Exploring new frontiers with next-generation sequencing

Pushing the limits of discovery

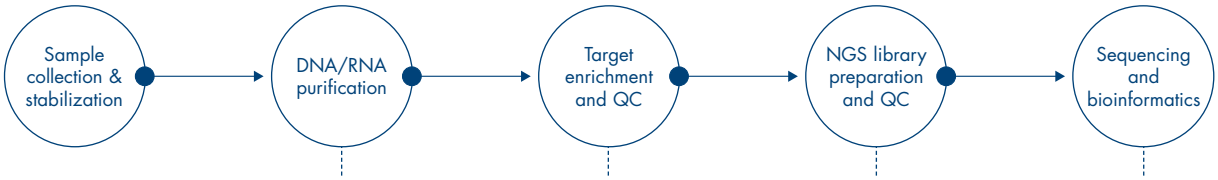
Next-generation sequencing (NGS) is being utilized for numerous new and exciting applications, such as single cell analysis, liquid biopsy research, circulating-free DNA (cfDNA) studies, metagenomics and targeted sequencing. Whether you're studying single cells or populations, selected genes or whole 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

QIAGEN

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.



DNA purification
- QIAseq FX Single Cell DNA Library Kit
- QIAseq cfDNA All-in-One Kit

RNA purification
- QIAseq FX Single Cell RNA Library Kit

Target enrichment
- QIAseq Targeted RNA Panels
- QIAseq Targeted DNA Panels
- QIAseq Targeted RNAscan Panels
- NGS Service & Analysis

QC
- QIAseq DNA QuantiMIZE Kits

DNA-seq library preparation
- QIAseq 1-Step Amplicon Library Kit
- QIAseq Ultralow Input Library Kit
- QIAseq FX DNA Library Kit
- QIAseq FX Single Cell DNA Library Kit
- QIAseq cfDNA All-in-One Kit

RNA-seq library preparation
- QIAseq FX Single Cell RNA Library Kit

Library QC
- QIAseq Library Quant Kits

Data analysis
- NGS Service & Analysis

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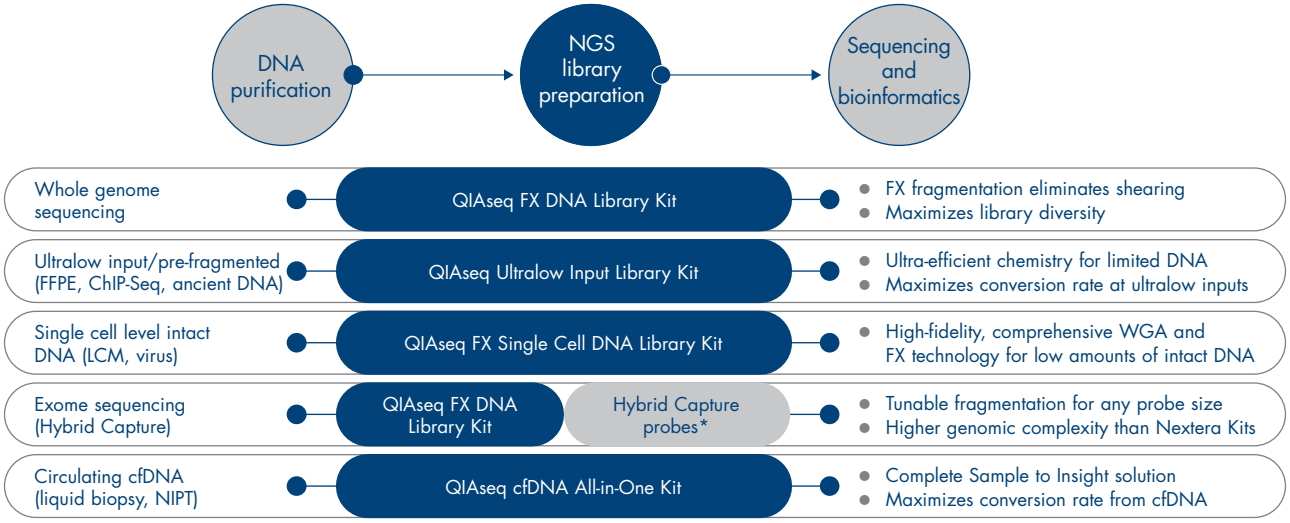
Whole genome sequencing and Hybrid Capture/exome sequencing



