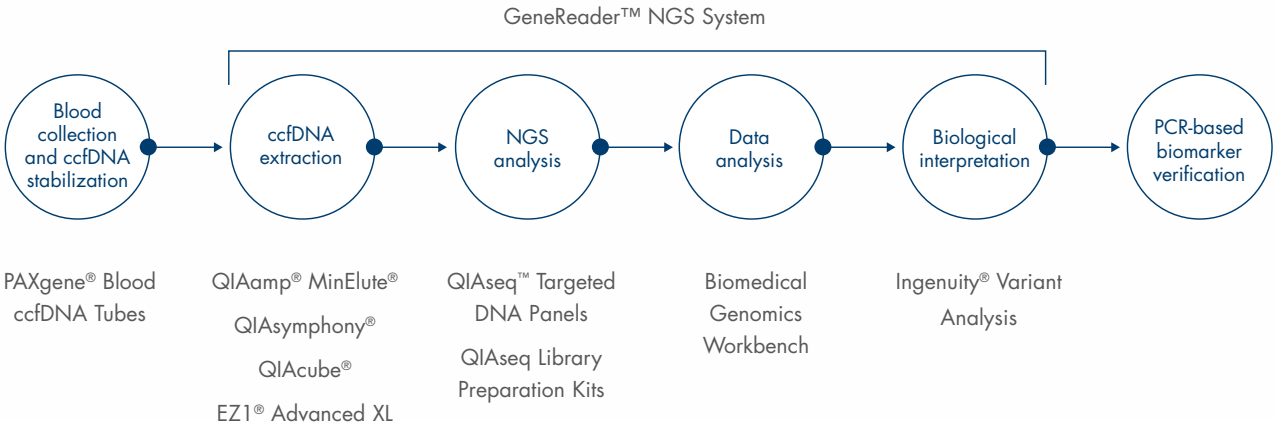
Cell-free DNA and NGS

Our expert solutions include a complete portfolio covering sample collection and extraction, next-generation sequencing (NGS) and analysis and interpretation. We aim to provide the highest quality tools to equip you to obtain invaluable insights from your liquid biopsy samples.



Research use only workflow

Sample to Insight

QIAGEN

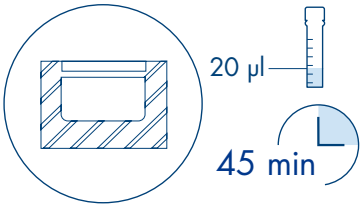
Blood collection and stabllization

PAXgene Blood ccfDNA Tube
(cat. no. varies)

- Cell-free DNA stabilization with non-crosslinking chemistry
- Suitable for a wide range of downstream applications
- Sample transport for up to 7 days at 2–30°C or up to 1 day at 37°C
- Standardized processing of samples with integrated isolation

Cell-free DNA (ccfDNA) preparation

Manual

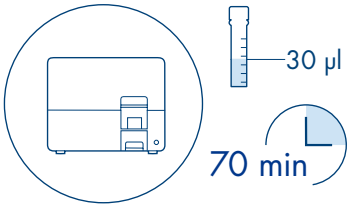


QIAamp MinElute ccfDNA Mini Kit
cat. no. 55204; 1–4 ml plasma

QIAamp MinElute ccfDNA Midi Kit
cat. no. 55284; 4–10 ml plasma

- High concentrations of ccfDNA with low (20 µl) elution volumes
- Low frequency variant detection with scalable sample input volumes (1–10 ml)
- High yields similar to the gold standard
- Automatable on QIAcube®

Automated on QIAcube – up to 12 samples



QIAcube
cat. no. 9001882

- Automation of the spin-column procedure
- All contained within a single square meter

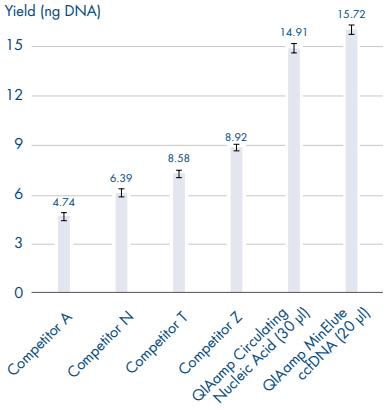
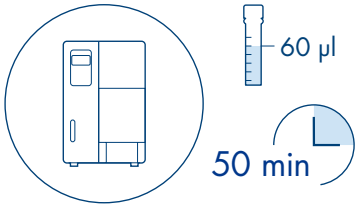


Figure 1. Higher DNA yields with the QIAamp MinElute ccfDNA Kit.
Total yield of a 66 bp ccfDNA fragment from 4 ml of plasma is shown using the QIAamp MinElute ccfDNA Kit compared with 5 other commercially available kits. Results show that the QIAamp MinElute ccfDNA Kit provided higher DNA yield than competitor solutions.

Automated on EZ1 Advanced XL – up to 14 samples

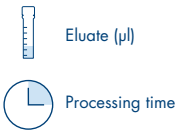


EZ1 ccfDNA Mini Kit
cat. no. 954134; 1–4 ml plasma

EZ1 ccfDNA Midi Kit
cat. no. 954154; 4–10 ml plasma

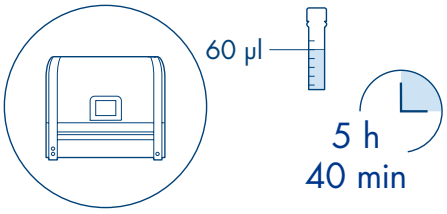
EZ1 Advanced XL System
cat. no. 9001874

- Convenient automation
- Standardized yields and efficient ccfDNA recovery
- Effortless data management and secure user environments



ccfDNA preparation on QIAsymphony SP for research applications

Up to 96 samples



QIAsymphony PAXgene Blood ccfDNA Kit (192)
cat. no. 768536

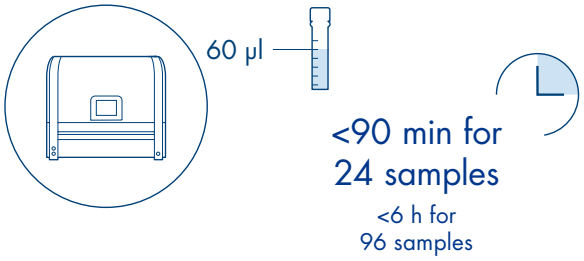
- Optimized isolation chemistry for plasma generated in PAXgene Blood ccfDNA Tubes
- Option for direct primary tube processing of PAXgene Blood ccfDNA Tubes

QIAsymphony SP
cat. no. 9001297; 2.4 ml or 4.8 ml plasma

- Fully automated sample preparation
- Prefilled, ready-to-use reagent cartridges
- Bar code reader for reagents and sample tracking

ccfDNA preparation on QIAsymphony SP for diagnostic applicatons

Up to 96 samples

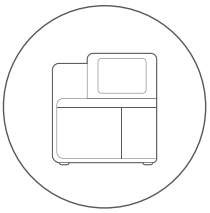


QIAsymphony DSP Circulating DNA Kit
cat. no. 937556; 2 ml or 4 ml plasma or urine

- Automated purification of ccfDNA from human plasma and urine
- Workflow compatibility with a wide range of blood collection tubes

Cell-free DNA (ccfDNA) sequencing

Whole genome/whole exome sequencing

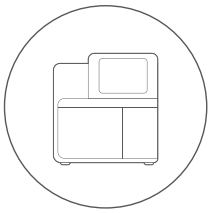


QIAseq cfDNA Library Kit
cat. no. 180015
For use on Illumina® sequencers

QIAseq cfDNA Library T Kit
cat. no. 1102308
For use on Ion Torrent™ Sequencers

- Superior conversion of ccfDNA through highly efficient ligation chemistry
- NGS library preparation optimized for variable cell-free DNA input amounts

