Introduction to Single-Cell RNA-seq

The CCDL

What can bulk RNA-seq vs single-cell RNA-seq help us determine?

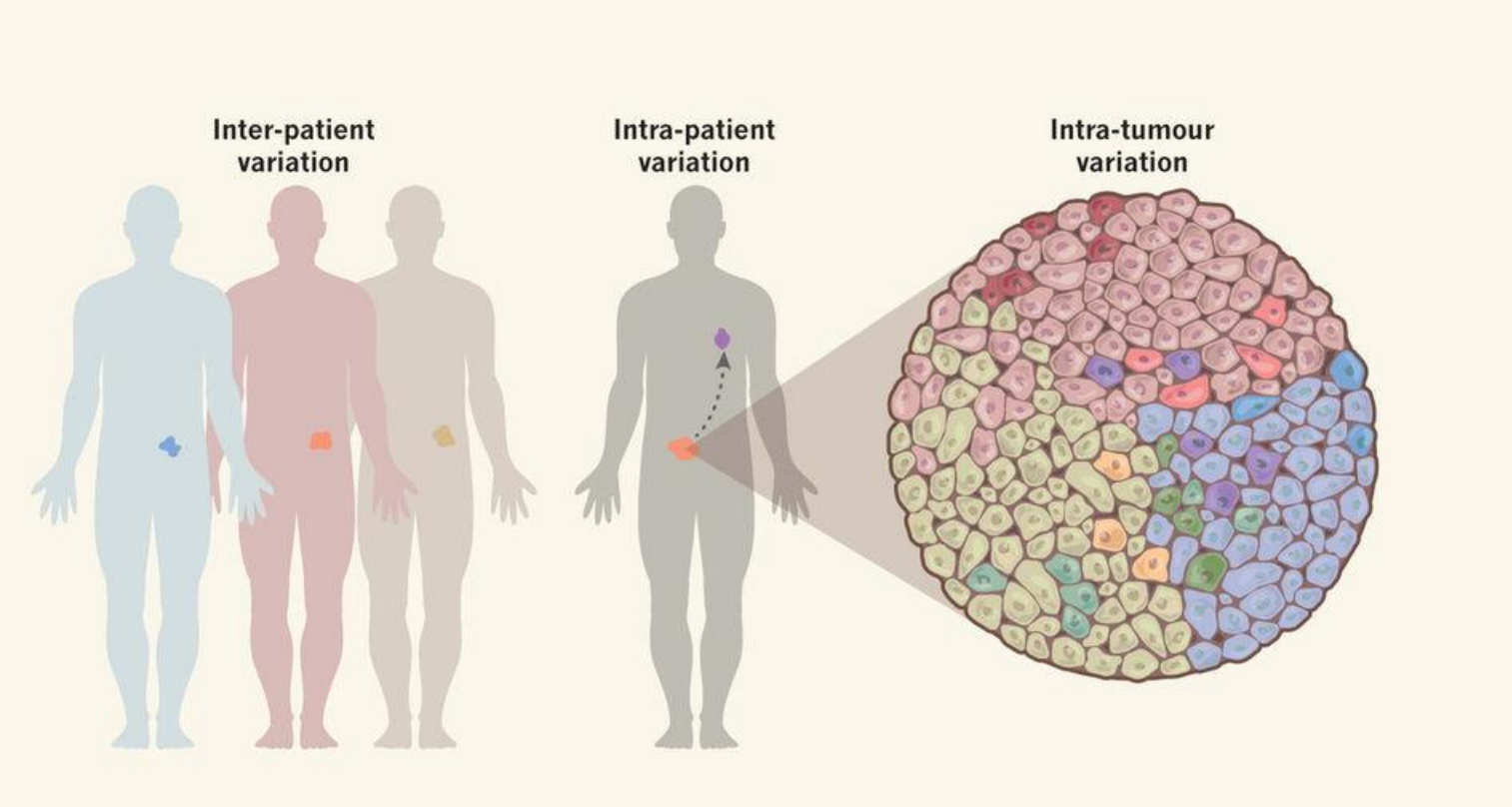


Image from Tanaka *et al*. 2018 https://doi.org/10.1038/s41551-017-0162-1.

