

# ForenSeq mtDNA Whole Genome Kit

Reference Guide

VEROGEN PROPRIETARY

Document # VD2020006 Rev. B

November 2020

## Revision History

Document #	Date	Description of Change
VD2020006 Rev. B	November 2020	Refreshed the format of the guide: <ul style="list-style-type: none"><li>• Updated the layout and formatting.</li><li>• Updated fonts, table styles, and other design elements.</li></ul> Updated instructions to prepare reagents for denaturing and diluting libraries. Updated the safety data sheet (SDS) link to <a href="http://verogen.com/product-documentation">verogen.com/product-documentation</a> . Updated patent information in the legal notice. Removed instruction to flick FEM and HL60. Corrected instructions on denaturing HSC. Corrected preparation instructions for bead-based normalization to indicate that LNB1 must be fully resuspended. Corrected plate labeling for the normalize libraries (manual quantification) process. Corrected the RSB cap color to purple and the SPB2 cap color to red.
VD2020006 Rev. A	August 2020	Initial release

## Table of Contents

Revision History .....	2
Table of Contents .....	3
<b>Chapter 1. Overview .....</b>	<b>5</b>
Introduction .....	5
DNA Input Recommendations .....	6
Protocol Steps .....	7
Acronyms .....	8
Additional Resources .....	9
<b>Chapter 1. Protocol .....</b>	<b>10</b>
Introduction .....	10
Tips and Techniques .....	11
Amplify and Tag Targets .....	12
Enrich Targets .....	16
Purify Libraries .....	19
Perform Second Purification (Optional) .....	22
Normalize Libraries Using a Bead-Based Method (Option 1) .....	24
Normalize Libraries Using Manual Quantification (Option 2) .....	26
Pool Libraries .....	27
Denature and Dilute Bead-Normalized Libraries (Option 1) .....	28
Denature and Dilute Manually Normalized Libraries (Option 2) .....	29
<b>Chapter 2. Materials .....</b>	<b>32</b>
Kit Contents and Storage .....	32
Consumables and Equipment .....	35
<b>Technical Support .....</b>	<b>37</b>

## ForenSeq mtDNA Whole Genome Kit Reference Guide

---

This document and its contents are proprietary to Verogen, Inc. and its affiliates, and are intended solely for the contractual use of its customer in connection with the use of the product(s) described herein and for no other purpose. This document and its contents shall not be used or distributed for any other purpose and/or otherwise communicated, disclosed, or reproduced in any way whatsoever without the prior written consent of Verogen. Verogen does not convey any license under its patent, trademark, copyright, or common-law rights nor similar rights of any third parties by this document. Patents: US Patent No. US10422002B2, Chinese Patent No. CN106164298B, and pending patents.

The instructions in this document must be strictly and explicitly followed by qualified and properly trained personnel in order to ensure the proper and safe use of the product(s) described herein. All of the contents of this document must be fully read and understood prior to using such product (s).

FAILURE TO COMPLETELY READ AND EXPLICITLY FOLLOW ALL OF THE INSTRUCTIONS CONTAINED HEREIN MAY RESULT IN DAMAGE TO THE PRODUCT(S), INJURY TO PERSONS, INCLUDING TO USERS OR OTHERS, AND DAMAGE TO OTHER PROPERTY.

VEROGEN DOES NOT ASSUME ANY LIABILITY ARISING OUT OF THE IMPROPER USE OF THE PRODUCT(S) DESCRIBED HEREIN (INCLUDING PARTS THEREOF OR SOFTWARE).

© 2020 Verogen, Inc. All rights reserved.

All other names, logos, and other trademarks are the property of their respective owners.

**For Research, Forensic, or Paternity Use Only.** Not for any clinical or therapeutic use in humans or animals.

Notice to Purchaser: Limited License

The purchase price of the product includes a limited, nontransferable license under US and foreign patents owned by BIO-RAD Laboratories, Inc., to use this product. No other license under these patents is conveyed expressly or by implication to the purchaser by the purchase of this Product.

The Product is sold under license from Affibody AB, Sweden.

Phusion DNA Polymerase is manufactured by Thermo Fisher Scientific. Phusion is a trademark or registered trademark of Thermo Fisher Scientific, or its subsidiaries.

# Overview

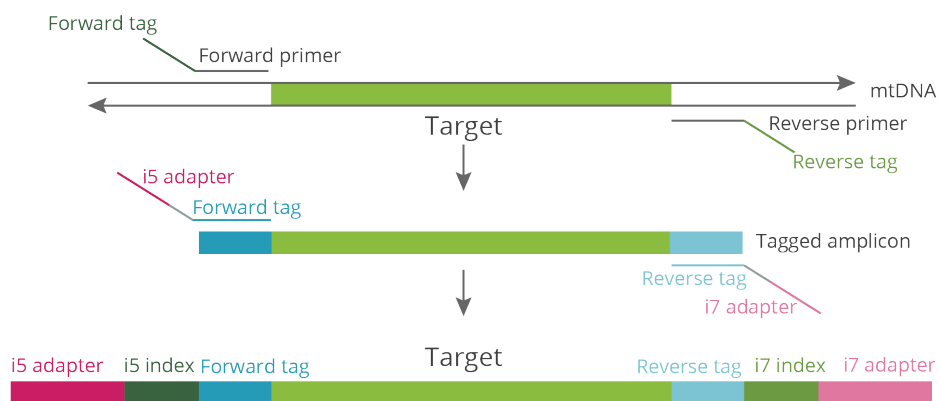
Introduction ..... 5  
 DNA Input Recommendations ..... 6  
 Protocol Steps ..... 7  
 Acronyms ..... 8  
 Additional Resources ..... 9

## Introduction

The Verogen ForenSeq™ mtDNA Whole Genome Kit prepares up to 48 paired-end, dual-indexed libraries for sequencing and analysis of the entire human mitochondrial genome (mtGenome). The protocol divides each sample into two PCR pools, a strategy that promotes efficient amplification of overlapping amplicons to allow complete coverage.

A primer mix containing tagged oligos for each target sequence mixes with each sample. PCR cycles link the tags to copies of each target, forming DNA templates consisting of regions of interest flanked by universal primer binding sequences. Index adapters then attach to the tags. The resulting libraries are amplified, purified, and pooled into one tube for sequencing.

**Figure 1** Assay overview



## Kit Features

The ForenSeq mtDNA Whole Genome Kit offers the following features:

- An efficient protocol that simultaneously prepares all libraries in one plate. Each library is a collection of tagged, amplified DNA fragments from one sample.
- Flexible input requirements allow preparation of libraries from samples that range from high-quality, single-source to degraded.
- Two options for library normalization support high-throughput workflows that can be automated or low-throughput workflows for low-input samples.

## ForenSeq mtDNA Whole Genome Kit Reference Guide

- A small amplicon size of < 210 bp with a minimum overlap of 3 bp improves recovery of mitochondrial DNA (mtDNA) from degraded samples.
- Two tiled primer mixes provide balanced coverage of the whole mtGenome. More than 500 primers efficiently amplify degenerate bases.

**Figure 2** Tiled amplicons for complete coverage



## DNA Input Recommendations

The ForenSeq mtDNA Whole Genome Kit is optimized for input of 100 pg human genomic DNA (gDNA) per sample. Each sample is **divided into two 50 pg reactions** early in the protocol. Before starting the protocol, quantify input DNA using a fluorometric-based method or qPCR and assess quality.

The kit is compatible with mtDNA extracted from hair, bone, tooth, and buccal samples. For hair, use DNA extracted from 0.5–2 cm of hair shaft.

## Controls

Each preparation must include Control DNA HL60 (HL60) as a positive template control and a negative amplification control. If these controls are not included, troubleshooting support is limited.

The kit includes HL60 and the negative amplification control is nuclease-free water. The protocol includes instructions to prepare each control and a reagent blank. Like the input DNA, each control is divided into two reactions.

