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See further—achieve clarity in RNA biomarkers

Clariom assays—next-generation transcriptome profiling tools

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The power of Clariom assays

Translational scientists don't have the luxury of time. Accelerate your expression biomarker discovery research with Applied Biosystems™ Clariom™ assays, the next generation of transcriptome profiling tools offering a fast path to results.

Recent advanced transcriptome analyses have uncovered thousands of splice variants and long noncoding (lnc)RNAs, providing new sources for biomarker discovery. Given the complexity of the transcriptome, however, finding informative expression biomarkers can be challenging, time-consuming, and costly. Clariom assays, built using the latest transcriptome knowledge from multiple public data sources, are simple and fast tools for finding expression biomarkers. They are compatible with challenging and precious samples, available in scalable formats for different throughput needs, and include 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

- Confidently identify complex biomarker signatures and investigate significantly altered pathways
- Quickly find key biomarkers with transcriptome-level assays that detect coding and long noncoding genes, exons, and alternative splicing events, including rare transcripts
- Get answers fast with gene-level assays that measure changes in well-annotated genes and pathways
- Gain important insights quickly from large-scale cohort studies

Robust results even from precious samples

- 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

Applied Biosystems™ Transcriptome Analysis Console (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. For example, Figure 1 shows how transcriptome-level assays identified dysregulated lncRNAs in human gastric epithelial cells infected with *Helicobacter pylori*.

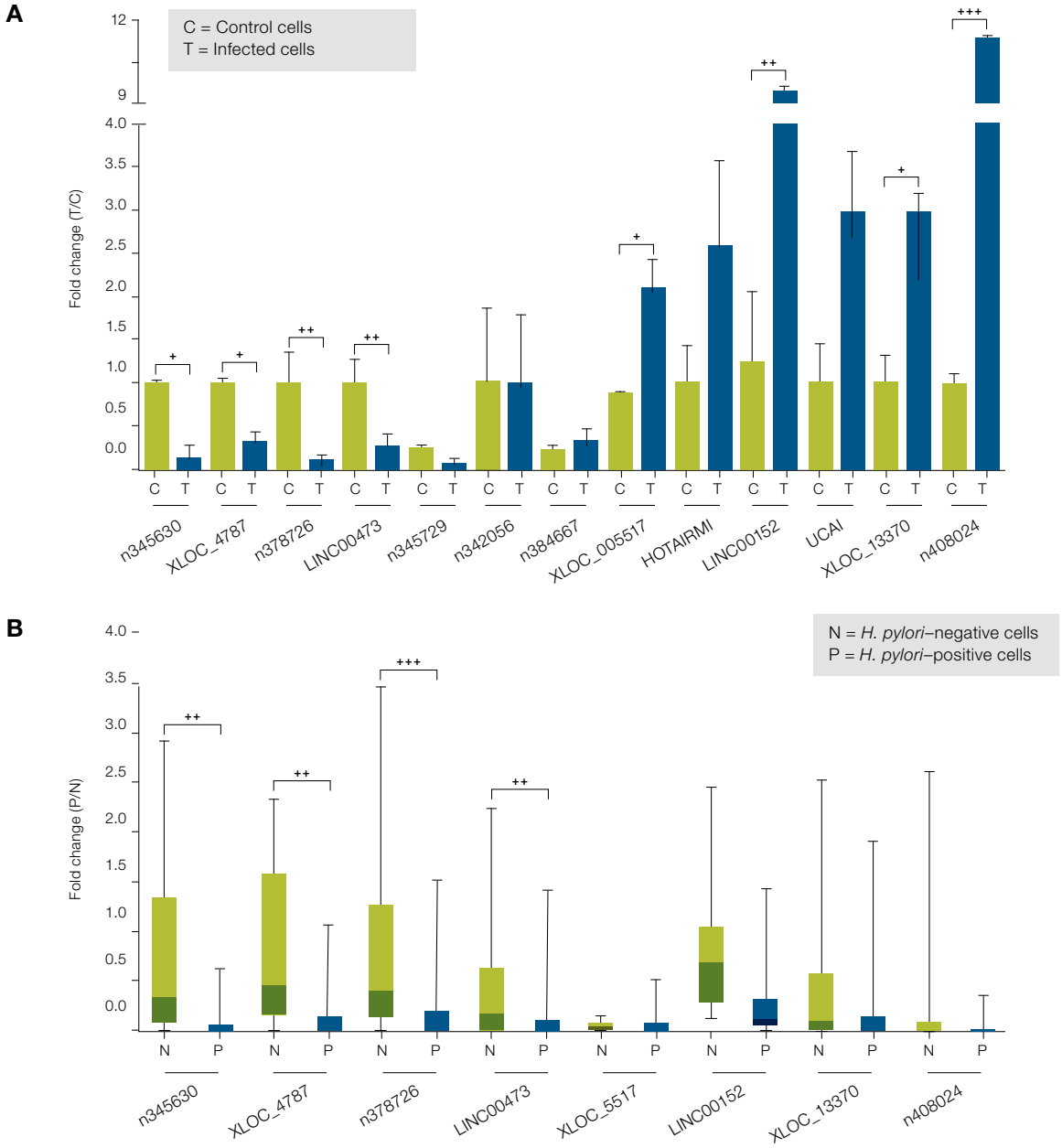

Figure 1. Identification and validation of dysregulated lncRNAs. (A) 13 candidate dysregulated lncRNAs identified by transcriptome-level assays were validated by qRT-PCR. Of those, eight samples expressed statistically significant differences in infected (T) vs. control (C) cells. **(B)** qRT-PCR validation 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. (2015) Microarray analysis of long noncoding RNA expression profiles in human gastric cells and tissues with *Helicobacter pylori* infection. *BMC Med Genomics* 8:84.*

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 principal investigators ask how they can get fast, publishable results, Dr. Chittur recommends transcriptome-level assays. With quick and intuitive Applied Biosystems™ Transcriptome Analysis Console (TAC) Software and no need for ribosomal RNA 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 data sources, researchers can use these assays to identify all known expressed isoforms, increasing the likelihood of finding transcripts of interest.

"Principal 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 help research the potential to overcome resistance to endocrine therapies, especially in estrogen receptor breast cancer. She is especially interested in understanding how alternatively spliced 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 future 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. Intuitive TAC Software lets you convert your data into insights in minutes. Explore your data using multiple interactive visualizations and analysis workflows to quickly and easily reach biological conclusions.

Share it now

With Clariom assays, you won't have to wait on answers. 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 potential future clinical application.

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

Trust it now

Clariom assays, built on proven technologies, provide data reproducibility, giving you confidence in your data. With comprehensive content derived from the largest number of public data sources, have confidence that your discoveries are real and biomarkers won't be missed. Clariom assays push the boundaries of transcriptome analysis so you can push the boundaries of your human health research.

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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 informative and relevant results. Now.

Go deep into the transcriptome with Clariom™ D assays

- Perform comprehensive, detailed analysis of coding and long noncoding genes, exons, and splice variants
- Get coverage of all known transcripts, regardless of abundance
- Rapidly discover complex signatures and help 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.

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

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

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

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