
March 2021

QIAseq[®] Targeted DNA Panel Handbook

For ultrasensitive targeted next-generation
sequencing (NGS) of DNA for Illumina[®]
NGS systems

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Kit Contents

QIAseq Targeted DNA Panel Catalog no. Number of samples	333502 12	HC 333512 12	333505 96	HC 333515 96	Extended 333545 96	Custom 333525 96
One pool of region-specific primers	75 µl	75 µl	600 µl	600 µl	600 µl	600 µl
Fragmentation Buffer, 10x	40 µl	40 µl	300 µl	300 µl	300 µl	300 µl
Fragmentation Enzyme Mix	75 µl	75 µl	600 µl	600 µl	600 µl	600 µl
FERA Solution	15 µl	15 µl	110 µl	110 µl	110 µl	110 µl
FG Solution	170 µl	170 µl	170 µl	170 µl	170 µl	170 µl
Ligation Buffer, 5x	160 µl	160 µl	1250 µl	1250 µl	1250 µl	1250 µl
DNA Ligase	75 µl	75 µl	600 µl	600 µl	600 µl	600 µl
Ligation Solution	125 µl	125 µl	970 µl	970 µl	970 µl	970 µl
Nuclease-free Water	1.5 ml	1.5 ml	10 ml	10 ml	10 ml	10 ml
TEPCR Buffer, 5x	60 µl	60 µl	500 µl	500 µl	500 µl	500 µl
UPCR Buffer, 5x	60 µl	60 µl	500 µl	500 µl	500 µl	500 µl
HotStarTaq® DNA Polymerase	30 µl	30 µl	240 µl	240 µl	240 µl	240 µl
One bottle containing QIAseq Beads	10 ml	10 ml	55 ml	55 ml	55 ml	55 ml

QIAseq Targeted DNA Booster Panel Catalog no. Number of samples	(96) 333535 96
One pool of region-specific primers	80 µl

Cat. no.	Product name	Total number of primers*	Panel size (kb)
DHS-001Z	Human Breast Cancer Panel	4831	370,942
DHS-002Z	Human Colorectal Cancer Panel	2929	215,328
DHS-003Z	Human Myeloid Neoplasms Panel	5887	436,672
DHS-005Z	Human Lung Cancer Panel	4149	318,059
DHS-101Z	Human Actionable Solid Tumor Panel	651	15,160
DHS-102Z	Human BRCA1 and BRCA2 Panel	223	16,405
DHS-103Z	Human BRCA1 and BRCA2 Plus Panel	348	25,590
DHS-104Z	Human Pharmacogenomics Panel	146	3313
DHS-105Z	Human Mitochondria Panel	222	16,570
DHS-3011Z	Human Inherited Disease Panel	11,579	838,627
DHS-3501Z	Human Comprehensive Cancer Panel	11,311	836,670

* The number of primers in Custom, Extended, and Booster panels is represented by the last digits of the catalog number. For example, a custom panel with catalog number CDHS-00100Z-1256 has 1256 primers.

QIAseq 96-Unique Dual Indices

QIAseq 96-Unique Dual Index Set* Catalog no. Number of samples	QIAseq 96-Unique Dual Index Set A 333725 384	QIAseq 96-Unique Dual Index Set B 333735 884
UDIN-96AA [†]	4 x 10 µl	N/A
UDIN-96BA [†]	N/A	4 x 10 µl
UDIS-96AK [§]	4	N/A
UDIS-96BK [§]	N/A	4
IL-Forward Primer (384)	310 µl	310 µl
QIAseq A Read1 Primer I (100 µM)	4 x 24 µl	4 x 24 µl
8-cap strips (24/bag)	4	4

* 10 bp dual indices.

[†] Adapter Plate (UDIN-96AA or UDIN-96BA); each plate contains 96 molecularly indexed adapters, with each well corresponding to one NQDIB### sample index; each index is single use.

[§] Dried Primer Plate (UDIS-96AK or UDIS-96BK); each array well contains one SQDIB### index primer and IL-universal PCR primer pair for PCR amplification and sample indexing; kit can process up to 384 total samples.

QIAseq Combinatorial Dual Indices

QIAseq 12-Index I* (12 sample index for 48 samples on Illumina® platform)	(48)
Catalog no.	333714
Number of samples	48
IL-N7## Adapter contains 12 tubes of molecularly indexed adapters, with each tube corresponding to one sample index; each index can be used for up to 4 samples	20 µl
IL-S502 Index Primer	40 µl
IL-Forward Primer	40 µl
IL-Universal Primer	40 µl
QIAseq A Read1 Primer I (100 µM)	24 µl

* 8 bp dual indices.

QIAseq 96-Index I Set A, B, C, or D*	QIAseq 96-Index I Set A	QIAseq 96-Index I Set B	QIAseq 96-Index I Set C	QIAseq 96-Index I Set D
Catalog no.	333727	333737	333747	33757
No. of sample	384	384	384	384
IL-701NJ [†]	160 µl	N/A	160 µl	N/A
IL-716NJ [†]	N/A	160 µl	N/A	160 µl
IL-502SK [§]	4	4	N/A	N/A
IL-513SK [§]	N/A	N/A	4	4
IL-Forward Primer (384)	310 µl	310 µl	310 µl	310 µl
QIAseq A Read1 Primer I (100 µM)	4 x 24 µl	4 x 24 µl	4 x 24 µl	4 x 24 µl
12-cap strips	16	16	16	16

* 8 bp dual indices

[†] Adapter Plate (IL-7##NJ); each plate contains 12 molecularly indexed adapters, with each well corresponding to one sample index; each index can be used for up to 4 samples.

[§] Dried Primer Plate with 4 index primer arrays (IL-5##K); each array well contains one IL-5## index primer and IL-universal PCR primer pair for PCR amplification and sample indexing; kit can process up to 384 total samples.

QIAseq 8-Unique Dual Indices

QIAseq 8-Unique Dual Index Set* Catalog. No. Number of samples	QIAseq 8-Unique Dual Index Set A 333715 48	QIAseq 8-Unique Dual Index Set B 333716 48
UDIN-8AA†	40 µl	N/A
UDIN-8BA†	N/A	40 µl
UDIS-8AK§	Dried	N/A
UDIS-8BK§	N/A	Dried
IL-Forward Primer (48)	40 µl	40 µl
QIAseq A Read1 Primer I (100 µM)	24 µl	24 µl
8-cap strips (24/bag)	4	4

* 8 bp dual indices

† Adapter Plate (UDIN-8AA or UDIN-8BA); each plate contains 8 molecularly indexed adapters, with each well corresponding to one IL-N7## sample index; each index can be used for up to 6 samples.

§ Dried Primer Plate with 6 index primer arrays (UDIS-8AK or UDIS-8BK); each array well contains one IL-S5## index primer and IL-universal PCR primer pair for PCR amplification and sample indexing; kit can process up to 48 total samples.

Shipping and Storage

QIAseq Targeted DNA Panels (except Ligation Solution and QIAseq Beads) are shipped on dry ice and should be stored at -30 to -15°C in a constant-temperature freezer upon arrival. QIAseq Beads and Ligation Solution are shipped on cold packs and should be stored at 2 – 8°C except the Ligation Solution that should be removed immediately upon receipt and stored at -30 to -15°C in a constant-temperature freezer.

QIAseq Index kits are shipped on dry ice and should be stored at -30°C to -15°C upon arrival. When stored correctly, the QIAseq Index kits are good until the expiration date printed on the kit label.

Intended Use

The QIAseq Targeted DNA Panels and QIAseq Index Kits are intended for molecular biology applications. These products are 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 the QIAseq Targeted DNA Panel is tested against predetermined specifications, to ensure consistent product quality.

Introduction

The QIAseq Targeted DNA Panels enable Sample to Insight®, targeted next-generation sequencing (NGS) of DNA. This highly optimized solution facilitates ultrasensitive variant detection using integrated unique molecular indices (UMIs) from cells, tissue, and biofluids. The required amount of template for a single QIAseq Targeted sequencing reaction ranges from 10 to 40 ng for fresh DNA or 40 to 250 ng for formalin-fixed paraffin-embedded (FFPE) DNA.

The NGS of DNA is a powerful tool for the detection of genetic variations, including somatic mutations, single nucleotide polymorphisms, copy number variation, and small insertions/deletions. Target enrichment technology enhances DNA NGS by enabling users to sequence specific regions of interest – instead of the entire genome – which effectively increases sequencing depth and sample throughput while minimizing cost. Many commercially available target enrichment, library preparation, and sequencing methods all use DNA polymerase and amplification processes that introduce substantial bias and artifacts. This results in artifactual errors that greatly limit the detection of true low-frequency variants in heterogeneous samples, such as tumors. The QIAseq Targeted DNA Panels overcome these biases/artifacts by utilizing a highly optimized reaction chemistry whereby UMIs are integrated into a single gene-specific, primer-based targeted enrichment process. The QIAseq Targeted DNA Panels have also been optimized in combination with a specially formulated enrichment chemistry to achieve highly efficient enrichment on both regular and GC-rich regions at high multiplex levels. In addition, the panels are compatible with most medium- and high-throughput Illumina sequencers.

Data analysis tools have been developed to perform all steps necessary to generate a DNA sequence variant report from NGS data. Collectively, the QIAseq Targeted DNA Panels are a Sample to Insight solution for precision variant detection of targeted genomic regions using NGS (Figure 1).

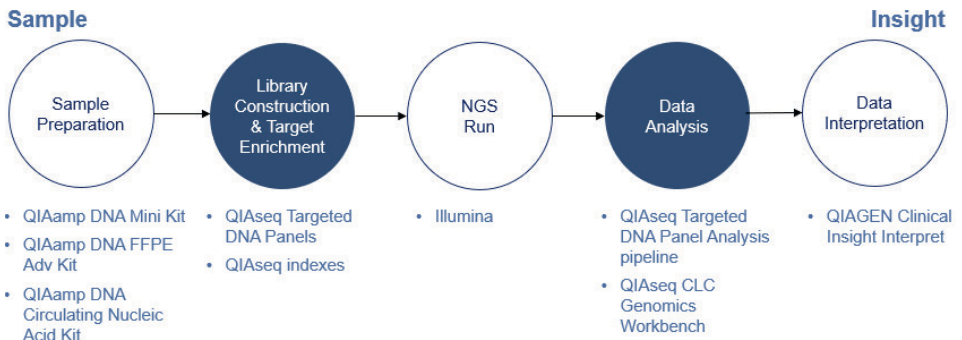


Figure 1. Overview of the Sample to Insight NGS workflow with the QIAseq Targeted DNA Panels. The complete Sample to Insight procedure begins with DNA extraction. Next is library construction and target enrichment with QIAseq Targeted DNA Panels. Following NGS, data analysis is performed using the QIAseq Targeted DNA Panel Analysis Software pipeline or QIAGEN CLC Genomics Workbench. Ultimately, detected variants can be interpreted with the QIAGEN Clinical Insight Interpret for QIAseq.

Principle and procedure

The QIAseq Targeted DNA Panels are provided as single tube primer mixes, with up to 20,000 primers per panel. The QIAseq Targeted DNA Panels are designed to enrich selected genes and regions using 10 to 40 ng fresh DNA or 40 to 250 ng FFPE DNA (Figure 2). Lower input amounts are possible; however, this will lead to fewer sequenced UMI and reduced variant detection sensitivity.

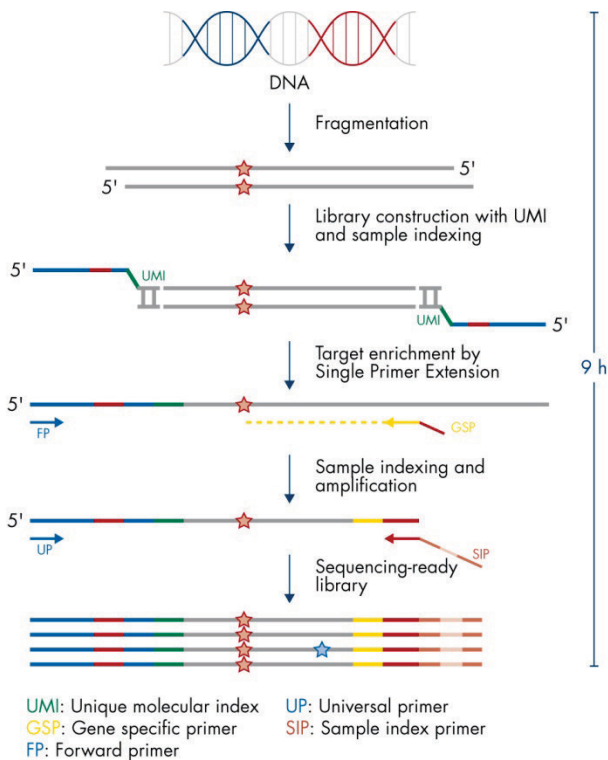


Figure 2. QIAseq Targeted DNA Panels workflow.