Targeted DNA panel sequencing



QIAseq Targeted DNA Panels
A wide range of catalogued, extended, booster or custom DNA panels

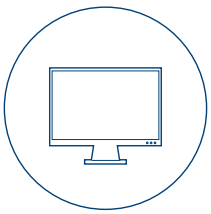
- Low frequency variant detection with unique molecular indices and single primer extension
- The Human Comprehensive Cancer QIAseq DNA Panel – a large gene panel covering 275 genes for identifying the major mutations in each tumor, plus potentially novel molecular mechanisms

Data analysis and interpretation

Software solutions built for biologists and configured specifically to help you detect and interpret variants

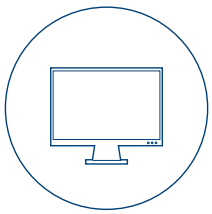
New release

Biomedical Genomics Workbench 5

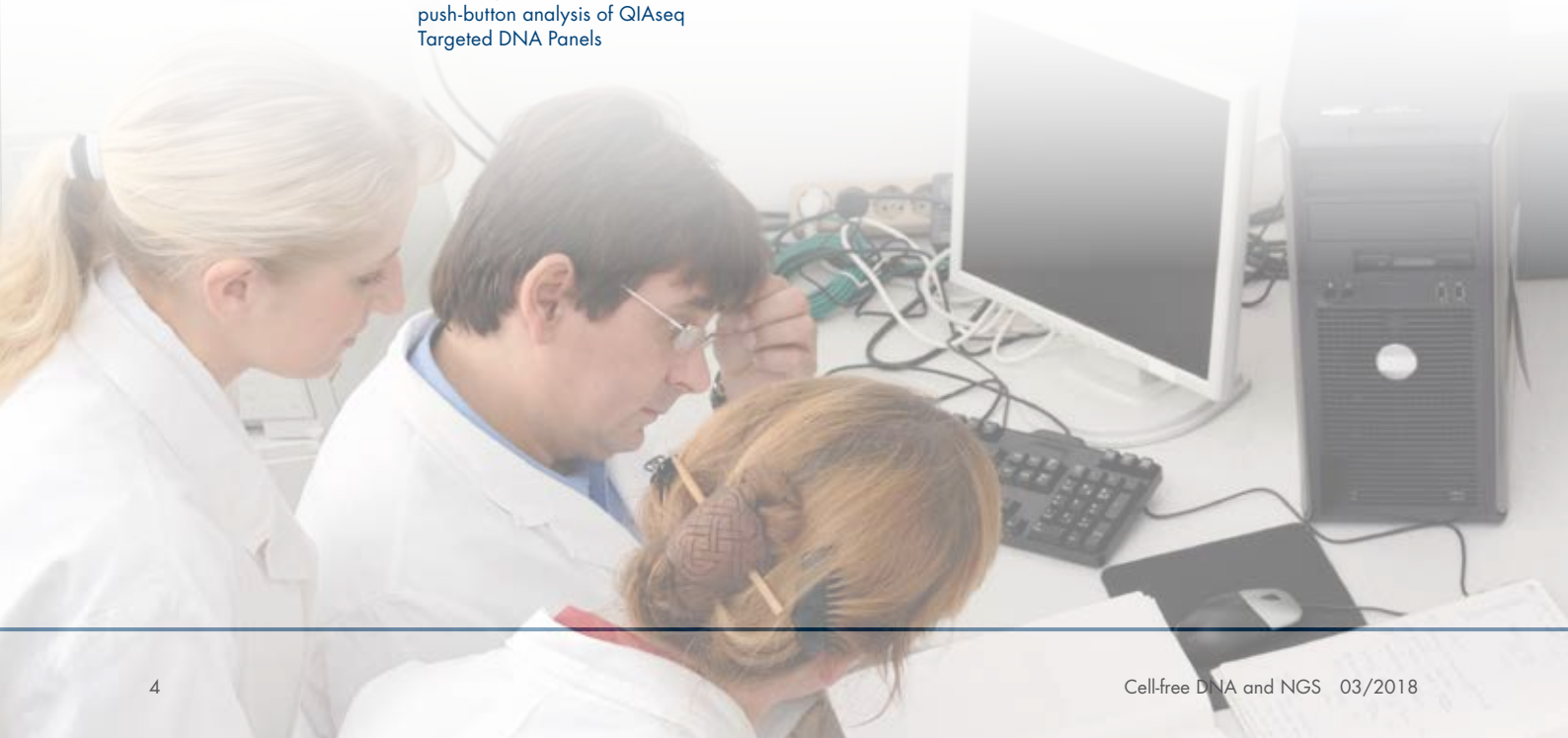


- Accurate variant detection at 1% minor allele frequency (MAF) or lower
- Identification of multiple types of variation, from single nucleotide to copy number to insertions and deletions
- Pre-configured workflows for push-button analysis of QIAseq Targeted DNA Panels

Ingenuity Variant Analysis



- Cancer-driver variations uncovered with more confidence
- Powered by the world's most comprehensive knowledge base for genome interpretation
- Intuitive options for filtering variants like biological context and statistical association



Methylation analysis by sequencing

QIAseq Methyl Library Kit (24)
cat. no. 180502

- High-quality libraries
- Low DNA input requirements

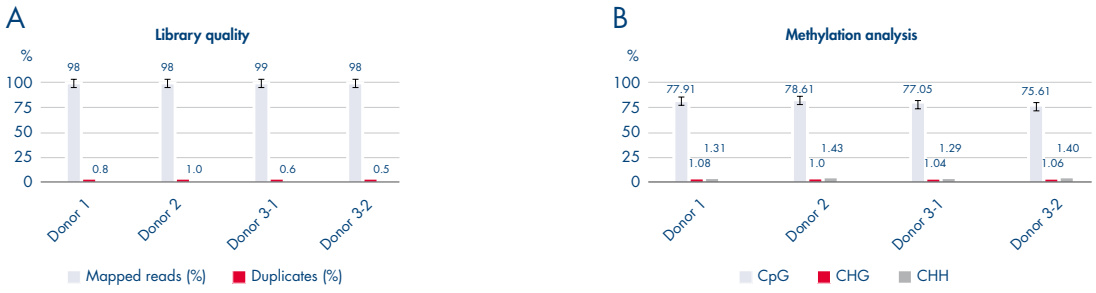
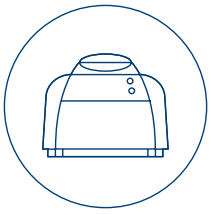


Figure 2. High mapping rate for accurate methylation analysis from low input ccfDNA. ccfDNA was purified using the QIAamp MinElute ccfDNA Kit. Purified ccfDNA from different donors was processed through the QIAseq Methyl WGBS workflow. ccfDNA was converted using the EpiTect fast kit. Total converted DNA was used to prepare libraries using the QIAseq Methyl DNA library kit. Libraries were sequenced on MiSeq®. Data was analyzed using the CLC Genomics Workbench Bisulfite sequencing Plugin.
A. High-quality libraries can be generated as evidenced by the high percentage of mapped reads, and the low percentage of duplicate reads. **B.** Accurate methylation analysis can be achieved across 4 donors.

