

Spotlight:

NGS

Exploring new frontiers with next-generation sequencing

Pushing the limits of discovery

Next-generation sequencing (NGS) is being utilized for numerous new and exciting applications, such as single cell analysis, liquid biopsy research, circulating-free DNA (cfDNA) studies, metagenomics and targeted sequencing. Whether you're studying single cells or populations, selected genes or whole genomes, our innovative high-quality products harness the power of NGS to help reveal meaningful insights for results that make an impact. Use QIAGEN® solutions and push the boundaries of your scientific research!

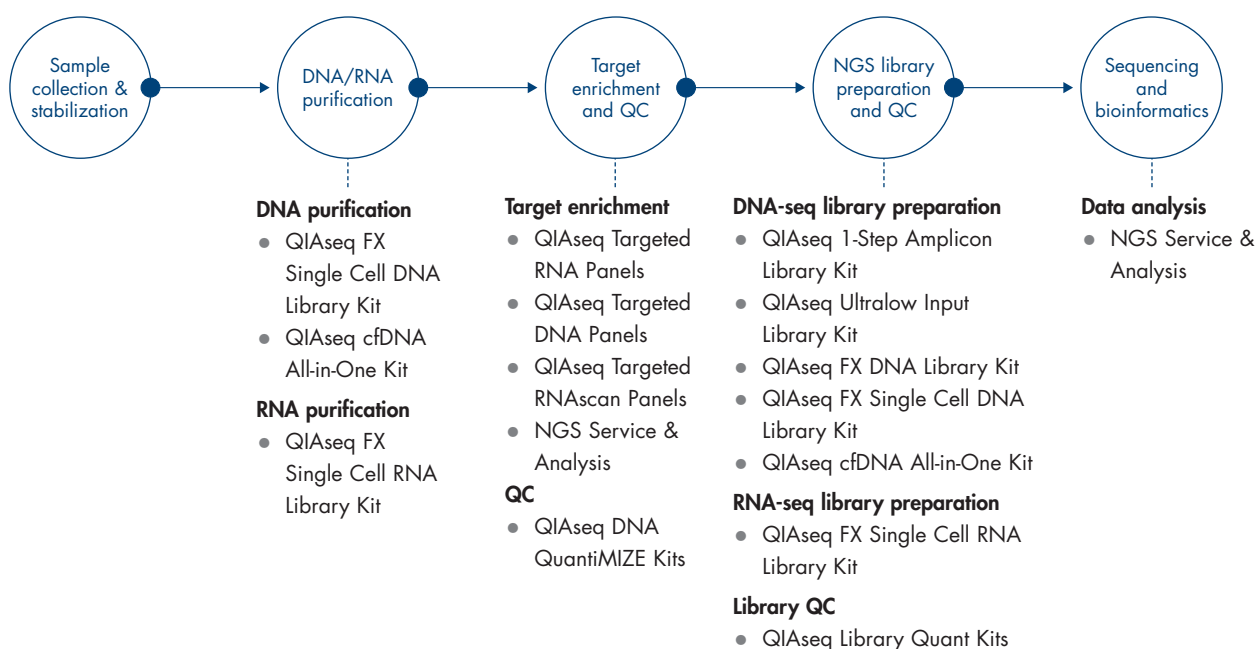
Sample to Insight



New QIAseq solutions provide the answers you seek!

QIAseq NGS products have been carefully designed to simplify and speed-up complicated workflows into simple, highly reproducible protocols allowing everyone to harness the power of NGS. We offer a simple path from Sample to Insight regardless of whether your application is whole genome, exome, metagenomics or targeted sequencing.

Starting with RNA, DNA or miRNA samples from tissues, exosomes, or single cells requires dedicated isolation, library construction and bioinformatics solutions. Our goal with QIAGEN's QIAseq product line is to guide you along the path to NGS success.

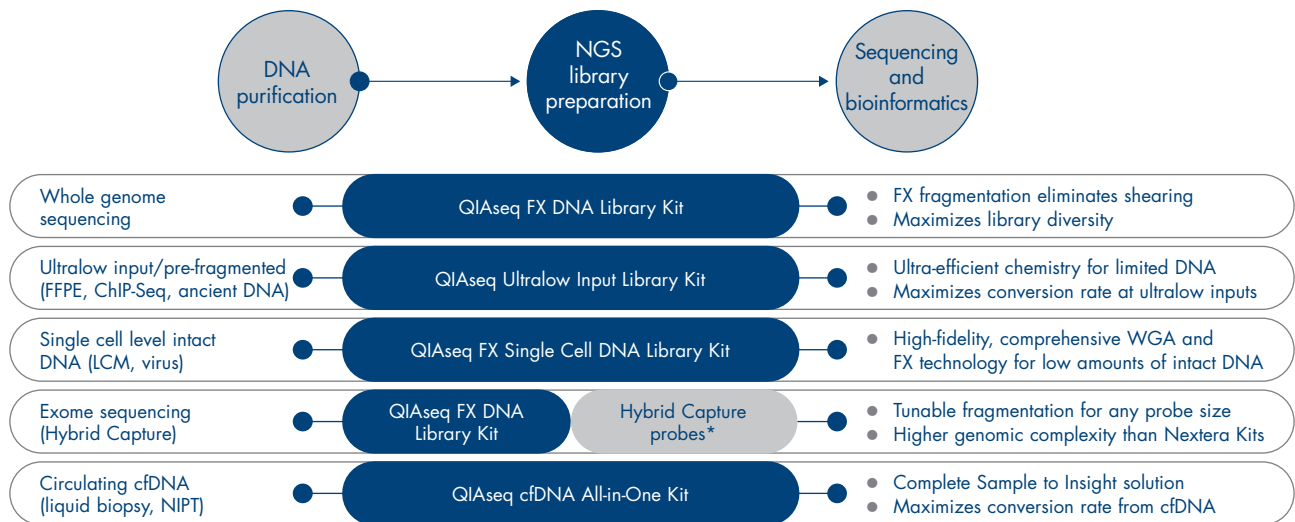


Introducing QIAseq.

Sample to Insight for all.