Fragmentation

Genomic DNA samples are first fragmented, end repaired, and A tailed within a single, controlled multienzyme reaction. The prepared DNA fragments are then ligated at their 5' ends with a sequencing platform-specific adapter containing UMIs and sample index.

UMI assignment

Prior to target enrichment and library amplification, each original DNA molecule is assigned a unique sequence or index, commonly referred to as a UMI. This assignment is accomplished by ligating fragmented DNA with an adapter containing a 12-base fully random sequence (i.e., the UMI). Statistically, this process provides 4^{12} possible indices per adapter, and each DNA molecule in the sample receives a unique UMI sequence. In addition, this ligated adapter also contains the first sample index.

Target enrichment and final library construction

Target enrichment is performed post-UMI assignment to ensure that DNA molecules containing UMIs are sufficiently enriched in the sequenced library. For enrichment, ligated DNA molecules are subject to several cycles of targeted PCR using one region-specific primer and one universal primer complementary to the adapter. A universal PCR is ultimately carried out to amplify the library and add platform-specific adapter sequences and additional sample indices.

NGS adapter and index technologies

The QIAseq Targeted DNA Panel Library Kits have the option of using either unique dual index (UDI) adapters or combinatorial dual index (CDI) adapters. The UDI adapters significantly reduce the risk of index-bleeding issues associated with different Illumina sequencing instruments, as well as reducing the impact of low-level contamination during oligo synthesis, and kit manufacturing, as well as carry over on the Illumina sequencing instrument itself. Hence, each sample will be assigned two unique indices to overcome the error introduced by image analysis, sequencing error, demultiplexing, and oligo synthesis contamination to reduce the reads mis-assignment to wrong samples.

Next-generation sequencing

The QIAseq Targeted DNA Panels are compatible with most medium- and high-throughput sequencers including Illumina NGS systems (MiniSeq®, MiSeq®, NextSeq® 500/550, HiSeq® 2500, HiSeq 3000/4000, and NovaSeq™ 6000). When using Illumina NGS systems, QIAseq Targeted DNA libraries require a custom sequencing primer for Read 1 (QIAseq A Read 1 Primer I).

Principle of variant detection with UMIs

The principle of variant detection with UMIs is described in Figure 3. Due to intrinsic noise and sequence-dependent bias, indexed molecules may be amplified unevenly across the target regions. Target region coverage can be better achieved, however, by counting the number of UMIs rather than counting the number of total reads for each region. Sequence reads having different UMIs represent different original molecules, while sequence reads having the same UMIs are the result of PCR duplication from one original molecule. Errors from PCR amplification and from the sequencing process may also be present in final reads that lead to false positive variants in sequencing results. These artifactual variants can be greatly reduced by calling variants across all reads within a unique UMI instead of picking up variants at the original read level.

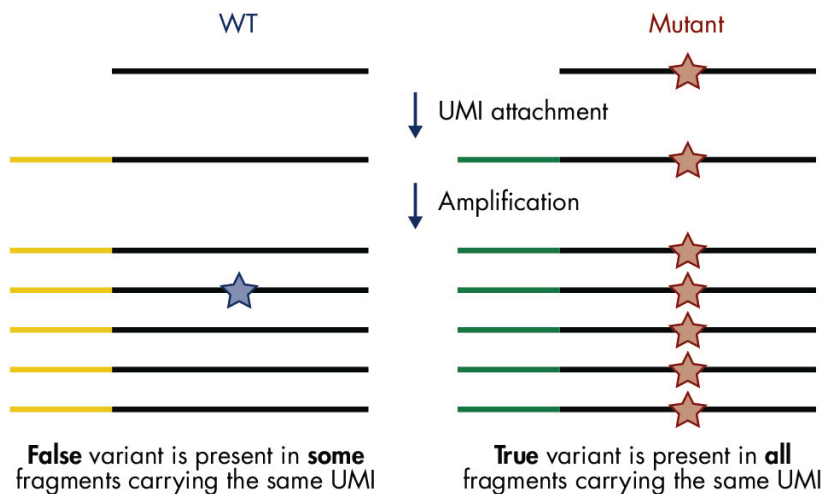


Figure 3. Principle of variant detection with UMIs. Each original molecule is tagged by a UMI. True variants are those mutations present in the majority of reads within a UMI, while false positives are mutations present in only one or a few reads within a UMI.

Data analysis

Data for QIAseq Targeted DNA Panels can be analyzed using the Biomedical Genomics Analysis plugin to the QIAGEN CLC Genomics Workbench. The plugin provides workflows and tools for all steps from the initial data processing and quality assurance through data analyses, annotation, and reporting. A detailed guide to UMI-directed variant detection in CLC Genomics Workbench can be found in Biomedical Genomics Analysis Plugin User Manual. Alternatively, the QIAseq Targeted DNA Panel Analysis pipeline is available at [www.qiagen.com/ shop/genes-and-pathways/data-analysis-center-overview-page/](http://www.qiagen.com/shop/genes-and-pathways/data-analysis-center-overview-page/). The pipeline automatically performs all steps necessary to generate a DNA sequence variant report from your raw NGS data. An explanation of the principles of UMI-directed variant detection and the features of the primary sequence analysis output can be found at Xu et al (1).

All detected variants can be further interpreted using and QCI Interpret.

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.

In addition to the QIAseq Targeted DNA Panels and the QIAseq Index Kit, the following are required:

- Ethanol, 80% (made fresh daily)*
- Nuclease-free pipette tips and tubes
- 1.5 ml LoBind® tubes (Eppendorf®, cat. no. 022431021)
- PCR tubes (0.2 ml individual PCR tubes [VWR, cat. no. 20170-012], or tube strips [VWR, cat. no. 93001 118]) or 96-well PCR plates and caps
- Ice
- Microcentrifuge
- Thermal cycler
- Multichannel pipettes
- Single-channel pipettes
- QIAxcel® or Agilent® 2100 Bioanalyzer® (Agilent, cat. no. G2939BA) or Agilent TapeStation® (Agilent, cat. no. G2991AA)
- Agilent High Sensitivity DNA Kit (Agilent cat. no. 5067-4626)
- DynaMag™-96 Side Magnet (Thermo Fisher Scientific Inc., cat. no. 12331D)
- QIAseq DNA QuantiMIZE Kits, if using FFPE samples (cat. no. 333404 or 333414)
- QIAxpert® or Thermo-Fisher Scientific Qubit Fluorometer
- Quanti-iT™ dsDNA Assay Kit (Thermo Fisher Scientific, cat. no. Q33120)

* Do not use denatured alcohol, which contains other substances, such as methanol or methylethylketone.

Important Notes

For optimal results, all DNA samples should demonstrate consistent quality according to the following criteria.

DNA isolation and quality check

The most important prerequisite for DNA sequence analysis is consistent, high-quality DNA from every experimental sample. Therefore, sample handling and DNA isolation procedures are critical to the success of the experiment. Residual traces of proteins, salts, or other contaminants may either degrade the DNA or decrease the efficiency of, if not block completely, the enzymatic activity necessary for optimal targeted enrichment. Sample purity can be checked with the QIAxpert®.

The QIAGEN kits listed in Table 1 are recommended for the preparation of genomic DNA samples from cells, tissues, FFPE tissues, and serum/plasma samples. For best results, all DNA samples should be resuspended in DNase-free water, or alternatively in DNase-free 10 mM Tris buffer pH 8.0.

Important: Do not use DEPC-treated water.

Important: Ensure that samples have been treated to remove RNA. RNA contamination will cause inaccuracies in DNA concentration measurements. Do not omit the recommended RNase treatment step to remove RNA.

Note: If genomic DNA samples must be harvested from biological samples for which kits are not available, please contact Technical Support representatives for suggestions.

Table 1. Recommended kits for purification of genomic DNA

Kit	Starting material	Cat. no.
QIAamp® DNA Mini Kit	Small amounts of cells and tissue	51304
QIAamp DNA FFPE Adv Kit	Animal/human tissues and cells	56604
QIAamp Circulating Nucleic Acid Kit	Animal and human plasma and serum	55114

For best results, all DNA samples should also demonstrate consistent quality according to the following criteria:

DNA quantification

The concentration and purity can be determined by measuring the absorbance in a spectrophotometer such as a QIAxpert. As the spectral properties of nucleic acids are highly dependent on pH, we recommend preparing dilutions and measure absorbance in 10 mM Tris-Cl, pH 8.0. The A_{260}/A_{280} ratio should be >1.8 .

DNA integrity

DNA integrity can be checked using the QIAxcel or Agilent Bioanalyzer or Agilent TapeStation. Although DNA is enzymatically fragmented before target enrichment PCR, intact DNA generally yields better results than fragmented DNA due to tiling space between primers. Intact DNA usually has better coverage uniformity, more UMIs captured, and more sensitive variant detection.

DNA quantification can also be performed using the high-sensitivity Quant-iT™ dsDNA Assay Kit (Thermo Fisher Scientific, cat. no. Q33120).

Specific recommendations for FFPE DNA

If FFPE DNA is used for QIAseq Targeted DNA Panels, the QIAseq DNA QuantiMIZE Array or Assay Kit is strongly recommended for determining the optimal DNA amount for each FFPE DNA sample. Quantification based on mass calculations (OD, NanoDrop™) can be very inaccurate. Appendix B (page 65) provides detailed information for FFPE DNA quality assessment and input amount.

DNA input amount and sequencing depth

The number of UMIs captured from the original DNA sample correlates with the DNA input amount and sequencing depth. Adequate sequencing of captured UMIs requires relatively deep sequencing coverage. Table 2~~Error! Reference source not found.~~ provides guidance on variant detection with fresh DNA amounts at different depths of coverage.

Table 2. Suggested fresh DNA input amount and sequencing depth for variant detection*

Variant frequency	Input (ng)	Read pairs/UMI	Mean read
5%	10	4	7200
1%	40	4	25,600

* Variant detection is based on 90% sensitivity on the entire region of the QIAseq Targeted DNA Panel.

Variant detection

The number of UMIs sequenced directly impacts the variant detection sensitivity. Therefore, low-frequency mutation detection usually requires more DNA input and sequencing at deeper coverage (i.e., more/reads/UMI) to generate a sufficient amount of UMIs.

Sequencing capacity and sample multiplex level

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; as a consequence, 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.

The QIAseq Targeted DNA Panel Library Kits include either a fully compatible UDI or CDI indexing solution. We recommend using the QIAseq 96-Unique Dual Index sets. Each QIAseq Targeted DNA Panel Library index kit includes one of the following:

- QIAseq 96-Unique Dual Index Set A (384): UDIN-96AA paired with UDIS-96AK
- QIAseq 96-Unique Dual Index Set B (384): UDIN-96BA paired with UDIS-96BK
- QIAseq 12-Index I (48): IL-N701 – IL-N707, IL-N710 – IL-N712, IL-N714 – IL-N715 all paired with IL-S502
- QIAseq 96-Index I Set A (384): IL-701NJ paired with IL-502SK
- QIAseq 96-Index I Set B (384): IL-716NJ paired with IL-502SK
- QIAseq 96-Index I Set C (384): IL-701NJ paired with IL-513SK
- QIAseq 96-Index I Set D (384): IL-716NJ paired with IL-513SK
- QIAseq 8-Unique Index Set A (48): UDIN-8AA paired with UDIS-8AK
- QIAseq 8-Unique Index Set B (48): UDIN-8BA paired with UDIS-8BK

QIAseq UDI kits use a fixed combination of 2 unique barcode motives per adapter molecule. Therefore, each single-index motive is only used once on any UDI adapter plate. In contrast, CDI adapters use twelve i7 and eight i5 barcode motives that can be combined to form up to 96 CDIs.

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.

