



# Arima Library Prep Module

## User Guide: Library Preparation for the Arima HiC+ for Genome Wide HiC Kit

16 reactions

**Material Part Numbers:** A510008, A303011

**Document Part Number:** A160432 v02

**Release Date:** May 2023

This product is intended for research use only. This product is not intended for diagnostic purposes. This document and its contents are proprietary to Arima Genomics, Inc (“Arima Genomics”).

Use of this document is intended solely for Arima Genomics customers for use with the Arima-HiC Kit, PN A510008 and the Arima Library Prep Module, PN A303011 and for no other purpose. This document and its contents shall not be used, distributed or reproduced in whole or in part and/or otherwise communicated or disclosed without the prior written consent of Arima Genomics.

This user manual must be read in advance of using the product and strictly followed by qualified and properly trained personnel to ensure proper use of the Arima Library Prep Module. Failure to do so may result in damage to the product, injury to persons, and/or damage to other property. Arima Genomics does not assume any liability resulting from improper use of its products or others referenced herein.

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

#### TRADEMARKS

Illumina<sup>®</sup>, MiSeq<sup>®</sup>, NextSeq<sup>®</sup>, HiSeq<sup>®</sup>, and NovaSeq<sup>™</sup> are trademarks of Illumina, Inc.

AMPure<sup>®</sup> is a trademark of Beckman Coulter, Inc.

Qubit<sup>®</sup> is a trademark of Molecular Probes, Inc.

SSIIbio<sup>®</sup> is a trademark of Scientific Specialties, Inc.

Bio-Rad<sup>®</sup> is a trademark of Bio-Rad Laboratories, Inc.

Fisher Scientific<sup>®</sup> is a trademark of Fisher Scientific Company, LLC.

Bioanalyzer<sup>®</sup> and TapeStation<sup>®</sup> are trademarks of Agilent Technologies, Inc.

Covaris<sup>®</sup> is a trademark of Covaris, Inc.

Diagenode<sup>®</sup> is a trademark of Diagenode S.A.

© 2022, Arima Genomics, Inc. All rights reserved.

## Revision History

Document	Date	Description of Change
<b>Material Part Number: A510008, A303011 Document Part Number: A160432 v01</b>	April 2022	Initial Release
<b>Material Part Number: A510008, A303011 Document Part Number: A160432 v01</b>	June 2023	Added instructions for accessing sample sheets for Illumina sequencing platforms. Standardized PCR cycle numbers to optimize performance and consistency.

# Table of Contents

<b>Section 1: Getting Started</b> .....	<b>5</b>
1.1 Handling and Preparation .....	5
1.2 Arima materials checklist .....	5
1.3 User-supplied reagents, consumables, and equipment checklist .....	6
1.4 How to cite Arima HiC in publications .....	6
<b>Section 2: Library Preparation</b> .....	<b>7</b>
2.1 DNA Fragmentation .....	7
2.2 DNA Size Selection .....	8
2.3 Biotin Enrichment .....	9
2.4 Library Preparation of Enriched Ligation products .....	11
2.5 Purify Amplified Library with Purification Beads .....	15
<b>Section 3: Warranty and Contact Info</b> .....	<b>17</b>

# Section 1: Getting Started

## 1.1 Handling and Preparation

- Several steps during the *Arima Library Prep Protocol* require preparation of a master mix. Sufficient reagent has been included in the kit to make master mixes with 10% excess volume. Use the master mix calculation tables provided.
- When handling reagents, room temperature (RT) is defined as 20 to 25°C.
- All kit reagents should be fully thawed and thoroughly mixed before use.
- To protect samples and from Nucleases we recommend the use of gloves and sterilized filter tips.
- If possible, performing the pre-amplification steps in a “Pre-PCR” environment and the post-amplification steps in a “Post-PCR” environment will reduce PCR contamination.
- DNA Purification Beads (e.g. AMPure® XP Beads) should be warmed to RT and thoroughly mixed before each use.
- In steps with magnetic beads that require centrifugation, be careful not to pellet the beads.

