



ThruPLEX[®] Plasma-seq Kit Instruction Manual

ILLUMINA[®] NGS Library Preparation

Designed and Optimized for Cell-Free DNA

Product Use Limitations

ThruPLEX[®] Plasma-seq Kit is intended for **Research Use Only**. It may not be used for any other purposes including, but not limited to, use in diagnostics, forensics, therapeutics, or in humans. ThruPLEX Plasma-seq may not be transferred to third parties, resold, modified for resale or used to manufacture commercial products without prior written approval of Rubicon Genomics, Inc.

*Protected by U.S. Patents 7,803,550; 8,071,312; 8,399,199; 8,728,737 and corresponding foreign patents.
Additional patents are pending.

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Product Description

ThruPLEX[®] Plasma-seq is powered by ThruPLEX chemistry to generate high performance NGS libraries from cell-free DNA isolated from plasma. The repair and ligation chemistries have been reformulated for cell-free DNA to minimize duplicates providing maximum library complexity and to preserve the GC representation of the input DNA. ThruPLEX Plasma-seq libraries can be used directly for whole genome sequencing applications or enriched using your custom panel or the leading target enrichment platforms, such as Agilent SureSelect[®] and Roche NimbleGen[®] SeqCap[®] EZ. For more information please visit:

<http://rubicongenomics.com/products/thruplex-plasma-seq-kit/>.

Kit Contents

ThruPLEX Plasma-seq Kit contains sufficient reagents to prepare up to the specified number of reactions. Enough buffers and enzymes are provided to prepare master mixes for up to 4 separate uses. **Freeze thaw of reagents should be limited to no more than four times.** Contents of ThruPLEX Plasma-seq Kit are not interchangeable with other Rubicon Genomics products.

Table 1: ThruPLEX Plasma-seq Kit Contents

Name	Cap Color	12S Kit R400490 12 Single Indexes 12 Reactions	48S Kit R400491 48 Single Indexes 48 Reactions	96D Kit R400492 96 Dual Indexes 96 Reactions
Template Preparation Buffer	Red	1 Tube	1 Tube	2 Tubes
Template Preparation Enzyme	Red	1 Tube	1 Tube	2 Tubes
Library Synthesis Buffer	Yellow	1 Tube	1 Tube	2 Tubes
Library Synthesis Enzyme	Yellow	1 Tube	1 Tube	2 Tubes
Library Amplification Buffer	Green	1 Tube	1 Tube	2 Tubes
Library Amplification Enzyme	Green	1 Tube	1 Tube	2 Tubes
Nuclease-Free Water	Clear	1 Tube	1 Tube	1 Tube
Indexing Reagents	Blue	12 Tubes	1 Single Index Plate (48S)	1 Dual Index Plate (96D)
Quick Protocol	N/A	1 Each	1 Each	1 Each

Shipping and Storage

ThruPLEX Plasma-seq Kit is shipped on dry ice. The kit must be stored at -20°C upon arrival.

Quality Control

ThruPLEX Plasma-seq Kit is functionally tested using Next Generation Sequencing (NGS) to ensure product quality and consistency.

Safety Information

Follow standard laboratory safety procedures and wear a lab coat, protective goggles and disposable gloves to ensure personal safety as well as to limit potential cross contaminations during the sample preparation and subsequent amplification reactions. For more information please refer to the appropriate Safety Data Sheets (SDS) available online at <http://rubicongenomics.com/resources/msds/>.

Technical Assistance

For technical support with any of Rubicon Genomics, Inc. products please contact technical support by email: support@rubicongenomics.com or call (734) 677-4845 (9 AM – 5:30 PM EST).

A. Introduction

Next-generation sequencing (NGS) of circulating cell-free DNA (cfDNA) from plasma is a rapidly growing application. Regardless of the specific application, a DNA library must be prepared from each sample in order to be sequenced on Illumina NGS platforms. Library preparation is a critical step in the NGS workflow (Figure 1) and has a direct impact on the quality of sequencing results. The process involves placing Illumina sequencing adapters on DNA fragments and adding Illumina-compatible indexes for identification of individual samples. Multiple samples are then pooled (multiplexed) and sequenced in parallel.

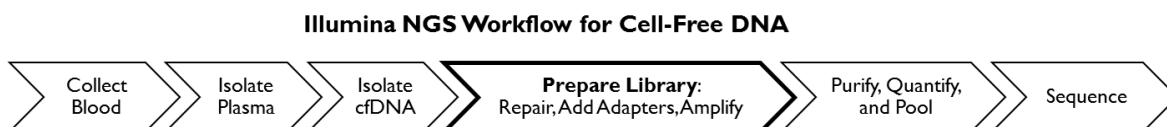


Figure 1. Illumina NGS workflow for cell-free DNA: Blood samples are collected, plasma is isolated, and cell-free DNA (cfDNA) purified. ThruPLEX Plasma-seq library preparation follows and consists of three steps: repair, ligation and amplification. Indexed libraries are purified, quantified, and pooled prior to sequencing on Illumina NGS platforms.

There are several key challenges in sequencing cfDNA from plasma. First, cfDNA is present in limited quantities in plasma samples. Second, the collected plasma samples can be highly variable in quality, DNA content, and composition. Lastly, the use of NGS samples necessitates careful tracking; a protocol in which the sample never leaves the tube is advantageous to ensure accurate sample tracking and to avoid contamination.

The commitment to overcome these challenges is the core of the ThruPLEX Plasma-seq Kit. It has been developed specifically for cfDNA derived from plasma by reformulating the repair and ligation reactions. The kit generates high-quality Illumina NGS libraries from variable amounts of cfDNA ranging from 1 to 30 ng* with a standard protocol. The performance of ThruPLEX Plasma-seq libraries is highly reproducible between replicates and sequencing runs and from sample to sample. ThruPLEX Plasma-seq's three-step, single-tube library preparation workflow (Figure 2) is the simplest in the industry, minimizing handling errors and loss of valuable samples.

* Libraries have been generated from input amounts less than 1 ng and over 30 ng. Contact technical support for further information (support@rubicongenomics.com).

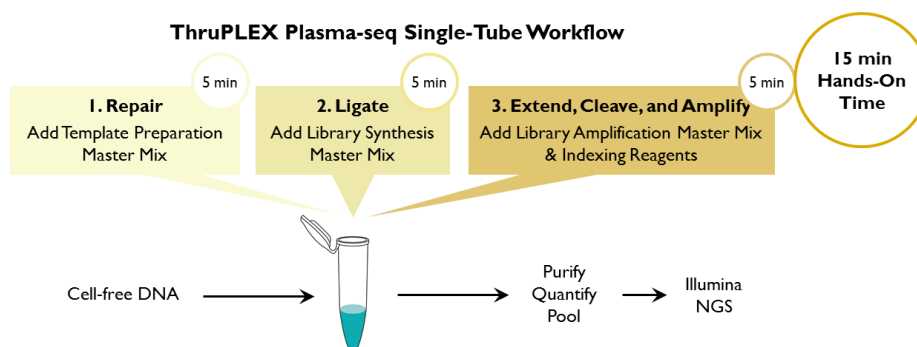


Figure 2. ThruPLEX Plasma-seq single-tube library preparation workflow: The ThruPLEX Plasma-seq workflow consists of 3 simple steps that take place in the same PCR tube or well and eliminates the need to purify and transfer the sample material.

B. ThruPLEX Plasma-seq Kit

I. Overview

ThruPLEX Plasma-seq Kit is designed to generate DNA libraries for Illumina NGS from cell-free DNA isolated from plasma. The ThruPLEX Plasma-seq chemistry is engineered and optimized to produce highly diverse libraries with reproducible sequencing performance from 1 to 30 ng of cell-free DNA. The entire three-step workflow takes place in a single tube or well in about 2 hours. No intermediate purification steps and no sample transfers are necessary, which prevent handling errors and loss of valuable samples.

ThruPLEX Plasma-seq Kit includes all necessary reagents including indexes for multiplexing up to 96 samples. Once purified and quantified, the resulting library is ready for Illumina NGS instruments using standard Illumina sequencing reagents and protocols. The kit provides quality libraries with highly reproducible results.

II. Principle

The ThruPLEX Plasma-seq Kit is based on Rubicon Genomics' patented ThruPLEX technology (Figure 3). Unlike other NGS library preparation kits, which are based on ligation of Y-adapters, ThruPLEX uses stem-loop adapters to construct high quality libraries in a fast and efficient workflow. In the first step, Template Preparation, the cell-free DNA (cfDNA) is repaired and yields molecules with blunt ends. In the next step, stem-loop adaptors with blocked 5' ends are ligated with high efficiency to the 5' end of the cfDNA, leaving a nick at the 3' end of the target fragment. The adaptors do not have single-strand overhangs and are prevented from ligating to each other, both of which contribute to non-specific background found with many other NGS preparations. In the final step, the 3' ends of the cfDNA are extended to complete library synthesis and Illumina-compatible indexes are added through a high-fidelity amplification. Any remaining free adaptors are destroyed. Hands-on time and risk of contamination are minimized by using a single-tube protocol and eliminating intermediate purifications.

