FLUIDIGM

TAKE THE PATH LESS TRAVELED

Simplified Transcriptome Analysis of Single Cells with the C1 System

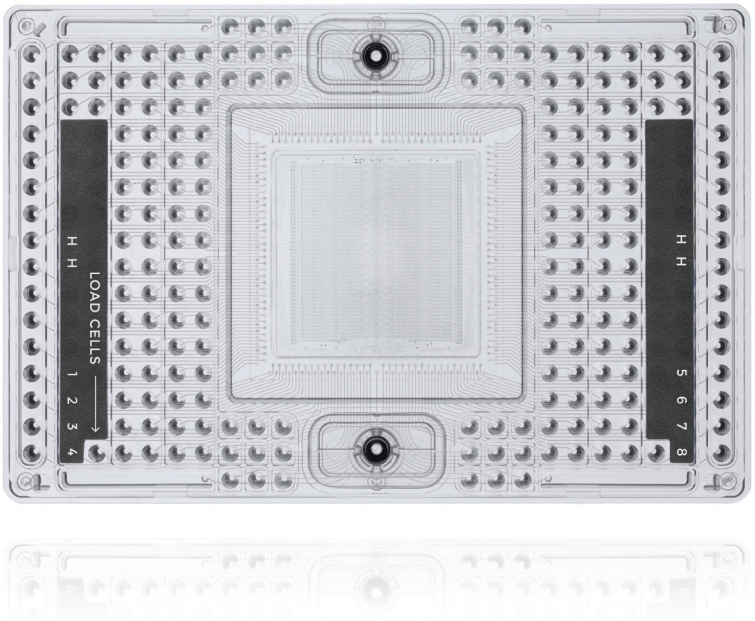
THE PATH LESS TRAVELED JUST GOT EASIER

THE C1 SOLUTION FOR mRNA SEQUENCING

- **Complete**—End-to-end workflow for whole transcriptome analysis of individual cells
- **Highest throughput**—Unprecedented parallel processing of 96 single cells per run
- **Easier**—Streamlined sample preparation directly from single cells with only three hours of hands-on time, and no fragmentation or purification steps
- **Affordable**—One-eighth the cost of other library preparation systems

Researchers are analyzing the transcriptome at greater depth to uncover new mechanisms of cell development, metabolism and disease. mRNA sequencing is a valuable tool to help researchers understand how subpopulations respond to signals and other environmental cues at critical stages of cell-fate determination or when they acquire aberrant phenotypes. Studying these gene expression patterns in single cells already has dramatically advanced cell biology.

Most methods, however, are impractical for single-cell analysis; they require large numbers of cells, are based on complex workflows that are too slow or generate highly variable results, and are too costly to generate significant results from single cells.



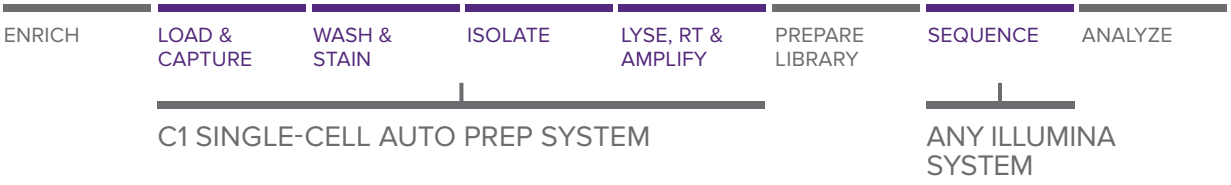
C1 IFC

The C1 Single-Cell mRNA Sequencing Application

- Measure expression levels of genes, alleles, and spliced variants.
- Compare expression profiles between individual cells and populations.
- Map transcription initiation sites.
- Characterize alternate splicing patterns.
- Evaluate post-transcriptional activity.
- Discover new transcripts and gene fusions.

Fluidigm C1 system mRNA Sequencing is designed specifically for detailed expression profiling in diverse cell populations. The C1 takes an entirely new approach, based on innovative microfluidic technology with nanoliter-scale reaction volumes. It delivers consistent results with the lowest sample requirements at a fraction of the cost of traditional library preparation methods.

This, simplified process leverages the Clontech® SMARTer™ Ultra Low RNA Input Kit for cDNA synthesis and the Illumina® Nextera™ XT DNA Sample Preparation Kit to provide the most comprehensive workflow with minimal hands-on time. Most traditional methods require total RNA as input, adding time, labor and cost. The C1 mRNA Sequencing application streamlines the process; it works directly from single cells, so you can eliminate the extra workflow steps of extensive RNA purification beforehand, such as magnetic beads, gel size selection or filter columns.