## Protocol Steps

The following diagram lists the steps to prepare libraries with hands-on times, total times, and reagents. Safe stopping points are marked between steps.

**Figure 3** Protocol overview



## Acronyms

Acronym	Definition
A50X	i5 Index Adapter
FEM	ForenSeq Enzyme Mix
HL60	Control DNA HL60
HP3	2 N NaOH
HSC	Human Sequencing Control
HT1	Hybridization Buffer
LNA1	Library Normalization Additives 1
LNB1	Library Normalization Beads 1
LNS2	Library Normalization Storage Buffer 2
LNW1	Library Normalization Wash 1
mtDNA	Mitochondrial DNA
mtGenome	Mitochondrial genome
mtPCR1	mtPCR1 Reaction Mix
mtPCR2	mtPCR2 Reaction Mix
NaOH	Sodium hydroxide
ProK	Proteinase K
R7XX	i7 Index Adapter
RSB	Resuspension Buffer
SPB2	Sample Purification Beads 2
WGS1	Whole Genome Mix Set 1
WGS2	Whole Genome Mix Set 2



### Additional Resources

This guide provides comprehensive information on the ForenSeq mtDNA Whole Genome Kit with detailed protocol instructions. Visit the [Documentation page](#) on the Verogen website to download additional kit documentation and access the latest versions.

Resource	Description
<i>ForenSeq mtDNA Whole Genome Kit Checklist (document # VD2020007)</i>	Provides concise protocol instructions for the experienced user.
<i>ForenSeq mtDNA Whole Genome Kit Materials List (document # VD2020008)</i>	Lists the consumables and equipment needed to perform the protocol.

# Protocol

Introduction .....	10
Tips and Techniques .....	11
Amplify and Tag Targets .....	12
Enrich Targets .....	16
Purify Libraries .....	19
Perform Second Purification (Optional) .....	22
Normalize Libraries Using a Bead-Based Method (Option 1) .....	24
Normalize Libraries Using Manual Quantification (Option 2) .....	26
Pool Libraries .....	27
Denature and Dilute Bead-Normalized Libraries (Option 1) .....	28
Denature and Dilute Manually Normalized Libraries (Option 2) .....	29

## Introduction

This chapter describes the ForenSeq mtDNA Whole Genome protocol with step-by-step instructions to prepare libraries for sequencing. For an overview of the protocol with reagents and durations for each step, see [Protocol Steps \(page 7\)](#).

Before starting, confirm kit contents and make sure that you have the necessary reagents, consumables, and equipment. For a list of items, see [Materials \(page 32\)](#).

## Number of Samples

Process at least eight samples at a time, including positive and negative amplification controls. Preparing master mixes for fewer than eight samples can introduce pipetting inaccuracies due to small volumes.

Plan on sequencing a maximum of 16 libraries on a standard MiSeq FGx<sup>®</sup> flow cell, which is provided in the MiSeq FGx Reagent Kit. You can prepare the full 48 libraries and split them between three flow cells, if desired.

## Index Adapter Strategy

The kit includes 24 index adapters that support either eight unique pairs or 64 total combinations. When preparing samples of varying input amounts and quality, using eight **unique** index adapter pairs mitigates cross-talk.

The following table provides example index adapter combinations to help with sensitivity for low-input samples, especially those in the presence of high-input samples.

Sample Type	Index 1 (i7) Adapter	Index 2 (i5) Adapter
Casework sample 1	R713	A501
Casework sample 2	R714	A502
Reference sample 1	R716	A503
Reference sample 2	R717	A503

## ForenSeq mtDNA Whole Genome Kit Reference Guide

Sample Type	Index 1 (i7) Adapter	Index 2 (i5) Adapter
Reference sample 3	R718	A503
Reference sample 4	R719	A503
Positive control	R720	A504
Reagent blank	R721	A505
Negative control	R721	A506

### Purification Options

The protocol includes two purification processes: the first is required and the second is optional. Verogen recommends the optional purification when preparing libraries from samples with  $\leq 20$  pg total input gDNA to enhance sensitivity and improve the performance of low-input samples.

### Normalization Methods

The protocol includes two methods for library normalization. Libraries must be normalized for sequencing, so choose the method that best suits your input and throughput needs:

- **Bead-based normalization**—The standard normalization method. Use this method when processing high-input samples of similar input, amount, and type. This method is optimized for high-sample throughput and can be automated.
- **Quantification-based normalization**—An alternative normalization method. Use this method for low-input samples and samples of varying inputs, such as when combining reference samples and casework samples. This method is optimized for low-sample throughput and can improve sequencing representation for low-input samples with  $\leq 20$  pg total input.

### Tips and Techniques

#### Protocol Continuity

- Follow the steps in the order indicated using the specified volumes and incubation parameters.
- Unless a safe stopping point is specified, proceed immediately to the next step.

#### Plate Setup

- Avoid using wells along the edge of the plate when preparing  $< 48$  samples.
- Create a sample sheet to record the position of each sample, control, and index adapter.
- Reference the sample sheet throughout the protocol to ensure proper plate setup.

The *ForenSeq Universal Analysis Software v2.0 Reference Guide (document # VD2019002)* provides detailed information on sample sheets and input of sample information.

#### Preventing Cross-Contamination

- Designate a separate workspace for mtDNA extraction and analysis from nuclear DNA extraction and analysis.

## ForenSeq mtDNA Whole Genome Kit Reference Guide

- Set up the [Amplify and Tag Targets \(below\)](#) process in a pre-PCR environment. Perform all other processes in a post-PCR environment.
- When adding or transferring samples, change tips between **each sample**.
- When adding adapters or primers, change tips between **each well**.
- When processing smaller sample batches of less than 96 libraries at a time, prevent aerosolization by resealing the utilized, pierced UDI wells with Microseal "B" adhesive seal. Trim excess seal with a scissors.
- Do not apply Microseal "B" to unused UDI wells as this will impact the integrity of the single-use pierceable foil.
- Remove unused index adapter tubes from the working area.

### Sealing the Plate

- Apply a microseal to cover the plate and seal with a rubber roller. After each use, discard seals from plates.
- Use Microseal 'A' pressure film for thermal cycling. When using fewer than 96 wells, you can cut the film to size.
- Use Microseal 'B' adhesive film for shaking, centrifuging, and long-term storage. These seals are effective at -40°C to 110°C.

### Handling Beads

- For optimal performance and yield, confirm that beads are at room temperature before use.
- Aspirate and dispense beads slowly due to viscosity.
- Do not centrifuge plates and tubes containing beads, except when indicated.
- Vortex beads before use and frequently throughout the protocol to resuspend. Resuspended beads are evenly distributed and homogenous in color.
- If beads aspirate into pipette tips during supernatant removal, dispense back to the plate on the magnetic stand and wait until the liquid is clear (~2 minutes).

## Amplify and Tag Targets

This process uses an oligonucleotide primer mix to amplify and tag regions specific to DNA sequences in the whole mtGenome.

### Consumables

- FEM (ForenSeq Enzyme Mix)
- HL60 (Control DNA HL60)
- mtPCR1 (mtPCR1 Reaction Mix)
- WGS1 (Whole Genome Mix Set 1)
- WGS2 (Whole Genome Mix Set 2)
- Input DNA
- Nuclease-free water
- 1.7 ml microcentrifuge tubes (4)
- 96-well PCR plate, skirted or semi-skirted
- Microseal 'A' film
- Microseal 'B' film
- [Optional] RNase/DNase-free 8-tube strips and caps (2)

### About Reagents

- Dispense mtPCR1 slowly to prevent bubbles.
- Do not vortex FEM, HL60, or input DNA.