PCR-based biomarker verification

Real-time PCR



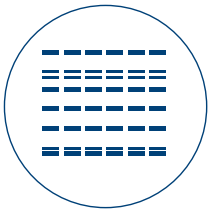
QuantiNova® Probe PCR Kit
cat. no. 208252

QuantiNova SYBR® Green PCR Kit
cat. no. 208052

QuantiNova Multiplex PCR Kits
cat. no. 208452)

- Highly sensitive, specific, real-time PCR
- For probe-based or SYBR Green-based PCR
- Singleplex or multiplex

Endpoint PCR

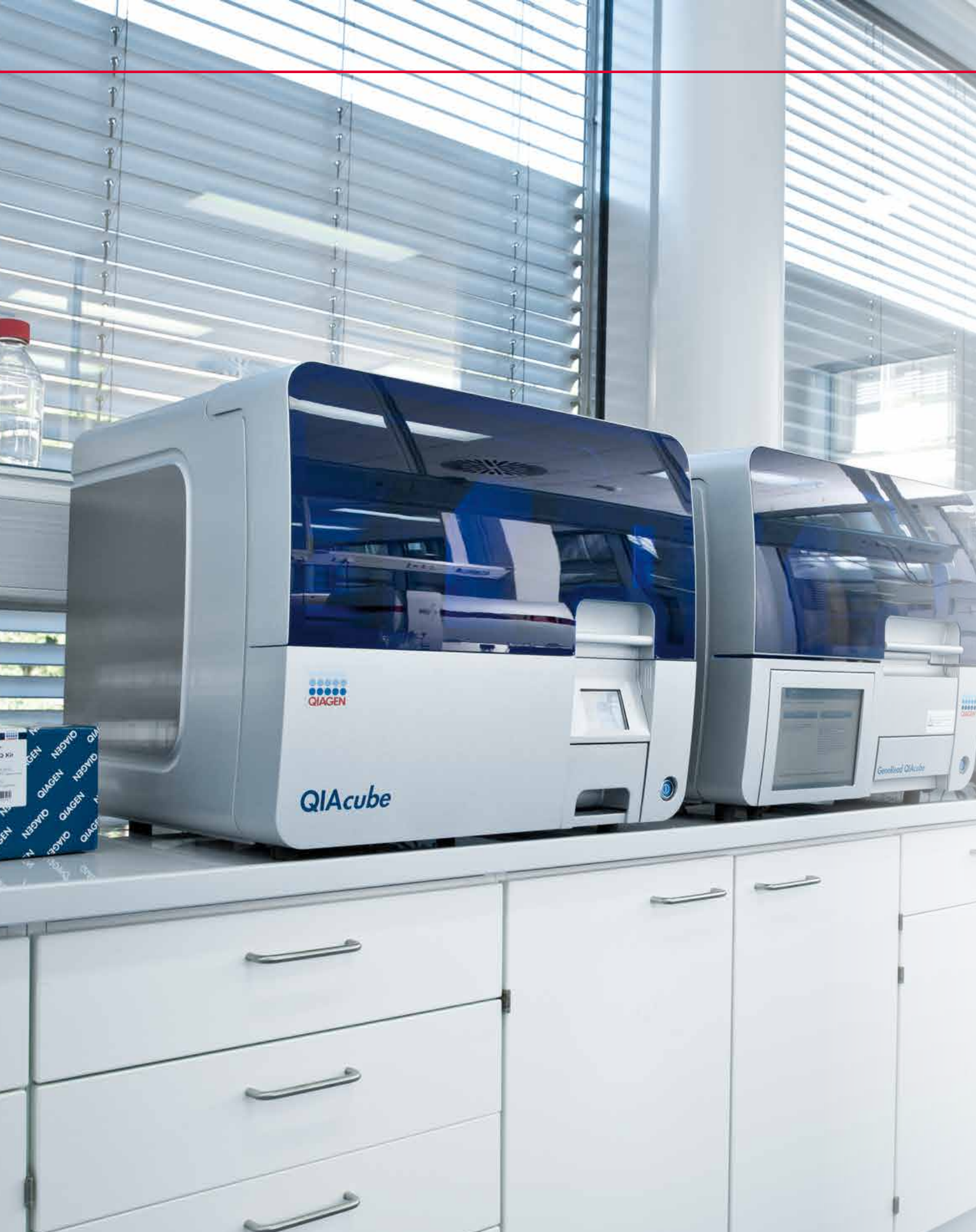


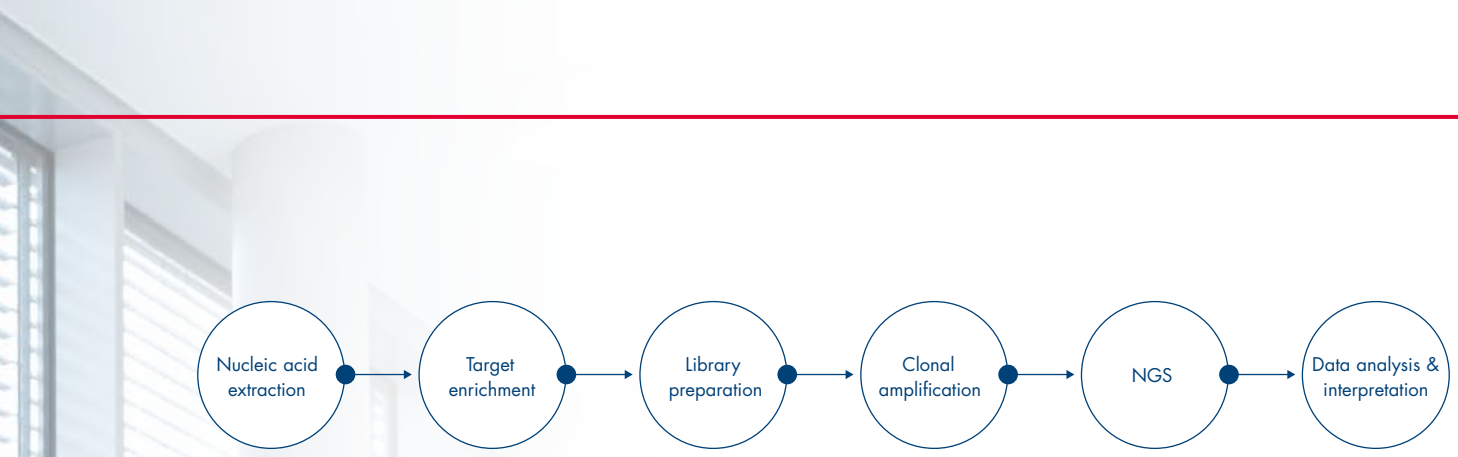
QIAGEN Multiplex PCR Kits
cat. no. 206143

- Highly specific and sensitive multiplex PCR without optimization requirements

QIAGEN AllTaq PCR Kits
cat. no. 203123

- Reliability for all routine PCR applications and assays with integrated safety and convenience features


QIAGEN
QIAcube
QIAGEN



GeneReader NGS System

Complete Sample to Insight® workflow takes you all the way to actionable insights

GeneRead QIAact Lung DNA UMI Panel Kit
cat. no. 181930

- One-stop NGS assay solution covering known actionable single nucleotide variants (SNV), InDels and CNVs
- Designed to detect 549 hotspot variants at 335 positions and 5 CNVs from 19 genes of known relevance to clinical lung cancer research