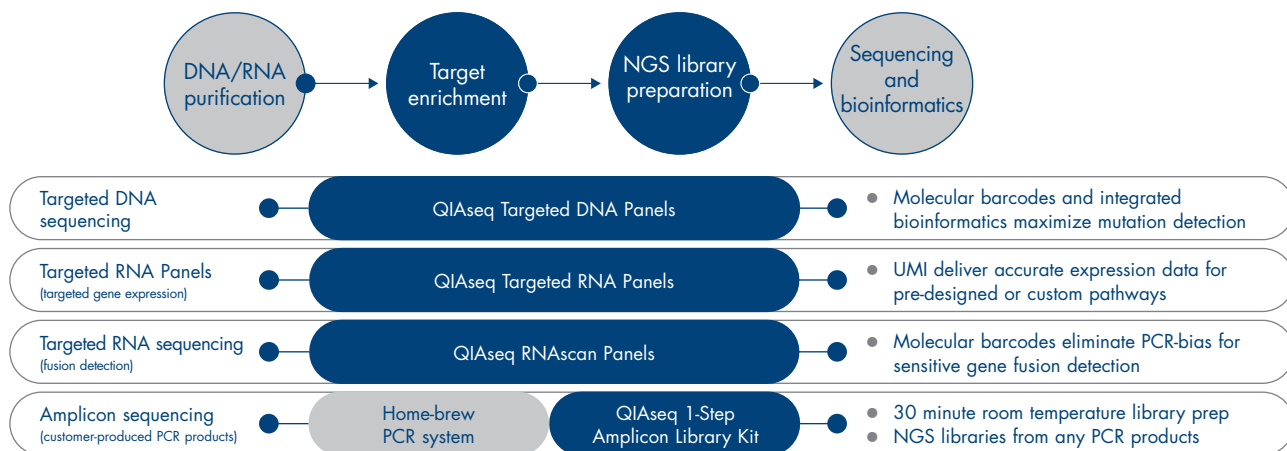


Whole genome sequencing and Hybrid Capture/exome sequencing

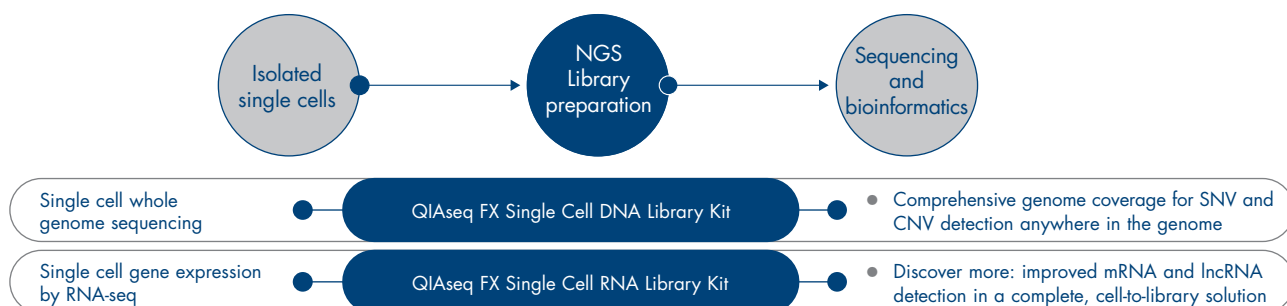


* From other manufacturers

Complete workflows for targeted sequencing



Single cell sequencing





Count unique transcripts, not PCR duplicates – enter the age of digital RNAseq for gene expression analysis

PCR duplicates and amplification bias can lead to inaccurate gene expression results using current RNA sequencing approaches. To address these technical limitations, we have developed **QIAseq Targeted RNA Panels** as a Sample to Insight® solution for quantitative gene expression profiling on any Illumina® or Ion Torrent™ NGS instrument.

QIAseq Targeted RNA Panels are the first gene expression kits to use unique molecular barcodes that tag each individual gene transcript prior to any amplification steps. By counting these molecular barcodes, instead of just the number of reads per transcript, unique gene transcripts are accurately accounted for. The resulting data reflects the original ratios

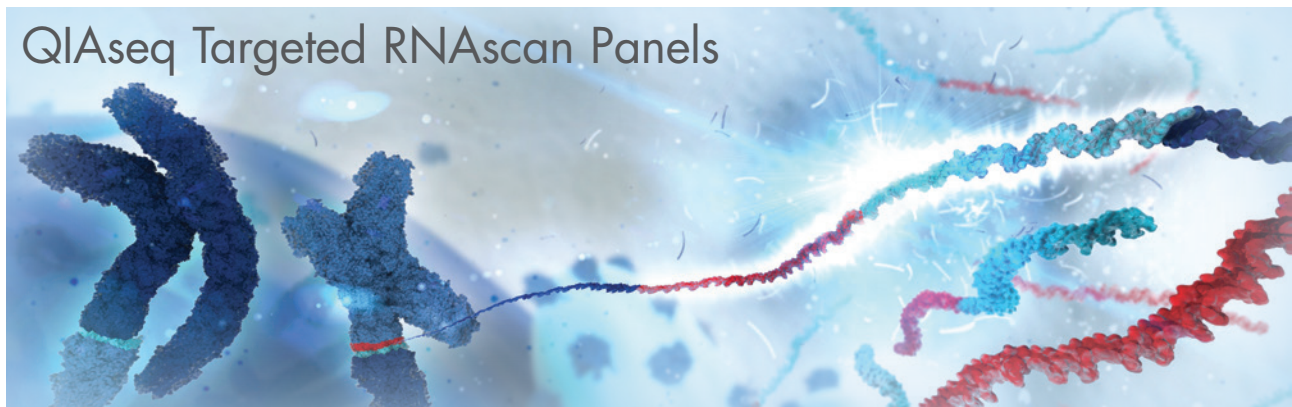
of RNA expression levels. **QIAseq Targeted RNA Panels** use a simple library construction workflow which allows you to have sequence ready libraries in less than 1 day. Starting from 25 ng of RNA, you can quantitatively measure up to 1000 mRNA, lncRNA or mt-RNA transcripts. For ultimate flexibility and customization, you can define your own content, and build your own unique panel using the custom builder at GeneGlobe.

Overwhelmed by downstream RNA-seq data analysis? **QIAseq Targeted RNA Panels** provide automated, free-of-charge online solutions that make data analysis easier than ever! Go from sequencing data to biologically relevant pathway analysis with our cloud-based solution.

QIAseq Targeted RNA Panels

| What's new? | How does this benefit you? |
|---|---|
| Unique molecular barcodes | Eliminate PCR duplicates and amplification bias for accurate quantitative gene expression results using NGS |
| Less than 25 ng of RNA required for up to 1000 targets | Preserve precious RNA samples for high-throughput gene expression analysis without amplification |
| 6 hours from extracted RNA sample to sequencing-ready libraries | Single day sample preparation leads to final results in days instead of weeks |
| Pathway or disease-related gene content for over 170 panels | Content to fit many applications which can be customized for each project |
| Online custom panel builder | Build your own custom panels to modify and expand as your studies change |
| Integrated bioinformatics pipeline | No need for specialized bioinformatics expertise |

Discover digital RNA-seq at www.qiagen.com/QIAseq-Targeted-RNA



Novel approach to detect and quantify fusion genes

A fusion gene is a hybrid gene formed when two separate genes fuse or become juxtaposed. About 20% of global cancer morbidity is a result of translocations and gene fusions. Improved detection and characterization of fusion genes will play a critical role in elucidating cancer mechanisms and aid in the development of targeted drugs.