What can bulk RNA-seq vs single-cell RNA-seq help us determine?

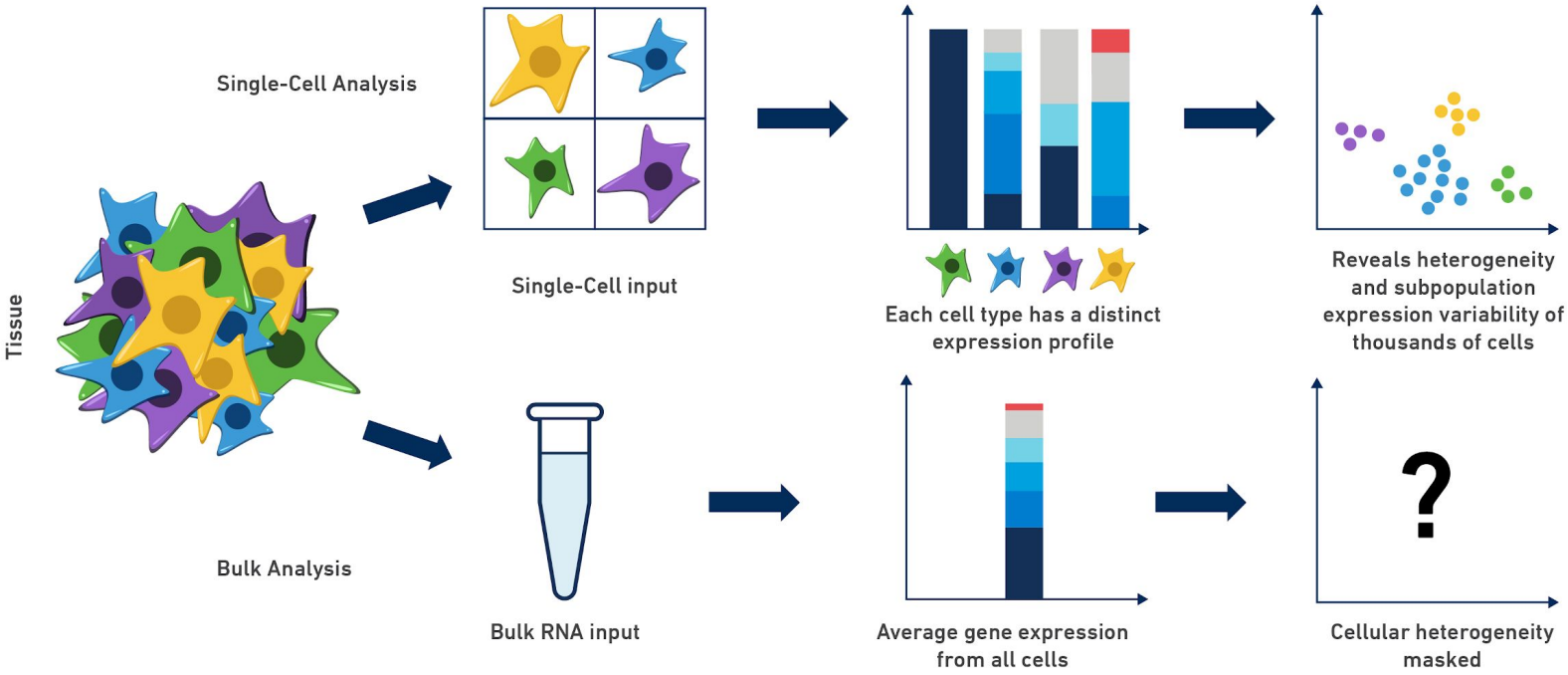


Image from 10X Genomics blog: https://www.10xgenomics.com/blog/single-cell-rna-seq-an-introductory-overview-and-tools-for-getting-started

