Trust QIAGEN Experts with Your Samples

Trust Service Core

Sample preparation,
gene expression research,
and genomic analyses

QIAGEN®

Sample & Assay Technologies

Let us process your samples!

Focus on your research goals instead of sample processing

Our complete service for genomic and expression analysis delivers robust and reproducible results. QIAGEN experts use cutting-edge technology that yields superior results for researchers in academic, governmental, and industrial settings. Our offer covers the whole workflow, from sample to result — and we provide the steps individually or as a full service, depending on your needs.

What is QIAGEN's Service Core?

Simply put, it is our expertise working for you!

As an innovative market leader, QIAGEN has long years of expertise in creating sample and assay technologies that enable you to obtain content from a whole range of biological samples. Now, QIAGEN Service Core combines these high-quality, reliable technologies with the unrivaled knowledge and experience of our scientists.

Free up your valuable time — let our scientists do your sample preparation, gene expression work, and genomic analyses. With QIAGEN processing your samples, you'll be sure of reliable answers from your precious samples.

We offer services for:

- DNA, miRNA, and RNA isolation
- Whole genome amplification
- Content-centered PCR assay panels
- Whole genome expression profiling and genotyping
- Sanger sequencing

DNA and RNA isolation

For isolation of high-quality genomic DNA, RNA, and miRNA

QIAGEN Service Core supports you with the preparation of high-quality nucleic acids for a whole range of downstream applications. We'll even support you with isolation from challenging samples, such as formalin-fixed, paraffin-embedded samples, laser capture microdissection samples, fine-needle aspiration biopsies, and inhibitor-laden samples. Trust us to obtain nucleic acids from your precious samples.

We offer:

- A broad portfolio of sample technologies to optimally suit your sample and application
- Full support of customer needs for automation, bar coding, or standardization
- Quantification and estimation of sample purity
- High-throughput capability
- A stand-alone service or a combination with other QIAGEN services

"Thank you for the excellent and remarkably efficient work."

DNA isolation service customer, UK

Starting material

Our standard offer covers blood, serum, plasma, PAXgene® stabilized blood, frozen tissue, FFPE tissue, cultured cells, buccal swabs, and saliva. We also process other sample types on request.

Results provided

Each purified sample is assessed with absorbance measurements for concentration and yield (A_{260}/A_{280}, A_{260}/A_{230}). Additional quality control assessments are available on request:

- Electrophoretic analysis of DNA or RNA integrity
- Comprehensive RNA quality control using PCR arrays
- qPCR amplification efficiency of purified DNA using proprietary, multi-copy loci

Whole genome amplification

For highly uniform DNA amplification from precious samples

Do you have small or precious samples for DNA work? Our team uses multiple displacement amplification based on our proven REPLI-g® technology to obtain large amounts of DNA from limited samples with minimal sequence bias. The resulting DNA is suitable for next-generation sequencing, qPCR, and microarray analyses (Figure 1).

