

ProxiMeta Hi-C Kit Protocol



For crude-sample proximity ligation library prep from metagenomic samples, for Illumina® sequencing.

This document can be used with the following Hi-C Kits:

Proximo (Microbe)	ProxiMeta
KT1045	KT1145
	KT5045

Please review this protocol thoroughly before you start processing your samples. If you have any questions, please contact us at support@phasegenomics.com.

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Introduction

Proximity ligation or Hi-C is one of a number of “chromosome conformation capture” (3C) methods, originally designed to study the spatial organization of chromatin.^{1,2} Hi-C employs cost-effective, high-throughput, short-read sequencing to identify the nucleotide sequences of genomic loci that are in close proximity in three-dimensional space, but may be megabases apart in the linear genome sequence. This powerful methodology has enabled significant improvements in genome assembly of humans and other species, as well as structural variant and epigenetic analysis.³ In addition, it has unlocked many applications in metagenomics and microbiology.⁴

Phase Genomics’ ProxiMeta Platform employs Hi-C to measure the physical proximity between DNA sequences in the same cell. This Hi-C kit is designed for the preparation of two (KT1045, KT1145) or eight (KT5045) dual-indexed Hi-C libraries from whole-cell microbial samples. The entire protocol, from sample to sequencing-ready library for Illumina paired-end sequencing can be completed in 1.5 to 3 days.

This kit is suitable for all types of whole-cell microbial inputs. Any microbial sample type (from soil to feces) may be used, but extracted DNA is not a suitable input. Please refer to the **Sample Types and Preparation** section to determine if your type of microbial sample requires additional preparation or reagents.

The ProxiMeta workflow is illustrated in Figure 1 on the next page.

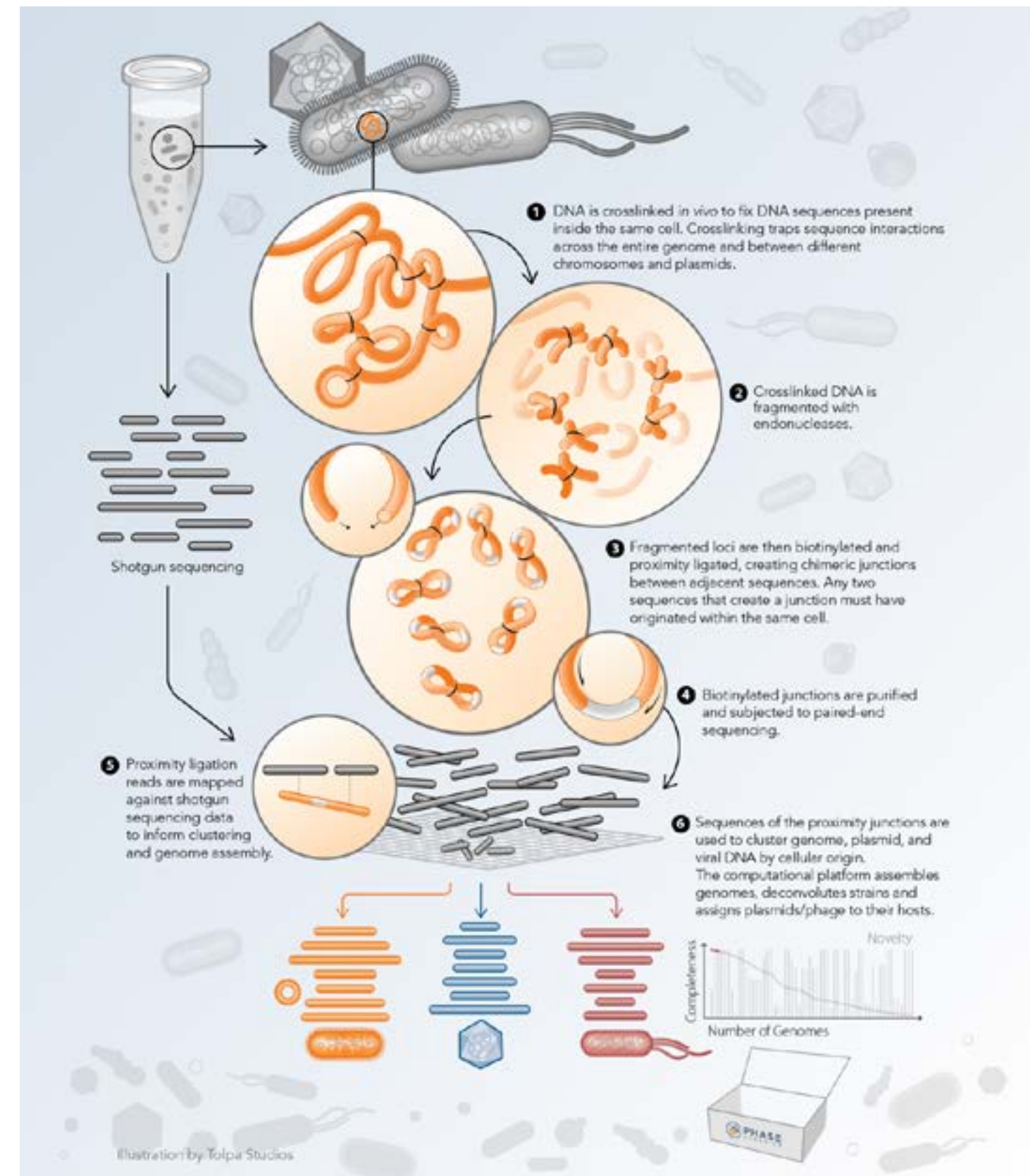


Figure 1. The ProxiMeta workflow

References

1. Lieberman-Aiden E, et al. Comprehensive mapping of long-range interactions reveals folding principles of the human genome. Science 2009; 326 (5950): 289-293. doi: 10.1126/science.1181369.

2. Van Berkum NL, et al. Hi-C: a method to study the three-dimensional architecture of genomes. J. Vis. Exp. 2010; 39: e1869. doi: 10.3791/1869.

3. <http://phasegenomics.com/applications/human-genomics-epigenomics/>

4. <http://phasegenomics.com/applications/metagenomics-microbiology/>

Kit Specifications

Reagent Storage and Preparation

Cap/Label Color	Top Label	Tube Label	Storage Temperature (°C)	Used in Step	Before Starting
	Crosslink Solution	Crosslinking Solution	-25 to +8°C	1.1	Thaw and warm to RT
	Quench Solution	Quenching Solution	-25 to +25°C	1.3	Thaw and warm to RT ¹
	Lysis Buffer 1	Lysis Buffer 1	-25 to +25°C	2.1-2.2	Thaw and warm to RT
	Lysis Buffer 2	Lysis Buffer 2	-25 to +25°C	2.7	Thaw and warm to RT
	Lysis Tube	Lysis Tube	-25 to +25°C	2.2	
	Fragment Buffer	Fragmentation Buffer	-25 to -15°C	3.3	Thaw on ice
	Fragment Enzyme	Fragmentation Enzyme	-25 to -15°C	3.4	Thaw on ice
	Ligation Buffer	10X Ligation Buffer	-25 to -15°C	4.2	Thaw on ice
	Ligation Enzyme	Ligation Enzyme	-25 to -15°C	4.3	Thaw and warm to RT
	RX Enzyme	RX Enzyme	-25 to -15°C	5.1	Thaw on ice
	Elution Buffer	Elution Buffer	-25 to +25°C	6.7, 10.10	Thaw and warm to RT
	Recovery Beads	Recovery Beads	+2 to +8°C	2.9, 6.2, 10.3, 10.6	Thaw and warm to RT
	Recovery Wash Buffer	Recovery Wash Buffer	+2 to +8°C	6.4, 6.5, 10.9	Warm to RT. Add 95%-100% Ethanol according to the instructions on the bottle. ²
	Strept Beads	Streptavidin Beads	+2 to +8°C	7.1	Thaw and warm to RT
	Bead Bind	Bead Binding Buffer	-25 to +25°C	7.4	Thaw and warm to RT
	Wash Buffer 1	Wash Buffer 1	-25 to +25°C	7.2, 7.3, 7.9, 8.15	Thaw and warm to RT
	Wash Buffer 2	Wash Buffer 2	-25 to +25°C	7.7, 7.9, 8.13, 8.15	Thaw and warmx to RT
	FERAT Buffer	Frag, End-Repair & A-Tail Buffer	-25 to -15°C	8.5	Thaw on ice
	FERAT Enzyme	Frag, End-Repair, & A-Tail Enzyme	-25 to -15°C	8.6	Thaw on ice
	Universal Adapter	Universal Adapter	-25 to -15°C	8.8	Thaw on ice
	Adapter Ligation Mix	Adapter Ligation Mix	-25 to -15°C	8.8	Thaw on ice
	PCR Mix	2X PCR Mix	-25 to -15°C	9.2	Thaw on ice
	Index	Index Mix	-25 to -15°C	9.3	Thaw on ice
	10X CRB	10X CRB	-25 to -15°C	1.6, 2.6, 2.11, 3.4, 3.5	Dilute to 1X in molecular biology-grade water before use. ⁴

