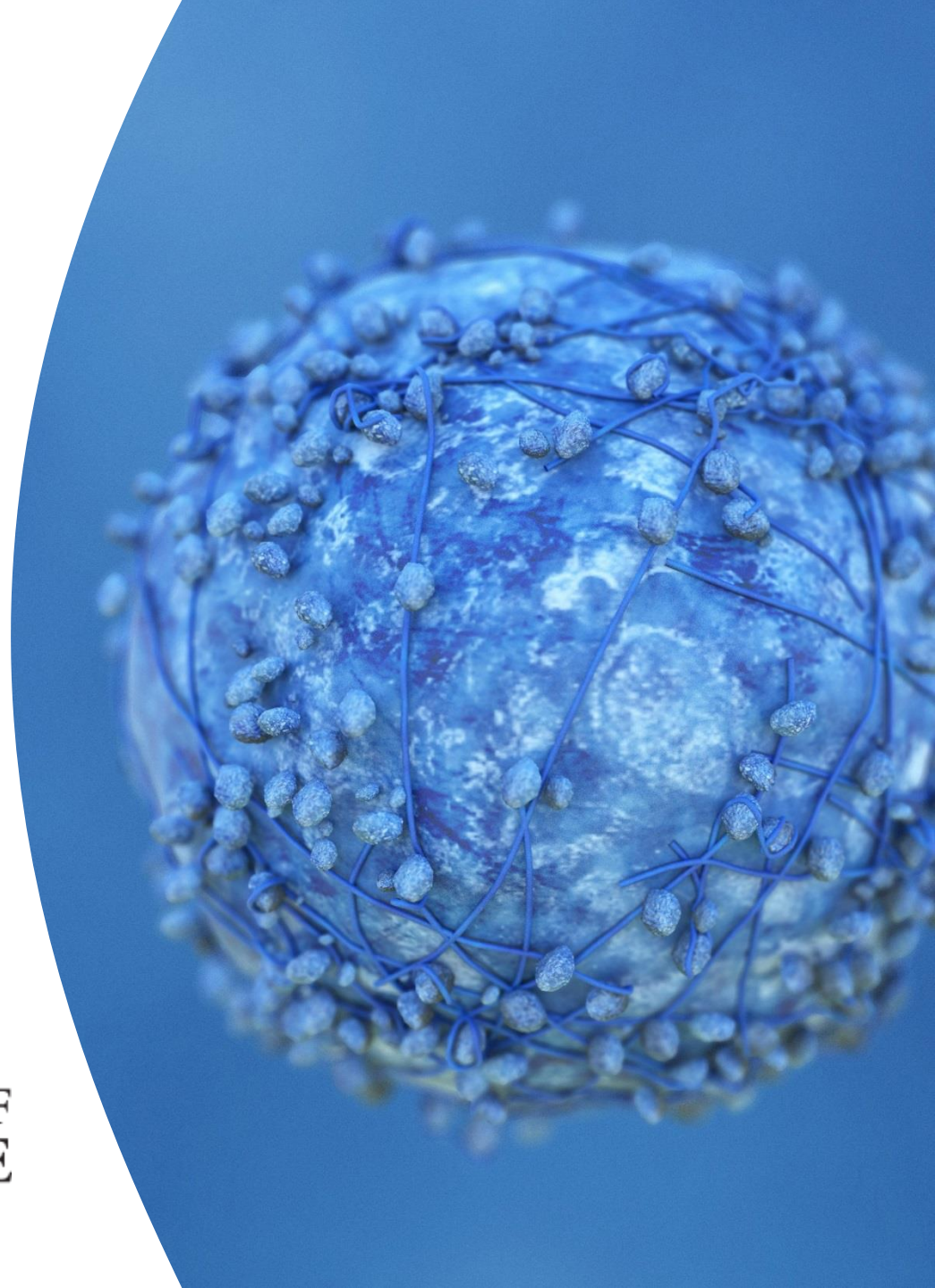
INTRODUCTION TO SINGLE CELL RNA-SEQ

Analysis of single cell RNA-seq data - online course

Katarzyna Kania (CRUK CI Genomics Core Facility)

17th June 2022



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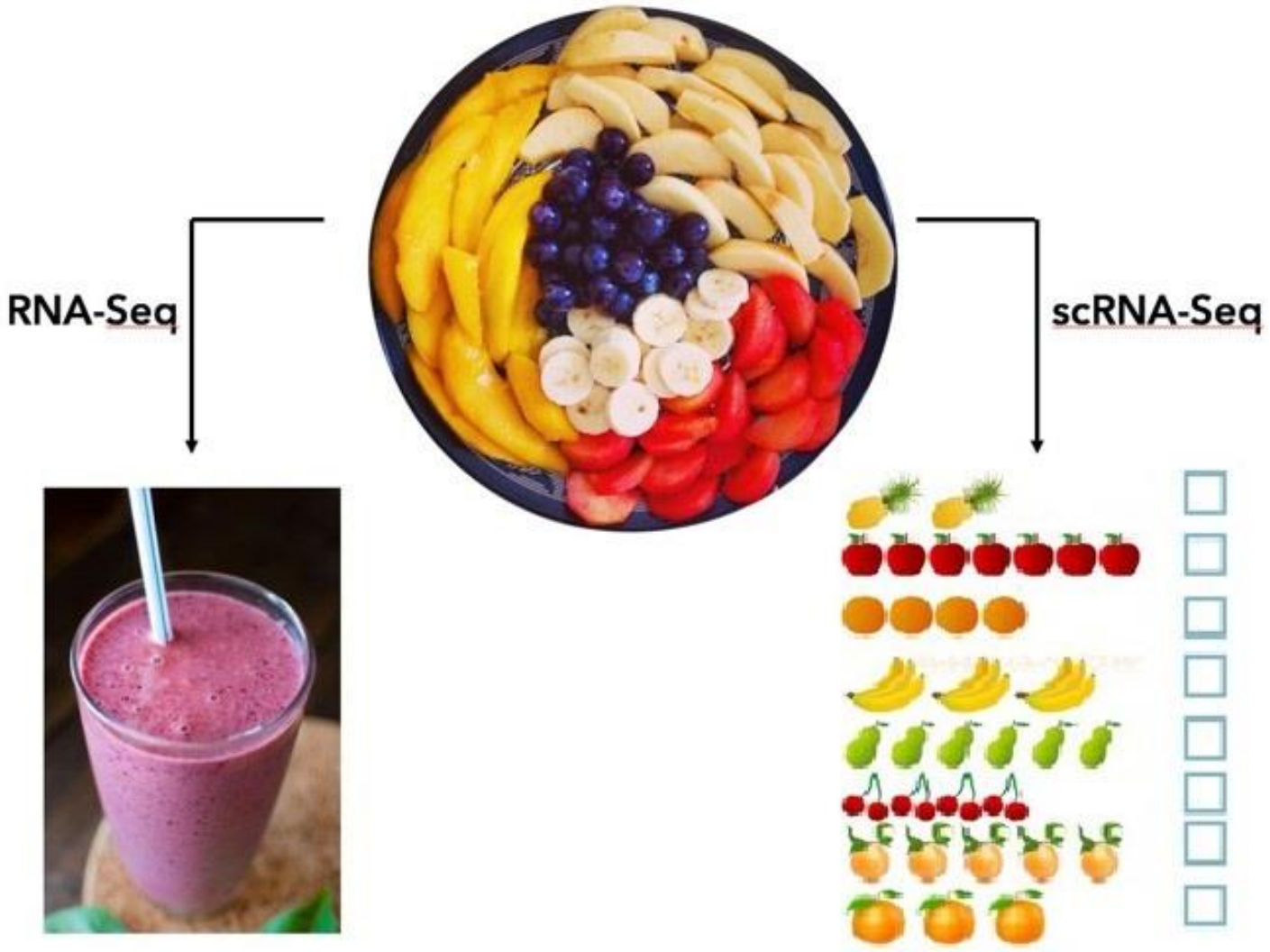
Together we will beat cancer

BULK VS SINGLE CELL RNA-SEQ

Average expression level
- Comparative transcriptomics
- Disease biomarker
- Homogenous systems



Separate populations
- Define heterogeneity
- Identify rare cell populations
- Cell population dynamics

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BULK VS SINGLE CELL RNA-SEQ

1. mRNA: TruSeq RNA-Seq (Gold Standard)
   - ~20,000 transcripts
     - More when consider splice variants / isoforms
   - Observe 80-95% of transcripts depending on sequencing depth

2. Low input methods ~3000 cells / well
   - 4000-6000 transcripts per sample
     - Limiting to transcripts observed across all samples
   - Observe 20-60% of the transcriptome

3. Single Cell Methods
   - 200 -10,000 transcripts per cell
   - Observe 10-50% of the transcriptome
   - Many transcripts will show up with zero counts in every cell. (even GAPDH)
   - If you only looked at transcripts observed in all cells numbers drop dramatically.

Source: Sarah Boswell, Harvard Medical School, September 2020

BULK VS SINGLE CELL RNA-SEQ

	Deep RNA-seq	Sort-seq	Low input	scRNA-seq
Transcriptome Coverage	High	High	Moderate	Low
Throughput	Moderate	Low	High	Low
Cell Subtype Information	None	Moderate	None	High
Sequencing Depth	Moderate	Moderate	Low	High
Cost per Sample	Moderate	Moderate	Low	High

Source: Sarah Boswell, Harvard Medical School, September 2020

Disadvantages of scRNA-seq

- Dropouts and noisy data
- Lowly expressed genes might be undetected
- Samples will contain doublets
- Replicates without batch effect are unlikely
- Expensive

APPLICATIONS

nature medicine

Letter | Published: 08 June 2020

A single-cell atlas of the peripheral immune response in patients with severe COVID-19

Aaron J. Wilk, Arjun Rustagi, Nancy Q. Zhao, Jonasel Roque, Giovanny J. Martínez-Colón, Julia L. McKechnie, Geoffrey T. Ivison, Thanmayi Ranganath, Rosemary Vergara,

LETTER

https://doi.org/10.1038/s41586-018-0394-6

A single-cell atlas of the airway epithelium reveals the CFTR-rich pulmonary ionocyte

Lindsey W. Plasschaert[1,5,7], Rapolas Žilionis[2,3,7], Rayman Choo-Wing[1,5], Virginia Savova[2,6], Judith Knehr[4], Guglielmo Roma[4], Allon M. Klein[2]* & Aron B. Jaffe[1,5]*

nature

Article | Published: 20 February 2019

A single-cell molecular map of mouse gastrulation and early organogenesis

Blanca Pijuan-Sala, Jonathan A. Griffiths, Carolina Guibentif, Tom W. Hiscock, Wajid Jawaid, Fernando J. Calero-Nieto, Carla Mulas, Ximena Ibarra-Soria, Richard C. V.

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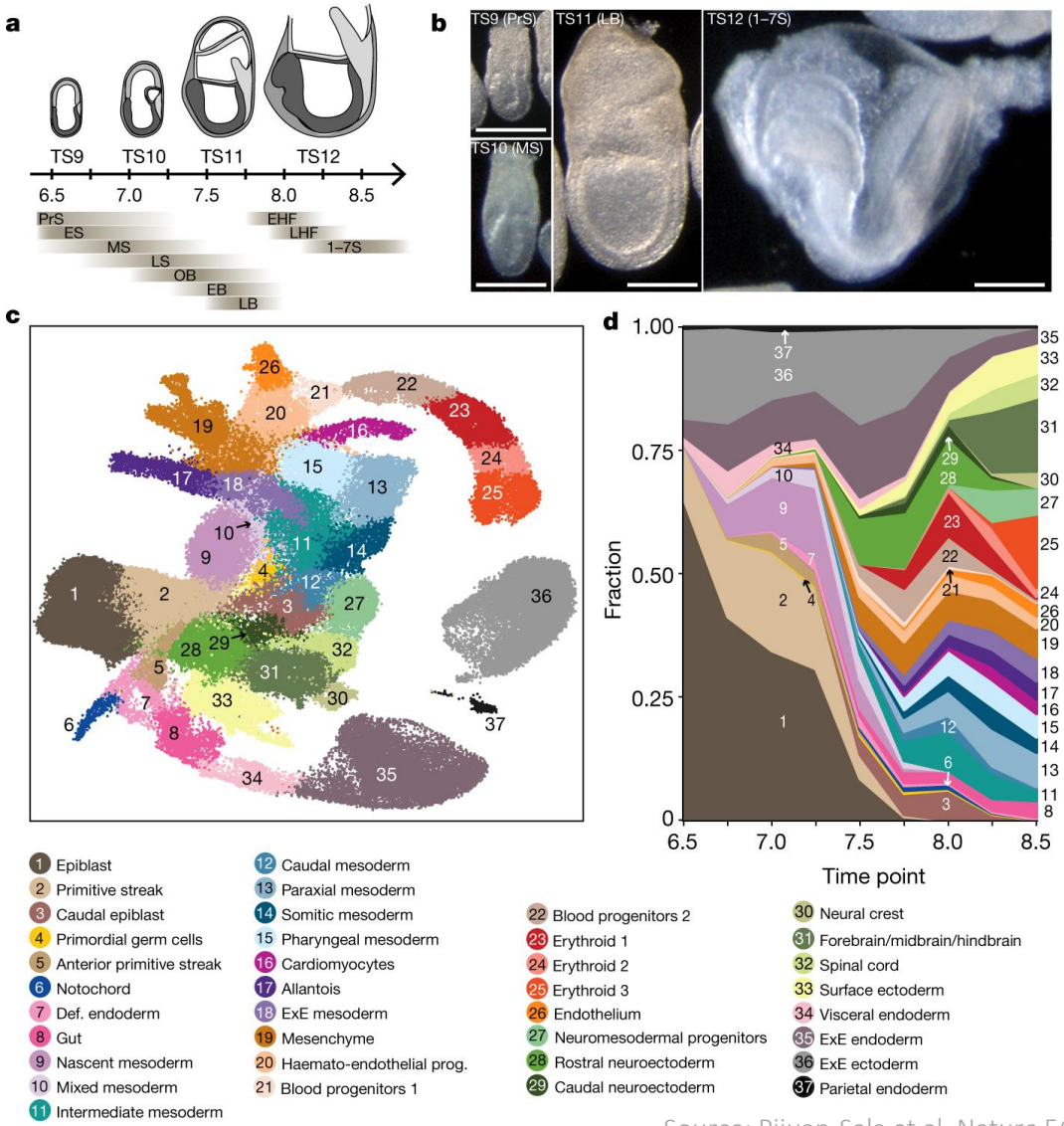
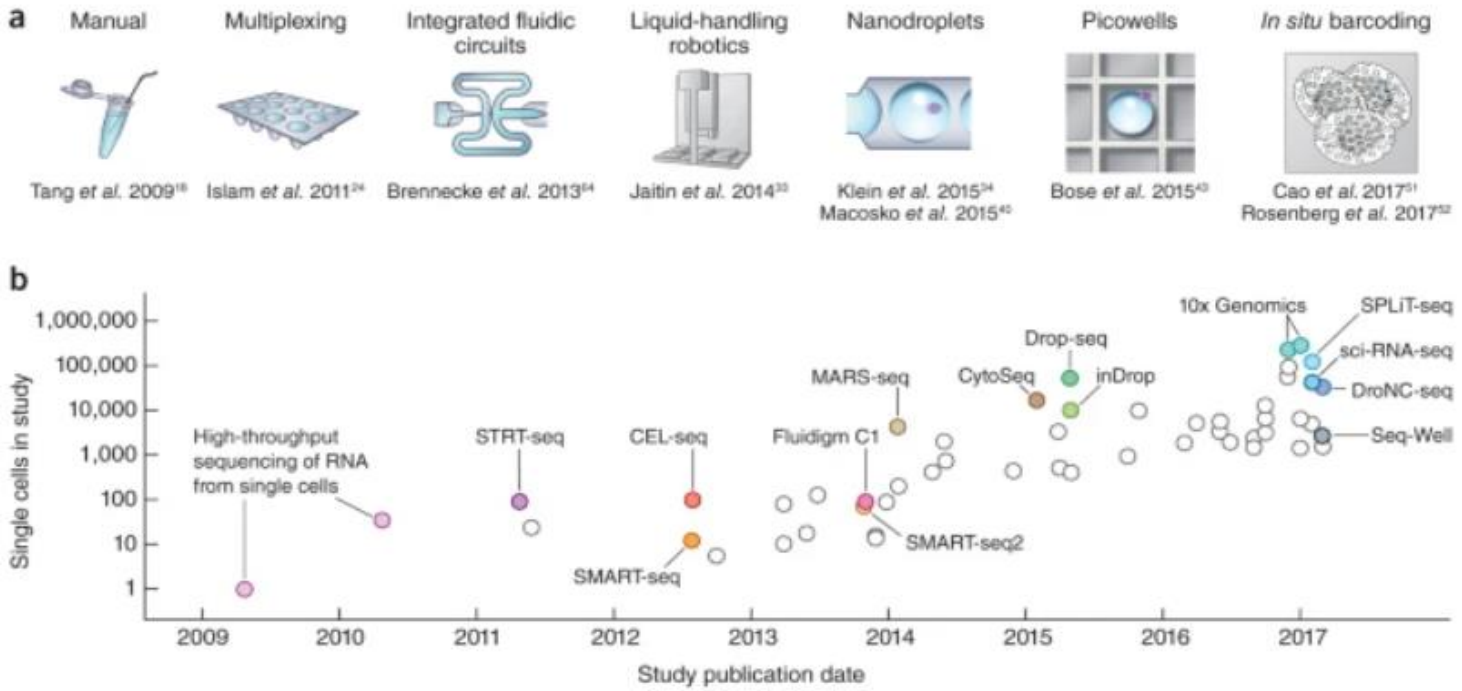