### Preparation

1. Prepare the following consumables:

Reagent	Storage	Instructions
FEM	-25°C to -15°C	Thaw at room temperature, and then centrifuge briefly. Return to storage immediately after use.
HL60	2°C to 8°C	Let stand for 30 minutes to bring to room temperature. Flick to mix, and then centrifuge.
mtPCR1	-25°C to -15°C	Thaw at room temperature. Vortex to mix, and then centrifuge briefly.
WGS1	2°C to 8°C	Let stand for 30 minutes to bring to room temperature. Vortex to mix, and then centrifuge.
WGS2	2°C to 8°C	Let stand for 30 minutes to bring to room temperature. Vortex to mix, and then centrifuge.

2. Save the following mtPCR1 program on the thermal cycler in the post-amplification area. See [Table 1](#) for ramp modes.
  - Choose the preheat lid option and set to 100°C
  - Reaction volume is 15 µl
  - 98°C for 3 minutes
  - 8 cycles of:
    - 96°C for 45 seconds
    - 80°C for 10 seconds
    - 54°C for 2 minutes, with applicable ramp mode
    - 66°C for 1.5 minutes, with applicable ramp mode
  - 10 cycles of:
    - 96°C for 30 seconds
    - 68°C for 2 minutes, with applicable ramp mode
  - 68°C for 10 minutes
  - Hold at 10°C

**Table 1 Ramp modes**

Thermal Cycler	Ramp Mode
ABI LTI thermal cycler 9700 9600 emulation mode	8%
Bio-Rad	0.2°C per second

## ForenSeq mtDNA Whole Genome Kit Reference Guide

Thermal Cycler	Ramp Mode
Eppendorf Mastercycler Pro S	2%
Proflex 96-well PCR System	0.2°C per second
QIAamplifier96 thermal cycler	0.1°C per second
Veriti 96-well thermal cycler	4%

Total program time is ~3.5 hours and can continue overnight.

3. Label tubes and the plate as follows.

Vessel	Label
1.7 ml microcentrifuge tube	Master Mix WGS1
1.7 ml microcentrifuge tube	Master Mix WGS2
1.7 ml microcentrifuge tube	Control DNA Dilution 1
1.7 ml microcentrifuge tube	Control DNA Dilution 2
96-well PCR plate	mtDNA WG Sample Plate

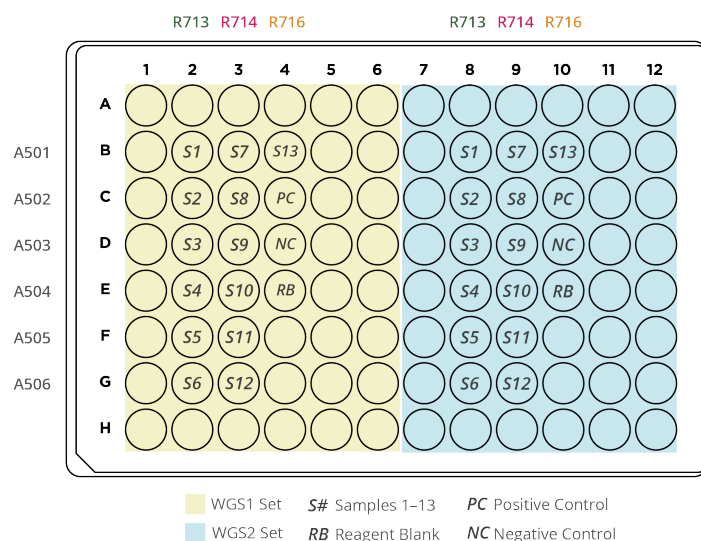
### Procedure

- Using nuclease-free water, dilute 100 pg gDNA to a volume of  $\geq 12 \mu\text{l}$  at 8.33 pg/ $\mu\text{l}$ . Gently pipette to mix.
- In the Master Mix WGS1 tube, combine the following volumes. Multiply each volume by the number of samples and add 10% for overage.
  - mtPCR1 (3.7  $\mu\text{l}$ )
  - FEM (0.3  $\mu\text{l}$ )
  - WGS1 (5  $\mu\text{l}$ )For example, for 16 samples prepare 158.4  $\mu\text{l}$  WGS1 Master Mix: 65.1  $\mu\text{l}$  mtPCR1, 5.3  $\mu\text{l}$  FEM, and 88  $\mu\text{l}$  WGS1.
- In the Master Mix WGS2 tube, combine the following volumes. Multiply each volume by the number of samples and add 10% for overage.
  - mtPCR1 (3.7  $\mu\text{l}$ )
  - FEM (0.3  $\mu\text{l}$ )
  - WGS2 (5  $\mu\text{l}$ )For example, for 16 samples prepare 158.4  $\mu\text{l}$  WGS2 Master Mix: 65.1  $\mu\text{l}$  mtPCR1, 5.3  $\mu\text{l}$  FEM, and 88  $\mu\text{l}$  WGS2.
- Pipette each master mix to mix, and then cap and centrifuge briefly.
- [Optional] For > 16 samples:
  - Transfer WGS1 Master Mix to an 8-tube strip, evenly distributing between tubes.
  - Transfer WGS2 Master Mix to an 8-tube strip, evenly distributing between tubes.

## ForenSeq mtDNA Whole Genome Kit Reference Guide

6. Using a multichannel pipette, add master mixes to the mtDNA WG Sample Plate:
  - a. Divide the plate into two even sections depending on the number of samples. See [Example plate setup for 16 samples \(below\)](#) for an example.
  - b. Add 9 µl WGS1 Master Mix to each well in the first section.
  - c. Add 9 µl WGS2 Master Mix to each well in the second section.

**Figure 4** Example plate setup for 16 samples



This step sets up the plate for samples and controls divided into two sets. A subsequent step splits each sample and control into two reactions: one for the WGS1 set and one for the WGS2 set. Both reactions must use the same i7 (R7XX) and i5 (A50X) index adapter combination.

7. Dilute 10 ng/µl HL60 stock:
  - a. In the Control DNA Dilution 1 tube, combine the following volumes to prepare 100 pg/µl HL60:
    - 10 ng/µl HL60 (2 µl)
    - Nuclease-free water (198 µl)
  - b. Gently pipette to mix, and then cap and centrifuge briefly.
  - c. In the Control DNA Dilution 2 tube, combine the following volumes to prepare 8.33 pg/µl HL60:
    - 100 pg/µl HL60 (5 µl)
    - Nuclease-free water (55 µl)
  - d. Gently pipette to mix, and then cap and centrifuge briefly.
8. Add the reagent blank:
  - a. Add 6 µl reagent blank to one well of the WGS1 set.
  - b. Add 6 µl reagent blank to the corresponding well of the WGS2 set.
  - c. Pipette to mix.
9. Divide each sample between the two sets:
  - a. Add 6 µl 8.33 pg/µl gDNA to one well of the WGS1 set.

## ForenSeq mtDNA Whole Genome Kit Reference Guide

- b. Add 6 µl 8.33 pg/µl gDNA to the corresponding well of the WGS2 set.
    - c. Pipette to mix.
10. Add the positive amplification control:
  - a. Add 6 µl 8.33 pg/µl HL60 to one well of the WGS1 set.
  - b. Add 6 µl 8.33 pg/µl HL60 to the corresponding well of the WGS2 set.
  - c. Pipette to mix.
11. Add the negative amplification control:
  - a. Add 6 µl nuclease-free water to one well of the WGS1 set.
  - b. Add 6 µl nuclease-free water to the corresponding well of the WGS2 set.
  - c. Pipette to mix.
12. Seal with microseal 'A' film, and then centrifuge at 1000 × g for 30 seconds.
13. Place on the preprogrammed thermal cycler and run the mtPCR1 program.

### SAFE STOPPING POINT

If you are stopping, seal the plate and store at 2°C to 8°C for up to 2 days. Alternatively, leave on the thermal cycler overnight.

