

# Reaching new Levels of Biological Insights with Single Cell Genomics Solutions

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**University of Minnesota – March 3<sup>rd</sup>, 2022**

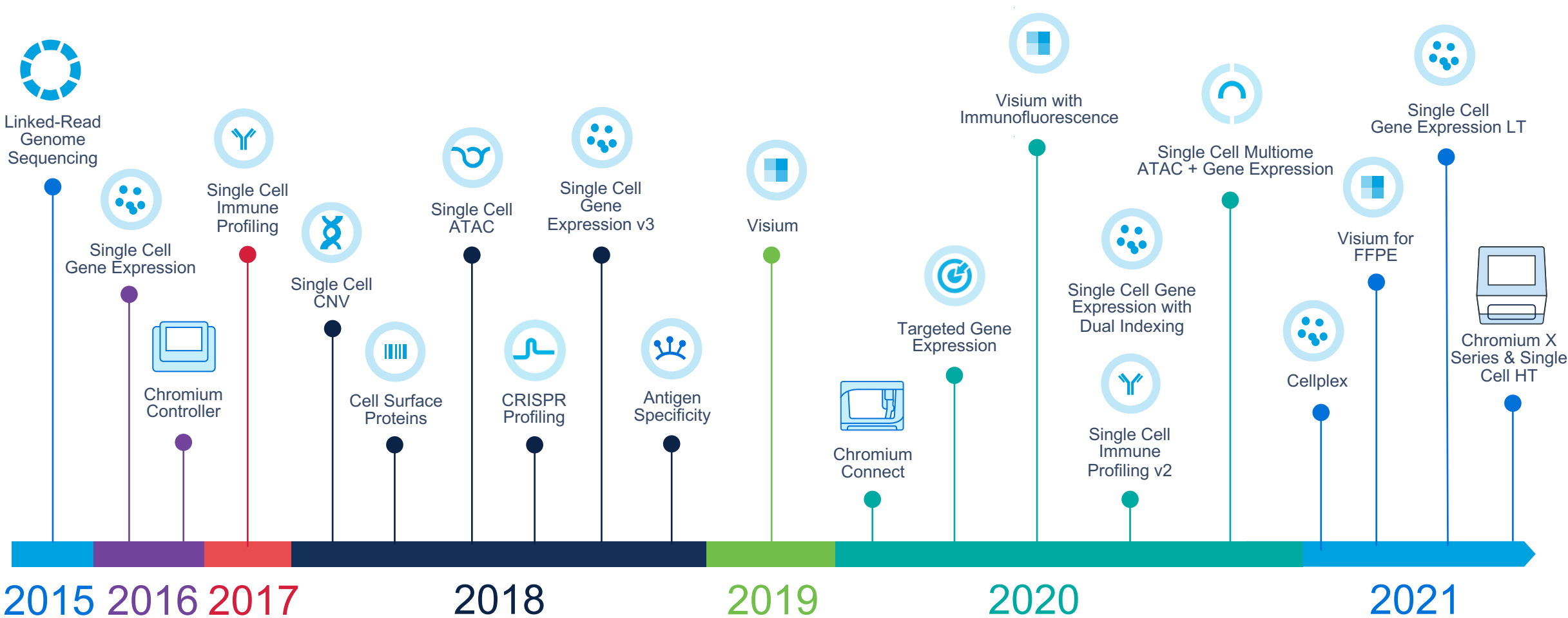
Egon J. Ranghini, PhD

Science & Technology Advisor - North Central

[egon.ranghini@10xgenomics.com](mailto:egon.ranghini@10xgenomics.com)



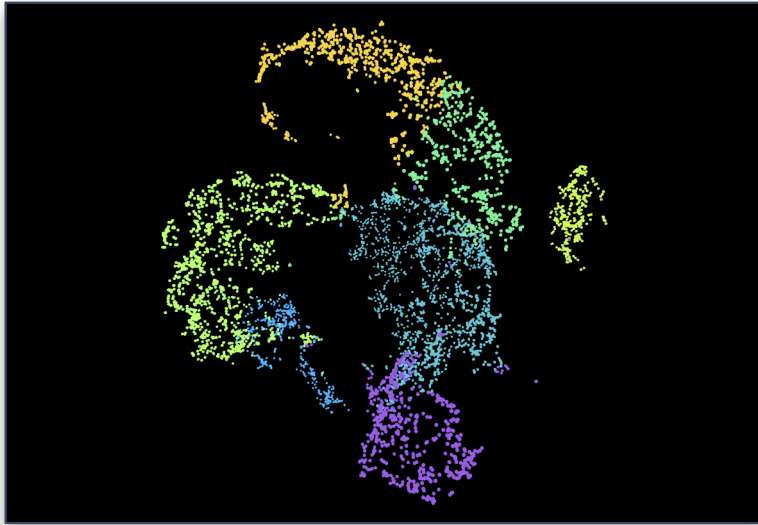
# 10x Genomics Innovation Engine



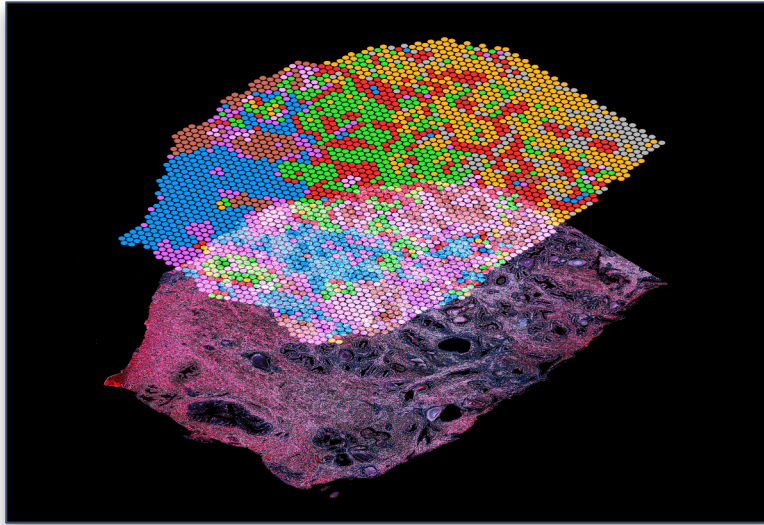


# From discovery to focused with three complementary workflows

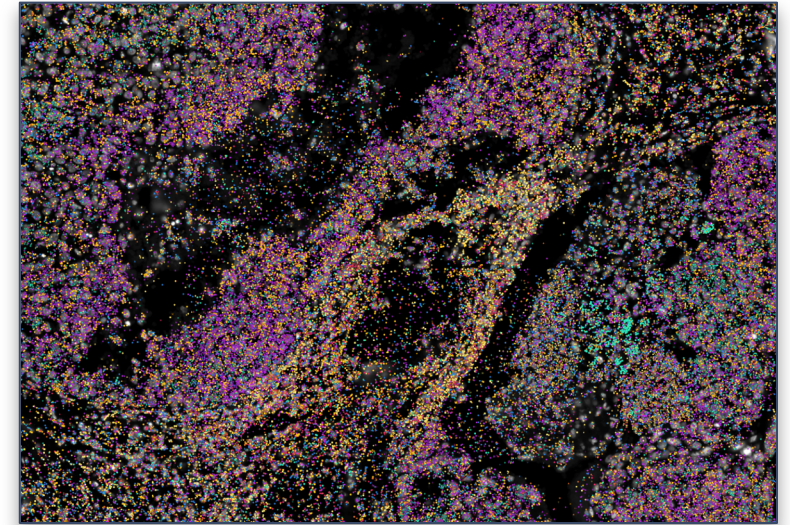
Chromium Single Cell



Visium Spatial



Xenium In Situ



Discovery

Focused



# Chromium Single Cell Platform



3,250+  
publications

TheScientist  
**TOP 10**  
INNOVATIONS

- 2021 Chromium X
- 2020 Single Cell Multiome, Total Seq C
- 2019 Single Cell ATAC
- 2018 Single Cell Immune Profiling
- 2017 Single Cell Gene Expression
- 2015 Gemcode



