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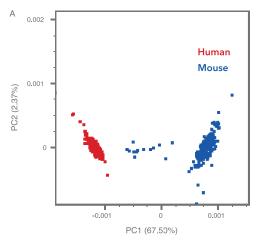# Introducing the ddSEQ™ Single-Cell Isolator, SureCell™ WTA 3' Library Prep Kit, and SeqGeq™ Analysis Software

Discover more with single-cell sequencing

RNA sequencing (RNA-Seq) of cell populations has revolutionized gene expression studies. Performed on bulk samples, RNA-Seq averages gene expression across thousands of cells and masks the individual contribution of a cell in complex networks. In contrast, single-cell RNA-Seq delivers higher resolution analysis of gene regulation for a deeper view of cell function in development and disease research. Now there is a robust, user-friendly workflow from the industry leaders in sequencing

and Droplet Digital™ technologies that accommodates high-throughput experiments and a wide range of experimental designs so researchers can discover more.

Sensitive assay chemistry delivers unbiased profiling of diverse cell populations with flexibility, as the droplet approach is agnostic to cell size. BaseSpace® Sequence Hub and SeqGeq Analysis Software from FlowJo, LLC enable powerful yet simple data analysis.
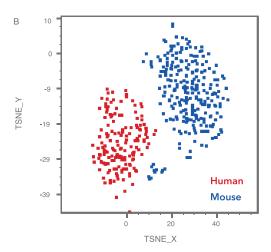

Fig. 1. Detection of Genes in a Heterogeneous Population of Cells. Principle Component Analysis (PCA) of 1,384 cells from a 1:1 ratio mixture of HEK293 and NIH3T3 cells (A) and a mixture of mouse cells spiked with human cells (B). The human cells (representing 7% of the total cell population) are identified as a distinct cluster in t-Distributed Stochastic Neighbor Embedding (t-SNE) analysis based on gene expression profile. Cells are colorcoded by gene expression of human RPL13 gene (red) or mouse Rpl13 (blue) to confirm the identity of the sub-population.

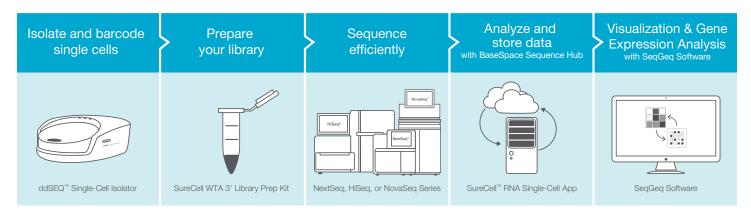| Isolate and barcode single cells	Prepare your library	Sequence efficiently	Analyze and store data with BaseSpace Sequence Hub	Visualization & Gene Expression Analysis with SeqGeq Software
ddSEQ™ Single-Cell Isolator	SureCell WTA 3' Library Prep Kit	NextSeq, HiSeq, or NovaSeq Series	SureCell™ RNA Single-Cell App	SeqGeq Software

Fig. 2. The Illumina Bio-Rad Single-Cell Sequencing Workflow. The workflow integrates industry-leading Bio-Rad Droplet Digital partitioning technology, Illumina next-generation sequencing (NGS) technology, and a user-friendly application from FlowJo, LLC. The solution enables high-throughput sequencing of thousands of individual cells quickly and cost effectively.

For Research Use Only. Not for use in diagnostic procedures.

SeqGeq Software Brings Flexible Exploration & Analysis for Deep Single-Cell Insight

SeqGeq™
from FlowJo, LLC

SeqGeq Software is a desktop application for data analysis, exploration, and visualization that enables you to extract insight from the individuality of single-cell gene expression. Built for and by biologists with 19+ year's of experience with single cell biology, SeqGeq Software features powerful data reduction and population identification tools.

SeqGeq Software directly integrates with BaseSpace Sequence Hub and enables visualization and analysis of expression data, so you can create, compare, and share gene sets.

Statistic color-mapping of individual cells, summary heatmaps, and drag and drop report editors help you rapidly summarize and communicate your results.
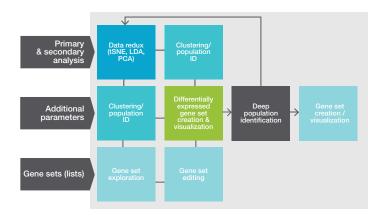

Fig. 3. Flexible, Robust Analysis Workflows in SeqGeq Software. SeqGeq Software can analyze and visualize gene expression data produced as a result of primary and secondary analysis, including any additional parameters. Gene sets may be dragged and dropped for rapid comparison between experiments and samples. An intuitive suite of tools enables an unprecedented level of analysis depth, getting you from gene expression data to new populations and differentially expressed genes in seconds.
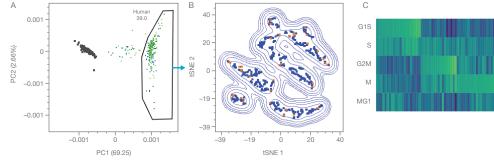

Fig. 4. Deep Single-Cell Analysis in SeqGeq Software Reveals Heterogeneity in HEK293 cells. PCA of 1:1 ratio mixture of HEK293 and NIH3T3 cells, color-mapped by expression of human RPL13 gene (A, mouse cells in gray) is shown. t-SNE analysis of the human cell subset where distinct clusters represent differences in gene expression profiles, revealing the heterogeneity of individual cells (B). Single cell heatmap reveals cell cycle state based on unique transcript counts of genes, normalized by total count for each cell. Expression is centered by the median and scaled by the median absolute deviation for each cell cycle (C). Analysis was performed using BaseSpace Sequence Hub and SeqGeq Software.

Accelerate your gene expression studies with this powerful, comprehensive single-cell sequencing solution.

Visit **www.bio-rad.com/ddSEQ** and **www.flowjo.com/seqgeq** for more information.

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