To multiplex more than 96 libraries in a single sequencing run, combine kits with different either QIAseq 96-Unique Dual Index or QIAseq 96-Index I (CDIs) sets. For example, combining the

unique dual QIAseq 96-Unique Dual Index Set A (or B) (96) kits will allow the generation of 192 libraries with different unique dual sample indexes for 192-plex sequencing. For example, combining the combinatorial QIAseq 96-Index I Set A (or B, or C, or D) (96) kits will allow the generation of 384 libraries with different combinatorial sample indexes for 384-plex sequencing. For more information on the unique dual QIAseq 8-Unique Dual Index Set A (or B) (48) kits, please refer to Appendix C, page 67.

Sample multiplexing level is determined by the size of the panel, required depth of coverage, and sequencing platform read capacity. General guidelines are provided for the number of samples that can be multiplexed in different sequencing platforms, based on panel size and read depth (Table 3, Table 4, and Table 5). Fine-tuning the read depth is possible after the first run.

Table 3. Number of multiplexed samples based on panel size with 500x mean coverage*

Instrument	Version	Capacity (paired-end reads)	1000 primers	2500 primers	5000 primers	12,000 primers
MiniSeq	Mid output	16 M	32	12	6	2
MiniSeq	High output	50 M	100	40	20	8
MiSeq	v2 Reagents	30 M	60	24	12	5
MiSeq	v3 Reagents	50 M	100	40	20	8
NextSeq 500	Mid output	260 M	520	208	104	43
NextSeq 500	High output	800 M	1600	640	320	133
HiSeq 2500 rapid run	Dual flow cell v2	1200 M	2400	960	480	200
HiSeq 3000	8 lanes per flow cell	5 B	10000	4000	2000	833
HiSeq 4000	8 lanes per flow cell	10 B	20000	8000	4000	1666
NovaSeq 6000	SP (2 lanes per flow cell)	1.6 B	3200	1280	640	266
NovaSeq 6000	S1 (2 lanes per flow cell)	3.2 B	6400	2560	1280	532
NovaSeq 6000	S2 (2 lanes per flow cell)	8.2 B	16400	6560	3280	1366
NovaSeq 6000	S4 (4 lanes per flow cell)	20 B	40000	16000	8000	3332

* Based on 2 x 149 bp paired-end reads for 96-UDIs and 2 x 151 bp reads for CDIs and 8-UDIs.

Table 4. Number of multiplexed samples based on panel size with 2500x mean coverage*

Instrument	Version	Capacity (paired-ends reads)	1000 primers	2500 primers	5000 primers	12,000 primers
MiniSeq	Mid output	16 M	6	2	1	N/A
MiniSeq	High output	50 M	20	8	4	1
MiSeq	v2 Reagents	30 M	12	4	2	1
MiSeq	v3 Reagents	50 M	20	8	4	1
NextSeq 500	Mid output	260 M	104	41	20	8
NextSeq 500	High output	800 M	320	128	64	26
HiSeq 2500 rapid run	Dual flow cell v2	1200 M	480	192	96	40
HiSeq 3000	8 lanes per flow cell	5 B	2000	800	400	166
HiSeq 4000	8 lanes per flow cell	10 B	4000	1600	800	333
NovaSeq 6000	SP (2 lanes per flow cell)	1.6 B	640	256	128	53
NovaSeq 6000	S1 (2 lanes per flow cell)	3.2 B	1280	512	256	106
NovaSeq 6000	S2 (2 lanes per flow cell)	8.2 B	3280	1312	656	273
NovaSeq 6000	S4 (4 lanes per flow cell)	20 B	8000	3200	1600	666

* Based on 2 x 149 bp paired-end reads for 96-UDIs and 2 x 151 bp paired-end reads for CDIs and 8-UDIs.
N/A: Not applicable, no samples can be run.

Table 5. Number of multiplexed samples based on panel size with 20,000x mean coverage*

Instrument	Version	Capacity (paired-ends reads)	1000 primers	2500 primers	5000 primers	12,000 primers
MiniSeq	Mid output	16 M	N/A	N/A	N/A	N/A
MiniSeq	High output	50 M	2	1	N/A	N/A
MiSeq	v2 Reagents	30 M	1	N/A	N/A	N/A
MiSeq	v3 Reagents	50 M	2	1	N/A	N/A
NextSeq 500	Mid output	260 M	13	5	2	1
NextSeq 500	High output	800 M	40	16	8	3
HiSeq 2500 rapid run	Dual flow cell v2	1200 M	60	24	12	5
HiSeq 3000	8 lanes per flow cell	5 B	250	100	50	20
HiSeq 4000	8 lanes per flow cell	10 B	500	200	100	40
NovaSeq 6000	SP (2 lanes per flow cell)	1.6 B	80	32	16	6
NovaSeq 6000	S1 (2 lanes per flow cell)	3.2 B	160	64	32	12
NovaSeq 6000	S2 (2 lanes per flow cell)	8.2 B	410	164	82	34
NovaSeq 6000	S4 (4 lanes per flow cell)	20 B	1000	400	200	80

* Based on 2 x 149 bp paired-end reads for 96-UDIs and 2 x 151 bp reads for CDIs and 8-UDIs.

N/A: Not applicable, no samples can be run.

Next-generation sequencing read-length recommendations

When using Illumina NGS systems, QIAseq Targeted DNA libraries require a custom sequencing primer for Read 1 (QIAseq A Read1 Primer I). QIAseq Targeted DNA Panel UDI libraries require 149 bp paired end reads and dual 10-bp indices, while QIAseq Targeted DNA Panel CDI libraries require 151-bp paired-end reads and dual 8-bp indices. However, QIAseq Targeted DNA Panel 8-UDI libraries require 151 bp paired end reads and dual 8-bp indices (see Appendix C, page 67, for more details).

Protocol: Fragmentation, End-Repair, and A-addition

Important points before starting

- This protocol covers all procedures required for the preparation of libraries for Illumina sequencers from “standard DNA” (i.e., cells or tissues), FFPE DNA, and cfDNA.
- Before setting up the reaction, it is critical to accurately determine the amount of the input DNA (10–40 ng for standard DNA or cfDNA; up to 250 ng of FFPE DNA can be used, if QIAseq QuantiMIZE kits have been used. If an alternative method was used to determine the concentration of FFPE DNA, then up to 100 ng DNA can be used). Lower input amounts are possible; however, this will lead to fewer sequenced UMIs and reduced variant detection sensitivity.
- Set up reactions on ice.
- Do not vortex any reagents or reactions.

Procedure: Fragmentation, end-repair, and A-addition

1. Thaw nucleic acid samples on ice. Gently mix, briefly centrifuge to collect residual liquid from the sides of the tubes, and then return to ice.
2. Prepare the reagents required for fragmentation, end-repair, and A-addition.
 - 2a. Thaw Fragmentation Buffer, 10x; FERA Solution and FG Solution if required at room temperature.
 - 2b. Mix by flicking the tube, and centrifuge briefly.

Note: The Fragmentation Enzyme Mix should be removed from the freezer just before use and placed on ice. After use, immediately return the enzymes to the freezer.

- On ice, prepare the fragmentation, end-repair, and A-addition mix according to Table 6. Briefly centrifuge, mix by pipetting up and down 7–8 times and briefly centrifuge again.

Note: In general, increasing the amount of DNA input will improve variant detection sensitivity – particularly for FFPE DNA. See Appendix B, page 65, for more details.

Table 6. Reaction mix for fragmentation, end-repair, and A-addition

Component	Volume/reaction (standard, FFPE or pure cfDNA)	Volume/reaction (cfDNA contaminated with cellular DNA)
DNA*	Variable	Variable
Fragmentation Buffer, 10x	2.5 µl	2.5 µl
FERA Solution	0.75 µl	0.75 µl
FG Solution	–	1.25 µl
Nuclease-free Water	Variable	Variable
Total	20 µl	20 µl

* 10–40 ng for standard DNA or cfDNA. Use up to 250 ng of FFPE DNA if QIAseq QuantiMIZE kits were used, or up to 100 ng of FFPE DNA if an alternative method was used.

- Add 5 µl Fragmentation Enzyme Mix to each reaction. Briefly centrifuge, mix by pipetting up and down 7–8 times (do not vortex), and briefly centrifuge again.

Important: Keep the reaction tubes/plate on ice during the entire reaction setup.

- Program the thermal cycler according to Table 7. Use the instrument’s heated lid.

Table 7. Cycling conditions for fragmentation, end-repair, and A-addition*

Step	Incubation temperature	Incubation time (standard DNA)	Incubation time (FFPE DNA)	Incubation time (cfDNA)
1	4°C	1 min	1 min	1 min
2	32°C*	24 min	14 min	14 min
3	72°C	30 min	30 min	30 min
4	4°C	Hold	Hold	Hold

* For Human Mitochondria Panel, use 8 min for both standard and FFPE DNA at 32°C incubation.

6. Before adding the tubes/plate to a thermal cycler, start the program. When the thermal cycler reaches 4°C, pause the program.

Important: The thermal cycler must be pre-chilled and paused at 4°C.

7. Transfer the tubes/plate prepared in step 2 to the pre-chilled thermal cycler and resume the cycling program.

8. Upon completion, allow the thermal cycler to return to 4°C.

9. Place the samples on ice and immediately proceed to “Protocol: Adapter Ligation”, page 28.

Protocol: Adapter Ligation

Important points before starting

- The 25 μ l product from “Protocol: Fragmentation, End-Repair, and A-addition”, page 25, is the starting material for this protocol.
- Set up reactions on ice.
- Do not vortex any reagents or reactions.
- **Important:** The QIAseq 96-Unique Dual Index Set Adapter Plate (UDIN-96#A): A or B used in the adapter ligation reaction must be paired with the matching QIAseq 96-Unique Dual Index Set (UDIS-96#K) Primer Plate: A or B used in the universal PCR amplification reaction.
 - The QIAseq 96-Unique Dual Index (UDIN-96#A) adapters are sealed in a 96-well plate with pierceable aluminum heat sealing film.
 - It does not need to be removed, instead puncture the film using standard 200 μ l pipet tips to withdraw the appropriate adapter and adapter volume.
 - **Important:** Thaw the adapter plate on ice or store at 4°C before usage. After it is fully thawed, centrifuge the plate at 1000 g for 1 min.
- **Important:** The QIAseq 12-Index I Adapters (IL-N7##) are in individual tubes.
 - **Important:** Thaw the tubes on ice or store at 4°C before usage. After the tubes are fully thawed, centrifuge the tubes.
- **Important:** The QIAseq 96-Index I Set Adapter Plate (IL-7##NJ): A, B, C, or D used in the adapter ligation reaction must be paired with the matching QIAseq 96-Index I (IL-5##SK) Primer Plate: A, B, C, or D used in the universal PCR amplification reaction.
 - The QIAseq 96-Index I Set (IL-7##NJ) adapters are sealed in a 96-well plate that needs to have the seal removed.
 - **Important:** Thaw the adapter plate on ice or store at 4°C before usage. After it is fully thawed, centrifuge the plate at 1000 x *g* for 1 min. Carefully withdraw the appropriate adapter and adapter volume.

- **Important:** The QIAseq 8-Unique Dual Index Set Adapter Plate (UDIN-8#A): A or B used in the adapter ligation reaction must be paired with the matching QIAseq 8-Unique Dual Index Set (UDIS-8#K) Primer Plate: A or B used in the universal PCR amplification reaction.
 - The QIAseq 8-Unique Dual Index (UDIN-8#A) adapters are sealed in a 96-well plate with pierceable aluminum heat sealing film.
 - It does not need to be removed, instead puncture the film using standard 200 µl pipet tips to withdraw the appropriate adapter and adapter volume.
 - **Important:** Thaw the adapter plate on ice or store at 4°C before usage. After it is fully thawed centrifuge the plate at 1000 x *g* for 1 min.
- QIAseq Beads are used for all reaction cleanups.
- **Important:** Prepare fresh 80% ethanol daily.
- Ensure that 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: Adapter ligation

1. Prepare the reagents required for the DNA ligation.
 - 1a. Thaw DNA Ligation Adapter; Ligation Buffer, 5x; and Ligation Solution at room temperature.
 - 1b. Mix by flicking the tube, and then centrifuge briefly.

Note: DNA 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 ligation mix according to Table 8. Briefly centrifuge, mix by pipetting up and down 10–12 times and briefly centrifuge again.

Important: Only one single-indexed adapter should be used per ligation reaction. The QIAseq 96-Unique Dual Index set adapter layout is described in Figure 4; use a multichannel pipette to pierce the foil prior to using a multichannel pipette to pipet the

appropriate amount of adapters. Open one adapter tube at a time if using QIAseq 12-Index I adapters and avoid cross-contamination. For QIAseq 96-Index I adapters supplied in a plate (layout described in Figure 7), use a multichannel pipette to pipet the appropriate amount of adapters. Refer to Appendix C, page 67, for the QIAseq 8-Unique Dual Index set adapter layout.

