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Biology for a better world

RNA biomarkers clarified. See further. Now.

Clariom™ assays

Next-generation transcriptome profiling tools

The power of Clariom assays

Patients don't have the luxury of time. Neither do translational scientists. Accelerate your expression biomarker discovery with Clariom assays, the next generation of transcriptome profiling tools providing the fastest path to actionable results.

Recent advanced transcriptome analyses have uncovered thousands of splice variants and long non-coding (lnc)RNAs, providing new sources for biomarker discovery. Given the complexity of the transcriptome, however, finding informative expression biomarkers is challenging, time-consuming, and costly. Clariom assays, built using the latest transcriptome knowledge from multiple databases, are the simplest and fastest tools for finding high-fidelity expression biomarkers. They are compatible with clinical samples, available in scalable formats for different throughput needs, and include flexible, intuitive software for fast and simple analysis.

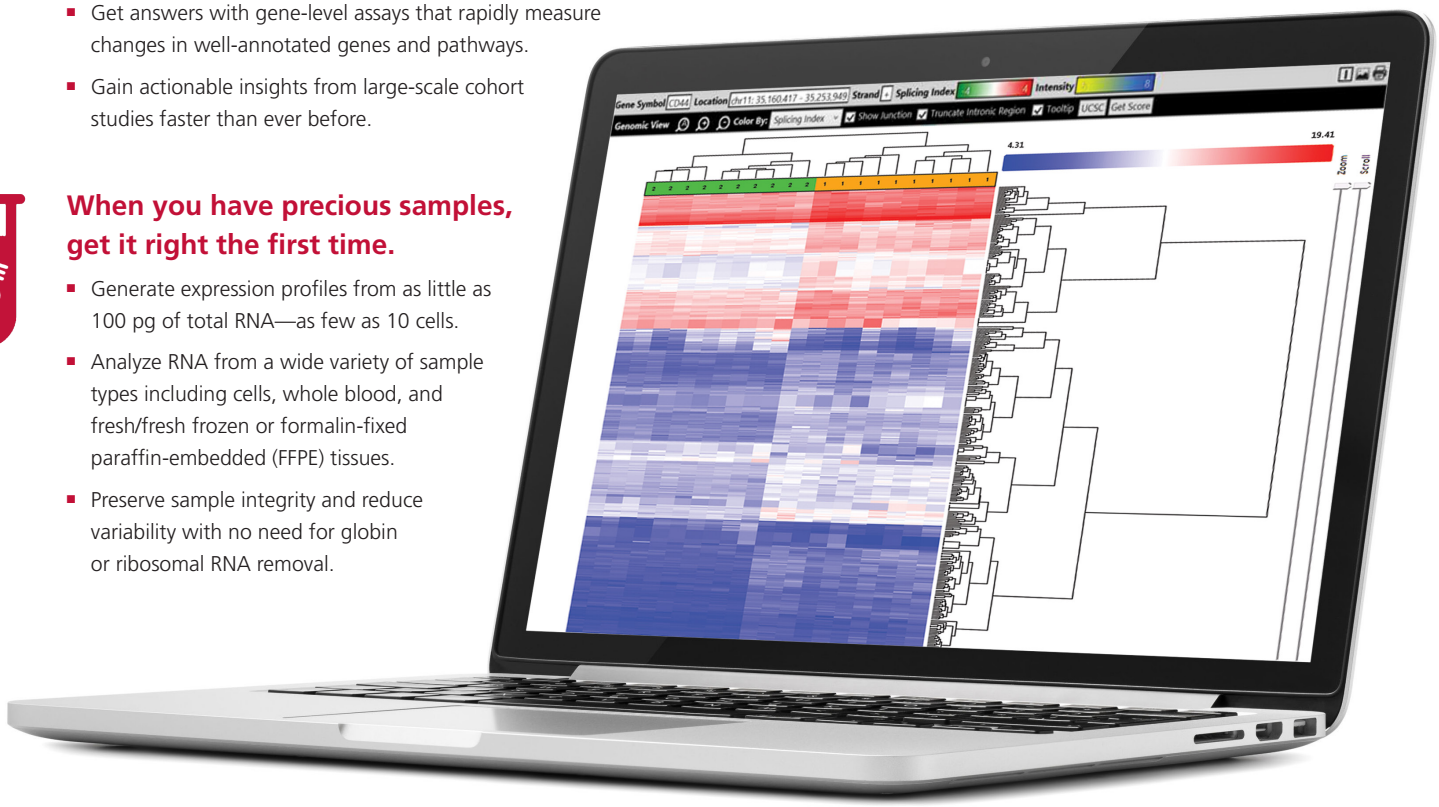
Get the comprehensive coverage you need, the reproducibility you require, and the insights you want to act quickly on your discoveries.