¹May be warmed to 37°C to dissolve any precipitate that is present after freezing and thawing

²Prepared Recovery Wash Buffer may be stored at +2 to +8°C for up to 6 months

³Reference code varies depending on your unique index mixes

⁴1X CRB is stable when stored at room temperature for up to 1 year

Kit Contents

		KT1045/KT1145			KT5045			
-25° to -15°C Box								
Cap/Label Color	Tube Label	Reference Code	Volume per tube	No. of Tubes	Reference Code	Volume per tube	No. of Tubes	
	Crosslinking Solution	KS0015/KS0024	1 mL/1.5 mL	2	KS0016	10 mL	1	
	Quenching Solution	KS0003/KS0026	1 mL/1.8 mL	1	KS0003/KS0026	1 mL/1.8 mL	1	
	Lysis Buffer 1	KB0036/KB0055	1.5 mL	1	KB0037/KB0073	6 mL/ 14 mL	1	
	Lysis Buffer 2	KB0003/KB0056	500 µL/1.2 mL	1	KB0003/KB0056	500 µL/1.2 mL	1	
	Lysis Tube	KC0001	500 µL	2	KC0001	500 µL	8	
	Fragmentation Buffer	KB0005	300 µL	1	KB0050	1.2 mL	1	
	Fragmentation Enzyme	KE0024	22 µL	1	KE0022	90 µL	1	
	10X Ligation Buffer	KB0051	20 µL	1	KB0053	80 µL	1	
	Ligation Enzyme	KE0026	10 µL	1	KE0028	40 µL	1	
	RX Enzyme	KE0007	10 µL	1	KE0017	40 µL	1	
	Elution Buffer	KB0015/KB0059	350 µL/1.7 mL	1	KB0028/KB0059	1.1 mL/1.7 mL	1	
	Bead Binding Buffer	KB0012/KB0061	250 µL/1.5 mL	1	KB0025/KB0061	800 µL/1.5 mL	1	
	Wash Buffer 1	KB0047/KB0062	7 mL/10 mL	1	KB0047/KB0062	7 mL/10 mL	1	
	Wash Buffer 2	KB0048/KB0063	7 mL/10 mL	1	KB0048/KB0063	7 mL/10 mL	1	
	Frag, End-Repair & A-Tail Buffer	KB0043	8 µL	1	KB0045	32 µL	1	
	Frag, End-Repair, & A-Tail Enzyme	KE0029	12 µL	1	KE0031	48 µL	1	
	Universal Adapter	KS0011	10 µL	1	KS0013	40 µL	1	
	Adapter Ligation Mix	KE0032	40 µL	1	KE0034	160 µL	1	
	2X PCR Mix	KE0035	50 µL	1	KE0037	200 µL	1	
	10X CRB	KB0054/KB0069	1.6 mL/1 mL	1	KB0054/KB0069	1.6 mL/1 mL	1	
	PCR Primer Mix	KP000N	5 µL each	2	KP000N³	5 µL each	8	
+2° to +8°C Box								
	Recovery Beads	KR0011	600 µL	1	KR0012	1.2 mL	2	
	Recovery Wash Buffer	KB0041/KB0060	500 µL/2 mL	1	KB0060	2 mL	1	
	Streptavidin Beads	KR0002	40 µL	1	KR0005	160 µL	1	
	PGShield™	KS0013	10 mL	1	KS0013	10 mL	2	

Shipping, Storage, and Handling

ProxiMeta and Proximo Hi-C Kits are shipped on cold packs. Upon receipt, remove the container with the **Recovery Beads and Streptavidin Beads**, and store at +2 to +8°C. If either the **Recovery Beads and Streptavidin Beads** are stored at freezing temperatures (below 0°C) they will no longer functional and should be replaced. Store the remainder of the kit between -25 and -15°C. When stored under these conditions and handled appropriately, all kit components will retain full activity until the expiration date indicated on the kit label.

Always ensure that all components are fully thawed and thoroughly mixed prior to use. Keep all enzymes and Adapter Ligation Mix on ice at all times during use.

Safety Information

When working with chemicals, always wear personal protective gear, such as a lab coat, disposable gloves, and safety glasses. For more information, consult the appropriate safety data sheets (SDS).

These are available online at <https://phasegenomics.com/product-literature/>

Phase Genomics PGShield™

Phase Genomics PGShield™ is a new preservative system for room temperature stabilization of biological samples. Unlike many lysis-based approaches, PGShield™ is designed to keep cells and cell structures intact until processing.

General Properties

- Nontoxic to humans and the environment
- Nonflammable
- Bacteriostatic/Bacteriocidal
- Slightly viscous
- Extended storage conditions
 - ▶ -80°C indefinitely
 - ▶ +4°C up to 1 year
 - ▶ Room temperature for up to 4 months

Sample types

- Bacterial pellets
 - ▶ Fresh cultured cells (media removed)
 - ▶ Environmental collection (water or liquid removed)
- Water filters
- Soil
- Rumen
- Fecal samples

Important Notes for Use

PGShield™ is best used as an immersive agent for cells/tissue at maximum concentration. Do not dilute PGShield™ before use and keep it at no less than 90% concentration. While the actual volume required may vary by sample type, we recommend starting with 1 mL PGShield™ to approximately 300 mg sample.

Other Reagents, Equipment and Consumables Required

Reagents

The following molecular-biology grade reagents are required to complete this protocol. Ensure that reagents are free of DNA, RNA and nucleases.

- 95 - 100% ethanol
- Molecular biology-grade water

Equipment and Consumables

The following general laboratory equipment and consumables are needed for this protocol.

- Calibrated 2 – 10 µL pipette and filtered tips
- Calibrated 10 – 100 µL pipette and filtered tips
- Calibrated 200 – 1000 µL pipette and filtered tips
- 1.5 or 2 mL microcentrifuge tubes
- 0.2 mL PCR tubes
- Magnetic tube rack/magnet for 0.2 mL PCR tubes and for 2 mL microcentrifuge tubes (if in step 3.9 the bead-bound material is in 2 mL tubes).
- Microcentrifuge capable of $\geq 10,000 \times g$
- Thermocycler
- Vortex mixer
- [Qubit™ Fluorometer](#) and [Qubit dsDNA DNA HS Assay Kit](#) (Thermo Fisher Scientific), or similar fluorometric assay for the quantification of double-stranded DNA

Additional Reagents and Equipment

The following molecular-biology grade reagents may be recommended or required for certain sample type inputs. See **Sample Types and Preparation** to determine what additional reagents your library prep may require.