## 1.2 Arima materials checklist

- Proximally Ligated DNA generated using the **Arima HiC+ Kit (PN A510008)**
- Arima Library Prep Module (PN A303011)**

**Table 1: Reagents Included in the Arima Library Prep Module**

Name	PN	Box	Storage	Cap Color
Ligation Buffer	A311035-01	A	-20°C	Purple
T4 DNA Ligase	A311035-02	A	-20°C	Blue
End Repair-A-Tailing Buffer	A311035-03	A	-20°C	Yellow
End Repair-A Tailing Enzyme Mix	A311035-04	A	-20°C	Orange
Herculase II Fusion DNA Polymerase	A311035-05	A	-20°C	Red
5x Herculase II Buffer with dNTPs	A311035-06	A	-20°C	Clear
Adaptor Oligo Mix	A311035-07	A	-20°C	White
Index 1-16	A311036-01 - A311036-16	B	-20°C	Foil cover
T1 Beads	A311042-01	C	4°C	White
Binding Buffer	A311041-01	D	RT	White

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

- Freshly prepared 80% Ethanol
- DNA Purification Beads (SPRI, e.g. Beckman Coulter Cat # A63880, Approx. 750 $\mu$ L per sample)
- Qubit Fluorometer, dsDNA HS Assay Kit and consumables (e.g. Thermo Fisher Scientific Cat # 32851, 32856)
- 1.7mL microcentrifuge tubes, PCR tubes (e.g. SSIbio Cat # 3247-00), or PCR plates (e.g. Bio-Rad Cat # HSS9641) and magnetic rack compatible with tube selection.
- Centrifuge
- Thermal cycler
- 8-well PCR Strip Tubes with Caps
- Optional: 8- or 12-channel 200  $\mu$ L Multi-Channel Pipette. Recommended when processing more than 4 samples at a time.
- Gel Electrophoresis System (e.g. Bioanalyzer, TapeStation, etc.)
- Deionized / Nuclease-free Water

### 1.4 How to cite Arima HiC in publications

When citing the Arima HiC protocol or kit, one may write: “Hi-C data was generated using the Arima-HiC+ kit, and the Arima Library Prep Module according to the manufacturer’s protocols”.

## Section 2: Library Preparation

**Input:** Proximally Ligated DNA generated using the **Arima HiC+ Kit (PN A510008)**

**Output:** Arima-HiC library ready for sequencing

**Components:**

- **Arima-HiC+, Box A (RT)**
  - Elution Buffer
  - Wash Buffer
- **Arima Library Prep Module Box A (-20°C)**
  - End Repair-A Tailing Enzyme Mix
  - End Repair-A Tailing Buffer
  - T4 DNA Ligase
  - Ligation Buffer
  - Adaptor Oligo Mix
  - 5X Herculase II Buffer with dNTPs
  - Herculase II Fusion DNA Polymerase
- **Arima Library Prep Module Box B (-20°C)**
  - Index Primer Pair 1 - 16
- **Arima Library Prep Module Box C (4°C)**
  - T1 Beads
- **Arima Library Prep Module Box D (RT)**
  - Binding Buffer
- **User Supplied Reagents**
  - DNA Purification Beads
  - 80% ethanol
  - Qubit assay and tubes

**Overview:** Library preparation begins with DNA fragmentation (Section 2.1), DNA size selection (Section 2.2), and biotin enrichment (Section 2.3). Afterwards, the Arima Library Prep Module reagents are used in a custom end-repair, dA-tailing and adapter ligation protocol (Section 2.4). This custom *Arima Library Preparation Protocol* constructs libraries while DNA is bound to T1 Beads. The final step is PCR amplification of the bead-bound Arima-HiC library using the library amplification reagents and index PCR primers from the Arima Library Prep Module, producing the final 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® sequencing instruments. Covaris® instruments are recommended for mechanical fragmentation of DNA, although Diagenode® instruments have also been tested and yield

comparable results. DNA should be fragmented in 100µL of **Elution Buffer (Arima HiC+, Box A)**. Some Covaris® protocols recommend DNA fragmentation in 130µL, but 100µL must be used for DNA fragmentation in the Arima-HiC library preparation protocol. It is recommended to fragment 1,500ng 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.

2.1.1 If necessary, add **Elution Buffer** to bring the sample volume to 100µL. Do not exceed 100µL of volume for DNA fragmentation.

2.1.2 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® publishes optimal DNA fragmentation Power, Duty Factor, Cycles per Burst, and Time for obtaining a target fragment size of 400bp.

2.1.3 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®, TapeStation®) 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® 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 T1 Beads provided in the Arima Library Prep. Module. For the ethanol washes performed below, use sufficient 80% ethanol to fully submerge the magnetized beads.

2.2.1 Transfer fragmented DNA sample from fragmentation tube to either a microfuge tube, PCR tube, or PCR plate. If necessary, add **Elution Buffer** to bring sample volume to 100µL.