Important: Pipet slowly to mix. The reaction mix is very viscous. Do not vortex.

Note: If setting up more than one reaction, prepare a volume of master mix 20% greater than what is required for the total number of reactions.

Table 8. Reaction mix for adapter ligation

Component	Volume/reaction		
	Standard DNA	FFPE DNA	cfDNA
Fragmentation, end-repair, and A-addition reaction (already in tube)	25 μ l	25 μ l	25 μ l
Ligation Buffer, 5x	10 μ l	10 μ l	10 μ l
UDIN-96#A or IL-N7## or IL-7##NJ or UDIN-8#A adapter*	2.8 μ l	2.8 μ l	0.5 μ l
DNA Ligase	5 μ l	5 μ l	5 μ l
Ligation Solution†	7.2 μ l	7.2 μ l	7.2 μ l
Nuclease-free Water	–	–	2.3 μ l
Total	50 μl	50 μl	50 μl

* This UDIN-96#A for QIAseq 96-Unique Dual Index Set A or B; or IL-N7## component applies to the adapters with up to a 12 sample index for QIAseq 12-Index I; or IL-7##NJ adapters with QIAseq 96-Index I A, B, C, or D set (CDIs); or UDIN-8#A for QIAseq 8-Unique Dual Index Set A or B.

† Ligation Solution is very viscous. It should be added into each reaction individually and not premixed with other components for a master mix. Do not coat the outside of the pipette tip with Ligation Solution or excess volume may be added.

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

Figure 4. Layout of the pierceable QIAseq 96-Unique Dual Index Set Adapter Plates. QIAseq 96-Unique Dual Index Set A (96) layout (NQDIB001-NQDIB096) and QIAseq 96-Unique Dual Index Set B (96) layout (NQDIB097-NQDIB192).

IL-701NJ Adapter Plate in QIAseq 96-Index I Set A or C set

	1	2	3	4	5	6	7	8	9	10	11	12
A	N701	N702	N703	N704	N705	N706	N707	N710	N711	N712	N714	N715
B	N701	N702	N703	N704	N705	N706	N707	N710	N711	N712	N714	N715
C	N701	N702	N703	N704	N705	N706	N707	N710	N711	N712	N714	N715
D	N701	N702	N703	N704	N705	N706	N707	N710	N711	N712	N714	N715
E												
F												
G												
H												

IL-716NJ Adapter Plate in QIAseq 96-Index I Set B or D set

	1	2	3	4	5	6	7	8	9	10	11	12
A	N716	N718	N719	N720	N721	N722	N723	N724	N726	N727	N728	N729
B	N716	N718	N719	N720	N721	N722	N723	N724	N726	N727	N728	N729
C	N716	N718	N719	N720	N721	N722	N723	N724	N726	N727	N728	N729
D	N716	N718	N719	N720	N721	N722	N723	N724	N726	N727	N728	N729
E												
F												
G												
H												

Figure 5. Layout of sample adapters in QIAseq 96-Index I Set A, B, C, or D. Rows A through D of each plate have adapters. Rows E through H are empty. Each well in each row contains one sample adapter, and the amount of adapter in each well is enough for 8 samples.

3. Incubate the reactions in thermal cycler according to Table 9.

Important: Do not use heated lid.

Table 9. Incubation conditions for DNA ligation

Step	Incubation temperature	Incubation time
1	4°C	1 min
2	20°C	15 min
3	4°C	Hold

4. Once the run has finished, for standard/FFPE samples, add 50 µl nuclease-free water to bring each sample to 100 µl. For cfDNA samples, add 30 µl nuclease-free water to bring each sample to 80 µl.

5. For standard/FFPE samples, add 100 µl QIAseq Beads. For cfDNA samples, add 112 µl QIAseq Beads. Mix well by pipetting up and down several times.

6. Incubate for 5 min at room temperature.

7. Place the tubes/plate on a magnetic rack for 2 min (for tubes) or 10 min (for plates). Once the solution has cleared, with the beads still on the magnetic stand, carefully remove and discard the supernatant.

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

8. With the beads still on the magnetic stand, add 200 µl 80% ethanol. Carefully remove and discard the wash.

9. Repeat the ethanol wash.

Important: Completely remove all traces of the ethanol after this second wash. Remove the ethanol with a 200 µl pipette first, and then use a 10 µl pipet to remove any residual ethanol.

10. With the beads still on the magnetic stand, air dry at room temperature for 10 min.

Note: Visually inspect that the pellet is completely dry.

11. Remove the beads from the magnetic stand, and elute the DNA from the beads by adding 52 μ l nuclease-free water. Mix well by pipetting.
12. Return the tubes/plate to the magnetic rack until the solution has cleared.
13. Transfer 50 μ l of the supernatant to clean tubes/plate.
14. For standard/FFPE samples, add 50 μ l QIAseq Beads (for Human Mitochondria Panel use 35 μ l). For cfDNA samples, add 70 μ l QIAseq Beads. Mix well by pipetting up and down several times.
15. Incubate for 5 min at room temperature.
16. Place the tubes/plate on a magnetic rack for 5 min (for tubes) or 10 min (for plates). Once the solution has cleared, with the beads still on the magnetic stand, carefully remove and discard the supernatant.

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

17. With the beads still on the magnetic stand, add 200 μ l 80% ethanol. Carefully remove and discard the wash.
18. Repeat the ethanol wash.

Important: Completely remove all traces of the ethanol after this second wash. Remove the ethanol with a 200 μ l pipette first, and then use a 10 μ l pipette to remove any residual ethanol.

19. With the beads still on the magnetic stand, air dry at room temperature for 15 min.

Note: Visually inspect that the pellet is completely dry. Ethanol carryover to the target enrichment PCR step will affect enrichment PCR efficiency.

Remove the beads from the magnetic stand, and elute the DNA from the beads by adding 12 μ l nuclease-free water. Mix well by pipetting.

20. Return the tube/plate to the magnetic rack until the solution has cleared.
21. Transfer 9.4 μ l of the supernatant to clean tubes or plate.
22. Proceed with "Protocol: Target Enrichment". Alternatively, the samples can be stored at -30 to -15°C in a constant-temperature freezer for up to 3 days.

Protocol: Target Enrichment

Important points before starting

- The 9.4 µl product from “Protocol: Adapter Ligation”, page 28, is the starting material for this protocol.
- Set up reactions on ice.
- Do not vortex any reagents or reactions.
- QIAseq Beads are used for all reaction cleanups.
- **Important:** Prepare fresh 80% ethanol daily.
- Ensure that 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: Target enrichment

1. Prepare the reagents required for the target enrichment.

1a. Thaw TEPCR Buffer, 5x; QIAseq Targeted DNA Panel; and IL-Forward Primer at room temperature.

1b. Mix by flicking the tube, and then centrifuge briefly.

Note: HotStarTaq DNA Polymerase should be removed from the freezer just before use and placed on ice. After use, immediately return the enzyme to the freezer.

Prepare the target enrichment mix according to Table 10. Briefly centrifuge, mix by pipetting up and down 7–8 times, and briefly centrifuge again.

Table 10. Reaction mix for target enrichment

Component	Volume/reaction
Sample (from "Protocol: Adapter Ligation")	9.4 μ l
TEPCR buffer, 5x	4 μ l
QIAseq Targeted DNA Panel	5 μ l
IL-Forward primer	0.8 μ l
HotStarTaq DNA Polymerase	0.8 μ l
Total	20 μl

2. Program a thermal cycler using the cycling conditions in Table 11 (panel with <1500 primers/tube) or Table 12 (panel with \geq 1500 primers/tube).

Table 11. Cycling conditions for target enrichment if number of primers <1500/tube

Step	Time	Temperature
Initial denaturation	13 min	95°C
	2 min	98°C
8 cycles	15 s	98°C
	10 min	68°C
1 cycle	5 min	72°C
Hold	5 min	4°C
Hold	∞	4°C

Table 12. Cycling conditions for target enrichment if number of primers \geq 1500/tube

Step	Time (1500–12,000 primers/tube)	Time (>12,000 primers/tube)	Temperature
Initial denaturation	13 min	13 min	95°C
	2 min	2 min	98°C
6 cycles	15 s	15 s	98°C
	15 min	30 min	65°C
1 cycle	5 min	5 min	72°C
Hold	5 min	5 min	4°C
Hold	∞	∞	4°C

3. Place the target enrichment reaction in the thermal cycler and start the run.
4. Once the run has finished, for standard/FFPE samples, add 80 μ l nuclease-free water to bring each sample to 100 μ l. For cfDNA samples, add 70 μ l nuclease-free water to bring each sample to 90 μ l.
5. For standard/FFPE samples, add 100 μ l QIAseq Beads (for Human Mitochondria Panel use 70 μ l). For cfDNA samples, add 108 μ l QIAseq Beads. Mix well by pipetting up and down several times.
6. Incubate for 5 min at room temperature.
7. Place the tubes/plate on a magnetic rack for 5 min (for tubes) or 10 min (for plates). After the solution has cleared, with the beads still on the magnetic stand, carefully remove and discard the supernatant.
Important: Do not discard the beads as they contain the DNA of interest.
8. With the beads still on the magnetic stand, add 200 μ l 80% ethanol. Carefully remove and discard the wash.
9. Repeat the ethanol wash.
Important: Completely remove all traces of the ethanol after this second wash. Remove the ethanol with a 200 μ l pipette first, and then use a 10 μ l pipette to remove any residual ethanol.
10. With the beads still on the magnetic stand, air dry at room temperature for 10 min.
Note: Visually inspect that the pellet is completely dry. Ethanol carryover to the next universal PCR step will affect PCR efficiency.
11. Remove the beads from the magnetic stand, and elute the DNA from the beads by adding 16 μ l nuclease-free water. Mix well by pipetting.

-
12. Return the tube/plate to the magnetic rack until the solution has cleared.
 13. Transfer 13.4 μ l of the supernatant to clean tubes/plate.
 14. Proceed with "Protocol: Universal PCR", page 40. Alternatively, the samples can be stored at -30 to -15°C in a constant-temperature freezer for up to 3 days.

Protocol: Universal PCR

Important points before starting

- The 13.4 µl product from “Protocol: Target Enrichment”, page 36, is the starting material for this protocol.
- Set up reactions on ice.
- Do not vortex any reagents or reactions.
- **Important:** The QIAseq 96-Unique Dual Index Set (UDIS-96#K) Index Primer Plate must be paired with the matching QIAseq 96-Unique Dual Index Set (UDIN-96#A) Adapter Plate: A or B used in the Adapter Ligation reaction.
 - The UDIS-96#K Index Primer Plate A or B contain pre-dispensed, dried index primers and the universal PCR primer and are sealed in a 96-well plate with pierceable aluminum heat sealing film.
 - Puncture the film using standard 200 µl pipet tips to add components directly in the UDIS-96#K Index Primer plates for the universal PCR reaction. See Figure 6 for the layout of the index primers in the plate.
- **Important:** The QIAseq 12-Index I Adapter (IL-S502) is in an individual tube and must be paired with the IL-N7## tubes.
 - **Important:** Thaw the tubes on ice or store at 4°C before usage. After the tubes are fully thawed centrifuge the tubes.
- **Important:** The QIAseq 96-Index I Set A, B, C or D (IL-5##SK) Plate must be paired with the matching QIAseq 96-Index I Set (IL-7##NJ) Adapter Plate: A, B, C or D used in the Adapter Ligation reaction.
- The QIAseq 96-Index I Set (IL-5##SK) Plates contain pre-dispensed, dried index primers and the universal PCR primer and are sealed in a 96-well plate that needs to have the seal removed.

- Add the universal PCR reaction components directly in the appropriate IL-5##SK Index Primer plates. See Figure 7 for the layout of the index primers in the plate.
- **Important:** The QIAseq 8-Unique Dual Index Set (UDIS-8#K) Index Primer Plate must be paired with the matching QIAseq 8-Unique Dual Index Set (UDIN-8#A) Adapter Plate: A or B used in the Adapter Ligation reaction.
 - The UDIS-8#K Index Primer Plate A or B contain pre-dispensed, dried index primers and the universal PCR primer and are sealed in a 96-well plate with pierceable aluminum heat sealing film.
 - Puncture the film using standard 200 µl pipet tips to add components directly in the UDIS-8#K Index Primer plates for the universal PCR reaction. See Appendix C, page 67 for more details.
- QIAseq Beads are used for all reaction cleanups.
- **Important:** Prepare fresh 80% ethanol daily.
- Ensure that 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: Universal PCR

1. Prepare the reagents required for the universal PCR.
 - 1a. Thaw UPCR Buffer, 5x, at room temperature and bring the appropriate IL-S502 tube, IL-5##SK plate, UDIS-96#K plate, or UDIS-8#K plate to room temperature.
 - 1b. Mix by flicking the tube, and then centrifuge briefly.

