

QIAGEN® Service Core

For gene expression and genomic analysis

QIAGEN provides a complete service for genomic and expression analysis that delivers robust and reproducible results. The Service Core at QIAGEN accepts and processes a variety of biological samples and then leverages cutting-edge tools for either pathway-focused or genomewide analysis, yielding superior results for scientists in academic, government, and industry settings.

Advantages of using the QIAGEN Service Core:

- Reliable results — experiments are performed by our technical experts
- Cost savings — no need to invest in capital equipment and reagents
- Time savings — we do the bench work for you, maximizing your efficiency

Table 1. Services provided by the QIAGEN Service Core

Type of service	RNA service	DNA service
Pathway-focused analysis	Gene expression miRNA expression	Mutation detection Gene copy number Methylation
Individual gene/locus analysis	Gene expression miRNA expression	Mutation detection Gene copy number Methylation
Whole genome analysis	Illumina® expression profiling miRNome profiling	SNP genotyping Copy number genotyping
Sample preparation	Cells or tissue Blood, plasma, sera Fixed tissue Small sample	Cells or tissue Blood, plasma, sera Fixed tissue Small sample

Applications

Pathway-focused analysis

Real-time PCR is a powerful tool for verifying results from whole genome expression profiling, genotyping, methylation, or pathway analysis. As an experienced leader in providing qPCR reagents and assay design, the Service Core delivers rapid and reproducible results for:

- RT² Profiler PCR Array analysis (pathway-focused and custom PCR arrays)
- miScript® miRNA PCR Array analysis (pathway-focused, miRNome, and custom PCR arrays)
- qBiomarker Somatic Mutation PCR Array analysis (pathway-focused and custom PCR arrays)
- qBiomarker Copy Number PCR Array analysis (pathway-focused and custom PCR arrays)
- EpiTect® Methyl II PCR Array analysis (pathway-focused and custom PCR arrays)



Whole genome analysis

The Service Core uses the Illumina Beadchip Platform to provide whole genome expression profiling, cytogenetic analysis, and single nucleotide polymorphism (SNP) genotyping. As an Illumina CPro® (certified service provider), our team of highly trained scientists has the necessary expertise to analyze your biological samples. Our Service Core has undergone a rigorous 2-phase certification process including minimum data generation, data certification, and an on-site audit of the facility.

Available analysis services include:

- Expression profiling (human, mouse)
- SNP genotyping and copy number variation analysis

Nucleic acid isolation

High-quality sample isolation and integrity are fundamental to the success of any biological analysis. The Service Core provides expertise in RNA and DNA isolation from a variety of biological samples. Each sample is evaluated for concentration and degradation to ensure successful future analysis.

Available sample isolation services include:

- RNA or DNA isolation from cells, tissue, FFPE samples, or biofluids
- Whole genome amplification
- Integrity/degradation testing for every sample
- Bisulfite conversion for DNA methylation

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.

Find out more about our Service Core today!

E-mail support@SABiosciences.com or visit www.SABiosciences.com.

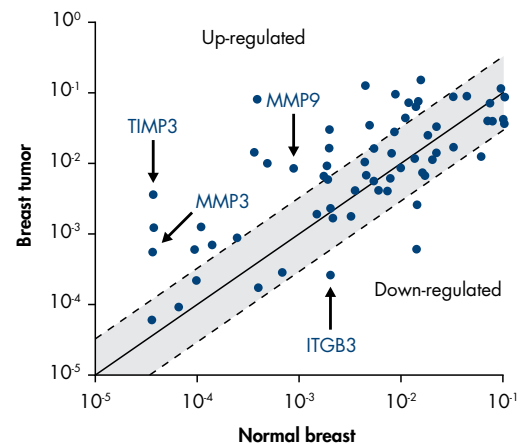


Figure 1. Example of gene expression profiling data that can be provided by the QIAGEN Service Core.

In this experiment, triplicate total RNA samples from normal human breast and a human breast tumor were characterized using the Human Extracellular Matrix and Adhesion Molecules RT² Profiler PCR Array. Genes encoding the matrix metalloproteinases (MMP3 and MMP9) and their inhibitors (TIMP3) are up-regulated, while genes encoding integrins (ITGB3 and ITGB4, not shown) are down-regulated by at least 3-fold in breast tumors relative to normal tissue.

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