2.2.2 Add 60µL of **DNA Purification Beads**, mix thoroughly by pipetting, and incubate at RT for 5 min.

2.2.3 Place sample against magnet and incubate until solution is clear.

2.2.4 Transfer ~160µL of *supernatant* to a new sample tube or well of a PCR plate. Discard beads.

2.2.5 Add 40µL of **DNA Purification Beads** to the ~160µL of supernatant, mix thoroughly by pipetting, and incubate at RT for 5 min.

- 2.2.6 Place sample against magnet and incubate until solution is clear.
- 2.2.7 Discard supernatant. While sample is still against magnet, add 200µL of **80% ethanol**, and incubate at RT for 1 min.
- 2.2.8 Discard supernatant. While sample is still against magnet, add 200µL of **80% ethanol**, and incubate at RT for 1 min.
- 2.2.9 Discard supernatant. While sample is still against magnet, incubate beads at RT for 1 min. to air-dry the beads.
- 2.2.10 Remove the sample from magnet, resuspend beads in 30µL of **Elution Buffer**, and incubate at RT for 5 min.
- 2.2.11 Place sample against magnet, incubate until solution is clear, and transfer supernatant to a new sample tube or well of a PCR plate.
- 2.2.12 Quantify sample using Qubit®. Record this value.
- 2.2.13 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 230µL 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.

**Note: T1 Beads used directly below are from the Arima Library Prep Module. They should not be mistaken for and are NOT interchangeable with the Arima-HiC+ Enrichment Beads nor the Arima-HiC+ QC Beads**

- 2.3.1 Mix T1 Beads very well before using, making sure that the solution is homogenous and there is nothing sticking to the bottom of the bottle.
- 2.3.2 Add 12.5µL of **T1 Beads** from the **Arima Library Prep Box C** into a well of a strip tube for each sample. **Note: These beads are NOT the Enrichment Beads that come with the Arima HiC+ kit.**
- 2.3.3 Wash the **T1 Beads** in each tube by:
- 2.3.4 Add 200uL of **Binding Buffer**.
- 2.3.5 Mix by pipetting up and down 20 times, cap the tubes, and vortex at high speed for 5 - 10 seconds.

2.3.6 Place tubes against a magnet and incubate 5 minutes or until solution is clear.

2.3.7 Discard supernatant and remove the tube from magnet.

2.3.8 Repeat steps 2.3.4 - 2.3.7 two more times for a total of three washes.

2.3.9 Resuspend beads in 200uL of **Binding Buffer**.

2.3.10 Transfer exactly 200ng\* of size-selected DNA into a new microfuge tube, PCR tube, or well of a PCR plate. If necessary, add Elution Buffer to bring sample volume to 30µL.

**\*Biotin enrichment and subsequent library preparation has been optimized to deliver peak performance for DNA inputs of 200ng. Using 200ng of DNA input has been shown to build libraries with sufficient complexity for up to 600M read-pairs of sequence data. If the amount of DNA is less than 200ng, add in the entire amount. (Refer to Table 11 for amplification guidance).**

2.3.11 Add 200µL of washed **T1 Beads** in **Binding Buffer**, mix thoroughly by pipetting, and incubate at RT for 15 min.

2.3.12 Place sample against magnet and incubate until solution is clear.

2.3.13 Discard supernatant and remove sample from magnet.

2.3.14 Wash beads by resuspending in 200µL of **Wash Buffer** and incubate at 55°C for 2 min. Set lid temperature to 85°C.

2.3.15 Place sample against magnet and incubate until solution is clear.

2.3.16 Discard supernatant and remove sample from magnet.

2.3.17 Wash beads by resuspending in 200µL of **Wash Buffer** and incubate at 55°C for 2 min. Set lid temperature to 85°C.

2.3.18 Place sample against magnet and incubate until solution is clear.

2.3.19 Discard supernatant and remove sample from magnet.

2.3.20 Wash beads by resuspending in 100µL of **Elution Buffer**.

2.3.21 Place sample against magnet and incubate until solution is clear.

2.3.22 Discard supernatant and remove sample from magnet.

2.3.23 Resuspend beads in 50µL of Deionized / Nuclease-free Water.

## 2.4 Library Preparation of Enriched Ligation products

**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.

### 2.4.1 End Repair

2.4.1.1 Thaw reagents and mix reagents according to **Table 2**.

Note: Thaw ligation buffer and vortex on high to make sure homogenous (buffer is highly viscous).