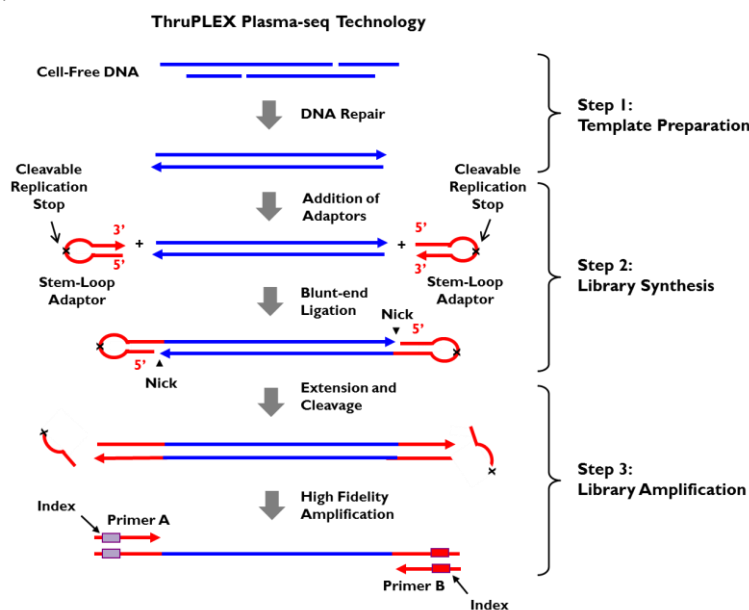


Figure 3. ThruPLEX Plasma-seq technology: A three-step, single-tube reaction that starts with isolated cell-free DNA. Stem-loop adapters are blunt-end ligated to the repaired input DNA. These molecules are extended, then amplified using a high-fidelity polymerase to yield an indexed Illumina NGS library.

III. ThruPLEX Plasma-seq Workflow

The highly streamlined ThruPLEX Plasma-seq Kit workflow (Figure 4) consists of the following three steps:

- **Template Preparation** for efficient repair of the input cell-free DNA
- **Library Synthesis** for ligation of Rubicon Genomics' patented stem-loop adapters
- **Library Amplification** for extension of the template, cleavage of the stem-loop adaptors, and amplification of the library. Illumina-compatible indexes are also introduced using a high-fidelity, low-bias DNA polymerase.

The three-step ThruPLEX Plasma-seq workflow takes place in a single tube or well and is completed in about 2 hours.

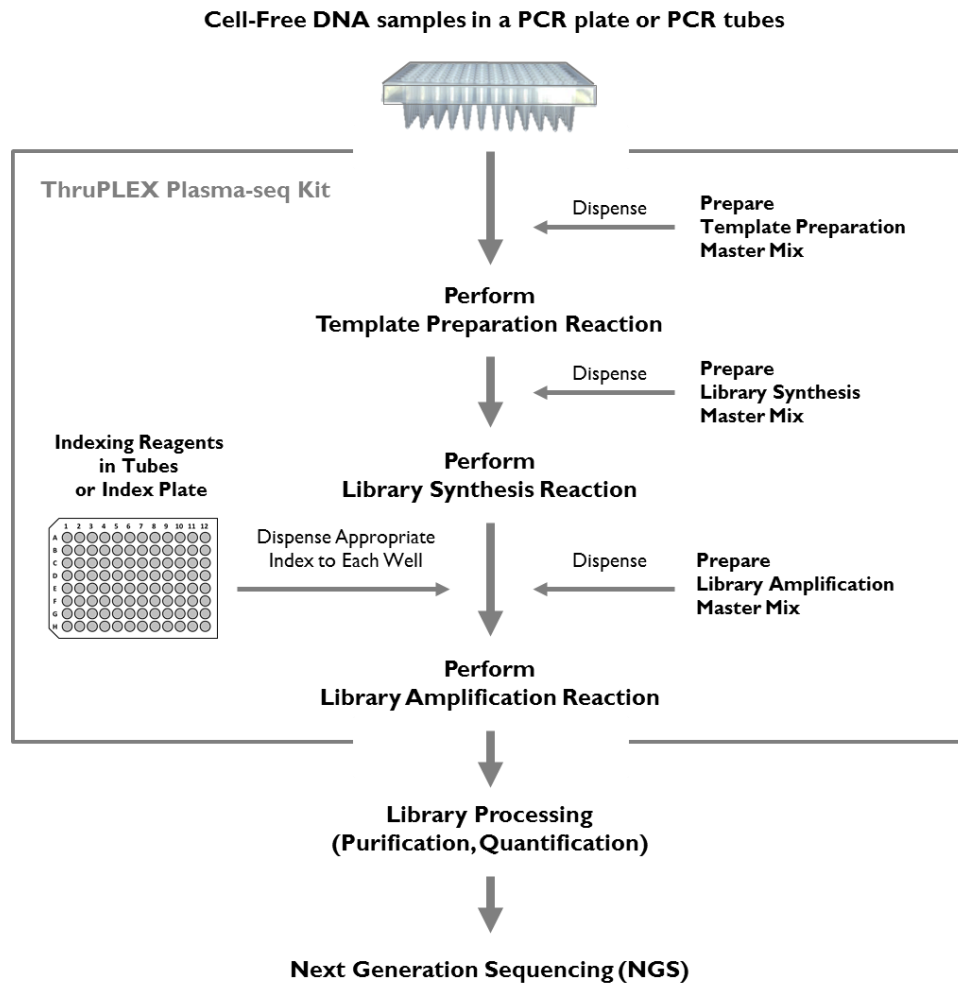


Figure 4. ThruPLEX Plasma-seq library preparation workflow overview: Steps involved in ThruPLEX library preparation for Illumina NGS starting with isolated cell-free DNA.

C. Getting Started

I. Additional Supplies and Equipment Needed

Required Supplies and Equipment

- Thermal cycler (real-time instrument recommended)

Note: See Thermal Cycler Considerations below.

- Centrifuge
- PCR tubes or 96-well PCR plates and seals

Note: Select appropriate tubes or plates that are compatible with the thermal cyclers and/or real-time thermal cyclers used. Use appropriate caps or sealing films and seal thoroughly to prevent cross-contamination and eliminate evaporation during cycling conditions. Evaporation could reduce robustness and reproducibility of the reactions.

- Low binding aerosol barrier tips
- Freshly prepared 80% (v/v) ethanol
- Agencourt[®] AMPure[®] XP beads (Beckman Coulter, CAT. NO. A63880)

Optional Supplies

- KAPA[®] Library Quantification Kit – Illumina (Kapa Biosystems, CAT. NO. specific to real time PCR system used)
- EvaGreen[®] Dye (20X in water, Biotium, CAT. NO. 31000-T)
- Fluorescein Calibration Dye (Bio-Rad Laboratories, CAT. NO. 170-8780)

II. Thermal Cycler Considerations

Thermal cycling and heated lid

Use a thermal cycler equipped with a heated lid that can handle 50 µL reaction volumes. Set the temperature of the heated lid to 101°C – 105°C to avoid sample evaporation during incubation and cycling.

Thermal cycler ramp rates

We recommend a ramp rate of 3°C/s – 5°C/s; higher ramp rates are not recommended and could impact the quality of the library.

Monitoring amplification during the Library Amplification Reaction

Amplification can be monitored using a real-time thermal cycler with the addition of fluorescent dyes (not provided with the kit, see Optional Supplies above) to the reaction. If a regular thermal cycler is used instead, there is no need to add the dyes; use an appropriate amount of nuclease-free water to prepare the Library Amplification Master Mix. In the absence of real-time monitoring, library amplification can be analyzed by gel or by analysis of an aliquot of the library using the Agilent[®] Bioanalyzer[®] (see Library Quantification, **Section E.II.**).

Depending on the real-time instrument used, select an appropriate calibration dye and mix with EvaGreen dye to prepare the dye mix (see Library Amplification Step, **Section D.III.**). For some real-time instruments, calibration dye may not be needed; please refer to the real-time thermal cycler instrument's manual.

III. Starting Material

DNA Sample Requirements	
Source	Plasma
Type	Isolated cell-free DNA
Recommended Input Amount	1 ng to 30 ng
Input Volume	10 μ L
Input Buffer	\leq 10 mM Tris, \leq 0.1 mM EDTA

Blood Collection and Plasma Preparation

A reference protocol can be downloaded at the ThruPLEX Plasma-seq Kit Product Page, under the Resources tab: <http://rubicongenomics.com/products/thruplex-plasma-seq-kit/>.