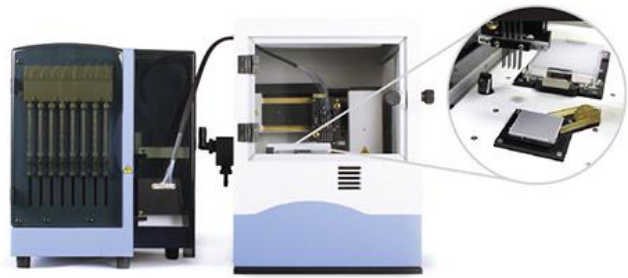
Source: Pijuan-Sala et al. Nature 566, 490–495 (2019)

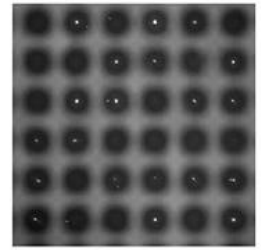
TECHNOLOGIES

Figure 1: Scaling of scRNA-seq experiments.



Source: Svensson et al. *Nat Protoc* 13, 599–604 (2018)





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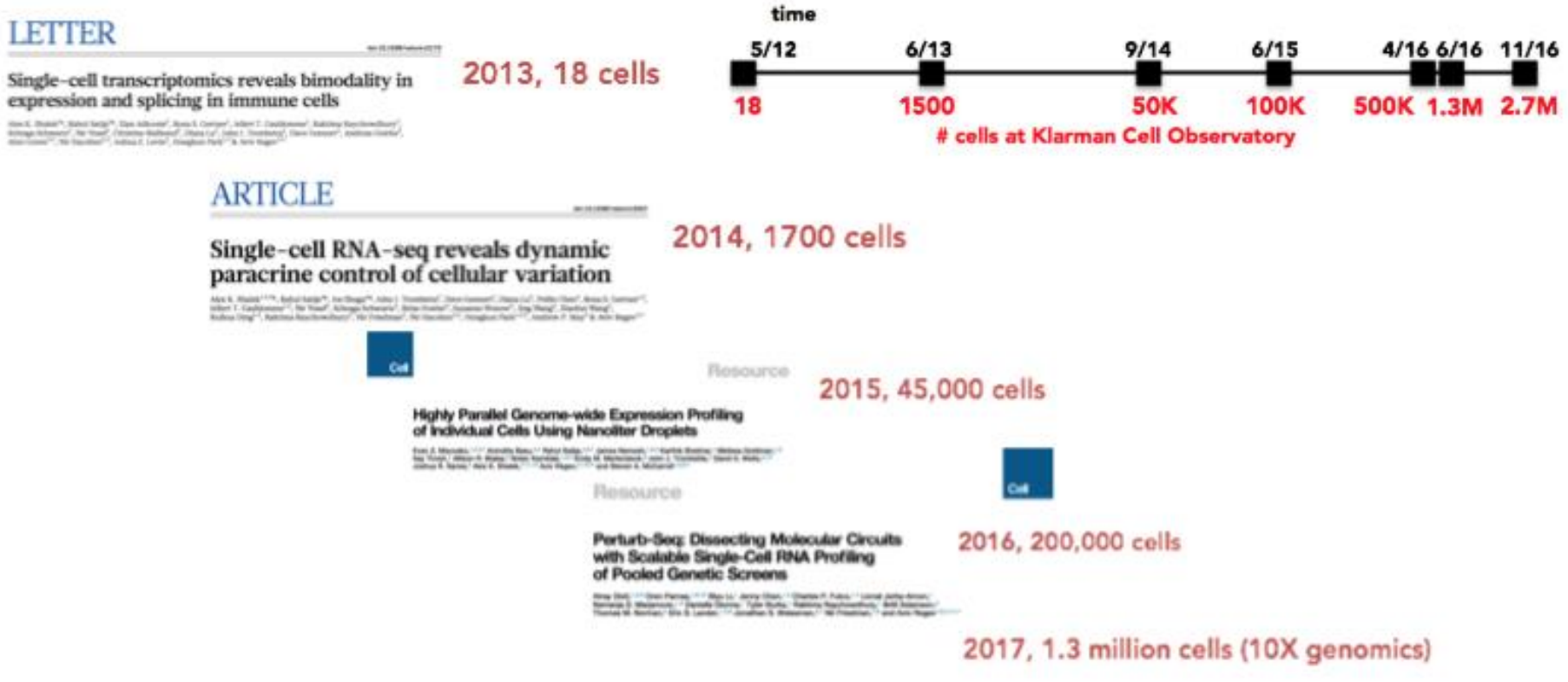
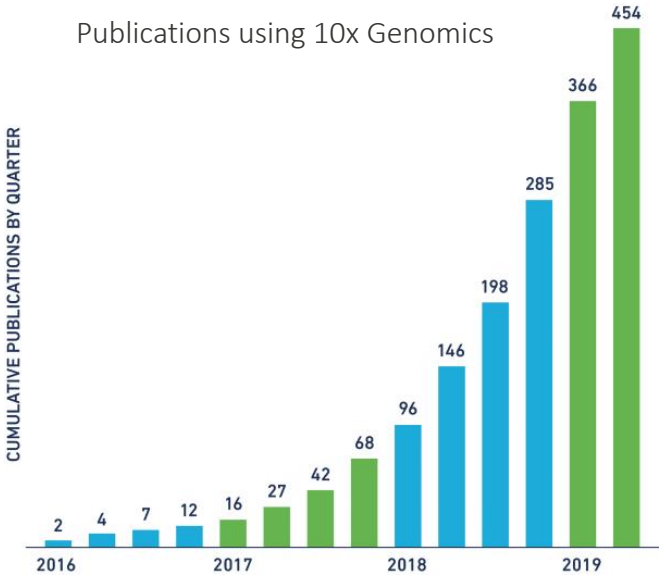
HISTORY AND PROGRESS

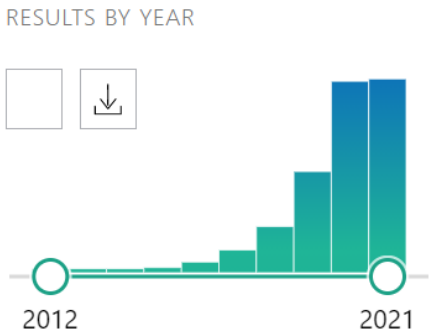


Source: Introduction to scRNASeq, Timothy Tickle & Brian Haas, Broad Institute, 2017

Publications using 10x Genomics



PubMed search for 'scRNA-seq'



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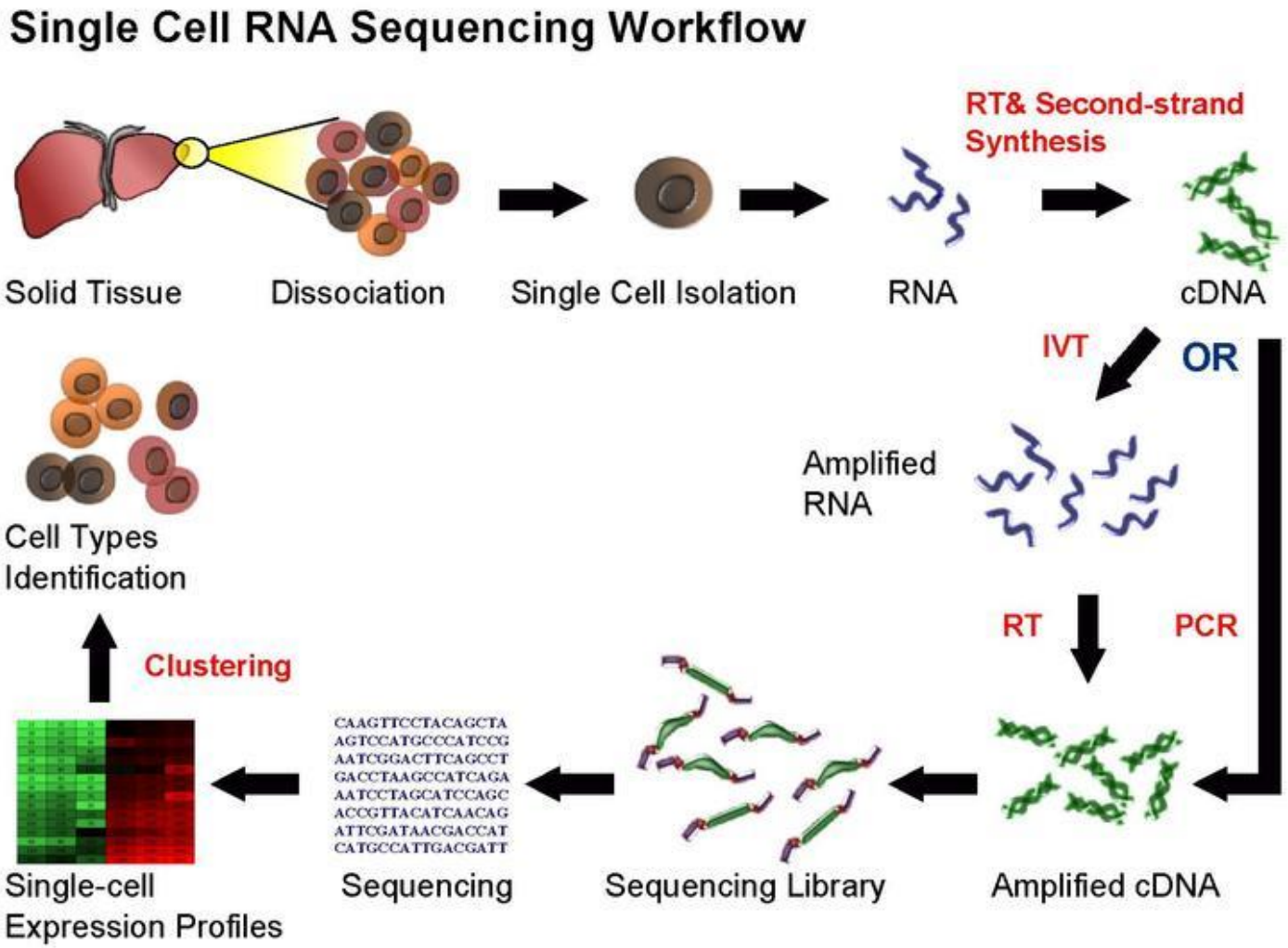
WORKFLOW

Good sample preparation is key to success!



Source: https://en.wikipedia.org/wiki/Single_cell_sequencing

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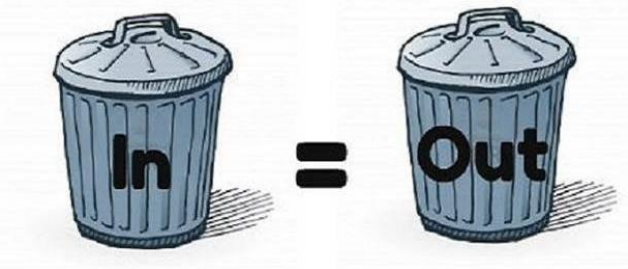
SAMPLE PREPARATION



- Understand well the nature of the sample (sampling conditions, preparation, purity)
- Identify the source of technical difficulties in order to resolve them first
- Practice your sample preparation, optimise the protocol well, do not rush to the final experiment
- A well planned pilot experiment is essential for evaluating sample preparation and for understanding the required number of cells.
- You need your cells to be highly viable (>90-95%), have no clumps and no debris. Cell membrane integrity is a must!
- Free-floating RNA will make analysis more challenging
- Be cautious about FACS (especially with more fragile cells). If FACS necessary for enrichment, remember that time is crucial factor
- Count with haemocytometer or cell counter (Countess II Automated Cell Counter) – do not trust sorter counts
- Fixation and cryopreservation are not compatible with many techniques

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TISSUE PRESERVATION

Research | Open Access | Published: 02 June 2020

Systematic assessment of tissue dissociation and storage biases in single-cell and single-nucleus RNA-seq workflows

Elena Denisenko, Belinda B. Guo, Matthew Jones, Rui Hou, Leanne de Kock, Timo Lassmann, Daniel Poppe, Olivier Clément, Rebecca K. Simmons, Ryan Lister & Alistair R. R. Forrest

Genome Biology **21**, Article number: 130 (2020) | Cite this article

14k Accesses | **39** Citations | **40** Altmetric | Metrics

Research | Open Access | Published: 10 May 2021

Cryopreservation of human cancers conserves tumour heterogeneity for single-cell multi-omics analysis

Sunny Z. Wu, Daniel L. Roden, [...]Alexander Swarbrick

Genome Medicine **13**, Article number: 81 (2021) | Cite this article

1757 Accesses | **34** Altmetric | Metrics

Immune Netw. 2020 Aug; 20(4): e34.
Published online 2020 Jul 15. doi: 10.4110/in.2020.20.e34

PMCID: PMC7458795
PMID: 32895621

Effects of Cryopreservation and Thawing on Single-Cell Transcriptomes of Human T Cells

Jeong Seok Lee,[1,†] Kijong Yi,[1,†] Young Seok Ju,[1,2] and Eui-Cheol Shin[✉1,2]

▸ Author information ▸ Article notes ▸ Copyright and License information Disclaimer

Genome Biol. 2020; 21: 1.
Published online 2019 Dec 31. doi: 10.1186/s13059-019-1906-x

PMCID: PMC6937944
PMID: 31892341

scRNA-seq assessment of the human lung, spleen, and esophagus tissue stability after cold preservation

E. Madissoon,[#1,2] A. Wilbrey-Clark,[#1] R. J. Miragaia,[1] K. Saeb-Parsy,[3] K. T. Mahbubani,[3] N. Georgakopoulos,[3] P. Harding,[1] K. Polanski,[1] N. Huang,[1] K. Nowicki-Osuch,[4] R. C. Fitzgerald,[4] K. W. Loudon,[5] J. R. Ferdinand,[5] M. R. Clatworthy,[5] A. Tsingene,[1] S. van Dongen,[1] M. Dabrowska,[1] M. Patel,[1] M. J. T. Stubbington,[1,6] S. A. Teichmann,[1] O. Stegle,[2] and K. B. Meyer[✉1]

