The QIAseq NGS Portfolio for Cancer Research: Sample-to-Insight for All

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The QIAseq NGS Portfolio: A Broad Range of Applications

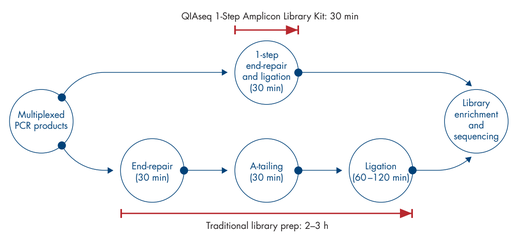
The QIAseq NGS portfolio offers a variety of NGS library prep products for a broad range of applications performed using any Illumina sequencer.

Targeted DNA amplicon-seq	Any PCR amplicon + QIAseq 1-Step Amplicon Library Kit	Off-the-shelf and custom DNA panels 1-tube, room temperature, 30-min library prep
Targeted gene expression	QIAseq Targeted RNA Expression Panels	Pre-PCR molecular transcript bar-coding Off-the-shelf, extended, and custom panels
Whole genome or hybrid capture sequencing	QIAseq FX DNA Library Kit	FX fragmentation step eliminates shearing 2.5 hour workflow from gDNA to library
Low-input ChIP-seq, LCM, FFPE	QIAseq Ultralow Input Library Kit	Ultra-efficient chemistry for 10–100 pg+ DNA Bar-coded adaptors for 96-plex sequencing
Cell-free DNA from liquid biopsy or non-invasive prenatal testing (NIPT)	QIAseq cfDNA All-in-One Kit	QIAamp® Circulating Nucleic Acid Isolation Optimized to maximize cfDNA conversion
Single-cell genomics	QIAseq FX Single Cell DNA/RNA Library Kits	PCR-free MDA amplification Sorted single cells or 6 pg DNA input

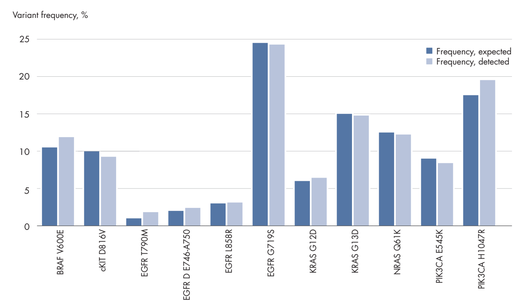
QIAseq 1-Step Amplicon Library Kit

High-quality amplicon-seq library in one room-temperature incubation step

- Ultimate convenience for amplicon sequencing: one single room-temperature, incubation step for combined end polishing and adaptor ligation.
- Compatible with any PCR product (QIAGEN gene panels, Ion AmpliSeq™, home-brew PCR assays)
- High adaptor ligation efficiency for sensitive and reliable mutation detection.



Comparison of the QIAseq 1-Step Amplicon Library Kit protocol with standard NGS library construction.

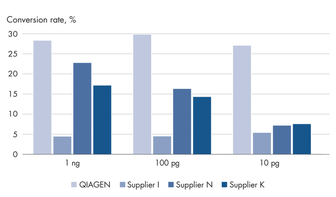


QIAseq 1-Step Amplicon Library Kit for reliable mutation detection. 40 ng FFPE DNA Standard Sample with defined mutations (Quantitative Multiplex Reference Standard, Formalin-Compromised DNA, Cat. No. HD-C749; Horizon) was subjected to PCR-based target enrichment with Ion AmpliSeq Cancer Hotspot Panel v2 (Thermo Fisher Scientific) and the PCR amplicons were constructed into a sequencing library with the QIAseq 1-Step Amplicon Kit and sequenced on MiSeq® (Illumina). Data were analyzed with CLC Biomedical Workbench (QIAGEN). All known mutations in the FFPE standard sample were accurately detected at expected frequencies using the procedure described above.

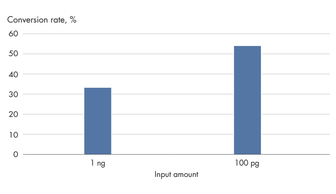
QIAseq Ultralow Input Library Kit

Highly efficient library construction for challenging and limited samples

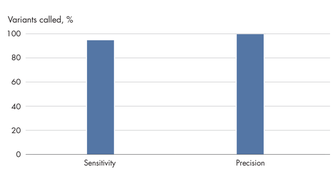
- Optimized chemistry formulation for optimal library complexity with minimal input amounts.
- Superior library conversion rate with sub-nanogram input DNA.
- Optimal solution for sequencing challenging samples: LCM, FFPE, cfDNA, and ancient DNA.



QIAseq Ultralow Input Kit delivers high library conversion rate with even sub-nanagram input DNA. Sequencing libraries were constructed with either QIAseq Ultralow Input Library Kit (QIAGEN) or dedicated low-input library kits from other suppliers. Conversion rate was calculated based on qPCR-quantified specific library amount prior to library amplification divided by input DNA amount. Input DNA: 10 pg or 100 pg of bacterial gDNA; equimolar mixture of gDNAs from *Bordetella pertussis* (67.7% GC), *Stretobacillus moniliformis* (26.3% GC) and *E. coli* DH10B (GC 50.79).



High library conversion rate with human gDNA sample. 100 pg or 1 ng of fragmented Genome-in-a-bottle (GIAB, RM8398; NIST) human reference DNA was constructed into an NGS sequencing library with QIAseq Ultralow Input Library Kit and sequenced on HiSeq™ 4000 (Illumina) to an average coverage of 23X and 25X, respectively. The conversion rate shown here was calculated as estimated library size (PicardTools) divided by the total number of input fragments.