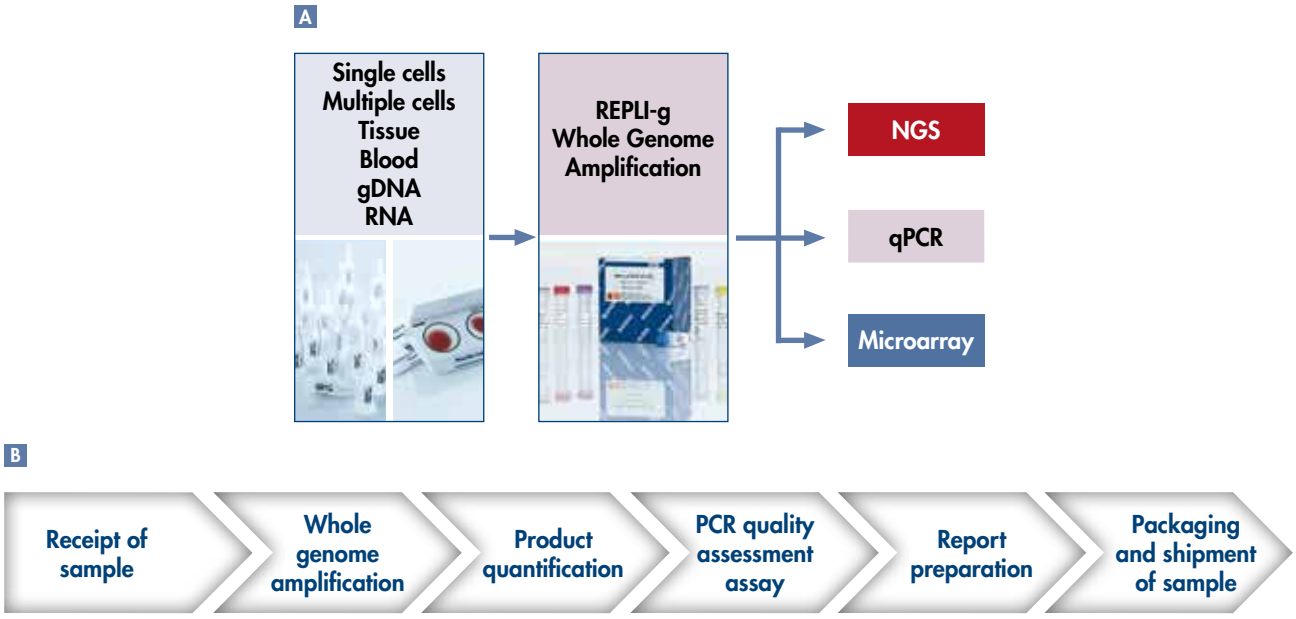

Figure 1. QIAGEN Service Core WGA workflow. A An overview of the starting material, core WGA process, and downstream processes. B The WGA workflow in detail.

What does our service include?

- Reproducible amplification from a variety of starting materials
- Scalable service, with 100 µg and 500 µg standard scales
- Extensive quality assessment, including detailed reports
- Customized workflows to meet your needs

Our stringent quality control assay provides information on the quality of the amplified DNA, enabling reliable predictions for the success of your downstream assays, such as assessments of tumor samples (Figures 2 and 3).

Starting material

A variety of samples can be submitted, including genomic DNA, whole blood, dried blood cards, buffy coat, buccal swabs, fresh or frozen tissue, and tissue culture cells.

Results provided

We provide results as Excel® files, including:

- A report with yields and assessment of the quality of the amplifications
- A work sheet with the results in a tabular format

We deliver data on a CD-ROM that is shipped together with the amplified DNA samples or via a secure Accellion® download server.

"QIAGEN has supported us with several service orders. For all of them, our customers were fully satisfied. Keep it up! Thank you for your excellent service."

Product specialist, PCR array and qPCR assay service customer, Le Perray en Yvelines, France