- OptiPrep™ (Or similar 60% iodixanol solution - not included)
- Formaldehyde
- Glycine

Sample Types and Preparation

This protocol is suitable for a wide range of microbial inputs, from soil to fecal samples. Consult the table below for required inputs and modifications to the standard protocol for your sample type. Please note that these are guidelines and optimization may still be required for your sample(s).

Sample Type	Suggested Input	Before you start:
Microbial cell pellet	1 - 50 million cells	- Centrifuge and pellet cells at 10,000 x g for 5 min, (or according to your standard pelleting protocol) and remove excess media or buffer - Proceed to 1. Recommended Pre-Processing or 2. Crosslinking.
Fecal sample	50 - 200 µL	- Centrifuge and pellet cells at 10,000 x g for 5 min, (or according to your standard pelleting protocol) and remove excess media or buffer - Proceed to 1. Recommended Pre-Processing or 2. Crosslinking.
Soil (High biodensity)	1 - 2 g	- See Appendix A-1 for bacterial enrichment protocol. - If you suspect your sample may contain contaminants that could interfere with PCR, use Appendix A-2. - Proceed to 1. Recommended Pre-Processing or 2. Crosslinking.
Soil (Low biodensity)	5 g or more	- If you suspect your sample may contain contaminants that could interfere with PCR, use Appendix A-2. - Appendix A-1 can also be used, but is only recommended if input sample is available in excess - Proceed to 1. Recommended Pre-Processing or 2. Crosslinking.
Water filters	1-2 filters	Filter processing requires additional reagents not included in the standard Hi-C kit. Contact us at support@phasegenomics.com for further assistance.
Rumen	50 - 100 µL	- Centrifuge and pellet cells at 10,000 x g for 5 min, (or according to your standard pelleting protocol) and remove excess media or buffer - Proceed to 1. Recommended Pre-Processing or 2. Crosslinking.

Workflow Overview

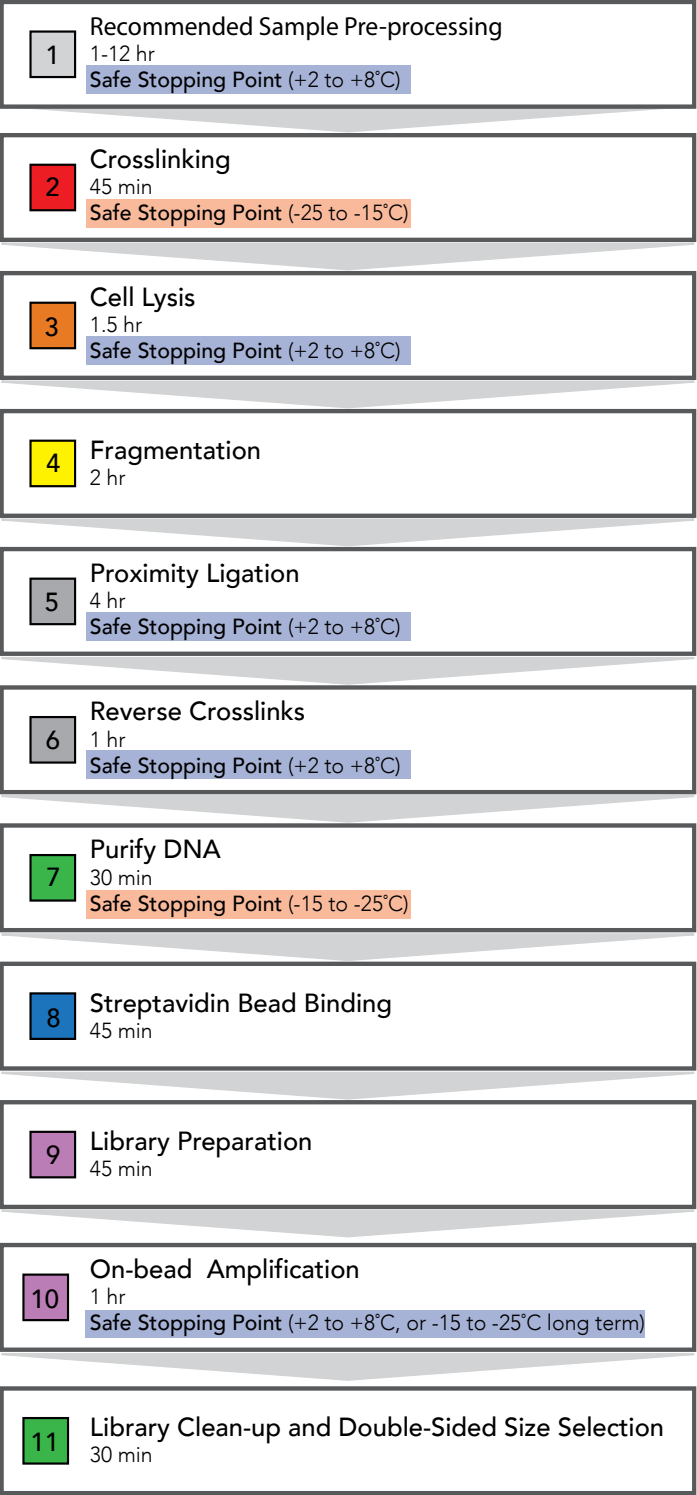
Protocol Notes and Recommended QC

Listed times and estimates, including incubations and time at-bench. The listed times assume familiarity with basic molecular biology techniques

Quantify streptavidin-bound DNA using Qubit dsDNA HS to determine the Universal Adapter dilution and number of PCR cycles.

Quantify library with Qubit dsDNA HS. Electrophoretic profile of library to assess fragment distribution.

Small amount of sequencing to assess number and quality of Hi-C contacts



Quick Protocol

This section provides a quick-step guide for experienced users. If this is your first time using the Proximo Hi-C Kit (Microbe) or ProxiMeta Kit, please refer to the detailed protocol on [p. 20](#).

Step	Protocol	Incubations and notes
1. Recommended Sample Pre-processing	- Centrifuge at 17,000 x g for 5 min to pellet all sample material. - Add 1 mL PGShield™ to pelleted sample and mix well.	Incubate at 4°C for 8-12 hours
2. Crosslinking (Red)	- Centrifuge at 17,000 x g for 5 min to pellet all sample material. - Remove and discard the supernatant.	
	Add 1 mL of Crosslinking Solution.	Incubate at room temperature for 20 min while rotating.
	Add 100 µL of Quenching Solution.	Incubate for room temperature for 15 min while rotating.
	- Centrifuge at 17,000 x g for 5 min to pellet all sample material. - Remove and discard the supernatant. - Wash the pellet with 1 mL of 1X CRB. - Centrifuge at 17,000 x g for 5 min. - Carefully remove and discard the supernatant.	SAFE STOPPING POINT: Pellet may be stored at -25 to -15°C for up to 1 month.