Article | Open Access | Published: 23 July 2019

DMSO cryopreservation is the method of choice to preserve cells for droplet-based single-cell RNA sequencing

Christian T. Wohnhaas, Germán G. Leparc, Francesc Fernandez-Albert, David Kind, Florian Gantner, Coralie Viollet, Tobias Hildebrandt & Patrick Baum

Scientific Reports **9**, Article number: 10699 (2019) | Cite this article

14k Accesses | **20** Citations | **49** Altmetric | Metrics

Chromium Single Cell Fixed RNA Profiling kits

Parse Biosciences, HIVE

Research article | Open Access | Published: 09 November 2020

Single-cell transcriptome conservation in a comparative analysis of fresh and cryopreserved human skin tissue: pilot in localized scleroderma

Emily Mirizio, Tracy Tabib, Xinjun Wang, Wei Chen, Christopher Liu, Robert Lafyatis, Heidi Jacobe & Kathryn S. Torok

Arthritis Research & Therapy **22**, Article number: 263 (2020) | Cite this article

2256 Accesses | **4** Citations | **4** Altmetric | Metrics

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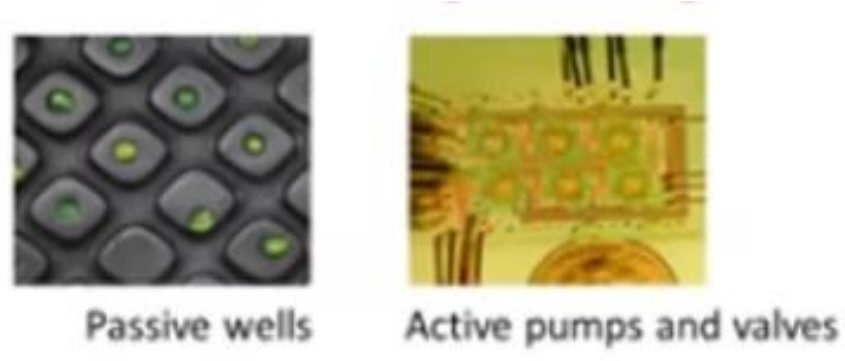
METHODS

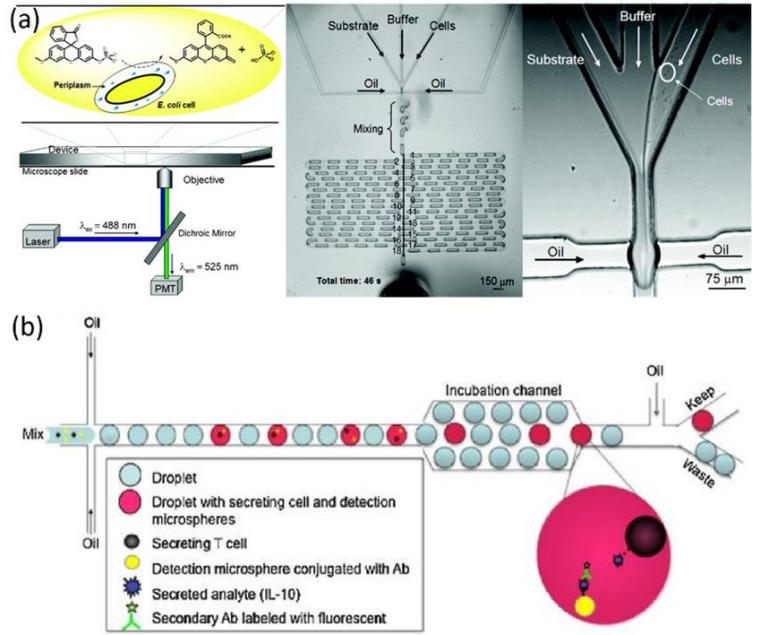
1) Cells in wells, traps and valves (nanowell, Flow sorting, CellenOne, Fluidigm C1, SmartSeq)
   - Screen for and retrieve single cells of interest
   - Enrich for rare cells with decided properties
   - Control the cellular microenvironment
   - Monitor and control cell-cell interactions
   - Precise/extensive manipulation of single cells

2) Droplets (Drop-seq, 10x Genomics)
   - Introduce distinct ‘packets’ of reagents to single cell (e.g. barcodes)
   - Perform amplification on individual cells
   - Sort large population of single cells

3) Combinatorial indexing (SCI-seq, SPLiT-seq)
   - Economic use of reagents for cell separation
   - Efficiency of handling larger population than Drop-seq
   - Maintain complexities of population without bias from droplet or well

4) ‘One tube’ solutions…





Source: Wen et al. Molecules (2016)

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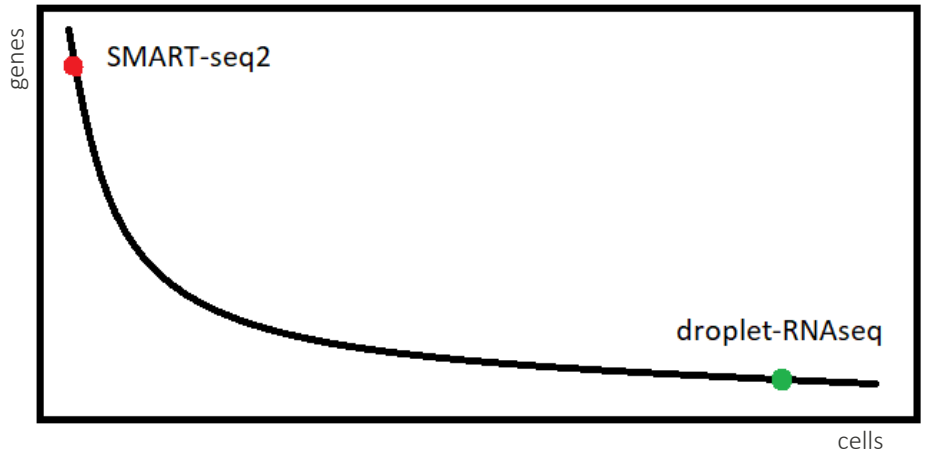
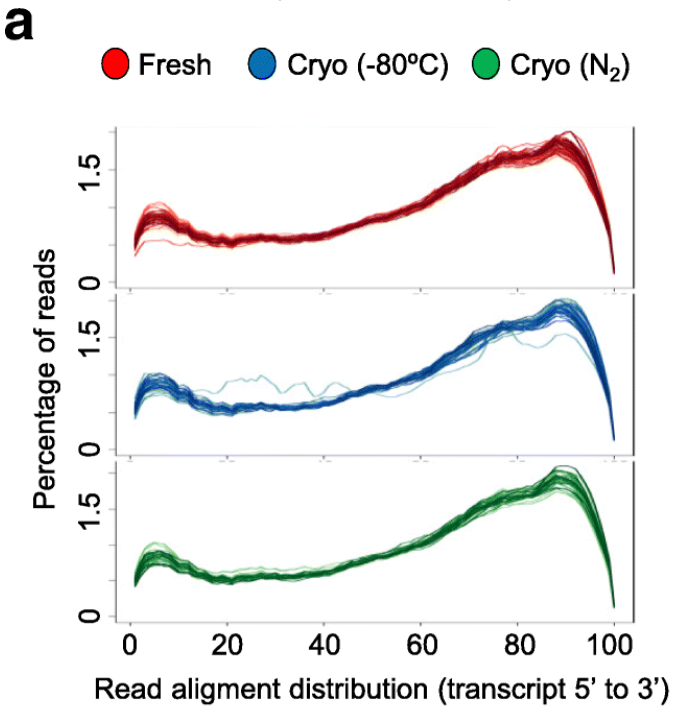
MORE CELLS OR MORE GENES?



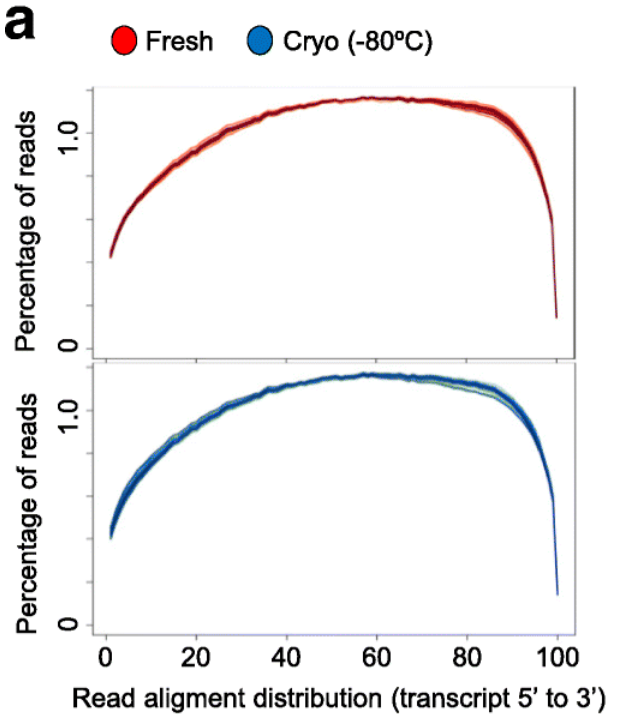
SMART-seq2
- 100 cells
- Full-length libraries
- 1M reads per cell

Droplet-RNAseq
- 10000 cells
- 50k reads per cell
- 3’/5’ bias

Droplet-RNAseq



SMART-seq2



Source: Guillaumet-Adkins, et al. Genome Biol 18, 45 (2017).

- Required number of cells increases with complexity of the sample.
- Number of reads will depend on biology of sample
- Cell-type classification of a mixed population usually requires lower read depth
- You can always re-sequence your samples.

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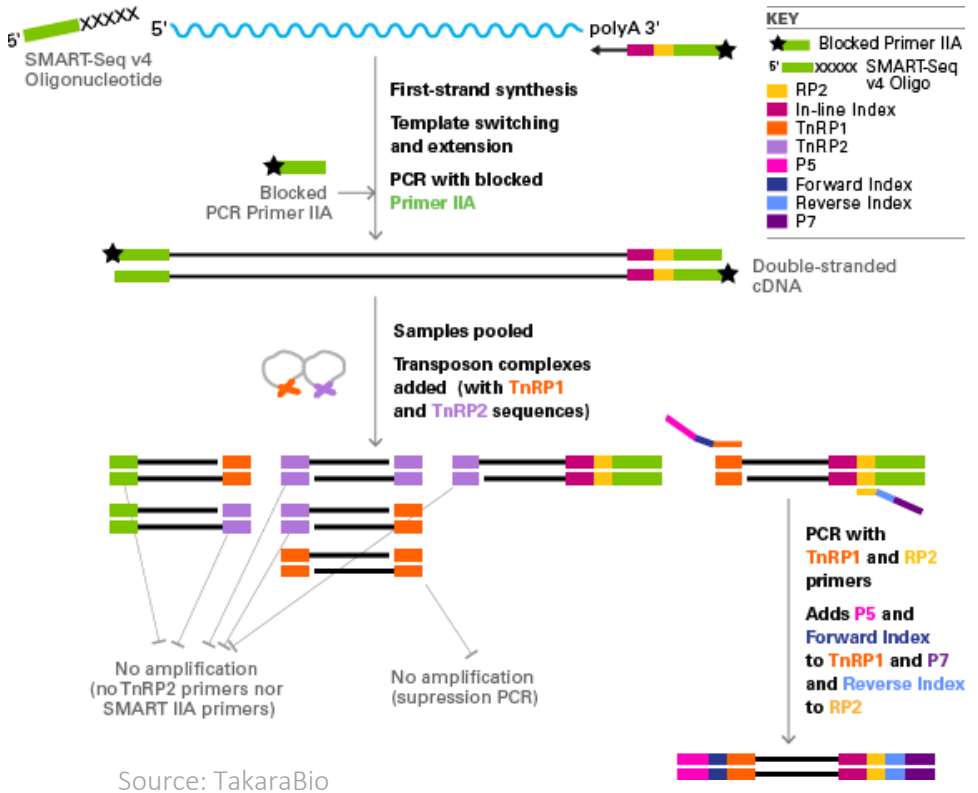
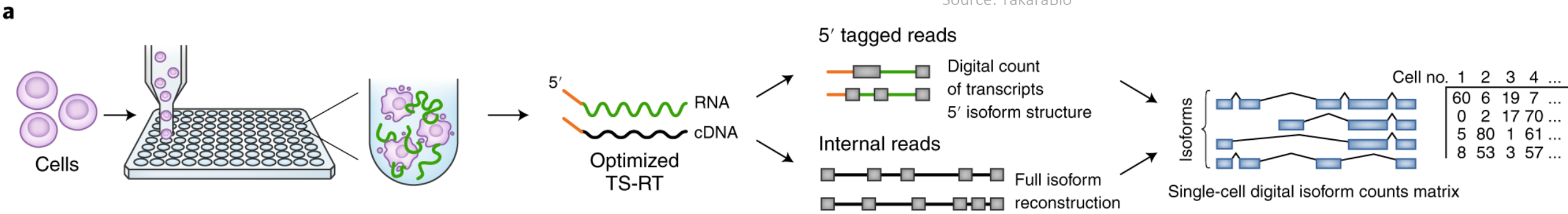
SMART-SEQ2/3/4 OVERVIEW

Developed for single cell but can performed using total RNA.

- Selects for poly-A tail.
- Full transcript assay.
- Uses template switching for 5' end capture.
- Standard Illumina sequencing.
- Plate-based solution so labour intensive, slow and costly (~$12/cell)

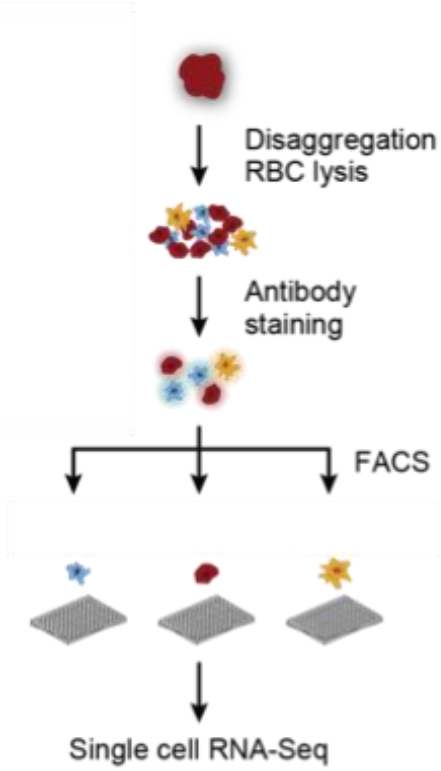


Source: TakaraBio

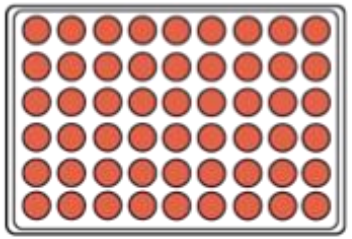


Source: Macosko, Nat Biotechnol 38 (2020).

