

# Arima-HiC Kit

Library Preparation using KAPA® Hyper Prep Kit

Material Part Number: A510008 Document Part Number: A160139 v00 Release Date: November 2018 This product is intended for research use only. This product is not intended for diagnostic purposes.

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U.S. Patent No. US 9,434,985 pertains to the use of this product.

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## **Revision History**

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## **Getting Started**

#### 1.1 Kit Contents and Storage

• The Arima-HiC Kit contains the following reagents to be used during Library Preparation:

Kit Location	Reagent	Storage Temperature
Box A	Wash Buffer	RT
	Elution Buffer	
Box C	Enrichment Beads	2 to 8°C

#### 1.2 Handling and Preparation

- The majority of required reagents for the *Library Preparation* protocol are included in the KAPA® Hyper Prep kit. Other required reagents are either supplied in the Arima-HiC kit, or, listed below in Section 1.3.
- Safe stopping points are indicated where the option is available.
- The **Enrichment Beads** should be thoroughly mixed by pipetting or vortexing until homogeneous directly before use.
- The **Wash Buffer** and **Elution Buffer** should be kept at room temperature during handling and preparation.

### 1.3 User-supplied reagents, consumables and equipment checklist

Kapa<sup>®</sup> Hyper Prep Kit with Library Amplification Module (e.g. Cat # KK8500, KK8502, or KK8504)

KAPA® Library Quantification Kit for Illumina® Platforms (e.g. KAPA® Cat # KK4824)

15µM Illumina<sup>®</sup> TruSeq<sup>®</sup> sequencing adapters (e.g. Illumina<sup>®</sup> Cat # 20020590)

DNA Purification Beads (e.g. Beckman Coulter Cat # A63880)

Qubit<sup>®</sup> Fluorometer, dsDNA HS Assay Kit and required consumables (e.g. Thermo Fisher Scientific Cat # 32851, 32856)

Freshly prepared 80% Ethanol

1.7mL microcentrifuge tubes, PCR tubes or PCR plates

Magnetic rack for 1.7mL microcentrifuge tubes, PCR tubes or PCR plates

Instrument for DNA Fragmentation (e.g. Covaris® or Diagenode®) and consumables.

Thermal cycler

Thermomixer (if doing some steps in 1.7mL microcentrifuge tubes)

Gel Electrophoresis System (e.g. Bioanalyzer®, TapeStation®, etc.)

## Library Preparation

Input: Proximally-ligated DNA Output: Bead-bound Arima-HiC library

**Overview:** Library preparation begins with DNA fragmentation (Section 2.1), DNA size selection (Section 2.2), and biotin enrichment (Section 2.3). Afterwards, KAPA® Hyper Prep reagents are used in a custom end-repair, dA-tailing and adapter ligation protocol (Section 2.4). This custom protocol contains specific modifications to the standard KAPA® Hyper Prep protocol that <u>must</u> be performed. All buffers and enzymes provided by the KAPA® Hyper Prep kit are used, and most additional required reagents are provided in the Arima-HiC kit. This custom *Library Preparation* protocol constructs libraries while DNA is bound to the **Enrichment Beads**. After the *Library Preparation* protocol, there is a recommended Arima-QC2 Quality Control checkpoint. The final step is PCR amplification of the bead-bound Arima-HiC library using KAPA® library amplification reagents, producing the final sequence-ready Arima-HiC library.

### 2.1 DNA Fragmentation

**Before you begin:** The output of the *Arima-HiC Protocol* is large proximally-ligated DNA molecules. These large DNA molecules must be fragmented using mechanical methods to limit sequence bias, and then prepared as a sequencing library that is compatible with Illumina<sup>®</sup> sequencing instruments. Covaris<sup>®</sup> instruments are recommended for mechanical fragmentation of DNA, although Diagenode<sup>®</sup> instruments have also been tested and yield comparable results. DNA should be fragmented in 100µL of **Elution Buffer**. Some Covaris<sup>®</sup> protocols recommend DNA fragmentation in 130µL, but 100µL <u>must</u> be used for DNA fragmentation in the Arima-HiC library preparation protocol. It is recommended to fragment at least 750ng of DNA per sample, or up to 5µg (depending on the DNA fragmentation instrument manufacturer recommendations). For certain applications, less than 750ng of DNA could be used.