Sample Type

ThruPLEX Plasma-seq Kit is optimized for cell-free DNA isolated from human plasma. This kit is **not** for use with single-stranded DNA (ssDNA) or RNA.

Cell-free DNA Isolation

ThruPLEX Plasma-seq Kit was optimized with cell-free DNA prepared using the QIAamp[®] Circulating Nucleic Acid Kit (Qiagen, CAT. NO. 55114).

Input DNA Amount

The recommended input amount is 1 ng to 30 ng of isolated cell-free DNA quantified by Qubit[®] Fluorometer or equivalent methods.

Libraries have been generated from input amounts less than 1 ng and over 30 ng, requiring the number of PCR cycles to be optimized. Contact technical support for further information (support@rubicongenomics.com).

Input Volume

The maximum input sample volume is 10 μ L. If a sample is in a larger volume, the DNA must be concentrated to 10 μ L or less. Care should be taken to ensure the buffer concentration is appropriate (see below).

Input Buffer

The concentrations of Tris and EDTA in the buffer containing the input DNA must not exceed 10 mM and 0.1 mM, respectively. Avoid phosphate containing buffers.

Fragment Size

Cell-free DNA (cfDNA) isolated from plasma samples contains both high and low molecular weight DNA fragments (Figure 5). The composition and concentration of the isolated cfDNA differ from sample to sample and may vary depending on the isolation method used. The cfDNA species of most interest is the mononucleosomal DNA fragments of about 170 bp in length, for which the concentration can be determined using the Agilent Bioanalyzer.

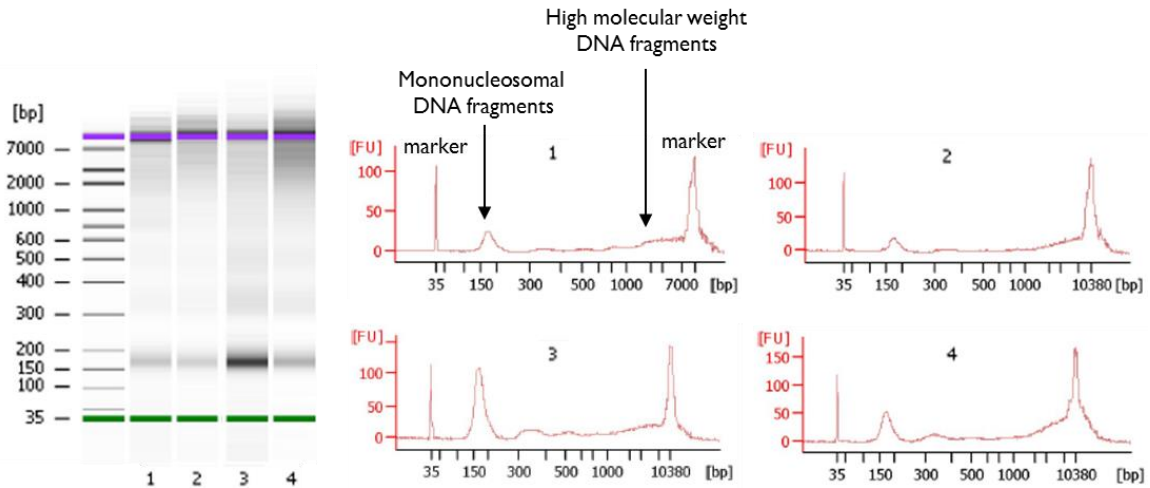


Figure 5. Fragment size distribution of cell-free DNA isolated from plasma: Cell-free DNA from 4 different human plasma samples was isolated and analyzed using the Agilent Bioanalyzer. One distinct feature of the isolated cfDNA is a peak (or band) centered around 170 bp and a distribution of higher molecular weight fragments.

IV. Positive and Negative Controls

If possible, include appropriate positive and negative controls in the experimental design to verify that reactions proceed as expected. If the experimental samples contain any carryover contaminant(s) in the buffer, the downstream reactions may be impacted, and the inclusion of controls will help elucidate such problems. Always prepare fresh dilutions of reference DNA. Include negative controls (No Template Control, NTC) in low TE buffer (10 mM Tris, 0.1 mM EDTA, pH 8.0) or nuclease-free water. The positive control and experimental samples should produce indexed libraries, while the NTC must not amplify.

V. Preparation of Master Mixes

A master mix with appropriate buffers and enzymes must be prepared just in time at each workflow step based on the number of reactions to be performed. Prepare ~5% excess of each master mix to allow for pipetting losses. Each kit contains sufficient reagents to prepare master mixes up to 4 separate times.

Transfer enzymes onto ice just prior to use and centrifuge briefly to collect contents at the bottom of the tube prior to use. Thaw the buffers, vortex briefly and centrifuge prior to use. Keep all the components and master mixes on ice. Once the master mix is prepared, thoroughly mix the contents several times with a pipette while avoiding introduction of air bubbles and briefly centrifuge prior to dispensing into the PCR plate or tube(s).

The Library Synthesis Master Mix and Library Amplification Master Mix can be prepared during the last 15 minutes of the previous step's cycling protocol and kept on ice until use.

VI. Indexing Reagents

ThruPLEX Plasma-seq Kit includes all necessary reagents including Indexing Reagents for multiplexing samples. The Indexing Reagents consist of amplification primers containing Illumina-compatible indexes. Index sequences can be downloaded as CSV files at the ThruPLEX Plasma-seq Kit Product Page, under the Resources tab: <http://rubicongenomics.com/products/thruplex-plasma-seq-kit/>.

Before starting the ThruPLEX Plasma-seq Library Preparation Protocol (**Section D**), refer to **Appendix I** for information on index sequences, Index Plate handling instructions, and multiplexing and index pooling guidelines.

ThruPLEX Plasma-seq 12S Kit

Indexing Reagents are pre-dispensed in 12 individual tubes with blue caps. Each tube contains sufficient volume for up to 4 uses. No more than 4 freeze/thaw cycles are recommended for the Indexing Reagent Tubes.

ThruPLEX Plasma-seq 48S and 96D Kits

Indexing Reagents are pre-dispensed and sealed in a linear barcoded Index Plate. The Index Plate is sealed with foil that can be pierced with a pipette tip to collect the required amount of index to assemble the reactions. Each well of the Index Plate contains sufficient volume for a single use. No more than 4 freeze/thaw cycles are recommended for the Index Plate.

VII. Using Illumina Experiment Manager

Make sure the latest version of the Illumina Experiment Manager (IEM) is installed (version 1.9 or later). Prior to starting the ThruPLEX Plasma-seq Library Preparation Protocol (**Section D**), create a Sample Sheet in the IEM to select and validate appropriate indexes to use in your experiments. Refer to **Appendix 1** for guidelines on using the IEM to validate your index combinations.

VIII. Target Enrichment

ThruPLEX Plasma-seq is compatible with the major exome and target enrichment products, including Agilent SureSelect, Roche NimbleGen SeqCap EZ and custom panels. ThruPLEX Plasma-seq target enrichment protocols and application notes can be assessed through the Applications section of the Rubicon Genomics website at: <http://rubicongenomics.com/applications/enrichment/>.

D. ThruPLEX Plasma-seq Library Preparation Protocol

I. Template Preparation Step

Template Preparation Reagents

Template Preparation Reagents	
Reagent	Cap color
Template Preparation Buffer	Red
Template Preparation Enzyme	Red

- **Note:** Assemble all reactions in thin-wall 96-well PCR plates or PCR tube(s) that are compatible with the thermal cycler and or real-time thermal cycler used.

Template Preparation Protocol

1. Prepare samples as described below.
 - **Samples:** Dispense 10 μL of isolated cell-free DNA into each PCR tube or well of a PCR plate.
 - **Positive control reactions using reference DNA:** If desired, include a positive control DNA.
 - **Negative control reactions/No Template Controls (NTCs):** If desired, assemble NTCs with 10 μL of nuclease-free water or low TE buffer (10 mM Tris, 0.1 mM EDTA, pH 8.0).
- **Note:** The maximum volume of DNA cannot exceed 10 μL .
2. Prepare **Template Preparation Master Mix** as described in the table below for the desired number of reactions. Mix thoroughly with a pipette. Keep on ice until used.

Template Preparation Master Mix		
Component	Cap color	Volume/Reaction
Template Preparation Buffer	Red	4 μL
Template Preparation Enzyme	Red	1 μL

- **Note:** Prepare 5% excess to allow for pipetting losses.
3. Assemble the **Template Preparation Reactions Mixture** as shown in the table below. To each 10 μL sample from step 1 above, add 5 μL of the **Template Preparation Master Mix**.