Note: HotStarTaq DNA Polymerase 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 universal PCR according to **Error! Reference source not found.** Table 13 or Table 14, depending in which index set is being used. Briefly centrifuge, mix by pipetting up and down 7–8 times and briefly centrifuge again.

Table 13. Reaction components for universal PCR if using QIAseq 96-Unique Dual Index Set A or B*[†]; or QIAseq 96-Index I Set A, B, C or D[†]; or QIAseq 8-Unique Dual Index Set A or B[§]

Component	Volume/reaction
Sample (from "Protocol: Target enrichment")	13.4 μ l
UPCR Buffer, 5x	4 μ l
HotStarTaq DNA Polymerase	1 μ l
Nuclease-free Water	1.6 μ l
Total	20 μl

* Applies to QIAseq UDIS-96#K Index Primer Plate in A, or B set. The final library dual sample index is determined by the unique UDIN-96#A Adapter Plate and the QIAseq UDIS-96#K Index Primer Plate. Total sample index level can be up to 192-plex if using QIAseq 96-Unique Dual Index Set A, and B together.

[†] Applies to QIAseq IL-5##SK Index Primer Plate in A, B, C, or D set. The final library dual sample index is determined by the combination of the IL-7##NJ Adapter Plate and the QIAseq IL-5##SK Index Primer Plate. Total sample index level can be up to 384-plex if using QIAseq 96-Index I Set A, B, C, and D together.

[§] Applies to QIAseq UDIS-8#K Index Primer Plate in A, or B set. The final library dual sample index is determined by the unique UDIN-8#A Adapter Plate and the QIAseq UDIS-8#K Index Primer Plate. Total sample index level can be up to 16-plex if using QIAseq 8-Unique Dual Index Set A, and B together.

Table 14. Reaction mix for universal PCR if using QIAseq 12-Index I (48)

Component	Volume/reaction (μ l)
Sample (from "Protocol: Target enrichment")	13.4
UPCR Buffer, 5x	4
IL-Universal Primer	0.8
IL-S502 Index Primer	0.8
HotStarTaq DNA Polymerase	1
Total	20

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

Figure 6. Layout of the pierceable QIAseq 96-Unique Dual Index Set Adapter Plates. QIAseq 96-Unique Dual Index Set A (96) layout (SQDIB001–SQDIB096) and QIAseq 96-Unique Dual Index Set B (96) layout (SQDIB097–SQDIB192).

IL-5025K Index Primer Plate in QIAseq 96-Index I Set A or B set

	1	2	3	4	5	6	7	8	9	10	11	12
A	S502	S502	S502	S502	S502	S502	S502	S502	S502	S502	S502	S502
B	S503	S503	S503	S503	S503	S503	S503	S503	S503	S503	S503	S503
C	S505	S505	S505	S505	S505	S505	S505	S505	S505	S505	S505	S505
D	S506	S506	S506	S506	S506	S506	S506	S506	S506	S506	S506	S506
E	S507	S507	S507	S507	S507	S507	S507	S507	S507	S507	S507	S507
F	S508	S508	S508	S508	S508	S508	S508	S508	S508	S508	S508	S508
G	S510	S510	S510	S510	S510	S510	S510	S510	S510	S510	S510	S510
H	S511	S511	S511	S511	S511	S511	S511	S511	S511	S511	S511	S511

IL-5135K Index Primer Plate in QIAseq 96-Index I Set C or D set

	1	2	3	4	5	6	7	8	9	10	11	12
A	S513	S513	S513	S513	S513	S513	S513	S513	S513	S513	S513	S513
B	S515	S515	S515	S515	S515	S515	S515	S515	S515	S515	S515	S515
C	S516	S516	S516	S516	S516	S516	S516	S516	S516	S516	S516	S516
D	S517	S517	S517	S517	S517	S517	S517	S517	S517	S517	S517	S517
E	S518	S518	S518	S518	S518	S518	S518	S518	S518	S518	S518	S518
F	S520	S520	S520	S520	S520	S520	S520	S520	S520	S520	S520	S520
G	S521	S521	S521	S521	S521	S521	S521	S521	S521	S521	S521	S521
H	S522	S522	S522	S522	S522	S522	S522	S522	S522	S522	S522	S522

Figure 7. Layout of IL-5##SK Index Primer Plate in QIAseq 96-Index I Set A, B, C, or D. Each well contains one pre-dispensed, dried sample index primer and universal primer pair for a single reaction. In universal PCR step, IL-7##NJ Adapter Plate in A, B, C, or D set used in ligation must be paired with the appropriate IL-5##SK Index Primer Plate in A, B, C, or D set, respectively.

3. Program a thermal cycler using the cycling conditions in Table 15 (cycling program) and Table 16 (cycle number).

Table 15. Cycling conditions for universal PCR

Step	Time	Temperature
Initial denaturation	13 min	95°C
	2 min	98°C
Number of cycles (see Table 16)	15 s	98°C
	2 min	60°C
1 cycle	5 min	72°C
Hold	5 min	4°C
Hold	∞	4°C

Table 16. Amplification cycles for universal PCR

Primers per pool	Cycle Number		
	Standard DNA	cfDNA	FFPE DNA
6–24	26	28	30
25–96	24	26	28
97–288	22	24	26
289–1056	21	23	25
1057–1499	20	22	24
1500–3072	21	23	25
3073–4999	20	22	24
5000–12,000	19	21	23
≥12,001	18	20	22

4. After the reaction is complete, place the reactions on ice and, for standard/FFPE samples, add 80 μ l nuclease-free water to bring each sample to 100 μ l. For cfDNA samples, add 70 μ l nuclease-free water to bring each sample to 90 μ l.
5. For standard/FFPE samples, add 100 μ l QIAseq Beads (for Human Mitochondria Panel use 70 μ l). For cfDNA samples, add 108 μ l QIAseq Beads. Mix well by pipetting up and down several times.
6. Incubate for 5 min at room temperature.
7. Place the tubes/plate on magnetic rack for 5 min (for tubes) or 10 min (for plates) to separate beads from supernatant. Once the solution has cleared, with the beads still on the magnetic stand, carefully remove and discard the supernatant.
Important: Do not discard the beads as they contain the DNA of interest.
8. With the beads still on the magnetic stand, add 200 μ l 80% ethanol. Carefully remove and discard the wash.
9. Repeat the ethanol wash.
Important: Completely remove all traces of the ethanol after this second wash. Remove the ethanol with a 200 μ l pipette first, and then use a 10 μ l pipette to remove any residual ethanol.
10. With the beads still on the magnetic stand, air dry at room temperature for 10 min.
Note: Visually inspect that the pellet is completely dry.
11. Remove the beads from the magnetic stand, and elute the DNA from the beads by adding 30 μ l nuclease-free water. Mix well by pipetting.

-
12. Return the tubes/plate to the magnetic rack until the solution has cleared.
 13. Transfer 28 μ l supernatant to clean tubes or plate.
 14. Proceed to “Recommendations: Library QC and Quantification”, page 48. Alternatively, the library can be stored in a -30 to -15°C in a constant freezer. Amplified libraries are stable for several months at -30 to -15°C . Once quantification is performed proceed to “Protocol: Sequencing Setup on Illumina MiSeq, NextSeq”, page 51.

Recommendations: Library QC and Quantification

NGS library QC

After the library is constructed and purified, QC can be performed with the QIAxcel or Agilent's Bioanalyzer or TapeStation to check for the correct size distribution of the library fragments and for the absence of adapters or adapter dimers (approx. < 200 bp) and concentration with the High Sensitivity DNA Kit. Libraries prepared for Illumina instruments demonstrate a size distribution between 300 and 1000 bp (Figure 8**Error! Reference source not found.** and Figure 9A, page 53). Library overamplification is normal (Figure 9B, page 53), and this should not affect the sequencing results. Overamplified libraries are usually single-stranded libraries with correct size but appear as "larger fragments" due to secondary structures. Amounts of DNA under the appropriate peaks can be used to quantify the libraries. However, due to the superior sensitivity of qPCR, we recommend quantifying the libraries using the QIAseq Library Quant System, especially when there are over-amplified libraries (See "Preferred library quantification method", page 50).

Recommended setting for checking QIAseq DNA Panel library on QIAxcel

- **Cartridge:** DNA High Resolution
 - Prepare libraries:** 1:5 dilution of libraries by using 1:1 mix of nuclease free water and QIAxcel dilution buffer.
 - Size marker:** 100 bp – 2.5 kb, 2.5 ng
- Alignment marker: 15 bp – 10 kb
- **Method:** OM500-AM10s (If library concentration is low, consider OL500.)
- Injection time: 40 seconds
- **Analysis:** Default Smear DNA
- **Peak calling:** 400 bp with 20% tolerance

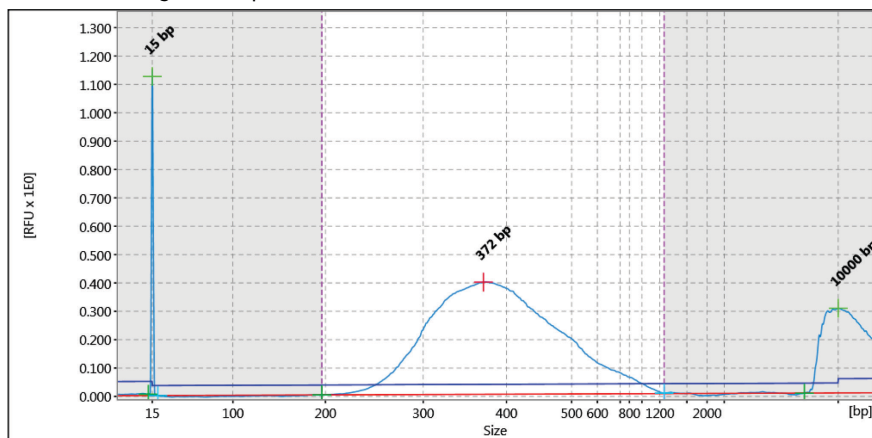
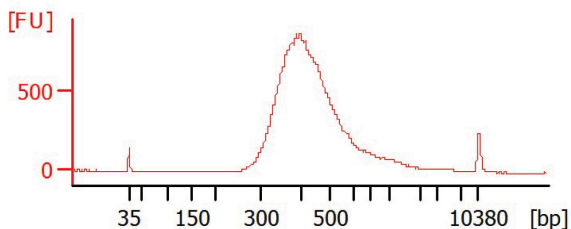


Figure 8. Sample QIAxcel image of QIAseq Targeted DNA Panel libraries for Illumina instruments. The library assessed using QIAxcel illustrates the size of the majority of the library fragments are between 300–1000 bp.

A: Library (without overamplification) prepared for Illumina instruments



B: Library (with overamplification) prepared for Illumina instruments

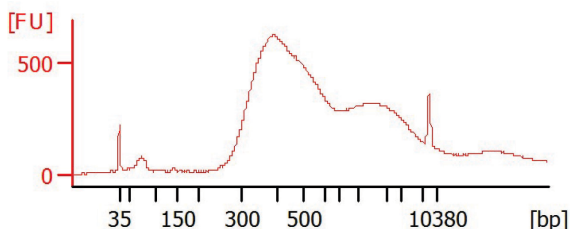


Figure 9. Sample Bioanalyzer images of QIAseq Targeted DNA Panel libraries for Illumina instruments. The size of the majority of the library fragments are between 300 and 1000 bp. A: Library without overamplification. B: Library with overamplification as indicated by the “larger fragment” peak.

Preferred library quantification method

The library yield measurements from the Bioanalyzer or TapeStation rely on fluorescence dyes that intercalate into DNA. These dyes cannot discriminate between molecules with or without adapter sequences, yet only complete QIAseq Targeted DNA libraries with full adapter sequences will be sequenced. Due to the superior sensitivity of qPCR, we recommend quantifying the libraries using, QIAGEN’s QIAseq Library Quant Assay Kit (cat. no. 333314), which contains laboratory-verified forward and reverse primers, together with a DNA standard. With this system, the correct dilution of the library can be determined for sequencing. Please refer to the relevant handbook (available at www.qiagen.com) for library quantification.

