throughput needs.

All reagents in the kit should be used in designated pre-PCR or post-PCR areas to prevent amplicon contamination. Each area designated for pre- and post-PCR should have dedicated equipment, supplies, and reagents to prevent contamination.

User-supplied Reagents

Reagent	Area use	Supplier
<i>10 N NaOH or 1 N NaOH</i>	Post-PCR	General lab supplier
<i>Agencourt AMPure XP Beads</i>	Post-PCR	Beckman Coulter, #A63881/ #A63880
<i>Ethanol, 200 proof for molecular biology</i>	Post-PCR	General lab supplier
<i>Nuclease-free water</i>	Pre- and Post-PCR	General lab supplier
<i>Qubit dsDNA High Sensitivity assay kit</i>	Post-PCR	Invitrogen, #Q32851/ #Q32854
<i>Agarose gel, 2% (optional)</i>	Post-PCR	General lab supplier
<i>DNA molecular weight markers (optional)</i>	Post-PCR	General lab supplier
<i>Or Bioanalyzer High Sensitivity DNA Analysis (optional)</i>	Post-PCR	Agilent #5067-4627/ #5067-4626
<i>Uracil-DNA glycosylase (UDG) (optional)</i>	Pre-PCR	NEB, #M0280S or #M0280L
<i>10 mM Tris-HCl w/ 0.1% Tween-20, pH 8.5 (optional)</i>	Post-PCR	Teknova, Cat#T7724

Compatible Illumina Reagent Kits

<i>MiSeq reagent Micro kit v2 (300 cycles)</i>	Illumina, #MS-103-1002
<i>MiSeq reagent kit v2 (300 cycles)</i>	Illumina, #MS-102-2002
<i>MiSeq reagent kit v3 (600 cycles)</i>	Illumina, #MS-102-3003
<i>NextSeq 500/550 Mid Output v2 kit (300 cycles)</i>	Illumina, #FC-404-2003

Consumables

Item	Area Use	Supplier
<i>1.5 mL microcentrifuge tubes</i>	Pre- and post-PCR	General lab supplier
<i>96-well PCR plates, 0.2 mL</i>	Pre- and post-PCR	Axygen, #6551 or equivalent
<i>Microplate sealing film</i>	Pre- and post-PCR	Axygen, #PCR-TS or equivalent
<i>Conical tubes, 15 mL</i>	Pre- and post-PCR	General lab supplier
<i>Conical tubes, 50 mL</i>	Post-PCR	General lab supplier
<i>Low retention, aerosol filter pipette tips</i>	Pre- and post-PCR	General lab supplier
<i>Solution basin (trough or reservoir)</i>	Pre- and post-PCR	Fisher, #13-681-506 or equivalent
<i>Qubit Assay tubes</i>	Post-PCR	Invitrogen, #Q32856

Equipment Requirements

Equipment	Area Use	Supplier
<i>Centrifuge adapted for PCR plates, tabletop</i>	Pre- and post-PCR	General lab supplier
<i>Gel electrophoresis apparatus (optional) or</i>	Post-PCR	General lab supplier
<i>2100 Bioanalyzer Instrument (optional)</i>	Post-PCR	Agilent. #G2939BA
<i>Magnetic stand for 96 wells</i>	Post-PCR	Life Technologies, #12331D/#12027
<i>Microfuge</i>	Pre- and post-PCR	General lab supplier
<i>Thermal cycler, heated lid capability</i>	Post-PCR	General lab supplier
<i>Pipettes, 0.5-1000 µL capabilities</i>	Pre- and post-PCR	General lab supplier
<i>Qubit Fluorometer</i>	Post-PCR	Invitrogen, #Q33216/Q33218
<i>Vortexer</i>	Pre- and post-PCR	General lab supplier

Other general lab supplies needed to carry out the protocol include laboratory gloves, ice, ice buckets, tube racks, etc.

For reagents, consumables, and equipment required in both pre- and post-PCR processes, dedicated supplies (including gloves, lab coats, etc.) should be located in both areas.

BEST PRACTICES

The following steps are recommended to improve consistency and reduce contamination:

- **Work areas:** To reduce the risk of contamination from PCR amplicons, supplies should not be moved from one area to another. Separate storage areas (refrigerator, freezer) should also be designated for pre- and post-PCR products.
- **Lab cleanliness:** To further reduce the possibility of contamination, clean work areas between experiments with laboratory cleaning solution (70% alcohol or freshly-made 10% hypochlorite solution). A periodic cleaning of the floor is also recommended.
- **Floor:** Items that have fallen to the floor are assumed to be contaminated and should be discarded. Gloves should also be changed after handling a contaminated item. If a sample tube or non-consumable item has fallen and remained capped, thoroughly clean the outside with a laboratory cleaning solution before use (70% alcohol or freshly-made 10% hypochlorite solution).
- **Aliquot reagents:** Aliquot frozen reagents into smaller volumes to prevent freeze/thaw cycles. For reagents stored at higher temperatures, aliquot from the stock and work from the aliquots to reduce the risk of stock contamination. In the case of contamination, aliquots can help to determine the source of contamination more quickly and easily.
- **Multichannel pipettes:** Use multichannel pipettes for consistency and efficiency among numerous samples.
- **Pipette tips:** Change tips between each sample to prevent cross-contamination. Discard any tips that may have become contaminated due to contact with gloves, lab bench, tube exteriors, etc.
- **Open containers and lids:** To prevent possible contamination from the air, keep tubes closed when not directly in use, avoid reaching over open containers, and cover plates with seals or lint-free laboratory wipes.

ONCO/Reveal Multi-Cancer Panel Workflow

The following chart (Figure 2) demonstrates the workflow for performing the ONCO/Reveal Multi-Cancer Panel library preparation.

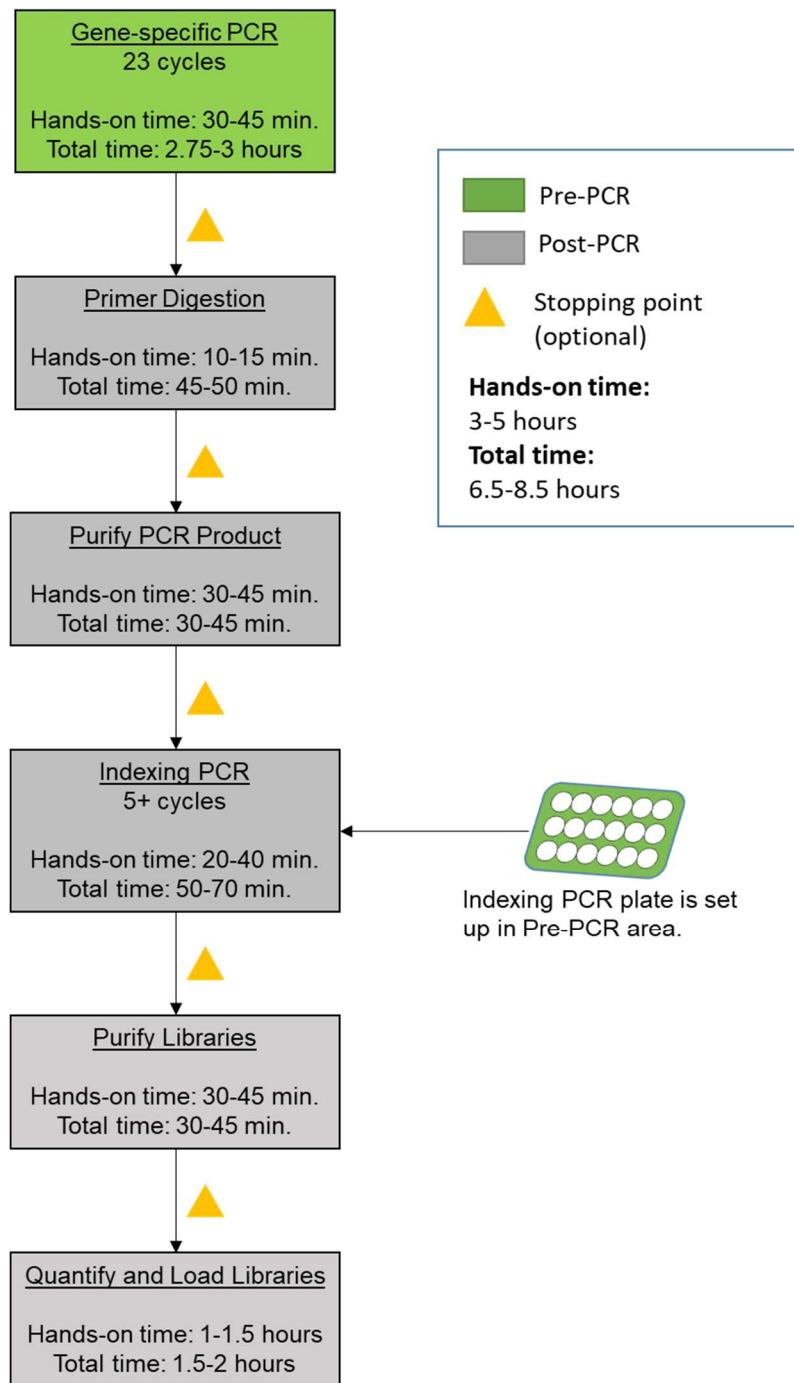


Figure 2. The ONCO/Reveal Multi-Cancer Panel workflow can be completed within a day but contains multiple stopping points for users with time constraints.

