

# ONCO/Reveal™ Multi-Cancer RNA Fusion v2 Panel Reference Guide

## Library Preparation User Guide

FOR RESEARCH USE ONLY

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version 0.1.1

## INTRODUCTION

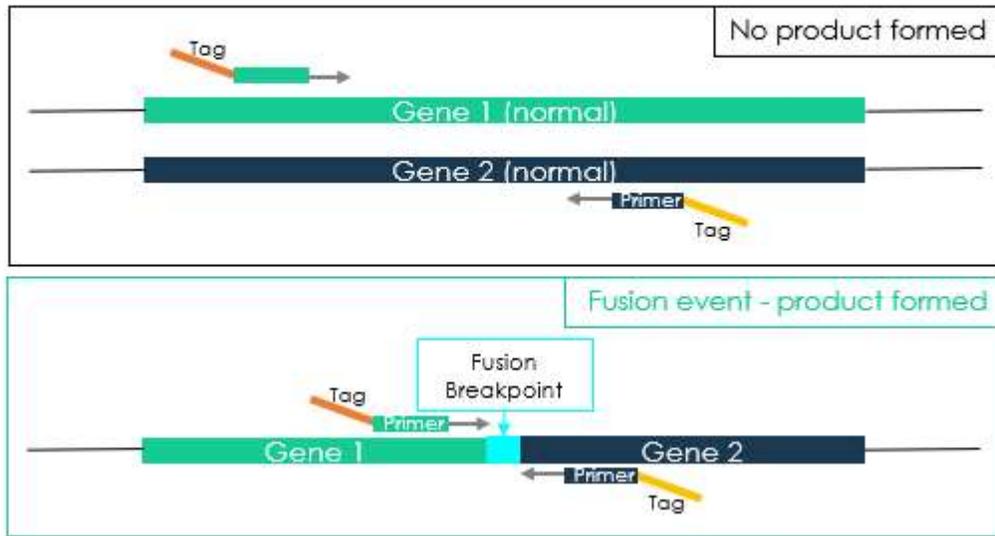
The ONCO/Reveal Multi-Cancer RNA Fusion v2 Panel utilizes Pillar Biosciences' proprietary SLIMamp® (**S**tem-**L**oop **I**nhibition **M**ediated **a**mplification) technology, allowing researchers to detect common Solid Tumor fusion transcripts in a simple, multiplex reaction. The assay was designed for the detection of common fusion variants including: ALK (NM\_004304), NTRK1 (NM\_002529), NTRK2 (NM\_006180), NTRK3 (NM\_00102338), NRG1 (NM\_013956), RET (NM\_020975), ROS1 (NM\_002944), FGFR3 (NM\_000142), and MET (NM\_000245) among others. It can also be used to detect exon 14 skipping in MET, and it contains two housekeeping genes as internal controls. The ONCO/Reveal Multi-Cancer RNA Fusion v2 Panel targets fusion variants of interest for researchers looking to explore fusion events using cDNA generated from FFPE (formalin-fixed paraffin-embedded) tissue, frozen tissue, or cell line samples. The prepared libraries are ready for sequencing on an Illumina sequencer using a paired-end read length of 150 (2x150).

The workflow of the ONCO/Reveal Multi-Cancer RNA Fusion v2 Panel can be performed and loaded for sequencing within about ten hours. The workflow contains numerous stopping points for users who have time limitations.

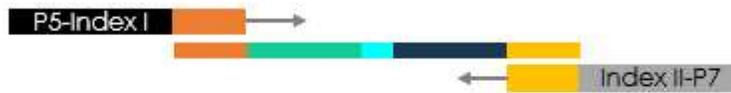
### How Does the ONCO/Reveal Multi-Cancer RNA Fusion v2 Panel Work?

A gene-specific primer was designed for each major breakpoint in the fusion genes (e.g. ALK), and another primer was designed for each partner gene (e.g. EML4). Additionally, amplicons were designed for each side of the breakpoint for the major driver genes. Using cDNA as input, the chimeric transcripts and wild-type transcripts of the driver genes are targeted in the first round of PCR. In the absence of a fusion event, 5' and 3' balance amplicons amplify distal regions of the driver gene transcripts and no fusion PCR product is formed. When a fusion event occurs, fusion primer binding sites are present on the same RNA transcript and allow for chimeric fusion amplicons to amplify. After GS PCR, the primers undergo digestion and the products are purified via bead-based size selection. After purification, indexing PCR using index adaptors adds indices for sample tracking and sequencing. The final libraries are purified and can be sequenced on the Illumina (Figure 1).

### GS PCR



### Indexing PCR



### Final Product



**Figure 1.** Overview of ONCO/Reveal Multi-Cancer RNA Fusion v2 Panel library preparation.

## **REVISION HISTORY**

2019-09: User Guide created.

