QIAGEN

Introducing QIAseq™

Accelerate your NGS performance through Sample to Insight® solutions

Sample to Insight

From Sample to Insight –

let QIAGEN enhance your NGS-based research

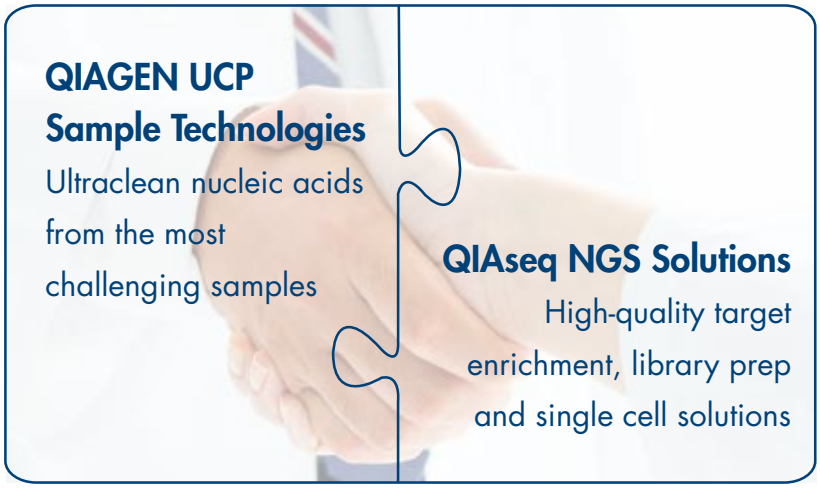
High-throughput next-generation sequencing (NGS) technologies continue to provide a wealth of sequence information, resulting in significant advances and new discoveries in a wide range of research areas. To enhance your specific NGS-based research and help you achieve your goals, QIAGEN has developed the broadest portfolio of dedicated NGS target enrichment, library preparation and single cell solutions: the QIAseq product family!

Accelerate your NGS performance with QIAseq

QIAseq NGS solutions are the perfect match to QIAGEN's gold standard sample technologies

The success of any NGS experiment is highly dependent on the upstream sample collection and nucleic acid extraction methods. QIAGEN, as the leading provider of sample technologies, offers a variety of NGS-grade sample preparation solutions that maximize yields of high-quality nucleic acids from virtually any sample type. QIAGEN instrumentation, including QIAcube® and QIAsymphony®, helps you start your NGS experiments on the right foot – offering platforms that fit your sample throughput for reliable and reproducible nucleic acid isolation.

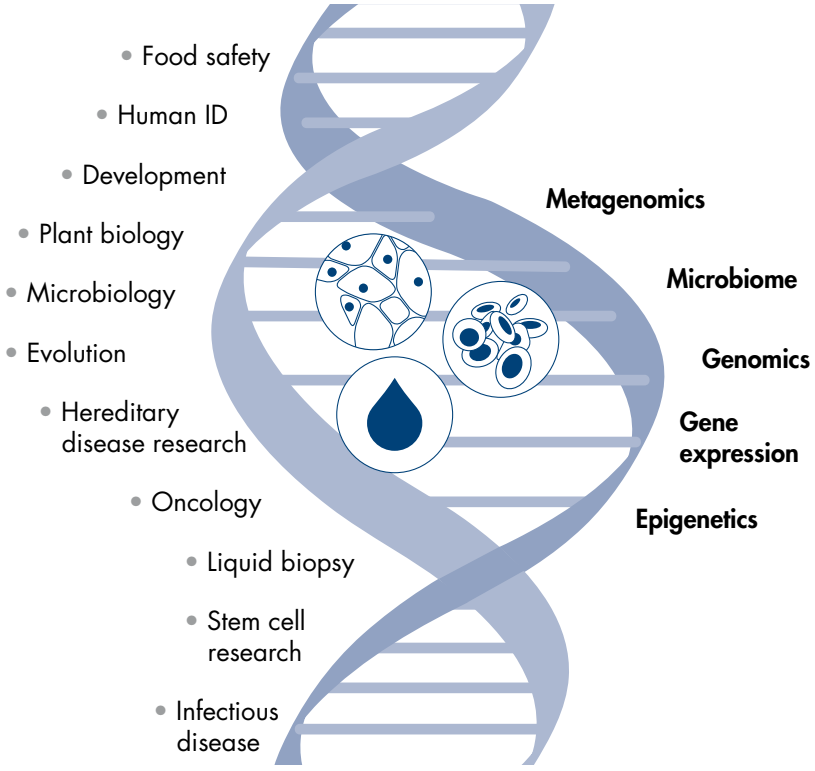
For NGS applications with special sensitivity requirements – such as ultra-deep sequencing, very limited or heterogeneous sample materials – QIAGEN offers "UCP" (ultraclean production) kits for RNA and DNA extraction, yielding ultrapure and high-quality nucleic acids.



The perfect match to achieve best-in-class NGS results

Find the right product for your sample type using our sample extraction selection guides at **www.qiagen.com/qec/selectiontoolsoverview**

QIAseq – the most comprehensive application-based NGS portfolio



Choose QIAGEN for every

QIAGEN sample technologies offer you effective solutions for manual and automated extraction of **NGS-grade nucleic acids** from a variety of samples.

Design your NGS research with QIAseq – the **broadest portfolio of best-in-class NGS** target enrichment, library prep and single cell solutions.

Track the quality of your NGS libraries throughout their preparation procedures with QIAGEN quality control solutions.

step of your NGS workflow

Enable biological discoveries with QIAseq NGS on any Illumina® or Ion Torrent™ sequencer.

Combine **reliable and robust** data analysis with data interpretation and the **most comprehensive** knowledge base through QIAGEN Bioinformatics.

