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QIAseq[®] Stranded RNA Library Kit Handbook

For stranded RNAseq library preparation with rRNA
and/or globin depletion for next generation sequencing
using dual indexing

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Kit Contents

QIAseq Stranded RNA Library Kit	UDI (24)	UDI-A(96)	UDI-B(96)	UDI-C(96)	UDI-D(96)
Catalog no.	180450	180451	180452	180453	180454
Number of reactions	24	96	96	96	96

Component	Tube cap color	Volume				
QIAseq Beads						
QIAseq Beads	N/A	10 mL	40 mL	40 mL	40 mL	40 mL
QIAseq Stranded RNA Lib Enzyme Kit						
RT Buffer, 5x	Blue	1 x 215 µL	1 x 860 µL			
RT Enzyme	Violet	1 x 28 µL	1 x 112 µL	1 x 112 µL	1 x 112 µL	1 x 112 µL
RNase Inhibitor	Green	1 x 55 µL	1 x 212 µL	1 x 212 µL	1 x 212 µL	1 x 212 µL
Second Strand Buffer, 10x	Blue	1 x 275 µL	1 x 1.1 mL			
Second Strand Enzyme Mix	Violet	1 x 175 µL	1 x 700 µL			
DTT, 1 M	Clear	1 x 1 mL				
Ultralow Input Ligase	Orange	2 x 65 µL	1 x 500 µL	1 x 500 µL	1 x 500 µL	1 x 500 µL
Ultralow Input Ligation Buffer, 4x	Yellow	1 x 900 µL	3 x 900 µL			
Primer Mix, 10uM	Clear	1 x 150 µL				
HiFi PCR Master Mix, 2x	Green	1 x 1.25 mL	2 x 1.25 mL			
CleanStart PCR Mix, 2x	Red	1 x 660 µL	2 x 1.4 mL			
CleanStart PCR Primer Mix	Clear	1 x 36 µL	1 x 150 µL	1 x 150 µL	1 x 150 µL	1 x 150 µL
Ligation Initiator	Black	1 x 210 µL	1 x 840 µL			
QIAseq UDI Adapter Kit						
QIAseq UDI Y-Adapter Plate (24)	N/A	1	N/A	N/A	N/A	N/A
QIAseq UDI Y-Adapter Kit A (96)	N/A	N/A	1	N/A	N/A	N/A
QIAseq UDI Y-Adapter Kit B (96)	N/A	N/A	N/A	1	N/A	N/A
QIAseq UDI Y-Adapter Kit C (96)	N/A	N/A	N/A	N/A	1	N/A
QIAseq UDI Y-Adapter Kit D (96)	N/A	N/A	N/A	N/A	N/A	1
QIAseq Y-Adapter Reference Card	N/A	1	1	1	1	1
Quick-Start Protocol	N/A	3	3	3	3	3

QIAseq Stranded Total RNA Lib Kit
Catalog no.
Number of reactions

(24)
180743
24

(96)
180745
96

Component	Tube cap color		Volume
QIAseq Beads			
QIAseq Beads	N/A	10 mL	40 mL
QIAseq Stranded RNA Lib Enzyme Kit			
RT Buffer, 5x	Blue	1 x 215 µL	1 x 860 µL
RT Enzyme	Violet	1 x 28 µL	1 x 112 µL
RNase Inhibitor	Green	1 x 55 µL	1 x 212 µL
Second Strand Buffer, 10x	Blue	1 x 275 µL	1 x 1.1 mL
Second Strand Enzyme Mix	Violet	1 x 175 µL	1 x 700 µL
DTT, 1 M	Clear	1 x 1 mL	1 x 1 mL
Ultralow Input Ligase	Orange	2 x 65 µL	1 x 500 µL
Ultralow Input Ligation Buffer, 4x	Yellow	1 x 900 µL	3 x 900 µL
CleanStart PCR Mix, 2x	Red	1 x 660 µL	2 x 1.4 mL
CleanStart PCR Primer Mix	Clear	1 x 36 µL	1 x 150 µL
Ligation Initiator	Black	1 x 210 µL	1 x 840 µL
QIAseq CDI Y-Adapter Kit			
QIAseq CDI Y-Adapter Plate (24)	N/A	1	N/A
QIAseq CDI Y-Adapter Plate (96)	N/A	N/A	1
QIAseq Y-Adapter Reference Card	N/A	1	1
Quick-Start Protocol	N/A	3	3

The QIAseq Stranded Library Kits ship with a QIAseq Y-Adapter plate with either unique dual-index (UDI) adapters or combinatorial dual-index (CDI) adapters. To multiplex more than 96 libraries in a single sequencing run, simply combine kits with different UDI Y-adapter plates. For example, to multiplex 384 samples in a single flow cell lane, prepare and combine libraries from the QIAseq Stranded RNA Library Kit UDI-A (96) with the QIAseq Stranded RNA Library Kit UDI-B (96), QIAseq Stranded RNA Library Kit UDI-C (96), and QIAseq Stranded RNA Library Kit UDI-D (96) Kits. For more information on the QIAseq Y-Adapter plates, please refer to Appendix A: QIAseq Dual-Index Y-Adapters, page 41.

Shipping and Storage

The QIAseq Stranded Total RNA Library Kit (cat. nos. 180743, 180745), QIAseq Stranded RNA Library Kit UDI (24) (cat. no. 180450), QIAseq Stranded RNA Library Kit UDI-A (96) (cat. no. 180451), QIAseq Stranded RNA Library Kit UDI-B (96) (cat. no. 180452), QIAseq Stranded RNA Library Kit UDI-C (96) (cat. no. 180453), and QIAseq Stranded RNA Library Kit UDI-D (96) (cat. no. 180454) are shipped in 3 boxes.

- Store the QIAseq Stranded RNA Lib Enzyme Kit (cat. nos. 1122418, 1122419) at -30 to -15°C .
- Store the QIAseq UDI Y-Adapter Kit (cat. nos. 180312, 180314, 180316, 180318, 180310) and QIAseq CDI Y-Adapter Kit (cat. nos. 180301, 180303) at -30 to -15°C .
- The QIAseq Beads (cat. nos. 1107149, 1107460) should be stored at 2 – 8°C (do not freeze).

Important: Do not use expired beads as this will significantly reduce library yield.

If stored under these conditions, the kit contents are stable until the date indicated on the box labels.

Intended Use

The QIAseq Stranded RNA Library Kit is intended for molecular biology applications. This product is not intended for the diagnosis, prevention, or treatment of a disease.

All due care and attention should be exercised in the handling of the products. We recommend all users of QIAGEN® products to adhere to the NIH guidelines that have been developed for recombinant DNA experiments, or to other applicable guidelines.

Safety Information

When working with chemicals, always wear a suitable lab coat, disposable gloves, and protective goggles. For more information, please consult the appropriate safety data sheets (SDSs). These are available online in convenient and compact PDF format at www.qiagen.com/safety, where you can find, view, and print the SDS for each QIAGEN kit and kit component.

Quality Control

In accordance with QIAGEN's ISO-certified Quality Management System, each lot of QIAseq Stranded RNA Library Kit is tested against predetermined specifications to ensure consistent product quality.

Introduction

NGS library preparation of RNA samples

The QIAseq Stranded RNA Library Kits enable one-day, accurate, stranded NGS library construction from a broad range of RNA inputs. This kit includes magnetized QIAseq Beads for fast and efficient reaction cleanups between protocol steps and Y-shaped sample index adapter plates, which enable sample multiplexing. A total of 384 samples can be sequenced together per lane on an Illumina NGS instrument by combining multiple different sets of UDI sample index plates.

Compared to other protocols, many novel advancements are included in the kit. During reverse transcription, the optimized RT enzyme and buffers do not require the usage of toxic reagents such as Actinomycin D to enhance strand specificity. In the second-strand synthesis reaction, a specialized combination of enzymes and optimized buffering not only enables degradation of the RNA strand, generation of a second cDNA strand, and generation of blunt DNA ends, but it also guarantees the A-base addition required for the efficient ligation of Illumina-compatible adapters. The novel strand-specific ligation step establishes the strand specificity of the QIAseq Stranded RNA Kit protocol without additional reagents or laborious and time-consuming protocol steps. Finally, the HiFi PCR Mix utilizes a high-fidelity, hot-start, DNA polymerase to efficiently amplify the library irrespective of GC content.

Ribosomal RNA (rRNA) and globin mRNA depletion

QIAseq FastSelect (sold separately) is a breakthrough technology that rapidly and efficiently removes rRNA and/or globin mRNA during NGS RNA library preparation. In one-step, QIAseq FastSelect removes up to 99% of all unwanted rRNA and/or globin mRNA even when starting with difficult samples or instances where the RNA is already degraded such as formalin-fixed paraffin-embedded (FFPE) samples. Simply add the QIAseq FastSelect reagent during the NGS library preparation, and unwanted RNAs are eliminated from the library.

Principle and procedure

The QIAseq Stranded RNA Library Kit comprises the QIAseq Stranded RNA Lib Enzyme Kit, QIAseq Beads, and QIAseq Y-Adapter Kits. QIAseq FastSelect (sold separately) is designed for fast and efficient removal of rRNA and/or globin mRNA during library preparation from FFPE, cells, tissues, or blood samples. Together, these kits enable preparation of strand-specific NGS libraries from total RNA in less than 5 hours (Figure 1)

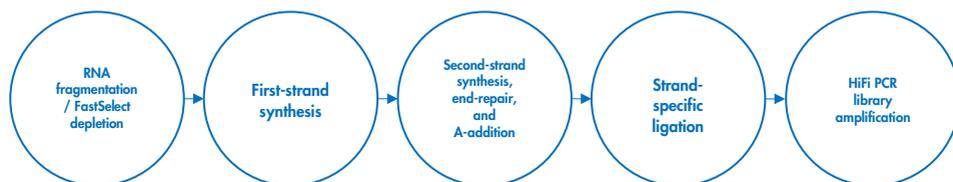


Figure 1. QIAseq Stranded RNA Library Kit workflow. The QIAseq Stranded RNA Library Kit, in combination with QIAseq FastSelect Kits, provides all necessary reagents for preparation of rRNA and/or globin mRNA-depleted strand-specific NGS libraries from total RNA. The HiFi PCR library amplification step utilizes a high-fidelity DNA polymerase to amplify the NGS libraries.