DNA INPUT INFORMATION

The following protocol includes information for preparing libraries using genomic DNA from tissue or FFPE samples.

The recommended DNA input is 20-60 ng per PCR reaction for standard genomic DNA and 20-80 ng for FFPE DNA.

For FFPE samples, it is recommended that Uracil-DNA glycosylase (UDG) be added to the initial gene-specific reaction. The deamination of cytosine to uracil is a common cause of the presence of artificial C>T (or G>A) variants. To reduce such artifacts due to DNA damage in FFPE samples, UDG can be added to the reaction during the initial setup of gene-specific PCR.

LIBRARY PREPARATION PROTOCOL

Hands-on time: 3-5 hours

Total time: 6.5-8.5 hours

Gene-specific PCR: Amplify Genomic DNA Targets

Hands-on time: 30-40 minutes

Total time: 2.75-3 hours

The following steps are performed in a pre-PCR area. For this portion of the protocol, have an ice bucket prepared. Keep the Gene-specific PCR MasterMix (GS PCR MMX) and Multi-Cancer oligo pool on ice.

1. **Prepare a PCR master mix:** Vortex and spin the GS PCR MMX and oligo pool before use. For each PCR reaction, the volume of each component is listed on the next page.

Note: The Gene-specific PCR Mastermix is viscous. Ensure the mix is fully homogenized before adding other reaction components. Vortexing is recommended and will not adversely affect enzyme activity.

- a. To prepare the PCR master mix, add components except genomic DNA to a 1.5 mL microtube and keep on ice.

For example, to prepare enough mixture for 10 samples, mix 125 µL of GS-PCR MMX, 50 µL of primer pool, 10 µL UDG (optional; see DNA input note), and the appropriate amount of water. Add reagent overage appropriately.

- b. Mix the PCR master mix by vortexing on medium speed for 10 seconds and spin down the solution in a microfuge. Transfer (25-n) µL of master mix to each sample well in a PCR plate, strip tube, or PCR tube.

Reagent	Volume (μ L) (without UDG)	Volume (μ L) (with UDG)
Gene-specific PCR MasterMix	12.5	12.5
Multi-Cancer oligo pool v1	5.0	5.0
Genomic DNA (20 ng*)	n	n
UDG (5 units/ μ L)	0.0	1.0
Nuclease-free water	7.5-n	6.5-n
Total	25.0	25.0

*The DNA concentration can be determined by the Qubit dsDNA BR Assay Kit (Life Technologies, Cat. No. Q32850 or Q32853; Quantitation range 2-1,000 ng) or the Qubit dsDNA HS Assay Kit (Life Technologies, Cat. No. Q32851 or Q32854; Quantitation range 0.2-100 ng).

The recommended DNA input is 20-60 ng per PCR reaction for standard genomic DNA and 20-80 ng for FFPE DNA. It is recommended that the quality of FFPE DNA be checked by qPCR (Taqman RNase P Detection Reagents Kit (Life Technologies, Cat. No. 4316831)) or a Bio-analyzer. If the FFPE DNA is not severely degraded, the DNA input can be as little as 5 ng. However, if the FFPE DNA is severely degraded, it is recommended to increase the DNA input quantitated by qPCR or Bio-analyzer when possible.

Note about FFPE samples: For FFPE samples, it is recommended that UDG be added to the reaction to reduce artifacts from fixation and storage. The deamination of cytosine is a common cause of the presence of artificial C>T (or G>A) variants.

2. **Add DNA:** Add (n) μ L of genomic DNA (or water for a no-template control).
3. **Seal and mix:** Carefully seal the reactions and vortex for 10-15 seconds.
4. **Spin:** Briefly spin the reactions to remove any air bubbles from the bottom of the wells and spin down droplets from the seal or side walls.

5. Perform PCR: Perform the following program with the heated lid on:

Temperature	Time	Number of Cycles (without UDG)*	Number of Cycles (with UDG)
37°C	10 minutes	0	1
95°C	15 minutes	1	1
97°C	1 minute		
58°C	1 minute		
60°C	2 minutes	5	5
64°C	30 seconds		
72°C	1 minute		
95°C	30 seconds	18	18
66°C	3 minutes		
8°C	Hold	1	1

*If multiple sample types are being processed (non-FFPE vs FFPE DNA), reactions with and without UDG can be run simultaneously. The 37°C incubation will not adversely affect the PCR reaction. Therefore, reactions with and without UDG can be run with the same cycling conditions.

IMPORTANT: *Do not leave the reactions at 8 °C overnight. Precipitation may occur when the reactions are incubated at 8 °C overnight.*

STOPPING POINT: *The gene-specific PCR reactions may be stored at -20 °C after cycling.*

Gene-specific Primer Digestion

Hands-on time: 10-15 minutes

Total time: 50-55 minutes

The following steps are performed in a post-PCR area. For this portion of the protocol, have an ice bucket prepared. Keep the exonuclease on ice. Keep the sample reactions at ambient temperature.

1. Briefly spin the reactions to remove any droplets from the side walls. Carefully remove the seal or caps.
2. **Dilute Exonuclease:**
 - a. Invert the Exonuclease I to mix and spin in a microfuge to remove any droplets from the lid.
 - b. For 10 samples, dilute 30 µL of the exonuclease I in 20 µL nuclease-free water to prepare 50 µL of diluted exonuclease. Add reagent overage as appropriate. Any excess dilution can be stored at -20°C overnight for a second use.

IMPORTANT: *The exonuclease solution is viscous and requires careful attention when pipetting. The diluted exonuclease I is good for a second use the next day if stored overnight at -20°C. Otherwise, freshly dilute the exonuclease before adding it to the samples.*

3. **Add Exonuclease:** Add 5 µL of the diluted exonuclease to each sample, pipetting up and down to mix.
4. **Seal and mix:** Carefully seal the reactions. Pulse vortex the reactions on a medium setting for 5-10 seconds.
5. **Spin:** Briefly spin the reactions to remove any air bubbles from the bottom of the wells and spin down droplets from the seal or side walls.
6. **Perform digestion:** Perform the following program with the lid on:

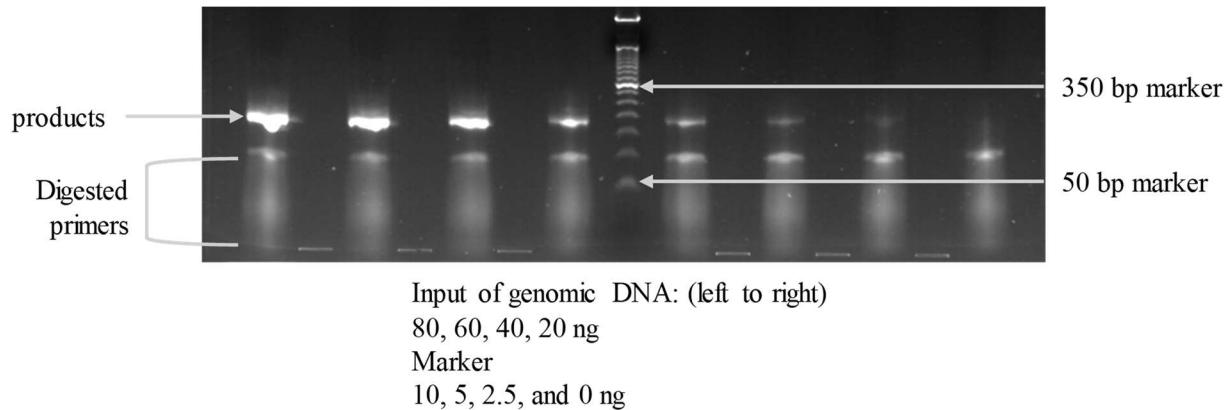
Temperature	Time	Number of Cycles
37°C	20 minutes	1
80°C	10 minutes	1
8°C	Hold	1

IMPORTANT: *Do not leave the reactions at 8°C overnight. Precipitation may occur when the reactions are incubated at 8°C overnight.*

STOPPING POINT: *The gene-specific PCR reactions may be stored at -20°C after primer digestion.*

Gel Image After Gene-specific PCR and Primer Digestion

The following image is an example of samples after gene-specific PCR and primer digestion using various inputs of genomic DNA on a 2% agarose gel.