Step	Protocol	Incubations and notes
3. Lysis (Orange)	Resuspend cells in 700 µL of Lysis Buffer 1 and transfer to Lysis Tube.	Vortex for at room temperature for 20 min, using a bead-beater attachment if available.
	Centrifuge for 10 sec in benchtop centrifuge or 500 x g for 30 sec - 1 min.	
	Transfer the supernatant to a clean microcentrifuge tube.	The chromatin is in the supernatant.
	- Centrifuge the supernatant at 17,000 x g for 5 min. - Discard the supernatant.	The chromatin is now in the pellet.
	- Resuspend the pellet in 500 µL of 1X CRB. - Centrifuge at 17,000 x g for 5 min. - Carefully remove and discard the supernatant.	SAFE STOPPING POINT: Pellet may be stored at -25°C to -15°C for up to 1 month.
	Resuspend the pellet in 100 µL of Lysis Buffer 2.	Incubate at 65°C for 15 min.
	Add 100 µL Recovery Beads to sample.	Incubate at room temperature for 10 min.
4. Fragmentation (Yellow)	- Wash the beads: - Place the sample tube on a magnetic rack - Once the solution has cleared, remove and discard the supernatant without disrupting the beads - Remove the tube from the magnetic rack and gently resuspend the beads in 150 µL 1X CRB.	SAFE STOPPING POINT: Store sample at +2 to +8°C overnight.
	- Place the sample tube on a magnetic rack - Once the solution has cleared, remove the supernatant without disrupting the beads - Remove the tube from the magnetic rack and gently resuspend the beads in 139 µL of Fragmentation Buffer.	
	Add 11 µL of Fragmentation Enzyme.	Incubate at 37°C for 1 hr.
	- Wash the beads: - Place the sample tube on a magnetic rack - Once the solution has cleared, remove and discard the supernatant without disrupting the beads - Remove the tube from the magnetic rack and gently resuspend the beads in 150 µL 1X CRB. - Repeat the bead wash steps for a total of 2 washes with 1X CRB.	SAFE STOPPING POINT: Store bead-bound sample in 1X CRB at +2 to +8°C overnight.

Step	Protocol	Incubations and notes
5. Proximity Ligation (Clear)	- Remove 1X CRB from beads. - Add 85 µL molecular biology-grade water. - Add 10 µL of 10X Ligation Buffer.	
	Add 5 µL of Ligation Enzyme.	Incubate at 25°C for 4 hr, followed by 65°C for 10 min
		SAFE STOPPING POINT: Store sample at +2 to +8°C overnight.
6. Reverse Crosslinks (Clear)	Add 4 µL of RX Enzyme.	Incubate at 65°C for 1 hr
		SAFE STOPPING POINT: Store sample at +2 to +8°C overnight.
7. Purify DNA (Green)	Add 100 µL of Recovery Beads to the sample tube.	Incubate at room temp for 10 min.
	- Rinse the beads: - Place the sample tube on a magnetic rack. - Once the solution has cleared, remove and discard the supernatant without disrupting the beads. - Keeping the beads on the magnet, gently rinse the beads with 200 µL of Recovery Wash Buffer without disrupting the beads, leaving the buffer on the beads for 30 sec - 1 min between washes. - Repeat the bead wash steps for a total of 2 washes with Recovery Wash Buffer - Remove Recovery Wash Buffer and air dry the beads.	To air dry, leave tubes with caps open on the magnet at room temperature for 5 - 15 min.
	Resuspend the beads in 100 µL of Elution Buffer.	Incubate at room temperature for 5 min.
	- Place the sample tube on a magnetic tube rack or magnet. - Once the solution has cleared, recover the DNA-containing supernatant and transfer to a fresh tube.	

Step	Protocol	Incubations and notes
8. Streptavidin Bead Binding (Blue)	Prepare the Beads - Transfer 20 µL of Streptavidin Beads into a new 2 mL microcentrifuge tube (or 0.2 mL PCR tube). - Place the tube on a magnetic tube rack or magnet for at least 30 sec. - Once the solution has cleared, remove and discard the supernatant without disrupting the beads. - Wash the beads: - Place the sample tube on a magnetic rack - Once the solution has cleared, remove and discard the supernatant without disrupting the beads - Remove the tube from the magnetic rack and gently resuspend the beads in 150 µL Wash Buffer 1. - Repeat the bead wash steps for a total of 2 washes with Wash Buffer 1. - Resuspend beads in 100 µL of Bead Binding Buffer.	
	Bind the Sample to the Beads. Transfer 100 µL of purified DNA from step 6 to the washed Streptavidin Beads.	Incubate at room temperature for 10 min.
	- Wash the beads: - Place the sample tube on a magnetic rack - Once the solution has cleared, remove and discard the supernatant without disrupting the beads - Remove the tube from the magnetic rack and gently resuspend the beads in 150 µL Wash Buffer 2. - Repeat the bead wash steps for a total of 2 washes with Wash Buffer 2. - Repeat the bead wash steps once with Wash Buffer 1. - Resuspend the beads in 200 µL of molecular biology-grade water. - Measure the concentration of DNA (while still bound to the streptavidin beads) using a Qubit™ dsDNA HS Assay Kit or similar fluorometric assay.	

Step	Protocol	Incubations and notes
9. Library Preparation (Purple)	- Transfer no more than 500 ng of DNA-containing Streptavidin Beads to a fresh microcentrifuge tube. - Place the sample tube on a magnetic tube rack or magnet. - Once the solution has cleared, remove and discard the supernatant without disrupting the beads. - Place tube on pre-cooled thermocycler.	Pre-cool thermocycler to 4°C.
	- To beads add: 40 µL of Molecular biology-grade water - Cool to 4°C, then add: 4 µL of Frag, Repair, & A-Tail Buffer 6 µL of Frag, Repair, & A-Tail Enzyme	Fragment, end-repair, and A-tail using thermocycler program listed in Step 9 .
	- To sample add: 5 µL of Universal Adapter (diluted if necessary) 20 µL Adapter Ligation Mix	Dilute Universal Adapter according to the table listed in Step 9.10 .
		Incubate at 20°C for 15 min, no heated lid.
10. On-bead Amplification (Purple)	- Wash the beads: - Place the sample tube on a magnetic rack - Once the solution has cleared, remove and discard the supernatant without disrupting the beads - Remove the tube from the magnetic rack and gently resuspend the beads in 150 µL Wash Buffer 2. - Repeat the bead wash steps for a total of 2 washes with Wash Buffer 2. - Repeat the bead wash steps once with Wash Buffer 1. - Repeat the bead wash steps once with molecular biology-grade water for a total of 4 washes.	
	To beads add: 20 µL of molecular biology-grade water 25 µL Hot Start PCR Mix 5 µL of one PCR Primer Mix	Amplify with PCR protocol given in Step 10 of the detailed protocol.

Step	Protocol	Incubations and notes
11. Library Clean-up (Clean-up)	- Place the sample tube on a magnetic tube rack or magnet and allow solution to clear. - Transfer 50 µL of the library-containing supernatant to a new tube.	
	Add 57.5 µL of Recovery Beads.	Incubate at room temperature for 10 min.
	Place the sample tube on a magnetic tube rack or magnet.	Your library is in the supernatant. Do not discard.
	Transfer the supernatant (107.5 µL) to a new tube containing 15 µL of Recovery Beads.	Incubate at room temperature for 10 min.
	- Rinse the beads: - Place the sample tube on a magnetic rack. - Once the solution has cleared, remove the supernatant without disrupting the beads. - Keeping the beads on the magnet, gently rinse the beads with 200 µL of Recovery Wash Buffer without disrupting the beads, leaving the buffer on the beads for 30 sec - 1 min between washes. - Repeat the bead rinse steps for a total of 2 washes with Recovery Wash Buffer - Air dry the beads.	Leave tubes with caps open on the magnet at room temperature for 10 - 15 min.
	Resuspend the beads in 30 µL of Elution Buffer.	Incubate at room temperature for 5 min.
	- Place the sample tube on a magnetic tube rack or magnet. - Once the solution has cleared, recover the Hi-C library-containing-supernatant and transfer to a fresh microcentrifuge tube.	See Step 12 in detailed Protocol for recommended QC to determine if your library is sufficient.