GeneReader Platform
cat. no. 9002312

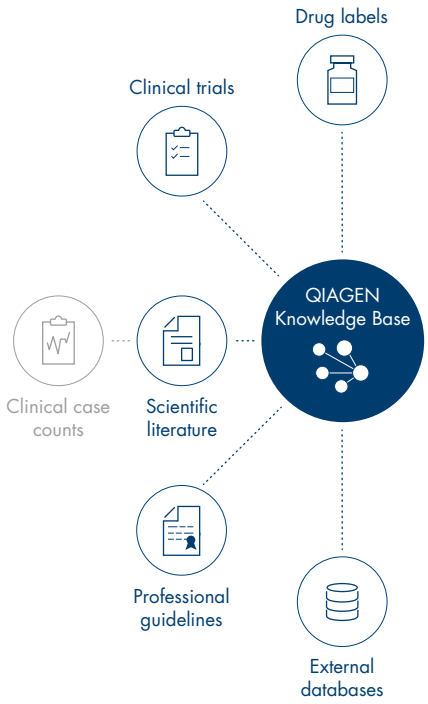
- NGS instrument
- Fully embedded into the Sample to Insight GeneReader NGS System

QCI Analyze
cat. no. 188001

- Bioinformatic complement to the GeneReader NGS System for variant identification

QCI Interpret
cat. no. 830371

- Advanced software enterprise
- Specifically designed for clinical-grade genomic testing laboratories
- Provides evidence-based clinical decision support solutions
- Enables interpretation and reporting of NGS cancer test results to your oncologists with confidence, accuracy and clinical utility



Gain additional insights from your liquid biopsy ccfDNA samples by visiting **www.qiagen.com/ccfdna**

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.

Ordering **www.qiagen.com/shop** | Technical Support **support.qiagen.com** | Website **www.qiagen.com**

QIAGEN

Identify the *PIK3CA* mutations that make a difference in breast cancer

The *therascreen*® PIK3CA Kit is the first FDA-approved and clinically validated companion diagnostic test for use as an aid in identification of breast cancer patients who could benefit from treatment with PIQRAY® (alpelisib)

Sample to Insight

종양 전문의가 신뢰할 수 있는 결과를 제공합니다.

therascreen PIK3CA RGQ PCR Kit (*therascreen* PIK3CA 검사)는 진행성/전이성 유방암 환자들 중 에스트로겐 수용체 길항제인 풀베스트란트(Furvestrant)와 병용하여 PI3K(Phosphatidylinositol-3-Kinase) α 특이적 억제제 PIQRAY(alpelsib) 치료가 가능한 환자를 선별하기 위한 FDA가 승인한 최초의 동반진단(CDx) 검사입니다. 이 검사는 진행성/전이성 유방암 환자에서 채취한 FFPE 종양 조직 또는 K_2EDTA 항응고 처리 혈장 검체에서 분리된 유전체 DNA에서 특정 PIK3CA 돌연변이의 검출을 기반으로 합니다. 이 빠르고 정확한 검사는 자동화된 검사 결과 보고와 함께 간단하고 신뢰할 수 있는 검사 과정의 일부입니다. 해당 검사는 분석적 타당성 및 임상적 타당성이 입증되었으며, 독립적인 SOLAR-1 임상시험을 통해 총 572명의 대상자들에서 평가된 알펠리십(alpelisib)에 대한 양성 반응을 예측하는 것으로 알려진 11개의 임상적으로 작용 가능한 돌연변이를 검출할 수 있었습니다 (1).

SOLAR-1: PIK3CA 돌연변이 상태에 따른 PIQRAY의 반응

SOLAR-1임상시험 (CBYL719C2301)은 아로마타제(aromatase) 억제제 치료 중 혹은 치료 이후에 진행된 호르몬 수용체 양성, HER2 음성인 진행성/전이성 유방암이 있는 남성 및 폐경 후 여성을 대상으로 PIQRAY+풀베스트란트(Fulvestrant) 및 위약+풀베스트란트, 두 그룹으로 나누어 각 그룹별 치료 효과를 비교한 무작위 배정, 이중 눈가림, 위약 대조 및 다국적 다기관 제 3상 임상시험입니다. 임상시험 대상자들은 PIQRAY 300mg과 풀베스트란트 또는 위약과 풀베스트란트를 투여받도록 1:1 비율로 무작위배정되었습니다. 1차 평가변수는 연구자의 평가에 기반하여 RECIST v1.1 기준을 사용한 무진행 생존 (PFS)이었습니다 (1).

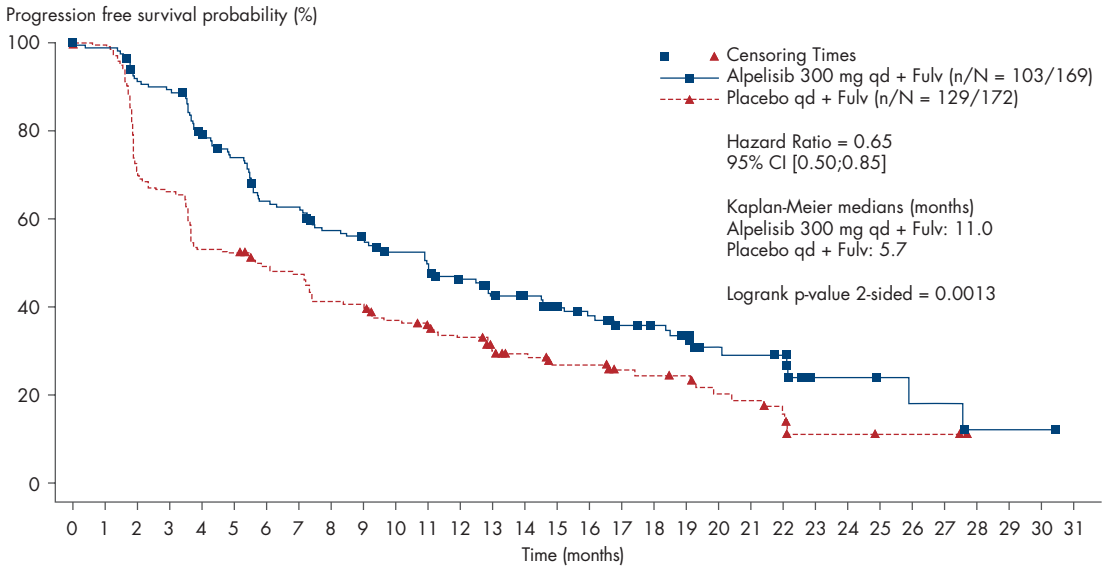


Figure 1. Kaplan-Meier plot of PFS by treatment in the *PIK3CA* mutant-positive patients randomized in SOLAR-1 (FFPE tissue samples) (1).

SOLAR-1은 종양에 특정 *PIK3CA* 돌연변이가 있는 대상자에서 위약과 풀베스트란트를 사용하여 치료한 그룹 대비 PIQRAY와 풀베스트란트를 사용해 치료한 그룹의 PFS 중앙값은 임상적으로 유의미한 5.3개월(전체 11개월) 연장했으며 질병 진행 또는 사망 위험이 약 35% 감소하는 것으로 나타냈습니다 (그림 1). *therascreen* PIK3CA RGQ PCR Kit에 의해 확인된 동반진단 *PIK3CA* 돌연변이 양성 대상자 하위 그룹 (347명의 대상자, 포르말린 고정 파라핀에 포매된 조직 검체, FFPET)의 분석에 따르면 PIQRAY와 풀베스트란트를 투여받은 대상자에서 위약과 풀베스트란트를 투여받은 대상자보다 질병 진행 또는 사망 위험이 36% 더 낮은 것으로 입증되었습니다 (HR = 0.64; 95% CI: 0.48, 0.85) (2).

대조적으로 *therascreen* PIK3CA RGQ PCR Kit 검사 결과 음성 그룹에서도 PFS가 추정되었으며 이러한 대상자들에게서 PFS 이점은 관찰되지 않았습니다 (HR = 0.85; 95% CI: 0.58, 1.25).

