Overcoming the clinical research sample bottleneck for expression studies

Using clinical research samples is a unique opportunity to make impactful discoveries since the rich annotation accompanying each sample can be directly correlated with genomic data and future clinical outcomes.

Common clinical research samples include formalin-fixed, paraffin-embedded (FFPE) tissues, blood, and small biopsies, all of which are technically challenging to work with, only available in limited amounts, and often of poor quality. Applied Biosystems™ Clariom™ Pico assays, the next generation of transcriptome profiling tools, are designed to produce accurate and reliable results from a wide spectrum of clinical research samples and very low input requirements, giving researchers the confidence needed to conduct experiments with precious samples.

Designed to reduce data variability from whole blood

Blood is a very desirable sample type for research because collection is relatively noninvasive and inexpensive, plus specimens are widely available. The most reproducible expression results from blood samples are produced when total RNA is extracted from isolated leukocytes. Unfortunately, this approach can affect the transcriptome profile, and is cumbersome and impractical in a clinical research setting. Therefore, researchers need easy and robust gene expression protocols that work with whole blood. However, 70% of the mRNA in whole blood is globin mRNA released from red blood cells, which can introduce noise and decrease transcript detection sensitivity. Most expression technologies that can use whole blood require the removal of globin mRNA from the sample before processing, which can be a time-consuming and costly step that introduces bias.

Clariom Pico assays generate robust transcriptome expression data from small amounts of whole blood without the need to eliminate globin mRNA, which helps save time and money while retaining data integrity.

Unlocking data from FFPE samples

It is estimated that there are more than 1 billion archived FFPE samples globally. Well-annotated FFPE samples provide a great resource for clinical researchers, as they provide the ability to conduct large-scale retrospective studies, particularly in cancer research. However, it can be challenging to generate reliable gene expression data from FFPE samples since the RNA yielded is often of poor quality and in low quantity.

Formalin is notoriously harsh on cellular and genetic material, and storage in paraffin causes degradation of nucleic acids over time; thus, RNA extracted from archived FFPE samples can be difficult to analyze due to excessive fragmentation, base modification, and cross-linking to protein within the sample matrix. Further, these samples typically produce a limited amount of total RNA, presenting challenges when multiple genes and replicate measurements are required. As such, researchers will benefit most from expression technologies that can perform well with small amounts of heterogeneous and often degraded nucleic acids.

Clariom Pico assays provide researchers with the ability to reliably profile the whole transcriptome from highly degraded FFPE samples with as little as 500 pg of total RNA.

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Working with limited and small input

Expression profiling is the most widely accepted and robust method to describe the physiological state of cells or tissue types. For accurate profiling, many techniques require RNA input amounts generated from thousands to millions of cells. However, many fields of research—such as stem cell research, oncology, neuroscience, and immunology—work with specialized cell types and have only a limited number of cells available.

Not only are researchers sometimes technically limited by the amount of material available, there is also a growing desire to unmask inherent gene expression differences among small, defined populations of cells. This is achieved by selecting cells of a particular phenotype, accurately partitioning the cells, and profiling their transcriptomes. However, challenges remain with current technologies to extract reliable expression data from small, isolated cell subpopulations.

We help solve the problems associated with transcriptome profiling of limited amounts of RNA by providing assays that generate detailed, robust, and accurate data from as few as 10 cells or 100 pg of total RNA from a wide range of challenging clinical research sample types.

Uncover the secrets of the transcriptome from a few cells and clinical research sample types

Transcriptome-wide analysis of coding and noncoding genes, exons, and splice variants:

- **Applied Biosystems™ Clariom™ D Pico Assay, human**
- **Applied Biosystems™ Clariom™ D Pico Assay, mouse**
- **Applied Biosystems™ Clariom™ D Pico Assay, rat**

Transcriptome-wide analysis of well-annotated genes:

- **Applied Biosystems™ Clariom™ S Pico Assay, human**
- **Applied Biosystems™ Clariom™ S Pico Assay, mouse**
- **Applied Biosystems™ Clariom™ S Pico Assay, rat**

Find out more at **thermofisher.com/microarrays**

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