2019-12: Update cycling conditions in cDNA protocol in version 0.1.0

2020-06: Add note about adaptor trimming and make minor edits in version 0.1.1

## GETTING STARTED

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

### Components of the ONCO/Reveal Multi-Cancer RNA Fusion v2 Panel

Reagent	Use	Area Use	Storage
Gene-specific PCR Master Mix (2x)	Gene-specific PCR	Pre-PCR	-15° to -25°C
SFv2 oligo pool (5x)	Gene-specific PCR	Pre-PCR	-15° to -25°C
Exonuclease I	Gene-specific PCR	Post-PCR	-15° to -25°C
Indexing PCR Master Mix (2x)	Indexing PCR	Pre-PCR	-15° to -25°C

### ONCO/Reveal Multi-Cancer RNA Fusion v2 Panel Indexing Kits

Reagent and Part Number	Use	Area Use	Storage
Pillar Custom Indexing Primers Kit A, indices PI501-8, PI701-4 (32 combinations - 96 reactions) PN: IDX-PI-1001-96	Indexing PCR	Pre-PCR	-15° to -25°C
Pillar Custom Indexing Primers Kit B, indices PI501-8, PI705-8 (32 combinations - 96 reactions) PN: IDX-PI-1002-96	Indexing PCR	Pre-PCR	-15° to -25°C
Pillar Custom Indexing Primers Kit C, indices PI501-8, PI709-12 (32 combinations - 96 reactions) PN: IDX-PI-1003-96	Indexing PCR	Pre-PCR	-15° to -25°C
Pillar Custom Indexing Primers Kit D, indices PI501-8, PI701-12 (96 combinations - 192 reactions) PN: IDX-PI-1004-192	Indexing PCR	Pre-PCR	-15° to -25°C
Pillar Custom Indexing Primers Kit E, indices PI501-8, PI701-12 (96 combinations - 384 reactions) PN: IDX-PI-1005-384	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.

**User-supplied Reagents**

<b>Reagent</b>	<b>Area use</b>	<b>Supplier</b>
<b>**cDNA Master Mix – (SuperScript VILO Master Mix)**</b>	<b>cDNA synthesis</b>	<b>Thermo Fisher #11755500</b>
<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
<b>Or</b> <i>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**

<b>Item</b>	<b>Area Use</b>	<b>Supplier</b>
<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**

<b>Equipment</b>	<b>Area Use</b>	<b>Supplier</b>
<i>Centrifuge adapted for PCR plates, tabletop</i>	Pre- and post-PCR	General lab supplier
<i>Gel electrophoresis apparatus (optional) <b>or</b></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 <math>\mu</math>L 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 FOR HANDLING RNA

Due to the prevalence of ribonucleases that will degrade RNA samples, RNA should be handled with care. RNases are not easily degraded and will quickly degrade precious RNA samples.

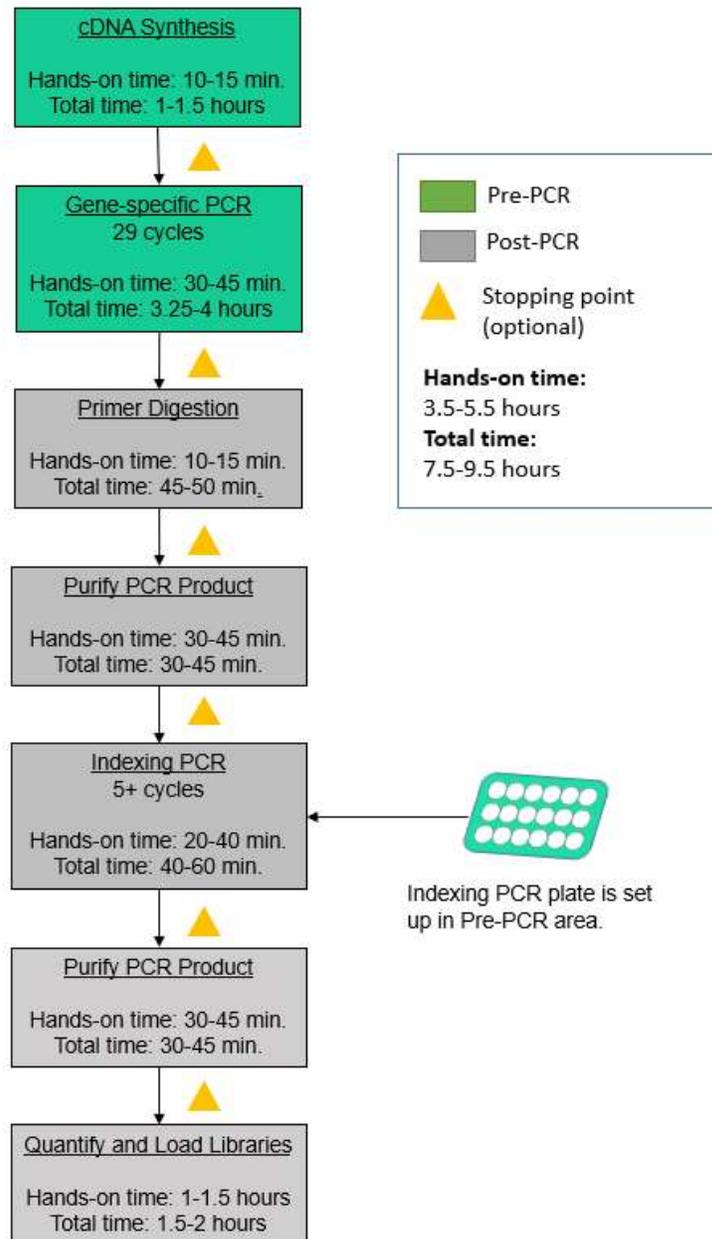
The following steps are recommended to improve consistency and reduce contamination:

- **Handling:** RNA is susceptible to degradation. When handling RNA, keep all components on ice and avoid repeated freeze/thaw cycles. Always wear gloves to avoid touching equipment used for RNA work with bare hands.
- **Work areas:** Work areas for RNA should be cleaned regularly and free of dust. Bacteria and skin are common sources of RNase enzymes; therefore, areas and equipment should be cleaned with a sterilizing solution (70% alcohol).
- **Hygiene:** When working with RNA, use aseptic techniques. Change gloves regularly and spray them often with a laboratory cleaning solution of 70% alcohol. Avoid touching any parts or items on the body such as the face, hands, or glasses, as they can be sources of RNases.
- **Equipment and consumables:** All consumables used for RNA work should be ensured they are RNase-free. Equipment should be cleaned or treated to inactive RNases.
- **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 reduce cross-contamination. Discard any tips that come into contact with surfaces (gloves, bench, and tube exteriors) outside of the sample area.

- **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 use racks that contain lids or covers.

## ONCO/Reveal MULTI-CANCER RNA FUSION V2 PANEL WORKFLOW

The following chart (Figure 2) demonstrates the workflow for the ONCO/Reveal Multi-Cancer RNA Fusion v2 Panel library preparation protocol.



**Figure 2.** The ONCO/Reveal Multi-Cancer RNA Fusion v2 Panel workflow can be completed from extracted RNA in about ten hours but contains multiple stopping points for users with time constraints.

**cDNA SYNTHESIS**

Hands-on time: 10-15 minutes

Total time: 1.5-1.75 hours

**IMPORTANT NOTE:** For cDNA synthesis from RNA extracted from total circulating nucleic acid see Appendix B.

Before performing the library preparation, prepare cDNA from total RNA extracted from FFPE samples, tissue, or cell lines. Additionally, cDNA may be prepared from total circulating nucleic acid extracted from blood. For the preparation from RNA, the cDNA should be prepared using random primers, not exclusively oligo d(T). Using only oligo d(T) may result in low or no coverage of the 5' end of transcripts. The cDNA Master Mix provided in the kit uses random hexamers for the synthesis of cDNA.

Up to 15  $\mu\text{L}$  of undiluted cDNA reaction can be added to the Gene-Specific PCR without inhibiting the reaction. Alternatively, with a higher RNA input, the cDNA reaction can be diluted with low TE or nuclease-free water. The recommend minimum input equivalent of FFPE RNA is 25 ng. For instance, using an initial RNA input of 50 ng into a 10  $\mu\text{L}$  cDNA reaction, 5  $\mu\text{L}$  would go into the initial PCR for an equivalent input of 25 ng of RNA. The recommended minimum input equivalent of cfRNA is 20 ng.

An example of the cDNA synthesis follows (see manufacturer's protocol for complete details). Set up the reaction on ice and keep all components chilled.

1. **Dilute RNA:** Dilute RNA\* in nuclease-free water to a final volume of 16.0  $\mu\text{L}$  (for a 20  $\mu\text{L}$  reaction) or 8.0  $\mu\text{L}$  (for a 10  $\mu\text{L}$  reaction) to each sample well in PCR plate, strip tube, or PCR tube. Add nuclease-free water to the no-template control well.
2. **Add cDNA Master Mix:** Add cDNA Master Mix to each sample well containing diluted RNA and no-template control well.

<b>Reagent</b>	<b>Volume (<math>\mu\text{L}</math>) (20 <math>\mu\text{L}</math> reaction)</b>	<b>Volume (<math>\mu\text{L}</math>) (10 <math>\mu\text{L}</math> reaction)</b>
cDNA Master Mix	4.0	2.0
Diluted RNA (or water)	16.0	8.0
<b>Total</b>	<b>20.0</b>	<b>10.0</b>

\*The RNA concentration can be determined by the Qubit RNA BR Assay kit (Life Technologies, Cat. Q10211 and Q10210; Quantitation range 20-1,000 ng) or

Qubit RNA HS Assay kit (Life Technologies, Cat. Q32852 and Q32855; Quantitation range 5-20 ng). The recommended minimum RNA input of FFPE RNA is 25 ng. For degraded FFPE samples, the initial RNA should be increased to 75-100ng.

For cfRNA, the RNA concentration can be assumed to be equal to the DNA concentration of the total circulating nucleic acid sample. The DNA concentration can be determined by the Qubit dsDNA HS Assay kit (Life Technologies, Cat. No. Q32851 or Q32854; quantitation range 0.2-100 ng). The recommended minimum input of cfRNA is 20 ng. For poor quality samples, a higher input amount may be necessary.

3. Perform the reverse transcription in a thermal cycler with the lid on according to the conditions below.

Temperature	Time
25°C	10 min
42°C*	30 min*
85°C	5 min
8°C	Hold

**\*Note:** For a 10 µL and 20 µL reaction, only the above cycling conditions with 42 °C for 30 minutes have been tested. However, 50 °C for 10 minutes may be used without affecting performance of the assay due to the short size of RNA fragments.