따라서 PIQRAY와 풀베스트란트 병행 요법으로 치료할 환자들을 선별할 때 *PIK3CA* 돌연변이 상태를 확인하는 것이 중요합니다. 작용 가능한 *PIK3CA* 돌연변이가 있는 종양을 가진 환자만이 임상적으로 의미 있는 PFS 증가를 경험할 가능성이 있습니다.

Sample to Insight®의 완전한 검사 과정

간단한 검사 작업 과정은 포르말린 고정 파라핀 포매(FFPE) 유방 종양 조직(QIAamp® DSP DNA FFPE Kit 사용) 또는 K_2EDTA 항응고 처리 혈장 (QIAamp DSP Circulating Nucleic Acid Kit 사용)에서의 수동으로 DNA 추출로 시작하여 민감한 real-time PCR인 Rotor-Rotor-Gene® Q MDx (US) 기기 및 Rotor-Gene AssayManager® 소프트웨어를 사용한 자동 데이터 분석으로 이어집니다 (그림 2).

therascreen PIK3CA 검사는 PIK3CA 유전자의 엑손 7, 9 및 20에서 총 11개 돌연변이(엑손 7: C420R; 엑손 9: E542K, E545A, E545D[1635G>T 한정], E545G, E545K, Q546E, Q546R 및 엑손 20: H1047L, H1047R, H1047Y)를 검출합니다.

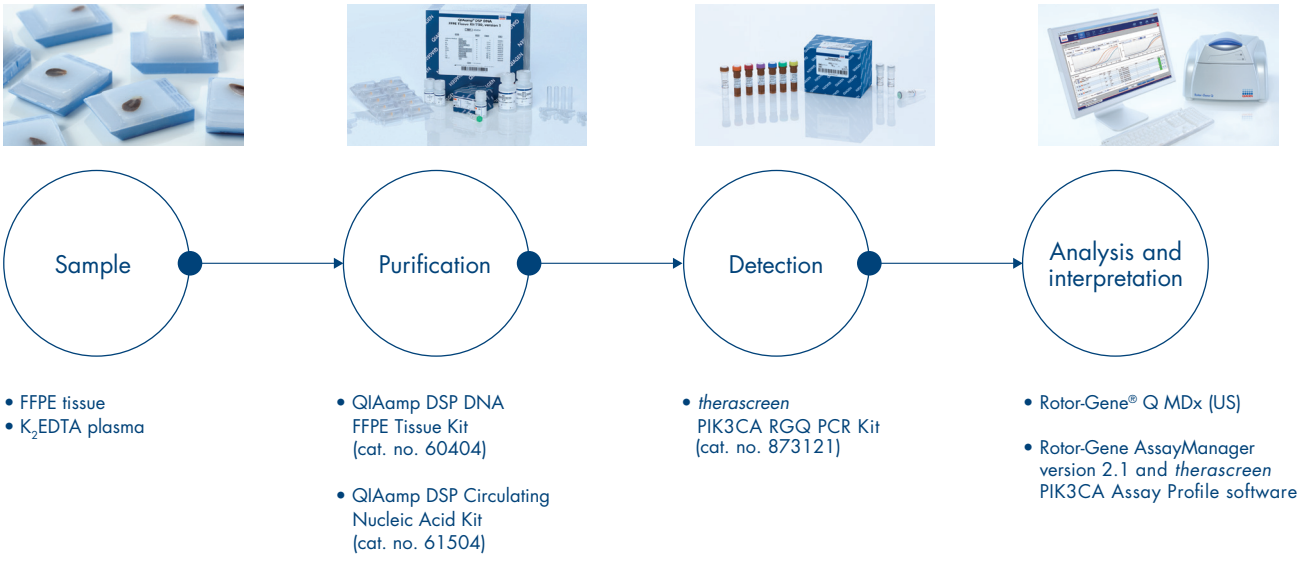


Figure 2. Simple, efficient workflow with the *therascreen* PIK3CA RGQ PCR System.

Ordering Information

Product	Contents	Cat. no.
therascreen PIK3CA RGQ PCR Kit (24)	For 24 reactions: Control Assay, 6 Assays, Positive Control, *Taq* DNA Polymerase, Water for NTC, and Water for Sample Dilution	873121
Related products		
QIAamp DSP DNA FFPE Tissue Kit (50)	For 50 DNA preps: QIAamp MinElute® columns, Proteinase K, Buffers, and Collection Tubes (2 ml)	60404
QIAamp DSP Circulating Nucleic Acid Kit (50)	For 50 DNA preps: QIAamp MinElute columns, Proteinase K, Buffers, and Collection Tubes (2 ml)	61504
Rotor-Gene Q MDx (US) System	Real-time PCR cycler with 6 channels, laptop computer, software, accessories, 1-year warranty on parts and labor, installation and training	9002036

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).

References

1. Andre, F. et al. (2019) Alpelisib for PIK3CA-Mutated, Hormone Receptor–Positive Advanced Breast Cancer. N. Engl. J. Med. 380, 1929.
2. *therascreen* PIK3CA RGQ PCR Kit Instructions for Use (Handbook). May 2019. Version 1, Revision 1.

Contact QIAGEN today to discover more about personalizing healthcare!
Learn more at **www.qiagen.com/pik3ca**

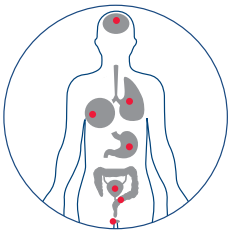
퀴아젠코리아
서울시 중구 한강대로 416번지 서울스퀘어 5층
주문문의 080-000-7146 **orders-KR@qiagen.com** | 학술문의 080-000-7145 **techservice-KR@qiagen.com** | Website **www.qiagen.com**

Single consolidated NGS workflow with DNA + RNA

QIAseq® Pan Cancer Multimodal cuts user interventions by 50%

Sample to Insight

QIAGEN



Challenges of pan cancer profiling

Pan cancer studies focus on profiling of relevant DNA and RNA alterations found across multiple cancers, as well as assessment of tumor mutational burden (TMB) and microsatellite instability (MSI) for solid tumors and heme malignancies. Recent advances in NGS chemistries, platforms and bioinformatics pipelines have empowered users to efficiently interrogate DNA and RNA alterations in biological samples. Current approaches, however, require the use of 2 separate workflows to prepare libraries from separate DNA and RNA isolates. Limitations of such approaches include:

- Precious samples must be split to extract DNA and RNA in separate sample prep protocols
- Large amounts of sample material are required to generate sufficient amounts of input DNA and RNA for multiple workflows
- Workflow has added complexity of deriving integrated insights from results of different technical approaches, each with its own innate bias
- Separate workflows result in inefficient use of resources and long turnaround times

Streamlined, consolidated one-day workflow

To overcome the limitations associated with current approaches, the QIAseq Pan Cancer Multimodal panel starts with total nucleic acids (or DNA + RNA) and prepares targeted DNA and RNA libraries containing Unique Molecular indices (UMIs) for Illumina® platforms using a one-day, consolidated workflow (see Figure 1).