**Table 2: Thawing and Mixing Instructions for End Repeat**

Reagent	Thaw Temp.	Mix	Cap
End Repair-A Tailing Buffer	On Ice	Vortex	Yellow
Ligation Buffer	On Ice	Vortex	Purple
End Repair-A Tailing Enzyme Mix	Ice Just Before Use	Inversion	Orange
T4 DNA Ligase	Ice Just Before Use	Inversion	Blue
Adaptor Oligo Mix	On Ice	Vortex	Clear

2.4.1.2 Prepare Ligation master mix to allow equilibration to room temperature before use (see **Table 3**, which includes 12.5% master mix overage for 8 reactions).

**Table 3: Ligation Master Mix Worksheet**

Reagent	Volume per reaction	12.5% extra		# reactions		Final
Ligation Buffer	23µL	25.88µL	x	8	=	207µL
T4 DNA Ligase	2µL	2.25µL	x	8	=	18µL
<b>Total</b>	25µL					225µL

Note: Ligation Master Mix will be used in Step 2.4.3.2 below (After End Repair and dA Tailing)

2.4.1.3 Keep Ligation Master Mix at room temperature for 30 - 45 minutes before use.

### 2.4.2 Prepare End Repair-A Tailing MasterMix using the table below

2.4.2.1 Vortex thawed vial of **End Repair-A Tailing Buffer** for 15 seconds - continue vortexing until no solids are observed.

2.4.2.2 Prepare End Repair/dA-Tailing master mix by combining reagents as listed in Table 4 below, mix well and spin down.

**Table 4: End Repair/dA Tailing Master Mix Worksheet**

Reagent	Volume per Reaction	12.5% extra		# Reactions	=	Final
End Repair-A Tailing Buffer	16 $\mu$ L	18 $\mu$ L	x	8	=	144 $\mu$ L
End Repair-A Tailing Enzyme Mix	4 $\mu$ L	4.5 $\mu$ L	x	8	=	36 $\mu$ L
<b>Total</b>	20 $\mu$ L					180 $\mu$ L

2.4.2.3 Add 20 $\mu$ L of the End Repair/dA-Tailing master mix to each sample containing 50 $\mu$ L of Bead bound HiC library from 2.3.23 in the previous section. Mix well.

2.4.2.4 Program thermal cycler for End Repair and dA-Tailing using the parameters in Table 5. Set reaction volume for 70 $\mu$ L, and the heated lid to 85°C, and press start. Total run time is approx. 30 min.

**Table 5: End Repair and dA-Tailing Thermal Cycler Program**

Temperature	Time
20°C	15 min
72°C	15 min
4°C	Hold

### 2.4.3 Adapter Ligation

- 2.4.3.1 Once thermal cycler has reached 4°C hold step, transfer samples to ice while preparing the ligation reaction.
- 2.4.3.2 Add 25µL of Ligation Master Mix, from step 2.4.1.3 above to the 70µL of bead bound, end repaired and dA-tailed HiC library. Mix well.
- 2.4.3.3 Add 5µL of **Adaptor Oligo Mix** to each sample. Mix well.
- 2.4.3.4 Briefly spin tubes with the bead-bound HiC library, Ligation master mix, and **Adaptor Oligo Mix**.
- 2.4.3.5 Program the thermal cycler for the ligation step with the program specified in **Table 6** below. Set the reaction volume to 100µL and the heated lid to 85°C, and press start. Total time is approx. 30 min.

**Table 6: Adapter Ligation Thermal Cycler Program**

Temperature	Time
20°C	30 min
4°C	Hold

- 2.4.3.6 After the “Ligation” program completes, remove the samples from the thermocycler and quick spin the tubes to remove any liquid from the caps.
- 2.4.3.7 Magnetize beads until liquid is clear. Remove and discard supernatant.
- 2.4.3.8 Resuspend beads in 200µL **Wash Buffer**. Mix by pipetting. Incubate at 55C for 2 min. Set lid temperature to 85°C
- 2.4.3.9 Magnetize beads until liquid is clear. Remove and discard supernatant.
- 2.4.3.10 Resuspend beads in 100µL **Elution Buffer**.
- 2.4.3.11 Magnetize beads until liquid is clear. Remove and discard supernatant.
- 2.4.3.12 Resuspend the beads in 34µL of **Deionized Water** and proceed immediately to Library Amplification below.

