Arima-HiC Kit

User Guide for Mammalian Cell Lines

8 reactions

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Revision History

Document	Date	Description of Change
Material Part Number: A510008 **Document Part Number:** A160134 v00	November 2018	Initial Release
Material Part Number: A510008 **Document Part Number:** A160134 v01	October 2019	• Added BSA to crosslinking buffer in *Crosslinking – Low Input* section. • Added a step to *Crosslinking – Low Input* section. • Added *Crosslinking – Cryopreserved Cells* section. • Added guidance for optional overnight Enzyme D incubation in *Arima-HiC Protocol* section.

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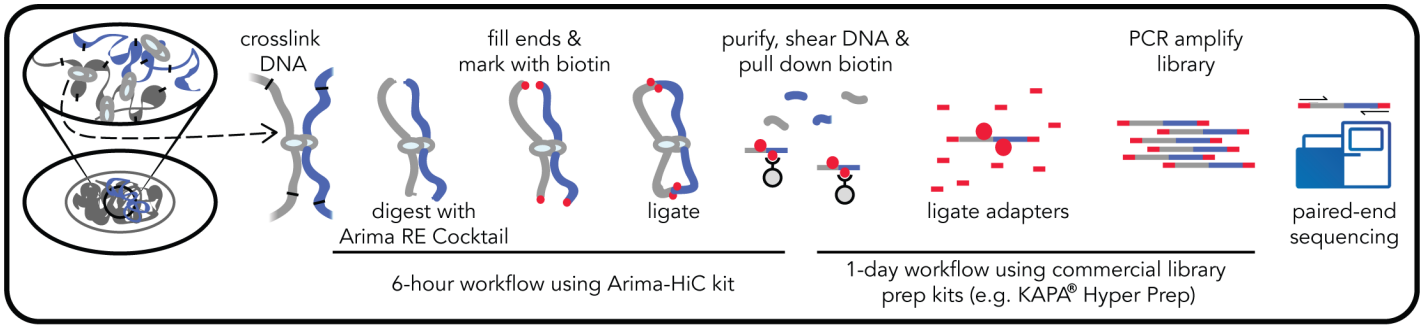

1.1 Arima-HiC Workflow Overview

Arima-HiC is an experimental workflow that captures the sequence and structure (three-dimensional conformation) of genomes. Arima-HiC has been successfully performed on a wide-range of species from the plant and animal kingdoms. As illustrated in the Arima-HiC workflow schematic above, chromatin from a sample source (tissues, cell lines, or blood) is first crosslinked to preserve the genome sequence and structure. The crosslinked chromatin is then digested using a restriction enzyme (RE) cocktail. The 5'-overhangs are then filled in, causing the digested ends to be labeled with a biotinylated nucleotide. Next, spatially proximal digested ends of DNA are ligated, capturing the sequence and structure of the genome. The ligated DNA is then purified, producing pure proximally-ligated DNA. The proximally-ligated DNA is then fragmented, and the biotinylated fragments are enriched. The enriched fragments are then subjected to a custom library preparation protocol utilizing a range of supported commercially available library prep kits. Depending on the choice of library prep kit, a separate Arima-HiC Library Prep user guide is provided that contains a custom protocol for converting proximally-ligated DNA to Arima-HiC libraries.

1.2 Sequencing and Data Analysis

Arima-HiC libraries are sequenced via Illumina® sequencers in "paired-end" mode. The resulting data is referred to as Arima-HiC data. The tools necessary for analyzing Arima-HiC data depend on the application. For example, for studying 3D genome conformation, Arima-HiC data can be processed using publicly available tools such as Juicer (Durand, 2016a) or Hi-C Pro (Servant, 2015), and genome organizational features such as compartments, TADs, and loops can be identified and visualized using tools such as Juicebox (Durand, 2016b). These tools require usage modifications and/or custom input files that are specific to Arima-HiC data, so please contact Technical Support for assistance implementing these tools. Additionally, because paired-end reads of Arima-HiC data can originate from distal sequences along the linear genome, these data capture short- and long-range DNA contiguity information that is valuable for applications such as *de novo* assembly and genome scaffolding. Therefore, Arima-HiC data can be mapped to contigs/unitigs using our mapping pipeline (https://github .com/ArimaGenomics) or Juicer, and then the contigs/unitigs can be scaffolded using tools such as SALSA (Ghurye, 2019) or 3D-DNA (Dudchenko, 2017). Please contact Technical Support for more information.