### Enrich Targets

This process amplifies the DNA and adds Index 1 (i7) Adapters, Index 2 (i5) Adapters, and the sequences required for cluster generation. The index adapters tag DNA with a unique combination of sequences that identify each sample.

When preparing eight samples, you can perform this process using an 8-tube strip instead of the 96-well PCR plate.

### Consumables

- Index 1 Adapters (R7XX) and green caps
- Index 2 Adapters (A50X) and white caps
- mtPCR2 (mtPCR2 Reaction Mix)
- ForenSeq Index Plate Fixture
- 1.7 ml microcentrifuge tubes (1 per index adapter tube)
- RNase/DNase-free 8-tube strip and caps
- Microseal 'A' film
- Microseal 'B' film

### About Reagents

- Dispense mtPCR2 slowly to prevent bubbles.
- Centrifuge index adapter tubes in the 1.7 ml microcentrifuge tubes.
- Use the same i7 and i5 index adapter combination for both reactions set up for a sample.



## ForenSeq mtDNA Whole Genome Kit Reference Guide

### Preparation

1. Prepare the following consumables:

Item	Storage	Instructions
Index adapters	-25°C to -15°C	Remove only the index adapters being used. Thaw at room temperature for 20 minutes. Vortex each tube to mix, and then centrifuge briefly.
mtPCR2	-25°C to -15°C	Thaw at room temperature, and then invert to mix.

2. Save the following mtPCR2 program on the thermal cycler:

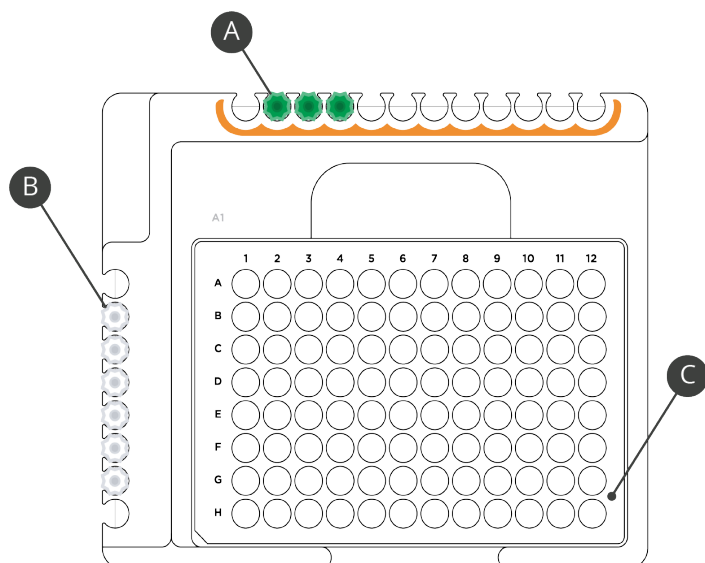
- Choose the preheat lid option and set to 100°C
- Reaction volume is 50 µl
- 98°C for 30 seconds
- 15 cycles of:
  - 98°C for 20 seconds
  - 66°C for 30 seconds
  - 68°C for 1.5 minutes
- 68°C for 10 minutes
- Hold at 10°C

Total program time is ~45 minutes.

### Procedure

1. Centrifuge the sealed mtDNA WG Sample Plate at 1000 × g for 30 seconds.
2. Arrange the index adapters in the ForenSeq Index Plate Fixture:
  - a. Place an Index 1 Adapter tube (green cap) in each column corresponding to the WGS1 set.
  - b. Place an Index 2 Adapter tube (white cap) in each row containing sample.
3. Place the mtDNA WG Sample Plate on the ForenSeq Index Plate Fixture.

**Figure 5** Example fixture setup for 16 samples



- A** Index 1 Adapter tubes in columns 2-4
- B** Index 2 Adapter tubes in rows B-G
- C** mtDNA WG Sample Plate

4. With a multichannel pipette, add Index 1 Adapters:
  - a. Down columns in the WGS1 set, add 4  $\mu$ l R7XX to each well.
  - b. Move the Index 1 Adapter tubes to the columns corresponding to the WGS2 set. Keep the same sequence used for the WGS1 set.
  - c. Down columns in the WGS2 set, add 4  $\mu$ l R7XX to each well.
  - d. Replace the cap on each Index 1 Adapter tube with a new green cap.
5. With a multichannel pipette, add Index 2 Adapters:
  - a. Add 4  $\mu$ l A50X across each row.
  - b. Replace the cap on each Index 2 Adapter tube with a new white cap.
6. Invert mtPCR2 several times to mix, and then centrifuge briefly.
7. [Optional] Evenly divide mtPCR2 among each tube of an 8-tube strip. Use a multichannel pipette to dispense.
8. Add 27  $\mu$ l mtPCR2 to each well.
9. Pipette to mix.
10. Seal with microseal 'A' film, and then centrifuge at 1000  $\times$  g for 30 seconds.
11. Place on the preprogrammed thermal cycler and run the mtPCR2 program.

### SAFE STOPPING POINT

If you are stopping, seal the plate and store at 2°C to 8°C for up to 7 days. Alternatively, leave on the thermal cycler overnight.

### Purify Libraries

This process combines purification beads with an enzyme to purify the amplified libraries from other reaction components. If you plan to perform the optional second purification, this process is the first of two purifications.

#### Consumables

- ProK (Proteinase K)
- RSB (Resuspension Buffer)
- SPB2 (Sample Purification Beads 2)
- [Second purification] 96-well midi plates (2)
- [No second purification] The following plates:
  - 96-well midi plate
  - 96-well PCR plate, skirted or semiskirted
- Freshly prepared 80% ethanol (EtOH)
- 1.7 ml microcentrifuge tube
- 50 ml reservoir
- Microseal 'B' film

#### About Reagents

- Aspirate and dispense SPB2/ProK slowly due to viscosity.

#### Preparation

1. Prepare the following consumables:

Item	Storage	Instructions
ProK	2°C to 8°C	Let stand for 30 minutes to bring to room temperature. Invert to mix, and then centrifuge.
RSB	2°C to 8°C	Let stand for 30 minutes to bring to room temperature. Vortex and invert to mix.
SPB2	2°C to 8°C	Let stand for 30 minutes to bring to room temperature. Vortex for <b>≥ 1 minute</b> and invert to mix.

2. For each sample, prepare 440 µl fresh 80% EtOH from absolute ethanol.
3. If you are performing the second purification, label plates as follows.

Plate Type	Label
Midi	Purification Bead Plate
Midi	Purification Bead Plate 2

4. If you are **not** performing the second purification, label plates as follows.

Plate Type	Label
Midi	Purification Bead Plate

## ForenSeq mtDNA Whole Genome Kit Reference Guide

Plate Type	Label
PCR	Purified Library Plate

- Prepare the SPB2 tube for a first or subsequent use:
  - For first-time use, add 25  $\mu$ l ProK to the SPB2 tube. Select the checkbox on the SPB2 label to indicate the addition.
  - For a subsequent use, make sure the checkbox on the SPB2 label is selected.
- Vortex and invert the ProK/SPB2 tube several times to mix.
- Prepare the appropriate volume of SPB2/ProK depending on how many samples you started the protocol with:

Number of Samples	Volume of SPB2/ProK ( $\mu$ l)	Instruction
$\leq 15$	$95 \times$ number of samples	Add the calculated volume to a 1.7 ml microcentrifuge tube.
$\geq 16$	$100 \times$ number of samples	Add the calculated volume to reservoir.