- If necessary, <u>add</u> Elution Buffer to bring the sample volume to 100μL. Do not exceed 100μL of volume for DNA fragmentation.
- Fragment DNA to obtain an average fragment size of 400bp. Please use the DNA fragmentation instrument manufacturer default settings for obtaining a target fragment size of 400bp. For example, Covaris<sup>®</sup> publishes optimal DNA fragmentation Power, Duty Factor, Cycles per Burst, and Time for obtaining a target fragment size of 400bp.
- 3. Samples may be stored at -20°C for up to 3 days.

**Recommended QC before proceeding:** Run an aliquot of fragmented DNA on a gel electrophoresis system (e.g. Bioanalyzer<sup>®</sup>, TapeStation<sup>®</sup>) to confirm an appropriate fragment size distribution centered around 400bp.

#### 2.2 DNA Size Selection

**Before you begin:** Fragmented DNA must be size-selected to have a size distribution between 200 – 600bp. This workflow can be performed in microfuge tubes as well as most PCR tubes and PCR plates. Ensure that your tubes or plates can hold up to 200µL of sample volume. Also ensure that you have a magnetic rack that fits your choice of sample tube/plate.

Note: DNA Purification Beads (e.g. AMPure<sup>®</sup> XP Beads) should be warmed to RT and thoroughly mixed before use. The DNA Purification Beads are a *user-supplied reagent* and should not be mistaken for the Enrichment Beads or QC Beads provided in the Arima-HiC kit. For the ethanol washes performed below, use sufficient 80% ethanol to fully submerge the magnetized beads.

- <u>Transfer</u> fragmented DNA sample from fragmentation tube to either a microfuge tube, PCR tube, or PCR plate. If necessary, <u>add</u> Elution Buffer to bring sample volume to 100µL.
- <u>Add</u> 60µL of **DNA Purification Beads**, <u>mix</u> thoroughly by pipetting, and <u>incubate</u> at RT for 5 min.
- 3. <u>Place</u> sample against magnet, and <u>incubate</u> until solution is clear.
- 4. <u>Transfer</u> ~160uL *of supernatant* to a new sample tube or well of a PCR plate. <u>Discard</u> beads.
- 5. <u>Add</u> 40μL of **DNA Purification Beads** to the ~160μL of supernatant, <u>mix</u> thoroughly by pipetting, and <u>incubate</u> at RT for 5 min.
- 6. <u>Place</u> sample against magnet, and <u>incubate</u> until solution is clear.
- <u>Discard</u> supernatant. While sample is still against magnet, <u>add</u> 200µL of 80% ethanol, and <u>incubate</u> at RT for 1 min.
- <u>Discard</u> supernatant. While sample is still against magnet, <u>add</u> 200µL of 80% ethanol, and <u>incubate</u> at RT for 1 min.
- <u>Discard</u> supernatant. While sample is still against magnet, <u>incubate</u> beads at RT for 3 5 min. to air-dry the beads.
- 10. <u>Remove</u> the sample from magnet, <u>resuspend</u> beads in 100µL of **Elution Buffer**, and <u>incubate</u> at RT for 5 min.
- 11. <u>Place</u> sample against magnet, <u>incubate</u> until solution is clear, and <u>transfer</u> supernatant to a new sample tube or well of a PCR plate.
- 12. <u>Quantify</u> sample using Qubit<sup>®</sup>.
- 13. Samples may be stored at -20°C for up to 3 days.

### 2.3 Biotin Enrichment

**Before you begin:** This workflow can be performed in microfuge tubes as well as most PCR tubes and PCR plates. Ensure that your tubes or plates can hold up to 200µL of sample volume. Also ensure that you have a magnetic rack that fits your choice of sample tube/plate. Set your thermal device (thermal cycler or thermomixer) to hold at 55°C.

1. <u>Transfer</u> **125ng – 2μg\*** of size-selected DNA into a new microfuge tube, PCR tube, or well of a PCR plate. If necessary, <u>add</u> **Elution Buffer** to bring sample volume to 100μL.