The QIAseq Pan Cancer Multimodal panel delivers:

- The ONLY single consolidated workflow for DNA + RNA library prep using total nucleic acids as input
- Operational efficiency with a 50% reduction in user interventions
- Confident detection of low-frequency variants with UMIs
- Reduced index hopping with Unique Dual Indices (UDIs)
- Comprehensive coverage of known and novel fusions as well as all relevant alterations
- 523 DNA gene targets, 56 RNA fusion gene targets and 26 microsatellite instability MSI loci (Tables 1–3)

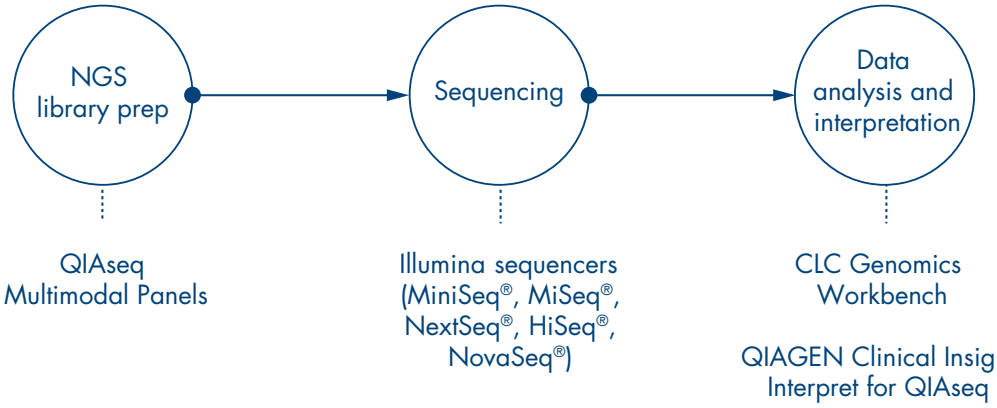


Figure 1. Extract more information, while reducing sample, time and cost with a simple, one-day workflow. This flexible solution enables the construction of libraries compatible with Illumina platforms from as little as 10 ng total nucleic acid isolated from a wide range of samples. The data analysis pipelines in CLC Genomics Workbench translate raw sequence data in FASTQ format to DNA and RNA variant files (VCFs), which can be further interpreted for biological significance through QCI® Interpret for QIAseq.

Confidently interpret NGS variants

Our software workflow makes it easy to extract, identify the variants of interest and deliver a comprehensive variant interpretation from your raw NGS data. The industry leading genomic analysis and interpretation software solutions, CLC Genomic Workbench and QCI Interpret for QIAseq, provide you with a comprehensive report to support your workflow, including variant classification, details on variant function, literature references, drug labels, drug interactions and relevant clinical trials. Accelerate your clinical research and go from raw NGS data to detailed and trusted insights in minutes – not hours.

Key differentiators

- The ONLY single consolidated workflow for DNA + RNA library prep using total nucleic acids as input
- Cuts user interventions by 50%
- Confident detection of low-frequency variants
- Detection of both known and novel fusions
- Increased target coverage of all relevant alterations

Table 1. 523 DNA gene targets (Part 1)

Genes targeted for SNP, InDel, and copy number variation (CNV) detection by DNA sequencing											
ABL1	*ASXL1*	*BCOR*	*CCND2*	*CENPA*	*DAXX*	*EP300*	*ETV5*	*FGF19*	*FOXA1*	*GPR124*	*HIST1H3I*
ABL2	*ASXL2*	*BCORL1*	*CCND3*	*CHD2*	*DCUN1D1*	*EPCAM*	*ETV6*	*FGF2*	*FOXL2*	*GPS2*	*HIST1H3J*
ACVR1	*ATM*	*BCR*	*CCNE1*	*CHD4*	*DDR2*	*EPHA3*	*EWSR1*	*FGF23*	*FOXO1*	*GREM1*	*HIST2H3A*
ACVR1B	*ATR*	*BIRC3*	*CD274*	*CHEK1*	*DDX41*	*EPHA5*	*EZH2*	*FGF3*	*FOXP1*	*GRIN2A*	*HIST2H3C*
AKT1	*ATRX*	*BLM*	*CD276*	*CHEK2*	*DHX15*	*EPHA7*	*FAM175A*	*FGF4*	*FRS2*	*GRM3*	*HIST2H3D*
AKT2	*AURKA*	*BMPR1A*	*CD74*	*CIC*	*DICER1*	*EPHB1*	*FAM46C*	*FGF5*	*FUBP1*	*GSK3B*	*HIST3H3*
AKT3	*AURKB*	*BRAF*	*CD79A*	*CREBBP*	*DIS3*	*ERBB2*	*FANCA*	*FGF6*	*FYN*	*H3F3A*	*HLA-A*
ALK	*AXIN1*	*BRCA1*	*CD79B*	*CRKL*	*DNAJB1*	*ERBB3*	*FANCC*	*FGF7*	*GABRA6*	*H3F3B*	*HLA-B*
ALOX12B	*AXIN2*	*BRCA2*	*CDC73*	*CRLF2*	*DNMT1*	*ERBB4*	*FANCD2*	*FGF8*	*GATA1*	*H3F3C*	*HLA-C*
AMER1	*AXL*	*BRD4*	*CDH1*	*CSF1R*	*DNMT3A*	*ERCC1*	*FANCE*	*FGF9*	*GATA2*	*HGF*	*HNF1A*
ANKRD11	*B2M*	*BRIP1*	*CDK12*	*CSF3R*	*DNMT3B*	*ERCC2*	*FANCF*	*FGFR1*	*GATA3*	*HIST1H1C*	*HNRNPK*
ANKRD26	*BAP1*	*BTG1*	*CDK4*	*CSNK1A1*	*DOT1L*	*ERCC3*	*FANCG*	*FGFR2*	*GATA4*	*HIST1H2BD*	*HOXB13*
APC	*BARD1*	*BTK*	*CDK6*	*CTCF*	*E2F3*	*ERCC4*	*FANCI*	*FGFR3*	*GATA6*	*HIST1H3A*	*HRAS*
AR	*BBC3*	*C11orf30*	*CDK8*	*CTLA4*	*EED*	*ERCC5*	*FANCL*	*FGFR4*	*GEN1*	*HIST1H3B*	*HSD3B1*
ARAF	*BCL10*	*CALR*	*CDKN1A*	*CTNNA1*	*EGFL7*	*ERG*	*FAS*	*FH*	*GID4*	*HIST1H3C*	*HSP90AA1*
ARFRP1	*BCL2*	*CARD11*	*CDKN1B*	*CTNNB1*	*EGFR*	*ERRFI1*	*FAT1*	*FLCN*	*GLI1*	*HIST1H3D*	*ICOSLG*
ARID1A	*BCL2L1*	*CASP8*	*CDKN2A*	*CUL3*	*EIF1AX*	*ESR1*	*FBXW7*	*FLI1*	*GNA11*	*HIST1H3E*	*ID3*
ARID1B	*BCL2L11*	*CBFB*	*CDKN2B*	*CUX1*	*EIF4A2*	*ETS1*	*FGF1*	*FLT1*	*GNA13*	*HIST1H3F*	*IDH1*
ARID2	*BCL2L2*	*CBL*	*CDKN2C*	*CXCR4*	*EIF4E*	*ETV1*	*FGF10*	*FLT3*	*GNAQ*	*HIST1H3G*	*IDH2*
ARID5B	*BCL6*	*CCND1*	*CEBPA*	*CYLD*	*EML4*	*ETV4*	*FGF14*	*FLT4*	*GNAS*	*HIST1H3H*	*IFNGR1*
IGF1	*KAT6A*	*LRP1B*	*MEF2B*	*MYD88*	*NSD1*	*PDGFRB*	*PMS1*	*PTPRS*	*REL*	*SDHD*	*SOX10*
IGF1R	*KDM5A*	*LYN*	*MEN1*	*MYOD1*	*NTRK1*	*PDK1*	*PMS2*	*PTPRT*	*RET*	*SETBP1*	*SOX17*