Protocol: Sequencing Setup on Illumina MiSeq, NextSeq500/550, MiniSeq, and NovaSeq

Important points before starting

- **Important:** Recommendations for library dilution concentrations and library loading concentrations are based on QIAseq Library Quant System (See Preferred library quantification method, page 50).
- **Important:** QIAseq A Read 1 Primer I (Custom Read 1 Sequencing Primer) **must** be used when performing sequencing on Illumina platform.
- **Important:** QIAseq A Read 1 Primer I (the Custom Read 1 Sequencing Primer) goes into the following specific reagent cartridge positions:
 - MiniSeq Position #15
 - MiSeq Position #18
 - NextSeq500/550 Position #7
 - NovaSeq Position #5
- **Important:** Paired-end sequencing **should** be used for QIAseq Targeted DNA Panel on Illumina platform.
- **Important:** To make sequencing preparation more convenient, download Illumina-compatible sample sheets for different sequencing instruments on www.qiagen.com, from the **Product Resources** tab of the QIAseq Targeted DNA Panel.
- **Important:** Paired-end sequencing of 149 bp should be used for QIAseq Targeted DNA 96-Unique Index Set libraries and dual 10 bp indices on Illumina platforms.
- **Important:** Paired-end sequencing of 151 bp should be used for QIAseq Targeted DNA 12-Index I, 96-Index I, and 8-Unique Index Set libraries and dual 8 bp indices on Illumina platforms.

- For complete instructions on how to denature sequencing libraries, prepare custom index primers, and set up a sequencing run, please refer to the system-specific Illumina documents.
- Instrument-specific imagery is included to aid in sequencing preparations.

Sequencing Preparations for MiSeq with QIAseq 96-Unique Dual Index Sets

1. When working with the QIAseq Targeted DNA Panel custom QIAseq 96-Unique Dual Index Sets, use Local Run Manager (LRM) v2 on the instrument to upload a sample sheet (see the **Product Resources** tab of the QIAseq Targeted DNA Panel and download the appropriate template) and proceed with sequencing: Read 1 is 149 bp, Read 2 is 149 bp, and each Index Read is 10 bp.

2. Sample dilution and pooling: Dilute libraries to 2 or 4 nM for MiSeq. Then, combine libraries with different sample indexes in equimolar amounts if similar sequencing depth is needed for each library.

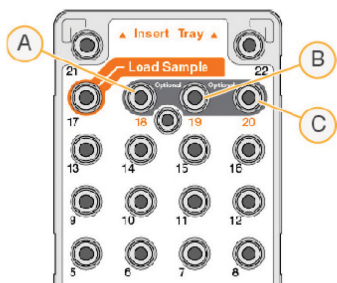
Note: Recommendations for library dilution concentrations are based on QIAseq Library Quant System.

Note: If combining libraries with the same number of primers, pool equal volumes of the individual libraries at 4 nM together. If the libraries have different primer numbers, then combine the libraries at volume ratios according to their number of primers. For example, Library A has 5000 primers at 4 nM and Library B has 600 primers at 4 nM; combining 50 μ l of Library A with 6 μ l of Library B will result in similar coverage depth for both Libraries A and B in the same sequencing run.

3. Library Preparation and loading: Prepare and load the library onto a MiSeq according to the MiSeq System Denature and Dilute Libraries Guide. The final library concentration is 10–12 μ M on the MiSeq.

Note: Recommendations for library loading concentrations are based on QIAseq Library Quant System.

4. Custom sequencing primer for Read 1 preparation and loading: Use 597 μl HT1 (Hybridization Buffer) to dilute 3 μl QIAseq A Read 1 Custom Primer I (provided) to obtain a final concentration of 0.5 μM . Load 600 μl of the diluted QIAseq A Read 1 Primer I to position 18 of the MiSeq reagent cartridge (Figure 10). For more details, please refer to the Illumina protocol: [miseq_using_custom_primers_15041638_b.pdf](#) for the MiSeq.



A Position 18 for Read 1 Custom Primer

Figure 10. MiSeq reagent cartridge. A: Position 18 for Read 1 Custom Primer; B and C: not relevant.

5. Upon completion of the sequencing run, proceed to Appendix D, page 69.

Sequencing Preparations for MiSeq with QIAseq 12-Index I, QIAseq 96 Index I Sets, and QIAseq 8-Unique Index Sets

1. When working with the QIAseq Targeted DNA Panel custom QIAseq 12-Index I, QIAseq 96-Index I Sets, and QIAseq 8-Unique Index Sets, use LRM v2 on the instrument to upload a sample sheet (see the **Product Resources** tab of the QIAseq Targeted DNA Panel and download the appropriate template) and proceed with sequencing: Read 1 is 151 bp, Read 2 is 151 bp, and each Index Read is 8 bp.

or

Set up the sample sheet with Custom Sequencing Read 1 primer using Illumina Experiment Manager v1.2, or later (Figure 11). Sample index of QIAseq Targeted DNA Panel is compatible with Illumina Nextera XT v2 adapter sample index system. Set the parameters as follows:

- **Category:** Select Other
- **Select Application:** Check FASTQ Only
- **Sample Prep Kit:** Select Nextera XT v2
- **Index Reads:** Select 2
- **Read Type:** Select Paired End Read
- **Cycles for both Read 1 and 2:** Select 151
- **Important:** Check Custom Primer for Read 1
- **Important:** Check Use Adapter Trimming

Sample Sheet Wizard - MiSeq Application Selection

Select Category

Targeted Resequencing Small Genome Sequencing RNA Sequencing Other

Select Application

TruSight HLA Library QC FASTQ Only ChIP-Seq

Sample Sheet Wizard - Workflow Parameters

FASTQ Only Run Settings

Reagent Cartridge Barcode* #####

Sample Prep Kit:

Index Reads: 0 1 2

Experiment Name:

Investigator Name:

Description:

Date:

Read Type: Paired End Single Read

Cycle Read 1:

Cycle Read 2:

* - required field

FASTQ Only Workflow-Specific Settings

Custom Primer for Read 1

Custom Primer for Index

Custom Primer for Read 2

Reverse Complement

Use Adapter Trimming

Figure 11. Sample sheet using Illumina Experiment Manager.

- Follow steps 2–5 in “Sequencing Preparations for MiSeq with QIAseq 96-Unique Dual Index Sets”.

Sequencing Preparations for NextSeq500/550 with QIAseq 96-Unique Index Sets

1. When working with the QIAseq Targeted DNA Panel custom QIAseq 96-Unique Dual Index Sets, use LRM v2 on the instrument to upload a sample sheet (see the **Product Resources** tab of the QIAseq Targeted DNA Panel and download the appropriate template) and proceed with sequencing: Read 1 is 149 bp, Read 2 is 149 bp, and each Index Read is 10 bp.
2. Sample dilution and pooling: Dilute libraries to 0.5, 1, 2, or 4 nM for NextSeq. Then, combine libraries with different sample indexes in equimolar amounts if similar sequencing depth is needed for each library.

Note: Recommendations for library dilution concentrations are based on QIAseq Library Quant System.

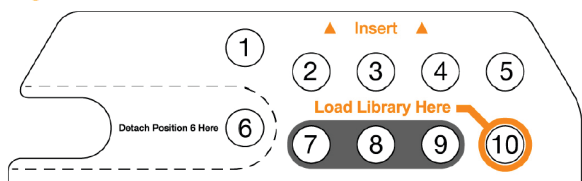
Note: If combining libraries with the same number of primers, pool equal volumes of the individual libraries at 4 nM together. If the libraries have different primer numbers, then combine the libraries at volume ratios according to their number of primers. For example, Library A has 5000 primers at 4 nM and Library B has 600 primers at 4 nM; combining 50 μ l Library A with 6 μ l Library B will result in similar coverage depth for both Libraries A and B in the same sequencing run.

3. Library preparation and loading: Prepare and load the library onto a NextSeq500/550 according to the NextSeq System Denature and Dilute Libraries Guide. The final library concentration is 1.2–1.5 pM on the NextSeq500/550.

Note: Recommendations for library loading concentrations are based on QIAseq Library Quant System.

4. Custom sequencing primer for Read 1 preparation and loading: Use 1994 μl HT1 (Hybridization Buffer) to dilute 6 μl QIAseq A Read 1 Primer I (provided) to obtain a final concentration of 0.3 μM . Load 2 ml of the diluted QIAseq A Read 1 Primer I to position 7 of the NextSeq reagent cartridge (Figure 12).

Note: All other steps refer to run setup workflow as described in the NextSeq 500 System Guide (part #15046563) or NextSeq 550 System Guide (part #15069765-02).



Position #	Custom Primer
7	Custom Read 1 primer

Figure 12. NextSeq reagent cartridge.

5. Upon completion of the sequencing run, proceed to “Appendix D”, page 69.

Sequencing Preparations for NextSeq500/550 with QIAseq 12-Index I, QIAseq 96-Index I Sets, and QIAseq 8-Unique Index Sets

1. When working with the QIAseq Targeted DNA Panel custom QIAseq 12-Index I, QIAseq 96-Index I Sets, and QIAseq 8-Unique Index Sets, use LRM v2 on the instrument to upload a sample sheet (see the Product Resources tab of the QIAseq Targeted DNA Panel and download the appropriate template) and proceed with sequencing: Read 1 is 151 bp, Read 2 is 151 bp, and each Index Read is 8 bp.
2. Follow steps 2–5 in “Sequencing Preparations for NextSeq500/550 with QIAseq 96-Unique Index Sets”.

Sequencing Preparations for MiniSeq with QIAseq 96-Unique Index Sets

1. When working with the QIAseq Targeted DNA Panel custom QIAseq 96-Unique Dual Index Sets, use LRM v2 on the instrument to upload a sample sheet (see the **Product Resources** tab of the QIAseq Targeted DNA Panel and download the appropriate template) and proceed with sequencing: Read 1 is 149 bp, Read 2 is 149 bp, and each Index Read is 10 bp.
2. Sample dilution and pooling: Dilute libraries to 0.5, 1, 2, or 4 nM for MiniSeq. Then, combine libraries with different sample indexes in equimolar amounts if similar sequencing depth is needed for each library.

Note: Recommendations for library dilution concentrations are based on QIAseq Library Quant System.

Note: If combining libraries with the same number of primers, pool equal volumes of the individual libraries at 4 nM together. If the libraries have different primer numbers, then combine the libraries at volume ratios according to their number of primers. For example, Library A has 5000 primers at 4 nM and Library B has 600 primers at 4 nM; combining 50 μ l Library A with 6 μ l Library B will result in similar coverage depth for both Libraries A and B in the same sequencing run.

3. Library preparation and loading: Prepare and load the library onto a MiniSeq according to the MiniSeq System Denature and Dilute Libraries Guide. The final library concentration is 1.2–1.5 pM on the MiniSeq.

Note: Recommendations for library loading concentrations are based on QIAseq Library Quant System.

4. Custom sequencing primer for Read 1 preparation and loading: Use 997 μ l HT1 (Hybridization Buffer) to dilute 3 μ l QIAseq A Read 1 Primer I (provided) to obtain a final concentration of 0.3 μ M. Load 1 ml of the diluted QIAseq A Read 1 Primer I to position 15 of the MiniSeq reagent cartridge (Figure 12).

Note: All other steps refer to run setup workflow as described in the MiniSeq System Guide (part #1000000002695).

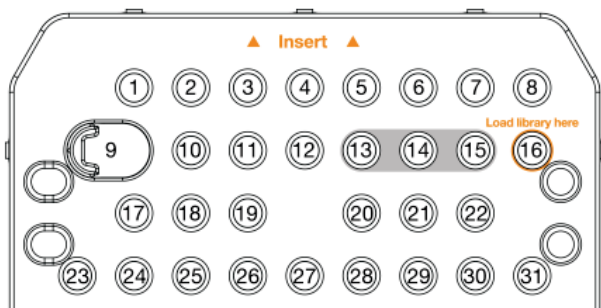


Figure 13. MiniSeq reagent cartridge.