2018  
Single Cell Genomics

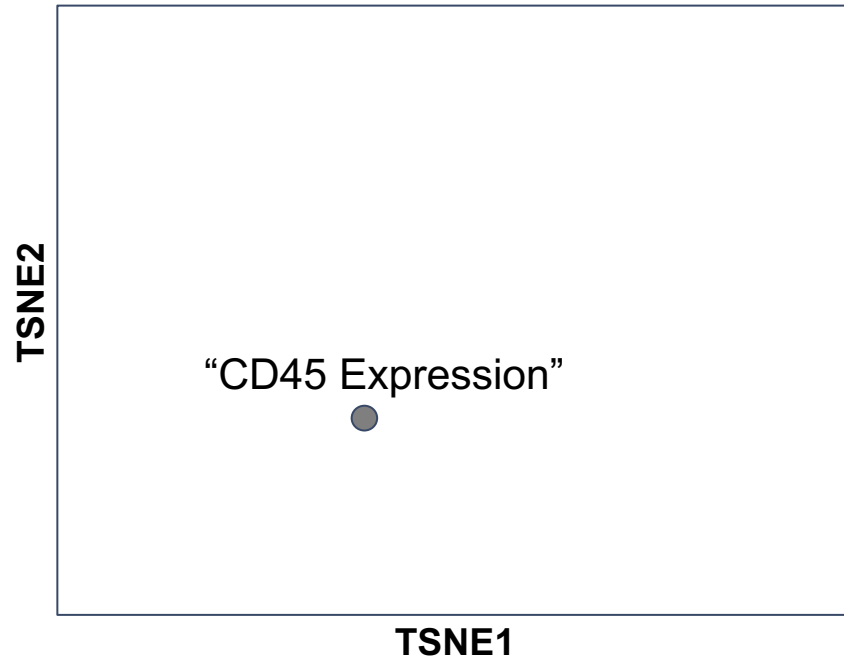


2019  
Single Cell  
Multimodal Omics



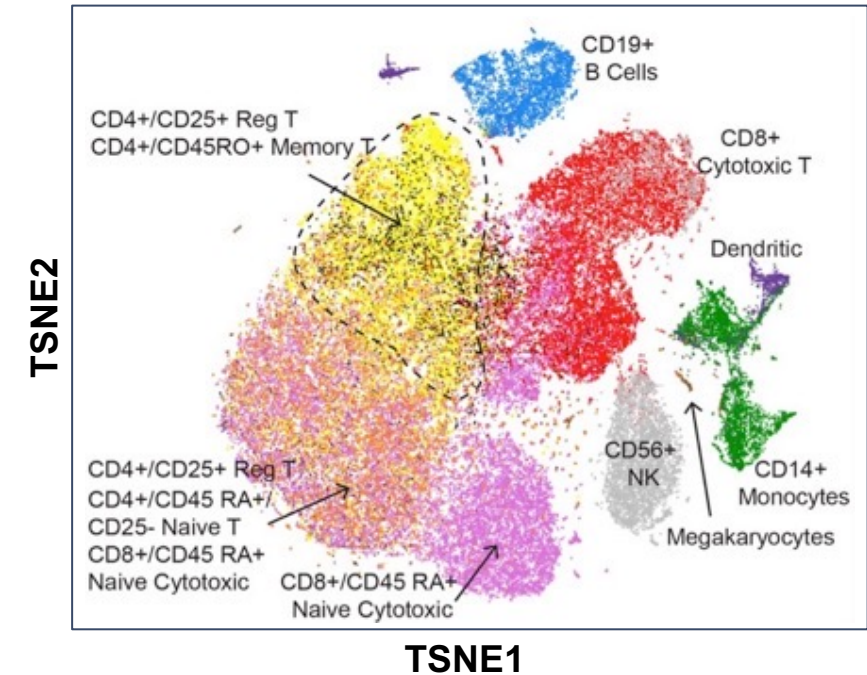
# Single Cell Gene Expression – Unbiased and scalable

## Conventional gene expression



One "average" data point from a mixture of cells

## 10x Genomics

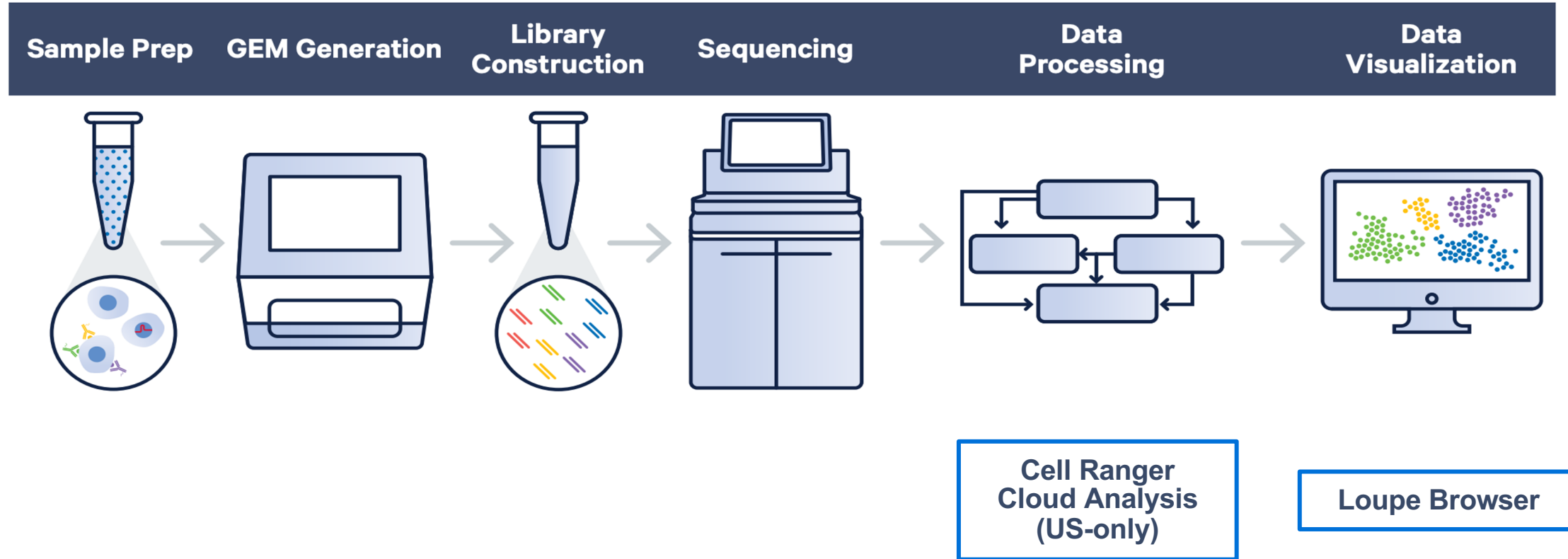


### Capture cells with:

- Diverse sizes
- Broad transcriptional activity
- Rare frequencies

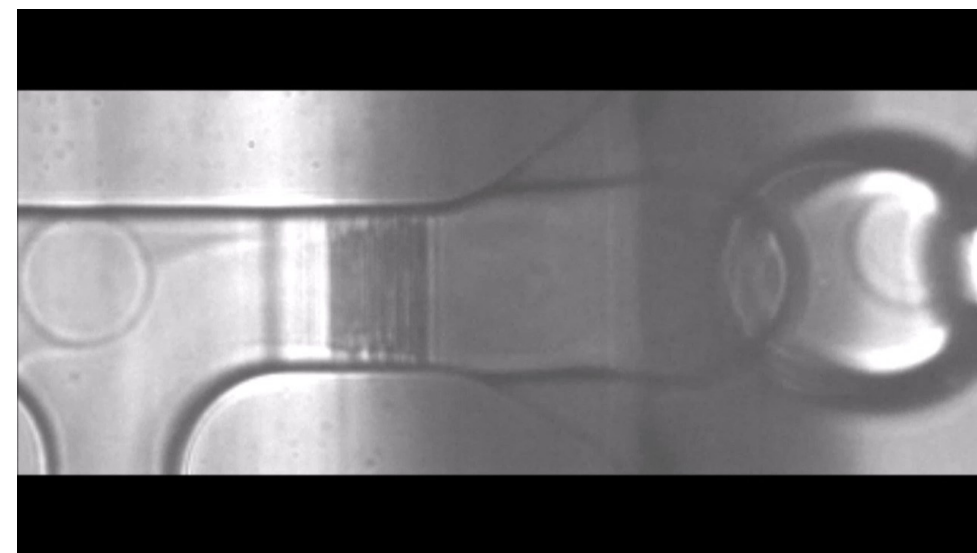
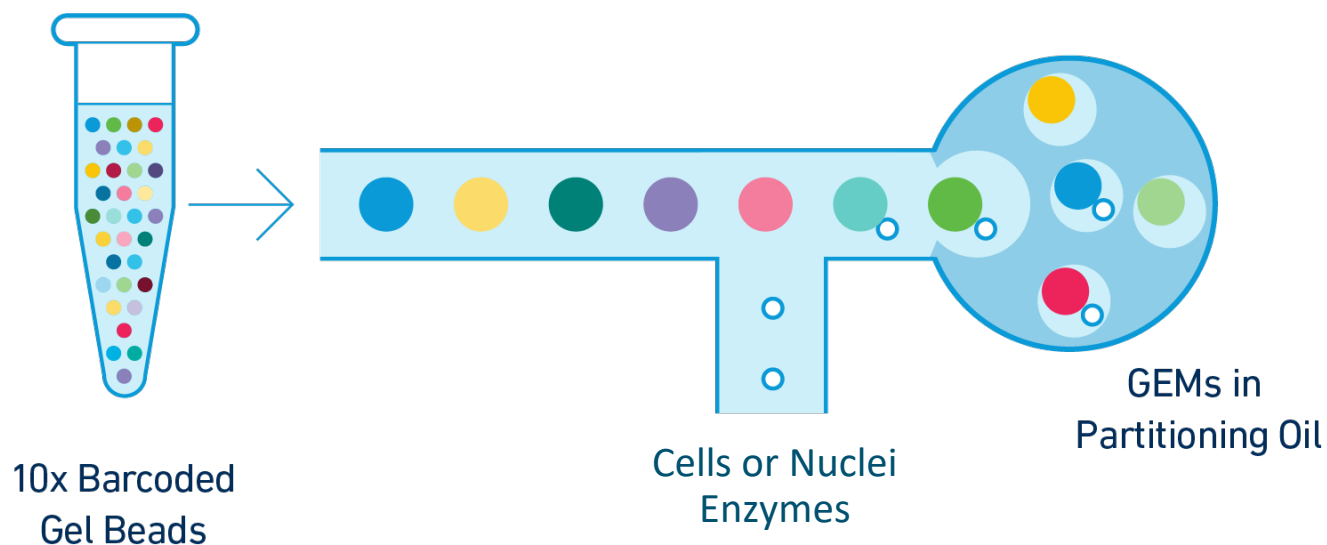