Template Preparation Reaction Mixture	
Component	Volume/Reaction
Cell-free DNA Sample	10 μL
Template Preparation Master Mix	5 μL
Total Volume	15 μL

4. Mix thoroughly with a pipette. Avoid introduction of air bubbles.
5. Seal the PCR plate using an appropriate sealing film or tightly cap the tube(s).
6. Centrifuge briefly to ensure the entire volume of the reaction is collected at the bottom of each well or tube.
7. Place the plate or tube(s) in a thermal cycler with heated lid set to 101°C – 105°C. Perform the **Template Preparation Reaction** using the conditions in the table below:

Template Preparation Reaction	
Temperature	Time
22°C	25 min
55°C	20 min
22°C	Hold for ≤ 2 hours

8. After the thermal cycler reaches 22°C, remove the plate or tube(s) and centrifuge briefly.
9. Proceed to the **Library Synthesis Step**.
 - **Note:** Following the Template Preparation Step, continue to Library Synthesis Step in the same plate or tube(s).

II. Library Synthesis Step

Library Synthesis Reagents

Library Synthesis Reagents	
Reagent	Cap Color
Library Synthesis Buffer	Yellow
Library Synthesis Enzyme	Yellow

Library Synthesis Protocol

1. Prepare **Library Synthesis Master Mix** as described in the table below for the desired number of reactions. Mix thoroughly with a pipette. Keep on ice until used.

Library Synthesis Master Mix		
Component	Cap Color	Volume/Reaction
Library Synthesis Buffer	Yellow	2.5 µL
Library Synthesis Enzyme	Yellow	2.5 µL

- **Note:** Prepare 5% excess to allow for pipetting losses.
2. Remove plate seal or open the tube(s) containing the Template Preparation Reaction Product.
 3. Assemble the **Library Synthesis Reaction Mixture** as shown in the table below. To each well or tube, add 5 µL of the **Library Synthesis Master Mix**.

Library Synthesis Reaction Mixture	
Component	Volume/Reaction
Template Preparation Reaction Product	15 µL
Library Synthesis Master Mix	5 µL
Total Volume	20 µL

4. Mix thoroughly with a pipette. Avoid introduction of air bubbles.
5. Seal the PCR plate using an appropriate sealing film or tightly cap the tube(s).
6. Centrifuge briefly to collect the contents at the bottom of each well or tube.

- Return the plate or tube(s) to the thermal cycler with heated lid set to 101°C – 105°C. Perform **Library Synthesis Reaction** using the cycling conditions in the table below:

Library Synthesis Reaction	
Temperature	Time
30°C	40 min
4°C	Hold for ≤30 min

- After the thermal cycler reaches 4°C remove the plate or tube(s) and centrifuge briefly.
- Continue to the **Library Amplification Step**.
 - Note:** Following the Library Synthesis step, continue Library Amplification Reaction in the same plate or tube(s) maintained at 4°C.

III. Library Amplification Step

Multiple stages occur during the **Library Amplification Reaction** (see table in step 8 below). Stage 1 and Stage 2 extend and cleave the stem loop adapters. **Proper programming of the thermal cycler is critical for these steps to be completed correctly, with no denaturation step until Stage 3.**

Illumina-compatible indexes are incorporated into the template library in Stage 4 using 4 amplification cycles. In Stage 5, the resulting template is amplified; the number of cycles required at this stage is dependent on the amount of cell-free DNA used. Samples are cooled to 4°C in Stage 6, after which they are pooled and purified or stored at –20°C.

- Note:** Refer to **Appendix 1** for selecting the appropriate indexes.

Selection of the optimal number of cycles for library amplification (Stage 5 ▲):

The number of PCR cycles required at Stage 5 of the Library Amplification Reaction is dependent on the amount of cell-free DNA and thermal cycler used. Use the table below as a guide for selecting the number of PCR cycles.

▲ Stage 5 Amplification Guide	
DNA Input (ng)	Number of Cycles
30	5
5	7
1	11

- Yield:** The amount of amplified library can vary depending upon sample condition, composition, and thermal cycler used. When starting with Qubit-quantified cell-free DNA and following the recommended number of amplification cycles, the typical yields range from 500 ng to 1000 ng.
- Note:** Libraries have been generated from input amounts less than 1 ng and over 30 ng, requiring the number of PCR cycles to be optimized. Contact technical support for further information (support@rubicongenomics.com)

Library Amplification Reagents

Library Amplification Reagents	
Reagent	Cap Color
Library Amplification Buffer	Green
Library Amplification Enzyme	Green
Nuclease-Free Water	Clear
Fluorescent Dyes	Not Provided
Indexing Reagents	Tubes (Blue) or Index Plate

- Note:** It is critical to handle the Index Plate following the instructions provided to avoid cross contamination of indexes. If the entire Index Plate is not used, please refer to **Appendix 1** for Index Plate handling instructions. No more than 4 freeze/thaw cycles are recommended for the Index Plate.

Library Amplification Protocol

- Prepare Indexing Reagents
 - Remove Indexing Reagents from freezer and thaw for ten minutes on the bench.
 - Spin Indexing Reagents briefly in a table top centrifuge to collect contents to the bottom.
 - Thoroughly wipe the Indexing Reagent Tubes or Index Plate foil seal with 70% ethanol and allow to dry.
- Prepare the **Library Amplification Master Mix** as described in the table below for the desired number of reactions. Mix thoroughly with a pipette. Keep on ice until used.

Library Amplification Master Mix		
Component	Cap Color	Volume/Reaction
Library Amplification Buffer	Green	21.5 μ L
Library Amplification Enzyme	Green	1.0 μ L
*Fluorescence Dyes (or Nuclease-Free Water)	Clear	2.5 μ L

- Note:** Prepare 5% excess to allow for pipetting losses.
 - If monitoring in real-time:** *Fluorescence dyes (for detection and optical calibration) are added when monitoring amplification in real time during cycling. Please refer to the real-time PCR instrument's user manual for calibration dye recommendations. The volume of detection and calibration dyes plus nuclease-free water must not exceed 2.5 μ L.
 - Example: Mix 90 μ L of EvaGreen dye (20X in water, Biotium, CAT. NO. 31000-T) with 10 μ L of 1:500 dilution of Fluorescein Calibration Dye (Bio-Rad Laboratories, CAT. NO. 170-8780). Add 2.5 μ L of this mix per reaction to prepare the Library Amplification Master Mix.
 - If NOT monitoring in real-time:** If a regular thermal cycler is used, there is no need to add the dyes; use 2.5 μ L of nuclease-free water per reaction in the Library Amplification Master Mix.
- Remove the seal on the PCR plate or open the tube(s) containing the Library Synthesis Reaction Product.
 - Add 25 μ L of the **Library Amplification Master Mix** to each well or tube.
 - Add 5 μ L of the appropriate Indexing Reagent to each well or tube:

Library Amplification Reaction Mixture	
Component	Volume/Reaction
Library Synthesis Reaction Product	20 µL
Library Amplification Master Mix	25 µL
Indexing Reagent	5 µL
Total Volume	50 µL

For ThruPLEX Plasma-seq 48S and 96D Kits containing Index Plate:

- Make sure the two corner notches of the Index Plate are on the left and the barcode label on the long side of the Index Plate is facing you.
 - Use a clean pipette tip to pierce the seal above the specific Indexing Reagent on the Index Plate; discard the tip used for piercing.
 - Use a clean pipette tip to collect 5 µL of the Indexing Reagent and add to the reaction mixture.
 - **Note:** Follow the Index Plate handling instructions in **Appendix 1** to avoid cross-contamination.
6. Mix thoroughly with a pipette. Avoid introducing air bubbles.
 7. Seal the PCR plate or tube(s) tightly and centrifuge briefly to collect the contents at the bottom of each well or tube.
 - **Note:** Use optical sealing tape if a real-time thermal cycler is used.
 8. Return the plate or tube(s) to the real-time PCR thermal cycler/thermal cycler with heated lid set to 101°C – 105°C. Perform **Library Amplification Reaction** using the cycling conditions in the tables below.
 - **Caution: Ensure that the thermal cycler does not have a denaturing step programmed until Stage 3.**

Library Amplification Reaction				
	Stage	Temperature	Time	Number of Cycles
Extension & Cleavage	1	72°C	3 min	1
	2	85°C	2 min	1
Denaturation	3	98°C	2 min	1
Addition of Indexes	4	98°C	20 s	4
		67°C	20 s	
		72°C	40 s	
Library Amplification	▲ 5	98°C	20 s	▲ 5 to 11 (see table on right)
		*72°C	50 s	
	6	4°C	Hold	1
*Acquire fluorescence data at this step, if monitoring amplification in real-time.				

▲ Stage 5 Amplification Guide	
DNA Input (ng)	Number of Cycles
30	5
5	7
1	11

9. Remove the PCR plate or tube(s) from the thermal cycler and centrifuge briefly to collect the contents at the bottom of each well.
 - **Note:** At this stage, samples can be processed for next generation sequencing (NGS) immediately or stored frozen at –20°C for up to 2 weeks. For instructions and recommendations on library pooling, purification, quantification, and sequencing, please refer to **Section E**.

