Setting the Standard in Drop-Sequencing Chips

Drop-sequencing (Drop-seq) developed by the McCarroll lab, Harvard Medical School, is a method designed for the parallel analysis of mRNA expression in thousands of individual cells following their encapsulation in tiny droplets. These droplets (nanolitre scale) are formed by precisely combining aqueous and oil flows in a specially designed microfluidic device (Drop-seq chip). Expression profiling can then be carried out in tens of thousands of cells in a matter of hours. The Drop-sequencing technique, including methodology is described in **Macosko *et al.* Cell. 2015**

OPTIMISE YOUR CHANCES OF SUCCESS! FlowJEM's Drop-sequencing chip offers exactly the same design as detailed in the latest McCarroll lab protocol.

Single Droplet Generation Device

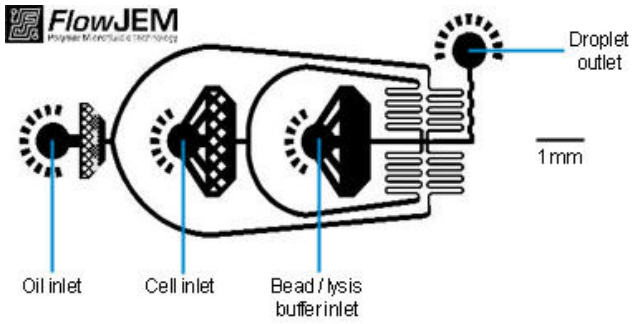


Fig. 1. Structure of the Droplet Generation Device showing inlets for oil, cells and beads / lysis buffer and droplet outlet.

Drop-Sequencing Chip



Fig. 2. Standard Drop-sequencing chip containing 26 individual Droplet Generation Devices.

Product Features & Benefits

- **Latest Design**

Each Droplet Generation Device is based on the design recommended in the latest McCarroll lab Drop-seq protocol, ensuring the best chances of success

- **Precision Engineered**

Robust Devices durable over a wide-range of pressures, temperatures and flow rates

- **26 Droplet Generation Devices Per Chip**

Provides value for money in a chip which lasts. When the life of one device is depleted, simply move onto the next one

- **Produces Highly Mono-Dispersed Droplets**

Reliable and consistent generation of droplets of optimal size for Drop-sequencing

- **Efficient Production Of Transcript Libraries**

Superior design promotes optimal mixing of component fluids, thereby minimizing bead shearing or premature lysis of cells and mRNA release

How It Works

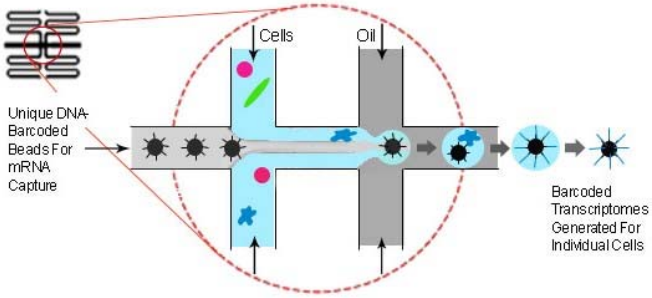


Fig. 3. Barcoded beads/lysis buffer, cells and oil enter the Droplet Generation Device in a specific sequence to produce barcoded mRNAs for individual cells. Tens of thousands of cells can be processed in this way and their entire transcriptomes sequenced in a matter of hours.

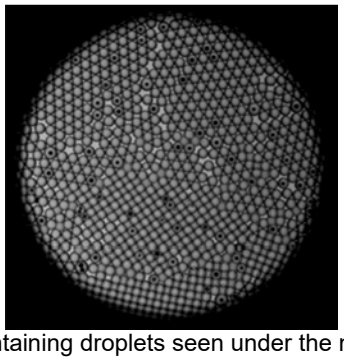


Fig. 4. Cell-containing droplets seen under the microscope. Reliable consistency is dependent on design. *Image courtesy of Hemant Suryawanshi, Tuschl Lab, Rockefeller University, NY.*

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