Purify the Gene-specific PCR Product

Hands-on time: 30-45 minutes

Total time: 30-45 minutes

The following steps are performed in a post-PCR area.

Pre-purification

Warm AMPure beads: Take out Agencourt AMPure XP beads from 4°C and incubate at room temperature for at least 30 minutes before use.

If samples were stored at -20°C, remove from the freezer to thaw to ambient temperature before purification.

IMPORTANT: *It is critical that the AMPure beads reach room temperature before performing the purification process. The temperature of the bead solution can alter the purification process.*

Gene-specific Product Purification

1. If the samples were stored at -20°C or condensation has formed, briefly spin the samples upon thawing to remove droplets from the side walls. Carefully remove the seal or caps.
2. **Mix beads:** Vortex AMPure XP beads thoroughly until all beads are well dispersed.

IMPORTANT: *It is critical that the AMPure beads solution is homogeneous before performing the purification process. A non-uniform distribution can affect the purification process.*

3. **Add water to sample:** Add 20 µL of nuclease-free water to each well or add enough water to bring the volume to 50 µL.

TIP: *Use a trough and multichannel pipette to quickly and easily add the water to each well. The same method can be applied to add the beads in step 4 and washes in steps 7-9.*

4. **Add beads:** Add 60 µL beads (1.2x beads if the volume is not currently 50 µL) to each well. Pipette the mixture up and down 10 times. If bubbles form on the bottom of the wells, briefly the samples and mix again.
5. **Bind PCR product to beads:** Incubate the samples for 5 minutes at room temperature.

TIP: *During the incubation time, prepare a 50 mL solution of 70% ethanol by combining 35 mL of ethanol and 15 mL of molecular biology grade water, which will be used to wash the beads in step 8.*

6. **Separate beads containing PCR product:** Place the samples on a magnetic rack until the solution appears clear, which can take up to 5 minutes.
7. **Remove supernatant:** Carefully remove the supernatant from each well without disturbing the beads from the wall of each well.

8. **Wash beads:** Leave the samples on the magnetic rack. Add 150 µL of freshly prepared 70% ethanol to each well without disturbing the beads. Incubate 30 seconds, and then remove the supernatant from each well.

IMPORTANT: *Do not allow the ethanol mixture to remain open to the air. The ethanol concentration will change over time, affecting the washing of the beads. Pour only enough solution for each wash.*

9. **Second wash:** Repeat step 8 for a second 70% ethanol wash. Remove the supernatant from each well. The unused solution of ethanol can be used to purify the libraries after indexing PCR.
10. **Remove remaining ethanol wash:** Remove trace amounts of ethanol completely from each well. Spin the samples in a benchtop centrifuge for 10-15 seconds, place the samples back on the magnetic rack, and use a 10 or 20 µL tip to remove the remaining ethanol solution at the bottom of the wells.
11. **Resuspend beads:** Remove the samples from the magnetic rack, and immediately resuspend the dried beads in each well using 64 µL nuclease-free water. Gently pipette the suspension up and down 10 times. If bubbles form on the bottom of the wells, briefly spin and mix again.

Note: *Do not allow the beads to over-dry. During the purification, the beads tend to clump and “fan.” Be sure to immediately resuspend the beads after removing the ethanol wash.*

12. Incubate the elution at room temperature for 5 minutes to fully elute the product.

TIP: *After resuspending the beads, cover the samples and prepare the reactions for indexing the libraries using the Indexing PCR Master Mix in the Pre-PCR area. Alternately, the purified gene-specific PCR product (on beads) may be stored at -20 °C after elution.*

STOPPING POINT: *The purified PCR product may be stored with the beads at -20 °C.*

Indexing PCR: Amplify the Libraries

Hands-on time: 20-40 minutes

Total time: 50-70 minutes

The following steps should be performed in a pre-PCR area. For this portion of the protocol, have an ice bucket prepared. The Indexing PCR Master Mix should be kept on ice.

1. **Add indexing primers:** For each indexing reaction, add 4 µL of the appropriate forward and reverse indexing primer to each sample well being used.
2. **Prepare a master mix:** Vortex and spin the Indexing PCR Master Mix before use. To prepare the PCR master mix, combine the Indexing PCR Master Mix and water sufficient for the samples being processed with overage.
 - a. For example, to prepare enough mixture for 10 samples, mix 250 µL of Indexing PCR MMX and 110 µL of water. Add reagent overage appropriately.
 - b. Mix the PCR master mix by vortexing on medium speed for 10 seconds and spin down the solution in a microfuge. Transfer 36 µL of master mix to each sample well in a PCR plate, strip tube, or PCR microtube. To prevent cross-contamination of indices, be sure to change tips between each well.

Reagent	Volume (µL)
Indexing PCR Master Mix (2x)	25.0
A700 TruSeq Amplicon Index	4.0
A500 TruSeq Amplicon Index	4.0
Nuclease-free water	11.0
Gene-specific PCR product, with or without beads*	6.0
Total	50.0

**Resuspend the beads by gently pipetting the entire solution up and down 10 times before the first PCR products (on beads) are added into the well. Alternately, the beads can be separated by placing the wells with the gene-specific PCR elution on the magnet before adding the PCR product. The indexing PCR is not affected by the presence of the beads. The remaining gene-specific PCR product can be stored with the beads at -20 °C.*

The following steps should be performed in a post-PCR area. **Important:** Cover or seal the reactions before transferring from the pre-PCR area to the post-PCR area.

3. **Add gene-specific PCR product:** Add 6 µL of the gene-specific PCR product with the beads to the corresponding wells and carefully seal the plate or cap the tubes.
4. **Mix and spin:** Pulse vortex the sealed reactions on a medium setting for 5-10 seconds to mix. Briefly spin down the reactions to remove any bubbles within the reaction solutions.

5. Perform PCR: Perform the following program with the heated lid on:

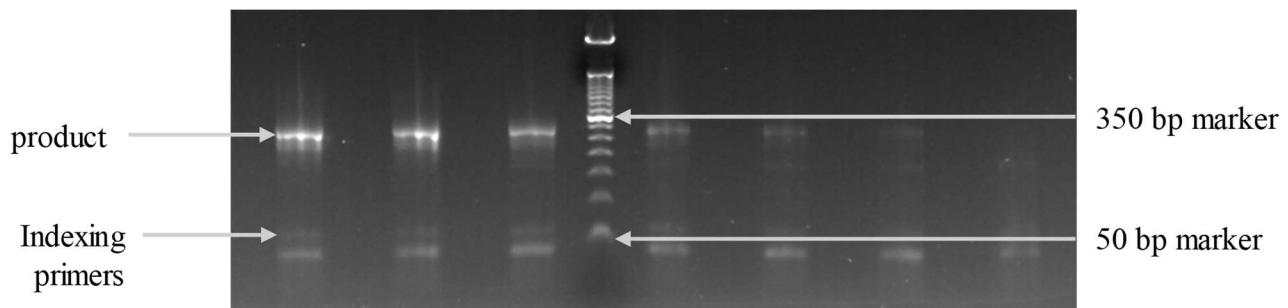
Temperature	Time	Number of Cycles
95°C	2 minutes	1
95°C	30 seconds	
66°C	30 seconds	5
72°C	60 seconds	
72°C	5 minutes	1
8°C	Hold	1

STOPPING POINT: The indexed libraries may be stored at -20 °C.

