

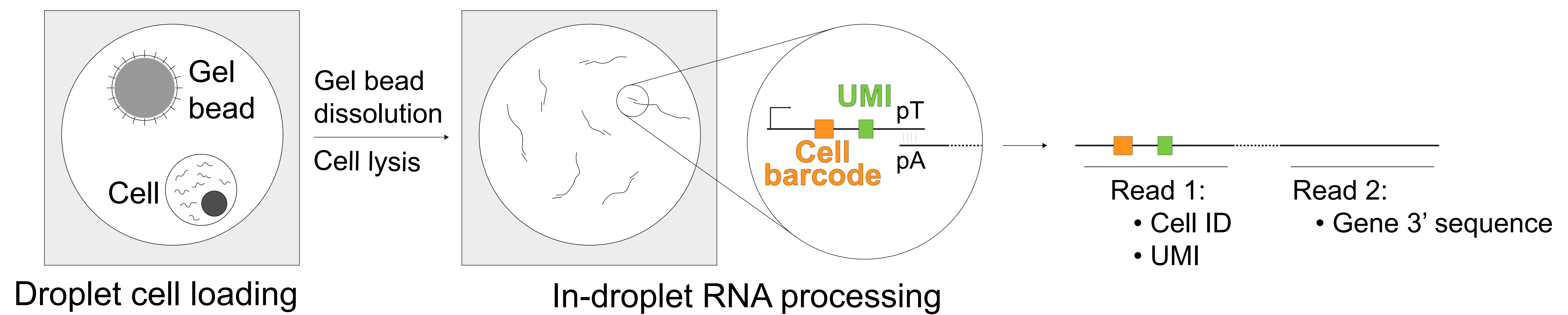
a

### 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)

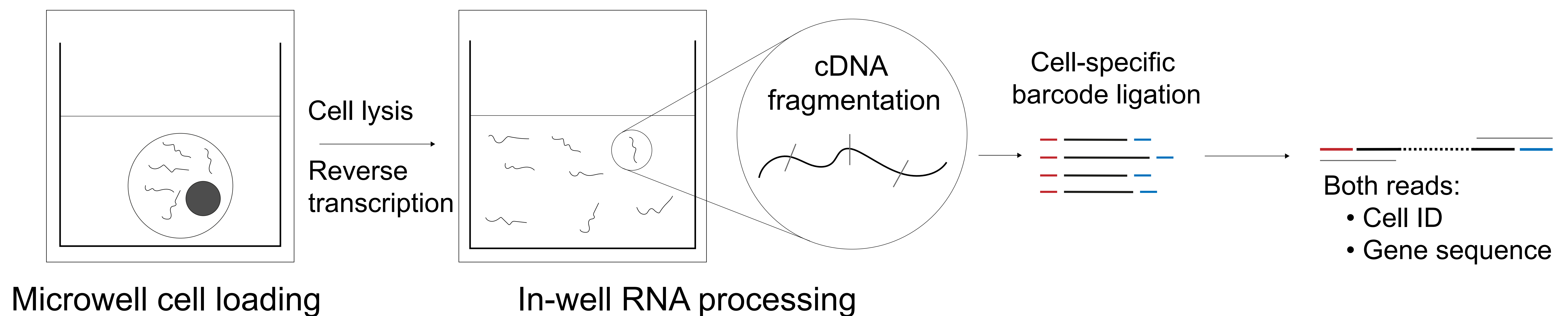


### Plate-based methods e.g. Smart-Seq2, MARS-seq

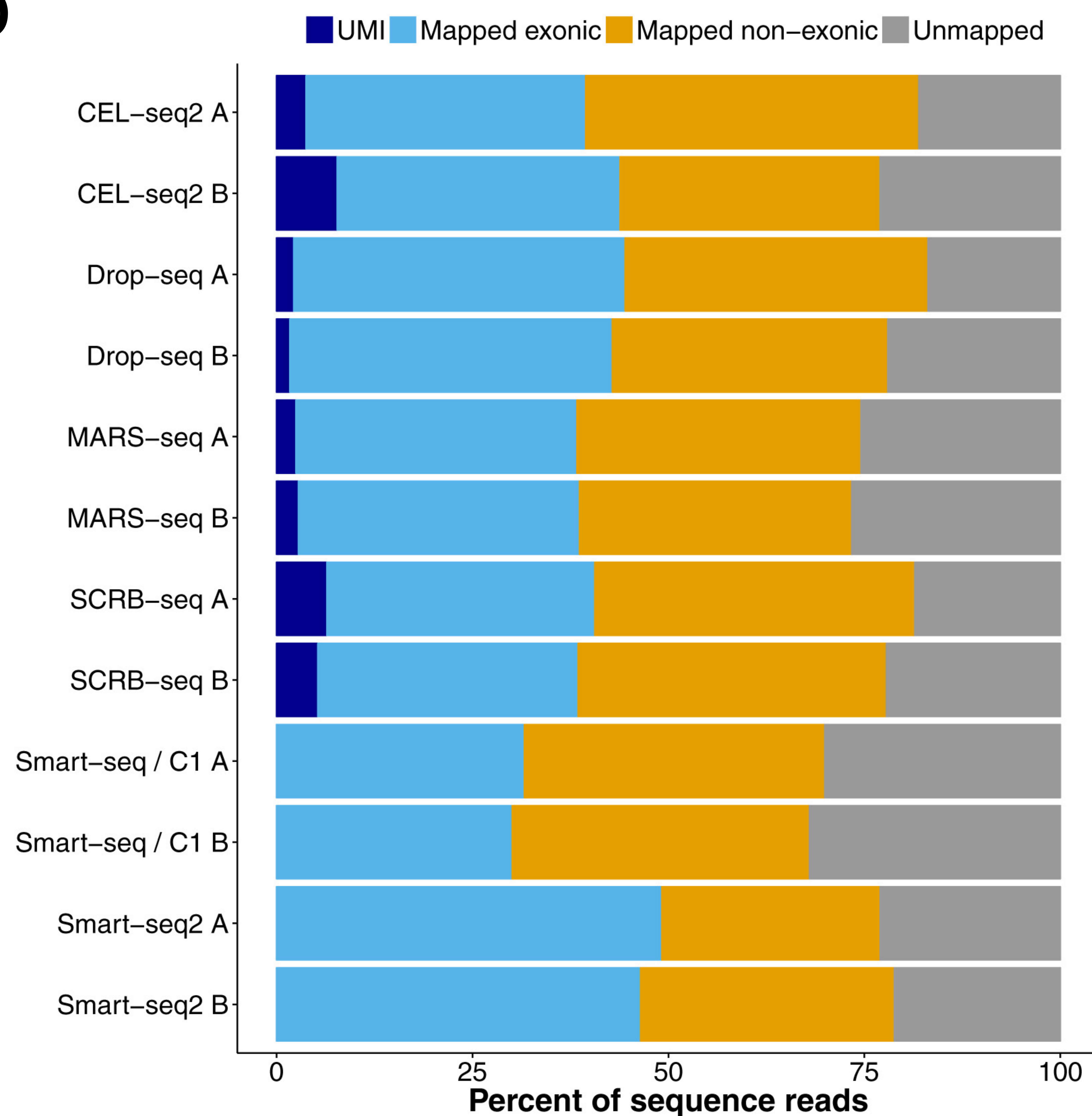
+ High read-depth per cell  
( $>10^6$  reads per cell)

+ Reads may be generated  
across whole transcript  
length

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



b



b