Detailed Protocol

1. Recommended Sample Pre-processing

PGShield™ treatment before crosslinking can contribute to improved library yield and quality for certain samples. While this quality improvement is not a guarantee, it does not negatively impact preparation of metagenomic Hi-C Libraries.

- 1.1 Prepare sample according to the recommendation specific to your sample type as described in **Sample Types and Preparation**.

- 1.2 Remove any remaining buffer or media from sample, being careful to remove as much as possible.

Too much residual buffer or other liquid carryover can negatively impact your library prep.

- 1.3 Resuspend sample in **PGShield™**, approximately 2X volume **PGShield™** to sample volume.

*Sample inputs as recommended in **Sample Types and Preparation** typically require no more than 1 mL **PGShield™**, but this can vary per sample type. Make sure enough **PGShield™** is added so that the sample is fully covered, but not in extreme excess.*

- 1.4 Allow cells to sit in **PGShield™** for 1-12 hours at +2 to +8°C.

*12 hours or more stored in **PGShield™** is recommended before proceeding, but 1 hour is sufficient to observe a positive impact. Samples can be stored in **PGShield™** at +2 to +8°C for up to 1 year.*

2. Crosslinking (Red)

*See **Sample Types and Preparation** for sample input and possible protocol modification recommendations based on sample type.*

Prepare 1X CRB from 10X CRB by diluting with molecular-biology grade water.

- 2.1 If **1. Recommended Sample Pre-processing** was skipped, prepare sample according to the recommendation specific to your sample type as described in **Sample Types and Preparation**, then proceed to step 2.2.
- 2.2 If sample is still stored in **PGShield™** or some other storage solution, centrifuge at 10,000 x g for 5 min to pellet all sample material. Remove and discard the supernatant.
- 2.3 Resuspend sample in 1 mL of **Crosslinking Solution**.
- 2.4 Incubate at room temperature for 20 min with occasional mixing by inversion or rotation.
- 2.5 Add 100 µL of **Quenching Solution**.
- 2.6 Incubate at room temperature for 15 min with occasional mixing by inversion or rotation.
- 2.7 Centrifuge at 17,000 x g for 5 min to pellet all sample material. Remove and discard the supernatant.
- 2.8 Wash the pellet with 1 mL of **1X CRB**, making sure the pellet has been fully disrupted and resuspended, then centrifuge at 10,000 x g for 1 min to gently compact the cellular material. Carefully remove and discard the supernatant.

To fully disrupt the pellet in 1X CRB, you do not need to be gentle. Vortex, pipette up and down, or physically break apart with a pipette tip as needed. However, some sample types are more likely to stick to pipette tips, so do your best to minimize sample loss.

SAFE STOPPING POINT: Pellet can be stored at -15 to -25°C

3. Cell Lysis (Orange)

Pre-heat a heating block, water bath, or thermocycler to 65°C (for use in Step 2.8)

- 3.1 Vortex **Lysis Buffer 1** to resuspend any particulates that may have settled out.
- 3.2 Resuspend cells in 700 µL of **Lysis Buffer 1** and add to **Lysis Tube**.
- 3.3 Vortex at room temperature for 20 min using a bead-beater attachment if available.

Other types of bead-beating shakers can be used. The appropriate duration and intensity will vary between instruments. Refer to manufacturer's recommendations.

However, do not perform any additional mechanical or motorized lysis. Mechanical or motorized homogenizers overly disrupt the sample and severely reduce yields of the final Hi-C library.

- 3.4 Centrifuge at 500 x g for 10 sec to collapse bubbles and pellet debris, then transfer the supernatant to a clean microcentrifuge tube. **The chromatin is in the supernatant.**
- 3.5 Centrifuge the supernatant from Step 2.4 at 17,000 x g for 5 min and discard the supernatant. **The chromatin is now in the pellet.**
- 3.6 Resuspend the pellet in 500 µL of **1X CRB** and centrifuge at 17,000 x g for 5 min. Discard the supernatant.

SAFE STOPPING POINT: Sample pellet may be stored at -15 to -25°C for up to 1 month.

- 3.7 Resuspend the pellet in 100 µL of **Lysis Buffer 2** and transfer the sample to a PCR tube.
 - 3.8 Incubate at 65°C for 15 min.
 - 3.9 Briefly allow sample tube to cool. Thoroughly resuspend **Recovery Beads** and add 100 µL of beads to sample tube. mix well by vortexing gently or pipetting thoroughly.
- Chromatin binds irreversibly to **Recovery Beads**. The crosslinked DNA-protein complexes will remain bound to the beads until completion of **Step 5: Reverse Crosslinks**.*
- 3.10 Incubate at room temperature for 10 min.

3.11 Wash the beads:

- Place the sample tube in a magnetic rack or on a magnet.
- Once the solution has cleared, remove and discard the supernatant without disrupting the beads.
- Remove the tube from the magnet and gently resuspend the beads in 200 µL of **1X CRB**.

If after several minutes your sample is not clearly adhering to the magnet, briefly centrifuge the sample to collect the bead-bound sample in the bottom of your tube and remove the supernatant, avoiding transfer of any particulate sample. Then resuspend the beads in 100 µL of 1X CRB. Repeat as needed until the beads better adhere to the magnet.

SAFE STOPPING POINT: Bead-bound sample may be stored in **1X CRB** at +2 to +8°C overnight.

4. Fragmentation (Yellow)

Pre-heat a heating block, water bath, or thermocycler to 37°C (for use in Step 3.3)

- 4.1 Place the sample tube on a magnetic rack
- 4.2 Once the solution has cleared, remove the supernatant without disrupting the beads.
- 4.3 Remove the tube from the magnetic rack and gently resuspend the beads in 139 µL of **Fragmentation Buffer** to the sample.

If your bead-bound sample was stored in 1X CRB, remove the buffer before adding Fragmentation Buffer.
- 4.4 Add 11 µL of **Fragmentation Enzyme** to the sample and mix by vortexing gently or pipetting thoroughly.
- 4.5 Incubate the sample at 37°C for 1 hr.
- 4.6 Wash the beads:

■ Place the sample tube in a magnet.

■ Once the solution has cleared, remove the supernatant without disrupting the beads.

■ Remove the tube from the magnet and gently resuspend the beads in 200 µL of 1X CRB.
- 4.7 Repeat the bead wash steps one more time with 200 µL of 1X CRB per wash, for a total of two washes.

SAFE STOPPING POINT: Store bead-bound sample in 1X CRB at +2 to +8°C overnight.

5. Proximity Ligation (Clear)

Set up the following **Ligation program**:

Step	Temperature (°C)	Time
Lid temperature	105	
Ligation	25	4 hr
Enzyme inactivation	65	10 min
Final hold	4	Hold

5.1 Prepare **Ligation Mix**:

Reagent	Volume 1 reaction (µL)	Volume 8.2 reactions (µL)
Water	85	697
10X Ligation Buffer	10	82
Ligation Enzyme	5	41
Total	100	820

- 5.2 Place the sample tubes in a magnetic rack or on a magnet.
- 5.3 Once the solution in each tube has cleared, remove the supernatant without disrupting the beads.
- 5.4 Remove the tubes from the magnetic rack and gently resuspend the beads for each sample in 100 µL of prepared **Ligation Mix**.
- 5.5 Place the samples on the thermocycler and initiate the **Ligation program** run (Programmed at the beginning of **Step 5. Ligation**).

SAFE STOPPING POINT: Store sample at +2 to +8°C overnight.

6. Reverse Crosslinks (Clear)

Set up the following Reverse Crosslinks program:

Step	Temperature (°C)	Time
Lid temperature	105	
Reverse crosslinks	65	1 hr
Final hold	4	Hold

- 6.1 Add 4 µL of **RX Enzyme** to each sample tube and mix well by vortexing or pipetting.
- 6.2 Place the samples on the thermocycler and initiate the run of the above **Reverse Crosslinks** program (Programmed at the beginning of **Step 6. Reverse Crosslinks**).