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Arima-HiC Quick Reference Protocol

Crosslink Sample

Resuspend cells in 20µL ● **Lysis Buffer** OR nuclei in 20µL water[1]
Incubate 15 min. at 4°C

Add 24µL ○ **Conditioning Solution**
Incubate 10 min. at 62°C

Add 20µL ● **Stop Solution 2**
Incubate 15 min. at 37°C

Add 7µL ○ **Buffer A** + 1µL ○ **Enzyme A1** + 4µL ○ **Enzyme A2**
Incubate 30 min. at 37°C followed by 20 min. at 62°C

Add 12µL ● **Buffer B** + 4µL ● **Enzyme B**
Incubate 45 min. at 25°C

Add 70µL ● **Buffer C** + 12µL ● **Enzyme C**
Incubate 15 min. at 25°C

Add 10.5µL ● **Buffer D** + 25µL ● **Enzyme D**
Add 20µL ● **Buffer E**
Incubate 30 min. at 55°C followed by 90 min. at 68°C

Purify DNA
Proceed to library prep using the unique protocol outlined in the User Guide

[1] If nuclei have been isolated prior to lysis step (e.g. from plant tissue, FAC-sorted nuclei)

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Arima-HiC Kit Contents and Storage Info

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Arima-HiC Box Contents & Storage Info

Box A		
Component	**Cap**	**Storage**
Stop Solution 1		20 to 25°C
Elution Buffer		
Wash Buffer*		
Conditioning Solution		
Stop Solution 2		
Buffer D		
Buffer E		

Box B		
Component	**Cap**	**Storage**
Lysis Buffer		-20°C
Buffer A		
Enzyme A1		
Enzyme A2		
Buffer B		
Enzyme B		
Buffer C		
Enzyme C		
Enzyme D		

Box C		
Component	**Cap**	**Storage**
Enrichment Beads*		2 to 8°C
QC Beads**		

* Required for library prep. Depending on choice of library prep kit, the User Guide has a unique library prep protocol to be followed

** Required for Arima-QC1. QC Beads are not interchangeable with Enrichment Beads

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2.1 Handling and Preparation

- Several steps during the *Arima-HiC 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.
- If the *Arima-HiC Protocol* is performed in PCR plates or PCR tubes, ensure to have a total volume capacity of at least 320µL. See Section 2.2 for recommended PCR plates and PCR tubes. Also, ensure that plates and/or tubes are compatible with thermal cyclers and other required equipment. Using seals and caps for PCR plates and tubes is required.
- All kit reagents should be fully thawed and thoroughly mixed before use.
- **Stop Solution 1**, ○**Conditioning Solution**, and ●**Buffer D** from **Box A** may contain precipitates. If present, these precipitates must be dissolved before use. Heating these reagents at 37°C for 5-15 minutes may be necessary to dissolve precipitates.
- During handling and preparation, reagents from **Box A** should be kept at RT.
- During handling and preparation, reagents from **Box B** should be kept on ice, except for **Enzyme D,** which should be kept on ice but warmed to room temperature just before use.
- Enzyme solutions from **Box B** are viscous and require special attention during pipetting.

2.2 User-supplied reagents, consumables, and equipment checklist

- ☐ 1X PBS, pH 7.4 (e.g. Fisher Scientific Cat # 50-842-949)
- ☐ 37% Formaldehyde (e.g. Fisher Scientific Cat # F79-500)
- ☐ Freshly prepared 80% Ethanol
- ☐ DNA Purification Beads (e.g. Beckman Coulter Cat # A63880)
- ☐ Qubit® Fluorometer, dsDNA HS Assay Kit and consumables (e.g. Thermo Fisher Scientific Cat # 32851, 32856)
- ☐ Liquid Nitrogen or dry ice
- ☐ 15mL conical tubes
- ☐ 1.7mL microcentrifuge tubes, PCR tubes (SSIbio® Cat # 3247-00), or PCR plates (Bio-Rad® Cat # HSS9641) and magnetic rack compatible with tube selection.
- ☐ Centrifuge
- ☐ Thermal cycler (if performing Arima-HiC in PCR tubes or PCR plate)
- ☐ Thermomixer (if performing Arima-HiC in 1.7mL microcentrifuge tubes)
- ☐ BSA (e.g. NEB® Cat # B9000S)