The following reactions are part of the workflow (Figure 2)

- **RNA fragmentation/FastSelect depletion**

Prior to RNA heat fragmentation, the FastSelect reagent is directly combined with the RNA and the library prep-specific buffers. Heat fragmentation (if necessary) is then performed, and the reaction temperature is gradually cooled to room temperature (15–25°C).

- **First-strand synthesis**

First-strand synthesis is performed using an RNase H- Reverse Transcriptase (RT) in combination with random primers.

- **Second-strand synthesis, end-repair, and A-addition**

Second-strand synthesis is performed using 5' phosphorylated random primers. This enables subsequent strand-specific ligation, as only one strand of the library is 5' phosphorylated.

- **Strand-specific ligation**

QIAseq adapters are efficiently asymmetrically ligated to the inserts due to the 5' phosphate that results from 5' phosphorylated second-strand synthesis reaction.

- **Library amplification**

QIAseq HiFi PCR reagents ensure high fidelity library amplification regardless of the GC content.

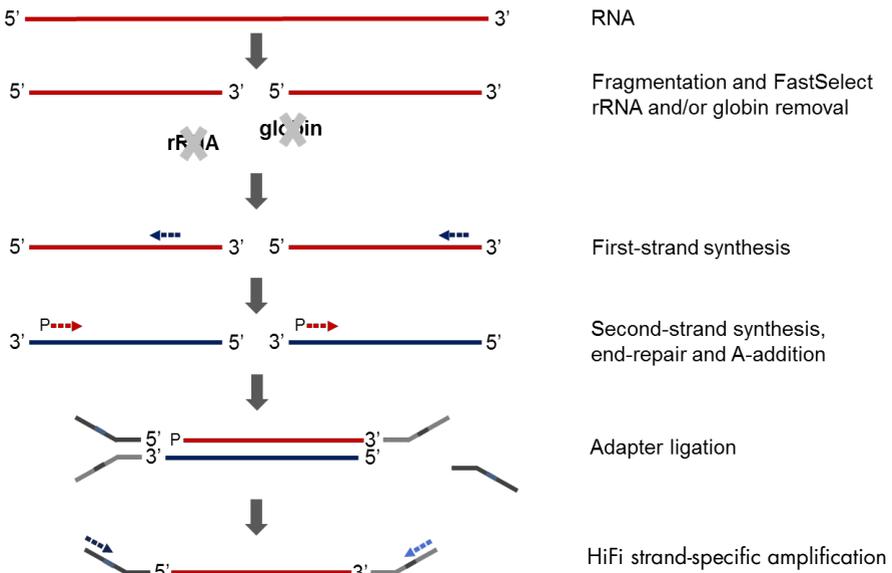


Figure 2. QIAseq Stranded RNA Library Kit with integrated QIAseq FastSelect rRNA and/or globin mRNA removal.

Library Amplification

Important: When preparing libraries for use on Illumina NGS instruments, care must be taken to identify the type of flow cells which will be utilized. For sequencing using newer Illumina instruments that utilize patterned flow cells, we recommend that the final library should be amplified using HiFi PCR Mastermix following the Hi-Fi PCR Library amplification protocol.

The CleanStart Library amplification ensures that the amplified library will not be able to contaminate subsequent rounds of library preparation. We recommend using this protocol if laboratories are worried about PCR contamination in the results. Researchers should test if the CleanStart library amplification method is compatible with their sequencing instrument and flow cell configurations.

Next-generation sequencing

Libraries prepared with the QIAseq Stranded RNA Library Kits can be sequenced with Illumina NGS systems (NextSeq® 500/550, HiSeq® 1000, HiSeq 1500, HiSeq 2000, HiSeq 2500, HiSeq 3000/4000, and NovaSeq™ 6000). When using unique dual indexes (cat. nos. 180450, 180451, 180452, 180453, 180454), 74 bp paired-end reads and dual 10 bp index reads are required. When using combinatorial indexes (cat. no. 180743 or 180745), 76 bp paired-end reads and dual 8 bp index reads are required.

Data analysis

The QIAseq Stranded RNA Library Kit is supported through two analysis pipelines: The QIAGEN CLC Genomics Workbench, and the RNA-seq Analysis & Biomarker Discovery Pipeline, a cloud-based RNAseq pipeline available in the QIAGEN GeneGlobe Analysis Portal (<https://geneglobe.qiagen.com/us/analyze/rnaseq-analysis-and-biomarker-discovery-portal>). Additionally, the QIAGEN CLC Genomics Workbench can be used.

The pipelines automatically perform all steps necessary for primary mapping, sample cluster analysis, and differential expression for bulk sequencing applications. When performing read alignment, the QIAseq Stranded Libraries represent the sense strand (or positive DNA strand) of the RNA sequence due to the strand-specific ligation during the second strand cDNA synthesis.

Equipment and Reagents to be Supplied by User

When working with chemicals, always wear a suitable lab coat, disposable gloves, and protective goggles. For more information, consult the appropriate safety data sheets (SDSs), available from the product supplier.

- 100% ethanol (ACS grade)
- Nuclease-free pipette tips and tubes
- PCR tubes (0.2 mL individual tubes or tube strips) (VWR cat. no. 20170-012 or 93001-118) or plates
- 1.5 mL LoBind® tubes (Eppendorf cat. no. 022431021)
- Ice
- Microcentrifuge
- Thermal cycler
- Vortexer
- Magnet for bead cleanups:
 - Tubes: MagneSphere® Technology Magnetic Separation Stand (Promega cat. no. Z5342)
 - Plates: DynaMag™-96 Side Magnet (Thermo Fisher Scientific cat. no. 12331D)
- **Optional spike-in:** ERCC RNA Spike-In Mix (Thermo Fisher Scientific cat. no. 4456740)
- Library QC: 2100 Bioanalyzer® (Agilent cat. no. G2939BA), Agilent High Sensitivity DNA Kit (Agilent cat. no. 5067-4626)
- Preferred qPCR library quantification method: QIAseq Library Quant Array (cat. no. 333304) or QIAseq Library Quant Assay Kit (cat. no. 333314)

Important Notes

High-quality RNA is essential for robust library preparation and sequencing. QIAGEN provides a range of solutions for purification of total RNA (Table 1)

Table 1. Recommended kits for purification of total RNA

Kit	Cat. no.	Starting material
RNeasy® Micro Kit	74004	Small amounts of cells and tissue
RNeasy Mini Kit	74104, 74106	Animal/human tissues and cells
RNeasy 96 Kit	74181, 74182	Animal/human tissues and cells
RNeasy FFPE Kit	73504	FFPE tissue samples
QIAamp® ccfDNA/RNA Kit	55184	Animal and human plasma and serum
exoRNeasy Midi Kit	77144	Animal and human plasma and serum
exoRNeasy Maxi Kit	77164	Animal and human plasma and serum

- Ensure that total RNA samples are of high quality relative to their sample type. For additional information, please see “Appendix C: General Remarks on Handling RNA”.
 - **RNA quantification:** The concentration and purity of total RNA isolated from cells and fresh/frozen tissues should be determined by measuring the absorbance in a spectrophotometer, such as the QIAxpert®. Since the spectral properties of nucleic acids are highly dependent on pH, we recommend preparing dilutions and measuring absorbance in 10 mM Tris-Cl, pH 7.5 instead of RNase-free water. Pure RNA has an $A_{260}:A_{280}$ ratio of 1.9–2.1 in 10 mM Tris-Cl, pH 7.5.
 - **RNA integrity:** The integrity and size distribution of total RNA from cells and fresh/frozen tissue can be confirmed using an automated analysis system (such as the Agilent 2100 Bioanalyzer) that assesses RNA integrity using an RNA integrity number (RIN). Although the RIN should ideally be ≥ 8 , successful library prep is still possible with samples with RIN values ≤ 8 .

- **Indexing recommendations:**

The QIAseq Stranded RNA Select Library UDI/CDI Kits include a fully compatible indexing solution containing a QIAseq Y-Adapter plate with either UDI or CDI index sequences. Each Stranded Total RNA Library UDI/CDI Kit includes one of the following:

- QIAseq Unique Dual-Index (UDI) Y-Adapter Plate (24)
- QIAseq Unique Dual-Index (UDI) Y-Adapter Plate A, B, C, or D (96)
- QIAseq Combinatorial Dual-Index (CDI) Y-Adapter Plate (24)
- QIAseq Combinatorial Dual-Index (CDI) Y-Adapter Plate (96)

- Sample multiplexing is one of the most important NGS tools for increasing throughput and reducing costs. It works by combining multiple samples to be processed together in a single sequencing run; therefore, sequencing reads need to be demultiplexed by reassigning each single read to its original source library. This is facilitated by the integration of index sequences into the individual adapter molecules.
- CDI adapters use twelve i7 and eight i5 barcode motifs that can be combined to form up to 96 combinatorial dual indices. In contrast, QIAseq UDI Adapters use a fixed combination of 2 unique barcode motifs per adapter molecule. Therefore, each single-index motif is only used once on any UDI adapter plate. To multiplex more than 96 libraries in a single sequencing run, combine kits with different UDI Y-adapter plates. Importantly, usage of UDI adapters effectively mitigates the risk of read misassignment due to index hopping. This is enabled by filtering misassigned reads during the demultiplexing of individual samples, thus generating highly accurate output data. For this reason, usage of UDI adapters is highly recommended. For more information on QIAseq Y-Adapter plates, please refer to “Appendix A: QIAseq Dual-Index Y-Adapters”.
- The protocol can be stopped at several steps and picked up on the following day. The stopping points are:
 - End of “Protocol: First-strand Synthesis”
 - End of “Protocol: Second-strand Synthesis, End-repair, and A-addition”
 - End of “Protocol: Strand-specific Ligation”
 - End of “Protocol: HiFi PCR Library Amplification”

Protocol: Fragmentation/FastSelect RNA Removal

Important points before starting

- The recommended total RNA input is 100 ng to 1 µg.
- QIAseq FastSelect kits for rRNA and/or globin mRNA removal are sold separately.
- Two different procedures, both integrated with QIAseq FastSelect, are provided:
 - **Option 1:** If using QIAseq FastSelect kits other than the QIAseq FastSelect – 5S/16S/23S Kit
 - **Option 2:** If using the QIAseq FastSelect –5S/16S/23S Kit alone or in combination with other FastSelect kits
- To generate optimal insert sizes, fragmentation time needs to be determined for each experiment, depending on the quality and origin of the RNA.