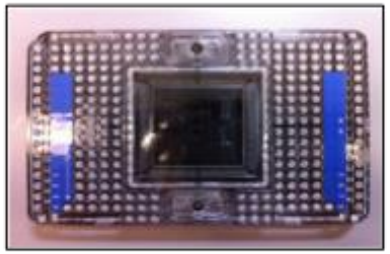
SMART-SEQ2/3/4 + MOSQUITO LV

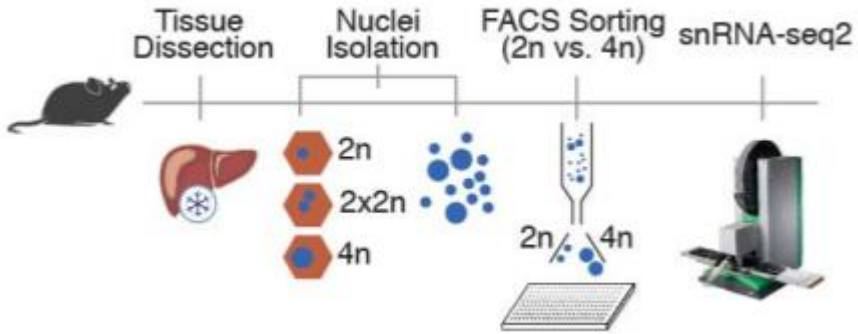


FACS sorting on 96/384-well plates

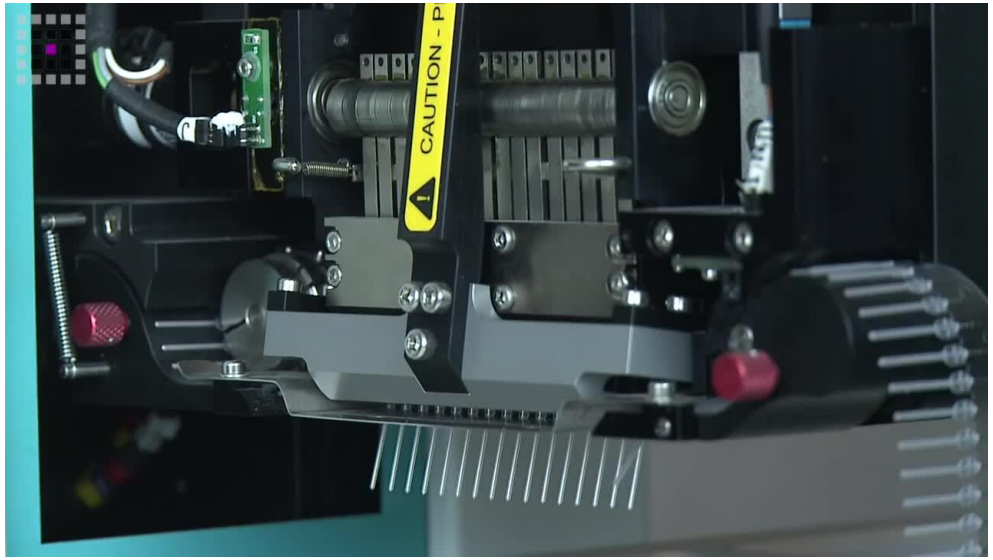


Fluidigm C1-autoprep system





Richter et al. Nat Commun 12, 4264 (2021)



Source: SPT Labtech

- Mosquito LV makes assay miniaturisation simple, leading to significant savings on precious reagents and time.
- Mosquito LV offers highly accurate and precise multichannel pipetting from 25 nL to 1.2 µL.
- SmartSeq2 cost reduced from $12 to $4 per cell

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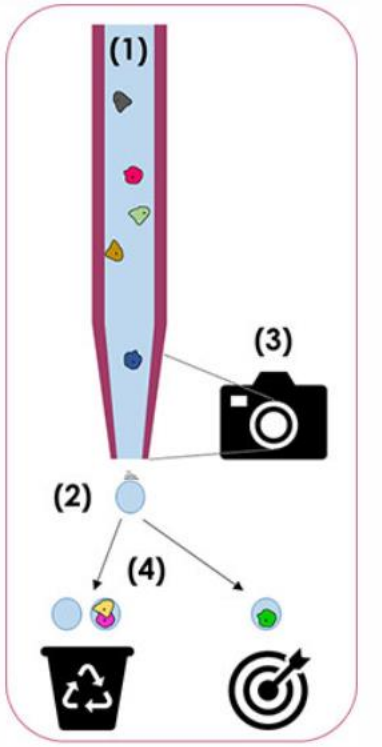
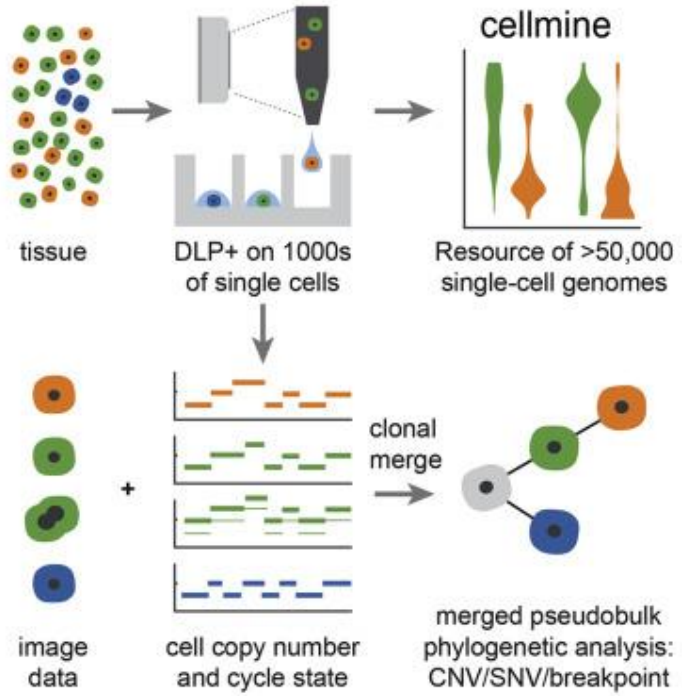
CELLENONE

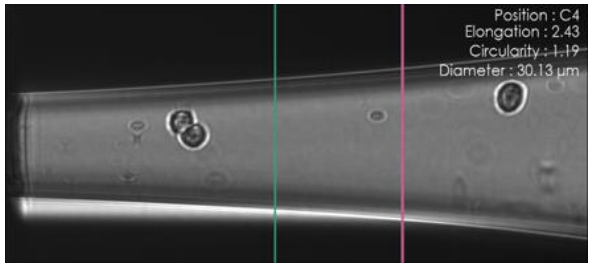


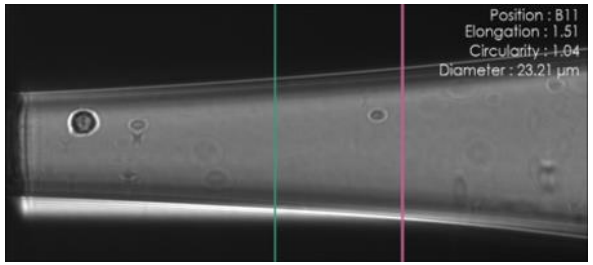
Source: Cellenion

1) Cell suspension is aspirated into a glass capillary
2) Generation of drops on demand, in air
3) Thanks to automated imagining, cellenONE tracks cells and determines if upcoming drops will contain or not a single cell
4) Drops containing single cells are dispensed into selected targets, drops without cells or with more than one cells are dispensed into recycling tube



Source: Laks et al. *Cell*. 179(5):1207-1221.e22. (2019)





Source: Cellenion

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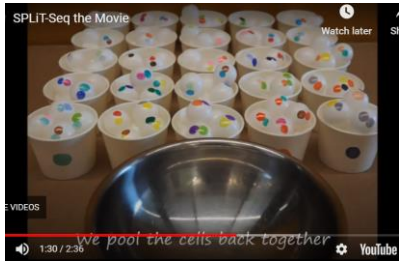
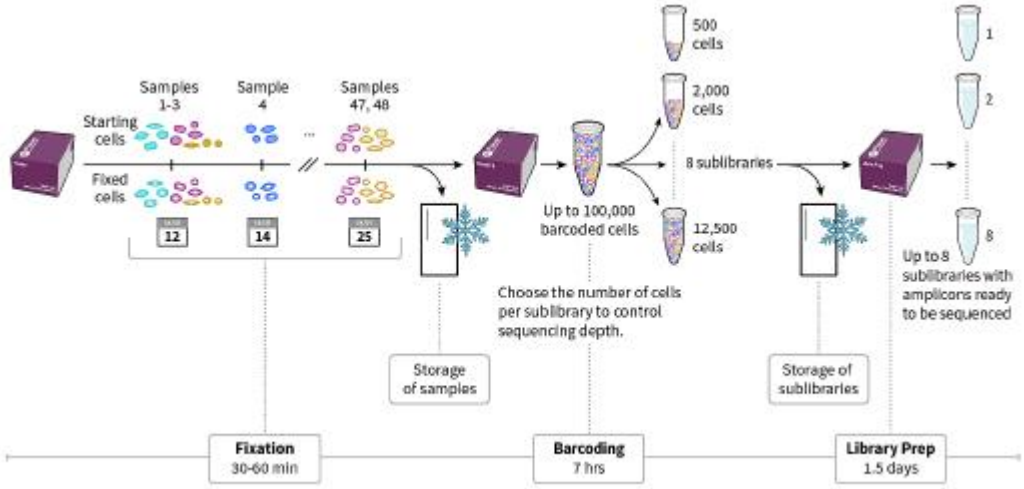
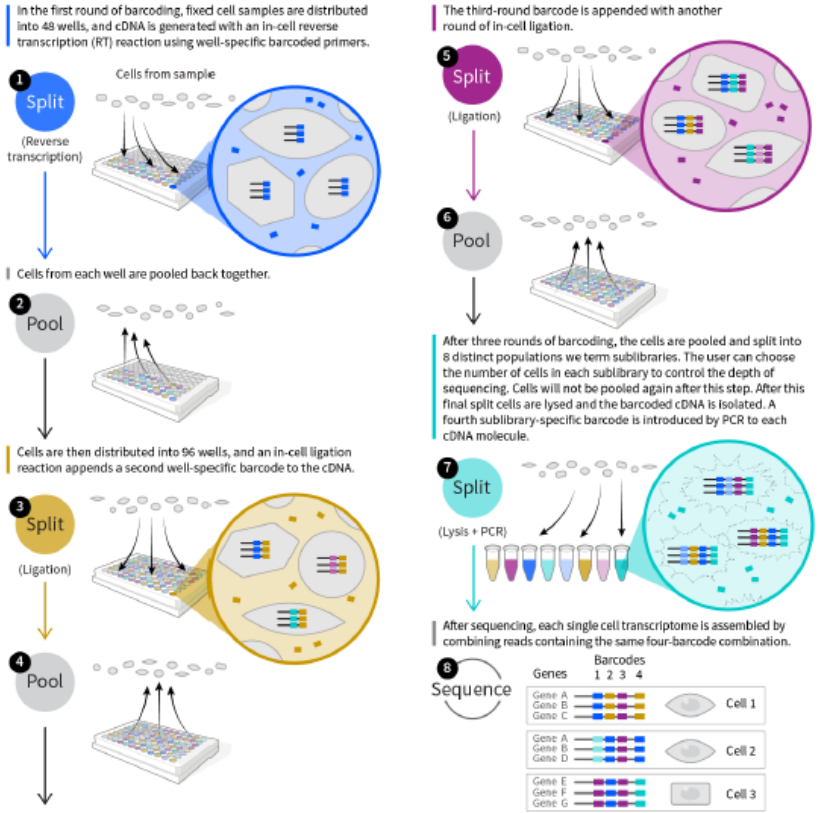
SPLIT-SEQ OVERVIEW (PARSE BIOSCIENCES)



Video available at: https://sites.google.com/uw.edu/splitseq





- Time flexibility – single experiment for samples collected on different dates (up to 6months storage)
- No instrument required for experiment. Computational pipeline available
- Up to 48 samples / 100k cells in total – kit has to be used at once
- Retail price of $9,800 per 100k cells or $16700 per million cells (+fixation kits)
- Doublet rate of 0.27% per 1000 cells (3.4% per library)
- No 3’/5’ bias – random hexamers method
- Median genes detection of about 12,000 genes
- Works with any species, any sizes of cells/nuclei & results in lower background noise

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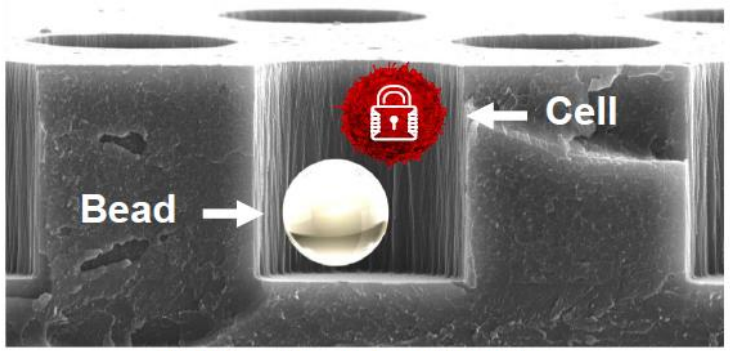
NEW PLAYERS (HIVE, SCIPIO)

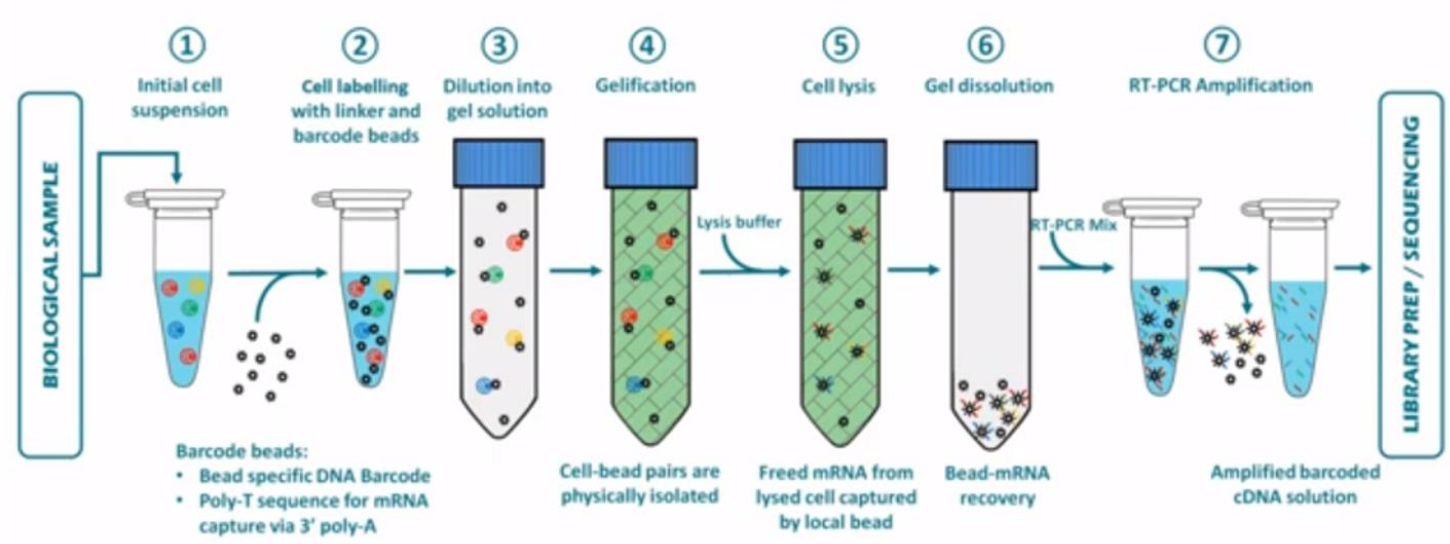
Honeycomb HIVE scRNAseq solution

- Collect - Obtain samples and prepare single-cell suspensions
- Capture Cells - Load cells into the HIVE and allow single cells to settle gently into HIVE picowells containing barcoded mRNA-capture beads
- The HIVE Difference: Store Or Ship - With cells in a stable environment, store HIVEs in the freezer and/or ship when ready to process
- Capture Transcripts - Seal the wells to create isolated chambers with one bead and one cell. Lyse cells and allow mRNA to bind to beads



~65,000 wells; ~60 µm diameter

Asteria (SciPio Bioscience) - hydrogel technology, a new era of instrument-free, ready-to-use scRNA-seq experiments