The sample is no longer bound to the beads and has been released into solution.

SAFE STOPPING POINT: The reaction may be stored at +2 to +8°C overnight, or the supernatant can be removed and stored at -25 to -15°C for up to 1 month.

7. Purify DNA (Green)

Prepare **Recovery Wash Buffer** according to the instructions on the bottle.

- 7.1 Allow sample tube to cool to room temperature.
- 7.2 Thoroughly resuspend the **Recovery Beads** and add 100 µL of **Recovery Beads** to the sample tube. Mix thoroughly by vortexing or pipetting.

*Recovering the supernatant from the used **Recovery Beads** before adding new **Recovery Beads** is acceptable but not necessary at this step. Removing used beads before the addition of new beads has not been found to notably impact the quality or yield of the final library for most sample types.*
- 7.3 Incubate at room temperature for 10 min.
- 7.4 Wash the beads:

- Place the sample tube in a magnetic rack or on a magnet.
 - Once the solution has cleared, remove and discard the supernatant without disrupting the beads.
 - Keeping the beads on the magnet, gently wash the beads with 200 µL of **Recovery Wash Buffer** without disrupting the beads, leaving the buffer on the beads for 30 sec to 1 min between washes.
- 7.5 Repeat the bead wash steps in Step 7.4 once more for a total of 2 washes with **Recovery Wash Buffer**.
- 7.6 Air dry the beads at room temperature for 5 - 15 min on the magnet with the cap open.

*Over-drying is not problematic for **Recovery Beads**. As soon as beads look sufficiently dry, proceed to Step 7.7. Sample type variation may impact required drying time. .*
- 7.7 Remove the sample tube from the magnet and thoroughly resuspend the beads in 100 µL of **Elution Buffer**.
- 7.8 Incubate at room temperature for 10 minutes to elute the DNA.
- 7.9 Place the sample tube in a magnetic tube rack or magnet.
- 7.10 Once the solution has cleared, recover the **DNA-containing supernatant** and transfer to a fresh tube. Discard the beads.

SAFE STOPPING POINT: Purified, proximity-ligated DNA may be stored at -25 to -15°C (indefinitely)

8. Streptavidin Bead Binding (Blue)

A. Prepare the Beads

Do not yet combine the beads with the DNA recovered in Step 7. DNA-binding will occur in section B after beads are prepared for binding.

- 8.1 Thoroughly resuspend the **Streptavidin Beads** and transfer 20 µL into a new microcentrifuge tube (or 0.2 mL PCR tube).
- 8.2 Wash the Beads:
 - Place the sample tube in a magnetic rack or on a magnet.
 - Once the solution has cleared, remove and discard the supernatant without disrupting the beads.
 - Remove the tube from the magnet and gently resuspend the beads in 150 µL of **Wash Buffer 1**.
- 8.3 Repeat the bead wash steps one more time with 150 µL of **Wash Buffer 1** for a total of two washes.
- 8.4 Remove beads from the magnet and resuspend in 100 µL of **Bead Binding Buffer**.

B. Bind the Sample to the Beads

- 8.5 Transfer 100 µL of purified DNA (from Step 7) to the washed **Streptavidin Beads** (from Step 8.4) and mix by vortexing gently or pipetting thoroughly.
- 8.6 Incubate at room temperature for 10 min, mixing occasionally by gentle vortexing or inversion.
- 8.7 Wash the beads:
 - Place the sample tube in a magnetic rack or on a magnet.
 - Once the solution has cleared, remove and discard the supernatant without disrupting the beads.
 - Remove the tube from the magnet and gently resuspend the beads in 150 µL of **Wash Buffer 2**.
- 8.8 Repeat the bead wash steps one more time with 150 µL of **Wash Buffer 2** for a total of two washes.
- 8.9 Repeat the bead wash steps one more time with 150 µL of **Wash Buffer 1**.
- 8.10 Repeat the bead wash steps one more time with 150 µL of **molecular biology-grade water**.
- 8.11 With your bead-bound sample suspended in 200 µL of water, measure the concentration of DNA (while still bound to the streptavidin beads) using a Qubit™ dsDNA HS Assay Kit or similar fluorometric assay.

It is essential that the beads are well-resuspended in the molecular biology-grade water prior to quantification by fluorometry. To ensure an accurate measurement, vortex the beads in the fluorometric assay tube immediately prior to measuring DNA concentration.

Beads will interfere with spectrophotometric quantitation of bound DNA. Use of fluorometric assay is a requirement.

*Use between 2-5 µL for quantification. If at this stage the quantity of bead-bound DNA is less than 10 ng (0.5ng/µL concentration if using 2 µL for quantification), including "too low - out of range" measurements, this does NOT necessarily indicate failure, proceed to **9. Library Preparation**. If you have any particular questions or concerns at this stage, we suggest reaching out to support@phasegenomics.com before proceeding.*

SAFE STOPPING POINT: Store bead-bound sample at +2 to +8°C overnight. Do not store longer than overnight before proceeding to **9. Library Preparation**.

9. Library Preparation (Purple)

Set up the following Fragmentation, End-repair, and A-tailing program:

Step	Temperature (°C)	Time (min)
Lid temperature	105	
Pre-cooling	4	Hold
Fragmentation, end-repair, and A-tailing	30	7
	65	30
Final hold	4	Hold

And set up the following Adapter Ligation Program:

Step	Temperature (°C)	Time (min)
Lid temperature	Off	
Adapter Ligation	20	15

- 9.1 Initiate the run of the **Fragmentation, End-repair, and A-tailing** program (Programmed at the beginning of **Step 9. Library Preparation**) to pre-cool the thermocycler.
- 9.2 Transfer no more than **500 ng of streptavidin-bound DNA** to a fresh microcentrifuge tube.
- 9.3 Place the sample tube in a magnetic rack or on a magnet.
- 9.4 Once the solution has cleared, remove and discard the supernatant without disrupting the beads.
- 9.5 Resuspend the beads in 40 µL of **molecular biology-grade water**.
- 9.6 Place the samples in the pre-cooled thermocycler and then cool to 4°C for at least 1 min.
- 9.7 Prepare **FERAT Master Mix**:

Reagent	Volume 1 reaction (µL)	Volume 8.2 reactions (µL)
Frag, Repair, A-Tail Enzyme	6	49.2
Frag, Repair, A-Tail Buffer	4	32.8
Total	10	82

- 9.8 Add 10 µL of **FERAT Mix** to each sample and mix by vortexing gently or pipetting thoroughly. Immediately place the samples back onto the thermocycler.

Vortex for at least 5 sec or pipette at least 25 µL of the reaction up and down a minimum of 10 times to ensure proper mixing.

Thorough mixing at this stage is extremely important! Improper mixing will result in a poorly fragmented library and will negatively affect your sequencable yield.
- 9.9 Advance the **Fragmentation, End-repair, and A-tailing** program from the Pre-cooling step to Fragmentation, end-repair, and A-tailing.
- 9.10 Every library for which the total mass of DNA measured at step 8.11 was less than 10 ng, prepare diluted **Universal Adapter** (provided tube is 15 µM) according to the table below.

Either molecular biology-grade water or 10 mM Tris-HCl, pH 8.0 can be used for the dilution.

Input Mass (ng)*	Adapter Concentration	Volume Water or Tris (µL)	Volume 15 µM Adapter (µM)
> 10	15 µM	Do not dilute	5
0 - 10	1 µM	14	1

*Measured in Step 8.11

- 9.11 Add 5 uL of appropriately diluted **Universal Adapter** to each sample and mix by vortexing gently or pipetting thoroughly.
- 9.12 Add 20 µL of **Adapter Ligation Mix** to each sample tube. Mix by pipetting thoroughly.