2.3 Optimal read length, sequencing depth, and number of Arima-HiC reactions per sample

Arima-HiC libraries must be sequenced in paired-end mode, and are compatible with most Illumina® sequencing machines (e.g. MiSeq®, NextSeq®, HiSeq®, NovaSeq™) and a variety of read lengths. We generally recommend 2x150bp read length on the HiSeq® or NovaSeq™ instruments to optimize for sequencing throughput and Arima-HiC data alignment quality, although shorter read lengths (e.g. 2x50bp, 2x100bp) and lower throughput instruments can certainly be used for certain applications of Arima-HiC data such as 3D genome conformation analysis and genome scaffolding.

The optimal sequencing depth for Arima-HiC libraries also depends on the application. For studying 3D genome conformation, the ability to detect certain genome organization features depends on the sequencing depth. For ~3Gb genomes such as mouse and human, we generally recommend obtaining at least 600 million read-pairs *per biological condition* for high-resolution analyses of A/B compartments, TADs, and chromatin loops. One way of obtaining at least 600 million read-pairs is by combining at least 300 million read-pairs from 2 biological replicates. In doing so, you will be able to assess the overall reproducibility of the Arima-HiC data across replicates, and then used the combined replicate Arima-HiC dataset for high-resolution chromatin conformation analyses. Alternatively, one can obtain at least 600 million read-pairs *per biological replicate* and then use the common set of identified genome conformational features across replicates as a "high confidence" set of structural features supported by their observation in both replicates. For lower resolution analyses of A/B compartments and TADs, we generally recommend obtaining at least 300 million read-pairs per biological condition. For help estimating the optimal sequencing depth for different genome sizes or analysis goals, please contact Technical Support.

For applications such as *de novo* assembly and genome scaffolding, the required sequencing depth can vary depending on the quality of contig/unitigs that are being scaffolded using Arima-HiC data. For a 3Gb genome, we recommend obtaining up to 600M read-pairs, as this is the amount of sequencing that is currently utilized from Arima-HiC libraries for genome scaffolding by the Vertebrate Genome Project (VGP) consortia. The amount of sequencing required scales linearly with the genome size (e.g. up to 200M read-pairs for a 1Gb genome).

Lastly, it is important to note that each Arima-HiC library should pass the Arima-QC2 assay and be evaluated for library complexity prior to deep sequencing. As a general rule, each Arima-HiC library should be complex enough to sequence up to ~600M read-pairs without reaching saturation. If >600M read-pairs of Arima-HiC data are needed, it may be more efficient to sequence a second Arima-HiC library than sequence deeper into the first Arima-HiC library.

2.4 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, according to the manufacturers protocols". Please reference the catalog number found on the kit packaging.

Crosslinking – Standard Input

Input: Cells collected from cell culture
Output: Crosslinked cells

Before you begin: The Arima-HiC workflow for mammalian cell lines begins with the harvesting and crosslinking of at least 1 million cells, but performs optimally with 5-10 million mammalian cells. If fewer than 1 million cells are available, please follow the *Crosslinking – Low Input* protocol in the following section. The crosslinking protocol below involves several cell pelleting centrifugations. During these centrifugations, pellet your specific cell types at a speed and duration as you normally would. Alternatively, we generally recommend centrifuging for 5 min at 500 x G.

1. Harvest cells from cell culture using standard protocols and pellet cells by centrifugation.
2. Resuspend in cell culture media, obtain a cell count by hemocytometer or automated cell counting methods.
3. Transfer 5-10 million cells to be crosslinked into a new 15mL conical tube, pellet cells by centrifugation and remove supernatant.
4. Resuspend cells in 5mL of RT **1X PBS**.
5. Add 286µL of **37% formaldehyde**, bringing the final formaldehyde concentration to 2%.
6. Mix well by inverting 10 times and incubate at RT for 10 min.
7. Add 460µL of **Stop Solution 1,** mix well by inverting 10 times and incubate at RT for 5 min.
8. Place sample on ice and incubate for 15 min.
9. Pellet cells by centrifugation.
10. Discard supernatant.
11. Resuspend cells in 5mL **1X PBS**.
12. Aliquot cells into several new tubes, with 1 x 10^6 cells per aliquot. Mix sample by inversion between aliquots to ensure all aliquots are equally homogeneous.
13. Pellet cells in all aliquots by centrifugation.
14. Discard supernatant leaving only the crosslinked cell pellet and no residual liquid.
15. Freeze samples on dry ice or liquid nitrogen, and store at -80°C until ready to proceed to the *Estimating Input Amount – Standard Input* protocol in a following section.

