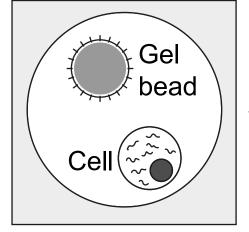
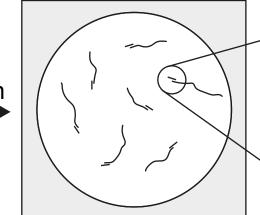
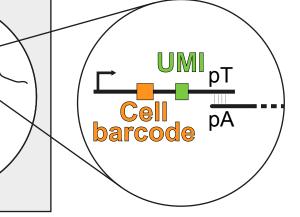
Droplet-based methods e.g. Drop-seq, 10X Chromium

- + Extremely high cell throughput (>10<sup>4</sup> cells per experiment)
- + Low cost per cell Smaller cell libraries (< \$0.01)
  - (~10<sup>4</sup> molecules per cell)



Gel bead dissolution Cell lysis







• UMI

- Cell ID
- Gene 3' sequence

Droplet cell loading

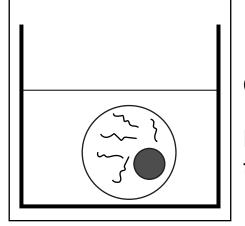
In-droplet RNA processing

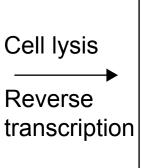
b

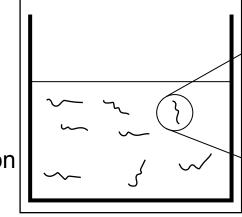
Plate-based methods e.g. Smart-Seq2, MARS-seq

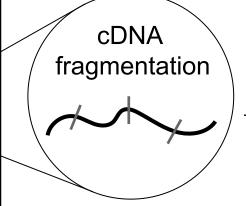
- + High read-depth per cell (>10<sup>6</sup> reads per cell)
- + Reads may be generated across whole transcript length
  - Moderate cell throughput (10<sup>2</sup> - 10<sup>3</sup> cells per experiment)

Read 2:









Cell-specific barcode ligation

Both reads:

- Cell ID
- Gene sequence

Microwell cell loading

In-well RNA processing