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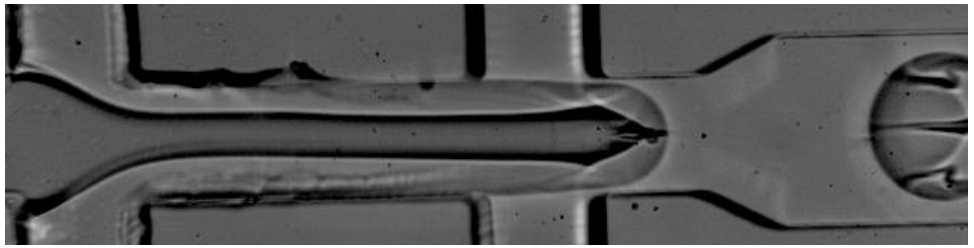
DROP-SEQ OVERVIEW

- Moved throughput from hundreds to thousands.
- Droplet-based processing using microfluidics
- Nanoliter scale aqueous drops in oil.
- 3' End
- Bead based (STAMPs).
- Single-cell transcriptomes attached to microparticles.
- Cell barcodes use split-pool synthesis.
- Uses UMI (Unique Molecular Identifier)
- Chance to have two cells within one droplet



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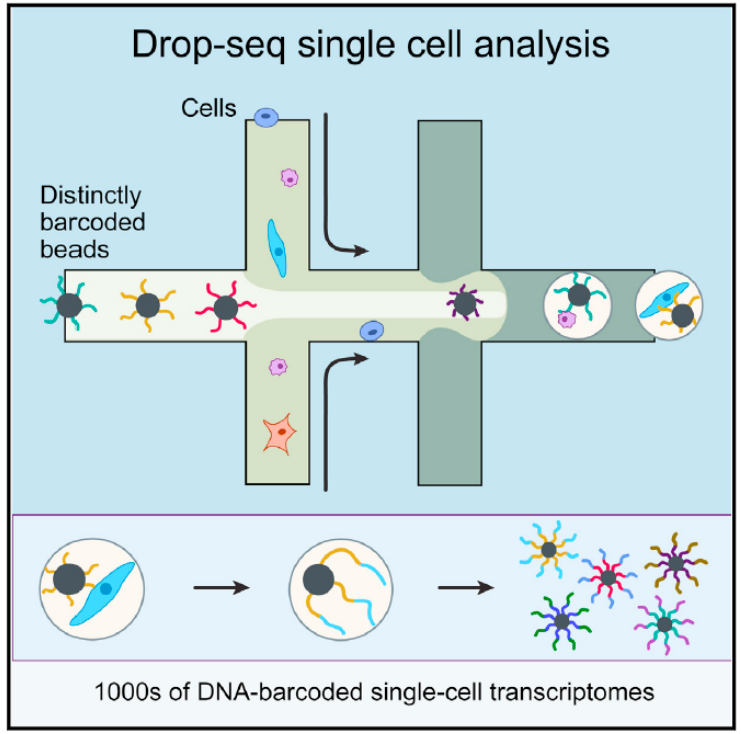
Resource

Cell

Highly Parallel Genome-wide Expression Profiling of Individual Cells Using Nanoliter Droplets

Graphical Abstract



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Correspondence

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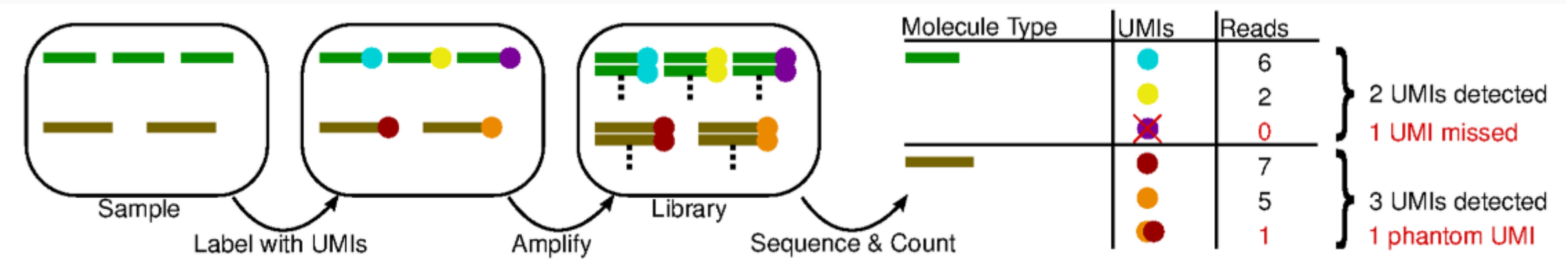
In Brief

Capturing single cells along with sets of uniquely barcoded primer beads together in tiny droplets enables large-scale, highly parallel single-cell transcriptomics. Applying this analysis to cells in mouse retinal tissue revealed transcriptionally distinct cell populations along with molecular markers of each type.

UMI – UNIQUE MOLECULAR IDENTIFIERS

After PCR enrichment, without UMIs, one can not distinguish if multiple copies of a fragment are caused by PCR clones or if they are real biological duplicated.
By using UMIs, PCR clones can be found by searching for non-unique fragment-UMI combinations, which can only be explained by PCR clones.
When performing variant analyses, these falsely overrepresented fragments can result in incorrect calls and thus wrong diagnostic findings



Source: Pflug et al. Bioinformatics (2018)

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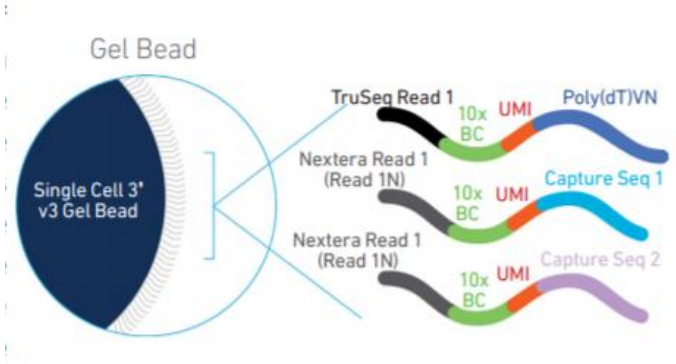
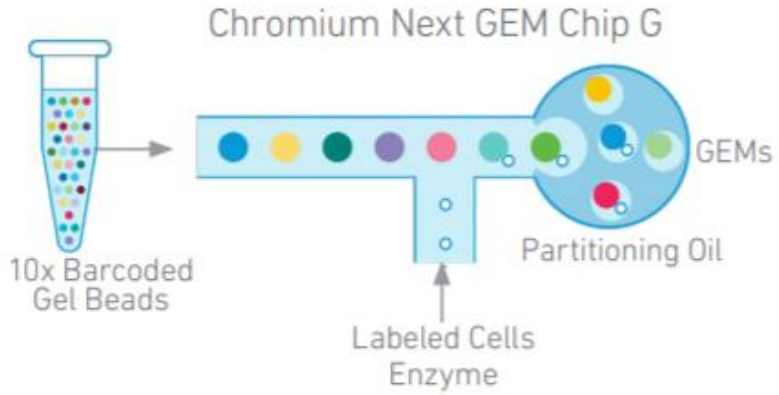
10X GENOMICS OVERVIEW

- Droplet-based similar to Drop-Seq, 3’ or 5’ mRNA
- In contrast to Drop-seq, where solid beads are used for RNA capture, 10X uses soft hydrogels containing oligos. These enable “single Poisson loading” leading to capture of >60% of input cells.
- Standardized instrumentation and reagents (unhackable so no customisation or control)
- Very easy to use and less processing time
- More high-throughput scaling - 8 samples can be processed simultaneously with up to 10000 cells captured per sample
- The doublet rate increases with number of cells loaded
- CellRanger and CellLoupe software are available and user friendly





Source: 10x Genomics

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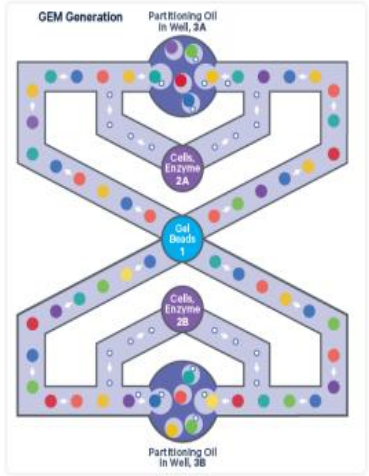
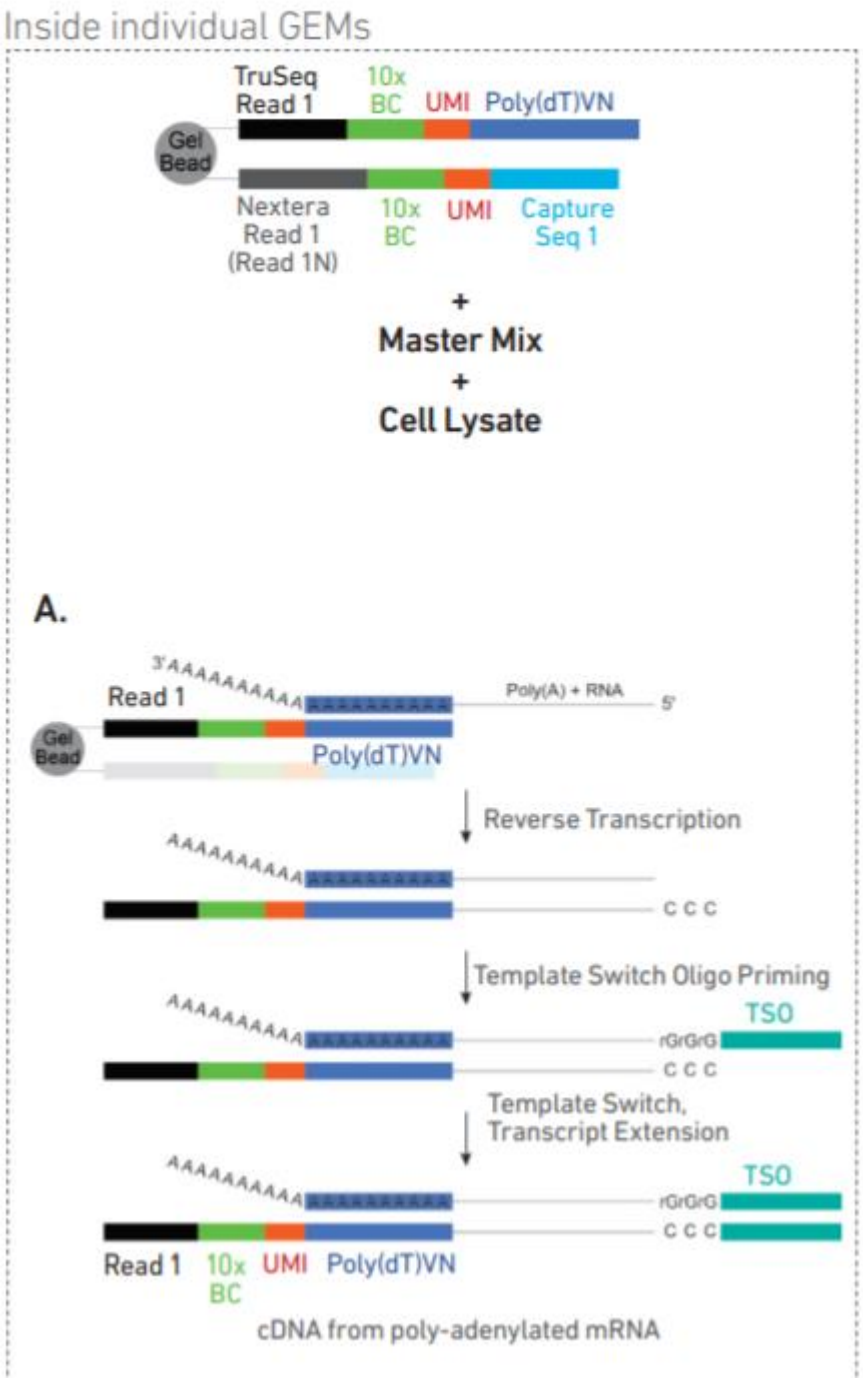
10X GENOMICS OVERVIEW



Chromium X

Making 1 million cell experiments routine



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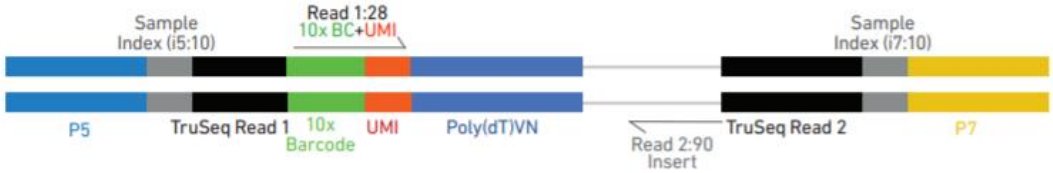
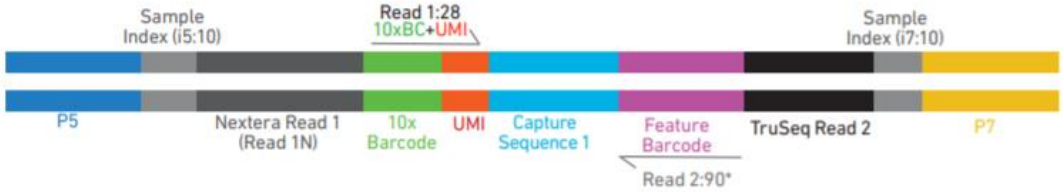
Source: 10x Genomics

10X GENOMICS LIBRARIES

Chromium Single Cell 3' Gene Expression Dual Index Library



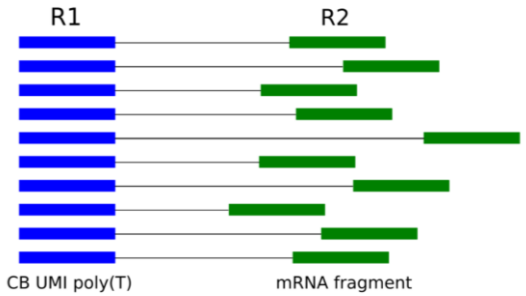
Chromium Single Cell 3' Cell Surface Protein Dual Index Library



Chromium Single Cell V(D)J Dual Index Library

Chromium Single Cell 5' Gene Expression Dual Index Library

Source: 10x Genomics



Sequencing Read	Description	Number of cycles
Read1	10x Barcode Read (Cell) + Randomer Read (UMI)	28bp
i7 index	Sample index read	10bp
i5 index	Sample index read	10bp
Read2	Insert Read (Transcript)	90bp

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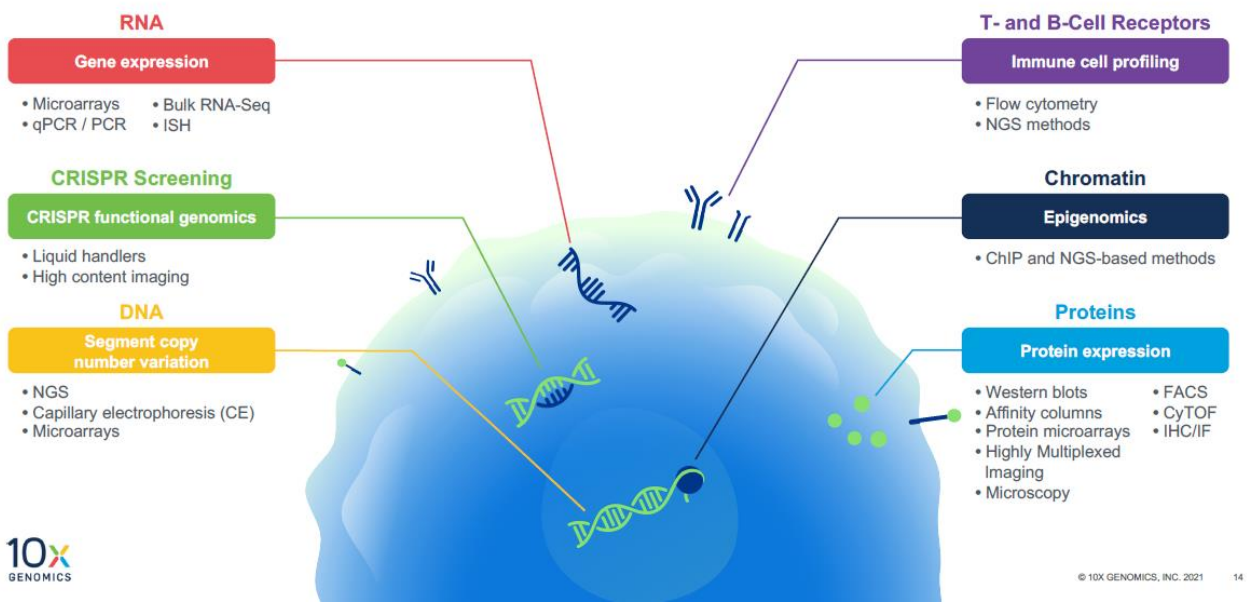
MULTIOMICS AGE