Crosslinking – Low Input

Input: Cells collected from cell culture, cell sorting, or other sources
Output: Crosslinked cells

Before you begin: The Arima-HiC workflow for low input mammalian cells begins with the collection and crosslinking of fewer than 1 million cells. The crosslinking protocol below involves several cell pelleting centrifugations. During these centrifugations, pellet your specific cell types at a speed and duration that is higher than you normally would to ensure minimal sample loss. Alternatively, we generally recommend centrifuging for a minimum of 5 min at 2500 x G, and faster speeds can be used to ensure maximum cell pelleting efficiency. The cell pellets may be very difficult or impossible to see by eye, so we advise to make special note of where the cell pellet would be expected in the bottom side of the sample tube after centrifugation and to avoid that region when pipetting.

Note: Steps 2-4 and Step 8 involve the addition of reagents pertaining to crosslinking or washing. Please note that each step involves mixing by *inversion*. Do not mix by pipetting to ensure minimal sample loss during the crosslinking workflow.

1. Collect cells in a 1.7mL microfuge tube and pellet cells by centrifugation.
2. Add 1mL of RT **1X PBS containing 3% BSA (v/v)** and mix by inverting 5 times.
3. Add 57µL of **37% formaldehyde**, mix well by inverting 10 times and incubate at RT for 10 min. with occasional inversion.
4. Add 91.9µL of **Stop Solution 1,** mix well by inverting 10 times and incubate at RT for 5 min. with occasional inversion.
5. Place sample on ice and incubate for 15 min.
6. Pellet cells by centrifugation.
7. Discard supernatant.
8. Add 1mL of RT **1X PBS containing 3% BSA (v/v)** and mix by inverting 5 times.
9. Pellet cells by centrifugation.
10. Discard supernatant leaving only the crosslinked cell pellet and no residual liquid.
11. Proceed directly to the *Arima-HiC Protocol* section, or freeze samples on dry ice or liquid nitrogen and store at -80°C until ready to proceed to the *Arima-HiC Protocol* section.

Crosslinking – Cryopreserved Cells

Input: Cryopreserved cells
Output: Crosslinked cells

Before you begin: We recommend that the Arima-HiC workflow for mammalian cell lines begin with the crosslinking of cells harvested from cell culture, however, under certain circumstances one can also crosslink cells preserved in a cryogenic "freeze" media such as a mixture of complete cell culture media, FBS, and DMSO. A typical example would be cells that were once cultured and then collected at 5 million cells per mL in cryogenic "freeze" media, and stored in a liquid nitrogen tank. The crosslinking protocol below involves several cell pelleting centrifugations. During these centrifugations, pellet your specific cell types at a speed and duration as you normally would. Alternatively, we generally recommend centrifuging for 5 min at 500 x G.

1. Fill a 15mL conical tube with 4mL of **1X PBS**.
2. Thaw the cryopreserved cells in a 37°C water bath.

Note: In the following step, the entire contents of the cryopreserved cell sample (i.e. cells *and* the cryogenic media) are transferred into the conical tube containing PBS. *Do not* centrifuge the cells to try and remove the cryogenic freeze media. The following step also assumes the cells are preserved in 1mL of cryogenic freeze media, and transferring the cells into the PBS will bring the total volume to 5mL. If the cells are not frozen in 1mL of cryogenic freeze media, adjust the volume of PBS so that the total sample volume after Step 3 will be 5mL.