TIP: Thaw the sequencing reagent cartridge in a water bath per the corresponding Reagent Kit Reagent Prep Guide, and prepare the sample sheet during indexing PCR (see page 29 for the MiSeq or page 32 for the NextSeq).

Gel Image After Indexing PCR

The following image is an example of samples after indexing PCR on a 2% agarose gel.



Input of genomic DNA: (left to right)
60, 40, 20 ng
Marker
10, 5, 2.5, and 0 ng

Purify the Libraries

Hands-on time: 30-45 minutes

Total time: 30-45 minutes

Pre-purification

Keep Agencourt AMPure XP beads at room temperature while the indexing PCR is being performed unless samples are going to be stored at -20°C.

If samples were stored at -20°C remove the samples from the freezer to thaw to ambient temperature before purification. Remove Agencourt AMPure XP beads from 4°C and incubate at room temperature for at least 30 minutes before use.

IMPORTANT: *It is critical that the AMPure beads reach room temperature before performing the purification process. The temperature of the bead solution can alter the purification process.*

Library Purification

The following steps should be performed in a post-PCR area.

1. If the samples were stored at -20°C or condensation has formed, briefly spin the samples once thawed to remove any droplets from the side walls. Carefully remove the seal or caps.
2. **Mix beads:** Vortex AMPure XP beads thoroughly until all beads are well dispersed.

IMPORTANT: *It is critical that the AMPure beads solution is homogeneous before performing the purification process. A non-uniform distribution can affect the purification process.*

3. **Add beads:** Add 50 µL beads (1.0x beads if reaction is not at 50 µL) to each well. Pipette the mixture up and down 10 times. If bubbles form on the bottom of the wells, briefly spin and mix again.

TIP: *Use a trough and multichannel pipette to quickly and easily add the beads to each well. The same method can be applied to the washes in steps 6-8.*

4. **Bind libraries to beads:** Incubate the samples for 5 minutes at room temperature to bind the libraries to the beads.
5. **Separate libraries on beads:** Place the samples on a magnetic rack until the solution appears clear, which can take up to 5 minutes.
6. **Remove supernatant:** Carefully remove the supernatant from each well without disturbing the beads from the wall of each well.
7. **Wash beads:** Leave the samples on the magnetic rack. Add 150 µL of freshly-prepared 70% ethanol to each well without disturbing the beads. Incubate 30 seconds, and then remove the supernatant from each well.

IMPORTANT: Do not allow the ethanol mixture to remain open to the air. The ethanol concentration will change over time, affecting the washing of the beads. Pour only enough solution for each wash.

8. **Second wash:** Repeat step 7 for a second 70% ethanol wash. Remove the supernatant from each well.

IMPORTANT: Remove trace amounts of ethanol completely from each well. If ethanol drops are attached to the sidewall of some wells, spin the samples in a benchtop centrifuge for 10-15 seconds and use a 10 or 20 μ L tip to remove the remaining solution from wells.

9. **Dry beads:** Let the beads air dry at room temperature for 2-5 minutes.

IMPORTANT: Do not over-dry the beads. The beads have sufficiently dried when the bead mass has small cracks in the middle. If large cracks have appeared among the entire bead ring or they are flaky, they are over-dried. Beads that are too dry may be difficult to resuspend.

10. **Resuspend beads:** Remove the samples from the magnetic rack, and resuspend the dried beads in each well using 32 μ L nuclease-free water. Gently pipette the beads suspension up and down 10 times. If bubbles form on the bottom of the wells, briefly spin and mix again.
11. **Elute libraries:** Incubate the resuspended beads at room temperature for 5 minutes to elute the final libraries.
12. **Separate libraries from beads:** Place the elutions on the magnetic rack at room temperature until the solution appears clear. Transfer 30 μ L of clear supernatant from each well of the PCR plate or tubes to the corresponding well of a new plate or tube.

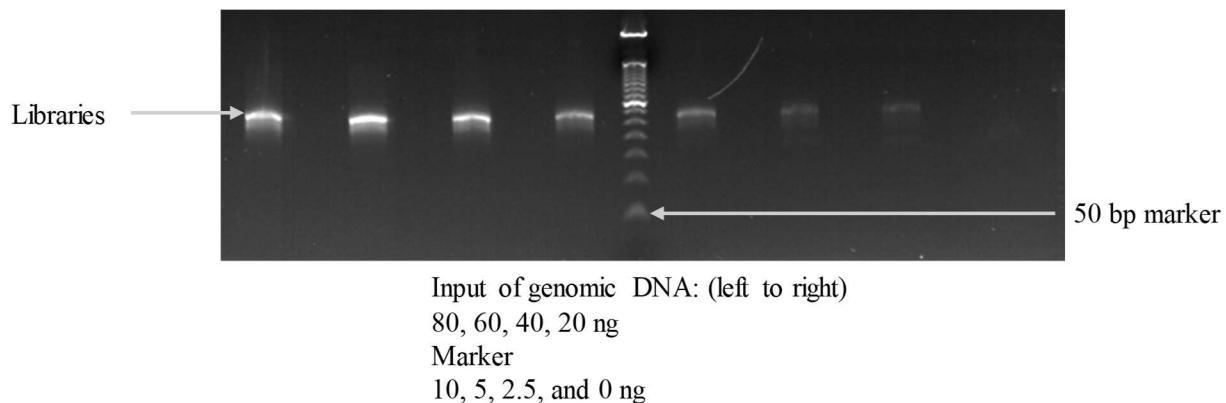
TIP: During the incubation and magnetic separation of the beads, cover the samples and prepare the solutions needed for quantitation in the next section. The purified libraries may also be stored at 4 °C for up to 3 days or at -20 °C for longer-term storage.

13. Analyze an aliquot of each library per the instructions in the next section.

STOPPING POINT: The purified libraries may be stored at 4 °C for up to 3 days. Store the purified libraries at -20 °C for longer-term storage.

Final Library Image

The following image is an example of final libraries after both rounds of PCR and purification on a 2% agarose gel.



Qubit Quantitation of Purified Libraries

Hands-on time: 30-45 minutes

Total time: 30-45 minutes

The following steps should be performed in a post-PCR area.

1. **Prepare buffer with dye:** Dilute the Qubit dsDNA HS reagent 1:200 in Qubit dsDNA HS buffer. Vortex briefly to mix Qubit working solution. For example, 2000 μ L is sufficient buffer for 10 readings (8 samples + 2 standards). Combine 1990 μ L of Qubit dsDNA HS buffer and 10 μ L HS reagent. Add reagent overage appropriately.

IMPORTANT: Fluorescent dyes are sensitive to light. Protect the Qubit buffer mixture with dye from light.

2. **Label tubes:** Set up 0.5 mL Qubit tubes for standards and samples. Label the tube lids.
3. **Prepare standards:** Transfer 190 μ L of Qubit working solution into two tubes for standard 1 and standard 2, and then add 10 μ L of each standard to the corresponding tube.

IMPORTANT: New standard dilutions should be prepared with the samples. Do not reuse standard dilutions from previous experiments.

4. **Prepare samples:** Transfer 198 μ L of Qubit working solution to each tube, and then add 2 μ L of each sample to the tube (1:100 dilution).
5. **Mix and spin:** Mix the tubes by vortexing and then spinning the tubes briefly.
6. Incubate the tubes at room temperature for 2 minutes.

7. **Measure concentration:** Measure the concentration of each sample on the Qubit 2.0 Fluorometer per the Qubit User Guide. Use the dsDNA High Sensitivity assay to read standards 1 and 2 followed by the samples.
 - a. If any sample concentrations are above the linear range of the instrument, prepare a new dilution using 199 μL Qubit buffer with dye and 1 μL sample (1:200 dilution). Repeat steps 5-7.
8. **Calculate concentration:** Calculate the concentration (in ng/ μL) of each undiluted sample. Convert the concentration of each sample to nM (1 ng/ μL of library is equal to 5 nM of library for the Multi-Cancer Panel).