Table 2. 56 RNA fusion gene targets

Genes targeted for fusion, exon skipping, and alternatively spliced variant detection by RNA sequencing											
ABL1	*BCL2*	*CSF1R*	*ESR1*	*EWSR1*	*FLI1*	*KIF5B*	*MSH2*	*NRG1*	*PAX3*	*PIK3CA*	*ROS1*
AKT3	*BRAF*	*EGFR*	*ETS1*	*FGFR1*	*FLT1*	*KIT*	*MYC*	*NTRK1*	*PAX7*	*PPARG*	*RPS6KB1*
ALK	*BRCA1*	*EML4*	*ETV1*	*FGFR2*	*FLT3*	*KMT2A*	*NOTCH1*	*NTRK2*	*PDGFRA*	*RAF1*	*TMPRSS2*
AR	*BRCA2*	*ERBB2*	*ETV4*	*FGFR3*	*JAK2*	*MET*	*NOTCH2*	*NTRK3*	*PDGFRB*	*RET*	*TP53*
AXL	*CDK4*	*ERG*	*ETV5*	*FGFR4*	*KDR*	*MLLT3*	*NOTCH3*				

Table 1. 523 DNA gene targets (Part 2)

Genes targeted for SNP, InDel, and copy number variation (CNV) detection by DNA sequencing											
IGF2	*KDM5C*	*LZTR1*	*MET*	*NAB2*	*NTRK2*	*PDPK1*	*PNRC1*	*QKI*	*RFWD2*	*SETD2*	*SOX2*
IKBKE	*KDM6A*	*MAGI2*	*MGA*	*NBN*	*NTRK3*	*PGR*	*POLD1*	*RAB35*	*RHEB*	*SF3B1*	*SOX9*
IKZF1	*KDR*	*MALT1*	*MITF*	*NCOA3*	*NUP93*	*PHF6*	*POLE*	*RAC1*	*RHOA*	*SH2B3*	*SPEN*
IL10	*KEAP1*	*MAP2K1*	*MLH1*	*NCOR1*	*NUTM1*	*PHOX2B*	*PPARG*	*RAD21*	*RICTOR*	*SH2D1A*	*SPOP*
IL7R	*KEL*	*MAP2K2*	*MLLT3*	*NEGR1*	*PAK1*	*PIK3C2B*	*PPM1D*	*RAD50*	*RIT1*	*SHQ1*	*SPTA1*
INHA	*KIF5B*	*MAP2K4*	*MPL*	*NF1*	*PAK3*	*PIK3C2G*	*PPP2R1A*	*RAD51*	*RNF43*	*SLIT2*	*SRC*
INHBA	*KIT*	*MAP3K1*	*MRE11A*	*NF2*	*PAK7*	*PIK3C3*	*PPP2R2A*	*RAD51B*	*ROS1*	*SLX4*	*SRSF2*
INPP4A	*KLF4*	*MAP3K13*	*MSH2*	*NFE2L2*	*PALB2*	*PIK3CA*	*PPP6C*	*RAD51C*	*RPS6KA4*	*SMAD2*	*STAG1*
INPP4B	*KLHL6*	*MAP3K14*	*MSH3*	*NFKBIA*	*PARK2*	*PIK3CB*	*PRDM1*	*RAD51D*	*RPS6KB1*	*SMAD3*	*STAG2*
INSR	*KMT2A*	*MAP3K4*	*MSH6*	*NKX2-1*	*PARP1*	*PIK3CD*	*PREX2*	*RAD52*	*RPS6KB2*	*SMAD4*	*STAT3*
IRF2	*KMT2B*	*MAPK1*	*MST1*	*NKX3-1*	*PAX3*	*PIK3CG*	*PRKAR1A*	*RAD54L*	*RPTOR*	*SMARCA4*	*STAT4*
IRF4	*KMT2C*	*MAPK3*	*MST1R*	*NOTCH1*	*PAX5*	*PIK3R1*	*PRKCI*	*RAF1*	*RUNX1*	*SMARCB1*	*STAT5A*
IRS1	*KMT2D*	*MAX*	*MTOR*	*NOTCH2*	*PAX7*	*PIK3R2*	*PRKDC*	*RANBP2*	*RUNX1T1*	*SMARCD1*	*STAT5B*
IRS2	*KRAS*	*MCL1*	*MUTYH*	*NOTCH3*	*PAX8*	*PIK3R3*	*PRSS8*	*RARA*	*RYBP*	*SMC1A*	*STK11*
JAK1	*LAMP1*	*MDC1*	*MYB*	*NOTCH4*	*PBRM1*	*PIM1*	*PTCH1*	*RASA1*	*SDHA*	*SMC3*	*STK40*
JAK2	*LATS1*	*MDM2*	*MYC*	*NPM1*	*PDCD1*	*PLCG2*	*PTEN*	*RB1*	*SDHAF2*	*SMO*	*SUFU*
JAK3	*LATS2*	*MDM4*	*MYCL*	*NRAS*	*PDCD1LG2*	*PLK2*	*PTPN11*	*RBM10*	*SDHB*	*SNCAIP*	*SUZ12*
JUN	*LMO1*	*MED12*	*MYCN*	*NRG1*	*PDGFRA*	*PMAIP1*	*PTPRD*	*RECQL4*	*SDHC*	*SOCS1*	*SYK*
TAF1	*TCF7L2*	*TET2*	*TGFBR2*	*TNFRSF14*	*TP63*	*TSC2*	*VHL*	*WT1*	*XRCC2*	*ZBTB2*	*ZNF217*
TBX3	*TERC*	*TFE3*	*TMEM127*	*TOP1*	*TRAF2*	*TSHR*	*VTCN1*	*XIAP*	*YAP1*	*ZBTB7A*	*ZNF703*
TCEB1	*TERT*	*TFRC*	*TMPRSS2*	*TOP2A*	*TRAF7*	*U2AF1*	*WISP3*	*XPO1*	*YES1*	*ZFHX3*	*ZRSR2*
TCF3	*TET1*	*TGFBR1*	*TNFAIP3*	*TP53*	*TSC1*	*VEGFA*					

Table 3. 26 MSI loci

Genes targeted for microsatellite length detection by DNA sequencing											
BAT25	*BAT40*	*D17S250*	*D17S787*	*D18S61*	*D18S69*	*D2S123*	*D5S107*	*D7S519*	*NR21*	*NR24*	*D18S35*
BAT26	*D10S196*	*D17S588*	*D18S55*	*D18S64*	*D20S100*	*D3S1029*	*D5S346*	*D8S87*	*NR22*	*MONO-27*	*HSP110-T17*
BAT34C4	*D13S175*										

Ordering Information

Product	Contents	Number of samples	Panel variant number	Cat. no.
QIAseq Multimodal HC Panel; Pan Cancer Panel	Kit containing ALL reagents (except indexes) for multimodal (DNA and RNA) sequencing	12	UHS-5000Z-12	333942
		96	UHS-5000Z-96	333945
QIAseq Multimodal Index I Set A SW (96)	Box containing adapters, enough to process a total of 96 samples, for Multimodal panel sequencing on Illumina platforms using separate enrichment workflows; one of two sets required for multiplexing 96 samples	96	N/A	333985
QIAseq Multimodal Index I Set B SW (96)	Box containing adapters, enough to process a total of 96 samples, for Multimodal panel sequencing on Illumina platforms using separate enrichment workflows; two of two sets required for multiplexing 96 samples	96	N/A	333995

Visit **go.qiagen.com/QIAseqmultimodal** and discover how youcan double your NGS insights and free up half of your resources.

The QIAseq Pan Cancer Multimodal Panel is intended for molecular biology applications. This product is not intended for the diagnosis, prevention, or treatment of a disease.