Get the data you need. Now.

- Confidently identify complex biomarker signatures and investigate significantly altered pathways.
- Quickly find key biomarkers with transcriptome-level assays that detect coding and long non-coding genes, exons, and alternative splicing events, including rare transcripts.
- Get answers with gene-level assays that rapidly measure changes in well-annotated genes and pathways.
- Gain actionable insights from large-scale cohort studies faster than ever before.

When you have precious samples, get it right the first time.

- Generate expression profiles from as little as 100 pg of total RNA—as few as 10 cells.
- Analyze RNA from a wide variety of sample types including cells, whole blood, and fresh/fresh frozen or formalin-fixed paraffin-embedded (FFPE) tissues.
- Preserve sample integrity and reduce variability with no need for globin or ribosomal RNA removal.

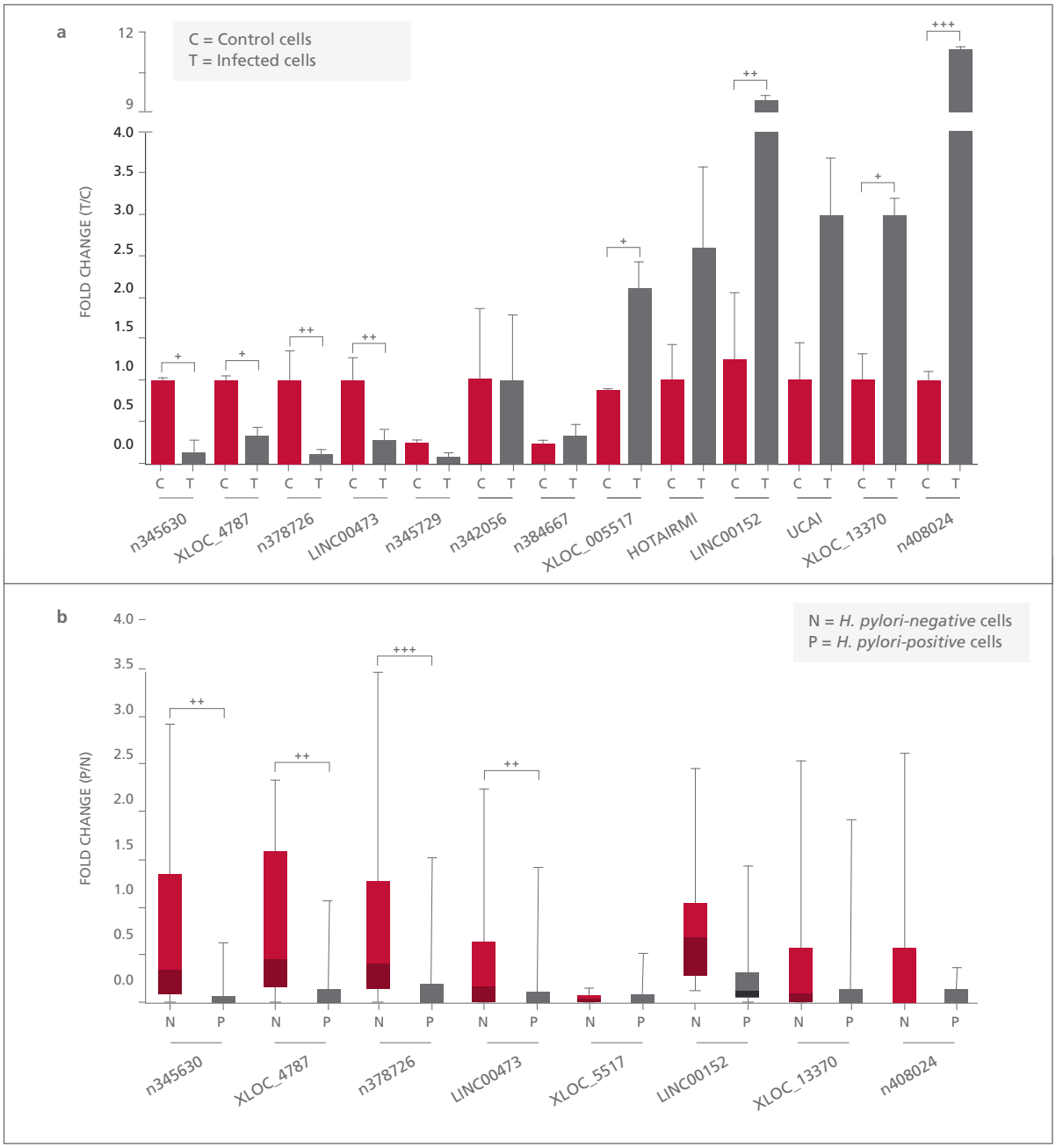


TAC Software hierarchical clustering view. Quickly arrange samples and genes into groups based on their expression levels.

The evidence

With increased knowledge of the transcriptome, a growing body of evidence has implicated lncRNAs as critical regulators of coding RNA and alternative splicing. Aberrant expression of these regulatory lncRNAs has been increasingly documented in a wide range of diseases, establishing their potential for use as biomarkers and therapeutic agents.

Transcriptome-level assays identified dysregulated lncRNAs in human gastric epithelial cells infected with *Helicobacter pylori*.



a) 13 candidate dysregulated lncRNAs identified by transcriptome-level assays were validated by qRT-PCR. Of those, eight samples expressed statistically significant differences in infected (T) vs. control (C) cells.

b) qRT-PCR validation of the same eight samples revealed four lncRNAs that were significantly differentially expressed in *H. pylori-positive* (P) vs. *H. pylori-negative* (N) cells.

Zhu, H., *et al.* Microarray analysis of long non-coding RNA expression profiles in human gastric cells and tissues with *Helicobacter pylori* infection. *BMC Medical Genomics* **8**:84 (2015).*

What researchers are saying

Transcriptome-level assays give all the information you need, without the wait.