Recent advances in NGS, especially in RNA sequencing technology and bioinformatics, have revolutionized the detection and quantification of fusion genes. Targeted RNA-seq is a method of choice when looking for highly relevant information instead of having to sort through large amounts of data after NGS.

PCR duplicates are a major issue in targeted RNA sequencing. Through PCR amplification, they turn unique RNA molecules into identical RNA molecules that cannot be distinguished from each other. This, in turn, results in the inability to confidently detect gene fusions.

QIAseq Targeted RNAscan Panels use digital sequencing principles such as incorporating molecular barcodes into the starting RNA material before any amplification takes place, thereby preserving the uniqueness of the starting RNA molecules. By taking advantage of the QIAseq Targeted RNAscan Panel, you can confidently overcome the issues of not only PCR duplicates but also amplification bias in your research.

QIAseq Targeted RNAscan Panel (cat. nos. 333602, 333605, 333625 and 333645)

| What's new? | How does this benefit you? |
|------------------------------------|--|
| Molecular barcoding of transcripts | Does not count PCR duplicates, accurate quantification of fusion transcripts, higher sensitivity |
| Single primer extension | Detect both known and novel fusion genes |
| Single pool of primers | Requires low amount of RNA |
| Short library fragments | Suitable for low yield, poor quality RNA samples |

Find out more about quantifying fusion genes at
www.qiagen.com/QIAseq-Targeted-RNAscan



Distinguish between errors and low-frequency mutations

Targeted DNA sequencing with panels is a powerful approach to detect low-frequency variants. However, if you are using many of the widely used targeted DNA sequencing methods out there, you are probably faced with one of their main drawbacks: PCR duplication during your amplification steps. Because of these PCR duplicates, all DNA fragments look exactly the same, making it impossible to distinguish between a unique DNA molecule or a duplicate. This limits your ability to confidently detect low-frequency DNA variants.

QIAGEN has been hard at work to help you distinguish whether your results are random fluctuations in your data or a truly novel insight that can help you propel your research

to a new level. The solution is **QIAseq Targeted DNA Panels**. These allow you to detect low-frequency variants to overcome issues associated with PCR duplicates such as false positives and library bias with confidence. QIAGEN's ingenious solution is based on the use of molecular barcodes and allows you to take advantage of a digital sequencing approach. With molecular barcodes, each unique DNA molecule is barcoded before any amplification takes place to accurately detect and remove PCR duplicates. Using **QIAseq Targeted DNA Panels**, you can now increase the sensitivity of your panel to confidently detect low-frequency DNA variants and increase your chance of making that next ground-breaking discovery!

QIAseq Targeted DNA panels (cat. nos. 333502, 333505, 333512, 333515, 333525, 333535 and 333545)

| What's new? | How does this benefit you? |
|-------------------------------------|--|
| Incorporation of molecular barcodes | Remove PCR duplicates to increase sensitivity of the panel |
| Single pool of primers | Reduce amount of input DNA |
| Single primer extension | Enhanced uniformity of enrichment and sequencing |
| Unique enrichment buffer | Coverage of GC-rich regions |

Start your discovery at www.qiagen.com/QIAseq-Targeted-DNA



Speed meets convenience – the latest innovation in library prep for targeted resequencing

The faster you can prepare high-quality NGS libraries, the faster you can proceed with sequencing your sample and uncovering insights that accelerate your understanding of its underlying biology. Traditional library prep can be laborious, taking anything from 2 to 3 hours to accomplish. The new **QIAseq 1-Step Amplicon Library Kit** offers a faster, more efficient 30-minute procedure that combines end-repair and ligation, allowing you to prepare high-quality, artifact-free libraries, ready for use on any Illumina platform!

The **QIAseq 1-Step Amplicon Library Kit** provides a simple, automatable one-tube solution that reliably converts PCR amplicons from target enrichment panels or other multiplexed PCR products into sequencer-ready libraries for NGS. For maximum convenience, reactions can be set up at room temperature and require minimal hands-on time or liquid transfers, reducing the risk of errors or contamination. Take advantage of the fastest library prep for targeted resequencing and amplicon sequencing applications and save time so you can focus on sequencing and data analysis!

QIAseq 1-Step Amplicon Library Kits (12) and (96) (cat. nos. 180412 and 180415, respectively)

| What's new? | How does this benefit you? |
|---|---|
| One-tube, benchtop library prep from PCR products in just 30 minutes | Save time with targeted resequencing and amplicon sequencing applications |
| One-reaction, room temperature setup | Maximum convenience and efficiency, with the potential for automation |
| High-quality, artifact-free libraries, ready for use on any Illumina NGS platform | Even representation of input amplicons; excellent evenness and specificity enables accurate variant detection |
| Compatible with any gene panel or PCR product, with just 1 ng input DNA | Increased flexibility; optionally PCR-free for reduced risk of sequence duplicates or PCR bias |
| Single-use barcoded Illumina adapters | Reduction in contamination potential and handling errors |

Discover the fastest library prep at www.qiagen.com/QIAseq-1Step-Amplicon



QIAseq Ultralow Input Library Kit

Limited samples, unlimited insights – high-quality library prep from just 10 pg input DNA!

If you're working with challenging samples such as FFPE material, cfDNA or tumor biopsies, the amount of DNA you retrieve can impede your progress in NGS applications. It doesn't have to be this way. Accelerate your quest for answers with the help of our attractive new solution for low-input DNA library prep – the **QIAseq Ultralow Input Library Kit!**

The **QIAseq Ultralow Input Library Kit** provides a streamlined solution for high-quality NGS library prep from as little as 10 pg DNA. Due to its optimized chemistry, high-diversity libraries with a <10% duplication rate can be prepared. For additional convenience, the kit can be readily automated, further accelerating the library preparation process and saving you valuable time that you can dedicate to sequencing and data analysis to gain actionable insights.