Alternatively, a 5 µL cDNA reaction may be performed according to the example below for FFPE RNA. After the cDNA synthesis reaction is complete, the master mix for the gene-specific reaction may be added directly to the cDNA synthesis plate and proceed with thermal cycling for the gene-specific PCR.

1. **Dilute RNA:** Dilute RNA in nuclease-free water to a final volume of 4.0 µL in each sample well of a PCR plate, strip tube, or PCR tube. Add nuclease-free water to the no-template control well.

Reagent	Volume (µL)
cDNA Master Mix	1.0
Diluted RNA (or water)	4.0
<b>Total</b>	<b>5.0</b>

2. Add cDNA Master Mix: Add cDNA Master Mix to each sample well containing diluted RNA and no-template control well.

3. Perform the reverse transcription in a thermal cycler with lid on according to the conditions below.

<b>Temperature</b>	<b>Time</b>
25°C	10 min
50°C	10 min
85°C	5 min
8°C	Hold

**STOPPING POINT:** After the completion of the cDNA synthesis, the reaction can be diluted with nuclease-free water or low TE and stored at -20°C if necessary.

## LIBRARY PREPARATION PROTOCOL

Hands-on time: 3.5-5.5 hours

Total time: 7.5-9.5 hours

### Gene-specific PCR: Amplify Transcript Targets

The following steps are performed in a pre-PCR area. For this portion of the protocol, have an ice bucket prepared. Vortex and spin the Gene-specific PCR Master Mix (GS PCR MMX) and Fusion oligo pool before use.

**IMPORTANT NOTE:** For performing Gene-Specific PCR from cfRNA samples, see Appendix B.

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 in the table below.

Reagent	Volume (μL)
Gene-specific PCR Master Mix	25.0
SF oligo pool (5x)	10.0
<b>Sub-Total</b>	<b>35.0</b>

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

2. **Transfer:** Transfer 35.0 μL of master mix to each sample well in a PCR plate, strip tube, or PCR tube.
3. **Dilute input:** Dilute cDNA in nuclease-free water to a final volume 15.0 μL of dilute cDNA\*. Add 15.0 μL of diluted cDNA to each sample well containing PCR master mix. Add 15.0 μL of nuclease-free water to the no-template control well.

\*Up to 15 μL of undiluted cDNA reaction may be added to the GS-PCR reaction. It is recommended that the volume added to the reaction corresponds to at least 25 ng of FFPE RNA. If using the entire cDNA reaction (5 or 10 μL reaction), the PCR master mix and supplementing water may be added directly to the cDNA reaction plate. The plate may proceed directly to GS-PCR. See previous section “cDNA SYNTHESIS” for more information regarding input.

Reagent	Volume (µL)
PCR Master Mix	35.0
Diluted cDNA (or water)	15.0
<b>Sub-Total</b>	<b>50.0</b>

4. **Seal and mix:** Carefully seal the reactions and vortex for 10-15 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 PCR:** Perform the following program with the heated lid on.  
**IMPORTANT NOTE:** See Appendix B for performing GS-PCR cycling with cfRNA samples. The cycling conditions below are optimized for FFPE RNA samples only.

Temperature	Time	Number of Cycles
95°C	15 min	1
95°C	1 min	5
58°C	1 min	
60°C	2 min	
64°C	30 sec	
72°C	1 min	
95°C	30 sec	24
66°C	3 min	
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 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 samples 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  $\mu\text{L}$  of the exonuclease I in 20  $\mu\text{L}$  nuclease-free water to prepare 50  $\mu\text{L}$  of diluted exonuclease. Add reagent overage as appropriate. Any excess dilution can be stored at  $-20^{\circ}\text{C}$  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  $-20^{\circ}\text{C}$ . Otherwise, freshly dilute the exonuclease before adding it to the samples.*

3. **Add Exonuclease:** Add 5  $\mu\text{L}$  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:

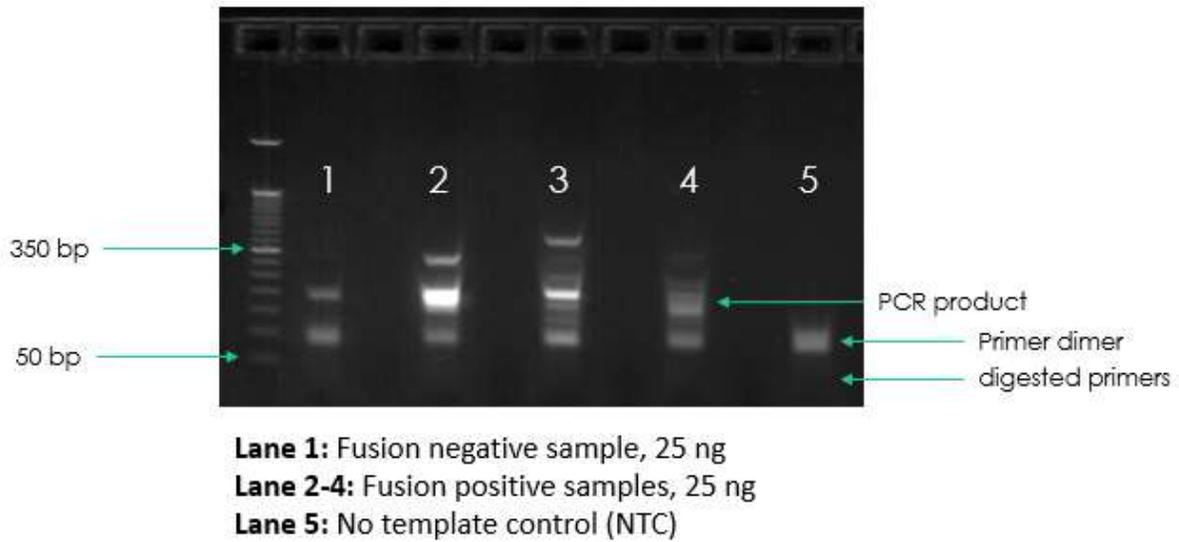
Temperature	Time	Number of Cycles
37°C	20 min	1
80°C	10 min	1
8°C	Hold	Hold

**IMPORTANT:** *Do not leave the reactions at  $8^{\circ}\text{C}$  overnight. Precipitation may occur when the reactions are incubated at  $8^{\circ}\text{C}$  overnight.*

**STOPPING POINT:** *The gene-specific PCR reactions may be stored at  $-20^{\circ}\text{C}$  after primer digestion.*

### Gel Image after Gene-Specific PCR

The following is a gel image of FFPE RNA samples after gene-specific PCR and primer digestion.



**Figure 3.** Gel analysis of GS PCR material on 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 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 66 µL beads (1.2x beads if the volume is not currently 55 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.

**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 6-9.*

4. **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 7.*

5. **Separate beads containing PCR product:** 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  $\mu$ L 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 supernatant from each well. The unused solution of ethanol can be used to purify the libraries after indexing PCR.
9. **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  $\mu$ L tip to remove the remaining ethanol solution at the bottom of the wells.
10. **Resuspend beads:** Remove the samples from the magnetic rack, and immediately resuspend the beads in each well using 64  $\mu$ L 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.
11. Incubate the elution at room temperature for 5 minutes to 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  $^{\circ}$ C after elution.

**STOPPING POINT:** The purified PCR product may be stored with the beads at -20  $^{\circ}$ C.

## Indexing PCR: Amplify the Libraries

Hands-on time: 20-40 minutes

Total time: 50-70 minutes

The following step 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.

**IMPORTANT:** The following protocol is for preparing libraries to be sequenced on the Illumina platform.

1. **Add indexing primers:** For each indexing reaction, add 4.0  $\mu\text{L}$  of the appropriate forward and reverse indexing primer to each sample well being used.

Reagent	Volume ( $\mu\text{L}$ )
Pi700 Pillar Index	4.0
Pi500 Pillar Index	4.0
<b>Total</b>	<b>8.0</b>

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. Transfer 30.0  $\mu\text{L}$  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 ( $\mu\text{L}$ )
Indexing PCR Master Mix (2x)	25.0
Nuclease-free water	5.0
<b>Total</b>	<b>30.0</b>

3. **Add master mix to wells:** Add prepared master mix to wells that contain indices from step 1.

Reagent	Volume (µL)
Pi500 and Pi700 Indices	8.0
Master Mix	30.0
<b>Total</b>	<b>38.0</b>

4. **Add gene-specific PCR product:** 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. Aliquot 12.0 µL of the separated supernatant (Gene-specific PCR product) into the appropriate wells containing indices and PCR Master Mix, being sure that no beads are transferred.

Reagent	Volume (µL)
Indices and PCR Master Mix	38.0
Gene-specific PCR product	12.0
<b>Total</b>	<b>50.0</b>

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

Temperature	Time	Number of Cycles
95°C	2 min	1
95°C	30 sec	5*
66°C	30 sec	
72°C	60 sec	
72°C	5 min	1
8°C	Hold	1

\*Additional Indexing PCR cycles can be performed if final library yield is low or initial DNA input is below recommended minimum.

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

## 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  $\mu\text{L}$  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 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  $\mu\text{L}$  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:** Removing the samples from the magnetic rack, resuspend the dried beads in each well using 32  $\mu\text{L}$  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  $\mu\text{L}$  of clear supernatant from each well of the PCR plate or tubes to the corresponding well of a new plate or tube.