Procedure

Option 1: If using QIAseq FastSelect kits other than the QIAseq FastSelect – 5S/16S/23S Kit

1. Thaw template RNA on ice. Gently mix, then briefly centrifuge to collect residual liquid from the sides of the tubes and return to ice.
2. Prepare the reagents required for the RNA fragmentation and QIAseq FastSelect rRNA and/or globin removal.
 - 2a. Thaw RT Buffer, 5x; Nuclease-Free Water; and the tube(s) from the appropriate QIAseq FastSelect RNA Removal Kits at room temperature.
 - 2b. Mix by vortexing and then briefly centrifuge to collect residual liquid from the sides of the tubes.
3. On ice, prepare the fragmentation/depletion reaction according to Table 2. Briefly centrifuge, mix by pipetting up and down 10 times, and centrifuge briefly again.

Note: If setting up more than one reaction, prepare a volume of master mix 10% greater than that required for the total number of reactions.

Table 2. Option 1: Setup of fragmentation/depletion reactions using QIAseq FastSelect –rRNA HMR and/or QIAseq FastSelect –Globin Kits

Component	Volume/reaction
Total RNA (100 ng – 1 µg)	Variable
RT Buffer, 5x	8 µL
QIAseq FastSelect –rRNA HMR*	1 µL
QIAseq FastSelect –Globin*	1 µL
ERCC Control†	Optional
Nuclease-Free Water	Bring total reaction volume to 37 µL
Total volume	37 µL

* Choose QIAseq FastSelect –rRNA HMR and/or QIAseq FastSelect –Globin. Other FastSelect kits, such as FastSelect –rRNA Plant or FastSelect Yeast, can also be substituted.

† ERCC Control RNA (see “Equipment and Reagents to be Supplied by User”) can be added according to the concentrations specified by the manufacturer. If added, the total reaction volume should remain 37 µL.

4. Incubate as described in Table 3, according to your input RNA quality and approximate insert size.

Table 3. Option 1: Fragmentation/depletion protocol

Input RNA quality	Step	Insert size 150–250 bp	Insert size 251–350 bp
High quality (RIN >9)	1*	15 min at 95°C	3 min at 95°C
Moderate quality (RIN 5–6)	1*	10 min at 95°C	3 min at 95°C
FFPE or degraded sample (RIN <3)	1*	No fragmentation†	No fragmentation†
Steps 2–9 are performed, regardless of input RNA quality. They need to be performed whether the RNA is high quality, moderate quality, FFPE, or degraded.	2	2 min at 75°C	2 min at 75°C
	3	2 min at 70°C	2 min at 70°C
	4	2 min at 65°C	2 min at 65°C
	5	2 min at 60°C	2 min at 60°C
	6	2 min at 55°C	2 min at 55°C
	7	2 min at 37°C	2 min at 37°C
	8	2 min at 25°C	2 min at 25°C
	9	Hold at 4°C	Hold at 4°C

* Choose one option for the Step 1 time, according to the input RNA quality and the desired insert size.

† Also suitable for exosomal RNA or RNA of other origin with a size between 80–500 bp.

5. Proceed immediately to “Protocol: First-strand Synthesis”.

Option 2: If using the QIAseq FastSelect – 5S/16S/23S Kit alone or in combination with other FastSelect kits

1. Thaw template RNA on ice. Gently mix, then briefly centrifuge to collect residual liquid from the sides of the tubes and return to ice.
2. Prepare the reagents required for the RNA fragmentation and QIAseq FastSelect rRNA removal:
 - 2a. Bring FastSelect –5S/16S/23S, FastSelect FH Buffer, and Nuclease-Free Water to room temperature.

Important: Only for FastSelect –5S/16S/23S, incubate the tube at 37°C for 5 min, and then vortex to dissolve the precipitate.
 - 2b. Mix all other reagents vigorously by vortexing, and then briefly centrifuge.

Note: Ensure the QIAseq Beads and QIAseq Bead Binding Buffer are brought to room temperature before using.

Note: Ensure the QIAseq Beads are thoroughly mixed at all times. This necessitates working quickly and resuspending the beads immediately before use. If a delay in the protocol occurs, simply vortex the beads.

Note: Make fresh 80% ethanol.

3. On ice, prepare the fragmentation/depletion reaction according to Table 4. Briefly centrifuge, mix by pipetting up and down 10 times, and centrifuge briefly again.

Note: If setting up more than one reaction, prepare a volume of master mix 10% greater than that required for the total number of reactions.

Table 4. Option 2: Setup of fragmentation/depletion reaction if using the QIAseq FastSelect –5S/16S/23S Kit

Component	Volume/reaction
Total RNA (100 ng – 1 µg)	Variable
FastSelect FH Buffer*	1.5 µL
QIAseq FastSelect Bacterial –5S/16S/23S*	1 µL
QIAseq FastSelect RNA Removal†	Optional
ERCC Control‡	Optional
Nuclease-Free Water	Bring total reaction volume to 15 µL
Total volume	15 µL

* From QIAseq FastSelect Bacterial –5S/16S/23S Removal Kit.

† Any QIAseq FastSelect RNA Removal Kit or combination can be supplemented or substituted here. If additional QIAseq FastSelect RNA Removal Kits are used, the total reaction volume should remain 15 µL.

‡ ERCC Control RNA (see “Equipment and Reagents to be Supplied by User”) can be added according to the concentrations specified by the manufacturer. If added, the total reaction volume should remain 15 µL.

4. Incubate as described in Table 5, according to your input RNA quality and approximate insert size.

Important: Regardless of the time and temperature chosen in step 1, steps 2–9 must be performed.

5. Add 19.5 µL of QIAseq Beads (prewarmed to room temperature and mixed by vortexing) to the 15 µL reaction. Mix thoroughly by vortexing, and then incubate for 5 min at room temperature.

6. Centrifuge in a tabletop centrifuge until the beads are completely pelleted (~2 min).

7. Place the tubes/plate on a magnetic rack for 2 min. Once the solution has cleared, with the beads still on the magnetic stand, carefully remove and discard the supernatant.

Note: You can completely avoid transferring beads by pipetting very slowly.

Important: Do not discard the beads, because they contain the RNA of interest.

Table 5. Option 2: Fragmentation/depletion protocol

Input RNA quality	Step	Insert size (bp)			
		125–175	175–225	275–325	325–375
High quality (RIN ≥8)	1*	12 min at 89°C	8 min at 89°C	5.5 min at 89°C	4 min at 89°C
Moderate quality (RIN 6–7)	1*		6 min at 89°C	4.5 min at 89°C	
4–5			4 min at 89°C	3 min at 89°C	
3			2 min at 89°C	2 min at 89°C	
FFPE or degraded sample (RIN ≤2)	1*		No fragmentation†	No fragmentation†	
Steps 2–9 are performed, regardless of input RNA quality. They need to be performed whether the RNA is high quality, moderate quality, FFPE, or degraded.	2	2 min at 75°C	2 min at 75°C	2 min at 75°C	2 min at 75°C
	3	2 min at 70°C	2 min at 70°C	2 min at 70°C	2 min at 70°C
	4	2 min at 65°C	2 min at 65°C	2 min at 65°C	2 min at 65°C
	5	2 min at 60°C	2 min at 60°C	2 min at 60°C	2 min at 60°C
	6	2 min at 55°C	2 min at 55°C	2 min at 55°C	2 min at 55°C
	7	2 min at 37°C	2 min at 37°C	2 min at 37°C	2 min at 37°C
	8	2 min at 25°C	2 min at 25°C	2 min at 25°C	2 min at 25°C
	9	Hold at 4°C	Hold at 4°C	Hold at 4°C	Hold at 4°C

* Choose one option for the Step 1 time, according to the input RNA quality and the desired insert size.

† Also suitable for exosomal RNA or RNA of other origin with a size between 80–500 bp.

8. Add 15 µL of Nuclease-Free Water and 19.5 µL of QIAseq Bead Binding Buffer (prewarmed to room temperature and mixed by vortexing). Mix vigorously by vortexing, and then incubate for 5 min at room temperature.
9. Centrifuge in a tabletop centrifuge until the beads are completely pelleted (~2 min).
10. Place the tubes/plate on a magnetic rack for 2 min. Once the solution has cleared, with the beads still on the magnetic stand, carefully remove and discard the supernatant.

Note: You can completely avoid transferring beads by pipetting very slowly

Important: Do not discard the beads, because they contain the RNA of interest.

11. With the tubes still on the magnetic stand, add 200 μ L of 80% ethanol. Wait for 30 s. Carefully remove and discard the wash.
12. Repeat the ethanol wash.
Important: Completely remove all traces of ethanol after this second wash. Remove the ethanol with a 200 μ L pipette tip first, and then use a 10 μ L pipette tip to remove any residual ethanol that will settle.
13. With the beads still on the magnetic stand, air-dry at room temperature for 6–10 min until all liquid has evaporated but without overdrying the beads.
Note: Visually inspect the pellet to confirm that it is completely dry.
14. Remove the beads from the magnetic stand and elute the RNA from the beads by adding 31 μ L Nuclease-Free Water. Mix well by pipetting or vortexing, and then allow the tubes to sit at room temperature for 2 min to appropriately hydrate the beads.
15. Return the tubes/plate to the magnetic rack until the solution has cleared.
16. Transfer 29 μ L supernatant to clean tubes/plate.
17. Proceed to “Protocol: First-strand Synthesis”.

Protocol: First-strand Synthesis

Important points before starting

- The entire product from “Protocol: Fragmentation/FastSelect RNA Removal” is the starting material for first-strand synthesis.
- Two different procedures are provided and should follow what was performed in “Protocol: Fragmentation/FastSelect RNA Removal”:
 - **Option 1:** If using QIAseq FastSelect kits other than the QIAseq FastSelect – 5S/16S/23S Kit
 - **Option 2:** If using the QIAseq FastSelect –5S/16S/23S Kit alone or in combination with other FastSelect kits
- Set up first-strand synthesis on ice.
- Do not vortex any first-strand synthesis reagents or reactions.
- Use thermal cycler with a heated lid.
- Ensure the QIAseq Beads are brought to room temperature before using.
- Ensure the QIAseq Beads are thoroughly mixed at all times. This necessitates working quickly and resuspending the beads immediately before use. If a delay in the protocol occurs, simply vortex the beads.
- Make fresh 80% ethanol.