# Streamlined and robust workflow for your experiment





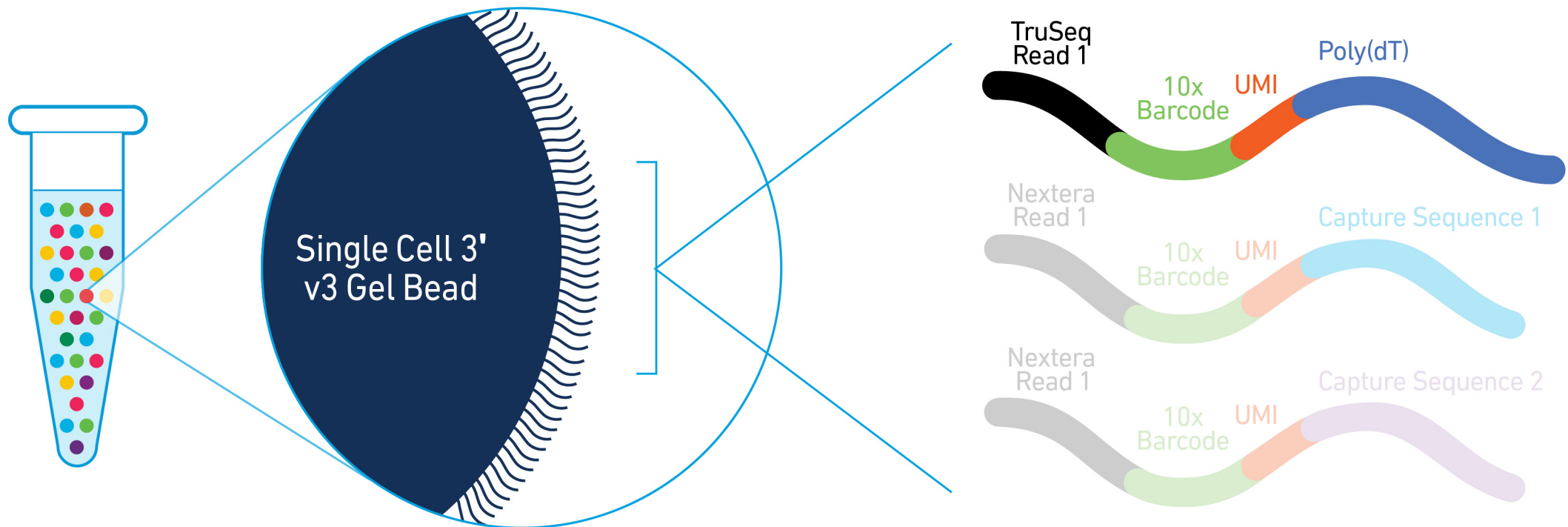
# Next GEM technology – creating Gel Beads in EMulsions (GEMs)





# 10x Genomics single cell technology

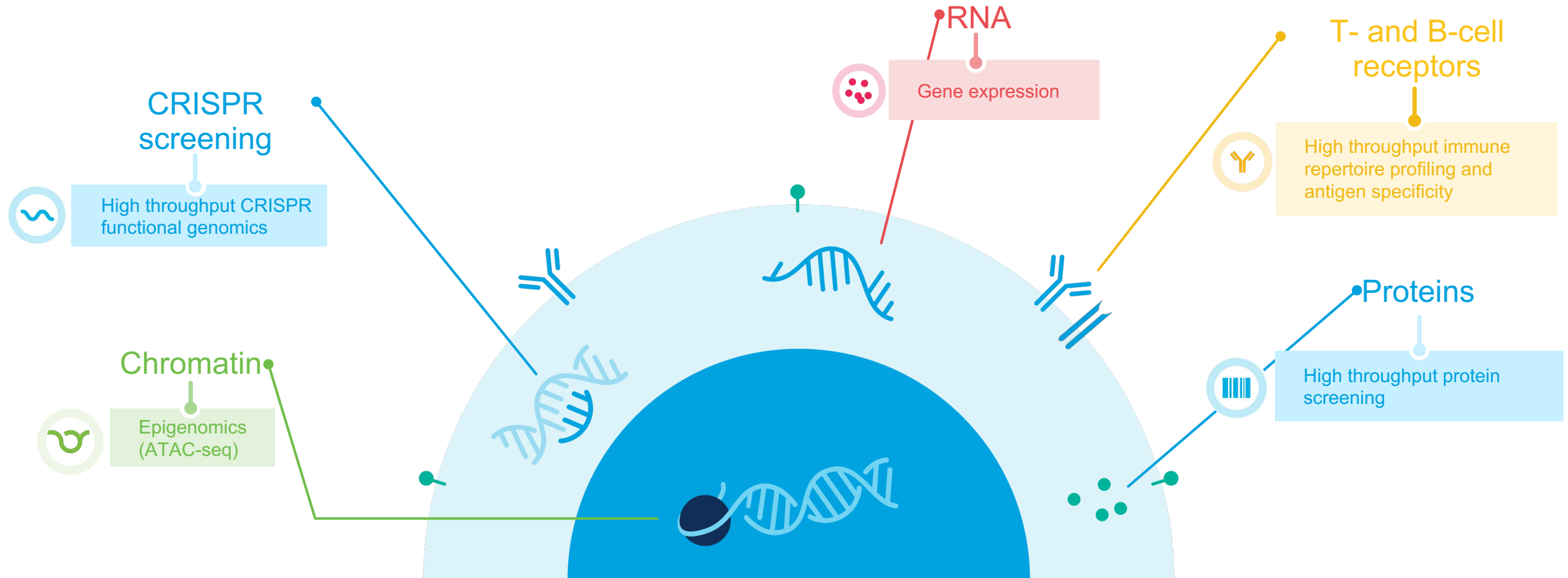
Barcoding single cell transcriptomes and other readouts