Benefit from QIAGEN's verification and validation solutions to **gain confidence in your NGS results.**

QIAseq
- **Targeted panels**
- Library prep
- Single cell

Targeted gene panels – superior variant detection through digital NGS

Enriching nucleic acids for specific genes of interest in targeted panels presents a cost-effective way to democratize NGS while keeping the complexity of data analysis and interpretation at a manageable level.

QIAseq targeted panels combine the advantages of target enrichment with advanced technical solutions to overcome biases:

- Leverage digital NGS through unique molecular indices (UMIs) to detect low-frequency variants with unmatched confidence and significantly reduce false positives.
- Avoid issues of PCR duplicates and library bias through single primer extension.
- Interrogate disease genes, quantify gene expression and detect known or novel fusion genes.

Discover our complete digital NGS solutions at **www.qiagen.com/QIAseq-Targeted-DNA**

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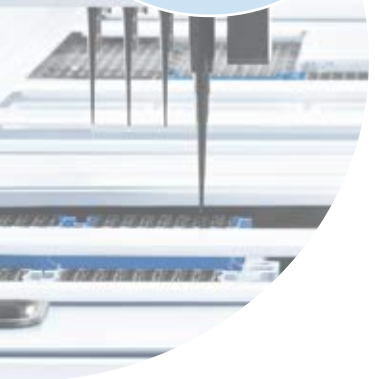


Whole genome, exome and transcriptome research – make exciting new discoveries from any sample

Genome- and transcriptome-wide sequencing from a sample paves the way for new research findings and requires no prior knowledge of known disease-causing genes – allowing for unbiased, hypothesis-free study of nucleic acids.

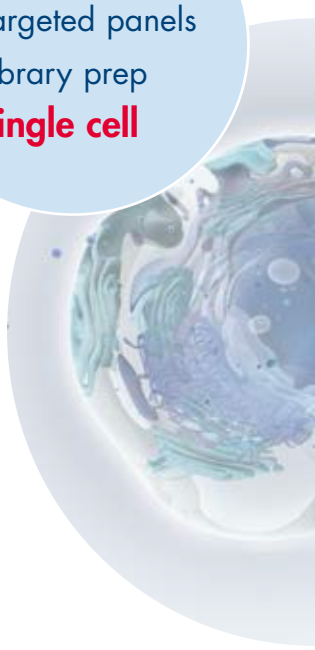
Overcome common sources of bias in GC content and coverage. Maximize confidence in your sequencing results with QIAseq NGS library preparation products:

- Dedicated library preparation solutions for any sample type – including whole blood, tissue, FFPE, liquid biopsy, metagenomics and ancient DNA or ultra-low sample amounts.
- High conversion rates, from sample to library, that maintain and capture the original complexity in your biological sample.
- Complete coverage to interrogate the genome or transcriptome without bias or sequencing gaps – enabling you to create exciting new insights.

Find out which QIAseq library prep solution fits your specific needs at **www.qiagen.com/QIAseq-NGS-Library**

Single cell analysis – uncover the full genome and transcriptome

QIAseq
- Targeted panels
- Library prep
- **Single cell**



Analyzing biological samples on an individual cell level uncovers hidden heterogeneity and enables new insights towards our understanding of cell types, cell function and the role of individual cells in normal or disordered development.

Experience our QIAseq cell-to-library solutions offering a streamlined, PCR-free workflow for the study of complete genomes or transcriptomes from single cells:

- Achieve complete, uniform genome coverage and sequence accuracy with diverse NGS libraries – set yourself up to analyze aneuploidy and sub-chromosomal copy number variations, or sequence variation analysis in single eukaryotic or bacterial cells.
- Gain confidence in your single cell RNA-seq data and reliably study differential gene expression with high transcript discovery rates for low-abundance RNA or RNA of varying lengths.

Find out more at **www.qiagen.com/SingleCellAnalysis**

Quality control and verification – success and confidence in NGS

NGS workflows are complex multistep procedures combining enzymatic reactions – and often PCR amplification – to prepare DNA or RNA fragments of specific concentrations, purities and lengths that are compatible with a particular sequencing platform. Each step of these complex workflows harbors risk for bias and experimental dropout.

To ensure success throughout each NGS workflow step and bring confidence to your data, QIAGEN offers a comprehensive set of quality control methods for both your sample and your NGS findings:

- The QIAxpert® spectrophotometer enables quick and accurate concentration measurements, while spectral content profiling provides a detailed insight into your sample's composition by detecting potential contaminants.
- The QIAxcel® Advanced capillary electrophoresis system simplifies and accelerates size distribution analysis, concentration and molarity assessment; comprehensive QC can be automated using objective QC criteria to make sure libraries are of highest quality prior to sequencing.
- The PyroMark® Pyrosequencing® system increases NGS data confidence by enabling verification and validation of sequencing results to detect false-positive variants and methylation results derived from the complex NGS procedure.

Find out more at **www.qiagen.com/NGS-QC**

QIAGEN Bioinformatics solutions – generate biological insights, not just data

While NGS platforms produce millions of individual datapoints, analyzing, interpreting, and managing this data in a standardized and reliable way is one of the major challenges in the NGS workflow.

QIAGEN Bioinformatics combines best-in-class NGS data analysis and interpretation software with access to a unique expert-curated knowledge base – for complete, optimized and streamlined end-to-end solutions:

- Identification of new and known disease driver variants in hereditary diseases and cancer from whole genome or exome
- Analysis of targeted panels with clinical reports
- Differential gene expression and whole transcriptome analysis, including pathway analysis
- Biomarker discovery through sample comparison
- Species and function mapping in metagenomics
- Epidemiological and outbreak analyses

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