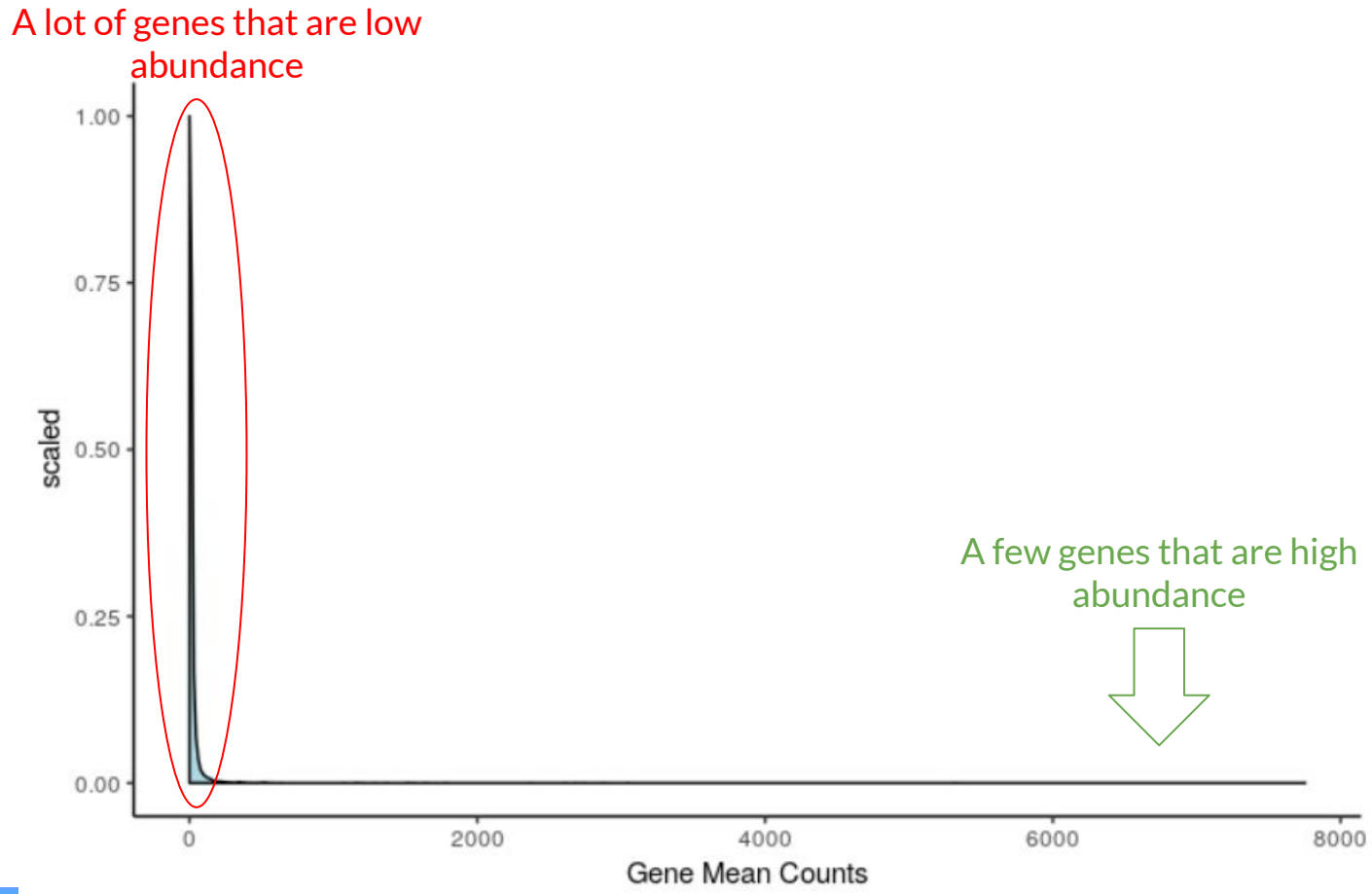
Single-cell RNA-seq quirks

Less starting material means:

- More PCR amplification (*and its associated biases*)
- More zero counts
  - Biology - Not every gene is expressed in every cell
  - Technical - Biased capture methods, Sequencing every RNA in every cell requires a lot more sequencing

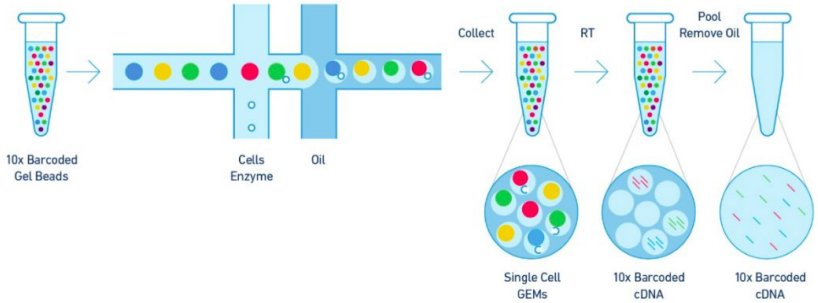
Choi *et al.* (Genome Biology, 2020) https://genomebiology.biomedcentral.com/articles/10.1186/s13059-020-02103-2

Single-cell gene mean density graph



Single Cell Basic Set-ups

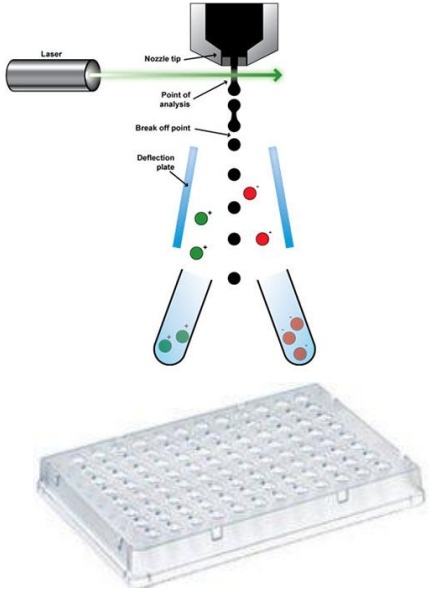
1. Tag-based scRNA-seq



Tag-based separation of cells' data *after* sequencing

Example: 10X Genomics Chromium
Zheng *et al.* 2017
https://www.ncbi.nlm.nih.gov/pubmed/28091601

2. Full-length scRNA-seq



Physical separation of cells *before* sequencing

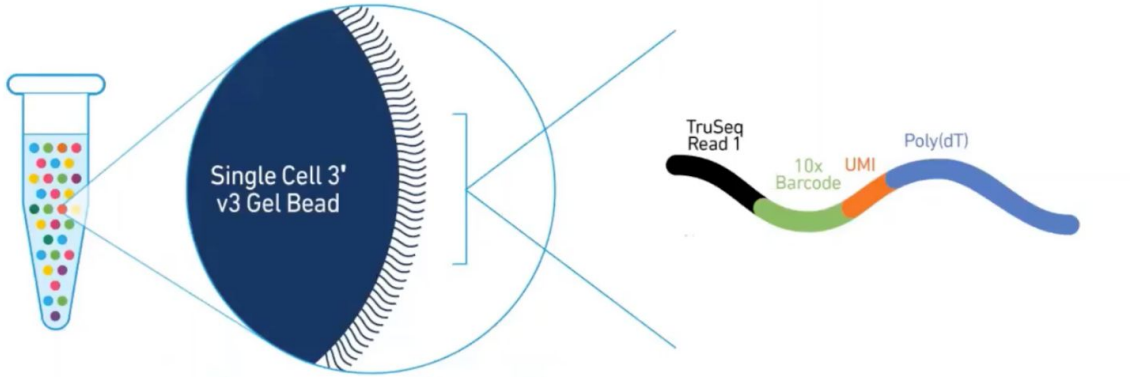
Example: Smart-seq2
Picelli *et al.* 2014
https://www.nature.com/articles/nprot.2014.006