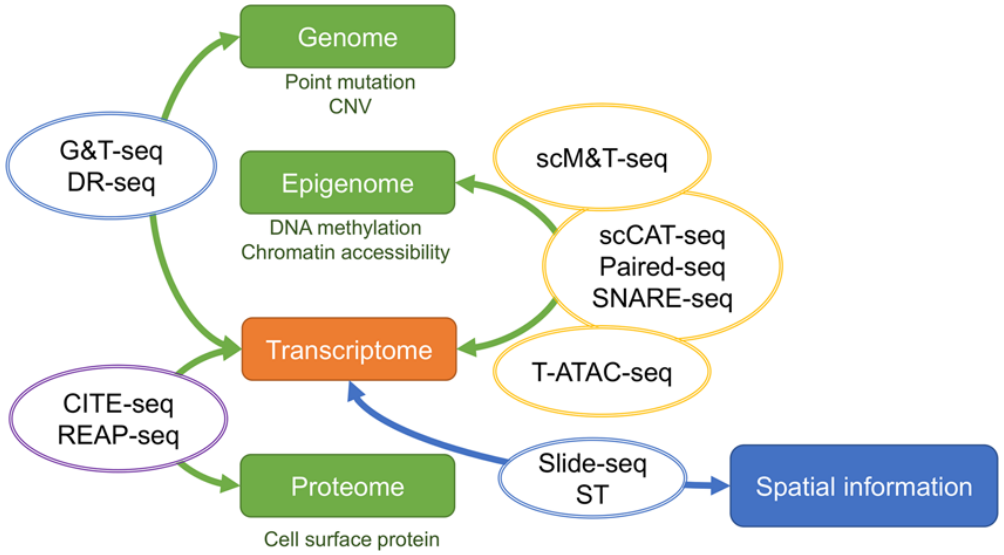


TECHNOLOGY FEATURE | 19 July 2021 | Correction 21 July 2021

Single-cell analysis enters the multiomics age

A rapidly growing collection of software tools is helping researchers to analyse multiple huge '-omics' data sets.

Jeffrey M. Perkel



Kashima Y et al. Exp Mol Med 52, 1419–1427 (2020)

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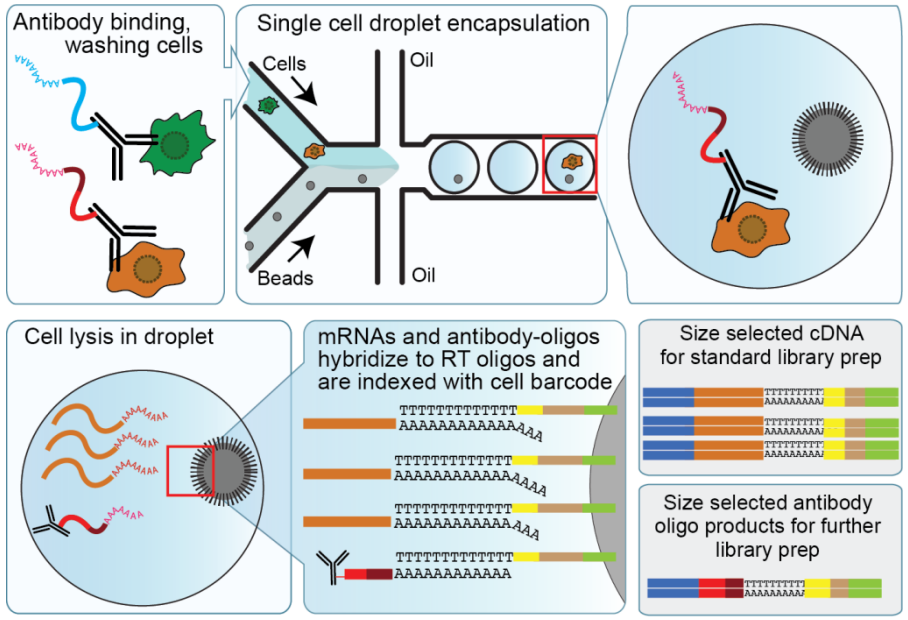
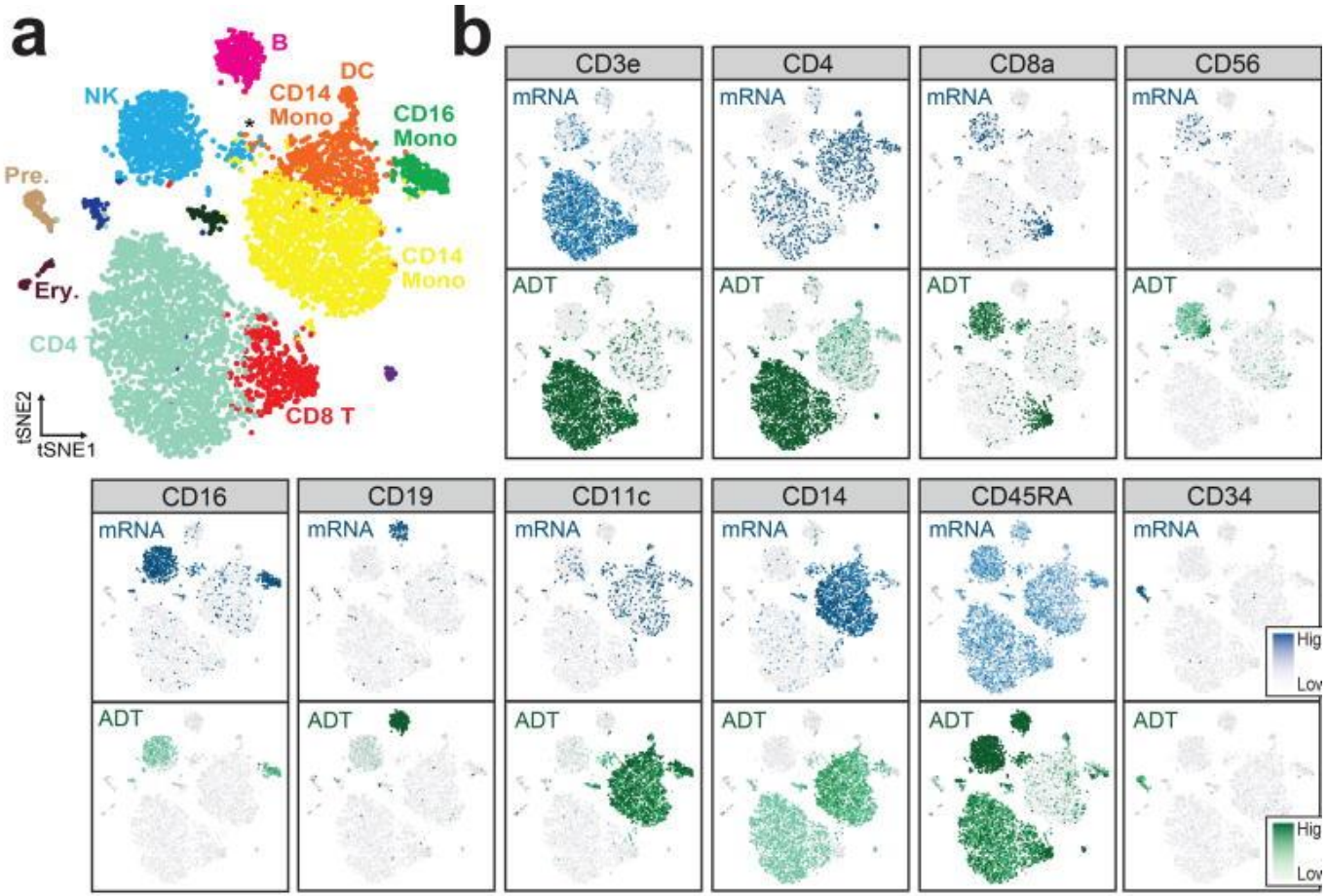
CITE-SEQ

- Cellular Indexing of Transcriptomes and Epitopes by Sequencing
- CITE-seq uses DNA-barcoded antibodies to convert detection of proteins into a quantitative, sequenceable readout



Source: cite-seq.com



BioLegend solutions:
TotalSeq-A – Poly(dT) based system
TotalSeq-B – 3’ v3.1 Feature barcode
TotalSeq-C – 5’ v2.0

Source: Stoeckius et al. *Nat Methods*. (2017)

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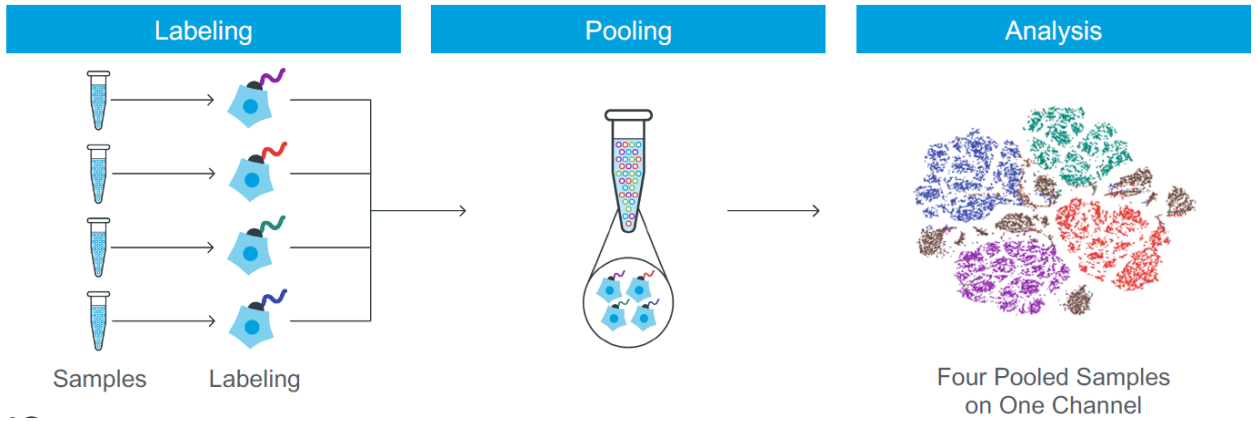
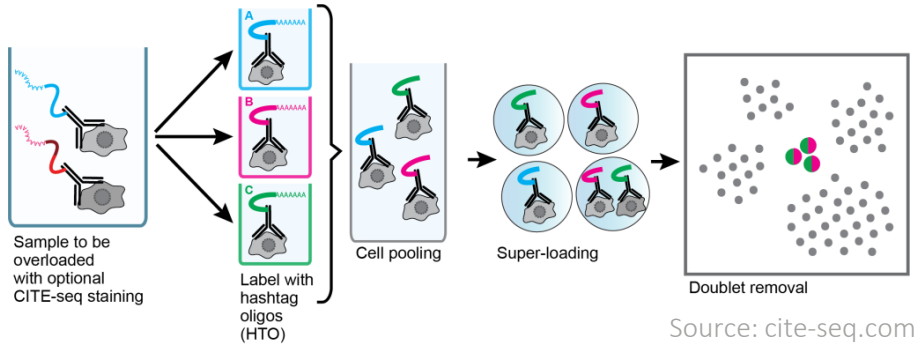
CELL HASHING

Reduces cost of running multiple samples by adding hashtag oligos and pooling into single channel of 10x chip (10x CellPlex or TotalSeq antibodies)



Allows overloading as by sequencing tags alongside the cellular transcriptome, we can assign each cell to its sample of origin, and robustly identify doublets originating from multiple samples



Source: cite-seq.com

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Genotype-free demultiplexing of pooled single-cell RNA-Seq

Jun Xu[a], Caitlin Falconer[b], Quan Nguyen[b], Joanna Crawford[b], Brett D. McKinnon[b,e], Sally Mortlock[b], Alice Pébay[f,g,h,i], Alex W. Hewitt[f,g,h,i], Anne Senabouth[d], Nathan Palpant[a,b], Han Chiu[b], Stacey Andersen[a,b], Grant W. Montgomery[a,b], Joseph Powell[c,d], Lachlan Coin[a,b,*]

nature methods

Article | Published: 17 June 2019

MULTI-seq: sample multiplexing for single-cell RNA sequencing using lipid-tagged indices

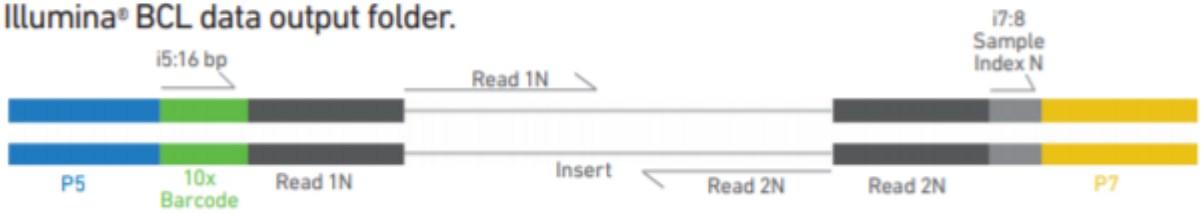
Christopher S. McGinnis, David M. Patterson, Juliane Winkler, Daniel N. Conrad, Marco Y. Hein, Vasudha Srivastava, Jennifer L. Hu, Lyndsay M. Murrow, Jonathan S. Weissman, Zena Werb, Eric D. Chow & Zev J. Gartner

Nature Methods **16**, 619–626(2019) | Cite this article

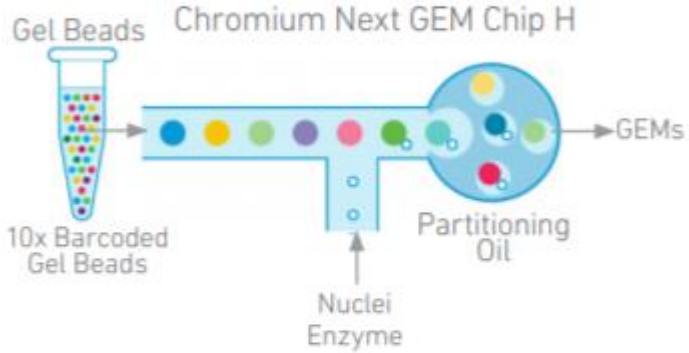
15k Accesses | **27** Citations | **85** Altmetric | Metrics

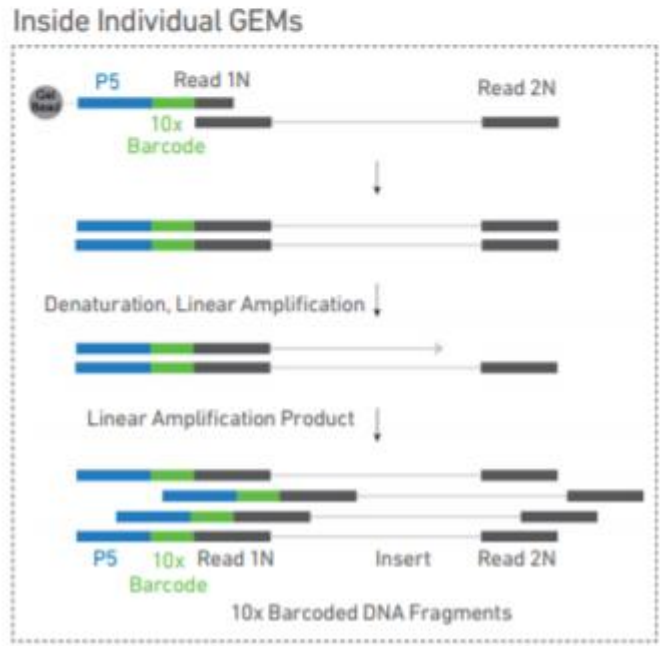
10X ATAC

Chromium Single Cell ATAC libraries comprise double stranded DNA fragments which begin with P5 and end with P7. Sequencing these libraries produces a standard Illumina® BCL data output folder.