* From other manufacturers

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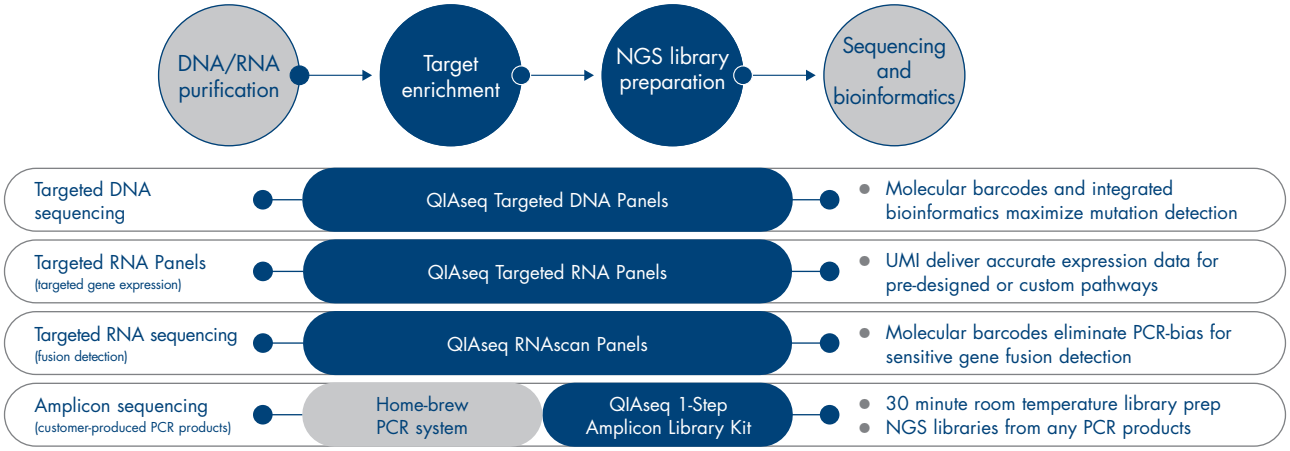
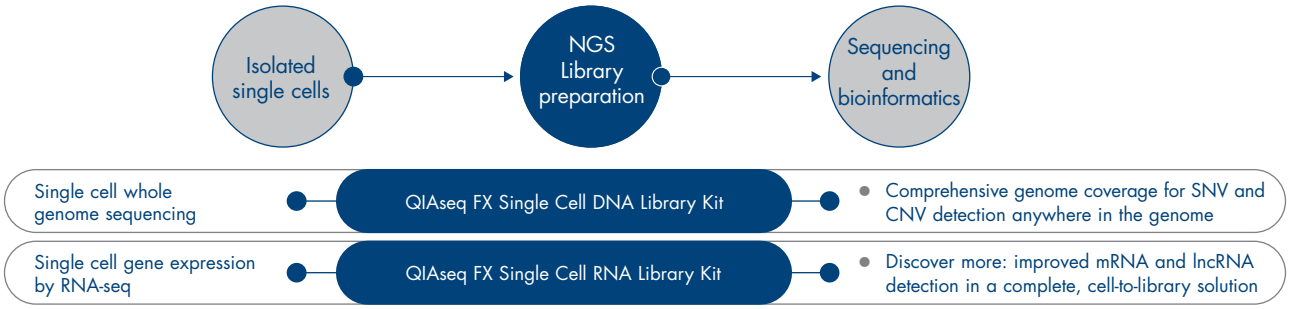
Complete workflows for targeted sequencing



Single cell sequencing



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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 quantitively 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 relevent 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**

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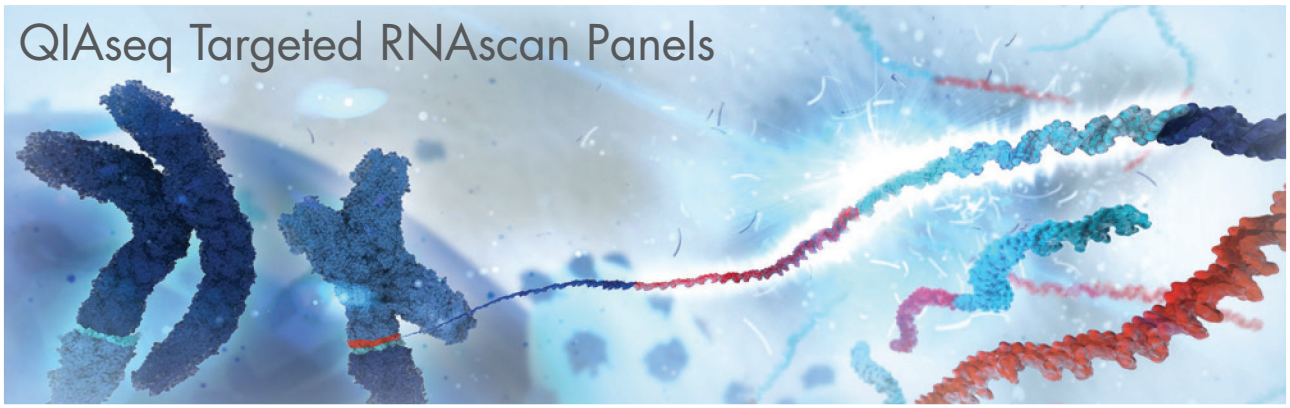

Novel approach to detect and quantify fusion genes

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**

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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**

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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

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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**

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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 form 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 to 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**

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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**

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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**

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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**

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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**

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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**

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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=HyqvMEqmkYk&index=12&list=PLnvL-JBxB4YvLhlW9qn6g_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