# Single cell multiomic cytometry

Simultaneous measurements of different cellular analytes

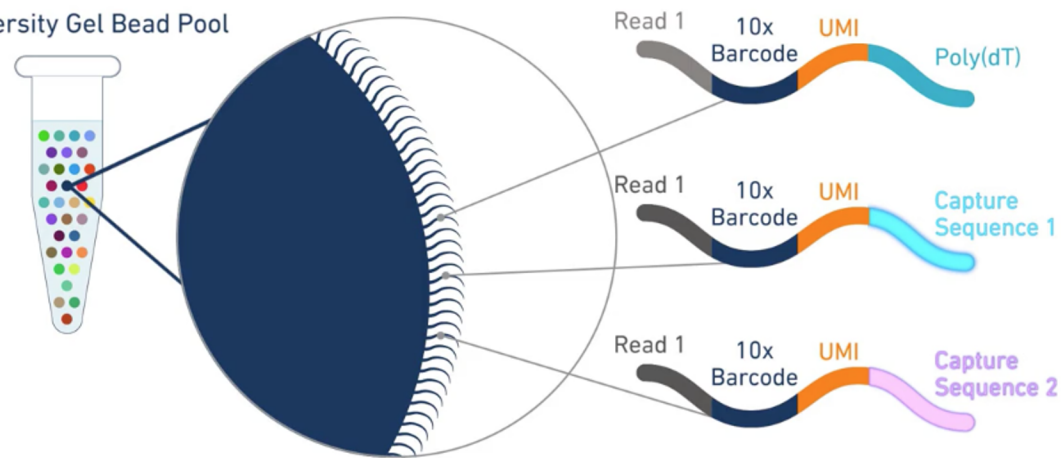




# Multimic cytometry with Feature Barcode technology

Barcoding biological analytes beyond mRNAs in single cells

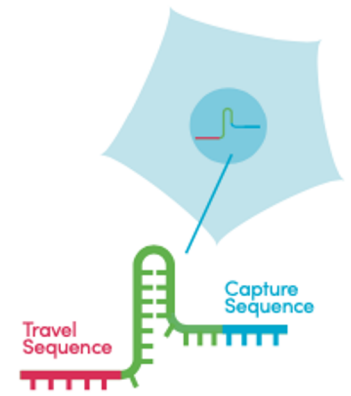
High-Diversity Gel Bead Pool



Antibodies for cell surface protein analysis



Peptide-MHC multimers to measure antigen specificity



Specific CRISPR perturbations for functional genomics screens

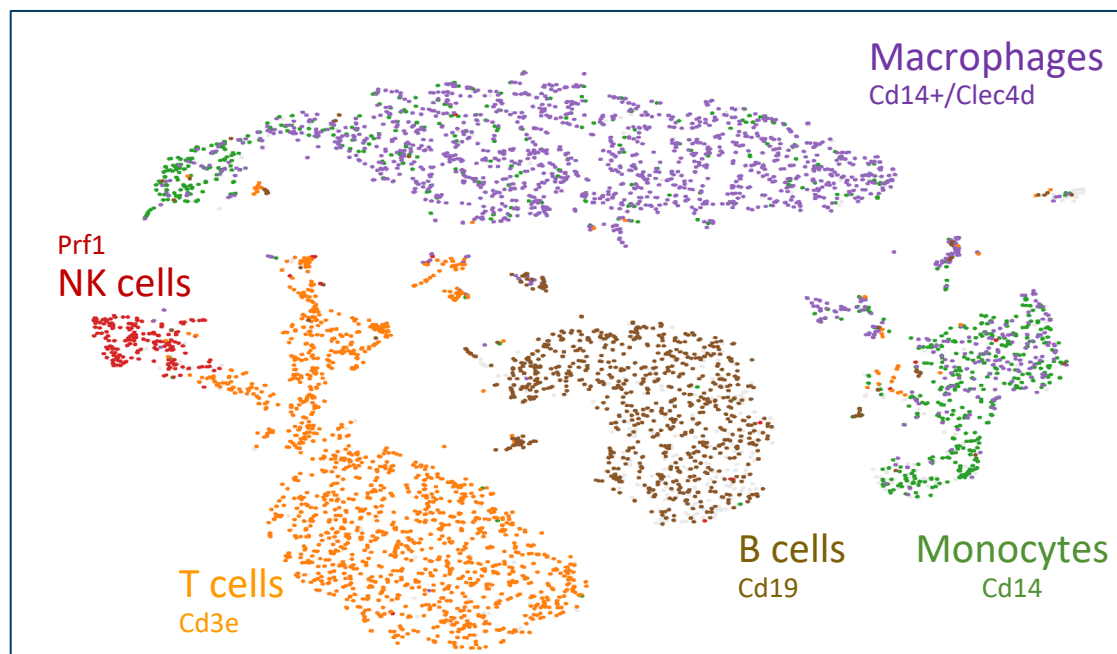




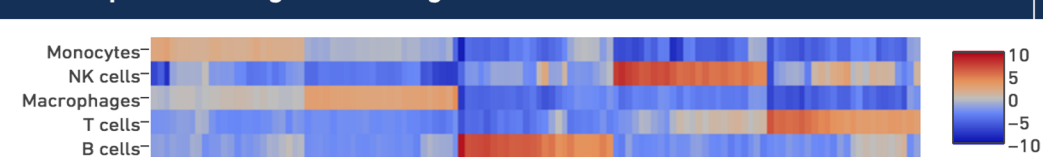
# Assess Cell Type Heterogeneity and the Immune Repertoire

## Mouse PBMCs

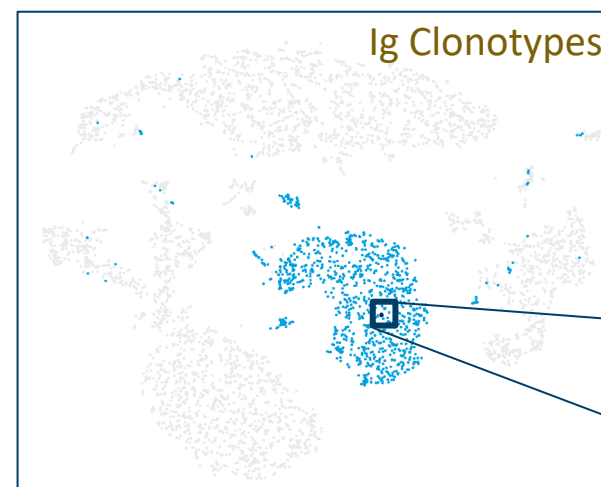
5' Gene Expression



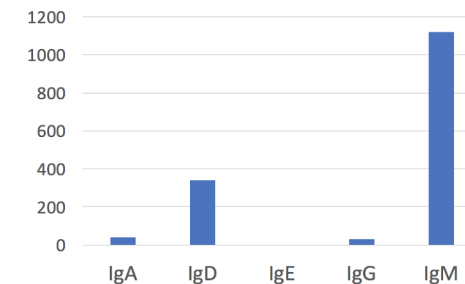
Heatmap of PBMC Log2 Fold Changes



V(D)J clonotypes overlapped with GEX

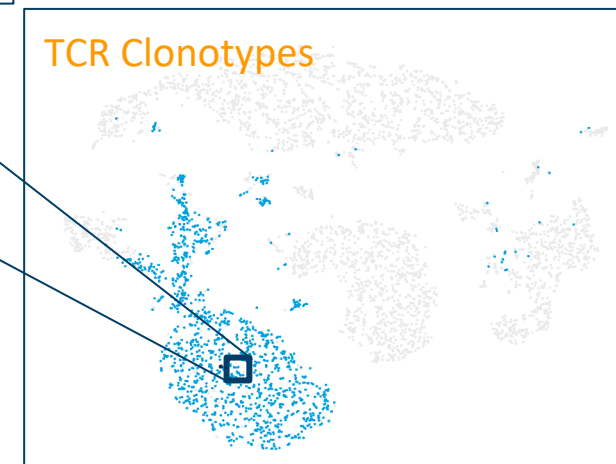


Isotype Distribution



	V	D	J	C	#
H	IGHV1-5	IGHD4-1	IGHJ2	IGHM	1
K	IGKV17-127		IGKJ4	IGKC	

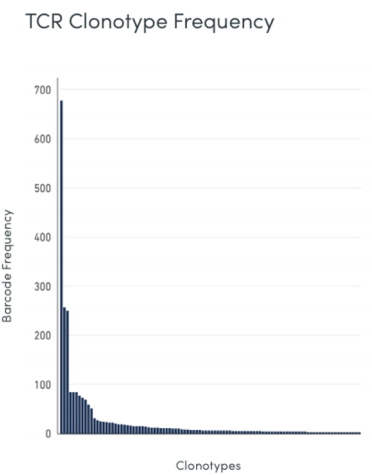
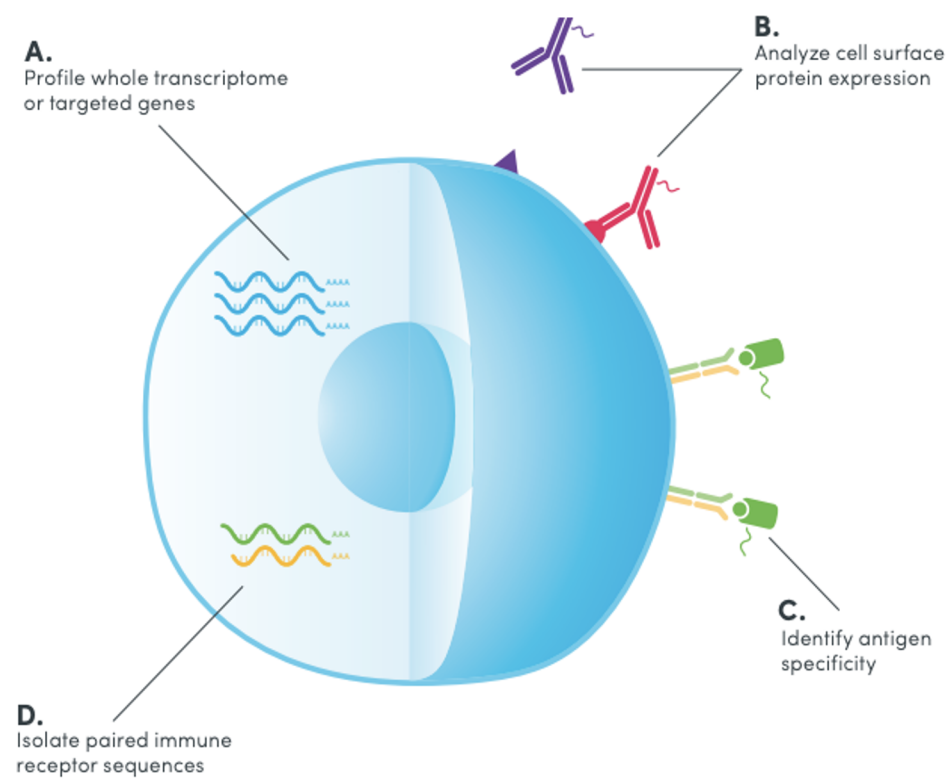
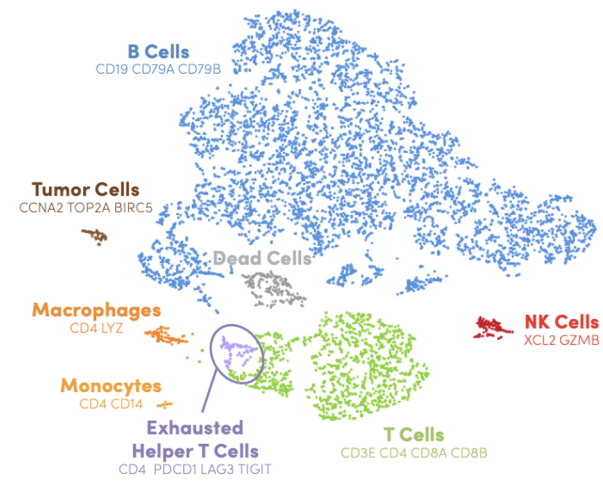
TCR Clonotypes