Sequencing Read	Description	Number of cycles
Read1	Insert Sequence 1N	50bp
i7 index	Sample index read	8bp
i5 index	10x Barcode Read (Cell)	16bp
Read2	Insert Sequence 2N (opposite end)	50bp





Source: 10x Genomics

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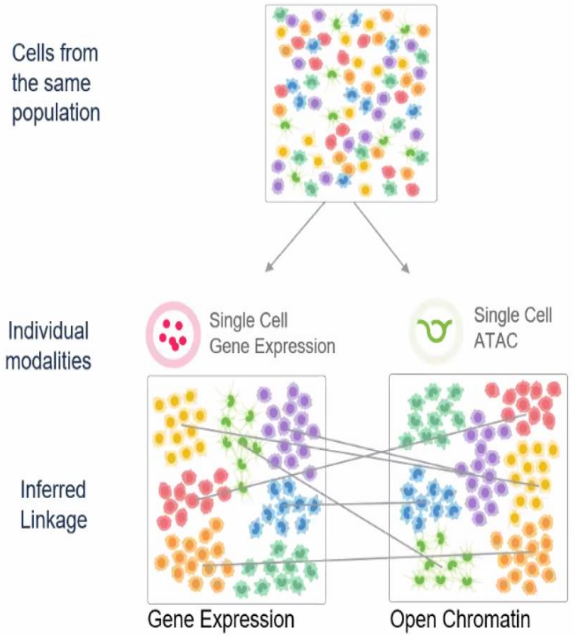
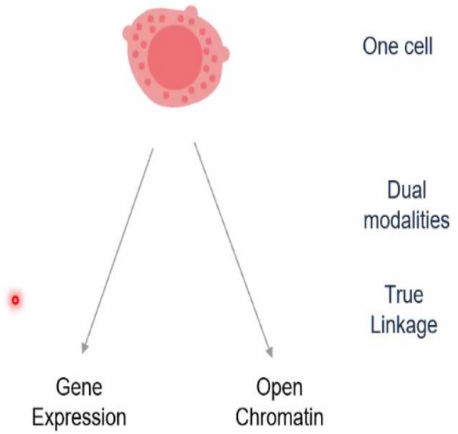
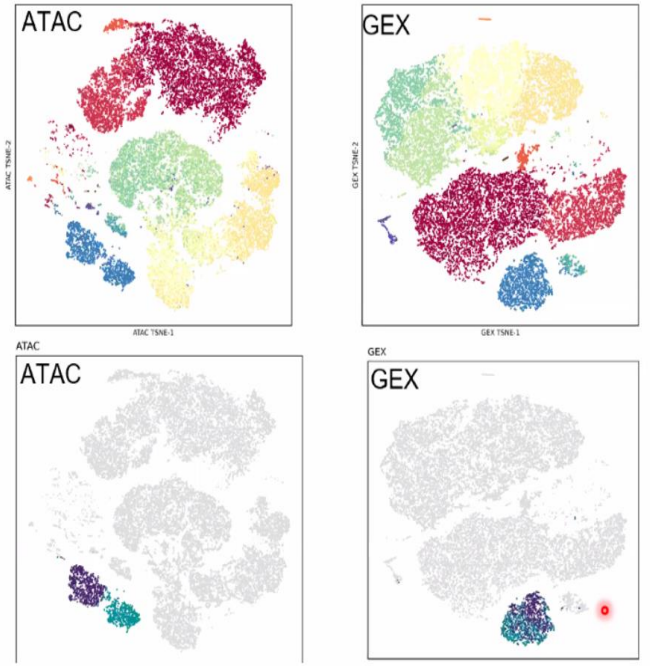
10X MULTIOME (RNA+ATAC)

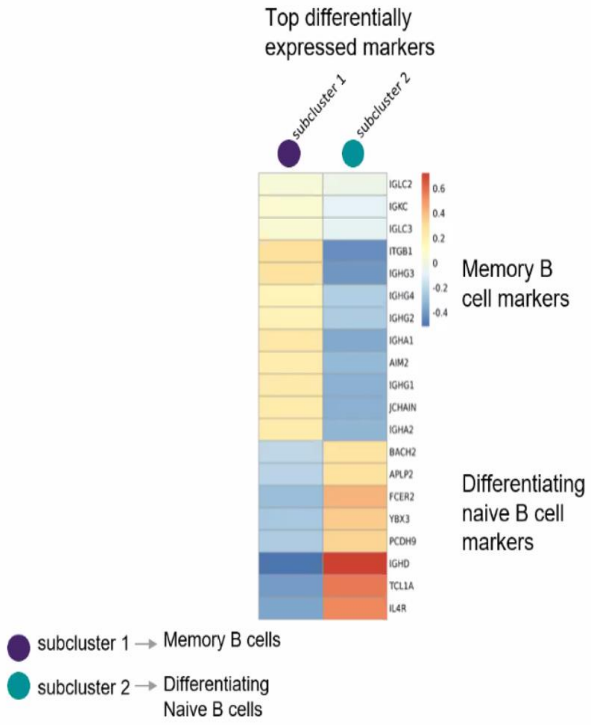
Profiling Different Modalities To Gain Deeper Insights





Dive Deep Where It Matters





Source: 10x Genomics

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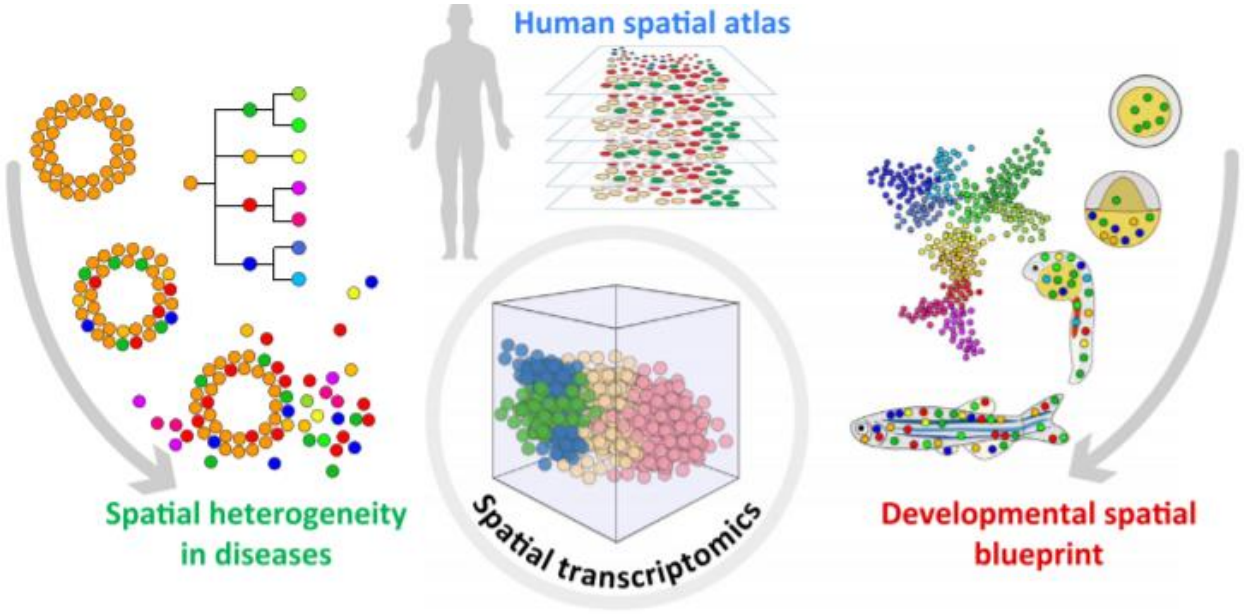
SPATIAL TRANSCRIPTOMICS

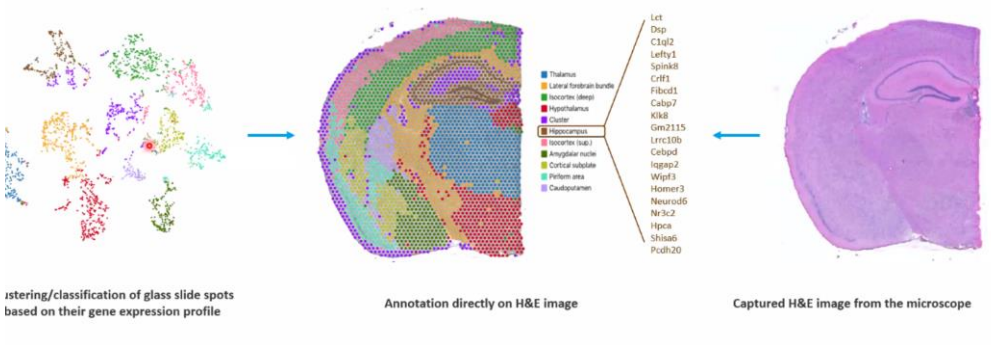


Trends in Biotechnology

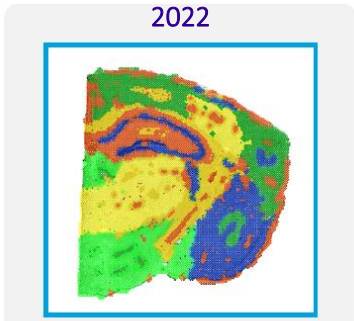
Figure 3. Applications for Spatially Resolved Transcriptomics. Three primary kinds of hot issues can be resolved by spatially resolved transcriptomics: left, discovering spatial heterogeneity of diseases; middle, establishing spatial transcriptome atlases for the human body; and right, delineating an embryonic developmental and spatial blueprint.

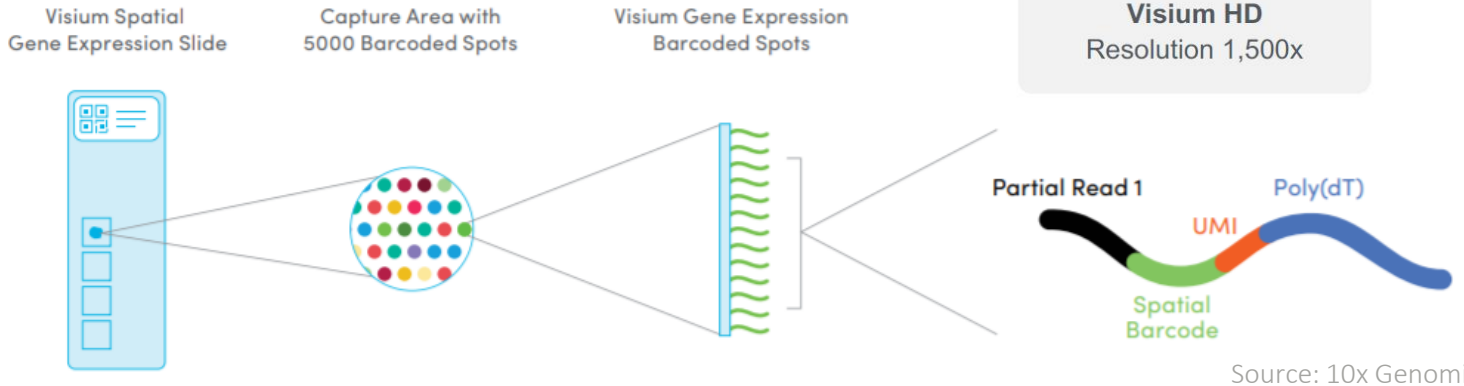
Source: Liao et al. Trends in Biotechnology. (2020)

55ul spots -> 1 and 10 cells captured per spot



Source: 10x Genomics





Source: 10x Genomics

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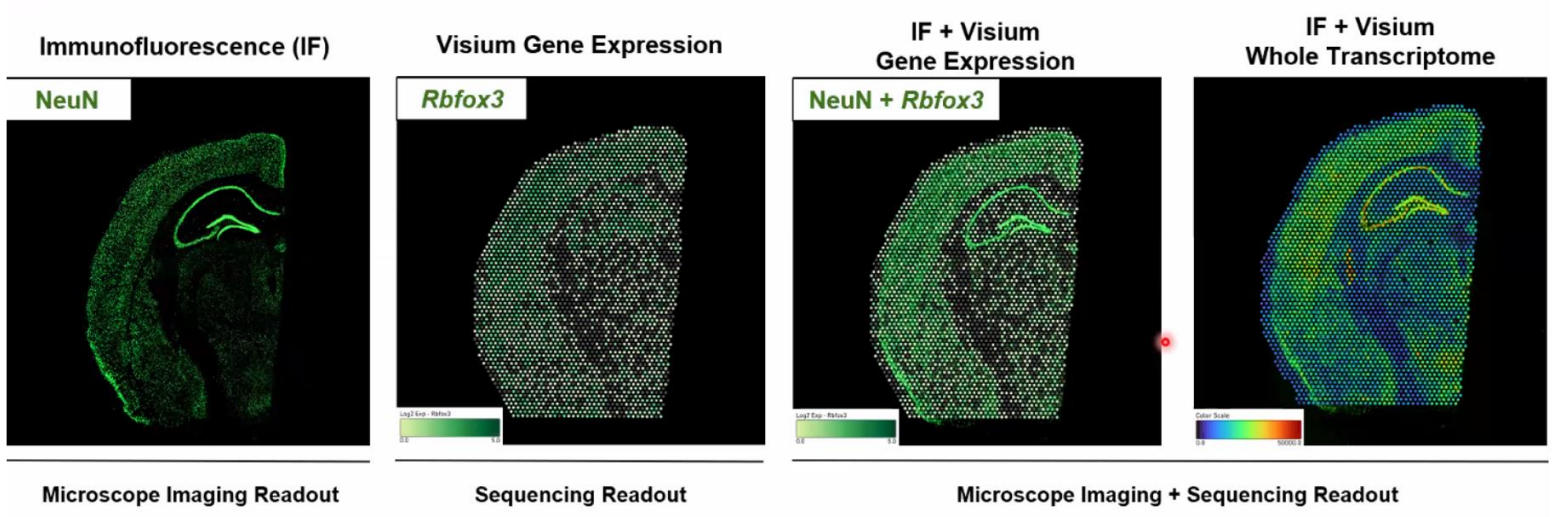
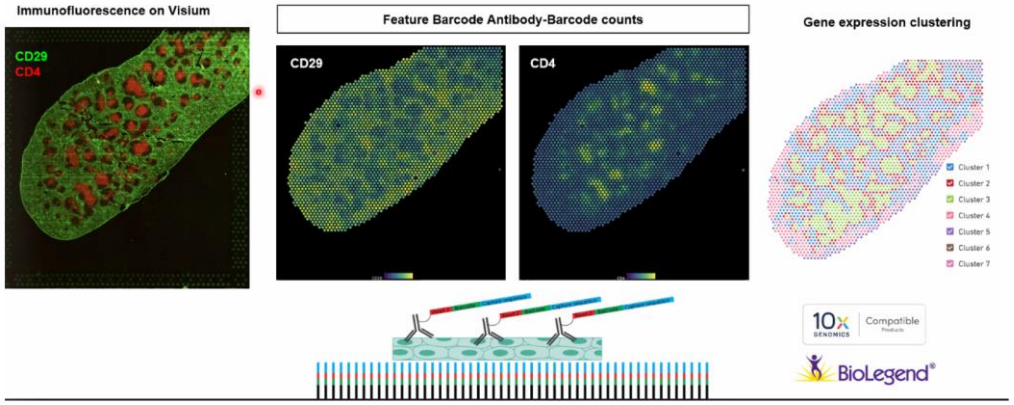
SPATIAL TRANSCRIPTOMICS