Procedure

Option 1: If using QIAseq FastSelect kits other than the QIAseq FastSelect – 5S/16S/23S Kit

1. Prepare the reagents required for first-strand synthesis.
 - 1a. Thaw 1 M DTT at room temperature.
 - 1b. Mix by flicking the tube.
 - 1c. Centrifuge to collect residual liquid from the sides of the tube.

Note: RT Enzyme and RNase Inhibitor should be removed from the freezer just before use and placed on ice. After use, immediately return the enzymes to the freezer.

2. Dilute 1 M DTT to 0.4 M for use in Table 6.
3. On ice, prepare the first-strand reaction according to Table 6. Briefly centrifuge, mix by pipetting up and down 10 times, and centrifuge briefly again.
Note: If setting up more than one reaction, prepare a volume of master mix 10% greater than that required for the total number of reactions.
4. Proceed to step 5 (incubate all first-strand synthesis reactions described in Table 8).

Table 6. Option 1: Setup of first-strand reaction

Component	Volume/reaction (μL)
Fragmentation/depletion reaction (already in tube)	37
Diluted DTT (0.4 M)	1
RT Enzyme	1
RNase Inhibitor	1
Total volume	40

Option 2: If using the QIAseq FastSelect – 5S/16S/23S Kit alone or in combination with other FastSelect kits

1. Prepare the reagents required for first-strand synthesis.
 - 1a. Thaw RT Buffer, 5x, and 1 M DTT at room temperature.
 - 1b. Mix by flicking the tube.
 - 1c. Centrifuge to collect residual liquid from the sides of the tube.**Note:** RT Enzyme and RNase Inhibitor should be removed from the freezer just before use and placed on ice. After use, immediately return the enzymes to the freezer.
2. Dilute 1 M DTT to 0.4 M for use in Table 7.

- On ice, prepare the first-strand reaction according to Table 7. Briefly centrifuge, mix by pipetting up and down 10 times, and centrifuge briefly again.

Note: If setting up more than one reaction, prepare a volume of master mix 10% greater than that required for the total number of reactions

- Proceed to step 5 (incubate all first-strand synthesis reactions described in Table 8).

Table 7. Option 2: Setup of first-strand reaction

Component	Volume/reaction
Fragmentation/depletion reaction from cleanup (already in tube)	29 μ L
RT Buffer, 5x	8 μ L
Diluted DTT (0.4 M)	1 μ L
RT Enzyme	1 μ L
RNase Inhibitor	1 μ L
Total volume	40 μ L

- Incubate all first-strand synthesis reactions described in Table 8.

Table 8. Option 2: First-strand reaction incubation protocol

Step	Temperature $^{\circ}$ C	Incubation time
1	25	10 min
2	42	15 min
3	70	15 min
4	4	Hold

- Add 56 μ L of resuspended QIAseq Beads. Vortex for 3 s and briefly centrifuge.
- Incubate for 5 min at room temperature.
- Place the tubes/plate onto a magnetic rack. After the solution has cleared (~10 min or longer), carefully remove and discard the supernatant.

Important: Do not discard the beads, because they contain the DNA of interest.

9. With the tubes still on the magnetic stand, add 200 μL of 80% ethanol. Rotate the tubes/plate 3 times to wash the beads. Carefully remove and discard the wash.
10. Repeat the ethanol wash.
Important: Completely remove all traces of the ethanol after this second wash. Briefly centrifuge and return the tubes to the magnetic stand. Remove the ethanol with a 200 μL pipette first, and then use a 10 μL pipette to remove any residual ethanol.
11. With the tubes/plate (caps opened) still on the magnetic stand, air-dry at room temperature for 5–10 min.
Note: Visually inspect that the pellet is completely dry and that all ethanol is evaporated.
12. Remove the tubes/plate from the magnetic stand and elute the DNA from the beads by adding 40 μL Nuclease-Free Water. Mix well by pipetting.
13. Return the tubes/plate to the magnetic rack until the solution has cleared.
14. Transfer 38.5 μL supernatant to clean tubes/plate.
15. Proceed to “Protocol: Second-strand Synthesis, End-repair, and A-addition”. Alternatively, the samples can be stored at -30 to -15°C in a constant-temperature freezer.

Protocol: Second-strand Synthesis, End-repair, and A-addition

Important points before starting

- The entire 38.5 μ L product from “Protocol: First-strand Synthesis” is the starting material for the second-strand synthesis, end-repair, and A-addition procedure.
- Set up reaction on ice.
- Do not vortex any second-strand synthesis, end-repair and A-addition reagents or reactions.
- Use a thermal cycler with a heated lid.
- Ensure the QIAseq Beads are brought to room temperature before using.
- Ensure the QIAseq Beads are thoroughly mixed at all times. This necessitates working quickly and resuspending the beads immediately before use. If a delay in the protocol occurs, simply vortex the beads.

Procedure

1. Prepare required reagents.
 - 1a. Thaw Second Strand Buffer, 10x, at room temperature.
 - 1b. Mix by vortexing.
 - 1c. Centrifuge to collect residual liquid from the sides of the tubes.

Note: Second Strand Enzyme Mix should be removed from the freezer just before use and placed on ice. After use, immediately return the enzyme to the freezer.
2. On ice, prepare the first-strand reaction according to Table 9. Briefly centrifuge, mix by pipetting up and down 10 times, and centrifuge briefly again.

Note: If setting up more than one reaction, prepare a volume of master mix 10% greater than that required for the total number of reactions.

Table 9. Setup of second-strand synthesis, end repair, and A-addition reaction

Component	Volume/reaction (μL)
Product from "Protocol: First-strand Synthesis"	38.5
Second Strand Buffer, 10x	5
Second Strand Enzyme Mix	6.5
Total volume	50

3. Incubate as described in Table 10.

Table 10. Second-strand synthesis, end-repair, and A-addition protocol

Step	Temperature (°C)	Incubation time
1	25	30 min
2	65	15 min
3	4	Hold

4. Add 70 μL or resuspended QIAseq Beads. Vortex for 3 s and briefly centrifuge.

5. Incubate for 5 min at room temperature.

6. Place the tubes/plate onto a magnetic rack. After the solution has cleared (~10 min or longer), carefully remove and discard the supernatant.

Important: Do not discard the beads, because they contain the DNA of interest.

7. With the tubes still on the magnetic stand, add 200 μL of 80% ethanol. Rotate the tubes/plate 3 times to wash the beads. Carefully remove and discard the wash.

8. Repeat the ethanol wash.

Important: Completely remove all traces of the ethanol after this second wash. Briefly centrifuge and return the tubes to the magnetic stand. Remove the ethanol with a 200 μL pipette first, and then use a 10 μL pipette to remove any residual ethanol.

9. With the tubes/plate (caps opened) still on the magnetic stand, air-dry at room temperature for 5–10 min.

Note: Visually inspect that the pellet is completely dry and that all ethanol is evaporated

10. Remove the tubes/plate from the magnetic stand and elute the DNA from the beads by adding 52 μL Nuclease-Free Water. Mix well by pipetting.
11. Return the tubes to the magnetic rack until the solution has cleared.
12. Transfer 50 μL supernatant to clean tubes/plate.
13. Proceed to “Protocol: Strand-specific Ligation”. Alternatively, the samples can be stored at -30 to -15°C in a constant-temperature freezer.

Protocol: Strand-specific Ligation

Important points before starting

- The entire 50 μ L product from “Protocol: Second-strand Synthesis, End-repair, and A-addition” is the starting material for the strand-specific ligation.
- Set up the reaction on ice.
- Do not vortex any strand-specific ligation enzymes or reactions.
- Use a thermal cycler without a heated lid.
- For UDI adapter plates, the layout of the 24-plex and 96-plex plates is described in “Appendix A: QIAseq Dual-Index Y-Adapters”. The index motifs used in the QIAseq Unique Dual-Index Kits are listed at www.qiagen.com, QIAseq UDI Y-Adapter Sequences.
- For CDI adapter plates, the layout and barcode sequences are described in Appendix A.
- Unused, undiluted adapters can be stored at -30 to -15°C . If desired residual diluted adapter can be removed and discarded before plate storage.
- Do not reuse diluted adapter due to the risk of barcode cross-contamination and lower than expected adapter concentration after storage of diluted material.
- Ensure the QIAseq Beads are brought to room temperature before using.
- Ensure the QIAseq Beads are thoroughly mixed at all times. This necessitates working quickly and resuspending the beads immediately before use. If a delay in the protocol occurs, simply vortex the beads.

Procedure

1. Prepare the required reagents.
 - 1a. Thaw Ultralow Input Ligation Buffer, 4x, and Ligation Initiator at room temperature.
 - 1b. Mix by vortexing.
 - 1c. Centrifuge to collect residual liquid from the sides of the tubes.

Note: Ultralow Input Ligase should be removed from the freezer just before use and placed on ice. After use, immediately return the enzyme to the freezer.

2. Prepare the adapter plate as follows. The layouts of the 24-plex and 96-plex single-use adapter plates are displayed in Appendix A: QIAseq Dual-Index Y-Adapters.

Note: If multiplexing 1–6 samples, consult the *Low-Plex Pooling Guidelines for Enrichment Protocols* document from Illumina to select the ideal adapter combinations.

- 2a. Thaw the adapter plate at room temperature. Vortex and centrifuge briefly before use.
- 2b. Remove the clear protective adapter plate lid and carefully pierce only the foil seal for each adapter well to be used, using a fresh tip to pierce each well.
- 2c. Remove an aliquot and dilute the adapters as suggested in Table 11.

Table 11. Dilution of QIAseq adapters

Total RNA Starting Amount	Adapter dilution
100 ng	1:100
500 ng	1:25
1 µg	1:12.5
5 µg	1:5

- 2d. Replace the plate lid and freeze unused, undiluted adapter at –30 to –15°C. Remove and discard residual diluted adapter before plate storage.
3. On ice, prepare the strand-specific ligation reaction according to Table 12. Briefly centrifuge, mix by pipetting up and down 15–20 times, and centrifuge briefly again.

Note: If setting up more than one reaction, prepare a volume of master mix 10% greater than that required for the total number of reactions.