	V	D	J	C	#
α	TRAV12D-3		TRAJ50	TRAC	1
β	TRBV1	TRBD2	TRBJ2-5	TRBC1	

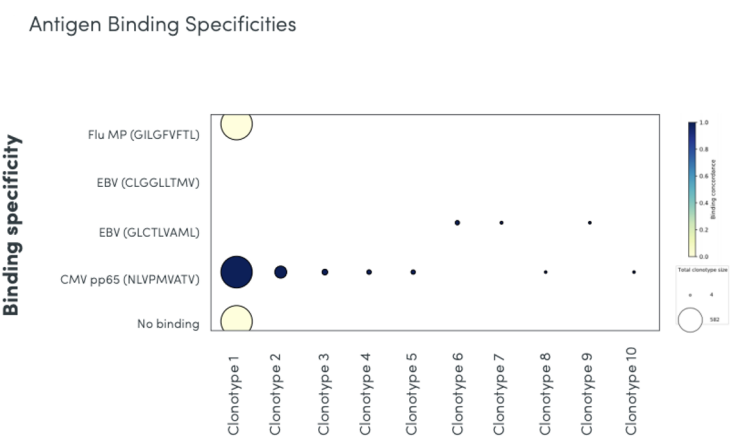
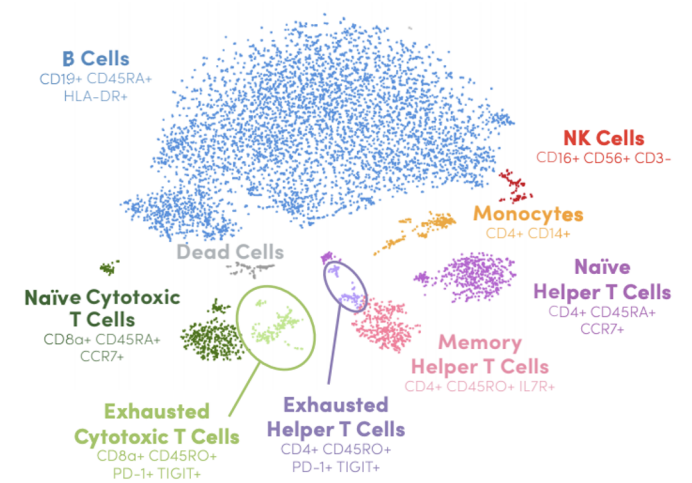


# Multiomic solution to study immunology



TCR Alpha  
TGGGGAGTCCACAGTTAGGCAGCGACCTCTGAAAGGGTGTCAATCTCGTTGTGTCCACACTCATGGGGGATTCCTCAAAGTTATGAAGTTGGCTGAAGA  
AAGCAGTTACTTGACCCCTCTTTGTGAACACAGAGGAAGCTGACATAGGGCAGAGCGTTCTAGGACATTTATGGAGCTGGTCTGCTGATTGGTAGGCAACCA  
GATGCGAGATCTCTTTTCTGAGGAGGATATTTCCACAGATTTGGGTGCAAGGTTTCTGCTGTGGTACCTGGAGGAGGAGAGATGGAGAGAGATCTTG  
CGAGCCCATCTACTACTCTCTGTTCTCTCTGACTGCTGAGCAGCATCTGAACCTGGAGCAAGCTCCTCAGTCACTGCTCATGTTGAGGAGGAGGAGCAGC  
AATTTCACTGCGAGCTGCTCTGAGCAGATTTTATGCTTACACTGTCAGATGGGAACTGCAAAAGGCGCCGAGGCTGTTTATGAGCTTAAATGGG  
ATGAAAGAGAGAGAGGAGATANGTGGCTGTTATACAGAGGAGGTTACAGCTATTGTCATGAGGATGCGAGCTGAGAGCTGAGCAGCATCTCTG  
TGGCTTCATCAGCGGTACACAGTTCTATTTGGGACAGGAGCAAGTTGACGGTCATTCAGAAATCCAGAACCCCTGACCTGCGCTGAGCAGTGAAGAG

TCR Beta  
GAGAGTCTGCTCCCTCTTCATCAATGACAGATACAGAGACCCCTCCGTCATGAGGATCTGGCATGAGCATGGGCTCTGCTGCTGAGCAGCTGTGTCTCT  
CTGTGGGAGGTCAGTGAATGCTGTGTCTCACTCAAGACCCAAATTCAGGTTCTGAGAGCAGGACAGCATGACACTGAGTGTGCGCAGGATATGAGCA  
TGAATACATCTGCTGTGTATGAGAGAGCCAGCAGCTGGGCTGAGGCTGATCTACTGATTTGGTGTGATATCAGTGAAGAGAGAGAGATCCCAATGAGCT  
CAATGCTCCAGATCAACCAAGAGGATTTCCGCTCAGGCTGCTGCGCTGCTCCCTCCAGACATCTGTGATCTCTGTCAGCAGCTGTTACCGGGA  
CAGGGGCTACCGGTACACCTTGGTTGGGAGCAGGTTACCGGTTAGAGAGCTGAGCAAGAGTTTCCACCGAGAGGCTGCTGTTGTTGAGCATACGA





# The local and systemic response to SARS-CoV-2 infection in children

**700,000 single cells**

nose  
trachea  
bronchi

5'10x  
TCR  
BCR

PBMCs

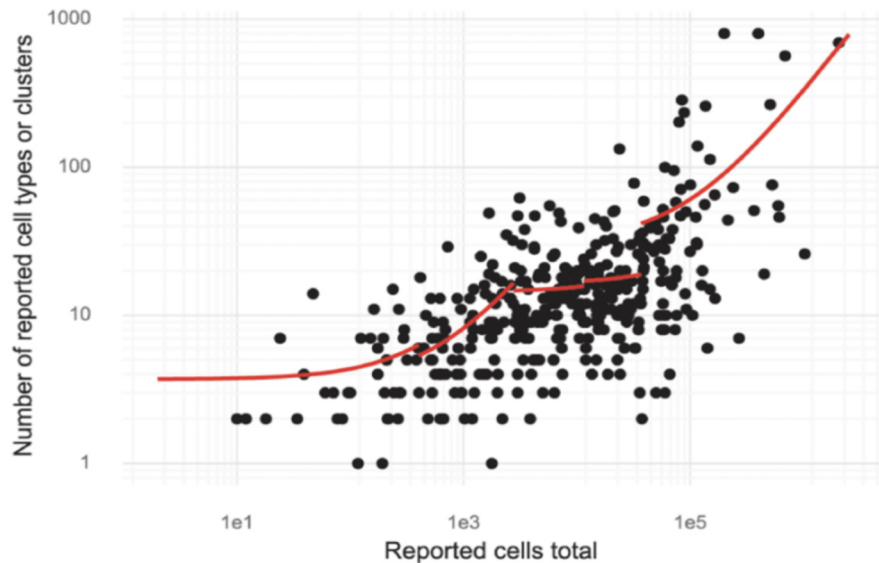
5'10x  
CITE-seq  
TCR  
BCR

- Protective pre-activated IFN state of airway
- Higher immune repertoire diversity
- Naive and less cytotoxic immune compartment
- Absence of systemic interferon stimulation

