

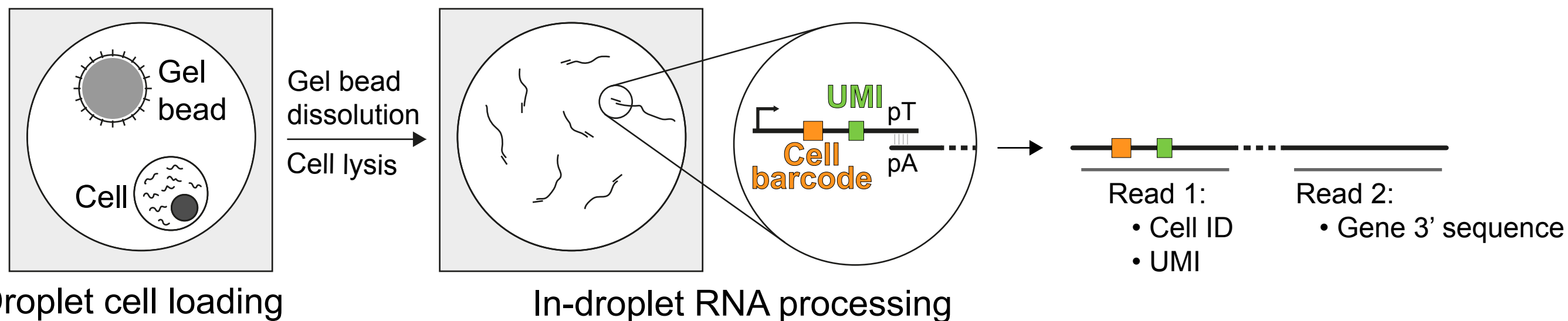
a

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

+ Extremely high cell throughput
($>10^4$ cells per experiment)

+ Low cost per cell
($< \$0.01$)

- Smaller cell libraries
($\sim 10^4$ molecules per cell)



b

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

+ High read-depth per cell
($>10^6$ reads per cell)

+ Reads may be generated
across whole transcript
length

- Moderate cell throughput
($10^2 - 10^3$ cells per
experiment)