Dr. Sridar Chittur (Center for Functional Genomics, University at Albany, State University of New York) finds the transcriptome-level assays very easy to use and intuitive to analyze. When principle investigators ask how they can get fast, publishable results, Dr. Chittur recommends transcriptome-level assays. With quick and intuitive TAC Software and no need for ribosomal reduction, he can go from samples to raw data in just a few days and obtain an analyzed gene list of differential expression with alternate splicing in a few hours. Dr. Chittur emphasized the value of analyzing expression of genes, transcripts, exons, and intergenic regions. With annotations for lncRNA, pseudogenes, and ribosomal RNA all derived from multiple sequence databases, researchers can use these assays to identify all known expressed isoforms, increasing the likelihood of finding transcripts of interest.

"Principle investigators come to the core lab and say, 'I have a grant that I am thinking of submitting next month. Would it be possible to get this piece of data because I want to put that in my grant?' With the arrays, it is doable."

Sridar Chittur, PhD, MBA
Research Associate Professor, Biomedical Sciences, Director, Microarray & HT Sequencing Core Facility,
Center for Functional Genomics, University at Albany, State University of New York

Microarray analysis reveals vital alternative splicing variants in endocrine-resistant breast cancer model cell lines. Dr. Yesim Gökmen-Polar (Indiana University School of Medicine) is investigating novel targets to overcome resistance to endocrine therapies, especially in estrogen receptor breast cancer. She is especially interested in understanding how alternative splicing isoforms affect responses to endocrine therapies. Dr. Gökmen-Polar chose transcriptome-level assays for her studies because she needs complete coverage of the entire transcriptome to analyze both high- and low-abundance transcripts of all known splicing isoforms. These studies revealed that Dr. Gökemen-Polar's resistant cell line models include the breast-cancer-specific variants that make a vital impact on the function of the CD44 invasion-resistance marker. Dr. Yesim Gökmen-Polar's goal is to translate these results into the clinical setting.

"I am a molecular biologist by training, and I can easily use this technology any time. I can go back to the software myself and further analyze other genes that are downstream."