QIAseq Ultralow Input Library Kit (cat. nos. 180492 and 180495)

| What's new? | How does this benefit you? |
|---|---|
| Ultra-efficient chemistry for limited DNA samples | NGS-ready libraries from just 10 pg input |
| Optimized protocol for cfDNA | Save time and get results faster in liquid biopsy and NIPT applications |
| Automation friendly | Greater convenience, flexibility and time savings, as well as standardization |
| High genetic diversity (<10% duplicate rate) | Reduced bias for greater coverage and uniformity |

Discover the kit at www.qiagen.com/QIAseq-ULI-DNA

QIAseq cfDNA All-in-One Kit



Designed for cfDNA from blood to NGS library to maximize your discoveries

The diagnostic promise of cell-free DNA (cfDNA) analysis from a liquid biopsy sample or non-invasive prenatal testing (NIPT) is highly recognized in the scientific community. But, if you are struggling with low signal-to-noise ratios, you can now be reassured knowing that QIAGEN is offering a solution based on a highly efficient and sensitive analysis system.

The **QIAseq cfDNA All-in-One Kit** is the first solution on the market designed from the ground up for cfDNA. Combining

highly efficient chemistries for cfDNA extraction and NGS library preparation, it ensures optimal sample conversion at every step in your workflow and maximizes NGS library yields. Get the most out of your cfDNA sample and increase mutation detection sensitivity so that you can find even the rarest of variants in your experiments. Barcoded adapters for either Illumina or Ion Torrent sequencers in convenient and automation-friendly plate format, are included in the kit. Gain confidence in your cfDNA results and open up new discoveries with the **QIAseq cfDNA All-in-One Kit!**

QIAseq cfDNA All-in-One Kit (cat. nos. 180025, 180023, 180015 and 180043)

| What's new? | How does this benefit you? |
|--|--|
| Protocol designed from the ground up for cfDNA | Optimal conversion of cfDNA at every step from blood to plasma is ensured to maximize NGS yields |
| Flexible cfDNA input range of library prep allows you to go directly from eluant to library prep without sample quantification | Eliminate a traditional roadblock in the cfDNA workflow and minimize sample loss |
| Highly efficient adapter ligation chemistry | Superior cfDNA conversion rate to detect even rarest variants |
| Enzyme and buffer formulations optimized for cfDNA | PCR-free libraries from as little as 10ng cfDNA minimize sequencing bias |
| Proprietary all-in-one library prep chemistry for Ion Torrent | Save time in your daily lab work and prepare NGS libraries for any Ion Torrent sequencer in 35 minutes |

Start your discovery at www.qiagen.com/QIAseq-cfDNA



High-quality whole genome libraries – no shearing required!

Go from DNA to high-quality libraries, ready for use on any Illumina NGS platform, in just 2.5 hours without the need for additional instrumentation or expensive glassware using the new **QIAseq FX DNA Library Kit**.

QIAseq FX incorporates one-step enzymatic fragmentation, end-repair and A-addition into a simple, three-reaction protocol for rapid manual library preparation or straightforward liquid handling automation for any whole genome sequencing or hybrid capture sequencing library prep workflow.

Start from any purified genomic DNA sample ranging from 1 ng – 1 µg and generate any custom DNA fragment

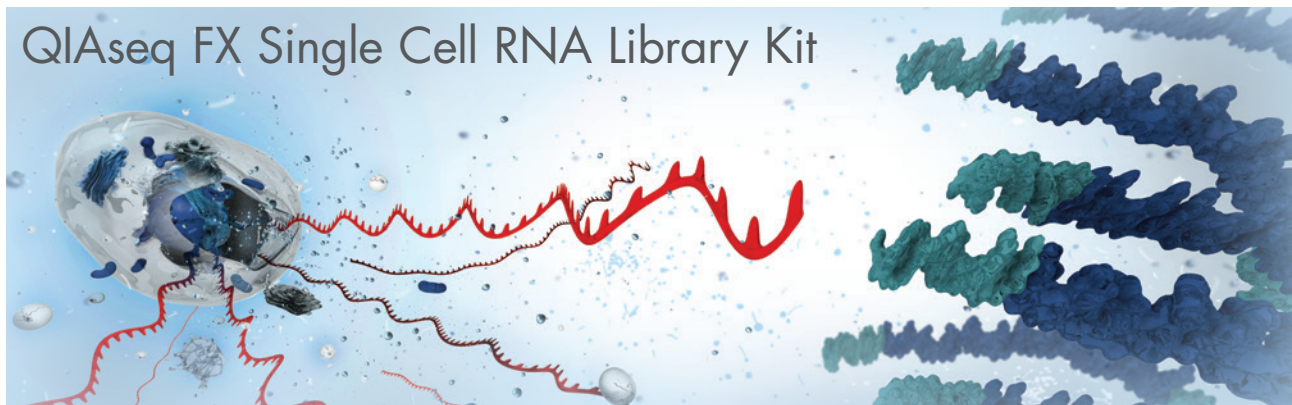
size compatible with Illumina sequencing platforms with no additional equipment beyond a standard laboratory thermocycler. Rely on highly random, low G/C bias enzymatic fragmentation that outperforms tagmentation-based methods. This will ensure that your genomic targets are evenly represented for high-quality data quality similar to that achieved by mechanical shearing.

Fully functional, dual-barcoded adapters in convenient 24- and 96-well plates enable 100% PCR-free libraries in under two hours, or, use the optional high-fidelity library amplification reagents to increase total library yield while introducing minimal PCR bias.

QIAseq FX DNA Library Kit (cat. nos. 180475 and 180473)

| What's new? | How does this benefit you? |
|---|---|
| FX Fragmentation technology | Customizable fragment size and flexible input amount for library quality that outperforms other enzymatic methods |
| Plate-format dual-barcoded adapters | Easy automation and support for 96- or 24-plex multiplexed sequencing |
| Optional library amplification reagents | Flexible protocol to support PCR-free workflows or high-fidelity library amplification in a single kit |

Discover gold-standard whole genome libraries with an all-enzymatic workflow at www.qiagen.com/QIAseq-FX



Discover higher-diversity mRNA-seq libraries from a single cell with the only library preparation kit on the market to capture both mRNA and lncRNA

The transcriptome of a cell is undoubtedly dynamic. It can reflect a cell's function, type, stage and even its response to intrinsic and external factors, such as signals or stressors. So how can you truly capture that type of detailed information in your studies? Only at a single cell level, can you eliminate the biological noise that is inherent to standard gene expression analysis – providing you with the key insights you'll need for a deeper understanding of transcription dynamics.