Cell Barcodes + Unique Molecular Identifiers (UMIs) are used to label individual transcripts

Each droplet contains 1 cell, all with the same cell barcode

Within each droplet, each bead contains millions of distinct UMIs

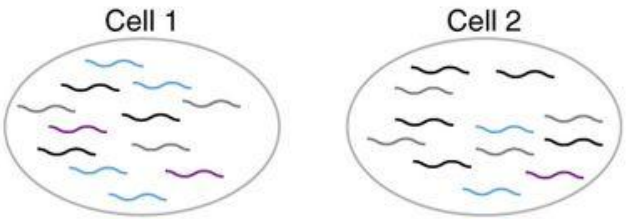
Each transcript within a cell is tagged with a cell barcode and unique molecular identifier (UMI)



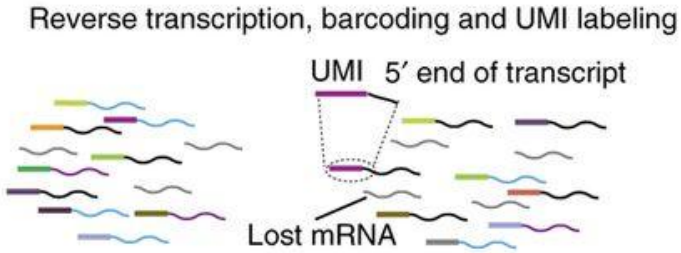
Unique Molecular Identifiers (UMIs):

a '*snapshot*' of the original molecules in the *pre-amplified* cell

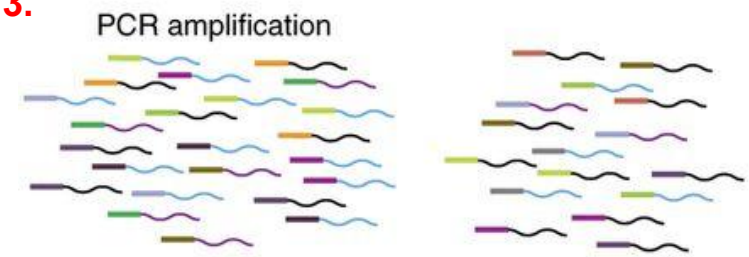
1.



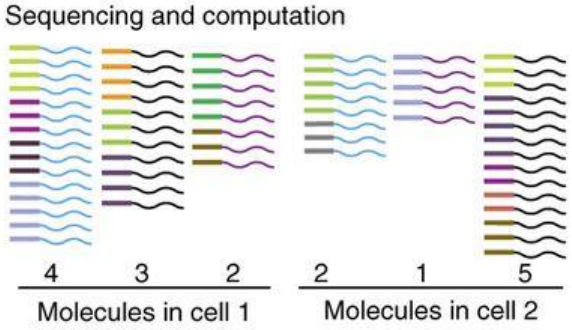
2.



3.

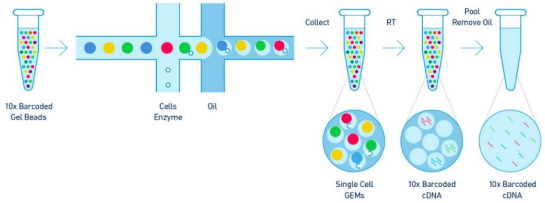


4.



Original image from: Islam *et al.* 2014 https://doi.org/10.1038/nmeth.2772

Tag-Based scRNA-seq



Pros:

- Can profile up to millions of cells.
- Takes less computing power.
- File storage requirements are smaller.
- Much less expensive.