2 in 200: $[X \text{ ng}\cdot\text{mL}^{-1}] \times [1 \text{ mL}\cdot 1000 \mu\text{L}^{-1}] \times \text{dilution factor [100]} = [Y \text{ ng}\cdot\mu\text{L}^{-1}]$

1 in 200: $[X \text{ ng}\cdot\text{mL}^{-1}] \times [1 \text{ mL}\cdot 1000 \mu\text{L}^{-1}] \times \text{dilution factor [200]} = [Y \text{ ng}\cdot\mu\text{L}^{-1}]$

$$[Y] \text{ ng}\cdot\mu\text{L}^{-1} \times [5 \text{ nM}\cdot\text{ng}^{-1}\cdot\mu\text{L}] = [Z \text{ nM}]$$

STOPPING POINT: *The undiluted libraries may be stored at 4 °C for up to 3 days. Store libraries at -20 °C for long-term storage.*

Prepare Diluted Libraries for Sequencing

Hands-on time: 30-70 minutes

Total time: 30-70 minutes

The following steps should be performed in a post-PCR area. For this portion of the protocol, have an ice bucket prepared.

Depending on the number of samples, samples can be multiplexed and sequenced using MiSeq v2 chemistry, MiSeq v3 chemistry, or a NextSeq. Please choose the appropriate workflow based on the number of samples and the desired sequencing depth.

The following table provides a general guideline for the performance of the ONCO/Reveal Multi-Cancer Panel. The total number of sequenced reads obtained is a function of the cluster density and the read quality passing filter. Generally, as the cluster density increases, the passing filter decreases. As an example, when using v3 chemistry on a MiSeq, a similar number of PE reads can be obtained with a (A) cluster density of approximately 1100 K/mm² and a passing filter of 94% or (B) cluster density of approximately 1300 K/mm² and a passing filter of 85%. Therefore, the estimates below are representative of libraries that obtain a cluster density from 830-1100 K/mm² and a passing filter >88% for v2 chemistry and 1100-1600 K/mm² with a passing filter >85% for v3 chemistry.

Kit	Cycles	Estimated PE reads	Est. Mean amplicon coverage (x) ^a	Est. Min. amplicon coverage (x) ^b	Estimated PE reads/sample	Est. Maximum # libraries
MiSeq Micro v2	2x150	8 Million	3500	350	2.0 Million	4
MiSeq v2	2x150	30 Million	3500	350	2.0 Million	15
MiSeq v3	2x150	50 Million	3500	350	2.0 Million	25
NextSeq Mid	2x150	260 Million	4800	480	2.7 Million	96

^a In paired end sequencing, each amplicon is sequenced from both the forward and reverse directions, generating two reads. Therefore, an amplicon coverage of 1x requires a read coverage of 2x.

^b The minimum coverage estimate is based on obtaining a minimum coverage of 10% of the mean amplicon coverage.

Sequencing Using v2 Chemistry (MiSeq Micro v2 or MiSeq v2 Kit)

For running a MiSeq kit using v2 chemistry (MiSeq Micro v2 or MiSeq v2 kits), dilute libraries to **5 nM**. The final concentration of the libraries for sequencing is **15 pM**.

1. **Normalize libraries to 5 nM:** Dilute an aliquot (i.e. 4 µL) of each sample library to 5 nM using nuclease-free water or 10 mM Tris-Cl with 0.1% Tween-20, pH 8.5.

The calculation uses the following equation:

$$\text{Concentration}_{\text{initial}} * \text{Volume}_{\text{initial}} = \text{Concentration}_{\text{final}} * \text{Volume}_{\text{final}}$$

$$(Z \text{ nM}) * (4 \text{ } \mu\text{L library}) / (5 \text{ nM}) = \text{Final volume of sample library}$$

$$\text{Final volume of sample library} - 4 \text{ } \mu\text{L library} = \text{volume of diluent}$$

STOPPING POINT: The normalized library products can be stored at 4°C overnight for loading the next day. For longer storage, the normalized samples can be stored at -20°C.

2. **Mix and spin:** Mix the 5 nM libraries thoroughly by vortexing followed by spinning.
3. **Prepare library mix:** Label a new 1.5 mL microtube for the library mix. Prepare a 5 nM mixture of libraries by combining each library at equal volume (i.e. mixing 5 µL of each 5 nM library). Quickly vortex the mix for 2-5 seconds and spin down.

The libraries prepared using the Multi-Cancer Panel cluster very efficiently on the MiSeq. It is recommended that the library mix be quantitated using Qubit or another library quantitation method (qPCR) to ensure the mix is at 5 nM to prevent over-clustering on the MiSeq. If the final dilution is not 5 nM ($\pm 10\%$), adjust the dilution in step 6 accordingly to obtain the desired concentration.

The following steps can be found in greater detail in Illumina's "Preparing Libraries for Sequencing on the MiSeq" (part # 15039740).

4. **Prepare 0.2 N NaOH:** Label a new 1.5 mL microtube for 0.2 N NaOH. Prepare the NaOH by combining 800 μ L nuclease-free water with 200 μ L of 1 N NaOH. Vortex the solution to mix.

Alternately, prepare a 1 N NaOH solution by combining 500 μ L 10 N NaOH into 4.5 mL of nuclease-free water. Vortex the solution to mix. If 1 N NaOH has not been prepared within the last week from a 10 N solution, prepare a new 1 N NaOH solution.

5. **Denature the library mix:** Label a new microtube for the denatured, 25 pM library mix.
 - a. Denature the library mix by combining 5 μ L of the library mix and 5 μ L of the freshly prepared 0.2 N NaOH.
 - b. Vortex the solution thoroughly for 10 seconds and centrifuge the solution in a microfuge for 1 minute.
 - c. Let the solution stand at room temperature for 5 minutes.
 - d. Add 990 μ L of Illumina's HT1 solution to the denatured library mix.
 - e. Invert the mixture several times, spin briefly, and place on ice.
6. **Dilute to 15 pM library mix:** Label a new 1.5 mL microtube for the 15 pM library mix. Combine 360 μ L of the 25 pM library mix (step 5) with 240 μ L of Illumina's HT1 solution. Adjust the volumes as needed for libraries that are over or under 25 pM. Invert the mixture several times, spin briefly, and place on ice.
7. **Combine library mix and PhiX control:** Label a new 1.5 mL microtube for the mixture that will be loaded. Combine 594 μ L of the 15 pM library mix (step 6) with 6 μ L of a 12.5 pM PhiX library control. Briefly vortex, spin, and place on ice.
8. **Load MiSeq cartridge:** Using a clean 1000 μ L tip, puncture the foil cap above the sample loading tube on the MiSeq cartridge. Load the 600 μ L library mix and PhiX mixture (step 7) into the cartridge and ensure the solution has reached the bottom of the tube by lightly tapping the tube if liquid remains on the side wall or there is an air bubble at the bottom of the tube.
9. **Run the MiSeq:** Run the libraries on the MiSeq per the manufacturer's instructions using a paired-end read length of 150 (2x150): "MiSeq System User Guide" (part #15027617). For instructions on preparing a sample sheet for the MiSeq, see page 29.
10. Store diluted libraries and mixtures at -20°C for long-term storage.

Sequencing using v3 chemistry (MiSeq v3 Kit)

For v3 chemistry (MiSeq v3 kit), dilute libraries to **5 nM**. The final concentration of the libraries for sequencing is **25 pM**.

1. **Normalize libraries to 5 nM:** Dilute an aliquot (i.e. 4 µL) of each sample library to 5 nM using nuclease-free water or 10 mM Tris-Cl with 0.1% Tween-20, pH 8.5.

The calculation uses the following equation:

$$\text{Concentration}_{\text{initial}} * \text{Volume}_{\text{initial}} = \text{Concentration}_{\text{final}} * \text{Volume}_{\text{final}}$$

$$(Z \text{ nM}) * (4 \mu\text{L library}) / (5 \text{ nM}) = \text{final volume of sample library}$$

$$\text{Final volume of sample library} - 4 \mu\text{L library} = \text{volume of diluent}$$

STOPPING POINT: The normalized library products can be stored at 4°C overnight for loading the next day. For longer storage, the normalized samples can be stored at -20°C.

2. **Mix and spin:** Mix the 5 nM libraries thoroughly by vortexing followed by spinning.
3. **Prepare library mix:** Label a new microtube for the library mix. Prepare a 5 nM mixture of libraries by combining each library at equal volume (i.e. mixing 5 µL of each 5 nM library). Quickly vortex the mix for 2-5 seconds and spin down.