The **QIAseq FX Single Cell RNA Library Kit** is an end-to-end library preparation solution for RNA-seq from single cells or low amounts of RNA. The kit includes all reagents you'll need for cell lysis, reverse transcription, cDNA amplification and PCR-free NGS library preparation. In only 5.5 hours with

approximately 1 hour of hands-on-time, you can produce high-quality NGS libraries as well as a tube of amplified cDNA that can be stored for follow-up experiments. Discover the transcriptome in greater detail with best-in-class transcript detection, and analyze both mRNA and long non-coding RNAs in a single dataset. The kit delivers excellent reproducibility and accuracy and is completely PCR-free to reduce bias and eliminate PCR duplicates, while ensuring an efficient use of sequencing depth. The kit is ideally suited to allow you to perform transcript discovery and differential expression from single eukaryotic cells, studies in inter-cellular heterogeneity, RNA-seq from limited amounts of difficult-to-obtain samples and studies in infectious diseases.

QIAseq FX Single Cell RNA Library kit (cat. nos. 180733 and 180735)

| What's new? | How does this benefit you? |
|---------------------------------|---|
| Higher library complexity | Discover a greater number of transcripts in same sequencing run |
| Effectively sequences long RNAs | Captures both mRNA and lncRNA in a single experiment |
| Higher amplification fidelity | Less sequencing errors, ideal for virus research |
| PCR-free workflow | Eliminate PCR bias or duplicate reads arising from PCR |
| Generates more amplified cDNA | Enables follow-up and confirmatory experiments |

Start your discovery at www.qiagen.com/QIAseq-FX-SC-RNA



PCR-free NGS libraries from single cell in only 3.5 hours! Try the new QIAseq FX Single Cell DNA Library Kit

Somatic genome variations are the cause of many diseases including cancer, autoimmune disease, brain disorders and more. Single cell next-generation sequencing enables cell-by-cell analysis of the genome, including the detection of single nucleotide variants, aneuploidy, copy number variations and structural variants for tumor or cell profiling and lineage analysis. Our streamlined PCR-free workflow takes you from one single cell (mammalian or bacterial) to a high-quality NGS library in just 3.5 hours!

The kit includes all reagents you'll need for cell lysis, whole genome amplification, enzymatic DNA fragmentation and PCR-free NGS library preparation. It delivers a high-quality,

artifact-free NGS library and μg levels of amplified gDNA for follow-up studies and confirmatory testing. Discover polymorphisms and structural variants in the genome no matter where they are with industry-leading genome coverage, and have greater confidence in your results with high-fidelity whole genome amplification.

The kit is ideally suited to analyze aneuploidy and sub-chromosomal copy number variation, sequence variation in single cells, intra-cellular genome heterogeneity, whole genome sequencing from rare samples and for new types of experiments such as low-pass consensus variant calling and de novo genome assembly from unculturable bacteria.

QIAseq FX Single Cell DNA Library Kit (cat. nos. 180713 and 180715)

| What's new? | How does this benefit you? |
|--|---|
| Comprehensive genome coverage | Low locus drop-out, suitable for low-pass consensus variant calling or CNV detection, and perfect for de novo bacterial genome assembly |
| Ultra-high amplification fidelity | Low sequence errors and false positives, high confidence in variant calling |
| PCR-free protocol | No PCR duplicates introduced, better coverage especially in regions with high or low GC content |
| Compatible with eukaryotic and bacterial cells | Perfect for metagenomics and de novo sequencing |
| Single-use adapter plates available in 24- and 96-reaction formats | Reduced chance of cross-contamination, regardless of your lab's throughput |

Start your discovery at www.qiagen.com/QIAseq-FX-SC-DNA

Quality input, quality output – NGS quality control to help you get the most out of your NGS run

NGS can be expensive and time consuming if you don't have sufficient amounts of high-quality library for definitive data acquisition. Accurate and sensitive quantification of DNA or RNA libraries can help you streamline your

NGS workflow and use resources more effectively. **QIAseq Library Quant Kits** offer a ready-to-go solution for reliable qPCR-based quantification. For increased flexibility, you can choose either an array or assay format.

QIAseq Library Quant Assay Kit (cat. no. 333314) and QIAseq Library Quant Array Kit (cat. no. 333304)

| What's new? | How does this benefit you? |
|--|---|
| Ready-to-use system for accurate quantification of RNA and DNA libraries | Get the most out of your NGS run |
| Available in array and assay format | Greater flexibility and convenience |
| Optimized solution based on qPCR | Increased accuracy and sensitivity, as well as time savings |

Discover more at www.qiagen.com/QIAseq-Library-Quant

Even if you have low-quality DNA samples, there's still hope! **QIAseq DNA QuantiMIZE Kits** rescue poor-quality DNA samples for NGS analysis by guiding the DNA input amount and number of cycles for target enrichment. The kit uses 2 qPCR assays to quantify and qualify amplifiable amounts of DNA

in a sample prior to NGS. Whether you're working with FFPE samples or fine-needle aspirates, **QIAseq DNA QuantiMIZE Kits** improve the likelihood of a successful NGS run by not only quantifying amplifiable DNA, but by also offering a cost-effective way to maximize your sequencer's output.

QIAseq DNA QuantiMIZE Array Kit (cat. no. 333404) and QIAseq DNA QuantiMIZE Assay Kit (cat. no. 333414)

| What's new? | How does this benefit you? |
|---|--|
| Provides 2 qPCR assays dispensed onto arrays or in individual tubes | No need for assay design – each assay interrogates 20 genomic loci to determine amounts of amplifiable DNA in biological samples |
| Quantifies and qualifies DNA that is amplifiable by PCR | Rescue low-quality samples for NGS analysis |
| Guides optimization of targeted enrichment conditions | Streamlines experiments for faster NGS data acquisition |
| Serial dilutions not required | Greater convenience and reliability |

Find out how to rescue low-quality DNA samples at www.qiagen.com/QIAseq-QuantiMIZE



Your vision, our expertise – NGS service for QIAseq targeted DNA, miRNA and fusion gene analysis

Are challenging samples and complicated library construction slowing down your NGS project? If so, consider sending your samples to QIAGEN's life science service core!

Our solutions are tailored to each individual project. Whether you are looking at miRNA, gene expression, fusion genes or DNA variants, we have targeted NGS panels that can be customized to your specific biological question. Do you need qPCR validation, or whole transcriptome sequencing to start?

We also offer these, and other services, to compliment any NGS project from Sample to Insight!

Our service cores located in Frederick, Maryland USA and Hilden, Germany offer you the unique ability to access samples from around the world to include in your studies, with the confidence that your results will be of the high quality that you expect from QIAGEN.