3. Gently transfer cells, including the cryogenic freeze media, into the conical tube containing 4mL of **1X PBS**, bringing the total volume to 5mL.
4. Add 286µL of **37% formaldehyde**, bringing the final formaldehyde concentration to 2%.
5. Mix well by inverting 10 times and incubate at RT for 10 min.
6. Add 460µL of **Stop Solution 1,** mix by inverting 10 times and incubate at RT for 5 min.
7. Place sample on ice and incubate for 15 min.
8. Pellet cells by centrifugation and discard supernatant.
9. Resuspend cells in 5mL **1X PBS**.
10. Aliquot cells into several new tubes, with 1 x 10^6 cells per aliquot. Mix sample by inversion between aliquots to ensure all aliquots are equally homogeneous.
11. Pellet cells in all aliquots by centrifugation.
12. Discard supernatant leaving only the crosslinked cell pellet and no residual liquid.
13. Freeze samples on dry ice or liquid nitrogen, and store at -80°C until ready to proceed to the *Estimating Input Amount – Standard Input* protocol in a following section.

Estimating Input Amount – Standard Input

Input: Crosslinked cells
Output: Purified genomic DNA

Before you begin: The *Estimating Input Amount* protocol is required if one does *not* know how many crosslinked cells will comprise 500ng-5µg of DNA, and if sufficient cells are available to perform this protocol. Arima-HiC reactions are optimally performed on crosslinked cells comprising ~500ng-5µg of DNA. The *Estimating Input Amount* protocol measures the amount of DNA obtained per 1 x 10^6 crosslinked cells, which guides the calculation of the optimal cellular input for an Arima-HiC reaction. The Arima-HiC kit contains enough reagents to perform this protocol on 8 samples. This protocol concludes with a descriptive example of how to estimate the optimal number of crosslinked cells to use per Arima-HiC reaction.

Note: Step 2 requires addition of several reagents in the same step. These reagents should be combined into master mixes with 10% excess volume before use.

1. Thaw one aliquot of 1 x 10^6 cells prepared during the *Crosslinking – Standard Input* or *Crosslinking – Cryopreserved Cells* protocol.
2. Add 209.5µL of a master mix containing the following reagents:

Reagent	Volume per reaction	10% extra		# reactions		Final
Elution Buffer	174µL	191.4µL	x	2	=	382.8µL
● Buffer D	10.5µL	11.55µL	x	2	=	23.1µL
● Enzyme D	25µL	27.5µL	x	2	=	55µL
Total	**209.5µL**					460.9µL

3. Add 20µL of ● **Buffer E**, mix gently by pipetting, and incubate as follows. If using a thermal cycler, set the lid temperature to 85°C.

Temperature	Time
55°C	30 min.
68°C	90 min.
4°C	∞

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-HiC kit.

4. Add 150µL of **DNA Purification Beads**, mix thoroughly, and incubate at RT for 5 min.

5. Place sample against magnet, and incubate until solution is clear.
6. Discard supernatant. While sample is still against magnet, add 400µL of 80% ethanol, and incubate at RT for 1 min.
7. Discard supernatant. While sample is still against magnet, add 400µL of 80% ethanol, and incubate at RT for 1 min.
8. Discard supernatant. While sample is still against magnet, incubate beads at RT for 3 – 5 min. to air-dry the beads.
9. Remove sample from magnet, resuspend beads thoroughly in 20µL of **Elution Buffer**, and incubate at RT for 5 min.
10. Place sample against magnet, incubate until solution is clear, and transfer supernatant to a new tube.
11. Quantify sample using Qubit®. The total DNA yield corresponds to the amount of DNA obtained from 1 x 10^6 mammalian cells.
12. Estimate how many mammalian cells to use per Arima-HiC reaction. See the example description below:

    Example: In the following *Arima-HiC Protocol*, it is recommended to use crosslinked cells corresponding to at least 500ng of DNA per Arima-HiC reaction, but no more than 5µg of DNA. If 250ng of DNA was obtained *per 1 x 10^6 mammalian cells* as calculated in step 11, one can estimate that *at least* 2 x 10^6 crosslinked cells should be used per Arima-HiC reaction (~500ng of DNA). More crosslinked cells should be used if available, as long as the total DNA per reaction is not more than 5µg. If possible, we recommend aiming to use crosslinked cells comprising 3µg of DNA per Arima-HiC reaction. Additionally, please note that the crosslinked cell pellet for one Arima-HiC reaction should occupy no more than 20µL of volume in the sample tube. If the crosslinked cell pellet comprises 500ng-5µg of DNA but occupies greater than 20µL of volume, aliquot the cells into multiple Arima-HiC reactions such that the sum of the DNA input from all reactions is at least 500ng and each cell pellet occupies no more than 20µL of volume, or contact Technical Support for additional guidance.