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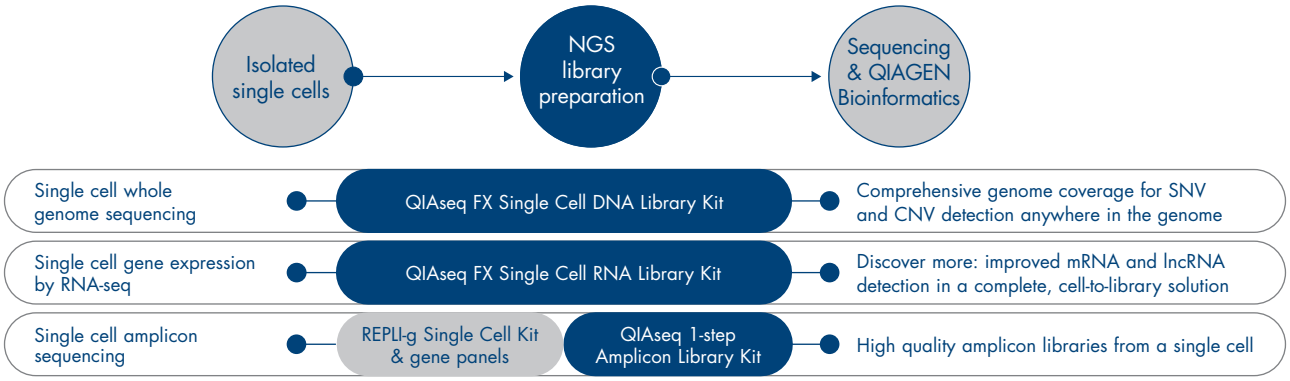
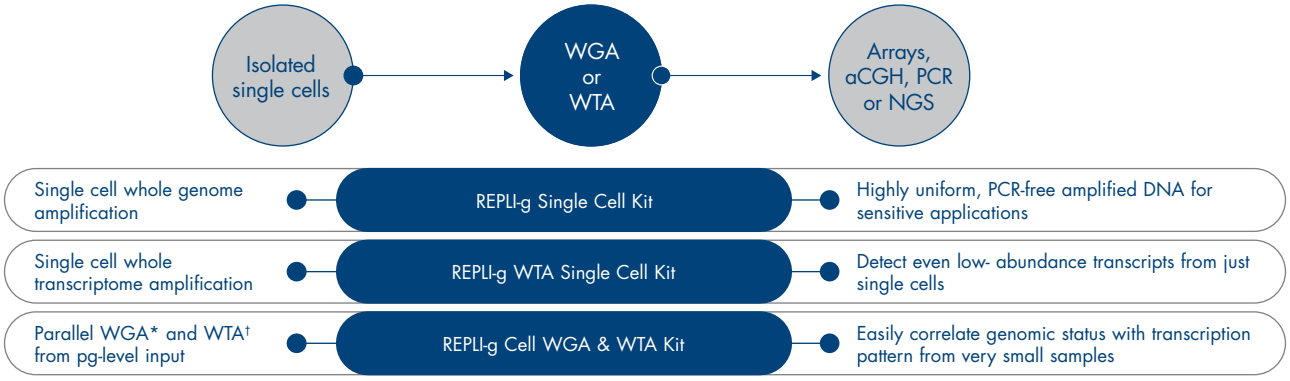
Single cells, multiple details – decipher the differences!

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

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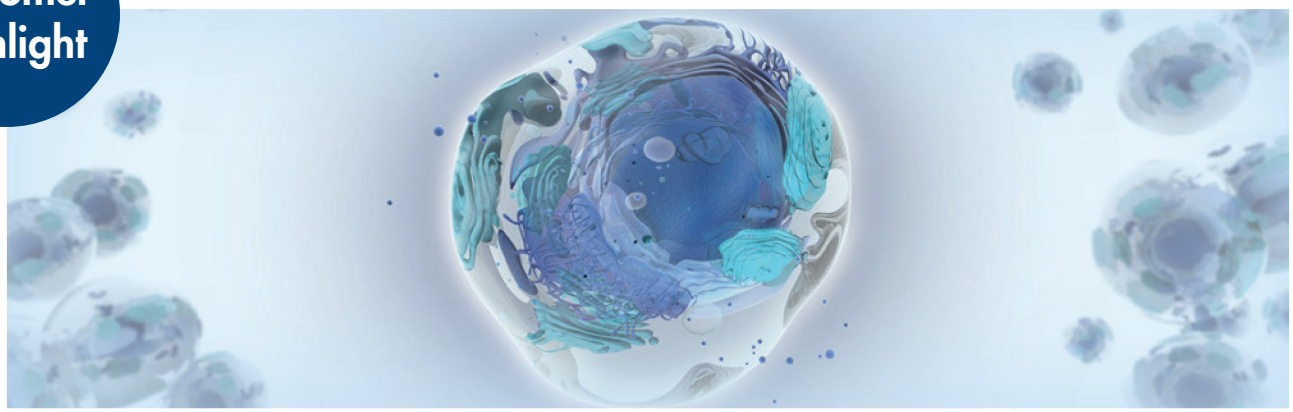
Customer highlight



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.

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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

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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

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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

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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

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

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