## 2.4.4 Amplification of Adaptor-Ligated HiC Library and Sample Indexing

- 2.4.4.1 Thaw and mix the reagents according to the Table 7 below and keep on ice.

**Table 7 : Thawing and Mixing Instructions**

Reagent	Thaw	Mix	Cap
Herculase II Fusion DNA Polymerase	Ice	Pipette	Red
5X Herculase II Buffer with dNTPs	RT	Vortex	Clear
Index Primer Pair 1 - 16	RT	Vortex	foil

2.4.4.2 Thaw only the index primers needed for experiment to minimize freeze-thaw cycles.

2.4.4.3 Determine the unique index pair assignment for each sample using **Table 8** as a reference.

**Table 8: Index Pairs included with the Arima Library Prep Module**

Primer Pair #	P7 Index Forward	P5 Index Forward
1	CAAGGTGA	ATGGTTAG
2	TAGACCAA	CAAGGTGA
3	AGTCGCGA	TAGACCAA
4	CGGTAGAG	AGTCGCGA
5	TCAGCATC	AAGGAGCG
6	AGAAGCAA	TCAGCATC
7	GCAGGTTC	AGAAGCAA
8	AAGTGTCT	GCAGGTTC
9	CTACCGAA	AAGTGTCT
10	TAGAGCTC	CTACCGAA
11	ATGTCAAG	TAGAGCTC
12	GATCATA	ATGTCAAG
13	GACTTGAC	GATCATA
14	CTACAATG	GACTTGAC
15	TCTCAGCA	CTACAATG
16	AGACACAC	TCTCAGCA

2.4.4.4 Prepare appropriate volume of PCR reaction mix in **Table 9** below. Mix well.

**Table 9: PCR Reaction Mix**

Reagent	Volume per Reaction	12.5% extra		# Reactions	=	Final
5x Herculase II Buffer with dNTPs (clear cap)	10 $\mu$ L	11.25 $\mu$ L	x	8	=	90 $\mu$ L
Herculase II Fusion DNA Polymerase (red cap)	1 $\mu$ L	1.125 $\mu$ L	x	8	=	9 $\mu$ L
<b>Total</b>	11 $\mu$ L					99 $\mu$ L

- 2.4.4.5 Add 11 µL of the PCR reaction mixture prepared from the table above to 34 µL of Adaptor Ligated Bead Bound HiC Library from step 2.4.3.12
- 2.4.4.6 Add 5 µL of the appropriate, unique, **Index Primer Pair** to each sample. Make sure to take note of which index was used with each sample.
- 2.4.4.7 Program thermal cycle according to the settings in **Table 10**
- 2.4.4.8 Place the PCR reaction in the thermocycler and press play

**Table 10: Library Amplification Thermal Cycle Program**

Cycles	Temperature	Time
1 X	98°C	2 min.
12 X*	98°C	30 sec.
	60°C	30 sec.
	72°C	1 min.
1 X	72°C	5 min.
1 X	4°C	Hold

Note: The cycle number entered into the thermocycler is typically X-1 (e.g., 12 cycles would be input as return to step 2, 11X) Set Lid Temp to 105°C and the reaction volume to 50 µL.

\*If you are working with challenging or lower-input samples (e.g. <200 ng), please contact technical support.

## 2.5 Purify Amplified Library with Purification Beads

Note: DNA Purification Beads (e.g., AMPure® 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 Library Prep kit.

- 2.5.1 Add 50 µL of **DNA Purification Beads** to each 50 µL Indexed sample. Mix well.
- 2.5.2 Incubate for 5 minutes at room temperature.
- 2.5.3 Place sample against magnet and incubate until solution is clear.
- 2.5.4 Discard supernatant. While sample is still against magnet, add 200 µL of **80% ethanol**, and incubate at RT for 1 min.
- 2.5.5 Discard supernatant. While sample is still against magnet, add 200 µL of **80% ethanol**, and incubate at RT for 1 min.
- 2.5.6 Discard supernatant. While sample is still against magnet, incubate beads at RT for 3 – 5 min. to air-dry the beads.

- 2.5.7 Remove the sample from magnet, resuspend beads in 15µL of Deionized / Nuclease-free Water, and incubate at RT for 5 min.
- 2.5.8 Place sample against magnet and incubate until solution is clear.
- 2.5.9 Remove purified and complete HiC library and transfer to a fresh PCR strip tube.
- 2.5.10 Quantify sample using Qubit® using 1uL.
- 2.5.11 Run the sample from the previous step on a gel or other platform to determine the size distribution of the HiC library.
- 2.5.12 Samples may be stored at -20°C for up to 6 months.