Important: Pipet slowly to mix. Ligation Initiator and the reaction mix are very viscous.

Table 12. Preparation of strand-specific ligation reactions

Component	Volume/reaction (µL)
Product from Protocol: Second-Strand Synthesis, End-repair, and A-addition	50
Diluted adapter*	2
Ultralow Input Ligation Buffer, 4x	25
Ultralow Input Ligase	5
Ligation Initiator	6.5
Nuclease-Free Water	11.5
Total volume	100

* Choose a unique adapter for each sample.

4. Incubate at 25°C for 10 min.

Important: Do not use a heated lid.

5. Add 80 µL of resuspended QIAseq Beads. Vortex for 3 s and briefly centrifuge.

6. Incubate for 5 min at room temperature.

7. Place the tubes/plate onto a magnetic rack. After the solution has cleared (~10 min or longer), carefully remove and discard the supernatant.

Important: Do not discard the beads, because they contain the DNA of interest.

8. With the tubes still on the magnetic stand, add 200 µL of 80% ethanol. Rotate the tubes/plate 3 times to wash the beads. Carefully remove and discard the wash.

9. Repeat the ethanol wash.

Important: Completely remove all traces of the ethanol after this second wash. Briefly centrifuge and return the tubes to the magnetic stand. Remove the ethanol with a 200 µL pipette first, and then use a 10 µL pipette to remove any residual ethanol.

10. With the tubes/plate (caps opened) still on the magnetic stand, air-dry at room temperature for 5–10 min.

Note: Visually inspect that the pellet is completely dry and that all ethanol is evaporated.

11. Remove the tubes/plate from the magnetic stand and elute the DNA from the beads by adding 92 μL Nuclease-Free Water. Mix well by pipetting.
12. Return the tubes/plate to the magnetic rack until the solution has cleared.
13. Transfer 90 μL supernatant to clean tubes/plate.
14. Add 108 μL or resuspended QIAseq Beads. Vortex for 3 s and briefly centrifuge.
15. Incubate for 5 min at room temperature.
16. Place the tubes/plate onto a magnetic rack. After the solution has cleared (~10 min or longer), carefully remove and discard the supernatant.

Important: Do not discard the beads, because they contain the DNA of interest.

17. With the tubes still on the magnetic stand, add 200 μL of 80% ethanol. Rotate the tubes/plate 3 times to wash the beads. Carefully remove and discard the wash.
18. Repeat the ethanol wash.

Important: Completely remove all traces of the ethanol after this second wash. Briefly centrifuge and return the tubes to the magnetic stand. Remove the ethanol with a 200 μL pipette first, and then use a 10 μL pipette to remove any residual ethanol.

19. With the tubes/plate (caps opened) still on the magnetic stand, air-dry at room temperature for 5–10 min.

Note: Visually inspect that the pellet is completely dry and that all ethanol is evaporated.

20. Remove the tubes/plate from the magnetic stand and elute the DNA from the beads by adding 25 μL Nuclease-Free Water. Mix well by pipetting.
21. Return the tubes/plate to the magnetic rack until the solution has cleared.
22. Transfer 23.5 μL supernatant to clean tubes/plate.
23. Proceed to “Protocol: HiFi PCR Library Amplification”. Alternatively, the samples can be stored at -30 to -15°C in a constant-temperature freezer.

Protocol: HiFi PCR Library Amplification

Important points before starting

- This protocol is compatible with all Illumina NGS instruments that use patterned and non-patterned flow cells.
- The entire 23.5 μL product from “Protocol: Strand-specific Ligation” is the starting material for the CleanStart Library Amplification.
- Set up the reaction on ice.
- Use a thermal cycler with a heated lid.
- Ensure the QIAseq Beads are brought to room temperature before using.
- Ensure the QIAseq Beads are thoroughly mixed at all times. This necessitates working quickly and resuspending the beads immediately before use. If a delay in the protocol occurs, simply vortex the beads.

Procedure

1. Prepare the reagents required for HiFi PCR library amplification.
 - 1a. Thaw Primer Mix, 10 μM at room temperature and thaw HiFi PCR Master Mix, 2x, on ice.
 - 1b. Mix by flicking the tube.
 - 1c. Centrifuge to collect residual liquid from the sides of the tubes.
2. On ice, prepare the library amplification reaction according to Table 13.
3. Briefly centrifuge, mix by pipetting up and down 10 times, and centrifuge briefly again.

Note: If setting up more than one reaction, prepare a volume of master mix 10% greater than that required for the total number of reactions.

Table 13. Setup of library amplification

Component	Volume/reaction (µL)
Product from "Protocol: Strand-specific Ligation"	23.5
HiFi PCR Master Mix, 2x	25
Primer Mix, 10 uM	1.5
Total volume	50

4. Select the number of PCR cycles, based on total RNA input, according to Table 14.

Important: When removing globin with QIAseq FastSelect Globin RNA Removal Kit, 2 additional cycles of library amplification need to be performed.

Table 14. Recommended number of PCR cycles, based on total RNA input

Total RNA Input	Number of amplification cycles*
100 ng	14–16†
500 ng	11–13†
1 µg	9–11†
5 µg	7–9†

* Use selected number of cycles for amplification in Table 16.

† **Important:** When removing globin with QIAseq FastSelect Globin RNA Removal Kit, add 2 additional cycles of amplification.

5. Incubate as described in Table 15.

Table 15. CleanStart library amplification cycling conditions

Step	Time	Temperature (°C)	Number of cycles
Initial denaturation	2 min	98	1
PCR	20 s	98	See Table 14
	30 s	60	
	30 s	72	
Final extension	1 min	72	1
Hold	∞	4	Hold

* For the reamplification of libraries, omit the CleanStart decontamination step. Start with incubation at 98°C for 2 min.

6. After amplification, add 60 μ L QIAseq Beads. Vortex for 3 s and briefly centrifuge.

7. Incubate for 5 min at room temperature.

8. Place the tubes/plate onto a magnetic rack. After the solution has cleared (~10 min or longer), carefully remove and discard the supernatant.

Important: Do not discard the beads, because they contain the DNA of interest.

9. With the tubes still on the magnetic stand, add 200 μ L of 80% ethanol. Rotate the tubes/plate 3 times to wash the beads. Carefully remove and discard the wash.

10. Repeat the ethanol wash.

Important: Completely remove all traces of the ethanol after this second wash. Briefly centrifuge and return the tubes to the magnetic stand. Remove the ethanol with a 200 μ L pipette first, and then use a 10 μ L pipette to remove any residual ethanol.

11. With the tubes/plate (caps opened) still on the magnetic stand, air-dry at room temperature for 5–10 min.

Note: Visually inspect that the pellet is completely dry, and that all ethanol is evaporated.

12. Remove the tubes/plate from the magnetic stand and elute the DNA from the beads by adding 22 μL Nuclease-Free Water. Mix well by pipetting.
13. Return the tubes/plate to the magnetic rack until the solution has cleared.
14. Transfer 20 μL to clean tubes/plate. This is the QIAseq Stranded Sequencing Library.
15. Proceed to “Recommendations: Library QC, Quantification, and Sequencing”.
Alternatively, the samples can be stored at -30 to -15°C in a constant-temperature freezer.

Recommendations: Library QC, Quantification, and Sequencing

NGS library QC

QC can be performed with the Agilent Bioanalyzer or TapeStation®. Check for the correct size distribution of library fragments (~300–500 bp median size) and for the absence of adapters or adapter-dimers (~130 bp). Figure 3 shows the library size distributions for 1 ng and 50 ng libraries prepared from UHRR input material. Both results show no traces of adapter-dimers. The 1 ng input RNAseq library shows optimal size distribution, while the 50 ng input RNAseq library shows broader library size distribution (but does not affect the NGS sequencing quality).

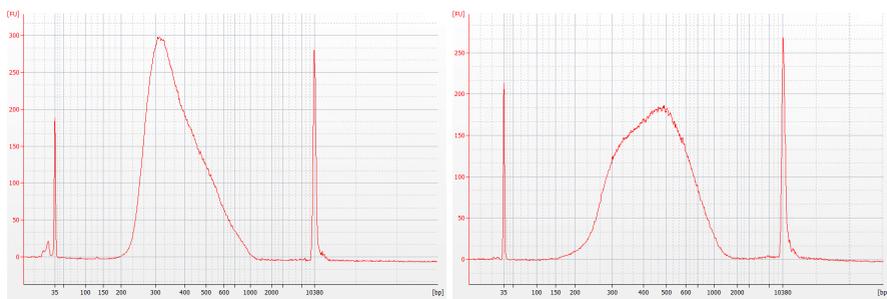


Figure 3. QIAseq Stranded RNAseq library size distributions measured with the Agilent Bioanalyzer High Sensitivity DNA Chip using standard protocol conditions with different input amounts. Left: 1 ng, right: 50 ng UHRR input material.

Important: If excessive adapter-dimers (~130 bp) are prominent after library QC (greater than 1–2% of total library yields), perform a second purification with QIAseq Beads. This can be accomplished by bringing the sample to a final volume of 55 μ l and repeating steps 6–14 of the HiFi PCR library amplification protocol.

Preferred library quantification method

The library yield measurements from the Bioanalyzer or TapeStation rely on fluorescence dyes that intercalate into DNA or RNA. These dyes cannot discriminate between cDNA with or without adapter sequences, so only complete QIAseq Stranded Total RNA libraries with full adapter sequences will be sequenced. As a result, QIAGEN's QIAseq Library Quant Array Kit or Assay Kit, which contains laboratory-verified forward and reverse primers, together with a DNA standard, is highly recommended for accurate quantification of the prepared QIAseq Stranded Total RNA library.

Sample dilution, pooling, sequencing, and data analysis

When the QIAseq Stranded libraries have been quantified with the QIAseq Library Quant Array or Assay Kit, typical QIAseq Stranded library yields are approximately 8–10 nM in 20 μ L volume, depending on the quality of the input starting RNA used. This yield is sufficient for an NGS sequencing run. Dilute the individual QIAseq Stranded libraries to a concentration of 4 nM. Then combine libraries with different sample indexes in equimolar amounts. The recommended starting concentration of the pooled QIAseq Stranded libraries to load onto a MiSeq is 9 pM, or 1.6 pM on a NextSeq.