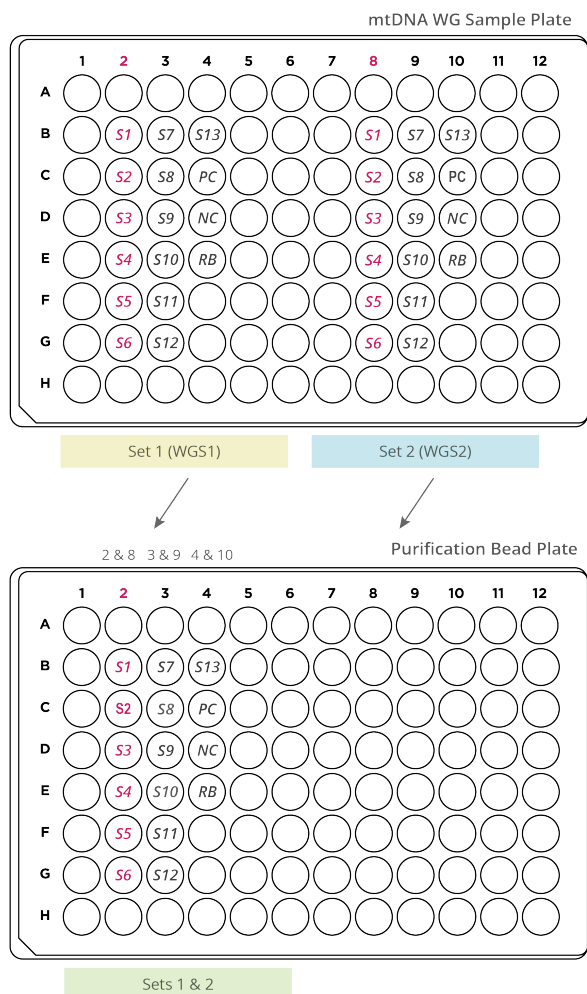
For example, for 16 samples add 1.6 ml SPB2/ProK to a reservoir.

### Procedure

- Add 90  $\mu$ l SPB2/ProK to each well of the Purification Bead Plate.
- Centrifuge the sealed mtDNA WG Sample Plate at  $1000 \times g$  for 30 seconds.
- With a multichannel pipette, transfer 45  $\mu$ l each reaction from the mtDNA WG Sample Plate to the corresponding column of the Purification Bead Plate to combine each reaction set in one well.

For example, transfer columns 2 and 8 of the mtDNA WG Sample Plate to column 2 of the Purification Bead Plate (see [Example transfer for 16 samples \(next page\)](#)). The resulting volume per well is 180  $\mu$ l (90  $\mu$ l sample + 90  $\mu$ l SPB2/ProK).

**Figure 6** Example transfer for 16 samples



4. Discard the mtDNA WG Sample Plate.
5. Seal the Purification Bead Plate and shake at 1800 rpm for 2 minutes.
6. Incubate at room temperature for 5 minutes.
7. Place on the magnetic stand and wait until the liquid is transparent (~5 minutes).
8. Remove and discard all supernatant.
9. Keep on the magnetic stand and wash as follows.
  - a. Add 200 µl fresh 80% EtOH to each well.
  - b. Incubate for 30 seconds.
  - c. Remove and discard all supernatant.
10. Wash a **second** time.
11. With a 20 µl pipette, remove residual EtOH from each well.
12. Remove from the magnetic stand.
13. Add 52.5 µl RSB to each well.

## ForenSeq mtDNA Whole Genome Kit Reference Guide

14. Seal and shake at 1800 rpm for 2 minutes.
15. If the beads are not fully resuspended, pipette to mix or reshake at 1800 rpm for 2 minutes.
16. Incubate at room temperature for 2 minutes.
17. Place on the magnetic stand and wait until the liquid is clear (~2 minutes).
18. Transfer 50  $\mu$ l supernatant from each well of the Purification Bead Plate to the applicable plate:
  - If you are performing the second purification, transfer to the Purification Bead Plate 2.
  - If you are not performing the second purification, transfer to the Purified Library Plate.
19. Seal and centrifuge at 1000  $\times$  g for 30 seconds.

### SAFE STOPPING POINT

If you are stopping, seal the plate and store at -25°C to -15°C for up to 1 year.

### Perform Second Purification (Optional)

This optional process repeats the preceding purification process, combining purification beads with an enzyme to further purify libraries. A second purification is highly beneficial for low-input samples ( $\leq$  20 pg gDNA).

### Consumables

- ProK (Proteinase K)
- RSB (Resuspension Buffer)
- SPB2 (Sample Purification Beads 2)
- Freshly prepared 80% ethanol (EtOH)
- 1.7 ml microcentrifuge tube
- 50 ml reservoir
- 96-well PCR plate, skirted or semi-skirted
- Microseal 'B' film

### About Reagents

- Aspirate and dispense SPB2/ProK slowly due to viscosity.

### Preparation

1. Prepare the following consumables:

Item	Storage	Instructions
ProK	2°C to 8°C	Let stand for 30 minutes to bring to room temperature. Invert to mix, and then centrifuge.
RSB	2°C to 8°C	Let stand for 30 minutes to bring to room temperature. Vortex and invert to mix.
SPB2	2°C to 8°C	Let stand for 30 minutes to bring to room temperature. Vortex for $\geq$ <b>1 minute</b> and invert to mix.

2. For each sample, prepare 440  $\mu$ l fresh 80% EtOH from absolute ethanol. Alternatively, use 80% EtOH prepared within the day.
3. Label a new PCR plate Purified Library Plate.

## ForenSeq mtDNA Whole Genome Kit Reference Guide

- Prepare the SPB2 tube for a first or subsequent use:
  - For first-time use, add 25  $\mu$ l ProK to the SPB2 tube. Select the checkbox on the SPB2 label to indicate the addition.
  - For a subsequent use, make sure the checkbox on the SPB2 label is selected.
- Vortex and invert the ProK/SPB2 tube several times to mix.
- Prepare the appropriate volume of SPB2/ProK depending on the number of samples:

Number of Samples	Volume of SPB2/ProK ( $\mu$ l)	Instruction
$\leq 15$	55 $\times$ number of samples	Add the calculated volume to a 1.7 ml microcentrifuge tube.
$\geq 16$	60 $\times$ number of samples	Add the calculated volume to a reservoir.

### Procedure

- Add 50  $\mu$ l SPB2/ProK to each sample well of the Purification Bead Plate 2. Each well contains a volume of 100  $\mu$ l.
- Seal and shake at 1800 rpm for 2 minutes.
- Incubate at room temperature for 5 minutes.
- Place on the magnetic stand and wait until the liquid is clear (~5 minutes).
- Remove and discard all supernatant.
- Keep on the magnetic stand and wash as follows.
  - Add 200  $\mu$ l fresh 80% EtOH to each well.
  - Incubate for 30 seconds.
  - Remove and discard all supernatant.
- Wash a **second** time.
- With a 20  $\mu$ l pipette, remove residual EtOH from each well.
- Remove from the magnetic stand.
- Add 52.5  $\mu$ l RSB to each well.
- Seal and shake at 1800 rpm for 2 minutes.
- If the beads are not fully resuspended, pipette to mix or reshake at 1800 rpm for 2 minutes.
- Incubate at room temperature for 2 minutes.
- Place on the magnetic stand and wait until the liquid is clear (~2 minutes).
- Transfer 50  $\mu$ l supernatant from each well of the Purification Bead Plate 2 to the Purified Library Plate.
- Seal and centrifuge at 1000  $\times$  g for 30 seconds.

### SAFE STOPPING POINT

If you are stopping, seal the plate and store at -25°C to -15°C for up to 1 year.

### Normalize Libraries Using a Bead-Based Method (Option 1)

This process normalizes the concentration of each library for even representation without the need for post-PCR quantification and individual normalization. Samples of varying type and input amounts achieve consistent cluster density, optimizing the resolution of individual libraries in a pool.

Use a bead-based method to normalize libraries from high-input samples of similar input, amount, and type. This method is optimized for high-sample throughput and can be automated.