NGS Service & Analysis

| What's new? | How does this benefit you? |
|--|--|
| Get instant access to QIAGEN's Sample to Insight expertise for NGS applications | Save time learning new protocols or waiting for NGS equipment with QIAGEN's NGS workflows |
| One PO number for the entire project | Greater convenience and ease of ordering |
| Custom project design using standard QIAGEN kits | Increased flexibility and proven quality and reliability with QIAGEN's optimized Sample to Insight workflows |
| Rely on QIAGEN's global organizational infrastructure for large-scale collaborative research | Support with large collaborations involving multiple samples from multiple locations |

For your next big Sample to Insight project, contact us at LifeScienceService_request@qiagen.com

Customer highlights

Library preparation using cell-free DNA – NGS with challenging samples

OURUI is a newly founded Diagnostics Company based in Shantou, China. Aiming to enter the market for non-invasive prenatal testing (NIPT) but with little experience in this field, they were looking for a professional partner to set up the complete test. QIAGEN's Sample to Insight library prep solutions for Illumina sequencers offered a simple, streamlined and standardized workflow that allowed

OURUI to significantly accelerate the implementation process. Today, OURUI uses QIAGEN's Sample to Insight products for all steps of the NIPT workflow – from DNA extraction to library prep. Valuing the excellent performance and stability of our NGS library prep kits and a direct technical service channel, OURUI is planning to expand its NIPT business in the near future.

QIAGEN's library preparation methods in metagenomics

»QIAGEN has been a great partner in the whole process from the DNA extraction to library prep all the way to data analysis. I have been using QIAGEN since I was a graduate student. I am excited to use these products for metagenomic and microbiome research.«

Christopher Mason, Ph.D.
Associate Professor, Weill Cornell Medical College, New York, USA

Listen to the full interview with Christopher Mason on his metagenomic research:

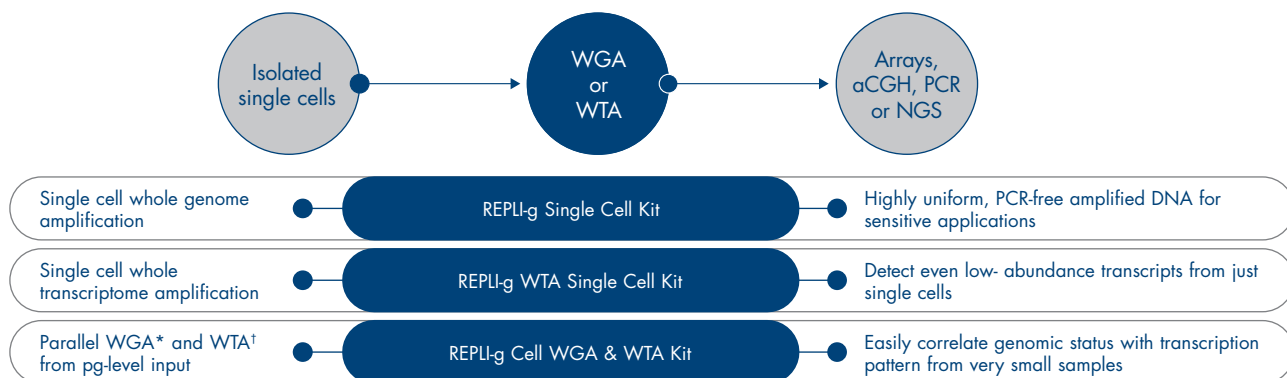
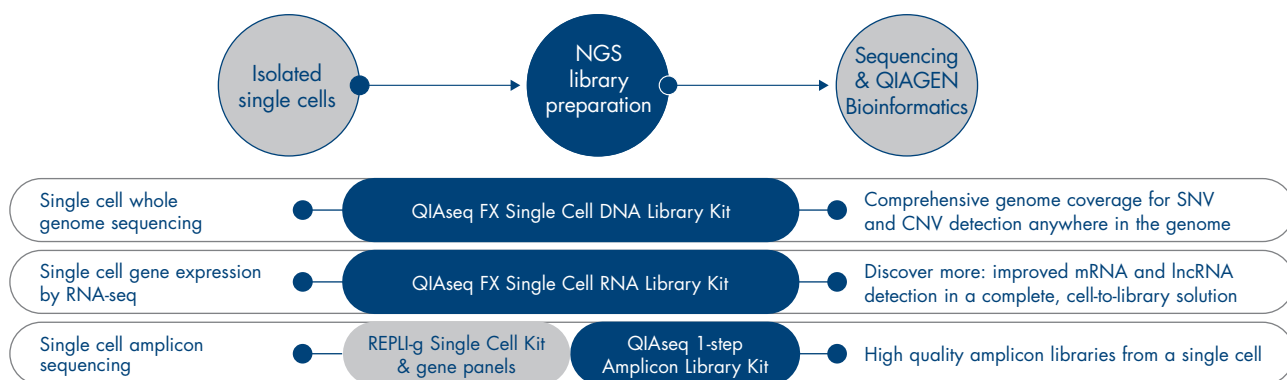
https://www.youtube.com/watch?v=HyqvMEqmYk&index=12&list=PLnVL-JBxB4YvLhIW9qn6g_z-VONCZvJFu

Read the publication by Christopher Mason's lab on metagenomics research:

Afshinnekoo, E. et al. (2015) Geospatial Resolution of Human and Bacterial Diversity with City-Scale Metagenomics. Cell Systems Jul 29, 72-87

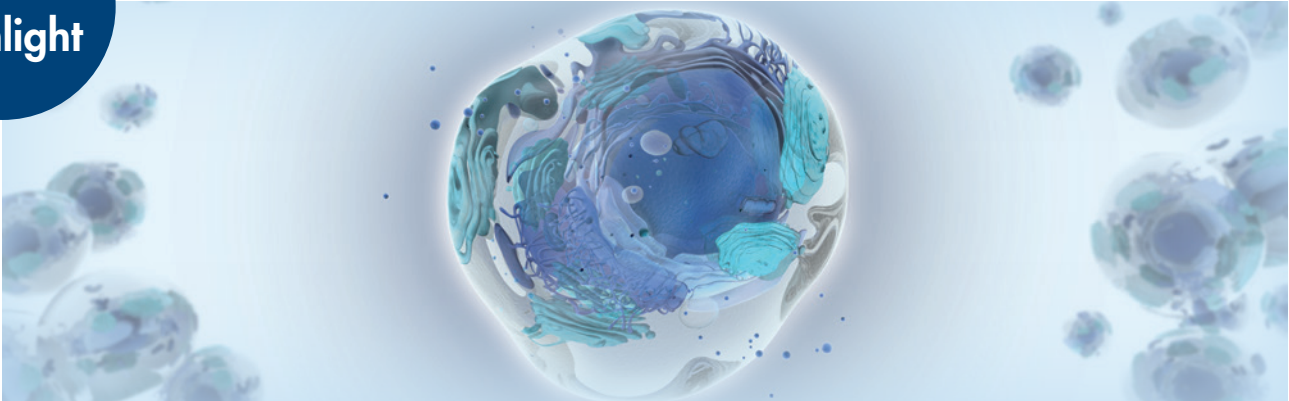
Single cells, multiple details – decipher the differences!