5. Upon completion of the sequencing run, proceed to "Appendix D", page 69.

Sequencing Preparations for MiniSeq with QIAseq 12-Index I, QIAseq 96-Index I Sets, and QIAseq 8-Unique Index Sets

1. When working with the QIAseq Targeted DNA Panel custom QIAseq 12-Index I, QIAseq 96-Index I Sets, and QIAseq 8-Unique Index Sets, use LRM v2 on the instrument to upload a sample sheet (see the **Product Resources** tab of the QIAseq Targeted DNA Panel and download the appropriate template) and proceed with sequencing: Read 1 is 151 bp, Read 2 is 151 bp, and each Index Read is 8 bp.
2. Follow steps 2–5 in "Sequencing Preparations for NextSeq500/550 with QIAseq 96-Unique Index Sets".

Sequencing Preparations for NovaSeq with QIAseq 96-Unique Index Sets

1. When working with the QIAseq Targeted DNA Panel custom QIAseq 96-Unique Dual Index Sets, upload a sample sheet (see the **Product Resources** tab of the QIAseq Targeted DNA Panel and download the appropriate template) and proceed with sequencing: Read 1 is 149 bp, Read 2 is 149 bp, and each Index Read is 10 bp.

2. Sample dilution and pooling: Dilute libraries to 10 nM for NovaSeq. Then, combine libraries with different sample indexes in equimolar amounts if similar sequencing depth is needed for each library.

Note: Recommendations for library dilution concentrations are based on QIAseq Library Quant System.

Note: If combining libraries with the same number of primers, pool equal volumes of the individual libraries at 10 nM together. If the libraries have different primer numbers, then combine the libraries at volume ratios according to their number of primers. For example, Library A has 5000 primers at 10 nM and Library B has 600 primers at 10 nM; combining 50 μ l Library A with 6 μ l Library B will result in similar coverage depth for both Libraries A and B in the same sequencing run.

3. Library preparation and loading: Prepare and load the library onto a NovaSeq according to the NovaSeq 6000 Sequencing System Guide (part #1000000019358). The final pooled library concentration recommendation is between 1.0 – 1.5 pM yielding a final loading concentration of between 200 – 300 pM on the NovaSeq.

Note: Recommendations for library loading concentrations are based on QIAseq Library Quant System.

4. Custom sequencing primer for Read 1 preparation and loading:

S4 Mode: Use 3489.5 μ l HT1 (Hybridization Buffer) to dilute 10.5 μ l QIAseq A Read 1 Primer I (provided) to obtain a final concentration of 0.3 μ M. Load 3.5 ml of the diluted QIAseq A Read 1 Primer I to position 5 of the NovaSeq reagent cartridge (Figure 14).

SP/S1/S2 Mode: Use 1994 μ l HT1 (Hybridization Buffer) to dilute 6 μ l QIAseq A Read 1 Primer I (provided) to obtain a final concentration of 0.3 μ M. Load 2 ml of the diluted QIAseq A Read 1 Primer I to position 5 of the NovaSeq reagent cartridge (Figure 14).

Note: All other steps refer to run setup workflow as described in the NovaSeq 6000 Sequencing System Guide (part #1000000019358).

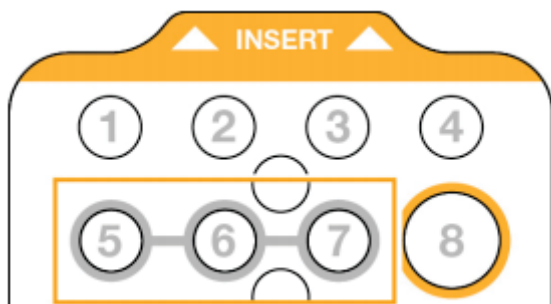


Figure 14. NovaSeq reagent cartridge.

5. Upon completion of the sequencing run, proceed to "Appendix D", page 69.

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 at 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 and/or protocols in this handbook or sample and assay technologies (for contact information, visit www.qiagen.com).

Comments and suggestions

Low library yield

- | | | |
|----|---|--|
| a) | Suboptimal reaction conditions due to low DNA quality | Make sure to use high-quality DNA to ensure optimal activity of library enzymes. |
| b) | Inefficient targeted enrichment or universal PCR | QIAseq Beads need to be completely dried before elution. Ethanol carryover to targeted enrichment and universal PCR will affect PCR reaction efficiency. |

Unexpected signal peaks

- | | | |
|----|--|---|
| a) | Short peaks around 75 and 180 bp | These are primer-dimers from targeted enrichment PCR (~75 bp) or universal PCR (~180 bp). The presence of primer dimers indicates either not enough DNA input or inefficient PCR reactions or handling issues with bead purifications. |
| b) | Larger library fragments after universal PCR | After the universal PCR, library fragments are larger than the intended peak and can be a PCR artifact due to over-amplification of the DNA library. Overamplification of the library won't affect the QIAseq Targeted DNA Panels sequencing performance. Decreasing the number of universal PCR cycle numbers can reduce over-amplification. |

Sequencing issues

- | | | |
|----|-------------------------------------|---|
| a) | Too low or too high cluster density | Accurate library quantification is the key for optimal cluster density on any sequencing instrument. PCR based quantification method is recommended. Other methods may lead to the incorrect quantification of the library especially when there is over-amplification. |
| b) | Very low clusters passing filter | Make sure the library is accurately quantified and that the correct amount is loaded onto the sequencing instrument. In addition, the QIAseq A Read 1 Primer I (100 µM) Custom Read 1 Sequencing primer must be used when sequencing on any Illumina platform. |

Variant detection issues

Comments and suggestions

Known variants not detected

Variant detection sensitivity is directly related to the input DNA and read depth. Check Table 2 **Error! Reference source not found.** to see if the required input DNA, UMI numbers, and read depth are met for the specific variant detection application.

References

1. Xu, C., Nezami Ranjbar, M.R., Wu, Z., DiCarlo, J., Wang, Y. (2017) Detecting very low allele fraction variants using targeted DNA sequencing and a novel molecular barcode-aware variant caller. *BMC Genomics*. **18**, 5.

Appendix A: Combining an Existing Panel with a Booster Panel

If additional primers need to be added into an existing panel, a Booster Panel with up to 100 primers can be ordered. To combine the existing panel with a Booster Panel, follow the volume ratio indicated in Table 17.

Table 17. Combining an existing panel (at 50 μ l) with a booster panel

No. of primers in existing panel	Volume of existing panel to combine	Volume of booster panel to combine
1–2000	50 μ l	5 μ l
2001–4000	50 μ l	3.75 μ l
4001–12,000	50 μ l	2.5 μ l
12,001–20,000	50 μ l	1.25 μ l

Appendix B: FFPE DNA Quality and Quantity

Genomic DNA present in FFPE archives is usually damaged and fragmented to an uncertain extent. Commonly used DNA quantification methods, including spectrometers or fluorometers, do not differentiate between amplifiable and nonamplifiable DNA. Therefore, they cannot reliably measure the amplifiable amounts of DNA that are able to participate in the targeted enrichment step in the NGS workflow involving multiplex PCR, such as the QIAseq Targeted DNA Panels.

The QIAseq DNA QuantiMIZE System is a qPCR-based approach that determines the quantity and quality of the DNA amenable to PCR-based targeted enrichment prior to NGS. The system provides a cost-effective approach to qualify and quantify the DNA isolated from biological samples – mainly for FFPE samples. Please refer to the corresponding handbook for determining FFPE DNA quantity and quality with the QIAseq DNA QuantiMIZE System.

The QIAseq DNA QuantiMIZE System is recommended for determining FFPE DNA input for the QIAseq Targeted DNA Panels. If FFPE DNA is defined as high quality (quality control (QC) score ≤ 0.04) by QuantiMIZE, then up to 100 ng of DNA can be used. If the DNA is determined as low quality (QC score > 0.04), then up to 250 ng of DNA can be used. The QC score of QuantiMIZE reflects the amount of amplifiable DNA present in the sample, therefore correlating with the number of UMIs that can be sequenced in the library (Figure 15, next page).

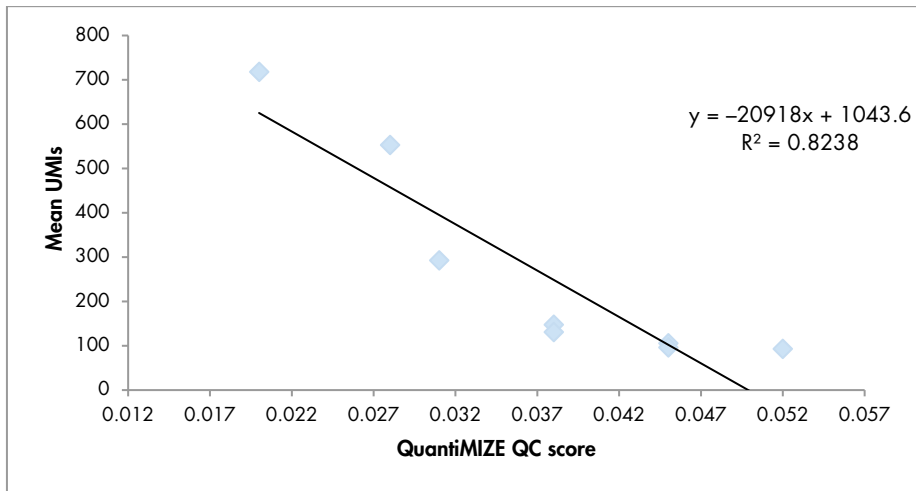


Figure 15. Correlation between QIAseq QuantiMIZE QC Score and the number of UMIs.

Compared to the same amount of fresh DNA, only 10–50% of UMIs can be captured from FFPE DNA, depending on the quality. This is due to a lower amplifiable DNA amount present in the FFPE samples. Therefore, a higher input amount is recommended for FFPE DNA samples to ensure that enough UMIs can be sequenced for variant detection.

However, if the quality of the FFPE DNA is not assessed by QIAseq QuantiMIZE kits, up to 100 ng can be used. If the FFPE DNA quality is high, an input of more than 100 ng will potentially overload the QIAseq Targeted DNA system.

Appendix C: QIAseq 8-Unique Dual Index Sets

The barcode sequences used in the QIAseq 8-Unique Dual Index Sets correspond to Illumina adapter barcodes from Nextera XT v2. The layout used in the QIAseq 8-Unique Dual Index Sets are described in Figure 16 and Figure 17.

UDIN-8AA Adapter Plate in QIAseq 8-Unique Dual Index Set A (48)

	1	2	3	4	5	6	7	8	9	10	11	12
A	N701											
B	N702											
C	N703											
D	N704											
E	N706											
F	N707											
G	N712											
H	N714											

UDIN-8BA Adapter Plate in QIAseq 8-Unique Dual Index Set B (48)

	1	2	3	4	5	6	7	8	9	10	11	12
A	N716											
B	N720											
C	N721											
D	N722											
E	N726											
F	N727											
G	N728											
H	N729											

Figure 16. Layout of sample adapters in QIAseq 8-Unique Dual Index Set A or B. Only Column 1 of each plate have adapters. Columns 2 through 12 are empty. Each well in column 1 contains one sample adapter, and the amount of adapter in each well is enough for 6 samples.

UDIS-8AK Index Primer Plate in QIAseq 8-Unique Dual Index Set A (48)

	1	2	3	4	5	6	7	8	9	10	11	12
A	S502	S502	S502	S502	S502	S502						
B	S503	S503	S503	S503	S503	S503						
C	S505	S505	S505	S505	S505	S505						
D	S506	S506	S506	S506	S506	S506						
E	S507	S507	S507	S507	S507	S507						
F	S508	S508	S508	S508	S508	S508						
G	S510	S510	S510	S510	S510	S510						
H	S511	S511	S511	S511	S511	S511						

UDIS-8BK Index Primer Plate in QIAseq 8-Unique Dual Index Set B (48)

	1	2	3	4	5	6	7	8	9	10	11	12
A	S513	S513	S513	S513	S513	S513						
B	S515	S515	S515	S515	S515	S515						
C	S516	S516	S516	S516	S516	S516						
D	S517	S517	S517	S517	S517	S517						
E	S518	S518	S518	S518	S518	S518						
F	S520	S520	S520	S520	S520	S520						
G	S521	S521	S521	S521	S521	S521						
H	S522	S522	S522	S522	S522	S522						

Figure 17. Layout of UDIS-8#K Index Primer Plate in QIAseq 8-Unique Dual Index Set A or B. Each well contains one pre-dispensed, dried sample index primer and universal primer pair for a single reaction. In the universal PCR step, the UDIN-8#A Adapter Plate in A, or B set used in the ligation reaction, must be paired with the appropriate UDIS-8#K Index Primer Plate in A, or B set, respectively. For the universal PCR step, mix the components directly into the single use pierceable plate.