    Recommended HiC Input Amount Explanation: The recommendation to use crosslinked cells comprising at least 500ng of DNA is only a *general* recommendation. If crosslinked cells comprising at least 500ng of DNA cannot be obtained, one should proceed with the *Arima-HiC Protocol* as described in this user guide and then use our validated low-input library prep protocol.

Input: Crosslinked cells containing ~500ng-5µg of DNA
Output: Proximally-ligated DNA

Before you begin: The cell pellet for one Arima-HiC reaction should occupy no more than 20µL of volume and should be devoid of any residual liquid. If the cell pellet occupies greater than 20µL of volume, aliquot the cells such that the sum of the DNA input from all reactions is between 500ng-5µg and each cell pellet occupies no more than 20µL of volume, or contact Technical Support for additional guidance. Note that steps 2 – 3 require consecutive heated incubations. Make sure your thermal device(s) are set to 62°C and 37°C for these incubations. The safe stopping point in this section is after completing Step 21.

Note: Choose to perform either Step 1a if the input sample type is crosslinked cells, or Step 1b only if the input sample type is crosslinked *nuclei* that have been previously purified from cells.

1a. Resuspend one reaction of crosslinked cells in 20µL of ● **Lysis Buffer** in a tube or a well of a PCR plate, and incubate at 4°C for 15 min.

1b. Resuspend one reaction of purified crosslinked nuclei in 20µL of **Water** in a tube or a well of a PCR plate and procced to the next step.

2. Add 24µL of ○ **Conditioning Solution**, mix gently by pipetting, and incubate at 62°C for 10 min. If using a thermal cycler, set the lid temperature to 85°C.

3. Add 20µL of ● **Stop Solution 2**, mix gently by pipetting, and incubate at 37°C for 15 min. If using a thermal cycler, set the lid temperature to 85°C.

Note: Steps 4, 6, 8 and 10 require addition of several reagents in the same step. These reagents should be combined into master mixes following the master mix tables.

4. Add 12µL of a master mix containing the following reagents:

Reagent	Volume per reaction	10% extra		# reactions		Final
○ Buffer A	7µL	7.7µL	x	2	=	15.4µL
○ Enzyme A1	1µL	1.1µL	x	2	=	2.2µL
○ Enzyme A2	4µL	4.4µL	x	2	=	8.8µL
Total	**12µL**					26.4µL

5. Mix gently by pipetting, and incubate as follows. If using a thermal cycler, set the lid temperature to 85°C. Note that there are sequential incubations at different temperatures:

Temperature	Time
37°C	30 min.*
65°C	20 min.
25°C	10 min.

* Optimal performance can be achieved with incubation durations between 30 and 60min.

6. Add 16µL of a master mix containing the following reagents:

Reagent	Volume per reaction	10% extra		# reactions		Final
● Buffer B	12µL	13.2µL	x	2	=	26.4µL
● Enzyme B	4µL	4.4µL	x	2	=	8.8µL
Total	**16µL**					35.2µL

7. Mix gently by pipetting, and incubate at room temperature (RT) for 45 min.

8. Add 82µL of a master mix containing the following reagents:

Reagent	Volume per reaction	10% extra		# reactions		Final
● Buffer C	70µL	77µL	x	2	=	154µL
● Enzyme C	12µL	13.2µL	x	2	=	26.4µL
Total	**82µL**					180.4µL

9. Mix gently by pipetting, and incubate at RT for 15 min.

Note: Enzyme D should be warmed to RT to prevent precipitation in the below master mix.

10. Add 35.5µL of a master mix containing the following reagents:

Reagent	Volume per reaction	10% extra		# reactions		Final
● Buffer D	10.5µL	11.55µL	x	2	=	23.1µL
● Enzyme D	25µL	27.5µL	x	2	=	55µL
Total	**35.5µL**					78.1µL

11. Add 20µL of ● **Buffer E**, mix gently by pipetting, and incubate as follows. If using a thermal cycler, set the lid temperature to 85°C.