## Section 3: Warranty and Contact Info

### WARRANTY DISCLAIMERS

THE EXPRESS WARRANTIES AND THE REMEDIES SET FORTH ABOVE ARE IN LIEU OF, AND ARIMA GENOMICS AND ITS LICENSORS, SUPPLIERS AND REPRESENTATIVES HEREBY DISCLAIM, ALL OTHER REMEDIES AND WARRANTIES, EXPRESS, STATUTORY, IMPLIED, OR OTHERWISE, INCLUDING, BUT NOT LIMITED TO, ANY WARRANTIES OF MERCHANTABILITY, SATISFACTORY QUALITY, NONINFRINGEMENT OR FITNESS FOR A PARTICULAR PURPOSE, OR REGARDING RESULTS OBTAINED THROUGH THE USE OF ANY PRODUCT OR SERVICE (INCLUDING, WITHOUT LIMITATION, ANY CLAIM OF INACCURATE, INVALID OR INCOMPLETE RESULTS), IN EACH CASE HOWEVER ARISING, INCLUDING WITHOUT LIMITATION FROM A COURSE OF PERFORMANCE, DEALING OR USAGE OF TRADE, OR OTHERWISE. TO THE MAXIMUM EXTENT PERMITTED BY APPLICABLE LAW, ARIMA AND ITS LICENSORS, SUPPLIERS AND REPRESENTATIVES SHALL NOT BE LIABLE FOR LOSS OF USE, PROFITS, REVENUE, GOODWILL, BUSINESS OR OTHER FINANCIAL LOSS OR BUSINESS INTERRUPTION, OR COSTS OF SUBSTITUTE GOODS OR SERVICES, OR FOR ANY SPECIAL, CONSEQUENTIAL, INCIDENTAL, EXEMPLARY OR INDIRECT DAMAGES FOR BREACH OF WARRANTY.

### WARRANTY

All warranties are personal to the Purchaser and may not be transferred or assigned to a third-party, including an affiliate of the Purchaser. The warranty described below excludes any stand-alone third-party goods that may be acquired or used with the Product. Arima Genomics only warrants that the kit reagents will be made and tested in accordance with Arima Genomics manufacturing and quality control processes. Arima Genomics makes no warranty that the reagents provided in this kit will work as intended by the Purchaser or for the Purchaser's intended uses. ARIMA GENOMICS MAKES NO OTHER WARRANTY, EXPRESSED OR IMPLIED. THERE IS NO WARRANTY OF MERCHANTABILITY OR FITNESS FOR A PARTICULAR PURPOSE. The warranty provided herein and the data and descriptions of Arima Genomics products appearing in Arima Genomics product literature and website may not be altered except by express written agreement signed by an officer of Arima Genomics. Representations, oral or written, which are inconsistent with this warranty or such publications are not authorized and if given, should not be relied upon.

The foregoing warranties do not apply to the extent a non-conformance is due to (i) abuse, misuse, neglect, negligence, accident, improper storage, or use contrary to the Documentation or Specifications, (ii) use that is an Excluded Use, (iii) improper handling, (iv) unauthorized alterations, (v) natural disasters, or (vi) use with a third-party's good that is not specified in the product documentation. In the event of a breach of the foregoing warranty, customer shall promptly contact Arima Genomics customer support to report the non-conformance and shall cooperate with Arima Genomics in confirming or diagnosing the non-conformance. Additionally, Arima Genomics may request return shipment of the non-conforming product at Arima Genomics cost. Arima Genomics sole obligation shall be to replace the applicable product or part thereof, provided the customer notifies Arima Genomics within 90 days of any such breach. If after exercising reasonable efforts, Arima Genomics is unable to replace the product, then Arima Genomics shall refund to the Purchaser all monies paid for such applicable product.

### CONTACT US

Website: [www.arimagenomics.com](http://www.arimagenomics.com)

Technical Support: [techsupport@arimagenomics.com](mailto:techsupport@arimagenomics.com)

Order Support: [ordersupport@arimagenomics.com](mailto:ordersupport@arimagenomics.com)

# Appendix A: Sample Sheets for Illumina Sequencing

## A.1 Sequencing Sample Sheets

A "Sample Sheet" is a comma-separated (CSV) document that is used to specify sequencing parameters and samples for Illumina sequencing systems. Arima has pre-filled sample sheets available on the company website under Support > Documentation. [Download](#)