\* Biotin enrichment and subsequent library preparation has been optimized to deliver peak performance for DNA inputs ranging from 125ng-2µg. While input amounts closer to 2µg will result in more complex Arima-HiC libraries, 125ng of input has been shown to build libraries with sufficient complexity for 600M read-pairs of sequence data.

- 2. <u>Add</u> 100µL of **Enrichment Beads**, <u>mix</u> thoroughly by pipetting, and <u>incubate</u> at RT for 15 min.
- 3. <u>Place</u> sample against magnet, and <u>incubate</u> until solution is clear.
- 4. <u>Discard</u> supernatant, and <u>remove</u> sample from magnet.
- 5. <u>Wash</u> beads by resuspending in 200µL of **Wash Buffer**, and <u>incubate</u> at 55°C for 2 min.
- 6. <u>Place</u> sample against magnet, and <u>incubate</u> until solution is clear.
- 7. <u>Discard</u> supernatant, and <u>remove</u> sample from magnet.
- 8. <u>Wash</u> beads by resuspending in 200µL of **Wash Buffer**, and <u>incubate</u> at 55°C for 2 min.
- 9. <u>Place</u> sample against magnet, and <u>incubate</u> until solution is clear.
- 10. <u>Discard</u> supernatant, and <u>remove</u> sample from magnet.
- 11. <u>Wash</u> beads by resuspending in 100µL of **Elution Buffer**.
- 12. <u>Place</u> sample against magnet, and <u>incubate</u> until solution is clear.
- 13. <u>Discard</u> supernatant, and <u>remove</u> sample from magnet.
- 14. <u>Resuspend</u> beads in 50µL of **Elution Buffer**.

### 2.4 End Repair, dA-tailing, and Adapter Ligation

**Before you begin**: This custom protocol *resembles* the standard KAPA<sup>®</sup> Hyper Prep protocol but has been modified for library preparation while DNA is bound to the **Enrichment Beads**. The **Wash Buffer** and **Elution Buffer** provided in the Arima-HiC kit are used during this protocol. This protocol can be performed in microfuge tubes as well as most PCR tubes and PCR plates. Ensure that your tubes or plates can hold up to 150µL of sample volume. Select a uniquely indexed Illumina<sup>®</sup> TruSeq<sup>®</sup> sequencing adapter for each sample.

Note: Steps 1 and 4 require the addition of buffer and enzyme reagents, which should be prepared as a master mix and added in a single pipetting step.

1. <u>Add</u> 10μL of a master mix containing the following reagents to 50μL of bead-bound, biotin-enriched DNA:

Reagent	Volume per reaction	10% extra		# reactions		Final
End Repair and A-Tailing Buffer	7μL	7.7µL	х	2	=	15.4µL
End Repair and A-Tailing Enzyme	3µL	3.3µL	х	2	=	6.6µL
Total	10µL					22µL

2. <u>Mix</u> thoroughly by pipetting until homogeneous, and <u>incubate</u> as follows in a thermal cycler with the lid temperature set to >75°C. Once completed, immediately proceed to the next step.

Temperature	Time
20°C	30 min.
65°C	30 min.
4°C	Hold

- 3. Add 1µL of Illumina<sup>®</sup> TruSeq<sup>®</sup> sequencing adapter (15µM).
- 4. Add  $49\mu$ L of a master mix containing the following reagents:

Reagent	Volume per reaction	10% extra		# reactions		Final
PCR-grade water	9µL	9.9µL	х	2	II	19.8µL
Ligase Buffer	30µL	33µL	х	2	II	66µL
DNA Ligase	10µL	11µL	х	2	II	22µL
Total	49µL					107.8µL

5. <u>Mix</u> thoroughly by pipetting until homogeneous, and <u>incubate</u> as follows in a thermal cycler with the heated lid turned off. Once completed, immediately proceed to the next step.

Temperature	Time
20°C	15 min.
4°C	Hold

Note: Steps 8 and 11 require incubations at 55°C. Set your thermal device to hold at 55°C.