Do not vortex Adapter Ligation Mix.
- 9.13 Place the samples on the thermocycler and initiate the run of the **Adapter Ligation** program (Programmed at the beginning of **Step 9. Library Preparation**)

9.14 Wash the beads:

- Place the sample tube in a magnetic rack or on a magnet.
- Once the solution has cleared, remove and discard the supernatant without disrupting the beads.
- Remove the tube from the magnet and gently resuspend the beads in 150 µL of **Wash Buffer 2**.

9.15 Repeat the bead wash steps one more time with 150 µL of **Wash Buffer 2** for a total of two washes.

9.16 Repeat the bead wash steps one more time with 150 µL of **Wash Buffer 1**.

9.17 Repeat the bead wash steps one more time with 150 µL of **molecular biology-grade water**.

10. On-bead Library Amplification (Purple)

Set up the following PCR Program:

Step	Temperature (°C)	Time (sec)	Cycles
Initial denaturation	98	45	1
Denaturation	98	15	12*
Annealing	60	30	
Extension	72	30	
Final extension	72	60	1
Hold	12	hold	

Use the table in step 10. 6 below to determine the number of PCR cycles to use for each sample.

- 10.1 Place the sample tubes in a magnetic rack or on a magnet.
- 10.2 Once the solution in each tube has cleared, remove the supernatant without disrupting the beads.
- 10.3 Thoroughly resuspend the beads in 20 µL of **molecular biology-grade water**.
- 10.4 Add 5 µL one **PCR Primer Mix** and mix by vortexing gently or pipetting thoroughly.
- Use a different primer for each sample. Sufficient primers with unique index sequences are provided with each kit. See [Index Sequences](#) for more information).*
- 10.5 Add 25 µL of **Hot Start PCR Mix** and mix by vortexing gently or pipetting thoroughly.

10.6 Determine how many PCR cycles each of your samples requires according to the following table:

Mass used at step 8.11 (ng)	Recommended Number of PCR Cycles
<10	14
10-50	12
50-200	10
200-500	8

Amplifying your libraries beyond the suggested number of cycles can negatively impact the final data quality. This may require you to separate your samples into separate PCR runs

10.7 Place the samples on the thermocycler and initiate the run of the **PCR program** (Programmed at the beginning of **Step 10. On-bead Library Amplification**).

SAFE STOPPING POINT: PCR reaction can be held overnight at +2 to +8°C, or stored at -25 to -15°C (indefinitely)

11. Library Clean-up and Double-sided Size Selection (Green)

Use Recovery Wash Buffer Prepared at Step 7.

- 11.1 Place the sample tube in a magnetic tube rack or magnet.
- 11.2 Once the solution has cleared, transfer the **library-containing supernatant** to a new tube.
Streptavidin beads can be stored in 1X CRB for troubleshooting if needed. Otherwise they can be discarded.
- 11.3 Add 57.5 µL (1.15X volume) of thoroughly resuspended **Recovery Beads** to the tube containing the library (from Step 10.2).
Unwanted high molecular weight fragments will be binding to the beads.
- 11.4 Incubate at room temperature for 10 min.
- 11.5 Place the sample tube in a magnetic tube rack or magnet. **Your library is in the supernatant. Do not discard.**
- 11.6 After 2 min, or once the solution has cleared, transfer the supernatant (105 µL) to a new tube containing 15 µL of **Recovery Beads**.
The library is now binding to the beads, leaving unwanted small fragments in the supernatant. Make sure no beads from the first incubation transfer over with the supernatant.
- 11.7 Incubate at room temperature for 10 min.

11.8 Wash the beads:

- Place the sample tube in a magnetic rack or on a magnet.
- Once the solution has cleared, remove and discard the supernatant without disrupting the beads.
- Keeping the beads on the magnet, gently wash the beads with 200 µL of **Recovery Wash Buffer** without disrupting the beads, leaving the buffer on the beads for 30 sec - 1 min between washes.

11.9 Repeat the bead wash steps from Step 11.8 for a total of two washes with **Recovery Wash Buffer**. Air dry the beads at room temperature 10 - 15 min on the magnet with the cap open.

*Over-drying is not problematic for **Recovery Beads**. Air dry the beads by leaving the tube on the magnet for 5 - 15 min with the cap open.*

11.10 Remove the sample tube from the magnet and thoroughly resuspend the beads in 30 µL of **Elution Buffer**.

11.11 Incubate at room temperature for 5-10 min to elute the DNA.

11.12 Place the sample tube in a magnetic tube rack or magnet.

11.13 Once the solution has cleared, recover the **Proximo Hi-C Library-containing supernatant** and transfer to a fresh microcentrifuge tube. Discard the beads.

12. Library QC (recommended)

11.1 Measure the concentration of DNA using a Qubit™ dsDNA HS Assay Kit or similar fluorometric assay.

Yields over 0.5 ng/µL are a strong indication that library preparation has been successful. The library can be stored at -15 to -25°C indefinitely.

11.2 Assess library fragment size using BioAnalyzer or similar instrument.

The expected average library size is between 400-500 bp.

Before performing a full sequencing run, it is highly recommended that you perform low-pass sequencing (approximately 1 million read pairs) to assess the quality of your Hi-C library. These data can be analyzed using our open-source Hi-C analysis tools (available from https://github.com/phasegenomics/hic_qc).

13. Sequencing

Proximo Hi-C libraries are compatible with any Illumina® sequencer.

Population Complexity	Hi-C Sequencing Recommendation
Low-to-mid-complexity communities (e.g. fecal microbiomes)	> 50 million pairs (2 x 100 bp or longer)
High-complexity communities (e.g. rumen, sludge, wastewater)	> 100 million pairs (2 x 100 bp or longer)

For mixed-community experiments, producing a shotgun library from the same input sample is recommended (not included in this kit).

Population Complexity	Shotgun Sequencing Recommendation
Low-to-mid-complexity communities (e.g. fecal microbiomes)	> 100 million pairs (2 x 100 bp or longer)
High-complexity communities (e.g. rumen, sludge, wastewater)	> 200 million pairs (2 x 100 bp or longer)

Note: these are meant as guidelines for the amount of data required to scaffold genomes. The actual requirements will vary between genomes and are dependent on assembly quality.

14. Analysis

ProxiMeta Metagenome Deconvolution Platform

Assemble high-quality genomes directly from the microbiome, or associate plasmids, phages and antimicrobial resistance genes (ARGs) with their hosts. Contact us directly for more information!

Other Hi-C Metagenomic Analysis Tools

Read Pre-processing

Both the shotgun and Hi-C reads should be quality filtered and adapter trimmed prior to utilizing them for the analysis. We recommend the following tools for this:

- [Fastp](#)
- [FastQC](#)

Metagenomic Assembly

The shotgun reads are assembled into a metagenomic assembly of sufficient quality prior to performing metagenomic binning and annotation. After generating an assembly, we recommend filtering the resulting contigs to only include contigs greater than 1kb.

- [MegaHit](#)
- [MetaSpades](#)

Hi-C Read Alignment

The quality-filtered and adapter-trimmed reads are aligned to the metagenomic assembly using bwa mem. Specific alignment parameters for aligning Hi-C read data should be used, which can be found [here](#).

- [BWA Mem](#)

Hi-C Metagenomic Binning

The contigs contained in the metagenomic assembly are combined into metagenomic bins using the proximity ligation signal obtained by mapping the Hi-C reads to the assembly. Some commonly used open source Hi-C binning tools are listed here:

- [Bin3C](#)
- [MetaCC](#)

Taxonomic Annotation

The metagenomic bins obtained from performing Hi-C binning can be taxonomically annotated using the following open source tool.