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.

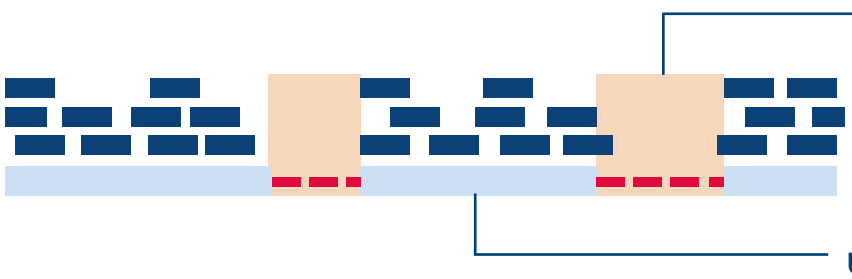
We've got you covered

With the **QIAseq® Human Exome** solution for rare variant detection

>60% of disease-causing mutations are found in protein-coding regions of the genome.

Compared to whole genome sequencing (WGS), **whole exome sequencing (WES)** focuses on coding regions, offering powerful variant detection power while **reducing time and expense**.

Uniform sequencing coverage is crucial

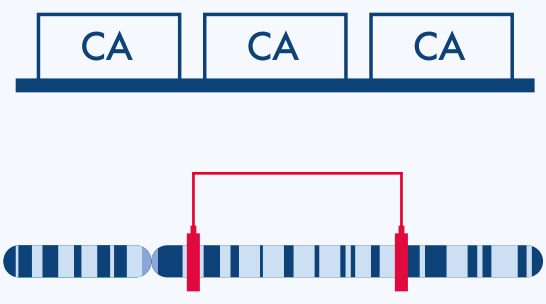


Uneven coverage can result in low coverage of important genomic regions.

Uniform coverage is required for efficient variant discovery.

Causes of uneven coverage

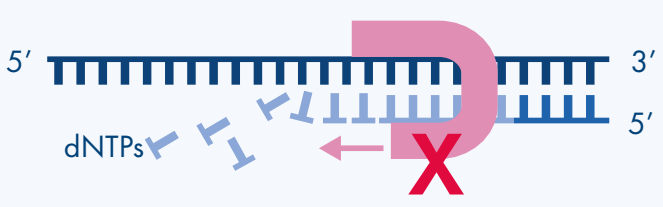
Uneven sequence coverage is linked to **repeat elements** and **segmental duplications**.



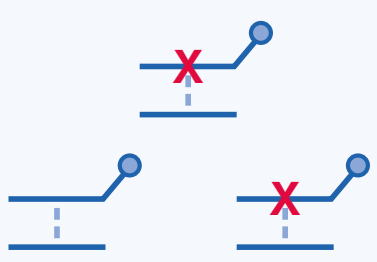
But is mainly attributed to **>65% GC content**

High GC content reduces the efficiency of:

01 PCR amplification



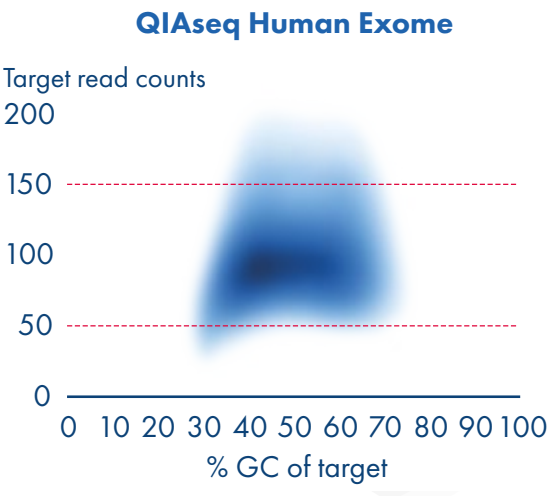
02 Capture probe hybridization

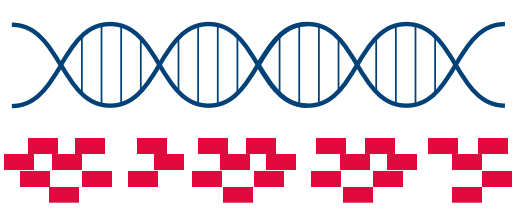


Overcoming GC bias

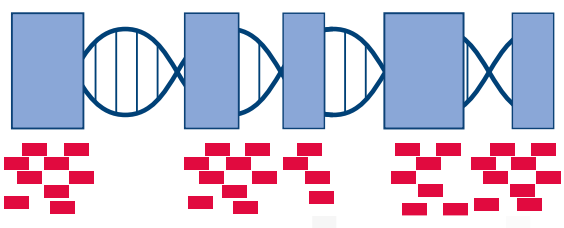
The **QIAseq Human Exome** solution is optimized to **minimize GC bias**, giving uniform exome coverage.

Plus, **QIAseq Human Exome** provides many reads per position, delivering WGS-quality variant data without the expense.



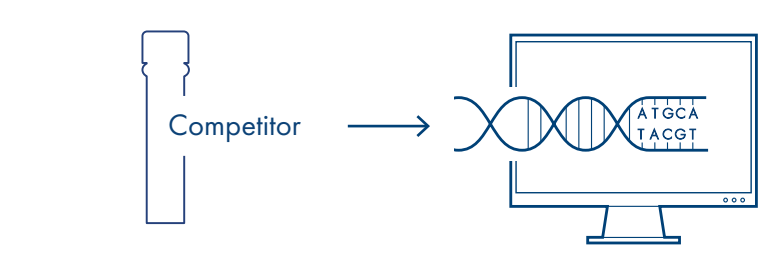


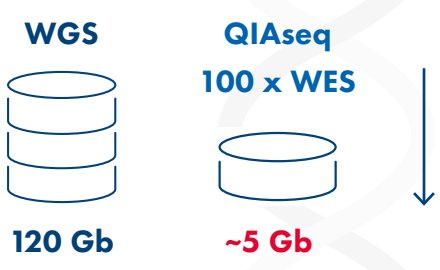
WGS

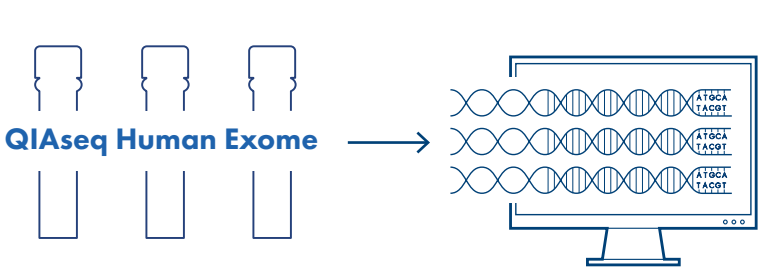


WES with QIAseq

QIAseq Human Exome reduces sequencing needs by **50%**, allowing more samples per run but produces just **~5 Gb** of data.







As a result, QIAseq Human Exome reduces costs by **30–50%**.

QIAseq Human Exome was built with researchers' needs in mind

6 sample types supported: gDNA derived from whole blood, cells, tissue, saliva, FFPE and cfDNA

1-day workflow, compatible with automation and scalable

50% reduction in sequencing costs

33% less time than competitors

References

1. Wang, Q. et al. (2017) Novel metrics to measure coverage in whole exome sequencing datasets reveal local and global non-uniformity. Sci. Rep. 7, 885.
2. Chilamakuri, C.S., et al. (2014) Performance comparison of four exome capture systems for deep sequencing. BMC Genomics. 15, 449.

Ordering **www.qiagen.com/shop** | Technical Support **support.qiagen.com** | Website **www.qiagen.com**