E. Library Processing for Illumina Next Generation Sequencing

I. Overview

This section contains guidelines for processing ThruPLEX Plasma-seq libraries for Illumina NGS. In some cases, recommended protocols are listed (Library Purification by AMPure XP beads) while in others, general guidelines are given. For more information, contact technical support at support@rubicongenomics.com.

Libraries prepared from each sample will contain the specific indexes selected at the time of amplification. Follow the recommended workflow (solid arrows) in Figure 6 to process the libraries for Illumina NGS. Alternative workflow paths (dashed arrows) may be followed as needed. If libraries are prepared from similar samples with equivalent input amounts, then an equal volume of each individual, uniquely indexed library can be pooled into one tube for further processing. This “pooled” library is then purified using AMPure XP to remove unincorporated primers and other reagents. Once purified, the library should be quantified accurately prior to NGS to ensure efficient clustering on the Illumina flowcell. Instructions and recommendations on library pooling, purification, quantification, and sequencing are described in the following sections.

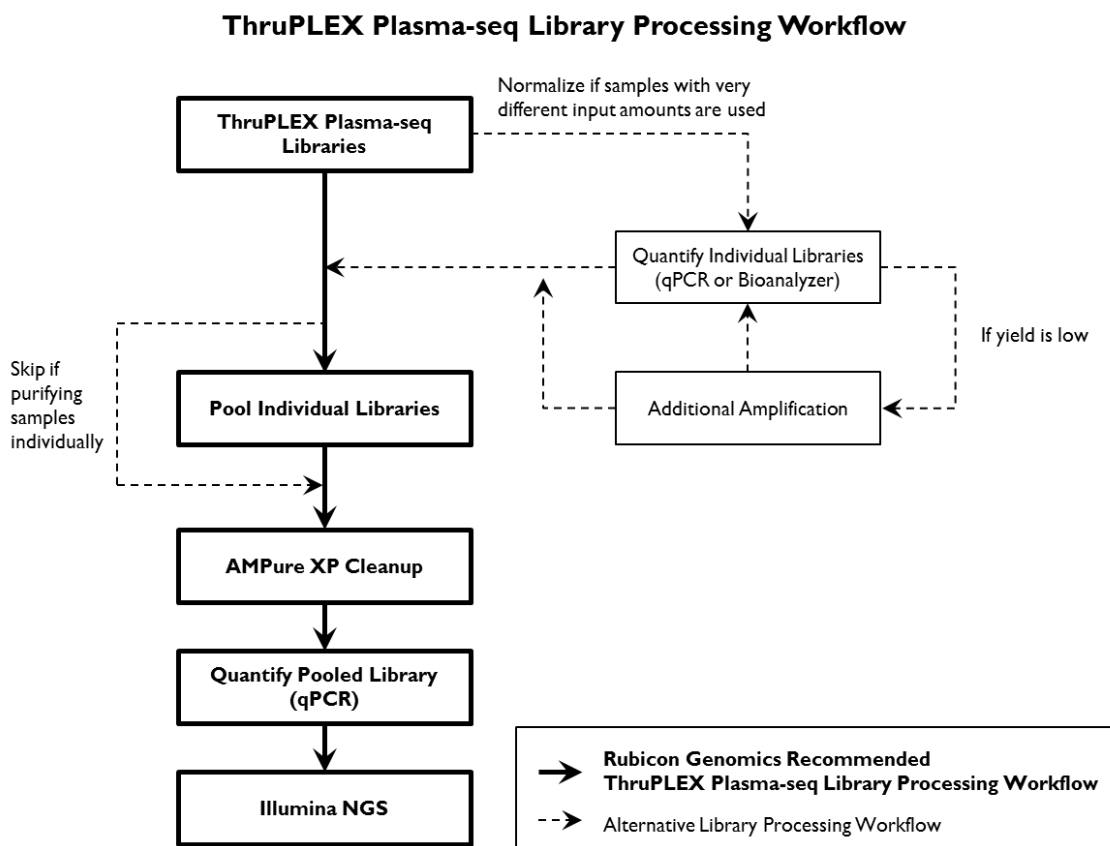


Figure 6. Workflow for processing the ThruPLEX Plasma-seq amplified libraries for Illumina NGS.

II. Library Quantification

There are several approaches available for library quantification including real-time PCR, UV absorption, fluorescence detection, and sizing and quantification using the Agilent Bioanalyzer. It is important to understand the benefits and limitations of each approach. Real-time PCR-based approaches (such as the KAPA Library Quantification Kit from Kapa Biosystems) quantify the library molecules that carry the Illumina adapter sequences on both ends and, therefore, reflect the quantity of the clustering competent library molecules. This approach assumes a relatively uniform size of distribution of input DNA used for library construction.

UV absorption/fluorescence detection-based methods (i.e., Nanodrop[®] (Thermo Scientific), Qubit Fluorometer (ThermoFisher), or Quant-iT[™] PicoGreen[®] dsDNA Assay Kit (Life Technologies)) quantify that total double-stranded nucleic acid concentration. These methods do not discriminate adapter presence and offer no information about the size of the library molecules. The Agilent Bioanalyzer system provides sizing and quantitation information about the library analyzed, but not about the clustering competency.

Quantification of ThruPLEX Plasma-seq libraries by real-time qPCR

Use the appropriate instrument-specific KAPA Library Quantification Kit for Illumina Sequencing Platforms (Kapa Biosystems). Dilute 2 – 5 μ L of the library 100,000-fold for the quantification procedure. Since the adapters result in about 140 bp increase in the DNA fragment size, the full length of the library fragments must be used to calculate the concentration of your library. For example, for a typical cfDNA input with fragments of about 170 bp in size, use 310 bp as the approximate size for calculating library concentration.

- **Note:** No purification of the template is necessary prior to qPCR due to the large dilution factor.

Quantification of ThruPLEX Plasma-seq libraries using the Bioanalyzer

Remove an aliquot of each library and dilute as appropriate in TE buffer. Load a 1 μ L aliquot of the diluted sample onto a Bioanalyzer high sensitivity DNA chip (Agilent Technologies, CAT. NO. 5067-4626).

III. Additional Amplification

If less than a desired yield of library was obtained and a plateau as measured by q-PCR was not reached, the remaining library can be further amplified to attain a higher yield. **Additional amplification can only be performed on unpurified libraries.** ThruPLEX Plasma-seq libraries can be further amplified with no extra reagents added after storage at 4°C for up to 6 hours or –20°C for up to 7 days. To perform this additional amplification, spin down the tube or plate containing the library (after thawing if the plate or tube was stored at –20°C), transfer it to a thermal cycler, and perform 2 – 3 PCR cycles as follows:

Number of Cycles	Temperature	Time
2 – 3 cycles	98°C	20 s
	72°C	50 s
1 cycle	4°C	Hold

IV. Library Pooling for Purification

When pooling libraries for sequencing, use the Illumina Experiment Manager (IEM) or BaseSpace to record information about your samples **before** beginning the ThruPLEX Plasma-seq Library Preparation Protocol.

Individual ThruPLEX Plasma-seq libraries containing different indexes can be pooled at desired molar ratios to allow multiplex sequencing. If libraries are prepared from similar input amounts, they can be pooled by combining equal volume aliquots of the individual libraries, each containing a unique index. Typically, a 10 μL aliquot from each library is adequate and the remainder of the library can be stored at -20°C . The total volume obtained at the end of pooling will vary depending on the number of libraries pooled. For example, if 12 libraries are pooled, then the final volume of the pool is 120 μL ; if 48 libraries are pooled, then the volume is 480 μL . A 100 μL aliquot of this pooled library is sufficient for AMPure XP purification purposes.

Some Illumina sequencing systems require balanced index combinations to ensure proper image registration and accurate demultiplexing of the pooled samples. Please see **Appendix I** for guidelines on selecting the appropriate indexes for pooling and multiplexing.

V. Library Purification with AMPure XP beads

AMPure XP is the recommended method of library purification. Do not use QIAquick[®] cleanup or other silica-based filters for purification as this will result in incomplete removal of primers.

The ratio of AMPure XP beads to library DNA is application dependent and determines the size-selection characteristics of the library. For post-amplification purification, a 1:1 bead to sample ratio is recommended.