With the C1 mRNA Sequencing application, you can parallel process up to 96 cDNA libraries from multiple individual cells, for relative quantitation of mRNA expression on any Illumina® sequencer. Key features of this system include:

- **Highest throughput.** Get higher efficiency with a massively parallel, sequence preparation of 96 individual cells and in-line barcoding to maximize multiplexing capacity during sequencing.
- **Easiest to use.** Hands-on time totals less than three hours working directly from single cells, with no RNA fragmentation and purification step.
- **Ultrasensitivity.** The system is compatible with single-cell input as low as 10 pg per reaction.
- **More mappable reads.** More than 70% of total reads are mapped to RefSeq.
- **Full gene analysis.** The application gives better read coverage across the entire transcript for better detailed analysis of alternative transcript isoforms and identification of single nucleotide polymorphisms.
- **Cost-effectiveness.** The application has one-eighth the cost of standard single-cell library prep due to innovative nanoliter reaction scale.
- **Compatible with any Illumina system.** It is supported on HiSeq®, HiScan®, GAII and MiSeq™ sequencing platforms.

The C1 System

The complete solution for mRNA sequencing for single cells

Product Name	Description
C1 IFCS FOR MRNA SEQUENCING	Our proprietary array and script for capture and cDNA amplification of 96 individual cells
C1 KIT FOR MRNA SEQ	Our reagent kit for lysis, wash, and stain of individual cells
C1 INSTRUMENT	Revolutionary technology to isolate, process and profile individual cells for analysis
CLONTECH SMARTER ULTRA LOW RNA KIT	To reverse transcribe and amplify cDNA
ILLUMINA NEXTERA XT DNA SAMPLE PREPARATION KIT	Simple, transposase-based method to streamline tag incorporation and amplification with in-line barcoding

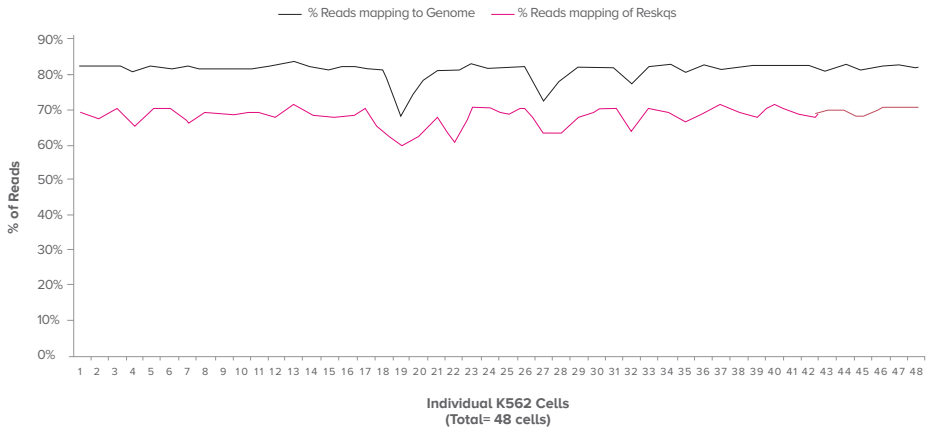


Figure 1. Percent of mapped reads to reference as a function of the total number of reads.

The data was generated from 48 individual K562 cells input to the SMARTer™ Ultra Low RNA Kit, processed on the C1 followed by library construction using the Nextera™ XT Kit. Average read depth is 3 million reads, >95% cells had >500,000 total read.

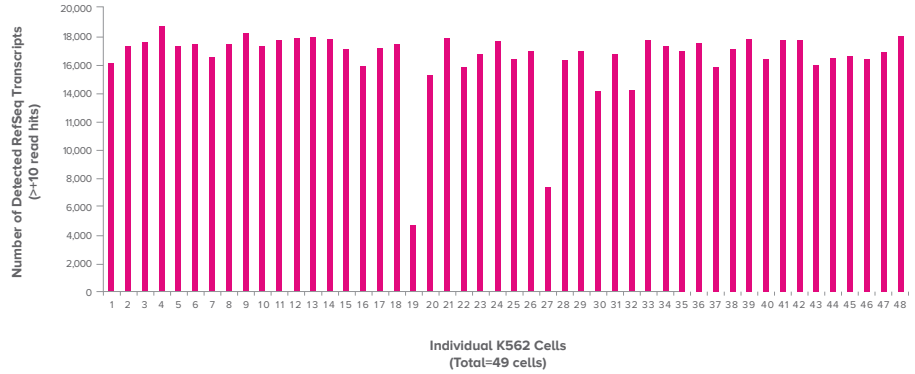


Figure 2. Number of detected RefSeq transcripts.

Number of detected transcripts across 48 single K562 cells with at least 10 reads per transcript. Number of transcripts detected is read-depth dependent; average read depth for these samples is ~3 million reads.