- [GTDB-TK](#)

Phage Annotation

Viral contigs can be identified by running the metagenomic assembly through one of the following viral annotation tools.

- [Vibrant](#)
- [VirSorter2](#)
- [ViralCC](#)
- [Genomad](#)

Plasmid Annotation

Plasmid contigs can be identified by running the metagenomic assembly through one of the following plasmid identification tools.

- [Genomad](#)
- [NCBI plasmid database \(PLSDB\)](#)

Mobile Element Host Interaction Analysis

Mobile element host associations can be identified using the Hi-C signal generated between microbial and mobile element contigs. The following tool can be used to identify these interactions.

- [ViralCC](#)

AMR and Virulence Gene Annotation

Antibiotic and virulence genes can be identified by running the metagenomic assembly through one of the following annotation tools.

- [AMRFinderPlus](#)
- [ResFinder](#)

Appendix A-1

This appendix describes modifications to the protocol for soil samples. If you are unsure about the optimal preparation for your sample, please reach out to support@phasegenomics.com.

Basic Soil Protocol

This protocol is designed for rich soil (i.e. top soil).

A1.1 Mix 5 mL of water per gram of sediment.

For rich soils use 1 - 2 g of soil.

A1.2 Vortex for 5 minutes.

A1.3 Centrifuge at 500 x g for 5 min to settle out heavy particles.

A1.4 Transfer the supernatant to a fresh microcentrifuge tube(s).

A1.5 Centrifuge the supernatant at 17,000 x g for 5 min.

A1.6 Remove and discard the supernatant.

A1.7 Proceed with pellet to step **1. Crosslinking**.

Appendix A-2

This protocol is intended for soils with low levels of live organisms. For soils with abundant microbial life, follow the soil protocol included in **Appendix A-1**.

Differential Centrifugation of Soil or Sludge Samples

Additional reagents not included in the kit are required.

A2.1 Mix 5 mL of water per gram of sediment.

A2.2 Vortex for 5 minutes.

Recommended starting amount: 2 tubes of 25 mL water + 5 g sediment.

A2.3 Spin tubes at 1,000 x g for 10 min to settle out heavy particles.

A2.4 Transfer the supernatant to a new tube.

A2.5 Add **Formaldehyde** to a final concentration of 1% (v/v)

A2.6 Incubate at room temperature for 20 min with occasional mixing by inversion or rotation.

A2.7 Add **glycine** to a final concentration of 1% (w/v) to quench the reaction.

A2.8 Incubate at room temperature for 20 min with occasional mixing by inversion or rotation.

A2.9 Carefully layer 1 mL of supernatant on top of 1 mL of **OptiPrep™** (or similar 60% iodixanol solution, not included).

*Alternatively, you can layer larger volumes over the **OptiPrep™** cushion if you have a centrifuge that can accommodate larger volumes.*

It is also possible to sequentially load sups 1 mL at a time over the OptiPrep™ cushion.

A2.10 Centrifuge the layered supernatant and OptiPrep™ at 10,000 x g for 20 min to pellet. Transfer the supernatant, including cloudy interface, to a new tube and centrifuge at 17,000 x g for 5 min.

A2.11 Remove and discard the supernatant avoiding the pelleted cells.

A2.12 Proceed to **2. Cell Lysis** with the pelleted cells.

Index Sequences

Your kit contains two sets of indexed primers which are used to generate unique dual-indexed Illumina®-compatible libraries with different sequence combinations. If you plan to pool your Hi-C libraries with other libraries for sequencing, please follow standard guidelines for multiplexed sequencing on your specific Illumina® instrument. Please reference the **Phase Genomics Index Sequences** document, available at info.phasegenomics.com/protocols

Please contact us at support@phasegenomics.com if additional indices or assistance with multiplexed sequencing are needed.

Restriction Enzymes

Restriction Enzyme	Cut Sequence
Sau3AI	GATC
MluCI	AATT

Revision History

Version	Date	Revision Description
3.0	2020-01	released
	2020-02	- tabulated incubation steps - expanded index table
4.0		- Library Preparation and On-bead Library Amplification steps protocol re-formulated - Increased Ligation Buffer concentration for better stability in long-term storage - Updated introduction - Updated links and redirects - Removed Bead Reagent addition in Streptavidin Bead Binding - Decreased sample input requirements - Added quick protocol for experienced users - Modified Workflow Overview - Adjusted index sequence IDs to match 96 well layout - moved liquid nitrogen grinding from before the lysis step to before crosslinking - added clarifying comments in crosslinking and lysis steps
4.5	2022-12	- Added restriction enzyme information - clarified buffer removal before fragmentation - decreased maximum recommended PCR cycle number from 16 to 14 - clarified dilution of CRB with molecular biology-grade water - updated formulation for crosslinking solution, 10X CRB, and Fragmentation Enzyme - Updated volumes for Wash Buffer 1 and Wash Buffer 2 - Corrected typo in step 8.9 - Updated color scheme and kit sticker image - Corrected font error in Kit Specifications - Updated formatting in quick protocol - Corrected typo in Equipment and Consumables (end of sentence was incorrectly deleted in previous iteration of the protocol) - Updated notes about DNA addition in step 8 - Step 8.9 - dilution information was moved to an in-line note. 9.2 - updated wording around number of provided primers
	2023-01	- corrected language in brief protocol in crosslinking and fragmentation steps for better clarify - Corrected capitalization error in step 2.11 - Corrected language and spelling error in subheader for streptavidin bead preparation - corrected "repar" to "repair" in table in step 8.8 - Corrected capitalization error in step 10.9 - Corrected grammatical error in Falcon-PHASE description - corrected typo in Notices section

Version	Date	Revision Description
4.5.1	2023-07	- Corrected numbering error at the beginning of step 4 - Corrected spelling of "botttom" to "bottom" on p19 - Added clarification about low on-bead measurements at step 7 - Updated final Recovery Bead clean up bead-to-volume ratios
4.5.2	2023-12	- Corrected discrepancies between quick and long protocol - Added more indexes and updated index IDs to new naming system - Converted font style - updated PCR cycle guidelines - updated adapter concentration dilution recommendations - updated index list to include more historical IDs
4.5.3	2024-04	- Increased fragmentation time from 5 to 7 min - Listed expected average fragment size in QC section
4.5.4	2024-06	- Corrected in-line Recovery Wash Buffer instructions to match instructions on bottle - Updated RX Enzyme time to 1 hour (removed extension up to 16 hours) - Added index plate locations
5.0	2026-08	- Decreased bead wash volumes from 200 uL to 150 uL - Updated sample input guidelines - Added PGShield™ use instructions - Updated contents to include PGShield™ - Added more in-line notes regarding sample preparation - Added dounce use instructions - Added master mix suggested volumes for 8 reaction volumes - Added thermocycler programs for fragmentation and setup instructions at the beginning of each step in which they are used - Expanded instructions to be useful for more than one kit variation - Increased base centrifugation speed from 6,000 to 10,000 x g. - Updated crosslink and quench time to sync up with other protocol versions - Updated sequencing recommendations - Adjusted formulation for Lysis Buffer 1 - Adjusted formulation for Crosslinking Solution and increased provided volume - Improved language consistency for bead washes and thermocycler protocol programming and use - Corrected PGShield™ trademark labeling and spacing. - Corrected "Purify" sp in quick protocol - Expanded analysis guidance - Updated workflow diagram - Merged multipack instructions into one unified protocol - Removed indexed adapter sequence information and moved to a separate document (Phase Genomics Index Sequences. Available at info.phasegenomics.com/protocols)

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