Every cell is unique. QIAGEN's QIAseq and REPLI-g® technology accelerates single cell analysis in diverse research areas, from oncology, immunology and microbiology to neuroscience, stem cell research and developmental biology, allowing you to access the smallest dimensions of biological research. Examine the genomic and transcriptomic differences between cells and uncover the heterogeneity in your sample for new biological insights with the help of QIAGEN's single cell solutions.



* Whole genome amplification.
 † Whole transcriptome amplification.

www.qiagen.com/SingleCellAnalysis



Two clever ideas to analyze rare cells in your samples

When analyzing bulk samples using whole genome sequencing (WGS) or whole exome sequencing (WES), the detection of low-frequency (subclonal) variants is commonly achieved by increasing sequencing depth. This strategy becomes prohibitively expensive when trying to capture mutations in rare cells present at 1% or lower fractions.

Two recent publications from Zhang et al. present clever ideas utilizing single-cell sequencing to overcome this challenge (1) (3). In a recent study (1), the authors selected individual cells based on live-cell imaging and performed single-cell whole-genome sequencing on these rare cells. Using this approach, called “LookSeq”, the authors identified the first molecular mechanism of chromothripsis – a new mutational phenomenon in cancer. For rare cells in cancer patients, such as circulating tumor cells (2), a low-pass census-based strategy makes accurate variant detection in these cells feasible and affordable (3). The census-based strategy described in this paper relies on sequencing many

single cells at low sequencing depth. Since the most interesting genetic variants are shared among these cells due to their common lineage, a census-based strategy can be used to combine data from multiple single cells to derive a mutational profile of the sample.

Using single-cell sequencing instead of bulk sample analysis, as described in their publications, opens a new dimension for comprehensive analysis of rare cells that seed metastases or drug-resistance.

Whole genome amplification (WGA) is a critical step for successful single-cell sequencing. An amplification method with highly uniform genome coverage is a prerequisite for success. The superior performance of QIAGEN’s **REPLI-g Single Cell Kit** has been critical for this milestone research. “...we achieved the best overall coverage uniformity with this latest version of REPLI-g from Qiagen [REPLI-g Single Cell Kit]...” (1)

1) Zhang, C.-Z. et al. (2015) Chromothripsis from DNA damage in micronuclei. *Nature* 522, 179–184.

2) Lohr, J. G. et al. (2014) Whole-exome sequencing of circulating tumor cells provides a window into metastatic prostate cancer. *Nature biotechnology* 32, 479–484.

3) Zhang, C. Z. et al. (2015) Calibrating genomic and allelic coverage bias in single-cell sequencing. *Nature Commun* 6, 6822.

Ordering Information

| Product | Contents | Cat. no. |
|--|---|----------|
| Digital RNA sequencing | | |
| QIAseq Targeted RNA Panel (12) | Kit containing reagents for first strand synthesis, molecular tagging, gene-specific amplification and library construction for targeted RNA sequencing; fixed panel for 12 samples | 333002 |
| QIAseq Targeted RNA Panel (96) | Kit containing reagents for first strand synthesis, molecular tagging, gene-specific amplification and library construction for targeted RNA sequencing; fixed panel for 96 samples | 333005 |
| QIAseq Targeted RNA Extended Panel (12) | Kit containing reagents for first strand synthesis, molecular tagging, gene-specific amplification and library construction for targeted RNA sequencing; extended panel for 12 samples | 333012 |
| QIAseq Targeted RNA Extended Panel (96) | Kit containing reagents for first strand synthesis, molecular tagging, gene-specific amplification and library construction for targeted RNA sequencing; extended panel for 96 samples | 333015 |
| QIAseq Targeted RNA Custom Panel (12) | Kit containing reagents for first strand synthesis, molecular tagging, gene-specific amplification and library construction for targeted RNA sequencing; customized panel for 12 samples | 333022 |
| QIAseq Targeted RNA Custom Panel (96) | Kit containing reagents for first strand synthesis, molecular tagging, gene-specific amplification and library construction for targeted RNA sequencing; customized panel for 96 samples | 333025 |
| QIAseq Targeted RNA Custom Panel (384) | Kit containing reagents for first strand synthesis, molecular tagging, gene-specific amplification and library construction for targeted RNA sequencing; customized panel for 384 samples | 333027 |
| QIAseq Targeted RNA 96-Index I (384) | Box containing oligos, enough for a total of 384 samples, for indexing up to 96 samples for targeted RNA sequencing on Illumina platforms | 333117 |
| QIAseq Targeted RNA 96-Index HT I (384) | Box containing oligos in arrays, enough for a total of 384 samples, for indexing up to 96 samples for targeted RNA sequencing on Illumina platforms | 333127 |
| QIAseq Targeted RNA 12-Index L (48) | Box containing oligos, enough for a total of 48 samples, for indexing up to 12 samples for targeted RNA sequencing on Ion Torrent platforms | 333214 |
| QIAseq Targeted RNA 96-Index HT L (384) | Box containing oligos in arrays, enough for a total of 384 samples, for indexing up to 96 samples for targeted RNA sequencing on Ion Torrent platforms | 333217 |
| QIAseq Targeted RNA Read 1 Primer I (48) | Kit containing primers necessary for sequencing RNA libraries generated by the QIAseq targeted RNA panels on MiSeq® platforms; enough for 48 sequencing runs | 333514 |



