



Cellecta Launches Targeted Expression Profiling Service for 19K Human Genes

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Premium

NEW YORK (GenomeWeb) – Cellecta has launched an expression profiling service that targets all 19,000 protein-coding genes of the human genome in a single-tube, multiplex reaction that reduces costs for large-scale projects.

Called Driver-Map, the custom service will cost around \$500 per sample for small-scale projects, on par with competing services, but will have a reduced cost as projects scale up, Alex Chenchik, Cellecta founder and CEO said in an interview.

This cost savings is due primarily to the firm's ability to multiplex up to 20,000 reactions in a single tube, Chenchik noted, enabling a single laboratorian at Cellecta to run between 200 and 500 samples each day. Next-generation sequencing follows the massively multiplexed amplification.

Typical RNA-seq can detect non-coding RNA as well as many transcripts that have no known biological function, and is sometimes dominated by the most abundant transcripts which may not necessarily have clinical relevance.

"Very often when you do expression profiling you don't need a snapshot of everything happening in the cells," Chenchik said, but rather it may be better to focus on things like growth factors and transcription factors.

The 10-year old genomics product and service provider reasoned a few years ago that biomarker discovery could be a growth opportunity, but it also saw a chance to improve sensitivity of RT-PCR reactions. Chenchik, who also has more than a decade of prior experience at Clontech developing PCR products, said a key was that the firm took a step beyond relying on computer-assisted primer design for Driver-Map.

"Most people believe that if you just take a standard program for primer design and design RT-PCR primers for 19,000 genes, it will be great, but our experience shows that is not the case," he said.

In particular, so many primers in a single tube winds up less like a solution and more like "some sort of soup," Chenchik said, adding, "The expectation that all of them will work together at very high efficiency is naive."

Cellecta's process was to design between five and 20 primer pairs for each of the 19,000 targets, and validate every assay for every gene in high-throughput testing in order to find the best pair. The firm was

also mindful of ways to decrease primer-dimer formation, which ultimately allowed for such massive multiplexing.

"Before, multiplex PCR was available for no more than a couple hundred genes because of just technical limitations of the technology, but we are able to overcome these limitations to scale up to 20,000 genes in one test tube," Chenchik said.

Cellecta spent several years and close to \$1 million in the process, but, "at the end, our assay is highly validated, which is actually not the case for everybody else," Chenchik said.

Because of the high sensitivity, he said, the assay can be used with as little as 10 picograms of total RNA, even working on single cells.

The Driver-Map service will also allow customers to make custom assays for smaller sets of the genes. The firm sees potential for complex clinical or research samples, like immunotherapy or human-mouse xenographs.

"To understand expression levels and find biomarkers which are related ... you need to have very high sensitivity because your signal is diluted by all the other cells" in the complex sample, Chenchik said. Meanwhile, global profiling may be overwhelmed and miss low levels of important molecules. Furthermore, Cellecta's assay primers are also designed to only amplify human complementary sequences, but not mouse, enabling xenograph profiling.

The single test tube protocol has also eliminated various purification steps, so it can be done for hundreds of samples per day. This could be particularly important to clinical researchers, Chenchik said, who sometimes require thousands of analyses to have confidence in biomarkers.

Customers will also have the option to include Cellecta's rigorous RNA quality control protocols in their custom service. "We find that it is extremely important to incorporate high-throughput RNA quality control using automation for every RNA sample," Chenchik said, noting a drawback is that some samples may be rejected after QC. The firm also offers options to provide raw data only, if an academic or industry partner already has access to bioinformatics facilities, but it can also provide comprehensive data analysis, statistical analysis, and biological interpretation.

Competitors for the service are many, and expression profiling is a quickly expanding field, Chenchik said. The Cellecta technology is compatible with Illumina sequencing platforms, for which the firm is considering launching a kit in the future. But, Chenchik said, there may not be much competition specifically for genome-wide, targeted expressing profiling. There are small panels available from firms like Qiagen; Illumina offers custom panels; and Thermo Fisher Scientific offers AmpliSeq which is only compatible with Ion Torrent, Chenchik said. Cellecta's validation efforts, however, could provide an edge over these other services, Chenchik said.

Currently, a few academic labs are already utilizing the Cellecta Driver-Map service, Chenchik said. Examples include Lester Kobzik at Harvard's School of Public Health, who focuses on lung responses to inhaled environmental particulates, pathogens, or allergens; [Luda Diatchenko](#), a pain genetics researcher at McGill University; and Costa Frangou at the Roswell Park Cancer Institute.

The firm hopes to build credibility and increased uptake as these academic collaborators using the service begin to publish their work.

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