#### Consumables

- HP3 (2 N NaOH)
- LNA1 (Library Normalization Additives 1)
- LNB1 (Library Normalization Beads 1)
- LNS2 (Library Normalization Storage Buffer 2)
- LNW1 (Library Normalization Wash 1)
- Nuclease-free water
- 1.7 ml microcentrifuge tubes (3)
- 15 ml conical tube
- 50 ml reservoir
- 96-well midi plate
- 96-well PCR plate, skirted or semi-skirted
- Microseal 'B' film

Warning: This set of reagents contains potentially hazardous chemicals. Personal injury can occur through inhalation, ingestion, skin contact, and eye contact. Wear protective equipment, including eye protection, gloves, and laboratory coat appropriate for risk of exposure. Handle used reagents as chemical waste and discard in accordance with applicable regional, national, and local laws and regulations. **For complete environmental, health, and safety information, see the safety data sheets (SDS) at [verogen.com/product-documentation](https://verogen.com/product-documentation).**

#### About Reagents

- The volumes to prepare LNA1/LNB1 Master Mix and 0.1 N HP3 include overage.

#### Preparation

1. Prepare the following consumables:

Item	Storage	Instructions
HP3	-25°C to -15°C	Thaw at room temperature.
LNA1	-25°C to -15°C	Thaw at room temperature. Vortex with intermittent inversion.
LNB1	2°C to 8°C	Let stand for 30 minutes to bring to room temperature. Vortex for at least 1 minute, inverting five times every 15 seconds. Pipette until the beads are fully resuspended.



## ForenSeq mtDNA Whole Genome Kit Reference Guide

Item	Storage	Instructions
LNW1	2°C to 8°C	Let stand for 30 minutes to bring to room temperature.
LNS2	15°C to 30°C	Remove from storage.

2. Hold LNA1 in front of a light. Make sure that no crystals are present and all precipitate has dissolved.
3. Make sure that LNB1 is fully resuspended with no pellet at the bottom of the tube. If necessary, use a 1000 µl pipette to fully resuspend.
4. Label tubes and plates as follows.

Vessel	Label
1.7 ml microcentrifuge tube	0.1 N HP3
1.7 ml microcentrifuge tube or 15 ml conical tube	LNA1/LNB1 Master Mix
Midi plate	Normalization Working Plate
PCR plate	Normalization Library Plate

5. Dedicate separate hazardous waste disposal containers for liquids and solids.

### Procedure

1. Vortex LNB1 to resuspend.
2. In the LNA1/LNB1 Master Mix tube, combine the following volumes without adding overage. Multiply each volume by the number of samples.
  - LNA1 (46.8 µl)
  - LNB1 (8.5 µl)
3. Cap and vortex the LNA1/LNB1 Master Mix tube, and then invert several times to mix.
4. Transfer all LNA1/LNB1 Master Mix to a reservoir.
5. Add 45 µl LNA1/LNB1 Master Mix to each sample well of the Normalization Working Plate.
6. Place the Purified Library Plate on the magnetic stand and wait until the liquid is clear (~2 minutes).
7. Transfer 20 µl from each well of the Purified Library Plate to the corresponding well of the Normalization Working Plate.

Each well contains a volume of 65 µl.
8. Seal the Purified Library Plate containing remaining libraries and store at -25°C to -15°C for up to 1 year from the date of purification.
9. Seal the Normalization Working Plate and shake at 1800 rpm for 30 minutes.
10. While the plate is shaking, perform steps 11–13 to save time later in the process.
11. In the 0.1 N HP3 tube, combine the following volumes without adding overage. Multiply each volume by the number of samples.
  - Nuclease-free water (33.3 µl)
  - HP3 (1.8 µl)
12. Invert several times to mix, and then set aside.
13. Add 30 µl LNS2 to each sample well of the Normalization Library Plate, and then set aside.

## ForenSeq mtDNA Whole Genome Kit Reference Guide

14. Immediately after shaking, place the Normalization Working Plate on the magnetic stand and wait until the liquid is clear (~2 minutes).
15. Remove and discard all supernatant.
16. Wash as follows.
  - a. Remove from the magnetic stand.
  - b. Add 45  $\mu$ l LNW1 to each well.
  - c. Seal and shake at 1800 rpm for 5 minutes.
  - d. If the beads are not fully resuspended, pipette to mix or reshake at 1800 rpm for 5 minutes.
  - e. Place on the magnetic stand and wait until the liquid is clear (~2 minutes).
  - f. Remove and discard all supernatant.
17. Wash a **second** time.
18. Remove from the magnetic stand.
19. Seal and centrifuge at  $1000 \times g$  for 30 seconds.
20. Place on the magnetic stand and wait until the liquid is clear (~2 minutes).
21. With a 20  $\mu$ l pipette, remove residual supernatant from each well.
22. Remove from the magnetic stand.
23. Add 32  $\mu$ l 0.1 N HP3 to each well.
24. Seal and shake at 1800 rpm for 5 minutes.
25. If the beads are not fully resuspended, pipette to mix or reshake at 1800 rpm for 5 minutes.
26. Place on the magnetic stand and wait until the liquid is clear (~2 minutes).
27. Transfer 30  $\mu$ l supernatant from the Normalized Working Plate to the Normalization Library Plate. Pipette to mix as you dispense.

The resulting volume is 60  $\mu$ l per sample well.
28. Seal and centrifuge at  $1000 \times g$  for 30 seconds.

### SAFE STOPPING POINT

If you are stopping, seal the plate and store at  $-25^{\circ}\text{C}$  to  $-15^{\circ}\text{C}$  for up to 30 days.

## Normalize Libraries Using Manual Quantification (Option 2)

This process quantifies libraries and checks the quality. Accurate quantification helps ensure optimum cluster density on the flow cell and a similar number of read counts.

Use a manual quantification method to normalize libraries from low-input samples and samples of varying inputs. This method is optimized for low-sample throughput and can improve sequencing representation for low-input samples ( $\leq 20$  pg gDNA).

### Consumables

- RSB (Resuspension Buffer)
- 96-well PCR plate, skirted or semi-skirted
- 1.7 ml microcentrifuge tube

## ForenSeq mtDNA Whole Genome Kit Reference Guide

### Preparation

1. Prepare the following consumable:

Item	Storage	Instructions
RSB	2°C to 8°C	Let stand for 30 minutes to bring to room temperature. Vortex and invert to mix.

2. Label a new 96-well PCR plate Quant Normalized Library Plate.

### Procedure

1. Quantify the library using a fluorometric method, such as QuantiFluor ONE (recommended), AccuClear, PicoGreen, or Qubit.
2. For libraries with a concentration > 0.75 ng/μl, calculate the volume of RSB required to dilute the library to 0.75 ng/μl as follows.
  - a. Use the formula  $C_1V_1=C_2V_2$  to calculate the value for  $V_2$ , where:
    - $C_1$  is the library quantification result
    - $V_1$  is 4 μl undiluted library
    - $C_2$  is 0.75 ng/μl
    - $V_2$  is the final volume of diluted library
  - b. Calculate the requisite amount of RSB ( $V_2 - 4 \mu\text{l}$ ).
3. Add the calculated volume of RSB to the corresponding well of the Quant Normalized Library Plate. If a library is  $\geq 42 \text{ ng}/\mu\text{l}$ , add RSB to a 1.7 ml tube instead.
4. Transfer 4 μl of each library from the Purified Library Plate to the corresponding well of the Quant Normalized Library Plate or 1.7 ml tube.

The result is a Quant Normalized Library Plate or 1.7 ml tube of 0.75 ng/ul libraries.

### SAFE STOPPING POINT

If you are stopping, seal the plate and store at -25°C to -15°C for up to 30 days.

### Pool Libraries

This process combines equal volumes of normalized libraries to create a pool of libraries that are sequenced together on the same flow cell. Only pool libraries normalized with the same method.