Yesim Gökmen-Polar, PhD
Assistant Research Professor, Department of Pathology and Laboratory Medicine,
Indiana University School of Medicine

Understand it now

Clariom assays use a novel and sophisticated array-based approach to generate results that are easy to analyze and interpret. The intuitive Transcriptome Analysis Console (TAC) Software lets you convert your data into insights in minutes. Explore your data using multiple visual representations and analysis workflows to quickly and easily build biological conclusions.

Share it now

With Clariom assays, you won't have to wait on answers. You can take control of your research and analyze your data to quickly generate results for grant applications, publications, sharing with colleagues, or moving forward to translate your discoveries into clinical application.

Clariom assays are the ideal tool for clinical and pre-clinical human disease research as well as large-cohort and biobank studies.

Trust it now

Clariom assays, built on established technologies with a proven path to clinical use, provide data reproducibility, giving you confidence in your data. With comprehensive content derived from the largest number of public databases, trust that your discoveries are real and key biomarkers won't be missed. Clariom assays push the boundaries of transcriptome analysis so you can push the boundaries of your insights into human health.

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An assay for every need

Whether you need a deep and broad high-resolution transcriptome profile, or are focused on gene-level changes on the surface of the transcriptome, Clariom assays generate reproducible data and offer the level of coverage you need to find biomarkers. Fast analysis yields actionable and clinically relevant results. Now.

Go deep into the transcriptome with Clariom™ D assays.

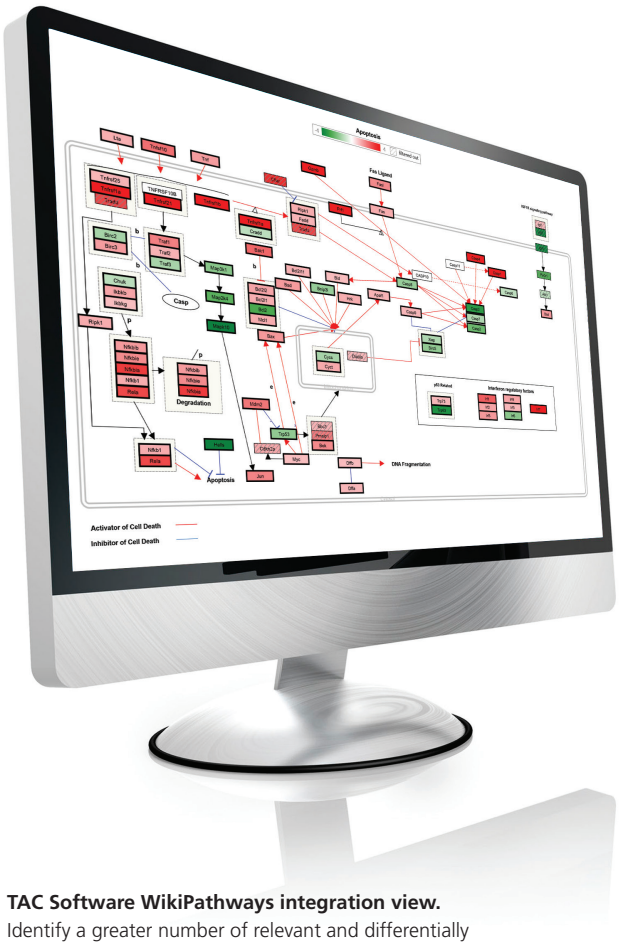
- Perform comprehensive and detailed analysis of coding and non-coding genes, exons, and splice variants.
- Get coverage of all known transcripts, regardless of abundance.
- Rapidly discover complex signatures and ensure biomarkers are not missed.

Keep biomarker discovery simple and swift with Clariom™ S assays.

- Rapidly generate robust expression profiles from all well-annotated genes.
- Identify important gene signatures and pathways quickly and easily.
- Discover gene-level signatures and quickly screen large numbers of samples with high-throughput, automated formats.

Clariom assays are available for human, mouse, and rat analyses. Custom designs are available for other species.

Learn more about Clariom assays at
www.affymetrix.com/clariom



TAC Software WikiPathways integration view.
Identify a greater number of relevant and differentially expressed genes with pathway visualizations.

*Study used GeneChip® Human Transcriptome Assay 2.0, part of the family of next-generation transcriptome-level assays.

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