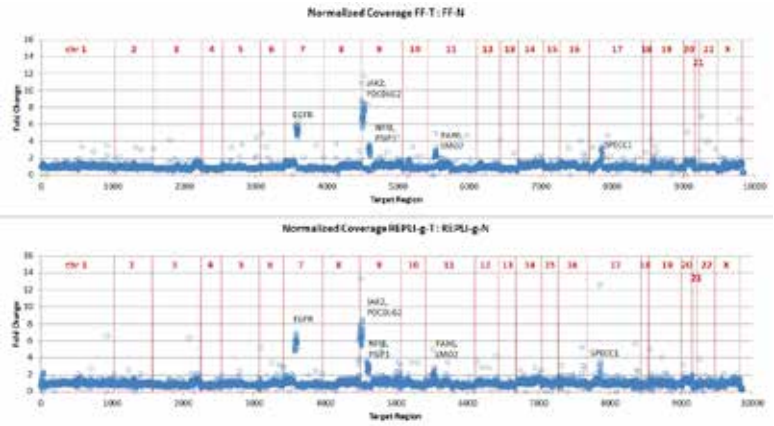

Figure 2. Copy number changes in tumor and normal samples. A comparison of the copy number changes in a bladder tumor sample compared to those in normal tissue obtained after sequencing of TruSeq™ libraries generated from genomic DNA (upper panel) and REPLI-g DNA (lower panel). Genomic DNA was isolated from tumor (**T**) and normal tissue (**N**) using the DNeasy® Blood & Tissue Kit (QIAGEN, cat. no. 69504). Subsequently, 10 ng of purified genomic DNA was amplified with the REPLI-g Mini Kit (QIAGEN, cat. no. 150025). The DNA was sheared with ultrasound and shotgun TruSeq libraries were generated from both the genomic DNA and REPLI-g DNA for normal and tumor samples according to the manufacturer's protocol. After targeted enrichment of the coding regions from 587 cancer genes using NimbleGen™ hybrid capture technology and subsequent sequencing on a Illumina® MiSeq®, the copy number changes in the tumor sample were calculated for the 9860 target regions. Comparable changes in the copy numbers were detected for the tumor samples of both library pairs in regions on chromosome 7 (EGFR gene), chromosome 9 (JAK2, PDCDLG2, NFIB, and PSIP1 genes), chromosome 11 (PAX6 and LMO2 genes), and chromosome 17 (SPECC1 gene).

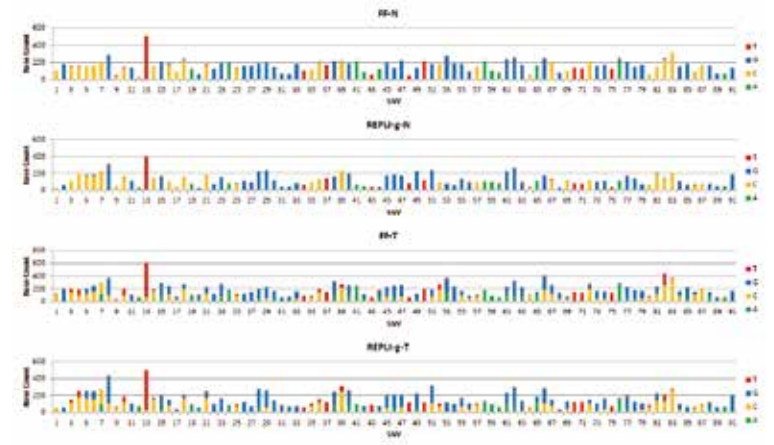

Figure 3. Comparison of somatic mutations in samples. After the process described in Figure 2, the samples were analyzed using CLC Cancer Workbench software. Ninety-one SNVs were found in the target regions of both library pairs after sequence alignment to the human reference sequence hg19, local realignment, duplicate removal, low-frequency variant calling, removal of germline and reference variants, and manual inspection of the aligned sequence data. For SNV positions all 4 bases were counted and plotted as stacked columns. The upper two panels show the 4 bases of the 91 positions from normal tissue and the lower two panels show the base counts from the same positions of the tumor sample for both library pairs.

Content-centered PCR assay panels

For pathway-focused, disease-focused, and custom gene profiling

QIAGEN offers content-centered PCR assays that allow simultaneous monitoring of the expression of up to 84 or 370 pathway-focused genes on a single plate. Our wet-lab verified assays and optimized processes yield outstanding data quality and have a rapid turnaround time. Assays can be custom designed to analyze any gene, even those not currently within our broad gene and species coverage.

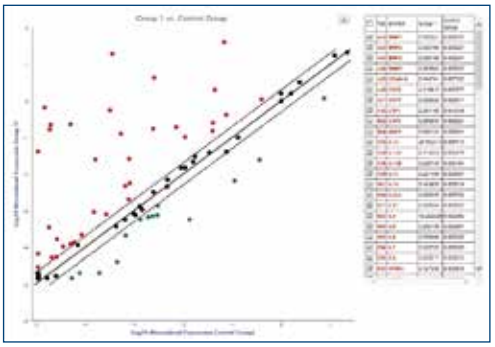

Figure 4. Example of a miScript PCR Array report.

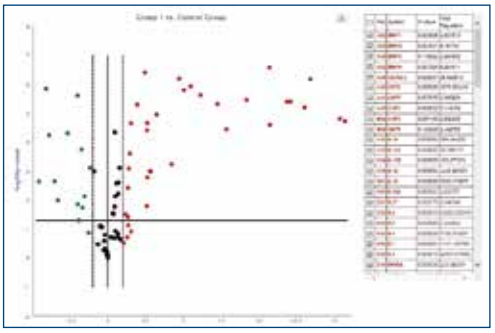

Figure 5. Example of an RT² Profiler Array report.