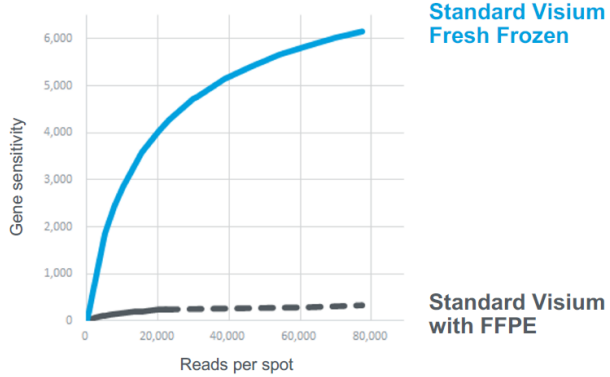


Feature Barcode Correlates with Immunofluorescence



The Challenge of FFPE Samples

FFPE tissue preservation degrades RNA



Source: 10x Genomics

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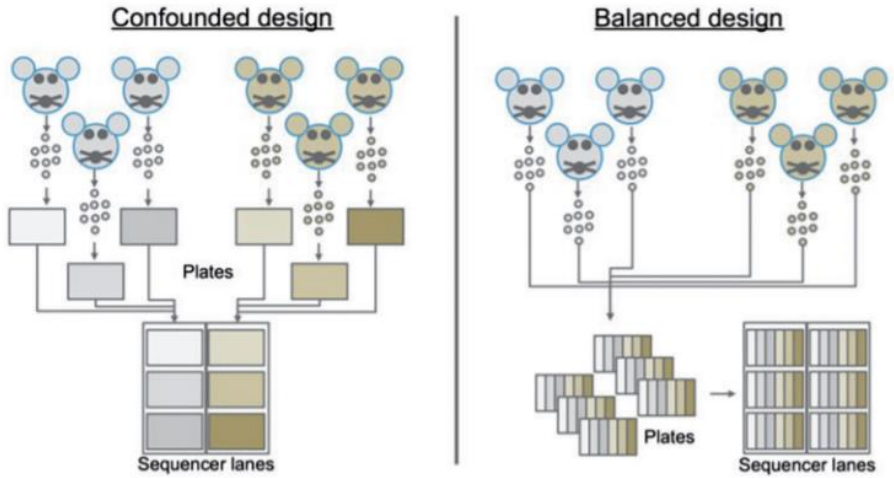
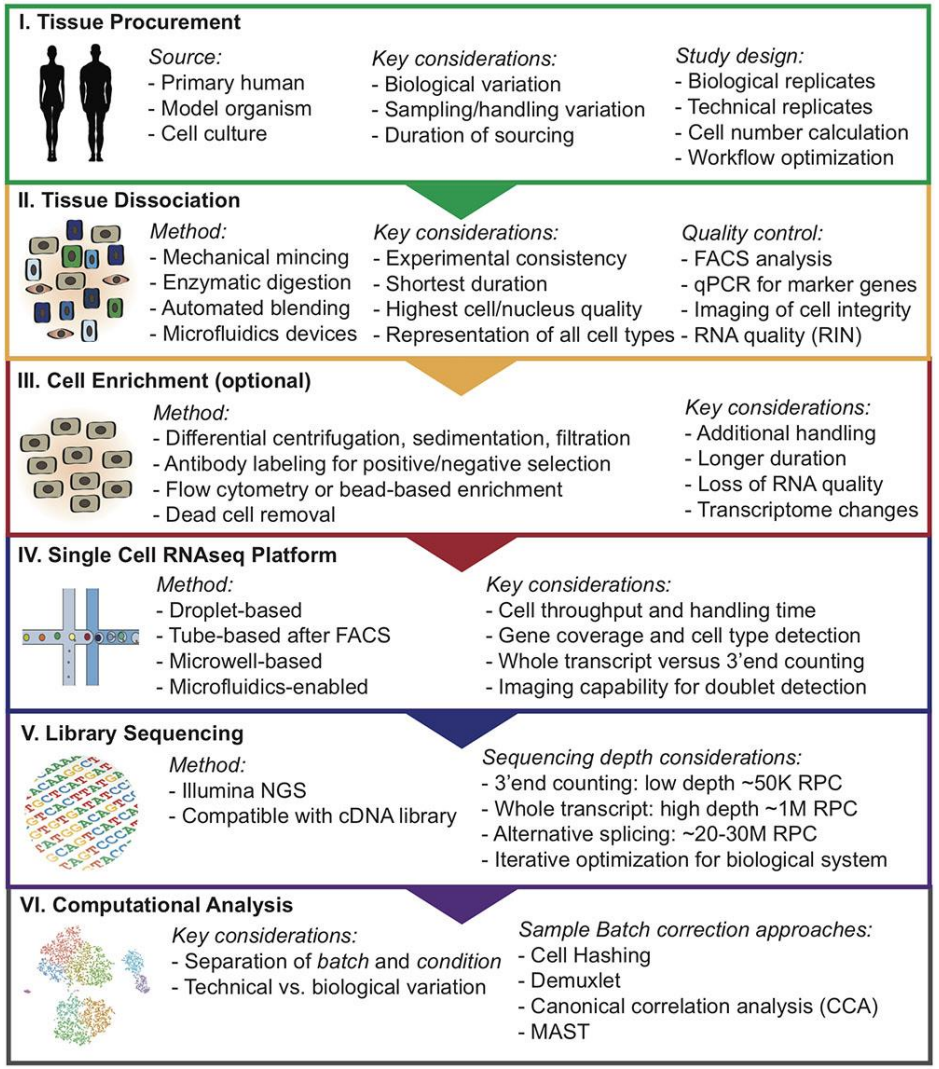
EXPERIMENTAL DESIGN



Source: Baran-Gale et al. Brief Func Genomics. 17 (4):233–239. (2018)



Source: Nguyen QH et al. *Front Cell Dev Biol* 6:108. (2018)

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WHAT PLATFORM SHOULD I USE?

Choose protocol based on:

- Throughput (number of cells per reaction)
- Sample of origin
- Cost / Labour / Time limitations
- Gene body coverage: 5'/ 3' biased or full-length?
- UMI vs no-UMI
- Sequencing depth per cell

Examples:

- If you sample is fairly homogeneous – bulk RNAseq
- If your sample is limited in cell number – plate-based method
- If you want re-annotate the transcriptome and discover new isoforms – full-length coverage (SMART-seq2)
- If you are looking to classify all cell types in a diverse tissue - high throughput
- If you have only archival human samples – nuclei isolation

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LITERATURE:

- https://hbctraining.github.io/scRNA-seq/slides/Single_Cell_2_27_20.pdf.
- https://www.slideshare.net/TimothyTickle/introduction-to-singlecell-rnaseq
- Arzalluz-Luque et al. A. Single-cell RNAseq for the study of isoforms—how is that possible?. Genome Biol 19, 110 (2018).
- Ding et al. Systematic comparison of single-cell and single-nucleus RNA-sequencing methods. Nat Biotechnol 38, 737–746 (2020).
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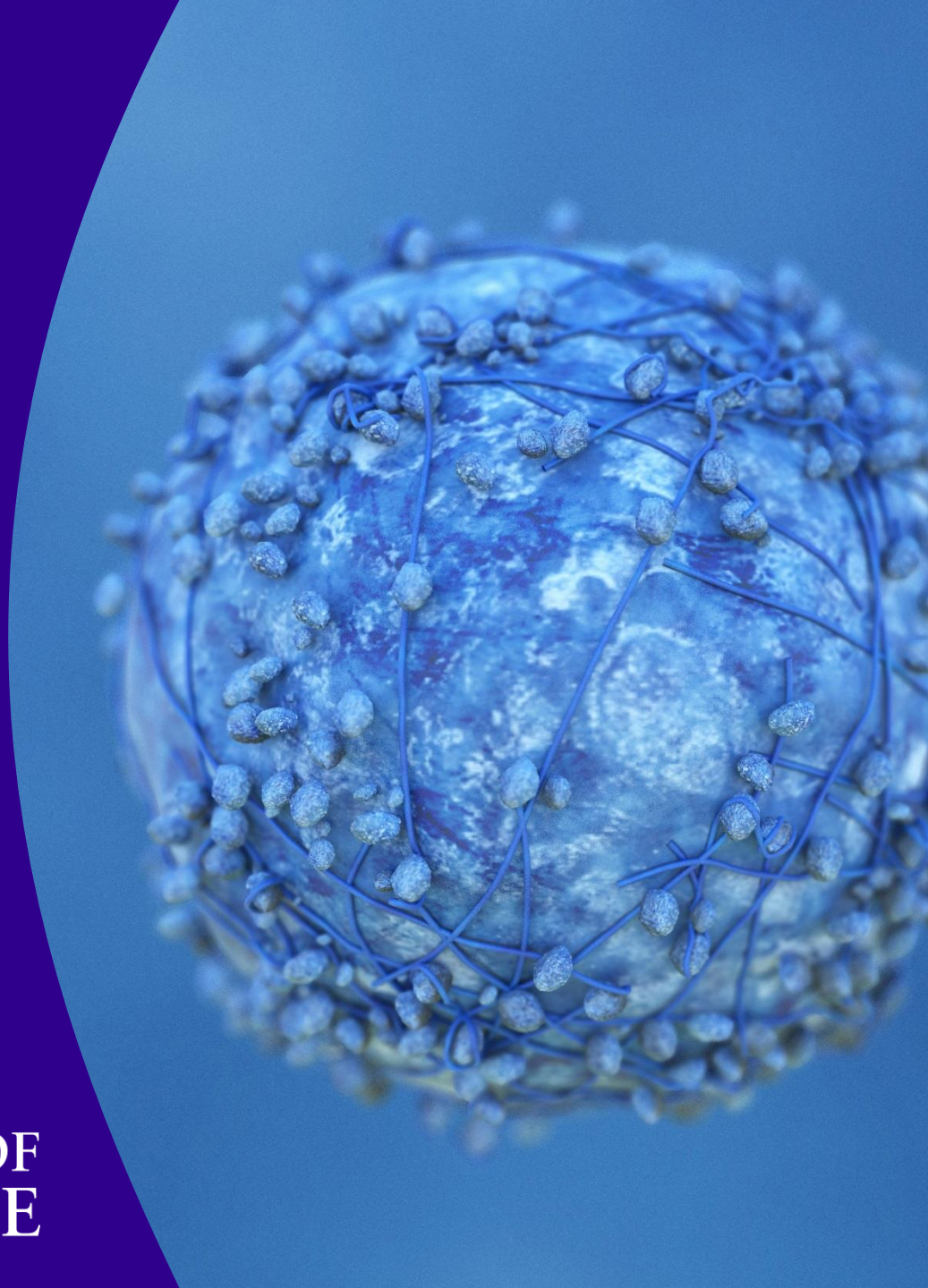
- Ziegenhain et al. Comparative Analysis of Single-Cell RNA Sequencing Methods. Mol Cell. 65(4):631-643.e4. (2017).

USEFUL RESOURCES:

- Haque et al. A practical guide to single-cell RNA-sequencing for biomedical research and clinical applications. *Genome Med*. 2017;9(1):75.
- Single cell course by Hemberg Lab, Wellcome Sanger Institute (http://hemberg-lab.github.io/scRNA.seq.course/index.html)
- Tabula Muris (https://tabula-muris.ds.czbiohub.org/)
- Human Cell Atlas (https://www.humancellatlas.org/)
- 10x Genomics demonstrated protocols for sample preparation (https://support.10xgenomics.com/single-cell-gene-expression/sample-prep)
- Worthington Tissue Dissociation Guide
- (http://www.worthington-biochem.com/tissuedissociation/default.html)
- Broad Institute Single Cell Portal (https://singlecell.broadinstitute.org/single_cell)
- List of software packages for single cell data analysis (https://github.com/seandavi/awesome-single-cell)
- SPLIT-seq (https://sites.google.com/uw.edu/splitseq)
- CITE-seq (https://cite-seq.com/)
- Biolegend TotalSeq (https://www.biolegend.com/en-us/totalseq)



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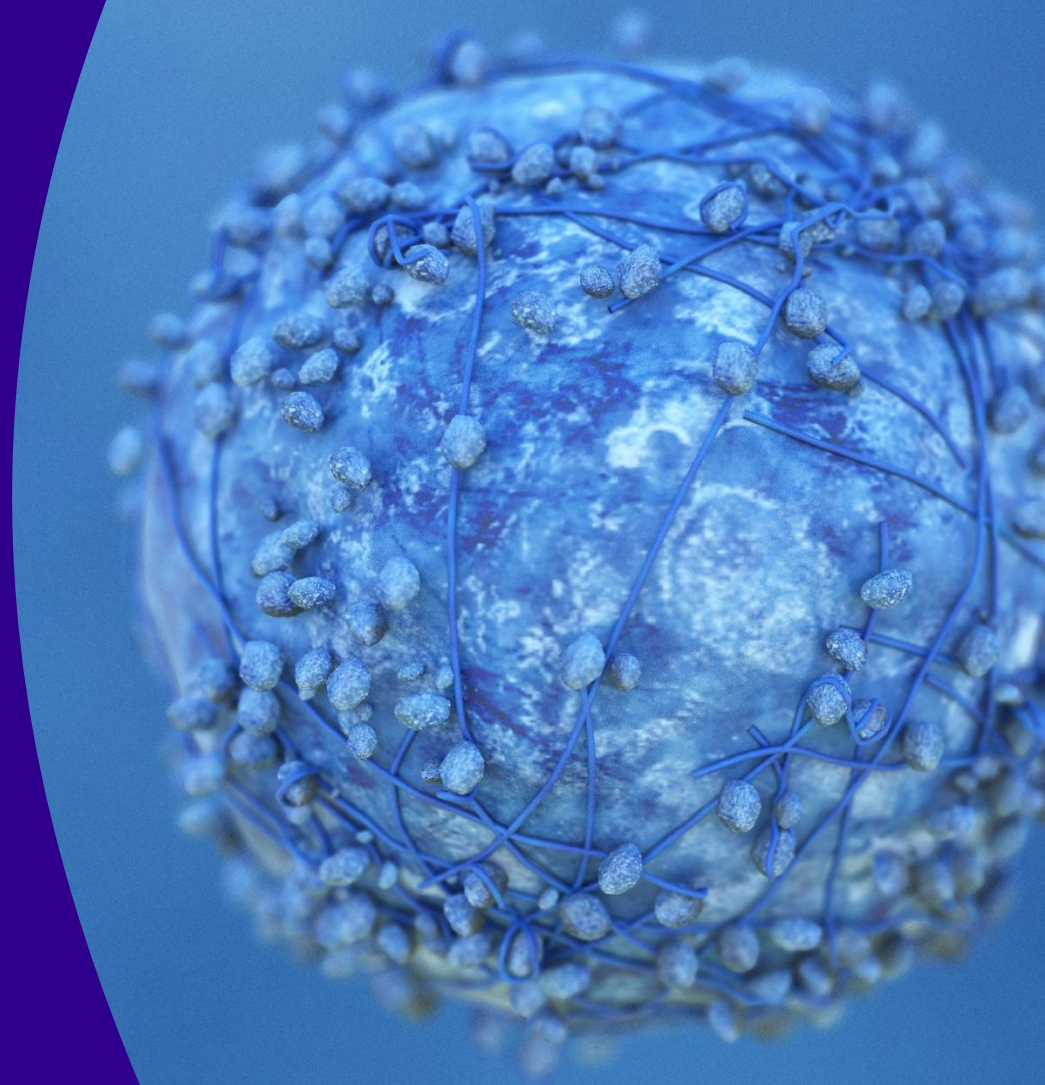
THANK YOU FOR YOUR ATTENTION!



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