Appendix D: Data Analysis Using QIAGEN's QIAseq Targeted Sequencing Data Analysis Portal or CLC Genomics Workbench

After sequencing, the results can be analyzed using QIAGEN's QIAseq targeted sequencing data analysis portal. Our data analysis pipeline will perform mapping to the reference genome, UMI counting, read trimming (removing primer sequences), and variant identification. Alternatively, data from QIAseq Targeted DNA Panels can be analyzed using CLC Genomics Workbench, which allows you to optimize analysis parameters to your specific panel. The parameters can then be locked for routine use. Contact your account manager for further details.

1. Log in to the GeneGlobe Data Analysis Center at <https://geneglobe.qiagen.com/us/product-groups/qiaseq-targeted-dna-panels>.
2. Make selection as highlighted in Figure 18.

The screenshot shows a web interface titled "Start Analyzing Your Data". It contains three numbered steps for selection:

- 1. Select analysis type: Two buttons are shown, "Next-Generation Sequencing" (highlighted in blue) and "PCR".
- 2. Select your analyte: Three buttons are shown, "miRNA", "mRNA/lncRNA", and "DNA" (highlighted in blue).
- 3. Select your panel: Five buttons are shown, "QIAseq Targeted DNA Panels" (highlighted in blue), "GeneRead DNAseq Panels", "QIAseq Targeted Methyl Panels", "QIAseq 16S Demultiplexer", and "EpiTect Hi-C".

At the bottom of the form is a large blue button labeled "START YOUR ANALYSIS". In the top right corner, there is a link that says "GO TO MY ANALYSIS".

Figure 18. GeneGlobe Analysis pipeline selections for QIAseq Targeted DNA Panels.

3. Click **START YOUR ANALYSIS**.

- In the **Read Files** tab, select BaseSpace to upload files from BaseSpace or select **Uploaded > Upload New Files** to upload files from your local drive (Figure 19).

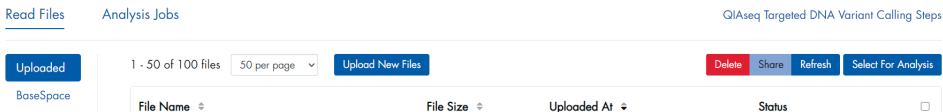


Figure 19. File Upload tab of the QIAseq Targeted DNA Panel Data Analysis Pipeline.

Note: All files that have been uploaded to GeneGlobe are listed under the Read Files tab. Using this tab, it is possible to delete files that are no longer needed and share files with collaborators.

- Select the boxes next to the files that will be analyzed, and then click **Select For Analysis** (Figure 20).

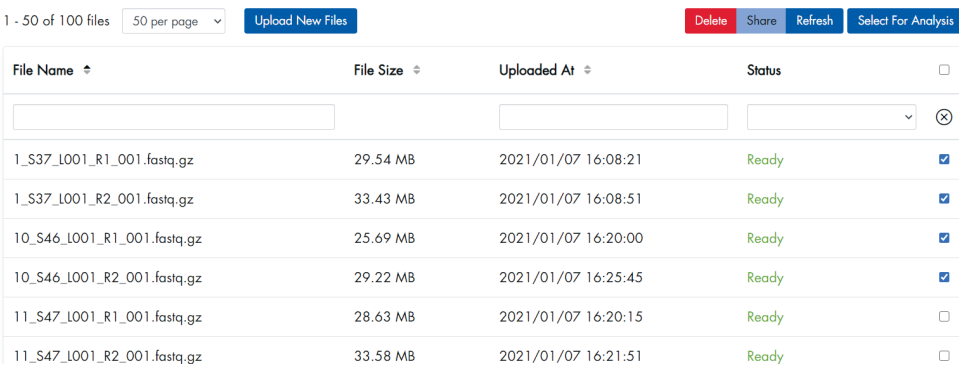


Figure 20. File selection for QIAseq Targeted DNA Panel data analysis pipeline

Under the **Analysis Jobs** tab, configure the analysis per the drop-down menus as described below:

The screenshot shows the 'Analysis Jobs' tab in the QIAseq Targeted DNA Variant Calling Steps interface. At the top, there are two tabs: 'Read Files' (selected) and 'Analysis Jobs'. The page title is 'QIAseq Targeted DNA Variant Calling Steps'. Below the tabs is a 'View All Jobs' button. The main form contains several fields: 'Read Files *' with a dropdown showing '4 read files selected'; 'Job Title *' with a text input 'Input job title'; 'Catalog # *' with a dropdown and a checkbox for 'Custom Catalog #'; 'Job Type' with a dropdown showing 'Single'; 'File Lanes' with a dropdown showing '1-lane'; and 'Copy Number Reference Job IDs' with a text input 'Input reference job ids, e.g. 3456, 3567'. A 'JSON Request' field is also present with a text input 'Input extra JSON request'. An 'ANALYZE' button is located at the bottom right of the form.

Figure 21. Analysis Jobs tab of the QIAseq Targeted DNA Panel data analysis pipeline

- Read Files: Verify that the correct read files have been selected.
 - Job Title: Enter a title for the analysis job.
 - Catalog #: If using a catalog panel, select the number from the dropdown menu. If using a custom panel, enter the custom catalog number manually.
 - **Job type:** Single or matched tumor/normal.
 - **File lanes:** For Illumina, choose 1-lane if you set up your runs using MiSeq/HiSeq/NextSeq concatenated. Choose 4-lane if you set up your runs using NextSeq individual lane files. Choose 1-lane for Ion Torrent™ files.
 - **Copy Number Reference Job IDs:** For copy number analysis, normal sample(s) need(s) to be analyzed with the portal before case samples are set up. Enter the job ID corresponding to your control samples for copy number analysis.
6. Click **ANALYZE**. The analysis job status changes from **Queued** to **In progress**, and then **Done successfully**.
7. Once the analysis is completed, output files can be downloaded by clicking **Download**.
- Note:** Ultimately, detected variants can be interpreted with QCI Interpret.

Ordering Information

Product	Contents	Cat. no.
QIAseq Targeted DNA Panel (12)	ALL reagents (except indexes) for targeted DNA sequencing; fixed panel for 12 samples; less than 200 genes	333502
QIAseq Targeted DNA Panel (96)	ALL reagents (except indexes) for targeted DNA sequencing; fixed panel for 96 samples; less than 200 genes	333505
QIAseq Targeted DNA HC Panel (12)	ALL reagents (except indexes) for targeted DNA sequencing; fixed panel for 12 samples; more than 200 genes	333512
QIAseq Targeted DNA HC Panel (96)	ALL reagents (except indexes) for targeted DNA sequencing; fixed panel for 96 samples; more than 200 genes	333515
QIAseq Targeted DNA Custom Panel (96)	ALL reagents (except indexes) for targeted DNA sequencing; Custom panel for 96 samples	333525
QIAseq Targeted DNA Extended Panel (96)	ALL reagents (except indexes) for targeted DNA sequencing; Extended panel for 96 samples	333545
QIAseq Targeted DNA Booster Panel (96)	Pool of primers used in combination with either cataloged or custom panels	333535 *
QIAseq Unique Dual Indices		
QIAseq 96-Unique Dual Index Set A (384)	Box containing unique molecularly indexed adapters and primers, enough for a total of 384 samples, for indexing up to 96 samples for targeted panel sequencing on Illumina platforms; Set A (of A and B) required for multiplexing 192 samples in one run	333725

* Visit www.qiagen.com/GeneGlobe to search for and order these products.

Product	Contents	Cat. no.
QIAseq 96-Unique Dual Index Set B (384)	Box containing unique molecularly indexed adapters and primers, enough for a total of 384 samples, for indexing up to 96 samples for targeted panel sequencing on Illumina platforms; Set A (of A and B) required for multiplexing 192 samples in one run	333735
QIAseq 8-Unique Dual Index Set A (48)	Box containing unique molecularly-indexed adapters and primers, enough for a total of 48 samples, for indexing up to 8 samples for targeted panel sequencing on Illumina platforms; Set A (of A and B) required for multiplexing 16 samples in one run	333715
QIAseq 8-Unique Dual Index Set B (48)	Box containing unique molecularly-indexed adapters and primers, enough for a total of 48 samples, for indexing up to 8 samples for targeted panel sequencing on Illumina platforms; Set A (of A and B) required for multiplexing 16 samples in one run	333716
QIAseq Combinatorial Dual Indices		
QIAseq 12-Index I (48)	Box containing molecularly indexed adapters and primers, enough for a total of 48 samples, for indexing up to 12 samples for targeted panel sequencing on Illumina platforms	333714

Product	Contents	Cat. no.
QIAseq 96-Index I Set A (384)	Box containing molecularly indexed adapters and primers, enough for a total of 384 samples, for indexing up to 96 samples for targeted panel sequencing on Illumina platforms; one of 4 sets required for multiplexing 384 samples	333727
QIAseq 96-Index I Set B (384)	Box containing molecularly indexed adapters and primers, enough for a total of 384 samples, for indexing up to 96 samples for targeted panel sequencing on Illumina platforms; 2 of 4 sets required for multiplexing 384 samples	333737
QIAseq 96-Index I Set C (384)	Box containing molecularly indexed adapters and primers, enough for a total of 384 samples, for indexing up to 96 samples for targeted panel sequencing on Illumina platforms; 3 of 4 sets required for multiplexing 384 samples	333747
QIAseq 96-Index I Set D (384)	Box containing molecularly indexed adapters and primers, enough for a total of 384 samples, for indexing up to 96 samples for targeted panel sequencing on Illumina platforms; 4 of 4 sets required for multiplexing 384 samples	333757

Related products

QIAseq Library Quant Assay Kit	Reagents for quantification of libraries prepared for Illumina or Ion Torrent platforms; assay format	333314
QIAseq DNA QuantiMIZE Array Kit	qPCR arrays for optimizing amount of input DNA and PCR cycling conditions for targeted enrichment of FFPE DNA	333404
QIAseq DNA QuantiMIZE Assay Kit	qPCR assays for optimizing amount of input DNA and PCR cycling conditions for targeted enrichment of FFPE DNA	333414

Product	Contents	Cat. no.
QIAamp DNA Mini Kit (50)	For 50 DNA preps: 50 QIAamp Mini Spin Columns, QIAGEN Proteinase K, Collection Tubes (2 ml), reagents and buffers	51304
QIAamp Circulating Nucleic Acid Kit (50)	For 50 DNA preps: QIAamp Mini Columns, Tube Extenders (20 ml), QIAGEN Proteinase K, Carrier RNA, Buffers, VacConnectors, and Collection Tubes (1.5 ml and 2 ml)	55114
GeneRead DNA FFPE Kit (50)	QIAamp MinElute columns, Proteinase K, UNG, collection tubes (2 ml), buffers, Deparaffinization Solution, RNase A	180134

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Document Revision History

Date	Description of changes
07/2016	Initial release.
05/2017	<p>Reagents added (use is highly recommended):</p> <p>FERA Solution (enhances efficiency)</p> <p>Ligation Buffer (enhances efficiency)</p> <p>FG solution (enables use of cfDNA containing cellular DNA)</p> <p>Panel sizes added. QIAseq Targeted DNA Panel Analysis pipeline portal updated. Biomedical Genomics Workbench added as an analysis option. Publication reference added for the QIAseq Targeted DNA Panel Analysis pipeline. QIAxpert added as recommendation for assessing sample purity. QIAxcel added as recommendation for assessing library quality. Sample-specific reaction mixes and conditions added for procedures. Fragmentation, end-repair and A-addition updated. Volumes and bead ratios updated. Adapter ligation procedures updated. Library over-amplification addressed in Appendix E. Figures and text updated.</p>
02/2020	QIAseq bead component size changed from 7 ml to 10 ml.
03/2021	<p>Introduction of UDIs. Updated the Kit Contents section. Updated Figure 1. Updated Table 1. Qubit added as recommendation for DNA quantification. GeneRead Library Quant Array removed from Preferred library quantification method. Protocol: Sequencing Setup on Illumina MiSeq and, NextSeq500/550, MiniSeq and NovaSeq updated to include sequencing preparations for MiniSeq and Novaseq. QIAseq Targeted DNA Panel Analysis pipeline portal updated in Appendix D.</p>

Notes

Notes

Limited License Agreement for QIAseq Targeted DNA Panels

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