### Consumables

- 1.7 ml microcentrifuge tube
- RNase/DNase-free 8-tube strip and caps
- Microseal 'B' film

### Preparation

1. Select  $\leq 16$  libraries to pool for sequencing.

## ForenSeq mtDNA Whole Genome Kit Reference Guide

Sixteen is the maximum number of ForenSeq mtDNA Whole Genome libraries the MiSeq FGx standard flow cell supports.

2. Label a new 1.7 ml microcentrifuge tube Pooled Normalized Libraries.

### Procedure

1. Transfer 5 µl each library to a new 8-tube strip.
2. Seal the Normalized Library Plate and store in the post-PCR area at -25°C to -15°C for up to 30 days.
3. Transfer libraries from the 8-tube strip to the Pooled Normalized Libraries tube.
4. Cap and vortex to mix, and then centrifuge briefly.
5. Follow the applicable instructions to denature and dilute libraries:
  - For bead-based normalized libraries, see [Denature and Dilute Bead-Normalized Libraries \(Option 1\)](#) (below).
  - For manually normalized libraries, see [Denature and Dilute Manually Normalized Libraries \(Option 2\)](#) (next page).

### SAFE STOPPING POINT

If you are stopping, seal the plate and store at -25°C to -15°C for up to 30 days.

### Denature and Dilute Bead-Normalized Libraries (Option 1)

This process adds a sequencing control and uses a heat-based method to denature and dilute libraries normalized with the bead-based method.

Start this process when you are ready to prepare sequencing reagents and set up the run. Delays can impact template loading.

### Consumables

- HP3 (2 N NaOH)
- HSC (Human Sequencing Control)
- Reagent Kit contents:
  - HT1 (Hybridization Buffer)
  - Reagent cartridge
- Nuclease-free water
- Pooled bead-based normalized libraries
- 1.7 ml microcentrifuge tubes (2)

### Preparation

1. Prepare the reagent cartridge per instructions in the *MiSeq FGx Sequencing System Guide* (document # VD2018006).
2. Prepare the following consumables:

Item	Storage	Instructions
HP3	-25°C to -15°C	Thaw at room temperature. Vortex to mix, and then centrifuge briefly.

## ForenSeq mtDNA Whole Genome Kit Reference Guide

Item	Storage	Instructions
HSC	-25°C to -15°C	Let stand for 30 minutes to bring to room temperature. Invert to mix, and then centrifuge.
HT1	-25°C to -15°C	Thaw at room temperature, and then vortex to mix.

3. Preheat the heat block to 96°C.
4. Label two new 1.7 ml microcentrifuge tubes as follows.
  - Denatured HSC
  - Denatured Normalized Libraries

### Procedure

1. In the Denatured HSC tube, combine the following volumes:
  - HSC (2 µl)
  - HP3 (2 µl)
  - Nuclease-free water (36 µl)
2. Pipette gently to mix. Cap and centrifuge briefly to mix
3. Incubate at room temperature for 5 minutes.
4. Add 600 µl HT1 to the Denatured Normalized Libraries tube.
5. Place the Pooled Normalized Libraries tube on the preheated heat block and incubate for 2 minutes.
6. Immediately transfer 5 µl library from the Pooled Normalized Libraries tube to the Denatured Normalized Libraries tube.
7. Pipette to mix.
8. Cap the Pooled Normalized Libraries tube and store at -25°C to -15°C for ≤ 30 days. Exceeding 30 days can significantly reduce cluster density.
9. Add 4 µl denatured HSC to the Denatured Normalized Libraries tube. You can store denatured HSC at room temperature for ≤ 1 day.
10. Pipette to mix.
11. Cap and vortex to mix, and then centrifuge briefly.
12. Immediately transfer the entire volume to the reagent cartridge per instructions in the *MiSeq FGx Sequencing System Guide (document # VD2018006)*.

### Denature and Dilute Manually Normalized Libraries (Option 2)

This process adds a sequencing control and uses an NaOH-based method to denature and dilute libraries normalized with the manual quantification method. The denaturation process ensures that the concentration of NaOH in the final library does not exceed 1 mM. Higher concentrations can inhibit hybridization to the flow cell and decrease cluster density.

Start this process when you are ready to prepare sequencing reagents and set up the run. Delays can impact template loading.

## ForenSeq mtDNA Whole Genome Kit Reference Guide

### Consumables

- HP3 (2 N NaOH)
- HSC (Human Sequencing Control)
- Reagent Kit contents:
  - HT1 (Hybridization Buffer)
  - Reagent cartridge
- Nuclease-free water
- Pooled manually quantified libraries
- 1.7 ml microcentrifuge tubes (4)

### Preparation

1. Prepare the reagent cartridge per instructions in the *MiSeq FGx Sequencing System Guide (document # VD2018006)*.
2. Prepare the following consumables:

Item	Storage	Instructions
HP3	-25°C to -15°C	Thaw at room temperature. Vortex to mix, and then centrifuge briefly.
HSC	-25°C to -15°C	Let stand for 30 minutes to bring to room temperature. Invert to mix, and then centrifuge.
HT1	-25°C to -15°C	Thaw at room temperature, and then vortex to mix.

3. Label three new 1.7 ml tubes as follows.
  - 6 pM Denatured Normalized Libraries
  - 20 pM Denatured Normalized Libraries
  - Denatured HSC
4. In another new 1.7 ml tube, combine the following volumes to prepare 0.1 ml 0.2 N NaOH:
  - Nuclease-free water (90 µl)
  - HP3 (10 µl)
5. Invert the tube several times to mix. Use within **12 hours**.  
Freshly prepared NaOH is essential to the denaturation process.

### Procedure

1. In the Denatured HSC tube, combine the following volumes to prepare denatured HSC:
  - HSC (2 µl)
  - HP3 (2 µl)
  - Nuclease-free water (36 µl)You can store denatured HSC at room temperature for ≤ 1 day.
2. Cap and vortex to mix, and then centrifuge briefly.
3. Incubate at room temperature for 5 minutes.
4. In the 20 pM Denatured Normalized Libraries tube, combine the following volumes:

## ForenSeq mtDNA Whole Genome Kit Reference Guide

- 0.75 ng/μl normalized library pool (5 μl)
  - 0.2 N HP3 (5 μl)
5. Cap and vortex briefly.
  6. Centrifuge at 280 × g for 1 minute.
  7. Incubate at room temperature for 5 minutes.
  8. Add 990 μl HT1 to the 20 pM Denatured Normalized Libraries tube.  
The result is 1 ml 20 pM denatured library.
  9. In the 6 pM Denatured Normalized Libraries tube, combine the following volumes to dilute the 20 pM library to 6 pM:
    - 20 pM library (180 μl)
    - HT1 (416 μl)
    - Denatured HSC (4 μl)
  10. Cap and vortex to mix, and then centrifuge briefly.
  11. Immediately transfer the entire volume to the reagent cartridge per instructions in the *MiSeq FGx Sequencing System Guide (document # VD2018006)*.

# Materials

Kit Contents and Storage .....	32
Consumables and Equipment .....	35

## Kit Contents and Storage

Make sure that you have the reagents identified in this section before starting the protocol. Use the reagents provided in the ForenSeq mtDNA Whole Genome Kit without making substitutions. When you receive the kit, promptly store reagents at the indicated temperatures.