<https://doi.org/10.1038/s41586-021-04345-x>



# Paradigm-shifting studies require increased scale



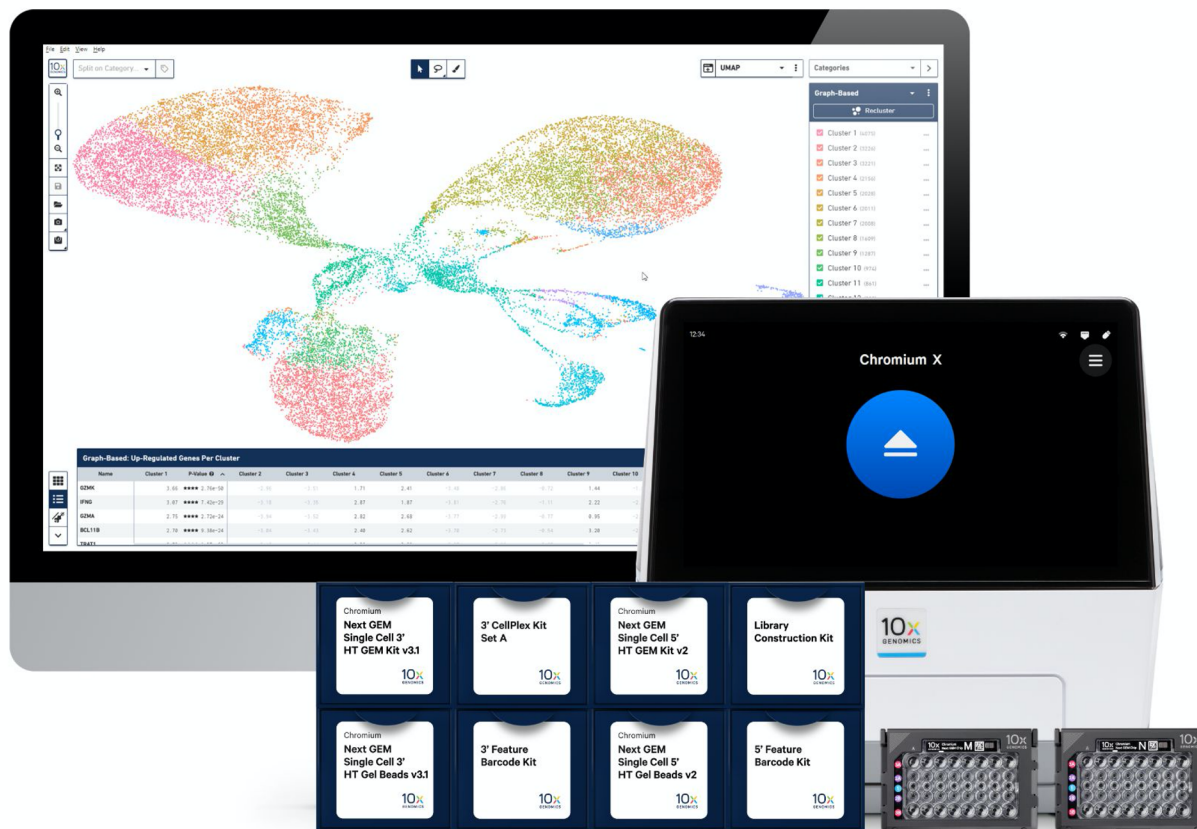
- Single cell publications have increased in cell number
- More cells > greater insights > more biology
- However, getting to very high cell numbers is challenging:
  - Profiling millions of cells is prohibitively expensive
  - Existing workflows for scaling are cumbersome, time-consuming and difficult to execute
- Robust methods for scaling up in a cost-effective manner are needed for science to move forward

*A curated database reveals trends in single cell transcriptomics*  
Valentine Svensson, Eduardo da Veiga Beltrame, & Lior Pachter  
Database, Volume 2020, 2020, baaa073; doi: 10.1093/database/baaa073



# Introducing...the Chromium X and Single Cell HT

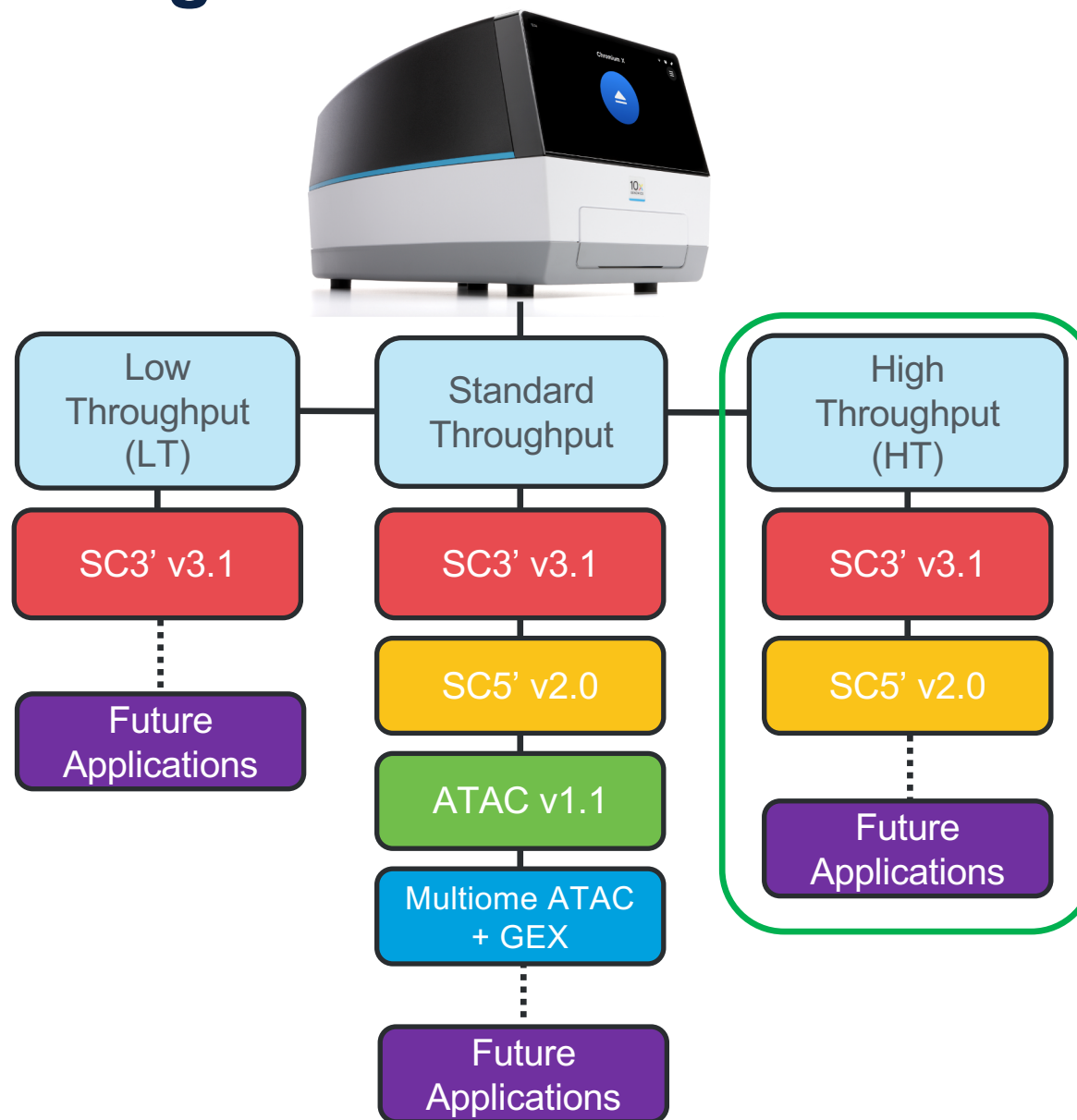
TheScientist  
**TOP 10**  
INNOVATIONS



- Chromium X + high-throughput (HT) assays offer:
  - Single cell experiments at scale, with an up to 7-fold reduction in cost per cell
  - Profiling transcripts of hundreds of thousands to millions of cells with high-dimensional multiomic outputs
  - Robust, fully supported, end to end workflow solutions
- Available now!



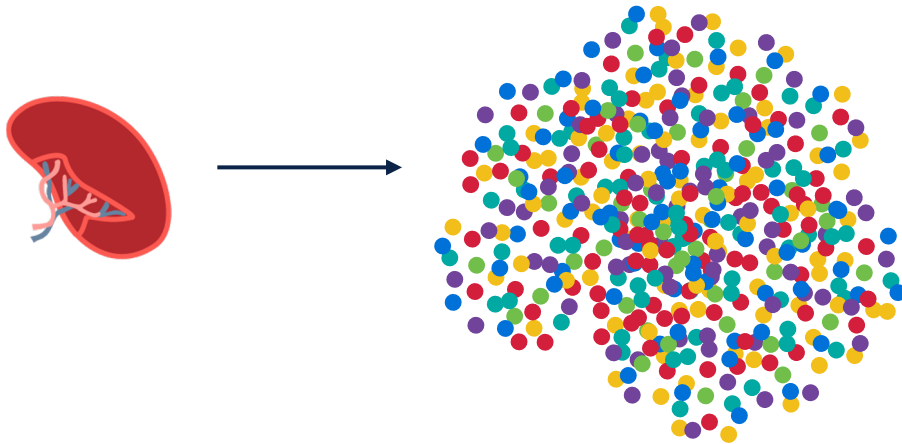
# Our most flexible single cell instrument to date