- 6. <u>Place</u> sample against magnet, and <u>incubate</u> until solution is clear.
- 7. <u>Discard</u> supernatant, and <u>remove</u> sample from magnet.
- 8. <u>Wash</u> beads by resuspending in 150µL of **Wash Buffer**, and <u>incubate</u> at 55°C for 2 min.
- 9. <u>Place</u> sample against magnet, and <u>incubate</u> until solution is clear.
- 10. <u>Discard</u> supernatant, and <u>remove</u> sample from magnet.
- 11. <u>Wash</u> beads by resuspending in 150µL of **Wash Buffer**, and <u>incubate</u> at 55°C for 2 min.
- 12. <u>Place</u> sample against magnet, and <u>incubate</u> until solution is clear.
- 13. <u>Discard</u> supernatant, and <u>remove</u> sample from magnet.
- 14. <u>Wash</u> beads by resuspending in  $100\mu$ L of **Elution Buffer**.
- 15. <u>Place</u> sample against magnet, and <u>incubate</u> until solution is clear.
- 16. <u>Discard</u> supernatant, and <u>remove</u> sample from magnet.
- 17. <u>Resuspend</u> beads in 22µL of **Elution Buffer**.
- 18. Samples may be stored at 4°C for up to 3 days.

# Arima-QC2 Quality Control

**Before you begin**: The following protocol utilizes the KAPA<sup>®</sup> Library Quantification Kit (qPCR assay) to determine the **Arima-QC2** values and estimate the appropriate number of PCR cycles needed for library amplification. After completing the qPCR assay, use the provided **Arima-HiC QC Worksheet** to determine the Arima-QC2 values and PCR cycle numbers. If performing Capture-HiC, please contact Technical Support for additional guidance.

Note: Step 2 requires the addition of buffer and enzyme reagents, which should be prepared as a master mix and added in a single pipetting step.

- <u>Prepare</u> a 1:1000 dilution of each bead-bound Arima-HiC library. To do this, first <u>vigorously mix</u> a bead-bound Arima-HiC library by vortexing and pipetting until homogeneous. Then, immediately <u>add</u> 1µL of bead-bound library to 999 µL of water.
- 2. <u>Add</u> 16µL of a master mix containing the following reagents to each well of the qPCR plate that will receive either standards, water, or samples (see Step 3 for recommended plate layout):

Reagent	Volume per reaction	10% extra		# reactions		Final
qPCR Master Mix	10µL	11µL	х	27	=	297µL
Illumina <sup>®</sup> Primer Mix	2µL	2.2µL	х	27	Π	59.4µL
Water	4µL	4.4µL	х	27	=	118.8µL
Total	16µL					475.2µL

 <u>Add</u> 4µL of each Standard, 1:1000 diluted bead-bound Arima-HiC library, or water to each well containing 16µL of master mix prepared during Step 2. Use the same water source as was used to prepare the qPCR Master Mix. A suggested plate layout is provided below:

	Arima-QC2 Recommended Plate Layout										
Std_1	Std_1	Std_1	Std_2	Std_2	Std_2	Std_3	Std_3	Std_3	Std_4	Std_4	Std_4
Std_5	Std_5	Std_5	Std_6	Std_6	Std_6	H <sub>2</sub> O	H <sub>2</sub> O	H <sub>2</sub> O	Lib1	Lib1	Lib1
Lib2	Lib2	Lib2	Lib3	Lib3	Lib3	Lib4	Lib4	Lib4	Lib5	Lib5	Lib5
Lib6	Lib6	Lib6	Lib7	Lib7	Lib7	Lib8	Lib8	Lib8			

Note: "Std" refers to the qPCR Standards provided in the KAPA<sup>®</sup> Library Quantification Kit. "Lib" refers to each 1:1000 diluted, bead-bound Arima-HiC library.