Kit Name	Verogen Part #
ForenSeq mtDNA Whole Genome Kit (48 reactions)	V16000086

### ForenSeq mtDNA Whole Genome Kit (48 reactions) (V16000086)

#### Pre-PCR Box 1

Quantity	Reagent	Description	Cap	Storage
1	HL60	Control DNA HL60	Black	2°C to 8°C
1	WGS1	Whole Genome Mix Set 1	Blue	2°C to 8°C
1	WGS2	Whole Genome Mix Set 2	Red	2°C to 8°C

#### Pre-PCR Box 2

Quantity	Reagent	Description	Cap	Storage
1	FEM	ForenSeq Enzyme Mix	Yellow	-25°C to -15°C
2	mtPCR1	mtPCR1 Reaction Mix	Green	-25°C to -15°C

#### Post-PCR Box 3

Quantity	Reagent	Description	Cap	Storage
1	A501	A501 Index Adapter	White	-25°C to -15°C
1	A502	A502 Index Adapter	White	-25°C to -15°C
1	A503	A503 Index Adapter	White	-25°C to -15°C
1	A504	A504 Index Adapter	White	-25°C to -15°C
1	A505	A505 Index Adapter	White	-25°C to -15°C
1	A506	A506 Index Adapter	White	-25°C to -15°C
1	A507	A507 Index Adapter	White	-25°C to -15°C



## ForenSeq mtDNA Whole Genome Kit Reference Guide

Quantity	Reagent	Description	Cap	Storage
1	A508	A508 Index Adapter	White	-25°C to -15°C
1	HP3	2 N NaOH	Orange	-25°C to -15°C
1	HSC	Human Sequencing Control	Pink	-25°C to -15°C
1	LNA1	Library Normalization Additives 1	Clear	-25°C to -15°C
1	LNS2	Library Normalization Storage Buffer 2	Clear	15°C to 30°C*
1	LNW1	Library Normalization Wash 1	Clear	-25°C to -15°C
2	mtPCR2	mtPCR2 Reaction Mix	Purple	-25°C to -15°C
1	R713	R713 Index Adapter	Green	-25°C to -15°C
1	R714	R714 Index Adapter	Green	-25°C to -15°C
1	R716	R716 Index Adapter	Green	-25°C to -15°C
1	R717	R717 Index Adapter	Green	-25°C to -15°C
1	R718	R718 Index Adapter	Green	-25°C to -15°C
1	R719	R719 Index Adapter	Green	-25°C to -15°C
1	R720	R720 Index Adapter	Green	-25°C to -15°C
1	R721	R721 Index Adapter	Green	-25°C to -15°C
1	Not applicable	i7 Index Tube Caps	Green	15°C to 30°C*
1	Not applicable	i5 Index Tube Caps	White	15°C to 30°C*

\* Shipped at -25°C to -15°C.

### Post-PCR Box 4

Quantity	Reagent	Description	Cap	Storage
1	LNB1	Library Normalization Beads 1	White	2°C to 8°C
2	ProK	Proteinase K	Clear	2°C to 8°C
1	RSB	Resuspension Buffer	Purple	2°C to 8°C
2	SPB2	Sample Purification Beads 2	Red	2°C to 8°C

## Index Adapter Sequences

The following tables list the 8 bp sequences for the index adapters included in the kit.

### Index 1 (i7)

Index Name	Sequence
R713	AGTCAAAT

## ForenSeq mtDNA Whole Genome Kit Reference Guide

Index Name	Sequence
R714	AGTTCCAT
R716	CCGTCCAT
R717	GTAGAGAT
R718	GTCCGCAT
R719	GTGAAAAT
R720	GTGGCCAT
R721	GTTTCGAT

### Index 2 (i5)

Index Name	Sequence
A501	TGAACCTT
A502	TGCTAAGT
A503	TGTTCTCT
A504	TAAGACAC
A505	CTAATCGA
A506	CTAGAACA
A507	TAAGTTCC
A508	TAGACCTA

## Consumables and Equipment

Make sure that you have the following user-supplied consumables and equipment before starting the protocol. These items supplement the library prep reagents and index adapters provided in the kit.

### Consumables

Consumable	Supplier
1.7 ml microcentrifuge tubes	General lab supplier
15 ml conical tubes	General lab supplier
20 µl barrier pipette tips	General lab supplier
200 µl barrier pipette tips	General lab supplier
50 ml PVC reservoirs	VWR, catalog # 89094-688
96-well deepwell storage plates, 0.8 ml (midi plate)	Fisher Scientific, catalog # AB-0859
96-well twin.tec PCR plates, semi-skirted, 250 µl	One of the following suppliers: • Eppendorf, catalog # 951020303 • VWR, catalog # 89136-706
96-well twin-tec PCR Plate, skirted, 150 µl	Eppendorf, catalog # 951020401
Ethyl alcohol, 200 proof for molecular biology, 500 ml (absolute alcohol)	MilliporeSigma, product # E7023
Microseal 'A' sealing film	Bio-Rad, catalog # MSA5001
Microseal 'B' sealing film, adhesive, optical	Bio-Rad, catalog # MSB1001
Reagent Kit	Verogen, part # 15066817
Nuclease-free water	General lab supplier
RNase/DNase-free 8-tube strips and caps	General lab supplier
QuantiFluor ONE dsDNA System*	Promega, catalog # E4870 or E4871
[Optional] Index Adapter Replacement Caps	Verogen, part # 15026762

\* Or equivalent fluorometric method, such as AccuClear, PicoGreen, or Qubit.

### Equipment

Equipment	Supplier	Pre-PCR	Post-PCR
20 µl multichannel pipettes (8-channel)	General lab supplier	X	X
200 µl multichannel pipette (8-channel)	General lab supplier		X
Benchtop microcentrifuge	General lab supplier	X	X
ForenSeq Index Plate Fixture	Verogen, part # 15055269		X

## ForenSeq mtDNA Whole Genome Kit Reference Guide

Equipment	Supplier	Pre-PCR	Post-PCR
Magnetic stand-96	Life Technologies, catalog # AM10027		X
Microcentrifuge tube heat block	General lab supplier		X
Microplate centrifuge	General lab supplier	X	X
Thermal cycler, 96-well with heated lid	See <a href="#">Thermal Cyclers (below)</a>		X
Thermoshaker, BioShake iQ or BioShake XP	QInstruments, item # 1808-0506 or 1808-0505		X
Quantus Fluorometer	Promega, catalog # E6150	X	X*
Vortexer	General lab supplier	X	X

\* For normalization using the manual quantification method.

### Thermal Cyclers

The following table lists supported thermal cyclers with recommended settings. If your laboratory has an unlisted thermal cycler, evaluate the thermal cycler before performing the protocol.

Thermal Cycler	Temperature Mode	Lid Temperature	Vessel Type
ABI LTI thermal cycler 9700 <sup>1</sup>	9600 Emulation	Heated	Polypropylene plates and tubes
Bio-Rad	Calculated	Heated, constant at 100°C	Polypropylene plates and tubes
Eppendorf Mastercycler Pro S	Standard	Heated	Plate
Proflex 96-well PCR System	Not applicable	Heated, constant at 100°C	Polypropylene plates and tubes
Veriti 96-well thermal cycler <sup>2</sup>	Standard	Heated, constant at 100°C	Polypropylene plates and tubes

<sup>1</sup> Only the fast block (gold) is supported.

<sup>2</sup> Only the standard blocks is supported.

## Technical Support

For technical assistance, contact Verogen Technical Support.

### Contact Information

**Address** 11111 Flintkote Avenue  
San Diego CA 92121 USA

**Website** [www.verogen.com](http://www.verogen.com)

**Email** [techsupport@verogen.com](mailto:techsupport@verogen.com)

**Telephone** +1.833.837.6436 toll-free (North America)  
+1.858.285.4101 tel  
+44 (0) 208 054 8706 (United Kingdom)

**Safety data sheets (SDS)**—Available for download from [verogen.com/product-documentation](http://verogen.com/product-documentation).

**Product documentation**—Available for download from [verogen.com/product-documentation](http://verogen.com/product-documentation).

## Meet any challenge

Verogen is a dedicated developer of human identification products for sequencing and analysis of forensic genomic samples. Working closely with the forensics community, Verogen places exceptional value on flexible, scalable solutions that deliver results when you need them most.

Verogen

+1.833.837.6436 toll-free  
(North America)

+1.858.285.4101  
(outside North America)

[techsupport@verogen.com](mailto:techsupport@verogen.com)

[www.verogen.com](http://www.verogen.com)