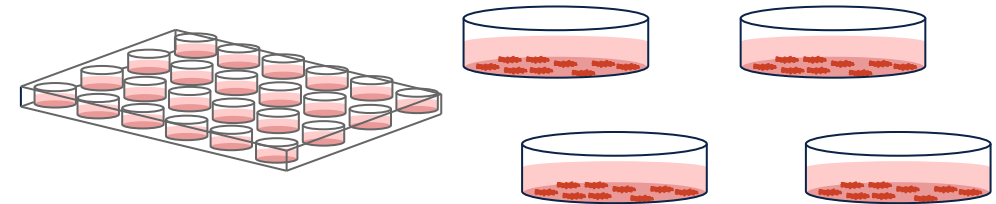
# Two types of high throughput

## Large number of cells



A few samples at a time, focus on high cell recovery

## Large number of samples



More samples, easily prepared at the same time



# Neuroscience

eLife Research article

Cell

Article

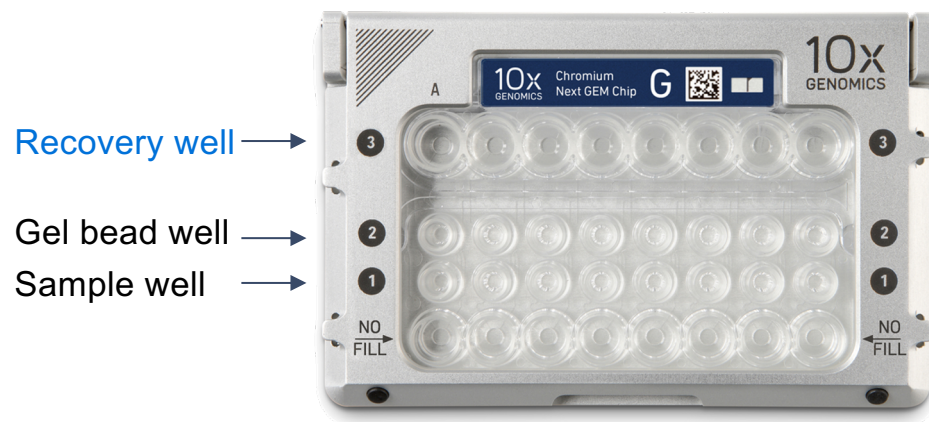
A taxonomy of transcriptomic cell types across the isocortex and hippocampal formation

Julien Y. Cheng<sup>1,2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20,21,22,23,24,25,26,27,28,29,30,31,32,33,34,35,36,37,38,39,40,41,42,43,44,45,46,47,48,49,50,51,52,53,54,55,56,57,58,59,60,61,62,63,64,65,66,67,68,69,70,71,72,73,74,75,76,77,78,79,80,81,82,83,84,85,86,87,88,89,90,91,92,93,94,95,96,97,98,99,100,101,102,103,104,105,106,107,108,109,110,111,112,113,114,115,116,117,118,119,120,121,122,123,124,125,126,127,128,129,130,131,132,133,134,135,136,137,138,139,140,141,142,143,144,145,146,147,148,149,150,151,152,153,154,155,156,157,158,159,160,161,162,163,164,165,166,167,168,169,170,171,172,173,174,175,176,177,178,179,180,181,182,183,184,185,186,187,188,189,190,191,192,193,194,195,196,197,198,199,200,201,202,203,204,205,206,207,208,209,210,211,212,213,214,215,216,217,218,219,220,221,222,223,224,225,226,227,228,229,230,231,232,233,234,235,236,237,238,239,240,241,242,243,244,245,246,247,248,249,250,251,252,253,254,255,256,257,258,259,260,261,262,263,264,265,266,267,268,269,270,271,272,273,274,275,276,277,278,279,280,281,282,283,284,285,286,287,288,289,290,291,292,293,294,295,296,297,298,299,300,301,302,303,304,305,306,307,308,309,310,311,312,313,314,315,316,317,318,319,320,321,322,323,324,325,326,327,328,329,330,331,332,333,334,335,336,337,338,339,340,341,342,343,344,345,346,347,348,349,350,351,352,353,354,355,356,357,358,359,360,361,362,363,364,365,366,367,368,369,370,371,372,373,374,375,376,377,378,379,380,381,382,383,384,385,386,387,388,389,390,391,392,393,394,395,396,397,398,399,400,401,402,403,404,405,406,407,408,409,410,411,412,413,414,415,416,417,418,419,420,421,422,423,424,425,426,427,428,429,430,431,432,433,434,435,436,437,438,439,440,441,442,443,444,445,446,447,448,449,450,451,452,453,454,455,456,457,458,459,460,461,462,463,464,465,466,467,468,469,470,471,472,473,474,475,476,477,478,479,480,481,482,483,484,485,486,487,488,489,490,491,492,493,494,495,496,497,498,499,500,501,502,503,504,505,506,507,508,509,510,511,512,513,514,515,516,517,518,519,520,521,522,523,524,525,526,527,528,529,530,531,532,533,534,535,536,537,538,539,540,541,542,543,544,545,546,547,548,549,550,551,552,553,554,555,556,557,558,559,560,561,562,563,564,565,566,567,568,569,570,571,572,573,574,575,576,577,578,579,580,581,582,583,584,585,586,587,588,589,590,591,592,593,594,595,596,597,598,599,600,601,602,603,604,605,606,607,608,609,610,611,612,613,614,615,616,617,618,619,620,621,622,623,624,625,626,627,628,629,630,631,632,633,634,635,636,637,638,639,640,641,642,643,644,645,646,647,648,649,650,651,652,653,654,655,656,657,658,659,660,661,662,663,664,665,666,667,668,669,670,671,672,673,674,675,676,677,678,679,680,681,682,683,684,685,686,687,688,689,690,691,692,693,694,695,696,697,698,699,700,701,702,703,704,705,706,707,708,709,710,711,712,713,714,715,716,717,718,719,720,721,722,723,724,725,726,727,728,729,730,731,732,733,734,735,736,737,738,739,740,741,742,743,744,745,746,747,748,749,750,751,752,753,754,755,756,757,758,759,760,761,762,763,764,765,766,767,768,769,770,771,772,773,774,775,776,777,778,779,780,781,782,783,784,785,786,787,788,789,790,791,792,793,794,795,796,797,798,799,800,801,802,803,804,805,806,807,808,809,810,811,812,813,814,815,816,817,818,819,820,821,822,823,824,825,826,827,828,829,830,831,832,833,834,835,836,837,838,839,840,841,842,843,844,845,846,847,848,849,850,851,852,853,854,855,856,857,858,859,860,861,862,863,864,865,866,867,868,869,870,871,872,873,874,875,876,877,878,879,880,881,882,883,884,885,886,887,888,889,890,891,892,893,894,895,896,897,898,899,900,901,902,903,904,905,906,907,908,909,910,911,912,913,914,915,916,917,918,919,920,921,922,923,924,925,926,927,928,929,930,931,932,933,934,935,936,937,938,939,940,941,942,943,944,945,946,947,948,949,950,951,952,953,954,955,956,957,958,959,960,961,962,963,964,965,966,967,968,969,970,971,972,973,974,975,976,977,978,979,980,981,982,983,984,985,986,987,988,989,990,991,992,993,994,995,996,997,998,999,1000</sup>