4. <u>Run</u> the following qPCR cycling protocol:

Cycles	Temperature	Time
1 X	95°C	5 min.
25.7	95°C	30 sec.
337	60°C	45 sec.
Melt	65°C - 95°C	-

5. <u>Extract</u> C<sub>q</sub> values from the qPCR instrument and follow the **Arima-HiC QC Worksheet** to calculate the Arima-QC2 values and estimate the required number of PCR cycles for library amplification. High-quality Arima-QC2 values are expected to be >0.2%. If Arima-QC1 and Arima-QC2 values both obtain a 'PASS' status, proceed to the *Library Amplification* protocol and subsequent sequencing analysis. If the Arima-QC2 value did not obtain a 'PASS' status, please contact Technical Support for troubleshooting assistance.

# Library Amplification

**Before you begin**: The following *Library Amplification* protocol utilizes the PCR reagents included in the Library Amplification Module of KAPA® Hyper Prep Kit. Determining how many PCR cycles to use for library amplification can be done in 1 of 2 ways – (1) determine the required PCR cycles empirically using the *Arima-QC2 Quality Control* protocol in the previous section, or (2) use the general guideline that 10 cycles of PCR should be sufficient to obtain enough library for DNA sequencing as long as >125ng of DNA was used as input in the *Biotin Enrichment* section. If the *Arima-QC2 Quality Control* protocol was not performed and the input into biotin enrichment was <125ng, please contact Technical Support for further guidance. Additionally, please contact Technical Support for recommended library amplification modifications for Capture-HiC.

Note: Step 1 requires the addition of buffer and enzyme reagents, which should be prepared as a master mix and added in a single pipetting step.

 <u>Add</u> 30μL of a master mix containing the following reagents to 20μL of bead-bound Arima-HiC library:

Reagent	Volume per reaction	10% extra		# reactions		Final
2X HiFi HotStart Ready Mix	25µL	27.5µL	х	2	=	55µL
10X Primer Mix	5µL	5.5µL	х	2	=	11µL
Total	30µL					66µL

2. <u>Mix</u> thoroughly by pipetting until homogeneous, and <u>run</u> the following PCR program in a thermal cycler with the lid temperature set to 105°C:

Cycles	Temperature	Time
1 X	98°C	45 sec.
	98°C	15 sec.
	60°C	30 sec.
(c.g. 107)	72°C	30 sec.
1 X	72°C	60 sec.
1 X	10°C	Hold

Note: DNA Purification Beads (e.g. AMPure<sup>®</sup> XP Beads) should be warmed to RT and thoroughly mixed before use. The DNA Purification Beads are a *user-supplied reagent* and should not be mistaken for the Enrichment Beads or QC Beads provided in the Arima-HiC kit.

- 3. Add 45µL of **DNA Purification Beads**, <u>mix</u> thoroughly, and <u>incubate</u> at RT for 5 min.
- 4. <u>Place</u> sample against magnet, and <u>incubate</u> until solution is clear.
- 5. <u>Discard</u> supernatant. While sample is still against magnet, <u>add</u> 150µL of **80% ethanol**, and <u>incubate</u> at RT for 1 min.

- 6. <u>Discard</u> supernatant. While sample is still against magnet, <u>add</u> 150µL of **80% ethanol**, and <u>incubate</u> at RT for 1 min.
- 7. <u>Discard</u> supernatant. While sample is still against magnet, <u>incubate</u> beads at RT for 3 5 min. to air-dry the beads.
- 8. <u>Remove</u> the sample from magnet, <u>resuspend</u> beads in 50µL of **Elution Buffer**, and <u>incubate</u> at RT for 5 min.
- 9. <u>Place</u> sample against magnet, <u>incubate</u> until solution is clear, and <u>transfer</u> supernatant to a new tube.
- 10. Repeat Steps 3-7. Once Step 7 has been completed, proceed to Step 11 below.
- 11. <u>Remove</u> the sample from magnet, <u>resuspend</u> beads in 25µL of **Elution Buffer**, and <u>incubate</u> at RT for 5 min.
- 12. <u>Place</u> sample against magnet, <u>incubate</u> until solution is clear, and <u>transfer</u> supernatant to a new tube.
- 13. <u>Quantify</u> sample using Qubit<sup>®</sup>.
- 14. <u>Store</u> Arima-HiC libraries at -20°C until standard library QC (Bioanalyzer<sup>®</sup>, qPCR) and sequencing.

## Warranty and Contact Info

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#### CONTACT US

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