The recommended starting point for rRNA-depleted samples is 50 M reads/sample. When using UDIs, 74 bp paired-end reads and dual 10 bp index reads are required. When using CDIs, 76 bp paired-end reads and dual 8 bp index reads are required. Longer paired-end reads (UDI libraries: 149 bp paired-end reads and dual 10 bp index reads, and CDI libraries: 151 bp paired-end reads and dual 8 bp index reads) are recommended for rare/novel transcripts, splice site isoforms, and fusion gene detection.

For data analysis recommendations, see “Appendix B: Data Analysis Recommendations”.

Troubleshooting Guide

This troubleshooting guide may be helpful in solving any problems that may arise. For more information, see also the Frequently Asked Questions page in our Technical Support Center: www.qiagen.com/FAQ/FAQList.aspx The scientists in QIAGEN Technical Services are always happy to answer any questions you may have about either the information or protocols in this handbook (for contact information, visit support.qiagen.com).

Comments and suggestions

Low library yields

- | | |
|---|--|
| a) Sub-optimal PCR cycle number | An increased number of PCR cycles in the HiFi PCR or CleanStart PCR library amplification enrichment step can increase library yields. |
| b) Insufficient RNA input amount | Higher RNA input amounts can lead to higher library yields; However, more RNA input could lead to a higher adapter dilution (see Appendix B: Data Analysis Recommendations). |
| c) Not enough adapter molecules in ligation (only if no adapter-dimers are visible) | Decrease adapter dilution. An increased number of adapter molecules during ligation can increase ligation efficiency and library yields but can also increase adapter-dimer formation. |

High Bioanalyzer peak at 120–140 bp (adapter-dimers)

- | | |
|---|--|
| a) Increase adapter dilution during ligation | Higher adapter dilutions decrease the adapter-dimer formation during the ligation step. |
| b) Decrease QIAseq Beads volume in cleanup after ligation | Lower QIAseq Bead volumes in cleanup step after ligation (e.g., 0.6x/1.1x instead of the standard volumes with 0.8x/1.2x) can increase adapter-dimer depletion but can lead to lower library yields. |
| c) Increase RNA input amount | Higher RNA input amounts can lead to higher library yields. |

Bioanalyzer peaks at higher molecular weight (>1000bp; PCR overamplification)

- | | |
|--|--|
| Reduce PCR cycle number in the HiFi PCR or CleanStart PCR Library amplification step | Single-stranded library products can self-anneal after too many PCR cycles when free PCR primers are no longer available. Reduced PCR cycle numbers are only necessary when the molarity of the high molecular peak is significantly elevated (>50% compared to library yields <700 bp). |
|--|--|

Comments and suggestions

Strong bias in transcript coverage plots after NGS data analysis

- | | |
|--|---|
| a) Keep input RNA on ice as much as possible | Degraded RNA can lead to stronger transcript coverage bias after NGS data analysis. Degradation can be caused by RNase contamination or prolonged storage of RNA at elevated temperatures (>4°C). |
| b) Add additional RNase Inhibitor into reactions | In cases of strong RNAseq contaminations, add additional RNase Inhibitor into the reactions to inhibit enzymatic activity of QIAseq Stranded RNA library enzymes. |

Very broad library size distributions

- | | |
|-----------------------------|---|
| Increase fragmentation time | If the library size distribution is very broad with library sizes >700 bp, increase RNA fragmentation time to 20 min, depending on the used RNA input material. |
|-----------------------------|---|

Appendix A: QIAseq Dual-Index Y-Adapters

Generation of sample sheets for Illumina instruments

Index sequences for QIAseq UDI and CDI Y-Adapters are available for download at www.qiagen.com

Sequencing on the NextSeq, HiSeq X™, or HiSeq 3000/4000 system follows a different dual-indexing workflow than other Illumina systems. If you are manually creating sample sheets for these instruments, enter the reverse complement of the i5 index adapter sequence. If you are using Illumina Experiment Manager, BaseSpace, or Local Run Manager for run planning, the software will automatically reverse complement index sequences when necessary.

Ready-to-use sample sheets containing all QIAseq UDI and CDI Y-Adapter barcode sequences are available for MiSeq, NextSeq, MiniSeq®, and HiSeq instruments. These can be conveniently downloaded from www.qiagen.com

These can be imported and edited using the Illumina Experiment Manager Software, Illumina Local Run Manager, or any text editor. Make sure to download the appropriate sample sheet for NextSeq, HiSeq X, or HiSeq 3000/4000 systems depending on whether you are using Local Run Manager or manually configuring the sequencing run.

Unique Dual-Index Y-Adapters

The layout of the 24-plex and 96-plex (A/B/C/D) single-use UDI adapter plate is shown in Figure 4 and Figure 5. The index motifs used in the QIAseq Unique Dual-Index Kits are listed at www.qiagen.com

To make sequencing preparation more convenient, you can download Illumina-compatible sample sheets for different sequencing instruments at www.qiagen.com

	1	2	3	4	5	6	7	8	9	10	11	12
A	001	009	017	-	-	-	-	-	-	-	-	-
B	002	010	018	-	-	-	-	-	-	-	-	-
C	003	011	019	-	-	-	-	-	-	-	-	-
D	004	012	020	-	-	-	-	-	-	-	-	-
E	005	013	021	-	-	-	-	-	-	-	-	-
F	006	014	022	-	-	-	-	-	-	-	-	-
G	007	015	023	-	-	-	-	-	-	-	-	-
H	008	016	024	-	-	-	-	-	-	-	-	-

Figure 4. QIAseq UDI Y-Adapter Plate (24) layout (UDI 1–24).

Plate A

	1	2	3	4	5	6	7	8	9	10	11	12
A	001	009	017	025	033	041	049	057	065	073	081	089
B	002	010	018	026	034	042	050	058	066	074	082	090
C	003	011	019	027	035	043	051	059	067	075	083	091
D	004	012	020	028	036	044	052	060	068	076	084	092
E	005	013	021	029	037	045	053	061	069	077	085	093
F	006	014	022	030	038	046	054	062	070	078	086	094
G	007	015	023	031	039	047	055	063	071	079	087	095
H	008	016	024	032	040	048	056	064	072	080	088	096

Plate B

	1	2	3	4	5	6	7	8	9	10	11	12
A	097	105	113	121	129	137	145	153	161	169	177	185
B	098	106	114	122	130	138	146	154	162	170	178	186
C	099	107	115	123	131	139	147	155	163	171	179	187
D	100	108	116	124	132	140	148	156	164	172	180	188
E	101	109	117	125	133	141	149	157	165	173	181	189
F	102	110	118	126	134	142	150	158	166	174	182	190
G	103	111	119	127	135	143	151	159	167	175	183	191
H	104	112	120	128	136	144	152	160	168	176	184	192

Plate C

	1	2	3	4	5	6	7	8	9	10	11	12
A	193	201	209	217	225	233	241	249	257	265	273	281
B	194	202	210	218	226	234	242	250	258	266	274	282
C	195	203	211	219	227	235	243	251	259	267	275	283
D	196	204	212	220	228	236	244	252	260	268	276	284
E	197	205	213	221	229	237	245	253	261	269	277	285
F	198	206	214	222	230	238	246	254	262	270	278	286
G	199	207	215	223	231	239	247	255	263	271	279	287
H	200	208	216	224	232	240	248	256	264	272	280	288

Plate D

	1	2	3	4	5	6	7	8	9	10	11	12
A	289	297	305	313	321	329	337	345	353	361	369	377
B	290	298	306	314	322	330	338	346	354	362	370	378
C	291	299	307	315	323	331	339	347	355	363	371	379
D	292	300	308	316	324	332	340	348	356	364	372	380
E	293	301	309	317	325	333	341	349	357	365	373	381
F	294	302	310	318	326	334	342	350	358	366	374	382
G	295	303	311	319	327	335	343	351	359	367	375	383
H	296	304	312	320	328	336	344	352	360	368	376	384

Figure 5. QIAseq UDI Y-Adapter Plates: Plate A (96) layout (UDI 1–96), Plate B (96) layout (UDI 97–192), Plate C (96) layout (UDI 193–288), and Plate D (96) layout (UDI 289–384).

Combinatorial Dual-Index Y-Adapters

The layouts for the 96-plex and 24-plex single-use CDI adapter plates are shown in Figure 6 and Figure 7. The barcode sequences used in the QIAseq Combinatorial Dual-Index Kits are listed in Table 16. Indices 501-508 and 701-712 correspond to the respective Illumina adapter barcodes, Illumina TruSeq® CD indexes (formerly TruSeq HT). To make sequencing preparation more convenient, you can download Illumina-compatible sample sheets for different sequencing instruments at www.qiagen.com

Follow *Low-Plex Pooling Guidelines for Enrichment Protocols* from Illumina to choose the correct combinations of D50x/D70x adapters for the corresponding instrument if loading between 1–6 samples onto one flow-cell lane.

Table 16. CDI Adapter barcode sequences used in the QIAseq CDI Y-Adapter Kits (24 and 96-plex Adapter Plates)

D50X barcode name	i5 barcode sequence*	D70X barcode name	i7 barcode sequence
D501	TATAGCCT	D701	ATTACTCG
D502	ATAGAGGC	D702	TCCGGAGA
D503	CCTATCCT	D703	CGCTCATT
D504	GGCTCTGA	D704	GAGATTC
D505	AGGCGAAG	D705	ATCAGAA
D506	TAATCTTA	D706	GAATTCGT
D507	CAGGACGT	D707	CTGAAGCT
D508	GTA CTGAC	D708	TAATGCGC
		D709	CGGCTATG
		D710	TCCGCGAA
		D711	TCTCGCGC
		D712	AGCGATAG

* Sequencing on the MiniSeq, NextSeq, and HiSeq 3000/4000 systems follow a different dual-indexing workflow than other Illumina systems, which requires the reverse complement of the i5 index adapter sequence.