Our miRNA PCR assays provide:

- Sensitive, highly specific miRNA profiling
- The broadest coverage available with up-to-date miRNome versions
- Preamplification for precious samples
- A variety of plant miRNA assays

Figure 4 shows an example of a QIAGEN miScript® PCR Array report.

Our mRNA PCR assays provide:

- Sensitive, highly specific mRNA profiling
- A choice of over 20,000 assays
- Preamplification for precious samples
- Option of lncRNA profiling

Figure 5 shows an example of a QIAGEN RT² Profiler Array report.

We also offer a high-throughput qPCR service for gene or miRNA expression profiling of more than 48 samples. It uses the Fluidigm® Biomark™ platform, with specifically designed, optimized, and verified assays and reagents for gene and miRNA expression. You may select either panels of mRNA or miRNA or screen the various versions of the miRBase miRNome for biomarker panel selection.

"I used QIAGEN's services for RNA purification and PCR array and was very happy with the results."

Stem cell and immunology researcher, RNA isolation and PCR array service customer, Boston, MA

Our DNA PCR assays provide:

- Somatic mutation detection, copy number analysis, microbial profiling
- Complete gene mutation panels
- Over 10 million qBiomarker copy number assays

The full workflow for PCR arrays begins with receipt of sample and ends with data delivery (Figure 6).

Starting material

Our standard offer covers purified nucleic acids, blood, serum, plasma, PAXgene-stabilized blood, frozen tissue, FFPE tissue, cultured cells, buccal swabs, and saliva. We also process other sample types on request.

Results provided

PCR assay data sets are provided as scientist-compiled reports with an Excel worksheet in a tabular format.

Data included in reports.

Data and analyses	C_T values, housekeeping gene selections, quality control reports, calculated results, 3D profiles, scatter plots (Figure 4), volcano plots (Figure 5)
	Pair-wise comparisons between groups of experimental replicates based on your definitions
	Analyses of differences in gene expression between samples based on $\Delta\Delta C_T$ change-fold calculations

Data delivery is via our secure Accellion download server. In addition, we offer a web-based software package that enables you to perform individual analyses (e.g., change the stringency of fold-change or statistical significance thresholds).

"We were very happy with the results of the serum array that QIAGEN performed for us. We'd like to expand the analysis to include more samples."

PCR array customer, UK.

Figure 6. Workflow for PCR arrays.

Whole genome expression profiling and genotyping

For whole genome SNP genotyping and genome-wide expression analysis

QIAGEN offers whole genome gene expression profiling services using the Illumina iScan® platform and direct hybridization assay-based whole genome expression BeadChips (standard and custom content). We are an Illumina-certified provider with fully trained and certified technical staff. We rapidly deliver outstanding data quality. Our workflow, from receipt of sample to data delivery, is illustrated in Figure 7.

Starting material

High-quality purified nucleic acids from a variety of tissue and biofluid sources can be used.

Results provided

We always provide scientist-compiled reports that are available via secure download. Report formats include:

- Raw data in Excel and text formats
- Fold changes in Excel and text formats
- Summary data using the fold-change cutoff and p-value of your choice

"The service was great. I am actually interested in sending 12 more samples that I would like to have analyzed using 3 pathways."

Psychiatry researcher, Service Core customer, Chicago, IL

Figure 7. Workflow for whole genome expression profiling and genotyping.

Sanger sequencing

For the highest standards in contract DNA sequencing

QIAGEN offers a wide range of Sanger sequencing services. Our single-read services enable routine sequencing of plasmids, PCR products, and siRNA expression vectors in the 96-well format. QIAGEN's verification services allow resequencing and comparison with reference sequences, and our de novo sequencing services enable analysis of unknown sequences, from single-stranded primer walking to patent quality. Optional template DNA purification is available for all services. Figure 8 illustrates our workflow.