Cons:

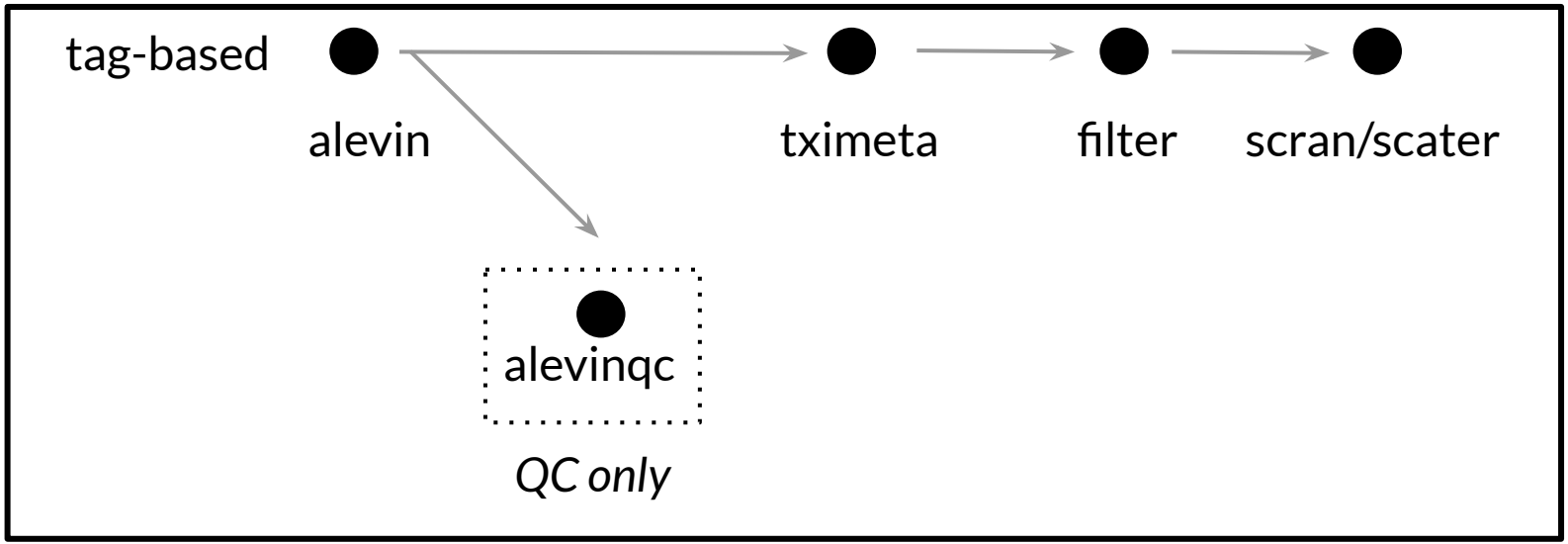
- More intense 3' bias because sequencing is not bidirectional.
- Coverage is generally not as deep as full-length scRNA-seq.

Pre-processing scRNA-seq

Step 1: Separate data by cell barcode and UMI
Step 2: Align reads to determine genes present in each cell
Step 3: Collapse duplicate UMI's to create gene x cell count matrix

- Many different pre-processing tools are available
- Cell Ranger, 10X supported tool, is popular mainly for being user friendly, but is very slow (aligns to the entire genome)
- Alevin is a faster salmon based pre-processing tool (aligns to the transcriptome)

Comparison of common alignment tools: https://doi.org/10.1093/gigascience/giac001


tag-based
alevin
tximeta
filter
scran/scater
alevinqc
QC only

Resources for you in `00-scRNA-seq_introduction.md`

- Hemburg lab scRNA-seq training course
- ASAP: Automated Single-cell Analysis Pipeline is a web server that allows you to process scRNA-seq data.
- Smith. Unique Molecular Identifiers – the problem, the solution and the proof - article on background of UMIs
- Literature on technologies