Ordering Information

| Product | Contents | Cat. no. |
|---|--|----------|
| Fusion gene detection | | |
| QIAseq Targeted RNAscan Panel (12) | Kit containing ALL reagents (except indexes) for targeted fusion sequencing; fixed panel for 12 samples; less than 100 fusions | 333602 |
| QIAseq Targeted RNAscan Panel (96) | Kit containing ALL reagents (except indexes) for targeted fusion sequencing; fixed panel for 96 samples; less than 100 fusions | 333605 |
| QIAseq Targeted RNAscan HC Panel (12) | Kit containing ALL reagents (except indexes) for targeted fusion sequencing; fixed panel for 12 samples; more than 100 fusions | 333612 |
| QIAseq Targeted RNAscan HC Panel (96) | Kit containing ALL reagents (except indexes) for targeted fusion sequencing; fixed panel for 96 samples; more than 100 fusions | 333615 |
| QIAseq Targeted RNAscan Custom Panel | Kit containing ALL reagents (except indexes) for targeted fusion sequencing; Custom panel for 96 samples | 333625 |
| QIAseq Targeted RNAscan Extended Panel | Kit containing ALL reagents (except indexes) for targeted fusion sequencing; Extended panel for 96 samples | 333645 |
| Digital DNA sequencing | | |
| QIAseq Targeted DNA Panel (12) | Kit containing ALL reagents (except indexes) for targeted DNA sequencing; fixed panel for 12 samples; less than 100 genes | 333502 |
| QIAseq Targeted DNA Panel (96) | Kit containing ALL reagents (except indexes) for targeted DNA sequencing; fixed panel for 96 samples; less than 100 genes | 333505 |
| QIAseq Targeted DNA HC Panel (12) | Kit containing ALL reagents (except indexes) for targeted DNA sequencing; fixed panel for 12 samples; more than 100 genes | 333512 |
| QIAseq Targeted DNA HC Panel (96) | Kit containing ALL reagents (except indexes) for targeted DNA sequencing; fixed panel for 96 samples; more than 100 genes | 333515 |
| QIAseq Targeted DNA Custom Panel (96) | Kit containing ALL reagents (except indexes) for targeted DNA sequencing; Custom panel for 96 samples | 333525 |
| QIAseq Targeted DNA Booster Panel (96) | Pool of primers used in combination with either cataloged or custom panels | 333535 |
| QIAseq Targeted DNA Extended Panel (96) | Kit containing ALL reagents (except indexes) for targeted DNA sequencing; Extended panel for 96 samples | 333545 |

| Product | Contents | Cat. no. |
|---|--|----------|
| DNA library prep for targeted resequencing | | |
| QIAseq 1-Step Amplicon Library Kit (12) | For 12 reactions: 1-Step Amplicon Enzyme Mix, 4x 1-Step Amplicon Buffer, Primer Mix Illumina Library Amp, HiFi PCR Master Mix, RNase-Free Water | 180412 |
| QIAseq 1-Step Amplicon Library Kit (96) | For 96 reactions: 1-Step Amplicon Enzyme Mix, 4x 1-Step Amplicon Buffer, Adapter Plate 96-plex Illumina, Primer Mix Illumina Library Amp, HiFi PCR Master Mix, RNase-Free Water | 180415 |
| High-quality library prep from limited DNA samples | | |
| QIAseq Ultralow Input Library Kit (12) | For 12 reactions: Buffers and reagents for Ultralow Input End Polishing, Ultralow Input Ligation and HiFi library amplification | 180492 |
| QIAseq Ultralow Input Library Kit (96) | For 96 reactions: Buffers and reagents for Ultralow Input End Polishing, Ultralow Input Ligation and HiFi library amplification. Includes 96-plex Adapter Plate with individually pierceable foil sealed wells. For use with Illumina instruments. | 180495 |
| cfDNA library prep | | |
| QIAseq cfDNA All-in-One Kit (96) | For 96 reactions on Illumina sequencers: QIAamp Mini Columns, tubes, reagents and buffers for cfDNA extraction for NGS. Enzymes and buffers for cfDNA library prep, Illumina Adapter Plate 96-plex, Illumina Library Amplification Primer and PCR Master Mix. | 180025 |
| QIAseq cfDNA All-in-One Kit (24) | For 24 reactions on Illumina sequencers: QIAamp Mini Columns, tubes, reagents and buffers for cfDNA extraction for NGS. Enzymes and buffers for cfDNA library prep, Illumina Adapter Plate 24-plex, Illumina Library Amplification Primer and PCR Master Mix. | 180023 |
| QIAseq cfDNA Library Kit (96) | For 96 reactions on Illumina sequencers: enzymes and buffers for cfDNA library prep, Illumina Adapter Plate 96-plex, Illumina Library Amplification Primer and PCR Master Mix | 180015 |
| QIAseq cfDNA All-in-One T Kit (24) | For 24 reactions on Ion Torrent sequencers: QIAamp Mini Columns, tubes, reagents and buffers for cfDNA extraction for NGS. Enzymes and buffers for cfDNA library prep, Ion Torrent Adapter Plate 24-plex, Ion Torrent Library Amplification Primer and PCR Master Mix. | 180043 |



Ordering Information

| Product | Contents | Cat. no. |
|---|---|----------|
| Whole genome/Hybrid Capture sequencing | | |
| QIAseq FX DNA Library Kit (24) | For 24 reactions: Buffers and reagents for DNA fragmentation, end-repair, A-addition, ligation and library amplification; for use with Illumina instruments; includes a plate containing 24 adapters with different barcodes (pierceable foil seal allowing usage of defined parts of plate) | 180473 |
| QIAseq FX DNA Library Kit (96) | For 96 reactions: One-tube enzymatic fragmentation, end repair and A-addition, plus ligation and library amplification reagents; for use with Illumina instruments; includes a plate containing 96 adapters with different barcodes (pierceable foil seal allowing usage of defined parts of plate) | 180475 |
| DNA and RNA library prep from single cells | | |
| QIAseq FX Single Cell RNA Library Kit (24) | REPLI-g SensiPhi DNA Polymerase, Buffers and Reagents for 24 x 60 µl whole transcriptome amplification reactions and subsequent enzymatic fragmentation end-repair, A-addition and ligation – for use with Illumina instruments | 180733 |
| QIAseq FX Single Cell RNA Library Kit (96) | REPLI-g SensiPhi DNA Polymerase, Buffers and Reagents for 96 x 60 µl whole transcriptome amplification reactions and subsequent enzymatic fragmentation end-repair, A-addition and ligation – for use with Illumina instruments | 180735 |
| QIAseq FX Single Cell DNA Library Kit (96) | For 96 reactions: Buffers and reagents for cell lysis, whole genome amplification and library preparation including DNA fragmentation, end-repair and adapter ligation. Includes a plate containing 96 barcoded adapters for use with Illumina instruments. | 180715 |
| QIAseq FX Single Cell DNA Library Kit (24) | For 24 reactions: Buffers and reagents for cell lysis, whole genome amplification, and library preparation including DNA fragmentation, end-repair and adapter ligation. Includes a plate containing 24 barcoded adapters for use with Illumina instruments. | 180713 |

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