- Template purification with QIAGEN technology
- Single-read services (96-well format only), verification sequencing, and de novo sequencing
- Outstanding data quality with fast delivery

Starting material

Your sequencing samples can be bacterial clones, PCR products, or plasmid DNA in 96-well plates (single-read services, verification, and de novo sequencing) or in tubes (verification and de novo sequencing).

Results provided

We always provide scientist-compiled reports that are available via secure download through our Accellion server (an example is shown in Figure 9).

Data included in reports.

For every sequence read	Phred20 analysis, .AB1, scf trace files, and seq files in txt format
Verification sequencing reports	Insertions, deletions, and mismatches between reference sequence and sequencing data, and alignment between reference sequence and sequencing data


QIAGEN | Genomic Services

Verification Sequencing Report

QSS3333 (Verification)

This report was generated on April 16th, 2014.
Of 801 bases in the alignment 793 matched the reference (99.00 %). 8 bases do not match, all bases in this report have been sequenced. Please Note: All positions are given relative to those of the original reference sequence. Dots represent a perfect match of the obtained sequence with the reference. Here are the results in more detail:

Insertions
An insertion of 3 bases has been detected at this site
84 +TAT

Deletions
A deletion of 3 bases has been detected at this site
213 -ATT

Mismatches
22 G>T; 55 G>A

Uncovered Regions
All bases have been verified.

Alignment

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Figure 9. Detailed Verification Sequencing Report. Insertions, deletions, and mismatches between reference sequence and sequencing data are marked in blue.

Figure 8. Workflow for Sanger sequencing.

Overview

Consultation

During the consultation, our trained application scientists discuss the goals of your project or study to develop a clear plan. Various technologies and platforms are assessed to provide the most appropriate and cost-effective options. Once the research plan takes shape, timelines are discussed. The Service Core also shares SOPs and protocols that may be relevant to the project. At the conclusion of the consultation, a representative from QIAGEN delivers a quotation for discussion and approval.

"I must say it has been a pleasure working with QIAGEN Service Core over the past couple of years. The sequences received have always been of the highest quality with a very fast turnaround time and extremely helpful interactions with your personnel."

Sequencing service customer, Heidelberg, Germany

Sample submission

During the consultation phase, you receive recommendations on how to package and ship samples to the appropriate QIAGEN laboratory. The Service Core handles projects of all sizes, from as few as six up to several thousand samples. We also supply an electronic sample submissions form. Simply ship the samples to the Service Core team, along with this sample submission form, and the purchasing information — ideally both as email and printout.

Sample preparation

As the samples for research studies arrive, they are delivered directly to Service Core scientists. We will contact you if there are questions about labeling or damage during shipment. Depending on the type of samples submitted and/or the downstream analysis, different protocols are initiated, such as RNA isolation. However, in all cases the samples are quantified and assessed for quality to ensure that each sample can reliably yield data. Any samples that fail quality control can be removed from the study or replaced with new samples. Typical quality assurance tests may include electrophoretic analysis of RNA or DNA, calculated integrity scores of RNA, or qPCR-based functional tests of nucleic acid integrity. If no downstream analysis is to be performed, then the samples are prepared for shipment and and we contact you to arrange receipt of the shipment.

Analysis

The prepared and quality controlled samples are analyzed using the previously agreed-upon research protocols and platforms. Raw data are collected and then analyzed using the appropriate software tools. Often these tools are software packages developed by QIAGEN for specific technologies. Sample data sets can be provided for most types of analysis.

Results delivered

Results are delivered via the secure Accellion download server with client-specific access, unless otherwise specified. After the data are delivered, you are invoiced for the completed and delivered results.

Contact QIAGEN for a personal consultation today!

Our Service Center for the United States is located in Frederick, MD. Our Service Center for worldwide clients is in Hilden, Germany.

USA: LifeScienceServiceUS@qiagen.com

Worldwide: LifeScienceService@qiagen.com

Visit www.qiagen.com/services for more details on our available services.

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Austria ▪ Orders 0800-28-10-10 ▪ Fax 0800-28-10-19 ▪ Technical 0800-28-10-11

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Canada ▪ Orders 800-572-9613 ▪ Fax 800-713-5951 ▪ Technical 800-DNA-PREP (800-362-7737)

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