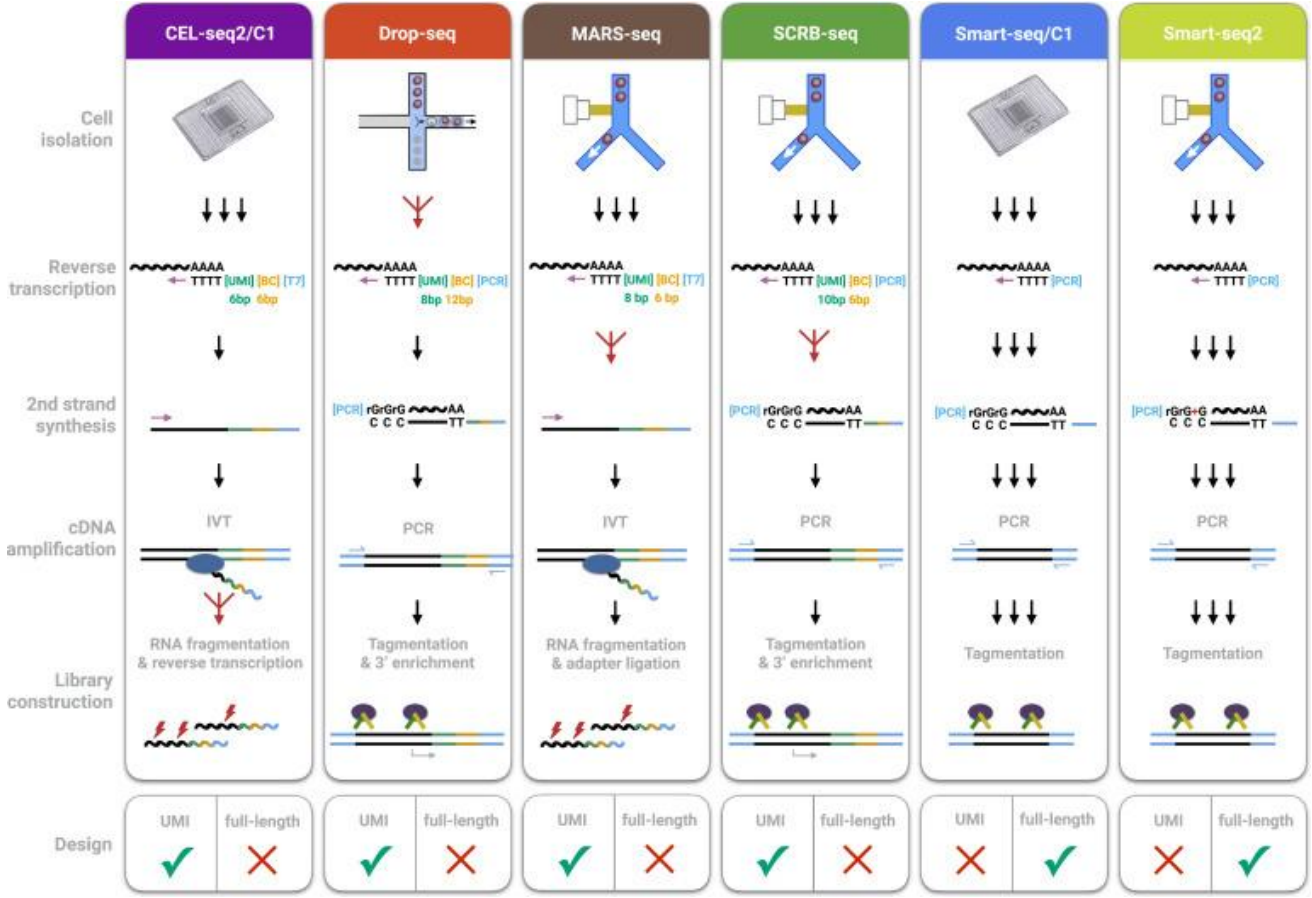


Image from: Zeigenhain et al. Mol Cell. 2018 (http://dx.doi.org/10.1016/j.molcel.2017.01.023)