Library purification reagents (supplied by the user)

Library Purification Reagents
AMPure XP beads
Magnetic rack for 1.5 mL centrifuge tubes
Freshly prepared 80% (v/v) ethanol
TE buffer, pH 8.0

AMPure XP Protocol

- **Note:**
 - It is important to bring all the samples and reagents to be used to room temperature.
 - Always use freshly prepared 80% (v/v) ethanol for Step 3 and Step 4 below.
 - Resuspend the AMPure XP reagent by gentle vortexing until no visible pellet is present at the bottom of the container.
1. In a 1.5 mL tube, combine AMPure XP reagent with an aliquot of the pooled library at 1:1 (v/v) ratio.
 2. Mix by pipetting 10 times to achieve a homogeneous solution; incubate for 5 min at room temperature.
 3. Place the tube in a magnetic stand for 2 min or until the beads are captured and the solution is clear.
 4. With the tube in the magnetic stand:
 - a) Without disturbing the pellet, use a pipette to remove and discard the supernatant.
 - b) Add 200 μ L of 80% (v/v) ethanol to the pellet; incubate for 30 s.
 - **Note:** The volume of 80% (v/v) ethanol should be at least the volume of the sample plus AMPure XP reagent (total volume from Step 1).
 - c) Without disturbing the pellet, use a pipette to remove and discard the supernatant.
 5. Repeat Step 4.
 6. Incubate the tube for 2 – 5 min at room temperature with the cap open to evaporate residual ethanol. DO NOT OVER DRY THE PELLETS.
 7. Remove the tube from the magnetic stand.
 8. Resuspend the beads in an appropriate volume of 1x TE buffer (pH 8.0) or nuclease-free water.
 - **Note:** Resuspend in nuclease-free water if a vacuum concentrator will be used to concentrate the sample.
 9. Mix by pipetting 10 times to achieve a homogeneous solution; incubate for 2 min at room temperature.
 10. Place the tube in a magnetic stand for 1 – 2 min or until the beads are captured and the solution is clear.
 11. With the tube in the magnetic stand and without disturbing the pellet, transfer the supernatant with a pipette into a new tube.
 - **Note:** If not used immediately, the purified library can be stored at -20°C .

VII. Sequencing Recommendations

ThruPLEX Plasma-seq Kit generates libraries that are ready for cluster amplification and sequencing on Illumina NGS platforms using standard Illumina reagents and protocols for multiplexed libraries. Libraries prepared using ThruPLEX Plasma-seq Kit result in a size distribution of library fragments centered at about 310 bp (Figure 7) when analyzed using the Agilent Bioanalyzer.

To achieve optimal cluster density on the Illumina flow cell, it is important to adjust the DNA concentration used for clustering based on these preferences. For example, for sequencing on the Illumina MiSeq[®], v3, load 14 – 15 pM of ThruPLEX Plasma-seq libraries.

Illumina recommends adding 1% PhiX control for most libraries. PhiX is a small genome that provides a balanced and diverse library to prevent sequencing problem and that can be quickly aligned to calculate error rates. For low diversity libraries and if experiencing sequencing issues, increase the PhiX control spike-in to at least 5%.

For sequencing on the HiSeq, please refer to Illumina's technical note [Using a PhiX Control for HiSeq[®] Sequencing Runs](#) (Illumina, Pub. No. 770-2011-041). For sequencing on the MiSeq, instructions for preparing a PhiX control can be found in Illumina's guide on [Preparing Libraries for Sequencing on the MiSeq](#) (Illumina, Part # 15039740 Rev. D, 2013).

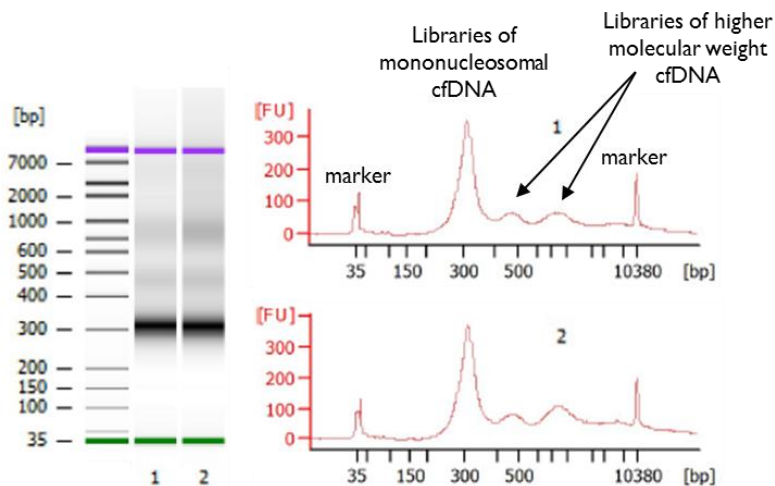


Figure 7. Bioanalyzer analysis of libraries prepared using ThruPLEX Plasma-seq: Cell-free DNA from plasma was isolated using the QIAamp Circulating Nucleic Acid Kit. Libraries were prepared using ThruPLEX Plasma-seq Kit and analyzed using the Agilent Bioanalyzer after library amplification. One distinct feature of the amplified libraries is a dominant peak (or intense band) around 310 bp containing library products of the mononucleosomal DNA fragments and a distribution of higher molecular weight library products.

Appendix I. Indexing Reagents

A. Overview

ThruPLEX Plasma-seq Kits contain all necessary reagents to generate amplified and indexed NGS libraries, including Indexing Reagents for multiplexing up to 96 samples. Table 3 below summarizes the characteristics of the included Indexing Reagents, which consist of amplification primers containing Illumina-compatible indexes. Indexing Reagents should be stored at -20°C and should not be subjected to more than 4 freeze/thaw cycles.

- **Note:** Indexing Reagents provided with ThruPLEX Plasma-seq Kit cannot be substituted with indexing reagents from any other sources.

Table 3: ThruPLEX Plasma-seq Kit – Indexing Reagents

	12S Kit	48S Kit	96D Kit
Number of Reactions	12	48	96
Number of Indexes	12	48	96
Index Type	Single	Single	Dual
Length of Indexes	8nt	8nt	8nt
Format	12 Tubes	96-Well Plate	96-Well Plate
Number of Uses	Up to 4	Single	Single
Illumina Experiment Manager or BaseSpace Kit Selection	TruSeq LT or Manual Input	Manual Input only	TruSeq HT

If libraries will be pooled for sequencing, use the Illumina Experiment Manager (IEM) or BaseSpace to record information about your samples **before** beginning the ThruPLEX Plasma-seq Library Preparation Protocol. Refer to Illumina's [TruSeq Library Prep Pooling Guide](#) (Illumina, Part # 15042173 v01, 2015) for Illumina sequencing systems that require balanced index combinations. For these Illumina sequencing systems, at each sequencing cycle of the index read, at least one of the two nucleotides for each colored laser should be present to ensure proper image registration and accurate demultiplexing of the pooled samples. Therefore, when libraries with **less than the full set** of ThruPLEX Plasma-seq indexes will be prepared and pooled, it is critical to follow the following steps **before** library preparation to ensure compatible index combinations are used:

1. Determine the number of libraries that will be pooled for sequencing.
2. Select the appropriate index combinations to use based on the multiplexing and index pooling guidelines provided below for each ThruPLEX Plasma-seq Kit. The IEM can be used to validate the compatibility of the chosen index combinations.

Appendices 1B to 1D provide index sequences, plate handling instructions, multiplexing and index pooling guidelines, and IEM Sample Sheet setup instructions specific for each ThruPLEX Plasma-seq Kit.

- For ThruPLEX Plasma-seq 12S Kit, proceed to Appendix 1B
- For ThruPLEX Plasma-seq 48S Kit, proceed to Appendix 1C
- For ThruPLEX Plasma-seq 96D Kit, proceed to Appendix 1D

B. ThruPLEX Plasma-seq 12S Kits

Single Index Sequences

ThruPLEX Plasma-seq single indexes (12S) use Illumina-compatible 8nt sequences developed by the Wellcome Trust Sanger Institute in Cambridge, UK. Each Indexing Reagent Tube contains a unique single index sequence. The first 6 bases of each 12S indexes are identical to the Illumina TruSeq LT indexes AD001 through AD012 (Figure 8), and they can be sequenced the same way as the TruSeq LT indexes. The prepared library has the structure shown in Figure 9.

- **Note:** Information about the Sanger index sequences can be found in *Nature Methods* 7, 111-118 (2010).

ThruPLEX Plasma-seq Single Indexes (12S)				
Tube	Sanger Tag	Sequence	TruSeq LT Index	TruSeq LT Sequence
1	iPCRtagT1	ATCACGTT	AD001	ATCACG
2	iPCRtagT2	CGATGTTT	AD002	CGATGT
3	iPCRtagT3	TTAGGCAT	AD003	TTAGGC
4	iPCRtagT4	TGACCACT	AD004	TGACCA
5	iPCRtagT5	ACAGTGGT	AD005	ACAGTG
6	iPCRtagT6	GCCAATGT	AD006	GCCAAT
7	iPCRtagT7	CAGATCTG	AD007	CAGATC
8	iPCRtagT8	ACTTGATG	AD008	ACTTGA
9	iPCRtagT9	GATCAGCG	AD009	GATCAG
10	iPCRtagT10	TAGCTTGT	AD010	TAGCTT
11	iPCRtagT11	GGCTACAG	AD011	GGCTAC
12	iPCRtagT12	CTTGTA	AD012	CTTGTA

Figure 8. ThruPLEX Plasma-seq Single Indexes: Each Indexing Reagent Tube contains a unique Illumina-compatible 8nt Sanger index sequence. The first 6 bases of each 12S indexes are identical to the Illumina TruSeq LT indexes AD001 through AD012.