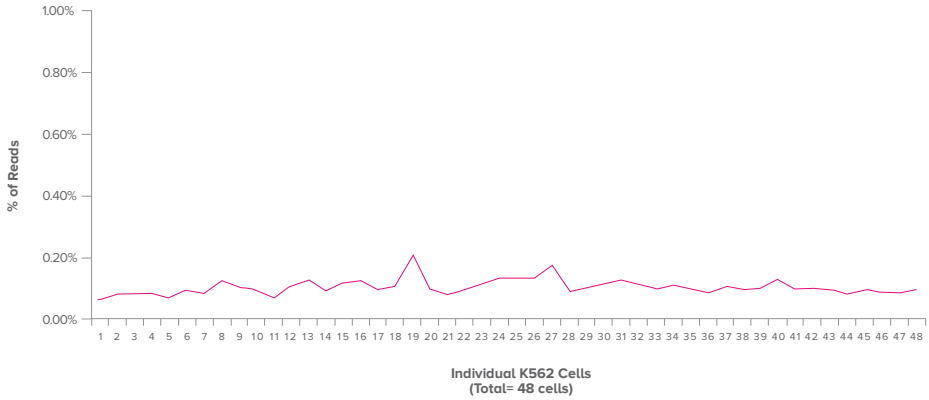


Figure 3. Percent of mapped reads to ribosomal RNA.

Non-rRNA sequences are preferentially primed and amplified, reducing the number of reads from rRNA sequences to less than 0.25% for each of 48 single K562 cells.

Figure 4a: Size distribution of cDNA after harvest from C1 array

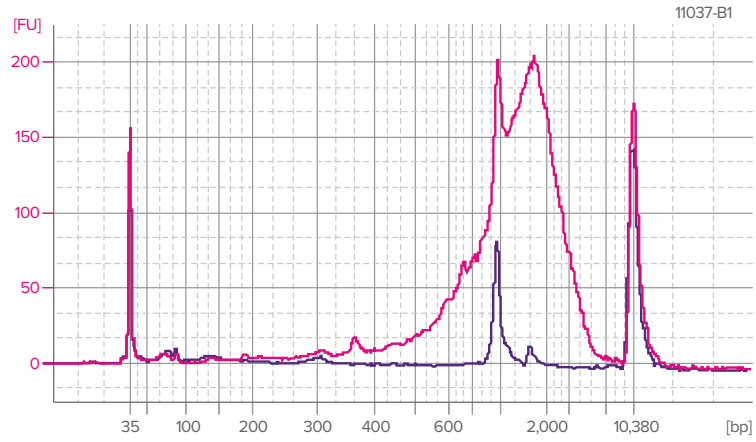


Figure 4b: Size distribution after library prep

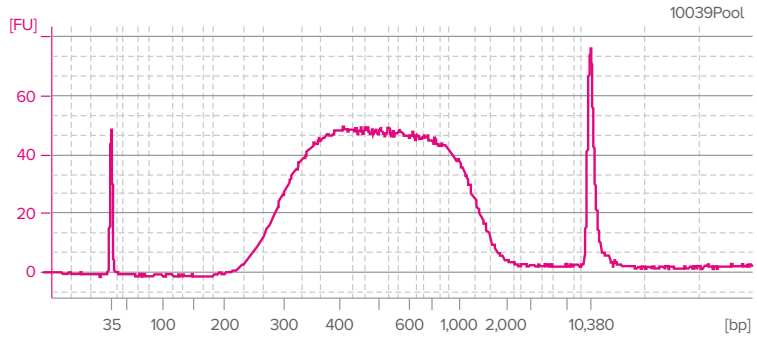


Figure 4. Size distribution of cDNA and libraries.

a). Bioanalyzer trace of cDNA product obtained from K562 cells using the DNA High Sensitivity Chip on the Agilent® Technologies Bioanalyzer® 2100. The average cDNA is approximately 2 kb long as measured on the Bioanalyzer 2100. The red line corresponds to the cDNA library of a single cell; blue corresponds to "no cell." The 800 bp fragment corresponds to RNA spike internal control.

b). Bioanalyzer traces of one single-cell library generated by Nextera XT kit and one round of cleanup by solid-phase reverse immobilization (SPRI).