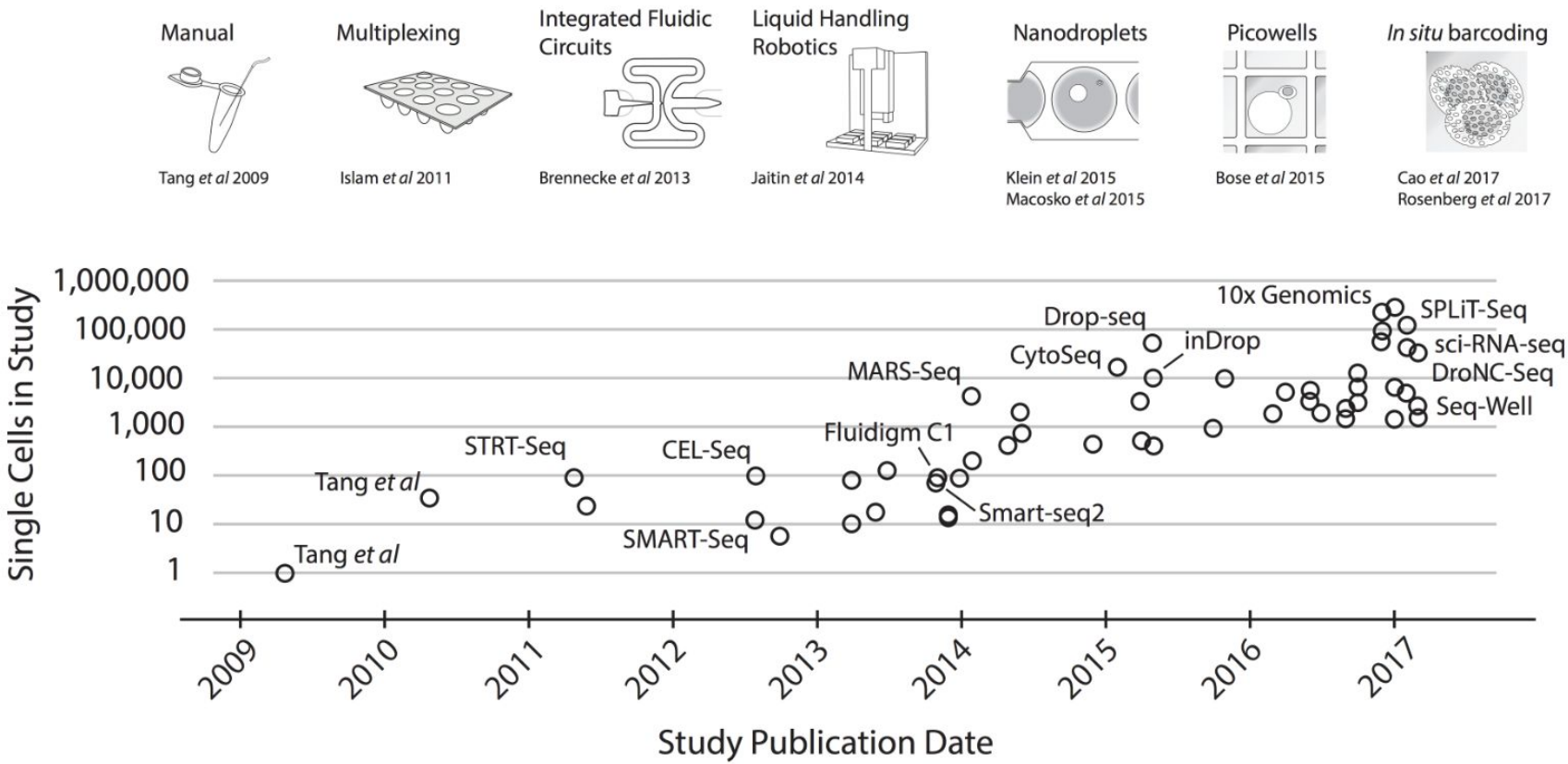


Image from Svensson et al: https://arxiv.org/abs/1704.01379