ThruPLEX Plasma-seq Single-Indexed Library Structure

5' AATGATACGGCGACCACCGAGATCTACACAGGCGAAGACACTCTTCCCTACACGACGCTCTTCCGATCT-----Insert-----
 -----Insert-----AGATCGGAAGAGCACACGTCTGAACTCCAGTCAC**NNNNNNNN**ATCTCGTATGCCGTCTTCTGCTTG 3'
 Sanger index

Figure 9. ThruPLEX Plasma-seq single-indexed library structure: Libraries prepared from the ThruPLEX Plasma-seq Kit contain the 8nt Sanger index sequence on the 3' end.

Multiplexing and Index Pooling

For Illumina sequencing systems that require balanced index combinations, select appropriate single indexes that are unique and meet the Illumina recommended compatibility requirements. In general, to ensure proper image registration on the sequencer, any low-plex combination should include Indexing Reagent Tube 6 (iPCRtagT6) and Indexing Reagent Tube 12 (iPCRtagT12); these correspond to the Illumina TruSeq LT indexes AD006 and AD012. For additional low-plex (2- to 11-plex) pooling guidelines and for Illumina sequencing systems that require balanced index combinations, refer to Illumina's [TruSeq Library Prep Pooling Guide](#) (Illumina, Part # 15042173 v01, 2015).

Sample Sheet Setup

The Illumina Experiment Manager (IEM) is a desktop tool that creates and edits Sample Sheets for Illumina sequencers. To use this tool with ThruPLEX indexes, ensure that the latest version of IEM (version 1.9 or later) is installed. There are two options for creating the Sample Sheet:

Option 1: In the IEM, on the “Workflow Parameters” page, select “TruSeq LT” in the dropdown menu for “Sample Prep Kit”. Add indexes to be used on the “Sample Selection” page by clicking “Add Blank Row” and then choosing the appropriate indexes from the “index 1 (I7)” dropdown menu.

- **Note:** If TruSeq LT is selected, only the first 6 bases of the 8nt sequence will be sequenced.

Option 2: Create a Sample Sheet using the IEM. Open the CSV file of the Sample Sheet in Microsoft Excel, then manually copy and paste the appropriate 8nt single index sequences to be used to the Sample Sheet.

The 8nt single index sequences can be downloaded as a CSV file at the ThruPLEX Plasma-seq Product Page, under the Resources tab: <http://rubicongenomics.com/products/thruplex-plasma-seq-kit/>.

- **Note:** The IEM will not check for color-balanced index combinations when index sequences are entered manually from the CSV file.

C. ThruPLEX Plasma-seq 48S Kit

Single Index Sequences

ThruPLEX Plasma-seq single indexes use Illumina-compatible 8nt sequences developed by the Wellcome Trust Sanger Institute in Cambridge, UK. Each well of the Single Index Plate (SIP) contains a unique single index sequence (Figure 10). The first 12 ThruPLEX Plasma-seq single indexes (wells A1 through A12) have sequences identical to the first 6 bases of the Illumina TruSeq LT indexes AD001 through AD012 (sequences provided in Appendix 1B). The prepared library has the structure shown in Figure 11.

- **Note:** Information about the Sanger index sequences can be found in *Nature Methods* 7, 111-118 (2010).

ThruPLEX Plasma-seq Single Indexes					
Well	Sanger Tag	Sequence	Well	Sanger Tag	Sequence
A1	iPCRtagT1	ATCACG TTT	B1	iPCRtagT13	TGGTTGTT
A2	iPCRtagT2	CGATGT TTT	B2	iPCRtagT14	TCTCGGTT
A3	iPCRtagT3	TTAGGC AT	B3	iPCRtagT15	TAAGCGTT
A4	iPCRtagT4	TGACCA CT	B4	iPCRtagT16	TCCGTCTT
A5	iPCRtagT5	ACAGTG GT	B5	iPCRtagT17	TGTACCTT
A6	iPCRtagT6	GCCAAT GT	B6	iPCRtagT18	TTCTGTGT
A7	iPCRtagT7	CAGATC TG	B7	iPCRtagT19	TCTGCTGT
A8	iPCRtagT8	ACTTGAT G	B8	iPCRtagT20	TTGGAGGT
A9	iPCRtagT9	GATCAG CG	B9	iPCRtagT21	TCGAGCGT
A10	iPCRtagT10	TAGCTT GT	B10	iPCRtagT22	TGATACGT
A11	iPCRtagT11	GGCTAC AG	B11	iPCRtagT99	GTGCTACC
A12	iPCRtagT12	CTTGTA CT	B12	iPCRtagT101	GGTTGGAC
Well	Sanger Tag	Sequence	Well	Sanger Tag	Sequence
C1	iPCRtagT25	TGCGATCT	D1	iPCRtagT102	GGCACAAC
C2	iPCRtagT26	TTCCTGCT	D2	iPCRtagT38	TCTCACGG
C3	iPCRtagT27	TAGTGACT	D3	iPCRtagT39	TCAGGAGG
C4	iPCRtagT28	TACAGGAT	D4	iPCRtagT40	TAAGTTCG
C5	iPCRtagT29	TCCTCAAT	D5	iPCRtagT41	TCCAGTCG
C6	iPCRtagT30	TGTGGTTG	D6	iPCRtagT42	TGTATGCG
C7	iPCRtagT31	TAGTCTTG	D7	iPCRtagT43	TCATTGAG
C8	iPCRtagT32	TTCCATTG	D8	iPCRtagT44	TGGCTCAG
C9	iPCRtagT33	TCGAAGTG	D9	iPCRtagT45	TATGCCAG
C10	iPCRtagT34	TAACGCTG	D10	iPCRtagT46	TCAGATTC
C11	iPCRtagT35	TTGGTATG	D11	iPCRtagT47	TACTAGTC
C12	iPCRtagT36	TGAACTGG	D12	iPCRtagT48	TTCAGCTC

Figure 10. ThruPLEX Plasma-seq Single Indexes: Each well of the Single Index Plate contains a unique Illumina-compatible 8nt Sanger index sequence. The first 12 ThruPLEX Plasma-seq single indexes have identical sequences to the first 6 bases (shown in BOLD) as the Illumina TruSeq LT indexes AD001 through AD012.

ThruPLEX Plasma-seq Single-Indexed Library Structure

5' AATGATACGGCGACCACCGAGATCTACACAGGCGAAGACACTCTTCCCTACACGACGCTCTTCCGATCT-----Insert-----
 -----Insert-----AGATCGGAAGAGCACACGTCTGAACTCCAGTCAC**NNNNNNNN**ATCTCGTATGCCGTCTTCTGCTTG 3'
 Sanger index

Figure 11. ThruPLEX Plasma-seq single-indexed library structure: Libraries prepared from the ThruPLEX Plasma-seq 48S Kit contain the 8nt Sanger index on the 3' end.

Plate Handling Instructions for Low Throughput Applications

It is recommended that experiments be designed to use the entire plate of Indexing Reagents. However, the SIP can also be used for low-level multiplexing of a small number of samples. The plate should not be frozen and thawed more than 4 times. If Indexing Reagents from the entire plate are not used at the same time, it is critical to follow the instructions below to avoid cross contamination:

- After removing Indexing Reagents of choice, cover any pierced or used index wells with scientific tape (e.g., VWR, CAT. NO. 89097-920, General-Purpose Laboratory Labeling Tape, 0.5”).
- Thoroughly wipe the seal with 70% ethanol and allow it to dry completely.
- Replace the plastic lid, return the SIP to its sleeve and store at -20°C .

Multiplexing and Index Pooling

For Illumina sequencing systems that require balanced index combinations, select appropriate single indexes that are unique and meet Illumina recommended compatibility requirements. To ensure proper image registration on the sequencer, follow the low-plex pooling guidelines below. Refer to Illumina's [TruSeq Library Prep Pooling Guide](#) (Illumina, Part # 15042173 v01, 2015) for Illumina sequencing systems that require balanced index combinations.