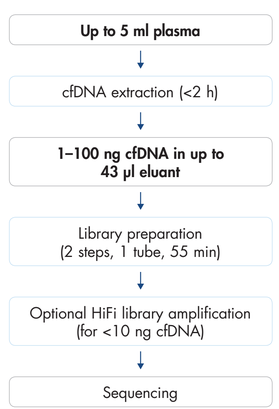


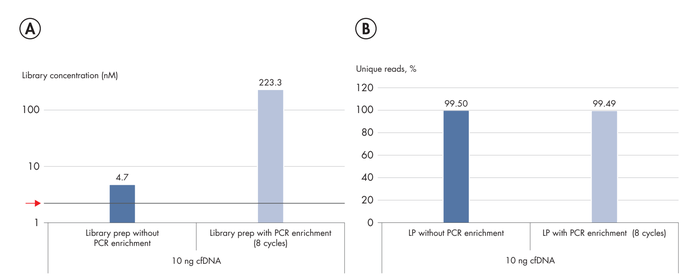
High SNP calling concordance from as little as 1 ng GIAB sample. Genome Analysis Toolkit (GATK) analysis pipeline was used for variant calling of the GIAB samples in the middle panel. With 1 ng gDNA input, 94.66% of the characterized high confident SNPs in the GIAB sample were detected with 99.70% precision (0.3% false-positive rate).

QIAseq cfDNA All-in-One Kit

Maximize your cfDNA discovery potential with the first dedicated solution for any liquid biopsy using NGS

- Designed for cfDNA analysis with NGS including highly efficient cfDNA extraction and library prep reagents to maximize mutation detection sensitivity.
- Flexible cfDNA input (1–100 ng) for library prep makes quantification after extraction unnecessary and eliminates potential source of sample loss.
- PCR-free libraries from 10 ng of cfDNA and HiFi amplification reagents minimizes PCR bias.



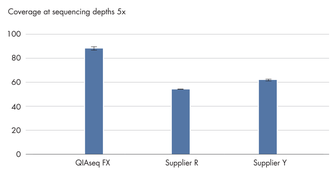


Comparison of amplified versus non-amplified libraries from 10 ng cfDNA. Ⓐ After library preparation from 10 ng cfDNA the final library concentration is >2 nM (red arrow) and thus sufficiently high for direct NGS without enrichment PCR. Ⓑ Comparison of normalized unique read distributions shows no differences of cfDNA samples with and without PCR.

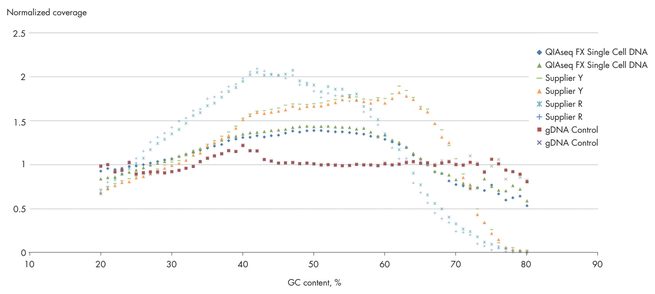
QIAseq FX Single Cell DNA Library Kit

Complete and comprehensive genome representation from single cells

- Optimal NGS library prep solution for single cells and low gDNA amounts.
- Uniform amplification ensures maximum and comprehensive genome coverage.
- PCR-free protocol eliminates duplicate reads and ensures high reproducibility of results.
- Best-in-class sequence fidelity reduces false positives and generates greater confidence in your results.
- Minimal sequence bias and GC-bias provides more accurate data.



Single-cell preparation from peripheral blood mononuclear cells (PBMC) were sequenced at low depth using an MiSeq. Data were analyzed according to Zhang, CZ, et al. (2015) Nat. Commun. **6**, 6822. Computed coverage at sequencing depths of 5x are plotted.

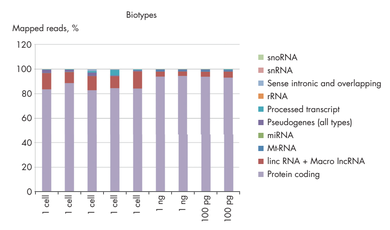


GC-bias of common single-cell whole genome sequencing kits. Libraries were generated from either bulk gDNA (control) using the QIAseq FX DNA Library Kit or from single PBMC using the QIAseq FX Single Cell DNA Library Kit or kits from two other suppliers. Single-cell preparations from PBMCs were sequenced at low depth using a MiSeq. Data were analyzed using a CLC Genomic workbench 8.5.1.

QIAseq FX Single Cell RNA Library Kit

Greater confidence and deeper insight into single-cell RNAseq results

- End-to-end solution for single cells and low RNA amounts.
- Complete workflow from sample to NGS library makes single-cell RNA-seq streamlined and routine.
- PCR-free protocol eliminates biases and maximizes confidence and reproducibility in transcript discoveries.
- Maximum transcript discovery potential provides deeper insights into transcriptome and unveils expression of important regulatory RNAs.
- Increasing statistical power in your conclusions by sequencing maximum number of single cells.



Evaluation of NextSeq Biotypes. mRNAs were amplified either from bulk RNA or from single PBMCs and libraries prepared using the QIAseq FX DNA Library Kit. Libraries were sequenced on NextSeq, Biotypes were evaluated and plotted as a percentage of the mapped reads.

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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Sample to Insight