Temperature	Time
55°C	30 min.
68°C	90 min.
25°C*	10 min.*

* To provide flexibility, this incubation can also be held overnight at 4°C. *Do not* incubate at 68°C for longer than 90 min. unless doing so using a thermal cycler with a heated lid.

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-HiC kit.

12. Add 100µL of **DNA Purification Beads**, mix thoroughly, and incubate at RT for 5 min.
13. Place sample against magnet, and incubate until solution is clear.
14. Discard supernatant. While sample is still against magnet, add 300µL of 80% ethanol, and incubate at RT for 1 min.
15. Discard supernatant. While sample is still against magnet, add 300µL of 80% ethanol, and incubate at RT for 1 min.
16. Discard supernatant. While sample is still against magnet, incubate beads at RT for 3 – 5 min. to air-dry the beads.
17. Remove sample from magnet, resuspend beads thoroughly in 100µL of **Elution Buffer**, and incubate at RT for 5 min.
18. Place sample against magnet, incubate until solution is clear, and transfer supernatant to a new tube.
19. Quantify sample using Qubit®.

Note: If the proximally-ligated DNA yield is less than 275ng, we recommend skipping the Arima-QC1 assay mentioned in Step 20 and described in the following *Arima-QC1 Quality Control* section, and strongly recommend performing the Arima-QC2 assay described in our *Arima-HiC Library Preparation* user guide for low input samples.

20. Transfer 75ng of sample into a new tube labelled "Arima-QC1**",** and add **Elution Buffer** to Arima-QC1 to bring the volume to 50µL. The "Arima-QC1" sample should now contain 75ng of proximally-ligated DNA in 50µL of **Elution Buffer**. Store at -20°C until use in the following *Arima-QC1 Quality Control* protocol.
21. Store all remaining samples at -20°C until ready to proceed to library preparation following an accompanying *Arima-HiC Library Preparation* user guide**.**

Arima-QC1 Quality Control

Before you begin: The following protocol quantifies the fraction of proximally-ligated DNA that has been labeled with biotin, and is a quality control metric after completing the *Arima-HiC Protocol* but before proceeding to library preparation. The *Arima-QC1 Quality Control* protocol involves using **QC Beads** to enrich an aliquot of proximally-ligated DNA, which is then quantified using a Qubit® fluorometer. Unlike standard Qubit® readings which involve quantifying a transparent unobstructed DNA sample, the Arima-QC1 value is obtained by quantifying DNA that is still bound to the **QC Beads**. This protocol can be performed in either plates or tubes. Set your thermal device (thermal cycler or thermomixer) to hold at 55°C. After completing the *Arima-QC1 Quality Control* protocol, use the provided **Arima-HiC QC Worksheet** to determine the Arima-QC1 values.

1. If necessary, thaw the "Arima-QC1" samples prepared during Step 20 of the *Arima-HiC Protocol* in the previous section.
2. Add 50µL of ● **QC Beads**, mix thoroughly by pipetting, and incubate at RT for 15 min.
3. Place sample against magnet, and incubate until solution is clear.
4. Discard supernatant, and remove sample from magnet.
5. Wash beads by resuspending in 200µL of **Wash Buffer**, and incubate at 55°C for 2 min.
6. Place sample against magnet, and incubate until solution is clear.
7. Discard supernatant, and remove sample from magnet.
8. Wash beads by resuspending in 200µL of **Wash Buffer**, and incubate at 55°C for 2 min.
9. Place sample against magnet, and incubate until solution is clear.
10. Discard supernatant, and remove sample from magnet.
11. Wash beads by resuspending in 100µL of **Elution Buffer**.
12. Place sample against magnet, and incubate until solution is clear.
13. Discard supernatant, and remove sample from magnet.
14. Resuspend beads in 7µL of **Elution Buffer.** Proceed to next step with resuspended beads.

Note: The following step involves the quantification of the *bead-bound* DNA using the Qubit® dsDNA HS Assay Kit.

15. Quantify the total amount of *bead-bound DNA* using Qubit®. Use 2µL of thoroughly mixed bead-bound DNA for the Qubit® assay.
16. Determine the **Arima-QC1** value by following the **Arima-HiC QC Worksheet**. High quality Arima-QC1 values are expected to be >15%. If the Arima-QC1 value did not obtain a 'PASS' status, please contact Technical Support for troubleshooting assistance.

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