C1

- **Comprehensive.** Supports a wide variety of single-cell genomics applications, including qPCR, mRNA and DNA sequencing, and epigenetic analysis.
- **Sensitive.** Allows you to reliably measure differences in gene expression profiles between individual cells using a simple automated workflow.
- **Fast.** Cell input to qPCR data in hours instead of days.
- **Proven.** Referenced by over 100 peer reviewed publications from around the world.

DEFY THE LAW OF AVERAGES

Individual cells are unique—they differ by size, protein levels, and expressed mRNA transcripts, even within nominally homogeneous cell populations. The tacit assumption that every cell in a sample behaves the same is a dangerous gamble. Taking averages of pooled cells can mask the dramatic variations in gene expression from cell to cell. Tracking the effects of these variations becomes essential for dynamic gene expression studies, especially in biomarker identification or expression profiling.

TRADITIONAL METHODS ARE TOO VARIABLE

Technical variability during sampling, storage, nucleic acid stabilization, extraction, reverse transcription, preamplification, and quantitative PCR can obscure true biological variability. And traditional methods are often limited to analysis of bulk samples.

SINGLE-CELL RESOLUTION WITH A SINGLE TECHNOLOGY

C1™ is an entirely innovative approach, based on Fluidigm microfluidic technology that enables geneticists and disease researchers to rapidly and reliably isolate, process, and profile individual cells across multiple genomic parameters. For the first time, you can extract, reverse-transcribe, amplify, and ultimately detect and analyze cell activity using just one technology, reducing the variability caused by multiplatform technical errors.

C1 System Design Advances

Breakthrough bench top automation for the isolation, lysis, and preparation of nucleic acid from single cells

Intuitive touchscreen to facilitate easy setup and monitoring of cell processing

SPECIFICATIONS

Instrument (Part Number 100-4072)

Dimensions	
Depth	66 cm (26 in)
Width	41 cm (16 in)
Height	48 cm (19 in)
Weight	45 kg (99 lb)
Thermal control	Peltier-based, 4–99 °C
IFC (integrated fluidic circuit) compatibility	96-cell and HT (high throughput) C1 IFC
Ports	4 USB 2.0
Power requirements	100–240 VAC, 50/60 Hz, 175 W (region-specific power cord provided)
Work Environment (indoor use only)	
Temperature	15–28 °C (59–82 °F)
Humidity	20%–80% relative humidity, non-condensing
Altitude	Not to exceed 2,000 m (6,562 ft) above sea level

Software

Data collection	C1 system software
Custom applications	Script Builder™ software Script Hub™
Analysis	Singular™ Analysis Toolset

Supported IFCs

DNA sequencing	C1 DNA Seq IFC
mRNA sequencing	C1 mRNA Seq IFC C1 mRNA Seq HT IFC
Targeted gene expression*	C1 Preamp IFC
Custom applications	C1 Open App™ IFC

* Compatible with Delta Gene™ assays and TaqMan® Gene Expression Assays (probe-based). Capture, stain, image, lyse, reverse-transcribe, preamplify, and harvest on C1. Perform real-time PCR analysis on the Biomark™ HD system.

C1 IFC Specifications

Sample sources	Primary and cultured cells
Sample input	200–1,000 cells (96-cell IFC) 2,000–5,000 cells (HT IFC)
Cell capture efficiency	
Small-cell (5–10 µm)	≥80% of capture sites will contain cells with 1,000 HL-60 cells input*
Medium-cell (10–17 µm)	≥90% of capture sites will contain cells with 1,000 (96-cell IFC) or 5,000 (HT IFC) K562 cells input*
Large-cell (17–25 µm)	≥90% of capture sites will contain cells with 1,000 BJ fibroblast cells input*

* Across a variety of cell types between 5 and 25 µm, with cells run in the correct-size IFC, we observe that on average >90% of occupied capture sites contain single cells.

Learn more at

fluidigm.com/c1

CORPORATE HEADQUARTERS
7000 Shoreline Court, Suite 100
South San Francisco, CA 94080 USA
Toll-free: 866 359 4354 in the US and Canada
Fax: 650 871 7152
fluidigm.com

SALES
North America | +1 650 266 6170 | info-us@fluidigm.com
Europe/EMEA | +33 1 60 92 42 40 | info-europe@fluidigm.com
China (excluding Hong Kong) | +86 21 3255 8368 | info-china@fluidigm.com
Japan | +81 3 3662 2150 | info-japan@fluidigm.com
All other Asian countries | +1 650 266 6170 | info-asia@fluidigm.com
Latin America | +1 650 266 6170 | info-latinamerica@fluidigm.com

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