The libraries prepared using the Multi-Cancer Panel cluster very efficiently on the MiSeq. It is recommended that the library mix be quantitated using Qubit or another library quantitation method (qPCR) to ensure the mix is at 5 nM to prevent over-clustering on the MiSeq. If the final dilution is not 5 nM ($\pm 10\%$), adjust the dilution in step 6 accordingly to obtain the desired concentration.

The following steps can be found in greater detail in Illumina's "Preparing Libraries for Sequencing on the MiSeq" (part # 15039740).

4. **Prepare 0.2 N NaOH:** Label a new 1.5 mL microtube for 0.2 N NaOH. Prepare the NaOH by combining 800 µL nuclease-free water with 200 µL of 1 N NaOH. Vortex the solution to mix.

Alternately, prepare a 1 N NaOH solution by combining 500 µL 10 N NaOH into 4.5 mL of nuclease-free water. Vortex the solution to mix. If 1 N NaOH has not been prepared within the last week from a 10 N solution, prepare a new 1 N NaOH solution.

5. **Denature the library mix:** Label a new 1.5 mL microtube for the denatured, 25 pM library mix.
 - a. Denature the library mix by combining 5 µL of the library mix and 5 µL of the freshly prepared 0.2 N NaOH.
 - b. Vortex the solution thoroughly for 10 seconds and centrifuge the solution in a microfuge for 1 minute.
 - c. Let the solution stand at room temperature for 5 minutes.

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- d. Add 990 µL of Illumina's HT1 solution to the denatured library mix.
 - e. Invert the mixture several times, spin briefly, and place on ice.
6. **Combine library mix and PhiX control:** Label a new 1.5 mL microtube for the mixture that will be loaded. Combine 594 µL of the 25 pM library mix (step 5) with 6 µL of a 20 pM PhiX library control. Adjust the volume as needed for libraries that are over or under 25 pM. Briefly vortex, spin, and place on ice.
7. **Load MiSeq cartridge:** Using a clean 1000 µL tip, puncture the foil cap above the sample loading tube on the MiSeq cartridge. Load the 600 µL library mix and PhiX mixture (step 6) into the cartridge and ensure the solution has reached the bottom of the tube by lightly tapping the tube if liquid remains on the side wall or there is an air bubble at the bottom of the tube.
8. **Run the MiSeq:** Run the libraries on the MiSeq per the manufacturer's instructions using a paired-end read length of 150 (2x150): "MiSeq System User Guide" (part #15027617). For instructions on preparing a sample sheet for the MiSeq, see page 29.
9. Store diluted libraries and mixtures at -20°C for long-term storage.

Sequencing on the NextSeq

For sequencing on the NextSeq, dilute libraries to **5 nM**. The final concentration of the libraries for sequencing is **1.8 pM**.

1. **Normalize libraries to 5 nM:** Dilute an aliquot (i.e. 4 µL) of each sample library to 5 nM using nuclease-free water or 10 mM Tris-Cl with 0.1% Tween-20, pH 8.5.

The calculation uses the following equation:

$$\text{Concentration}_{\text{initial}} * \text{Volume}_{\text{initial}} = \text{Concentration}_{\text{final}} * \text{Volume}_{\text{final}}$$

$(Z \text{ nM}) * (4 \mu\text{L library}) / (5 \text{ nM}) = \text{final volume of sample library}$

$\text{Final volume of sample library} - 4 \mu\text{L library} = \text{volume of diluent}$

STOPPING POINT: *The normalized library products can be stored at 4°C overnight for loading the next day. For longer storage, the normalized samples can be stored at -20°C.*

2. **Mix and spin:** Mix the 5 nM libraries thoroughly by vortexing followed by spinning.
3. **Prepare library mix:** Label a new 1.5 mL microtube for the library mix. Prepare a 5 nM mixture of libraries by combining each library at equal volume (i.e. mixing 4 µL of each 5 nM library). Quickly vortex the mix for 2-5 seconds and spin down.

It is recommended that the library mix be quantitated using Qubit or another library quantitation method (qPCR) to ensure the mix is at 5 nM to prevent over- or under-clustering on the NextSeq. If the final dilution is not 5 nM ($\pm 10\%$), adjust the dilution in step 6 accordingly to obtain the desired concentration.

The following steps can be found in greater detail in Illumina’s “NextSeq System: Denature and Dilute Libraries Guide” (part #15048776).

4. **Prepare 0.2 N NaOH:** Label a new 1.5 mL microtube for 0.2 N NaOH. Prepare the NaOH by combining 800 µL nuclease-free water with 200 µL of 1 N NaOH. Vortex the solution to mix.

Alternately, prepare a 1 N NaOH solution by combining 500 µL 10 N NaOH into 4.5 mL of nuclease-free water. Vortex the solution to mix. If 1 N NaOH has not been prepared within the last week from a 10 N solution, prepare a new 1 N NaOH solution.

5. **Denature the library mix:** Label a new microtube for the denatured, 25 pM library mix.
 - a. Denature the library mix by combining 5 µL of the library mix and 5 µL of the freshly prepared 0.2 N NaOH.
 - b. Vortex the solution thoroughly for 10 seconds and centrifuge the solution in a microfuge for 1 minute.
 - c. Let the solution stand at room temperature for 5 minutes.
 - d. Add 5 µL of 200 mM Tris-HCl, pH 7.0.
 - e. Vortex briefly and centrifuge the solution in a microfuge for 1 minute.

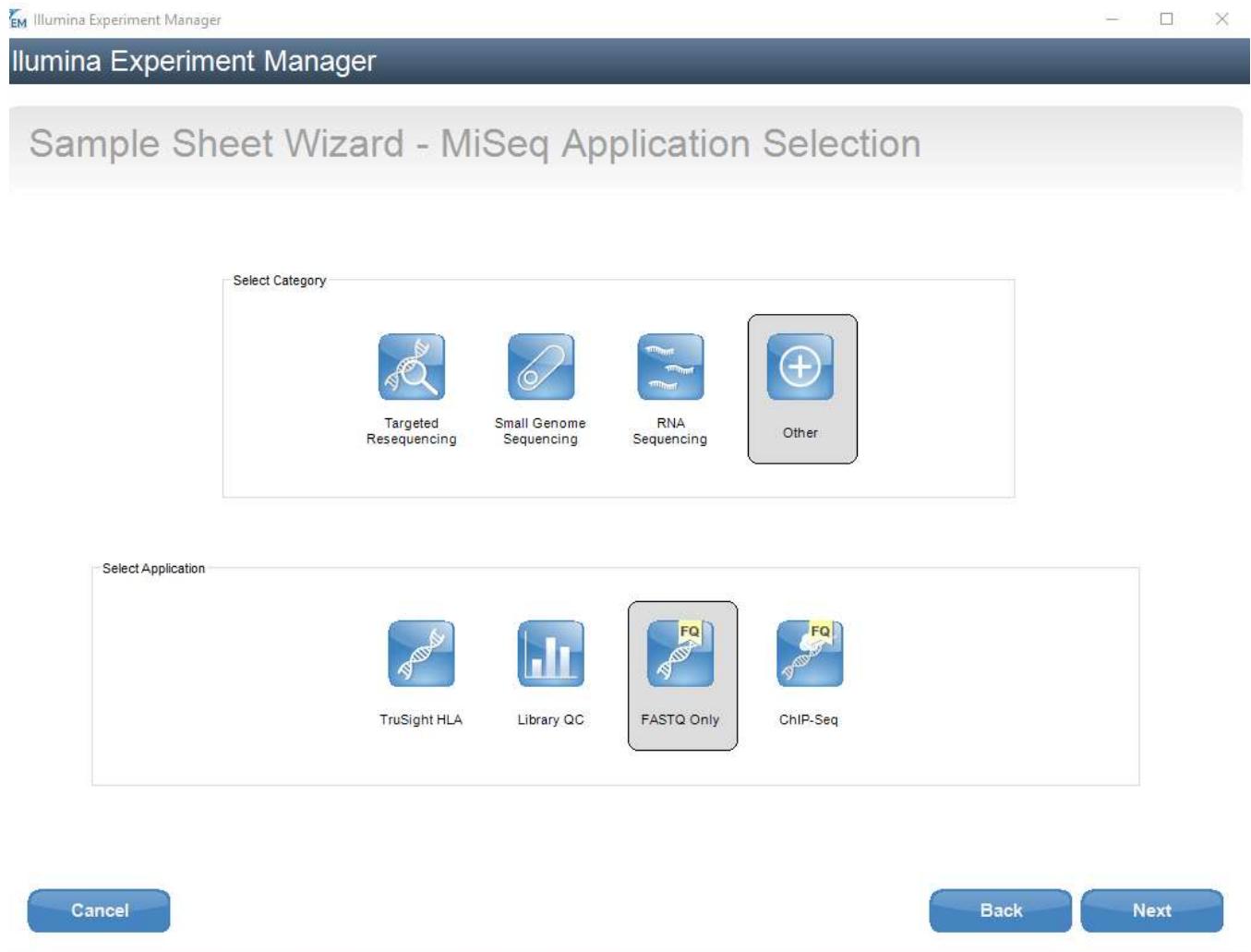
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- f. Add 985 µL of Illumina's HT1 solution to the denatured library mix.
 - g. Vortex briefly and centrifuge the solution in a microfuge for 1 minute.
6. **Dilute 25 pM library mix to 1.8 pM:** Dilute the denatured library to 1300 µL of a 1.8 pM solution by combining 101 µL of the 25 pM denatured library mix with 1299 µL of Illumina's HT1 solution. Invert to mix and spin briefly.
7. **Combine library mix and PhiX control:** Label a new 1.5 mL microtube for the mixture that will be loaded. Combine 1287 µL of the 1.8 pM library mix (step 6) with 13 µL of a 1.8 pM PhiX library control. Briefly vortex, spin, and place on ice.
8. **Load NextSeq cartridge:** Using a clean 1000 µL tip, puncture the foil cap above the sample loading well on the NextSeq cartridge. Load the 1300 µL library mix and PhiX mixture (step 7) into the cartridge and ensure the solution has reached the bottom of the cartridge well.
9. **Run the NextSeq:** Run the libraries on the NextSeq per the manufacturer's instructions using a paired-end read length of 150 (2x150) and two indexing reads of 8 cycles each: "NextSeq System User Guide" (part #15046563 or 15069765). For instructions on preparing a sample sheet for the NextSeq, see page 32.
10. Store diluted libraries and mixtures at -20°C for long-term storage.