	1	2	3	4	5	6	7	8	9	10	11	12
A	501 701	501 702	501 703	501 704	501 705	501 706	501 707	501 708	501 709	501 710	501 711	501 712
B	502 701	502 702	502 703	502 704	502 705	502 706	502 707	502 708	502 709	502 710	502 711	502 712
C	503 701	503 702	503 703	503 704	503 705	503 706	503 707	503 708	503 709	503 710	503 711	503 712
D	504 701	504 702	504 703	504 704	504 705	504 706	504 707	504 708	504 709	504 710	504 711	504 712
E	505 701	505 702	505 703	505 704	505 705	505 706	505 707	505 708	505 709	505 710	505 711	505 712
F	506 701	506 702	506 703	506 704	506 705	506 706	506 707	506 708	506 709	506 710	506 711	506 712
G	507 701	507 702	507 703	507 704	507 705	507 706	507 707	507 708	507 709	507 710	507 711	507 712
H	508 701	508 702	508 703	508 704	508 705	508 706	508 707	508 708	508 709	508 710	508 711	508 712

Figure 6. QIAseq CDI Y-Adapter Plate (96) layout (CDI 1–96).

	1	2	3	4	5	6	7	8	9	10	11	12
A	501 701	501 702	501 703	-	-	-	-	-	-	-	-	-
B	502 701	502 702	502 703	-	-	-	-	-	-	-	-	-
C	503 701	503 702	503 703	-	-	-	-	-	-	-	-	-
D	504 701	504 702	504 703	-	-	-	-	-	-	-	-	-
E	505 701	505 702	505 703	-	-	-	-	-	-	-	-	-
F	506 701	506 702	506 703	-	-	-	-	-	-	-	-	-
G	507 701	507 702	507 703	-	-	-	-	-	-	-	-	-
H	508 701	508 702	508 703	-	-	-	-	-	-	-	-	-

Figure 7. QIAseq CDI Y-Adapter Plate (24) layout (CDI 1–24).

Appendix B: Data Analysis Recommendations

RNAseq Analysis & Biomarker Discovery pipeline

RNA-seq Analysis & Biomarker Discovery pipeline Primary and secondary analysis tools are available at <https://geneglobe.qiagen.com/analyze>

The RNA-seq Analysis & Biomarker Discovery Pipeline uses QIAGEN CLC Biomedical Workbench for read alignment, and differential expression. QIAGEN Ingenuity® Pathway Analysis (IPA®) returns the top hits from the QIAGEN Knowledge Base for canonical pathways, upstream regulators, and diseases.

Using the RNA-seq Analysis & Biomarker Discovery Pipeline, FASTQ files can be uploaded, and RNA sequences aligned. Differential RNA expression will be calculated and visualized using interactive volcano plots. Differentially expressed RNAs will be queried against the QIAGEN Knowledge Base for canonical pathways, upstream regulators, and diseases and biological functions. Important RNAs can then be identified, and digital PCR and qPCR assays easily found for biological verification.

For each alignment, a credit is deducted from your account. Credits for using the RNA-seq Analysis & Biomarker Discovery Pipeline are included with QIAseq library kits. Credits can also be purchased for using the RNA-seq Analysis Portal with non-QIAGEN kits at www.qiagen.com.

Procedure

1. Go to <https://geneglobe.qiagen.com/>
2. Click Analyze Data.
3. Under Start Analyzing Your Data:

- 3a. Select analysis type: Next-Generation Sequencing
 - 3b. Select your analyte: mRNA/lncRNA
 - 3c. Select your kit: QIAseq Stranded RNA Kit
4. Click Start Your Analysis

RNAseq alignment using CLC Genomics Workbench

Downstream NGS data can be analyzed with CLC Genomics Workbench (see digitalinsights.qiagen.com). When doing alignment, the QIAseq Stranded libraries represent the sense strand of the RNA sequence.

CLC Genomics Workbench is a comprehensive analysis package for the analysis and visualization of data from all major NGS platforms. The workbench supports and seamlessly integrates into a typical NGS workflow. CLC Genomics Workbench is available for Windows®, Mac OS® X, and Linux® platforms. Incorporating cutting-edge technology and algorithms, CLC Genomics Workbench supports key NGS features within genomics, transcriptomics, and epigenomics research fields. Additionally, it includes all the classical analysis tools of CLC Main Workbench.

Gene expression interpretation

Ingenuity Pathway Analysis (IPA) is an all-in-one, web-based software application that enables analysis, integration, and understanding of data from gene expression, miRNA, and SNP microarrays, as well as metabolomics, proteomics, and RNAseq experiments. This application is a great tool for interpreting the data you generate from the new QIAseq Stranded RNAseq kit. IPA is the market leader in gene expression analysis, having been cited in over 18,000 scientific publications to date.

You will find that IPA data analysis and search capabilities help you understand the significance of data, specific targets, or candidate biomarkers in the context of larger biological or chemical systems. The software is backed by the Ingenuity Knowledge Base of highly structured, detail-rich biological and chemical findings. For information on IPA, visit digitalinsights.qiagen.com

Appendix C: General Remarks on Handling RNA

Handling RNA

Ribonucleases (RNases) are very stable and active enzymes that generally do not require cofactors to function. Since RNases are difficult to inactivate and even minute amounts are sufficient to degrade RNA, do not use any plasticware or glassware without first eliminating possible RNase contamination. Care should be taken to avoid inadvertently introducing RNases into the RNA sample during or after the purification procedure. To create and maintain an RNase-free environment, the following precautions must be taken during pretreatment and use of disposable and non-disposable vessels and solutions while working with RNA.

General handling

Proper microbiological, aseptic technique should always be used when working with RNA. Hands and dust particles may carry bacteria and molds and are the most common sources of RNase contamination. Always wear latex or vinyl gloves while handling reagents and RNA samples to prevent RNase contamination from the surface of the skin or from dusty laboratory equipment. Change gloves frequently and keep tubes closed whenever possible. Keep purified RNA on ice when aliquots are pipetted for downstream applications.

For removal of RNase contamination from bench surfaces, nondisposable plasticware and laboratory equipment (e.g., pipettes and electrophoresis tanks), general laboratory reagents can be used. To decontaminate plasticware, rinse with 0.1 M NaOH, 1 mM EDTA* followed by RNase-free water, or rinse with chloroform* if the plasticware is chloroform-resistant. To decontaminate electrophoresis tanks, clean with detergent (e.g., 0.5% SDS),* rinse with RNase-free water, rinse with ethanol (if the tanks are ethanol-resistant), and allow to dry.

* When working with chemicals, always wear a suitable lab coat, disposable gloves, and protective goggles. For more information, consult the appropriate material data sheets (SDSs), available from the product supplier.

Disposable plasticware

The use of sterile, disposable polypropylene tubes is recommended throughout the procedure. These tubes are generally RNase-free and do not require pretreatment to inactivate RNases.

Glassware

Glassware should be treated before use to ensure that it is RNase-free. Glassware used for RNA work should be cleaned with a detergent,* thoroughly rinsed and oven baked at 240°C for 4 hours or more (overnight, if more convenient) before use. Autoclaving alone will not fully inactivate many RNases. Alternatively, glassware can be treated with DEPC* (diethyl pyrocarbonate), as described in “Solutions” below.

Solutions

Solutions (water and other solutions)* should be treated with 0.1% DEPC. DEPC is a strong, but not absolute, inhibitor of RNases. It is commonly used at a concentration of 0.1% to inactivate RNases on glass or plasticware or to create RNase-free solutions and water. DEPC inactivates RNases by covalent modification. Add 0.1 mL DEPC to 100 mL of the solution to be treated and shake vigorously to bring the DEPC into solution. Let the solution incubate for 12 hours at 37°C. Autoclave for 15 minutes to remove any trace of DEPC. DEPC will react with primary amines and cannot be used directly to treat Tris* buffers. DEPC is highly unstable in the presence of Tris buffers and decomposes rapidly into ethanol and CO₂. When preparing Tris buffers, treat water with DEPC first, and then dissolve Tris to make the appropriate buffer. Trace amounts of DEPC will modify purine residues in RNA by carbethoxylation. Carbethoxylated RNA is translated with very low efficiency in cell-free systems. However, its ability to form DNA:RNA or RNA:RNA hybrids is not seriously affected unless a large fraction of the purine residues have been modified. Residual DEPC must always be eliminated from solutions or vessels by autoclaving or heating to 100°C for 15 minutes.

* When working with chemicals, always wear a suitable lab coat, disposable gloves, and protective goggles. For more information, consult the appropriate material data sheets (SDSs), available from the product supplier.

Appendix D:

Protocol: CleanStart Library Amplification

Important points before starting

- The CleanStart library protocol should be used when amplified library contamination may be an issue.
- Amplified libraries using the CleanStart protocol may exhibit abnormal clustering on illumina patterned flowcells and should be tested for compatibility with the specific instrument, flowcell and data analysis software.
- The entire 23.5 μL product from “Protocol: Strand-specific Ligation” is the starting material for the CleanStart Library Amplification.
- QIAseq CleanStart PCR reagents use a proprietary PCR reaction, in conjunction with modification enzymes, to ensure that previously constructed NGS libraries are removed.
Important: If a previously amplified CleanStart Library needs to be re-amplified - for instance, when an additional library is needed to replace a failed NGS run- omit the decontamination step of the PCR protocol (incubation for 15 min at 37°C) to disable selective degradation.
- Set up the reaction on ice.
- Do not vortex any CleanStart library amplification reagents or reactions.
- Use a thermal cycler with a heated lid.
- Ensure the QIAseq Beads are brought to room temperature before using.
- Ensure the QIAseq Beads are thoroughly mixed at all times. This necessitates working quickly and resuspending the beads immediately before use. If a delay in the protocol occurs, simply vortex the beads.

Procedure

1. Prepare the reagents required for CleanStart library amplification.

- 1a. Thaw CleanStart PCR Primer Mix at room temperature and thaw CleanStart PCR Mix, 2x, on ice.
 - 1b. Mix by flicking the tube.
 - 1c. Centrifuge to collect residual liquid from the sides of the tubes.
2. On ice, prepare the library amplification reaction according to Table 13.
 3. Briefly centrifuge, mix by pipetting up and down 10 times, and centrifuge briefly again.

Note: If setting up more than one reaction, prepare a volume of master mix 10% greater than that required for the total number of reactions.

Table 17. Setup of library amplification

Component	Volume/reaction (µL)
Product from "Protocol: Strand-specific Ligation"	23.5
CleanStart PCR Mix, 2x	25
CleanStart PCR Primer Mix	1.5
Total volume	50

4. Select the number of PCR cycles, based on total RNA input, according to Table 14.

Important: When removing globin with QIAseq FastSelect Globin RNA Removal Kit, two additional cycles of library amplification need to be performed.