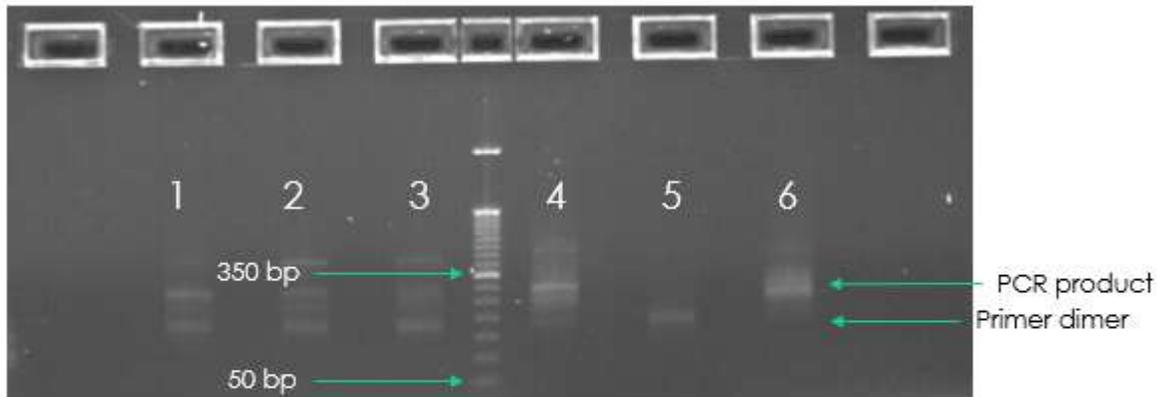
**TIP:** During the incubation and magnetic separation of the beads, cover the samples and prepare the solutions needed for quantitation in the next section. The purified libraries may also be stored at 4  $^{\circ}\text{C}$  for up to 3 days or at -20  $^{\circ}\text{C}$  for longer-term storage.

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

**STOPPING POINT:** The purified libraries may be stored at 4  $^{\circ}\text{C}$  for up to 3 days. Store the purified libraries at -20  $^{\circ}\text{C}$  for longer-term storage.

**Final Library Gel Image**

The following is a gel image of final libraries for sequencing on the Illumina platform after all rounds of PCR and purification.



**Lane 1-2:** Fusion negative sample, 25 ng  
**Lane 3-4,6:** Fusion positive samples, 25 ng  
**Lane 5:** No template control (NTC)

**Figure 4.** Gel analysis of Final Libraries on 2% agarose gel.

## Qubit Quantification 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. Ensure to prepare enough buffer for the number of samples being processed with overage.

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  $\mu\text{L}$  is sufficient buffer for 10 readings (8 samples + 2 standards). Combine 1990  $\mu\text{L}$  of Qubit dsDNA HS buffer and 10  $\mu\text{L}$  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  $\mu\text{L}$  of Qubit working solution into two tubes for standard 1 and standard 2, and then add 10  $\mu\text{L}$  of each standard to the corresponding tube.

**IMPORTANT:** New standard dilutions should be prepared with the samples. Do not re-use standard dilutions from previous experiments.

4. **Prepare samples:** Transfer 198  $\mu\text{L}$  of Qubit working solution to each tube, and then add 2  $\mu\text{L}$  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  $\mu\text{L}$  Qubit buffer with dye and 1  $\mu\text{L}$  sample (1:200 dilution). Repeat steps 5-7.
8. **Calculate concentration:** 1 ng/  $\mu\text{L}$  is equal to 5 nM. Example calculation is below. Adjust dilution factor accordingly.

2  $\mu\text{L}$  of library + 198  $\mu\text{L}$  Qubit solution:

$$\frac{\text{Qubit reading } \left(\frac{\text{ng}}{\text{mL}}\right)}{1,000} \times \text{dilution factor (100)} \times \text{conversion factor (5)} = \text{nM}$$

**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.

### Normalization and Pooling

Hands-on time: 30-45 minutes

Total time: 30-45 minutes

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

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.

$$\frac{\text{Library concentration (nM)} \times 4 \text{ uL library}}{5 \text{ nM}} = \text{final volume of library}$$

$$\text{Final volume of library} - 4 \text{ uL library} = \text{volume of diluent}$$

**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.
4. **Quantify final library pool (recommended):** The libraries prepared using the Multi-Cancer RNA Fusion v2 cluster very efficiently on the MiSeq. It is recommended that the library mix be quantified using Qubit or another library quantitation method (qPCR) to ensure the mix is at 5 nM to prevent over-clustering or under-clustering on the MiSeq. If the final dilution is not 5 nM ( $\pm 10\%$ ), adjust the dilution accordingly when loading the sequencer to obtain the desired concentration.

## Prepare Diluted Libraries for Sequencing

Hands-on time: 30-40 minutes

Total time: 30-40 minutes

Samples can be multiplexed and sequenced on the MiSeq using the v2 or v3 chemistry. The number of samples that can be loaded is dependent on the number of paired-end reads per sample and desired sequencing depth. Please choose the appropriate sequencing workflow and kit based on the number of samples to be sequenced.

Kit	Cycles	Estimated PE reads	Estimated PE reads/sample	Estimated max. # libraries
MiSeq nano v2	2x150	2 million	50,000	40
MiSeq micro v2	2x150	8 million	50,000	160
MiSeq v2	2x150	30 Million	50,000	600
MiSeq v3	2x150	50 Million	50,000	1000

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

### Sequencing with Additional ONCO/Reveal Panels (recommended)

It is recommended that Solid Tumor Fusion libraries should be loaded with libraries processed using Pillar's ONCO/Reveal Multi-Cancer or Lung & Colon Cancer Panel on a MiSeq Micro v2, MiSeq v2 kit, or MiSeq v3 kit. The final concentration of the libraries for sequencing is **15 pM** for v2 chemistry and **25 pM** for v3 chemistry.

