CELLECTA

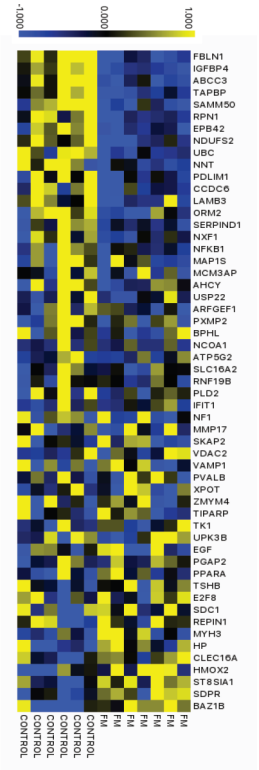
Discovery is yours™

DriverMap™ Targeted RNA Expression Profiling

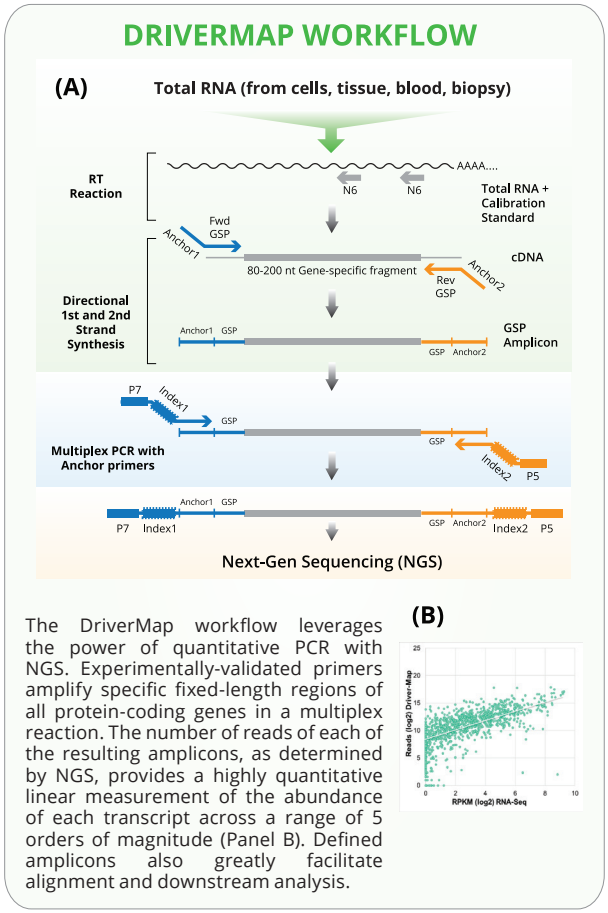
Complete Quantitative Transcriptome Analysis in a One-Tube Assay

- Convenient, one-tube, no-transfer protocol
- Start with as little as 10 pg total RNA—single-cell level
- Use total RNA from whole blood or tissues—no mRNA enrichment or globin-depletion
- 100-fold more sensitive than RNA-Seq—detect 20-30% more low-abundance transcripts

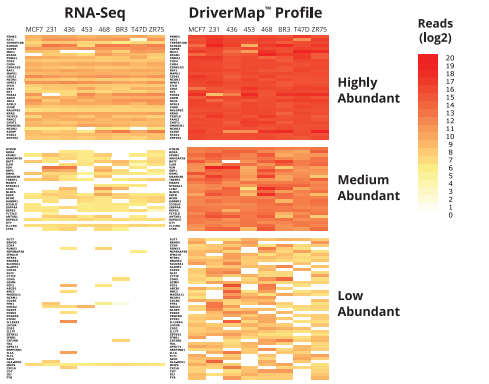
The Driver-Map Assay uses intelligently designed, empirically optimized targeted primers to amplify defined regions of each transcript for all human genes in a single multiplex RT-PCR reaction. The amplified products of this reaction are then analyzed using Next-Generation Sequencing (NGS) to assess abundance levels. This combination produces an assay that provides the sensitivity of RT-PCR with the dynamic range and quantitation of deep sequencing. Cellecta's novel approach uses total RNA as starting material and provides increased sensitivity for low- abundance genes and a broader linear range for more quantitative differential analysis than RNA-Seq.



A panel of 25 candidate pain biomarkers differentially expressed in individuals with fibromyalgia (FM) vs. healthy control cases. We used genome-wide Driver-Map to generate expression data from 50 ng of RNA isolated from whole blood from each of 6 negative controls (no pain) and 7 FM clinical specimens.



The DriverMap workflow leverages the power of quantitative PCR with NGS. Experimentally-validated primers amplify specific fixed-length regions of all protein-coding genes in a multiplex reaction. The number of reads of each of the resulting amplicons, as determined by NGS, provides a highly quantitative linear measurement of the abundance of each transcript across a range of 5 orders of magnitude (Panel B). Defined amplicons also greatly facilitate alignment and downstream analysis.



NGS read levels detected RNA-Seq and Driver-Map for selected high-abundant (10K-100K copies per sample), medium-abundant (1,000-10,000 copies per sample), and low-abundant transcripts (100-1,000 copies per sample) in 50ng of total RNA from seven common cancer cell lines.

For more information and to subscribe to updates, email us at info@cellecta.com.