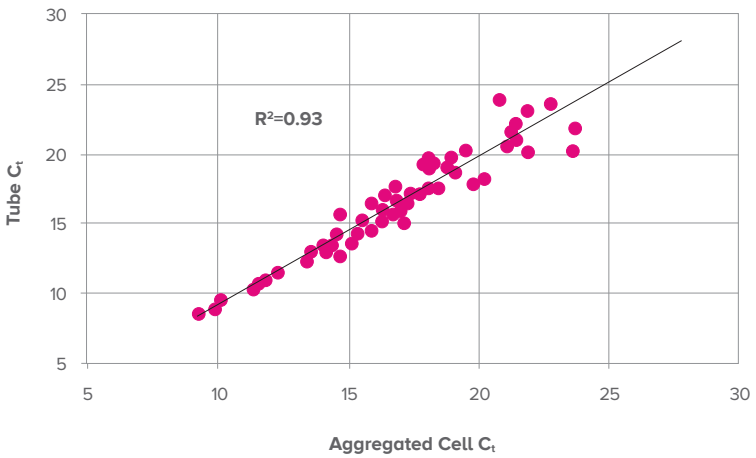
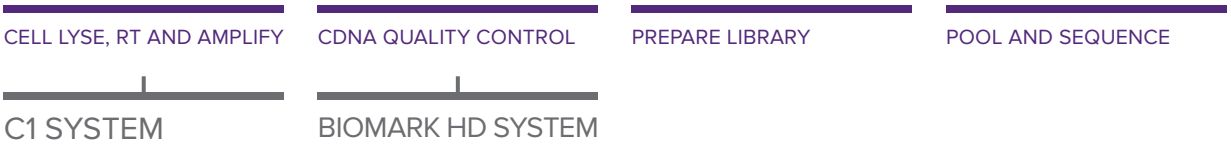


Figure 5. Correlation plot of aggregated cell C_ts vs tube C_ts.

Single-cell cDNA libraries and a multicell tube control were evaluated on the Biomark™ HD using Delta Gene™ Assays. Data aggregated from single-cell cDNA libraries correlate closely with data from a multicell tube control (R^2 = 0.93). Incorporating the Biomark HD into the routine analysis provides a rapid assessment of yield and quality of each library.

Fast and Easy Quality Control of cDNA Libraries: Biomark HD

The quality of single-cell mRNA sequencing data is directly proportional to the quality of each cDNA library. In order to produce the most reliable sequence data, a routine quality control step should be implemented. The Biomark™ HD System assesses the quality of each cDNA amplication, ensuring that each library is free of contamination and is not degraded. The system also will quantitate the level of each transcript.



Get a Clearer Picture with Single-Cell Analysis

Assuming that every cell in your sample behaves exactly the same is a dangerous gamble; taking averages of pooled cells masks dramatic variations in gene expression. Recognizing cellular variations in what appear to be homogenous populations has become crucial to advances in stem cell research, understanding cancer cells, identifying immune responses, determining the effectiveness of biological therapies, and discovering the mechanisms of neurodegenerative diseases. The drawbacks become particularly apparent in mRNA sequencing.

The C1 System enables you to rapidly and reliably isolate, process and profile individual cells for analysis. Our family of instruments, arrays, assays, software and kits are designed to take you from cellular isolation and extraction, through reverse transcription and amplification and ultimately to detection and analysis of cell activity using just one technology. The system opens the doors to studying cell differentiation, measuring individual cell responses to specific stimuli, verifying critical disease biomarkers, and conducting candidate drug screens.

Find the Path Less Traveled—with Ease

Great discoveries require blazing new trails. Single-cell analysis has the potential to find new transcriptome pathways, which could uncover new cellular roles in development, metabolism and disease. Finally, you can mRNA sequence more individual cells, with reduced technical noise and greater statistical significance. Discover how easy the path less traveled is at **fluidigm.com/products/c1-system.**

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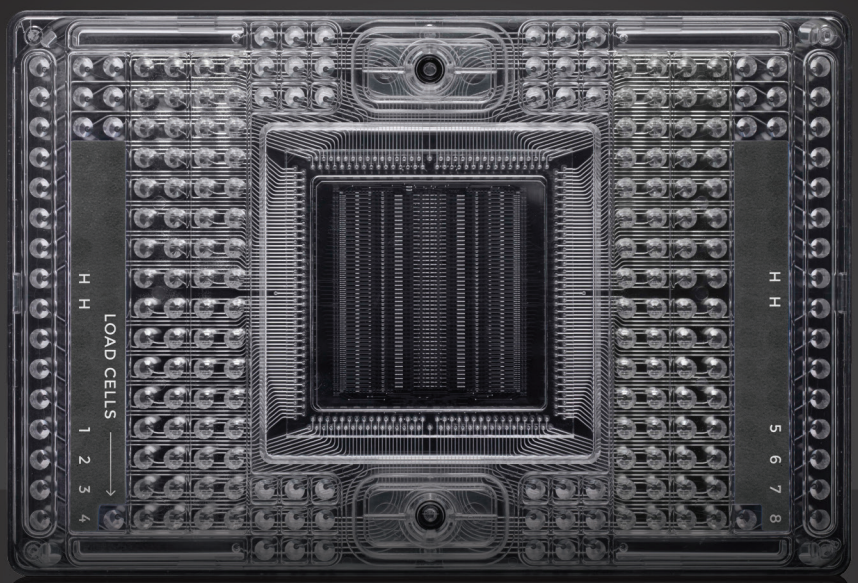

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