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

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

Alternately, prepare a 1 N NaOH solution by combining 500  $\mu$ 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.

2. **Denature the library mix:** Label a new microtube for the denatured, 25 pM library mix.
  - a. Denature the library mix by combining 5  $\mu\text{L}$  of the library mix and 5  $\mu\text{L}$  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  $\mu\text{L}$  of Illumina's HT1 solution to the denatured library mix.
  - e. Invert the mixture several times, spin briefly, and place on ice.
3. **Dilute to 15 pM library mix:** Label a new 1.5 mL microtube for the 15 pM library mix. Combine 360  $\mu\text{L}$  of the 25 pM library mix (step 2) with 240  $\mu\text{L}$  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.
4. **Combine library mix and PhiX control:** Label a new 1.5 mL microtube for the mixture that will be loaded. Combine 594  $\mu\text{L}$  of the 15 pM library mix (step 3) with 6  $\mu\text{L}$  of a 12.5 pM PhiX library control. Briefly vortex, spin, and place on ice.
5. **Load MiSeq cartridge:** Using a clean 1000  $\mu\text{L}$  tip, puncture the foil cap above the sample loading tube on the MiSeq cartridge. Load the 600  $\mu\text{L}$  library mix and PhiX mixture (step 4) 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.
6. **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 33.
7. Store diluted libraries and mixtures at  $-20^{\circ}\text{C}$  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**.

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

1. **Prepare 0.2 N NaOH:** Label a new 1.5 mL microtube for 0.2 N NaOH. Prepare the NaOH by combining 800  $\mu\text{L}$  nuclease-free water with 200  $\mu\text{L}$  of 1 N NaOH. Vortex the solution to mix.

Alternately, prepare a 1 N NaOH solution by combining 500  $\mu\text{L}$  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.

2. **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  $\mu\text{L}$  of the library mix and 5  $\mu\text{L}$  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  $\mu\text{L}$  of Illumina's HT1 solution to the denatured library mix.
  - e. Invert the mixture several times, spin briefly, and place on ice.
3. **Combine library mix and PhiX control:** Label a new 1.5 mL microtube for the mixture that will be loaded. Combine 594  $\mu\text{L}$  of the 25 pM library mix (step 2) with 6  $\mu\text{L}$  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.
4. **Load MiSeq cartridge:** Using a clean 1000  $\mu\text{L}$  tip, puncture the foil cap above the sample loading tube on the MiSeq cartridge. Load the 600  $\mu\text{L}$  library mix and PhiX mixture (step 3) 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.
5. **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 33.
6. Store diluted libraries and mixtures at  $-20^{\circ}\text{C}$  for long-term storage.

### Sequencing ONCO/Reveal Multi-Cancer RNA Fusion v2 Libraries only

The final concentration of the libraries for sequencing using v2 chemistry (MiSeq Nano v2, MiSeq Micro v2, or MiSeq v2 kit) is **10 pM**.

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

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

Alternately, prepare a 1 N NaOH solution by combining 500  $\mu$ 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.

2. **Denature the library mix:** Label a new microtube for the denatured, 25 pM library mix.
  - a. Denature the library mix by combining 5  $\mu$ L of the library mix and 5  $\mu$ 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  $\mu$ L of Illumina's HT1 solution to the denatured library mix.
  - e. Invert the mixture several times, spin briefly, and place on ice.
3. **Dilute to 10 pM library mix:** Label a new 1.5 mL microtube for the 10 pM library mix. Combine 240  $\mu$ L of the 25 pM library mix (step 2) with 360  $\mu$ 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.
4. **Combine library mix and PhiX control:** Label a new 1.5 mL microtube for the mixture that will be loaded. Combine 540  $\mu$ L of the 10 pM library mix (step 3) with 60  $\mu$ L of a 12.5 pM PhiX library control. Briefly vortex, spin, and place on ice.
5. **Load MiSeq cartridge:** Using a clean 1000  $\mu$ L tip, puncture the foil cap above the sample loading tube on the MiSeq cartridge. Load the 600  $\mu$ L library mix and PhiX mixture (step 4) 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.
6. **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 33.

7. Store diluted libraries and mixtures at -20°C for long-term storage.

## Preparing a Sample Sheet for Sequencing

**NOTE:** When creating the sample sheet and running BLC2FQ, do not select adapter trimming as this will interfere with analysis in PIVAT version 2020.1

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

The available Pillar indexing primers and their barcode sequences are listed in the attached Appendix A. For the i5 indexing primers, indexing on the NextSeq requires the reverse complement of the barcode sequence. The correct barcode sequence for sequencing on the MiSeq and the NextSeq is provided in Appendix A. Additionally, the Pillar sample sheet generator will automatically populate the correct barcode sequence when the indexing primer is selected.

In Appendix A, note that indexing primers highlighted in yellow have the same barcode sequences as Illumina TruSeq Custom Amplicon (TSCA) indices.

In the Pillar sample sheet generator, prepare a sample sheet that contains the information for the samples that are being loaded. Ensure that the appropriate sample sheet is being made for the MiSeq or the NextSeq.