Preparing a Sample Sheet for the MiSeq Using Illumina Experiment Manager

In the Illumina Experiment Manager, prepare a sample sheet that contains the information for the samples that are being loaded.

For best practice, prepare the sample sheet prior to loading the MiSeq cartridge. If an error has been made during indexing PCR where samples have the same indices, it can be remedied before loading the samples on the MiSeq.

1. Open Illumina Experiment Manager, select “Create Sample Sheet.”
2. **Instrument selection:** Select “MiSeq” and “Next.”
3. **Application selection:** Under “Category,” select “Other.” Under “Select Application,” select “FASTQ only” and “Next.”



4. **Reagent barcode:** Enter the reagent barcode number found on the cartridge being loaded onto the instrument. Example: For MSXXXXXXXXX-300v2 or MSXXXXXXXXX-600v3, enter the 7-digit number following MS.
5. **Library Prep Kit:** Use the menu to select “TruSeq Amplicon.”
6. **Index Reads:** Select to perform two index reads if not already selected.
7. **Experiment Name, Investigator Name, Description:** These fields can be filled out by the user per the laboratory’s standard operator procedure.
8. **Read type:** Select Paired End reads if not already selected.
9. **Cycle numbers:** Cycle numbers for both Read 1 and Read 2 should be 150. Select “Next.”

The screenshot shows the 'Sample Sheet Wizard - Workflow Parameters' window in the Illumina Experiment Manager. The window is divided into two main sections: 'FASTQ Only Run Settings' on the left and 'FASTQ Only Workflow-Specific Settings' on the right.

FASTQ Only Run Settings:

- Reagent Cartridge Barcode*:
- Library Prep Kit:
- Index Reads: 2 (radio buttons for 0, 1, 2)
- Experiment Name:
- Investigator Name:
- Description:
- Date:
- Read Type: Paired End (radio buttons for Paired End, Single Read)
- Cycles Read 1:
- Cycles Read 2:

* - required field

FASTQ Only Workflow-Specific Settings:

- Custom Primer for Read 1
- Custom Primer for Index
- Custom Primer for Read 2
- Reverse Complement

At the bottom of the window are three buttons: 'Cancel' (left), 'Back' (middle), and 'Next' (right).

- 10. Sample Information:** Prepare the sample sheet with the sample identifiers, indices, and other pertinent information and save the sample sheet to a MiSeq-accessible folder.
- Name the samples in the column labeled “Sample ID.” Illegal characters include spaces, periods, and other special characters.
 - (Optional) The plates and well numbers can be added in “Plate” and “Well.”
 - For each sample, indicate the TruSeq Custom Amplicon indices used during indexing PCR.

EM Illumina Experiment Manager

Sample Sheet Wizard - Sample Selection

Samples to include in sample sheet										* - required field	<input checked="" type="checkbox"/> Maximize
Sample ID*	Sample Name	Plate	Well	Index1 (I7)*	I7 Sequence	Index2 (I5)*	I5 Sequence	Sample Project	Description		
PositiveControl			A1	A708	CACCAAC	A501	TGAACCTT				
NegativeControl			C2	A708	CACCAAC	A503	TGTTCTCT				
sample1			A3	A710	TGTGACCA	A501	TGAACCTT				
sample2			B3	A710	TGTGACCA	A502	TGCTAAGT				
sample3			C3	A710	TGTGACCA	A503	TGTTCTCT				
sample4			D3	A710	TGTGACCA	A504	TAAGACAC				
sample5			E5	A711	AGGGTCAA	A505	CTAATCGA				
sample6			F5	A711	AGGGTCAA	A506	CTAGAACAA				
sample7			G5	A711	AGGGTCAA	A507	TAAGTTCC				
sample8			H5	A711	AGGGTCAA	A508	TAGACCTA				
NTC			H7	A712	AGGAGTGG	A508	TAGACCTA				

Add Blank Row Remove Selected Rows ?

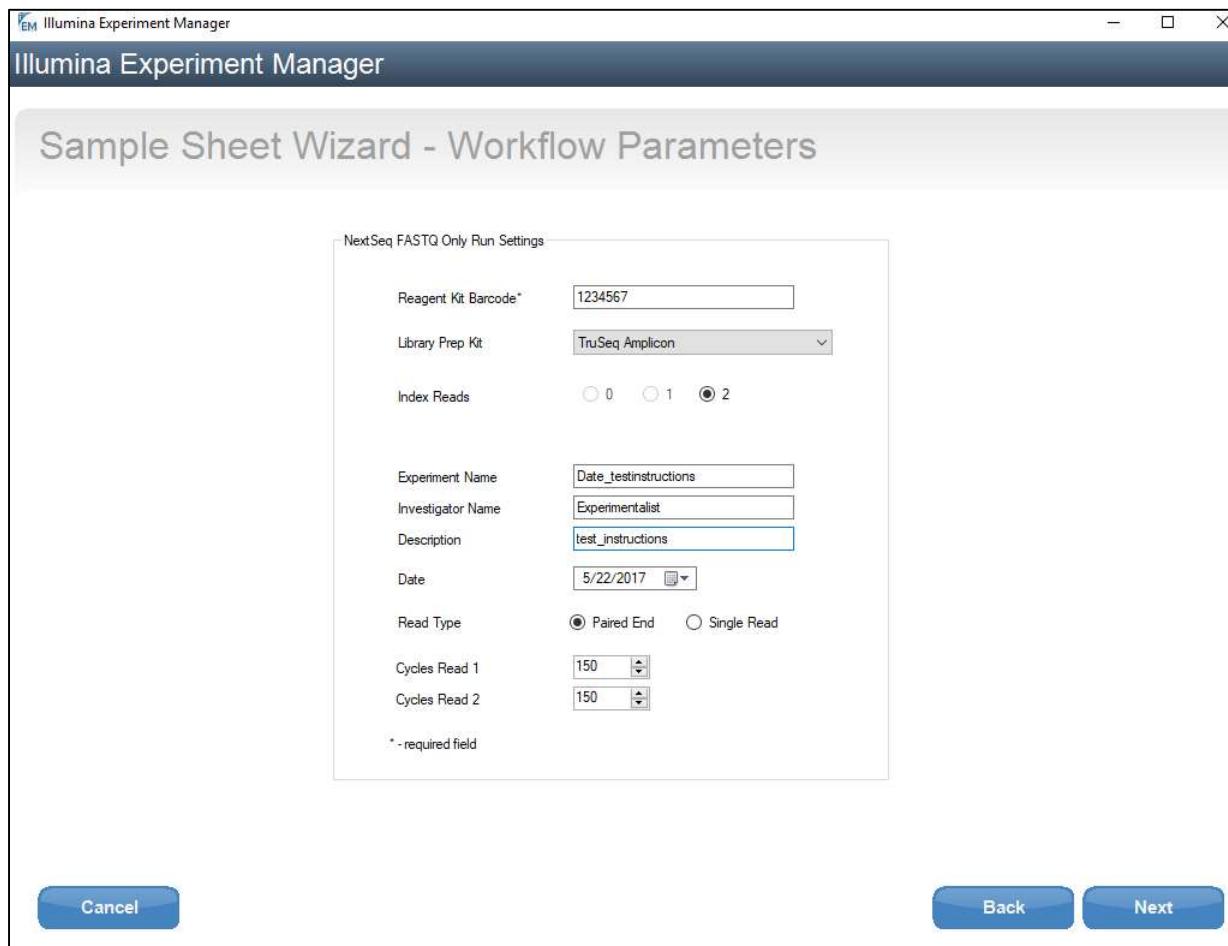
Sample Sheet Status: Valid
Reason:

