Quantitate and analyze expression levels of focused sets of key genes simply and easily

- Expertly curated key genes associated with specific human diseases or cell phenotypes.

- Ultra-sensitive quantitation of genes most likely to be involved in cellular processes and disease progression.

- Targeted gene sets increase next-generation sequencing (NGS) read numbers for gene targets which improves profiling statistics, specificity, and sensitivity.

### Five DriverMap™ Panels Target Biologically Relevant Gene Sets

The Predesigned Panel kits contain experimentally validated primers to specifically amplify selected sets of expertly curated genes whose expression provides insight on cancer and inflammatory disorders, cell signaling, cell lineages, processes of differentiation, and immune activation. Also included are all indexes required to prepare Illumina sequence-ready libraries, and Deconvolution software for easy analysis.

DriverMap Technology

The DriverMap Targeted Profiling Panels utilize the same single-tube, multiplex assay approach as the DriverMap Genome-Wide assay, which provides robust, quantitative, and reproducible measurements of each expressed protein-coding gene over as much as 5-orders of magnitude. The DriverMap approach overcomes the low sensitivity and specificity challenges of current RNA sequencing (RNA-Seq) technologies. It greatly simplifies the protocols for data generation and analysis.

Benefits of all Cellecta DriverMap Assays

- Functionally validated PCR primer sets selected for the highest sensitivity

- Rapid generation of transcript expression data from 100 or more samples in a single day

- Streamlined single-tube RT-PCR / NGS protocol yields robust results starting from 10 pg – 50 ng of total RNA.

- Direct use of total RNA isolated from whole blood without PBMC isolation, globin/rRNA depletion, or mRNA enrichment required.

- Human-specific transcript profiling for patient-derived xenograft (PDX), xenograft mouse, and other human-animal hybrid models.

- DriverMap Deconvolution Software that provides you with gene-specific expression data in an Excel spreadsheet format directly from the Illumina NGS Fastq raw data.
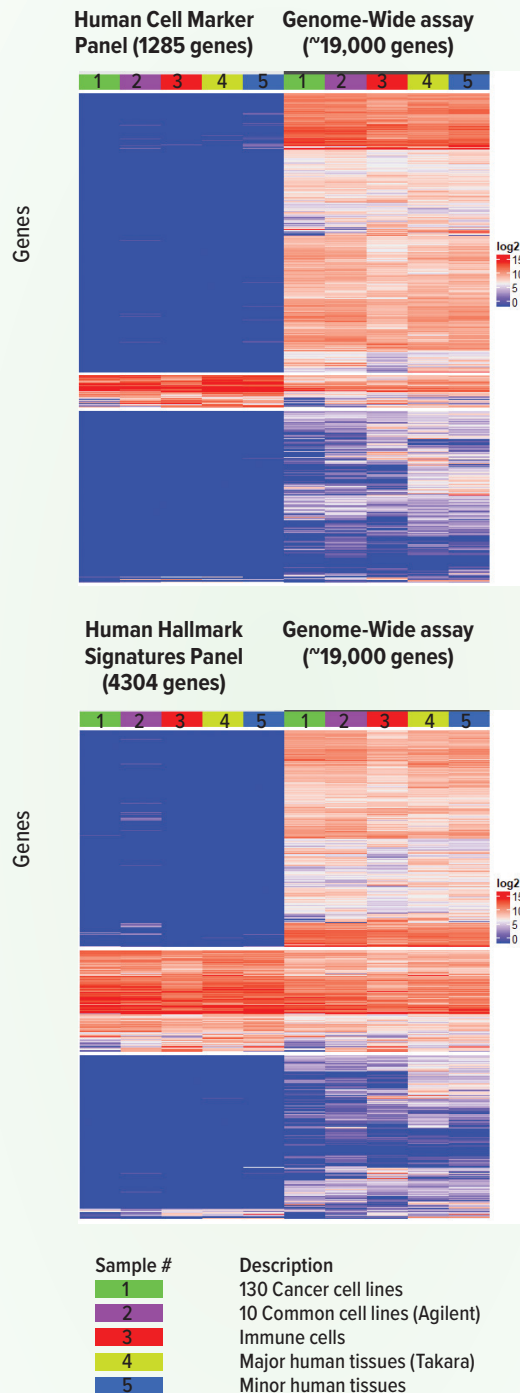
Heat Maps comparing performance of DriverMap Human Cell Marker Panel (1285 genes) and Human Hallmark Signatures Panel (4304 genes) with Driver Map Genome-Wide Assay (~19,000 genes). Significant improvement in sensitivity is seen with the focused panels vs. genome-wide. Samples 1-5 are Human Universal RNAs from a variety of tissues and cell lines.

Sample #	Description
1	130 Cancer cell lines
2	10 Common cell lines (Agilent)
3	Immune cells
4	Major human tissues (Takara)
5	Minor human tissues

DriverMap™ Human Predesigned Expression Profiling Panels

CELLECTA

PANEL	# GENES	SOURCES
Human Cell Marker Panel The Cell Marker Panel targets genes curated from 1000s of publications for 64 different cell types, spanning adaptive and innate immunity cells, hematopoietic progenitors, epithelial cells, and extracellular matrix cells.	1285	**ENCODE, FANTOM, ImmGen, Human Primary Cell Atlas (HPCA), Blueprint & IRIS projects**
Human Hallmark Signatures Panel The Hallmark Signatures Panel profiles genes involved in specific, well-defined molecular pathways, biological states, or disease processes. Each Hallmark set consists of a refined gene list, computationally derived from multiple founder sets based on gene set overlaps and coordinate expression.	4304	**Molecular Signatures Database (MSigDB)**
Human LINCSx Panel The LINCS 1000x Panel assesses expression of the landmark genes in LINCS database that are the most informative to catalog changes that occur when cells are exposed to drugs and other perturbing agents. Genes linked to targets for FDA-approved drugs as well as related targets and markers are included.	1573	**Library of Integrated Network-Based Cellular Signatures (LINCS), DrugBank**
Human Pan-Cancer Pathway Panel The Pan-Cancer Pathway Panel measures levels of genes in pathways often dysregulated in cancer. These gene targets were identified by curation of transcriptome data from scientific publications, the NCBI GEO, and Cellecta's profiling experiments (DECIPHER - http://www.decipherproject.net)	2094	**Cancer literature, NCBI GEO, DECIPHER project**
Human Transcription Factor Signatures Panel The Transcription Factor Panel analyzes gene expression of 343 key transcription factors and the activity of their known target genes. The Panel provides data for 6,401 possible regulatory pathways by linking 343 distinct transcription factors to 2649 distinct target genes.	2649	**JASPAR, PAZAR, TRANSFAC, TRED, TRRD databases**

Ordering Information

Catalog #	Description	Quantity
DMF-HCM-96	DriverMap™ Human Cell Marker Panel (96 multiplex)	1 kit (for 96 samples)
DMF-HHM-96	DriverMap™ Human Hallmark Signatures Panel (96 multiplex)	1 kit (for 96 samples)
DMF-HLX-96	DriverMap™ Human LINCS1000x Panel (96 multiplex)	1 kit (for 96 samples)
DMF-HPC-96	DriverMap™ Human PanCancer Panel (96 multiplex)	1 kit (for 96 samples)
DMF-HTF-96	DriverMap™ Human TransFactor Signatures Panel (96 multiplex)	1 kit (for 96 samples)

For more information visit **www.cellecta.com/drivermap** email **info@cellecta.com,** or call +1-650-938-3910
Order online at www.cellecta.com/e-Shop or quotes@cellecta.com