1. Open the Pillar sample sheet generator and enter user input in the shaded cells. Cells that are shaded blue are required and cells that are shaded grey are optional.
2. Enter the "Sample\_ID" for each sample. Each Sample\_ID must be unique and contain only alphanumeric characters, dashes (-), and underscores (\_). All other characters are not allowed. To check that the Sample\_ID meets all requirements click "Reset Sample\_ID color" and then click "Check Sample\_ID".
3. If text is green, the Sample\_ID is acceptable. If text is red, Sample\_ID is not acceptable. Change Sample\_ID accordingly and repeat step 2 until all text is green.
4. Next, enter indices into appropriate fields. Index sequences will be populated once the index\_ID is entered.
5. Check that all index combinations for each sample is unique. If "Check\_index\_uniqueness" column is green, then all index combinations are unique. If the column is red for a sample, then index combination is not unique. Do not load samples together in the same run that have the same index combination.
6. Once all requirements for the sample sheet are met, export the sample sheet as a comma-separated values (.csv) file by clicking "Export".

**TROUBLESHOOTING**

<b>Issue</b>	<b>Potential Cause</b>	<b>Solution</b>
Low yield of gene-specific product	RNA quantity or quality	The recommended minimum input for the assay is 25 ng of FFPE RNA and 20 ng of cfRNA. Higher quantities may be necessary for low or poor quality FFPE or cfRNA 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	RNA quantity or quality	<p>The recommended minimum input for the assay is 25 ng of FFPE RNA and 20 ng of cfRNA. Higher quantities may be necessary for low or poor quality FFPE or cfRNA samples.</p> <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) or 25 pM (v3)	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.
	Improper library quantitation	Improper library quantitation may result in artificially high or low yields, which affects downstream normalization.

		Re-quantify the final libraries and/or the normalized libraries to check for the expected values.
	Improper Ampure purification	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.
		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.
		The final libraries can be checked on an agarose gel for the proper product size and presence of primer dimers.
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>

## Appendix A

i7 Index	
Index Name	Index Barcode Sequence
Pi701	ATTACTCG
Pi702	TCCGGAGA
Pi703	CGCTCATT
Pi704	GAGATTCC
Pi705	ATTCAGAA
Pi706	GAATTCGT
Pi707	CTGAAGCT
Pi708	TAATGCGC
Pi709	ATCACGAC
Pi710	ACAGTGGT
Pi711	CAGATCCA
Pi712	ACAAACGG
Pi713	GAAACCCA
Pi714	TGTGACCA
Pi715	AGGGTCAA
Pi716	AGGAGTGG

i5 Index		
Index Name	Index Barcode Sequence for Miseq	Index Barcode Sequence for NextSeq
Pi501	TATAGCCT	AGGCTATA
Pi502	ATAGAGGC	GCCTCTAT
Pi503	CCTATCCT	AGGATAGG
Pi504	GGCTCTGA	TCAGAGCC
Pi505	AGGCGAAG	CTTCGCCT
Pi506	TAATCTTA	TAAGATTA
Pi507	CAGGACGT	ACGTCCTG
Pi508	GTACTGAC	GTCAGTAC
Pi509	TGAACCTT	AAGGTTCA
Pi510	TGCTAAGT	ACTTAGCA
Pi511	TGTTCTCT	AGAGAACA
Pi512	TAAGACAC	GTGTCTTA
Pi513	CTAATCGA	TCGATTAG
Pi514	CTAGAACA	TGTTCTAG
Pi515	TAAGTTCC	GGAACTTA
Pi516	TAGACCTA	TAGGTCTA

## Appendix C - Preparing SF Libraries from cfrRNA (version 1.1)

### I. cDNA sythesis

Final Reaction Volumes		
Reagent	Volume (μL) (20 μL reaction)	Volume (μL) (10 μL reaction)
cDNA Master Mix	4.0	2.0
Diluted RNA* (or water)	16.0	8.0
<b>Total</b>	<b>20.0</b>	<b>10.0</b>

### Cycling Conditions

Temperature	Time
25°C	10 min
42°C	30 min
85°C	5 min
8°C	Hold

*\*For cfrRNA, the RNA concentration can be assumed to be equal to the DNA concentration of the total circulating nucleic acid sample. The DNA concentration can be determined by the Qubit dsDNA HS Assay kit (Life Technologies, Cat. No. Q32851 or Q32854; quantitation range 0.2-100 ng). The recommended minimum input of cfrRNA is 20 ng. For poor quality samples, a higher input amount may be necessary.*

### II. Gene-Specific PCR

Final Reaction Volumes	
Reagents	Volume (μL)
GS PCR MMX (2x)	25.0
SF oligo pool (5x)	10.0
Diluted cDNA (or water)	15.0
<b>total</b>	<b>50.0</b>

### PCR Cycling Conditions

Temperature	Time	Number of Cycles
95°C	15 min	1
95°C	1 min	5
58°C	1 min	
60°C	2 min	
64°C	30 sec	
72°C	1 min	24
95°C	30 sec	
66°C	3 min	
8°C	Hold	1

III. Proceed with the rest of the protocol as outlined in the Solid Tumor Fusion User Guide.