		Well	Sanger Tag	Sequence
3-plex	Option A	A1	iPCRtagT1	ATCACGTT
		A7	iPCRtagT7	CAGATCTG
		B12	iPCRtagT101	GGTTGGAC
	Option B	A2	iPCRtagT2	CGATGTTT
		A8	iPCRtagT8	ACTTGATG
		D1	iPCRtagT102	GGCACAAAC
	Option C	A5	iPCRtagT5	ACAGTGGT
		B11	iPCRtagT99	GTGCTACC
		D10	iPCRtagT46	TCAGATTC
	Option D	A12	iPCRtagT12	CTTGACT
		D11	iPCRtagT47	TACTAGTC
		D12	iPCRtagT48	TTCAGCTC
4-plex or greater	Use 3-plex options with any other available indexes			

Figure 12. Low-plex pooling guidelines for ThruPLEX Plasma-seq 48S indexes: For pooling 3 or more samples, use the 3 required indexes specified in one of the options above plus any other available index as needed.

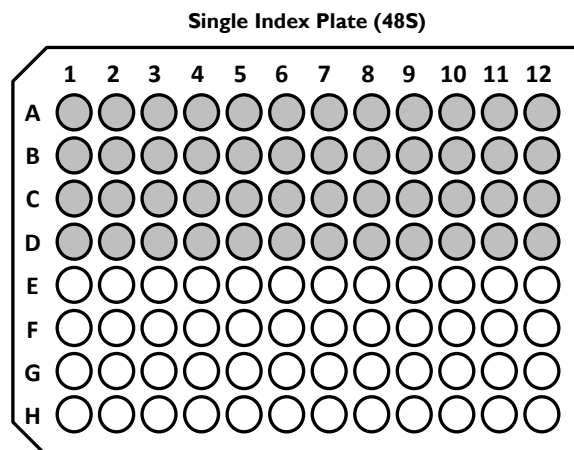


Figure 13. Single Index Plate maps with well locations: The 48S Single Index Plate contains Illumina-compatible indexes with 8nt Sanger sequences. The shaded wells indicate well positions containing Indexing Reagents.

Sample Sheet Setup

The Illumina Experiment Manager (IEM) is a desktop tool to create and edit Sample Sheets for Illumina sequencers. Make sure the latest version of IEM (version 1.9 or later) is installed.

Create a Sample Sheet using the IEM. Open the CSV file of the Sample Sheet in Microsoft Excel, then manually copy and paste the appropriate 8nt single index sequences to be used to the Sample Sheet.

Index sequences can be downloaded as a CSV file at the ThruPLEX Plasma-seq Product Page, under the Resources tab: <http://rubicongenomics.com/products/thruplex-plasma-seq-kit/>.

- **Note:** The IEM will not check for color-balanced index combinations when indexes are entered manually from the CSV file.

D. ThruPLEX Plasma-seq 96D Kits

Dual Index Sequences

ThruPLEX Plasma-seq dual indexes are 8nt long and identical to the Illumina TruSeq HT i5 and i7 dual indexes. Each well of the Dual Index Plate (DIP) contains a unique combination of the dual index sequences (Figure 14 and Figure 16). The prepared library has the structure shown in Figure 15.

ThruPLEX Plasma-seq Dual Indexes			
i7 Index	Sequence	i5 Index	Sequence
D701	ATTACTCG	D501	TATAGCCT
D702	TCCGGAGA	D502	ATAGAGGC
D703	CGCTCATT	D503	CCTATCCT
D704	GAGATTCC	D504	GGCTCTGA
D705	ATTCAGAA	D505	AGGCGAAG
D706	GAATTCGT	D506	TAATCTTA
D707	CTGAAGCT	D507	CAGGACGT
D708	TAATGCGC	D508	GTA CTGAC
D709	CGGCTATG		
D710	TCCGCGAA		
D711	TCTCGCGC		
D712	AGCGATAG		

Figure 14. ThruPLEX Plasma-seq Dual Indexes: Each well of the Dual Index Plate contains a unique combination of the 8nt Illumina TruSeq HT i7 and i5 dual index sequences.

ThruPLEX Plasma-seq Dual-Indexed Library Structure

5' AATGATACGGCGACCACCGAGATCTACAC**NNNNNNNN**ACACTCTTCCCTACACGACGCTCTTCCGATCT-----Insert-----
TruSeq HT i5 index
-----Insert-----AGATCGGAAGAGCACACGTCTGAACTCCAGTCAC**NNNNNNNN**ATCTCGTATGCCGTCTTCTGCTTG 3'
TruSeq HT i7 index

Figure 15. ThruPLEX Plasma-seq dual-indexed library structure: Libraries prepared from the ThruPLEX Plasma-seq 96D Kit contain the Illumina TruSeq HT i5 index on the 5' end and i7 index on the 3' end.

Plate Handling Instructions for Low Throughput Applications

It is recommended that experiments be designed to use the entire plate of Indexing Reagents. However, the DIP can also be used for low-level multiplexing of a small number of samples. The plate should not be frozen and thawed more than 4 times. If Indexing Reagents from the entire plate are not used at the same time, it is critical to follow the instructions below to avoid cross contamination:

- After removing Indexing Reagents of choice, cover any pierced or used index wells with scientific tape (e.g., VWR, CAT. NO. 89097-920, General-Purpose Laboratory Labeling Tape, 0.5”).
- Thoroughly wipe the seal with 70% ethanol and allow it to dry completely.
- Replace the plastic lid, return the DIP to its sleeve and store at -20°C .

Multiplexing and Index Pooling

For Illumina sequencing systems that require balanced index combinations, select appropriate dual index combinations that are unique and meet Illumina recommended compatibility requirements. In general, for pooling multiple samples, it is recommended to use indexes spanning as many columns and rows as possible to increase the diversity of the chosen combinations. For low-plex (2- to 16-plex) pooling guidelines and for Illumina sequencing systems that require balanced index combinations, refer to Illumina's [TruSeq Library Prep Pooling Guide](#) (Illumina, Part # 15042173 v01, 2015).

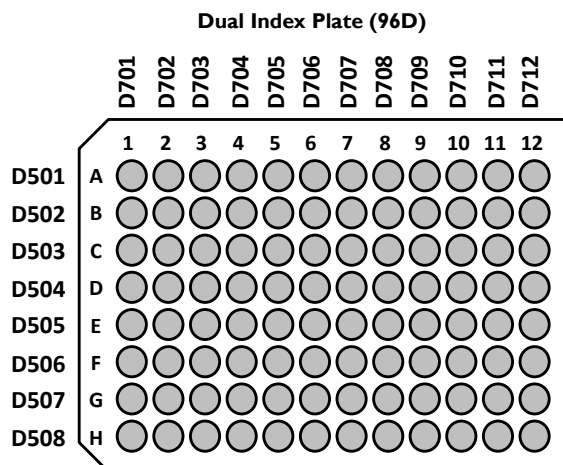


Figure 16. Dual Index Plate maps with well locations: The 96D Index Plate contains the 8nt Illumina TruSeq HT i7 and i5 dual index sequences. The dual index combination at each well position is indicated by the column (i7) and row (i5) labels on the plate maps. For low-plex (2- to 16-plex) pooling guideline, refer to Illumina's [TruSeq Library Prep Pooling Guide](#) (Illumina, Part # 15042173 v01, 2015).

Sample Sheet Setup

The Illumina Experiment Manager (IEM) is a desktop tool to create and edit Sample Sheets for Illumina sequencers. Index combinations may be validated using the IEM, which notifies user when improper combinations are used. Make sure the latest version of IEM (version 1.9 or later) is installed.

In the IEM, on the “Workflow Parameters” page, select “TruSeq HT” in the dropdown menu for “Sample Prep Kit”. Add indexes to be used on the “Sample Selection” page by clicking “Add Blank Row” and then choosing the appropriate indexes from the “index 1(I7)” and “index 2 (I5)” dropdown menus.

Appendix 2. Troubleshooting Guide

Problem	Potential Cause	Suggested Solutions
Sample amplification curve looks like No Template Control (NTC) amplification curve or does not produce amplified product	No input DNA added	Quantitate input before using the kit
	Incorrect library template used (e.g., RNA, ssDNA)	Adhere to DNA Sample Requirements (Section C.III.)
NTC amplification curve appears early or produces a yield similar to sample reaction products	NTC contaminated with DNA	Use a fresh control sample and check all reagents; replace kit if necessary. Clean area thoroughly and use PCR-dedicated plastics and pipettes.
After purification of the amplified library, Bioanalyzer traces shows broad peak(s) extending from less than 1,000 bp to greater than 1,000 bp	Library over-amplified or Bioanalyzer chip overloaded (common for high sensitivity chips)	Perform fewer PCR cycles at Stage 5 of the Library Amplification Reaction. For high sensitivity chips, load ≤ 500 pg/ μ L. Repeat Bioanalyzer run.

Technical Support

For technical support contact support@rubicongenomics.com or call +1.734.677.4845 (9 AM – 5:30 PM EST).

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