Table 18. Recommended number of PCR cycles, based on total RNA input

Total RNA Input	Number of amplification cycles*
100 ng	14–16 [†]
500 ng	11–13 [†]
1 µg	9–11 [†]
5 µg	7–9 [†]

* Use selected number of cycles for amplification in Table 16.

[†] **Important:** When removing globin with QIAseq FastSelect Globin RNA Removal Kit, add 2 additional cycles of amplification.

5. Incubate as described in Table 15.

Table 19. CleanStart library amplification cycling conditions

Step	Time	Temperature (°C)	Number of cycles
CleanStart decontamination*	15 min	37	1
Initial denaturation	2 min	98	1
PCR	20 s	98	See Table 14
	30 s	60	
	30 s	72	
Final extension	1 min	72	1
Hold	∞	4	Hold

* For the reamplification of libraries, omit the CleanStart decontamination step. Start with incubation at step 2: 98°C for 2 min.

6. After amplification, add 60 µL QIAseq Beads. Vortex for 3 s and briefly centrifuge.
7. Incubate for 5 min at room temperature.
8. Place the tubes/plate onto a magnetic rack. After the solution has cleared (~10 min or longer), carefully remove and discard the supernatant.

Important: Do not discard the beads, because they contain the DNA of interest.

9. With the tubes still on the magnetic stand, add 200 µL of 80% ethanol. Rotate the tubes/plate 3 times to wash the beads. Carefully remove and discard the wash.
10. Repeat the ethanol wash.

Important: Completely remove all traces of the ethanol after this second wash. Briefly centrifuge and return the tubes to the magnetic stand. Remove the ethanol with a 200 µL pipette first, and then use a 10 µL pipette to remove any residual ethanol.
11. With the tubes/plate (caps opened) still on the magnetic stand, air-dry at room temperature for 5–10 min.

Note: Visually inspect that the pellet is completely dry, and that all ethanol is evaporated.

12. Remove the tubes/plate from the magnetic stand and elute the DNA from the beads by adding 22 μL Nuclease-Free Water. Mix well by pipetting.
13. Return the tubes/plate to the magnetic rack until the solution has cleared.
14. Transfer 20 μL to clean tubes/plate. This is the QIAseq Stranded Sequencing Library.
15. Proceed to “Recommendations: Library QC, Quantification, and Sequencing”.
Alternatively, the samples can be stored at -30 to -15°C in a constant-temperature freezer.

Ordering Information

Product	Contents	Cat. no.
QIAseq Stranded RNA Library UDI Kits		
QIAseq Stranded RNA Library UDI-A Kit (96)	For 96 stranded RNAseq sequencing library prep reactions: buffers and reagents for fragmentation, reverse transcription, second-strand synthesis + end-repair + A-addition, adapter ligation, HiFi PCR and CleanStart PCR library amplification, and QIAseq Beads; for library cleanups for use with Illumina instruments; includes a plate containing 96 adapters with different barcodes (pierceable foil seal allowing usage of defined parts of the plate)	180451
QIAseq Stranded RNA Library UDI-B Kit (96)	For 96 stranded RNAseq sequencing library prep reactions: buffers and reagents for fragmentation, reverse transcription, second-strand synthesis + end-repair + A-addition, adapter ligation, HiFi PCR and CleanStart PCR library amplification, and QIAseq Beads; for library cleanups for use with Illumina instruments; includes a plate containing 96 adapters with different barcodes (pierceable foil seal allowing usage of defined parts of the plate)	180452

Product	Contents	Cat. no.
QIAseq Stranded RNA Library UDI-C Kit (96)	For 96 stranded RNAseq sequencing library prep reactions: buffers and reagents for fragmentation, reverse transcription, second-strand synthesis + end-repair + A-addition, adapter ligation, HiFi PCR and CleanStart PCR library amplification, and QIAseq Beads; for library cleanups for use with Illumina instruments; includes a plate containing 96 adapters with different barcodes (pierceable foil seal allowing usage of defined parts of the plate)	180453
QIAseq Stranded RNA Library UDI-D Kit (96)	For 96 stranded RNAseq sequencing library prep reactions: buffers and reagents for fragmentation, reverse transcription, second-strand synthesis + end-repair + A-addition, adapter ligation, HiFi PCR and CleanStart PCR library amplification, and QIAseq Beads; for library cleanups for use with Illumina instruments; includes a plate containing 96 adapters with different barcodes (pierceable foil seal allowing usage of defined parts of the plate)	180454

Product	Contents	Cat. no.
QIAseq Stranded RNA Library UDI Kit (24)	For 24 stranded RNAseq sequencing library prep reactions: buffers and reagents for fragmentation, reverse transcription, second-strand synthesis + end-repair + A-addition, adapter ligation, HiFi PCR and CleanStart PCR library amplification and QIAseq Beads; for library cleanups for use with Illumina instruments; includes a plate containing 96 adapters with different barcodes (pierceable foil seal allowing usage of defined parts of the plate)	180450
QIAseq Stranded Total RNA Lib CDI Kits		
QIAseq Stranded Total RNA Lib CDI Kit (24)	For 24 stranded RNAseq sequencing library prep reactions: fragmentation, reverse transcription, second-strand synthesis + end-repair + A-addition, adapter ligation, CleanStart PCR enrichment and QIAseq Beads for library cleanups	180743
QIAseq Stranded Total RNA Lib CDI Kit (96)	For 96 stranded RNAseq sequencing library prep reactions: fragmentation, reverse transcription, second-strand synthesis + end-repair + A-addition, adapter ligation, CleanStart PCR enrichment and QIAseq Beads for library cleanups	180745

Product	Contents	Cat. no.
QIAseq FastSelect Kits		
QIAseq FastSelect –rRNA HMR Kit	Cytoplasmic and mitochondrial rRNA removal reagent: supports human, mouse, and rat; available in 24, 96, or 384 reactions	334386 334387 334388
QIAseq FastSelect –Globin Kit	Globin mRNA removal reagent: supports human, mouse, and rat; available in 24, 96, or 384 reactions	334376 334377 334378
QIAseq FastSelect –rRNA/Globin Kit	Cytoplasmic and mitochondrial rRNA removal reagent and globin mRNA removal reagent: supports human, mouse, and rat; available in 24, 96, or 384 reactions	335376 335377 335378
QIAseq FastSelect –5S/16S/23S Kit	Bacterial rRNA removal reagent; available in 24, 96, or 384 reactions	335925 335927 335929
QIAseq FastSelect –rRNA Plant Kit	Cytoplasmic, mitochondrial, and chloroplast rRNA removal reagent: for plant samples, available in 24, 96, or 384 reactions	334315 334317 334319
QIAseq FastSelect –rRNA Yeast Kit	Cytoplasmic and mitochondrial rRNA removal reagent for yeast samples; available in 24, 96, or 384 reactions	334215 334217 334219

Related Products

QIAseq Y-Adapter Kits for Illumina

QIAseq UDI Y-Adapter Kit A (96)	Unique Dual-Index Adapters for Illumina (1–96)	180312
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QIAseq UDI Y-Adapter Kit B (96)	Unique Dual-Index Adapters for Illumina (97–192)	180314
QIAseq UDI Y-Adapter Kit C (96)	Unique Dual-Index Adapters for Illumina (193–288)	180316
QIAseq UDI Y-Adapter Kit D (96)	Unique Dual-Index Adapters for Illumina (289–384)	180318
QIAseq UDI Y-Adapter Kit (24)	Unique Dual-Index Adapters for Illumina (1–24)	180310
QIAseq CDI Y-Adapter Kit (96)	Combinatorial Dual-Index Adapters for Illumina	180303
QIAseq CDI Y-Adapter Kit (24)	Combinatorial Dual-Index Adapters for Illumina	180301

QIAseq Library Quantification Kits for use with Illumina instruments

QIAseq Library Quant Array Kit	Plate containing dried assay reagents for quantification of libraries prepared for Illumina; SYBR® Green Master Mix (1.35 mL x 2)	333304
QIAseq Library Quant Assay Kit	Laboratory-verified forward and reverse primers for 500 x 25 µL reactions (500 µL); DNA Standard (100 µL); Dilution Buffer (30 mL); SYBR Green Master Mix (1.35 mL x 5)	333314

For up-to-date licensing information and product-specific disclaimers, see the respective QIAGEN kit handbook or user manual. QIAGEN kit handbooks and user manuals are available at www.qiagen.com or can be requested from QIAGEN Technical Services or your local distributor.

Notes

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Notes

Document Revision History

Date	Changes
06/2019	Revised second header in cover page; added 5x to RT Buffer in Kit Contents; added Ribosomal RNA and/or globin mRNA removal topic; revised Principle and Workflow section; revised Equipments and Reagents Supplied by User; revised RNA integrity item in Important Notes; renamed and revised Protocol: NGS Library Preparation to Protocol: Fragmentation/FastSelect RNA Removal; revised Protocol: First-Strand Synthesis section to update procedure; revised Protocol: Second-Strand Synthesis, End Repair, and A-addition section to update procedure; revised Protocol: Strand-specific Ligation section to update procedure; revised Protocol: CleanStart Library Amplification section to update procedure; replaced high quality Poly(A)+ RNA isolated with libraries prepared in Recommendations; updated Sample dilution, pooling, sequencing, and data analysis topic; updated appendices A and B; deleted Adapter Plate Preparation appendix; updated Ordering Information section.
05/2020	Corrected the volume of QIAseq Beads for step 6 in "Protocol: HiFi PCR Library Amplification".
02/2021	Changed the main title to "QIAseq Stranded RNA Library Kit Handbook". Incorporated the UDIs in this handbook. Added QIAseq Stranded RNA Library Kit in the "Kit Contents" section. Revised the "Shipping and Storage", "Introduction", "Important Notes" sections. Added 100% ethanol (ACS grade) in the "Equipment and Reagents to Be Supplied by User" section. Updated tables and added new tables. Deleted Figure 3 and added new figures. Updated the procedures in all protocols. Revised "Important points before starting" in "Protocol: Strand-specific Ligation" and "Protocol: CleanStart Library Amplification". Updated Appendix A and changed the title to "QIAseq Dual-Index Y-Adapters". Updated the "Ordering Information" section.
05/2023	Updated handbook according to the new brand style guide. Added HiFi PCR Library amplification reagents and protocol to workflow. Updated tables and Kit Content. Moved CleanStart PCR library amplification protocol to appendix D.

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