Cancel Back Finish

Preparing a Sample Sheet for the NextSeq Using Illumina Experiment Manager

In the Illumina Experiment Manager, prepare a sample sheet that contains the information for the samples that are being loaded.

1. Open Illumina Experiment Manager, select “Create Sample Sheet.”
2. **Instrument selection:** Select “NextSeq” and “Next.”
3. **Application selection:** Select “NextSeq FASTQ only” and “Next.”
4. **Reagent barcode:** Enter the reagent barcode number found on the cartridge being loaded onto the instrument. For NSXXXXXXX, enter the 7-digit number following NS.
5. **Library Prep Kit:** Use the menu to select “TruSeq Amplicon.”
6. **Index Reads:** Select to perform two index reads if not already selected.
7. **Experiment Name, Investigator Name, Description:** These fields can be filled out by the user per the laboratory’s standard operator procedure.
8. **Read type:** Select Paired End reads if not already selected.
9. **Cycle numbers:** Cycle numbers for both Read 1 and Read 2 should be 150. Select “Next.”



10. Sample Information: Prepare the sample sheet with the sample identifiers, indices, and other pertinent information.

- a. Name the samples in the column labeled “Sample ID.” Illegal characters include spaces, periods, and other special characters.
- b. (Optional) The plates and well numbers can be added in “Plate” and “Well.” **Note:** *Information in the “Sample Name” column will be used to name the corresponding FASTQ files in BCL2FASTQ.*
- c. For each sample, indicate the TruSeq Custom Amplicon indices used during indexing PCR. **Note:** *The A500 indices are the reverse complement in the NextSeq workflow.*

The screenshot shows the "Sample Sheet Wizard - Sample Selection" interface in the Illumina Experiment Manager. The window title is "Illumina Experiment Manager". The main area displays a table titled "Samples to include in sample sheet". The table has columns: Sample ID*, Sample Name, Plate, Well, Index1 (I7)*, I7 Sequence, Index2 (I5)*, I5 Sequence, Sample Project, and Description. A note at the top right indicates "* - required field" and there is a checked "Maximize" checkbox. The table data is as follows:

Sample ID*	Sample Name	Plate	Well	Index1 (I7)*	I7 Sequence	Index2 (I5)*	I5 Sequence	Sample Project	Description
PositiveControl			A1	A708	CACCAAC	A501	TGAACCTT		
NegativeControl			C2	A708	CACCAAC	A503	TGTTCTCT		
sample1			A3	A710	TGTGACCA	A501	TGAACCTT		
sample2			B3	A710	TGTGACCA	A502	TGCTAAGT		
sample3			C3	A710	TGTGACCA	A503	TGTTCTCT		
sample4			D3	A710	TGTGACCA	A504	TAAGACAC		
sample5			E5	A711	AGGGTCAA	A505	CTAATCGA		
sample6			F5	A711	AGGGTCAA	A506	CTAGAACAC		
sample7			G5	A711	AGGGTCAA	A507	TAAGTTCC		
sample8			H5	A711	AGGGTCAA	A508	TAGACCTA		
NTC			H7	A712	AGGAGTGG	A508	TAGACCTA		

Below the table are buttons for "Add Blank Row" and "Remove Selected Rows". At the bottom left is a "Cancel" button, and at the bottom right are "Back" and "Finish" buttons. Status messages "Sample Sheet Status: Valid" and "Reason:" are also present.

TROUBLESHOOTING

Issue	Potential Cause	Solution
Low yield of gene-specific product	DNA quantity or quality	The recommended input for the assay is 20-80ng of genomic DNA. Higher quantities may be necessary for low or poor quality FFPE samples.
	Improper cycling	Check that the cycling protocol performed is the appropriate protocol for gene-specific amplification.
Low indexing efficiency	Improper Ampure purification	Incomplete Ampure purification or loss of gene-specific product will affect the indexing PCR reaction. The purified product can be checked on an agarose gel to ensure the gene-specific product was not lost or that clean-up was sufficient to remove excess primers.
		The Ampure bead ratio and ethanol concentration affect the PCR cleanup. Ensure the correct Ampure concentration was used for cleanup and fresh, 70% ethanol is used for the wash.
		Leftover ethanol from the wash steps can hinder the PCR reaction. Remove as much of the ethanol during the final wash step with a pipette and dry the beads to ensure the residual ethanol has evaporated.
	Partial primer digestion	Poor digestion of the gene-specific primers can hinder the indexing efficiency of the indexing PCR reaction. Check the primer digestion using an agarose gel.
	Incomplete deactivation of exonuclease	The inactivation of the nuclease and Ampure purification is necessary before performing indexing PCR. Leftover active exonuclease can digest the indexing PCR primers, reducing the yield of the indexing PCR reaction.
Low library yield	DNA quantity or quality	The recommended input for the assay is 20-60ng of genomic DNA. Higher quantities may be necessary for low or poor quality FFPE samples.

		<p>Run the product from the gene-specific PCR on agarose gel to check the yield.</p> <p>The product can also be checked on an agarose gel after indexing PCR before and after Ampure purification.</p>
	Improper Ampure purification	<p>Incomplete Ampure purification or loss of product will affect the final yield. The purified product can be checked on an agarose gel to ensure the product was not lost during PCR cleanup.</p> <p>The Ampure bead ratio and ethanol concentration affect the PCR cleanup. Ensure the correct Ampure concentration was used for cleanup and fresh, 70% ethanol is used for the wash.</p>
The libraries over-cluster or under-cluster on the MiSeq	Normalization and mix of libraries is not 15 pM (v2) 25 pM (v3), or 1.8 pM (NextSeq)	<p>Check the 5 nM library mix using Qubit or RT-PCR. Dilute the denatured library mix as needed to adjust for the difference in concentration.</p>
	Improper library quantitation	<p>Improper library quantitation may result in artificially high or low yields, which affects downstream normalization.</p> <p>Re-quantify the final libraries and/or the normalized libraries to check for the expected values.</p>
	Improper Ampure purification	<p>Changing the ratio of Ampure beads affects the purification of the products. Notably, the presence of primer dimers can cause an underestimation of total quantity, causing over-clustering.</p> <p>The Ampure bead ratio and ethanol concentration affect the PCR cleanup. Ensure the correct Ampure concentration was used for cleanup and fresh, 70% ethanol is used for the wash.</p>

		<p>The final libraries can be checked on an agarose gel for the proper product size and presence of primer dimers.</p>
No-template control contains amplicons	Cross-contamination	<p>Make sure to change tips between samples, and avoid waving over tubes or plates. When liquid handling, be careful to avoid waving used tips over samples. Poor sealing or residual liquid in tips can cause contamination of nearby samples. If possible, leave adjacent wells empty between samples.</p> <p>Work spaces and equipment for pre-PCR and post-PCR should be separated to prevent amplicon contamination.</p> <p>Periodically clean the work space, floor, equipment, and instrumentation with a laboratory cleaning solution (10% bleach, 70% isopropanol, or 70% ethanol) to break down amplicons on surfaces.</p>