# New HT chip allows for significant increase in throughput

**Chromium Next GEM Chip G**  
(standard 3' assay)

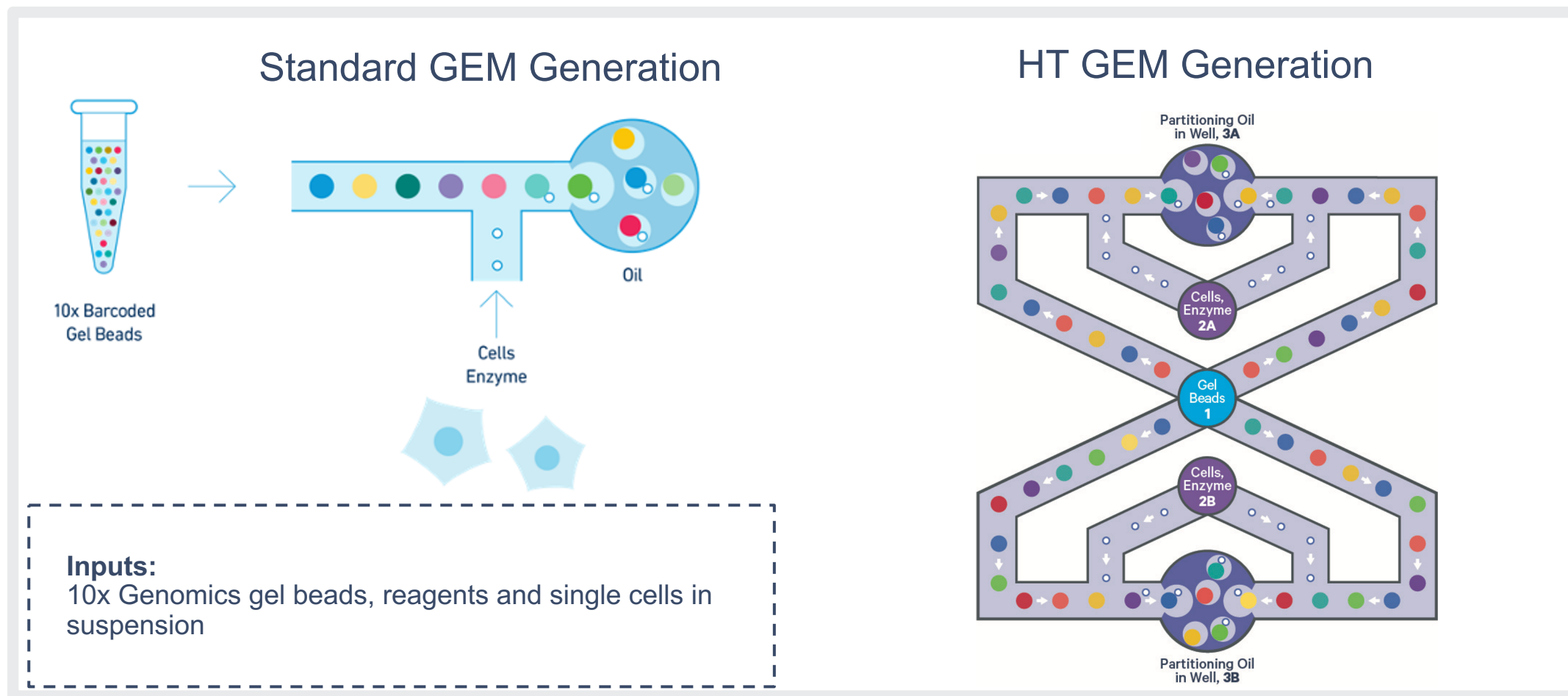


**Chromium Next GEM Chip M**  
(HT 3' assay)





# Comparing standard and HT single cell assays





# Comparing standard and HT single cell assays

Assay-level specifications without sample multiplexing

Sensitivity, mapping rates, gene length distributions, library quality, etc. are similar

	Standard assay		HT assay	
Supported Dynamic Range (per sample input well)	500 – 10,000		2,000 – 20,000*	
Optimal Cell Stock Concentration (cells/μL)	700 - 1,200			
Cell Multiplet Rate per 1,000 cells	~0.8%		~0.4%	
Cell Recovery Efficiency	Up to 65%			
Number of GEMs per recovery well	~100k		~200K	
Number of reactions per kit	4 rxn	16 rxn	8 rxn	48 rxn
Number of chips per kit	2	6	1	5

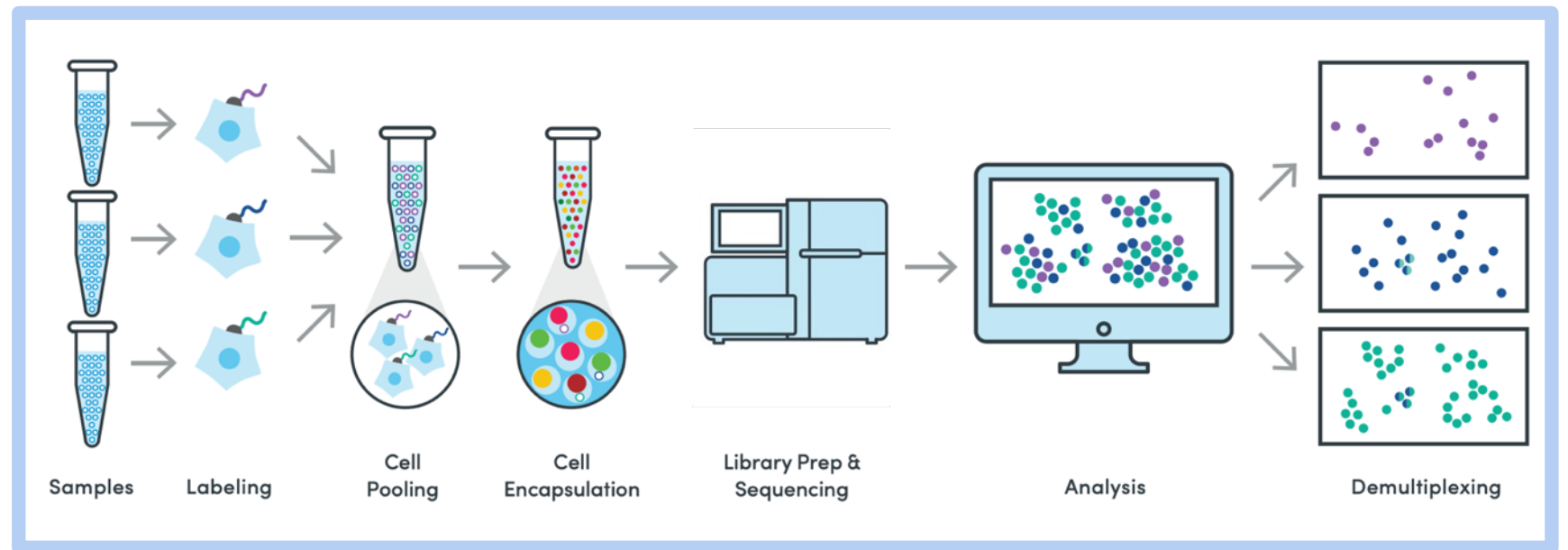
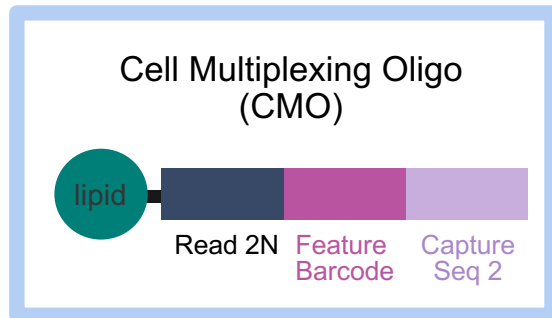
*\*Up to 320,000 cells/chip*



# Cell multiplexing

Increase experimental efficiency

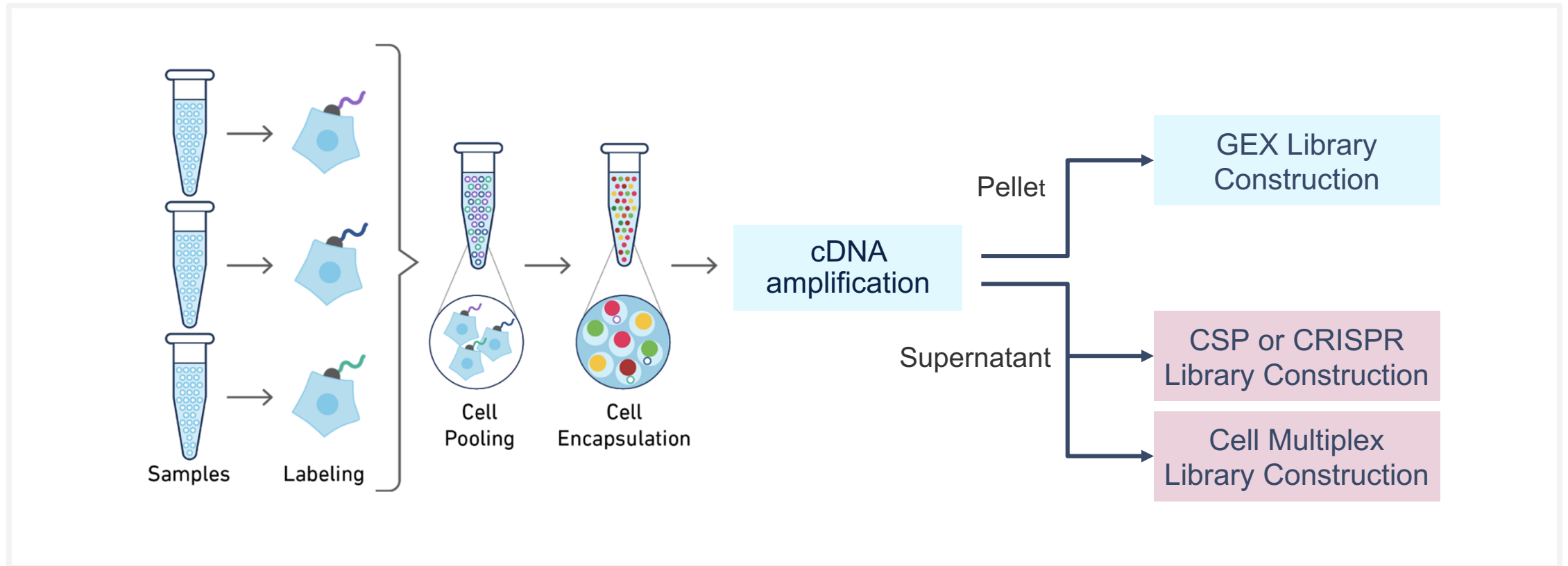
- Label cells (or nuclei) with lipids conjugated to Feature Barcode oligos (Cell Multiplexing Oligos)
- Pool labeled cells/nuclei together to run in a single well of a 10x Genomics chip (pool up to 12 samples)
- Load more cells in a single well, bioinformatically filtering out cell multiplets (target up to 60,000 cells with 3' HT v3.1)





# 3' CellPlex workflow

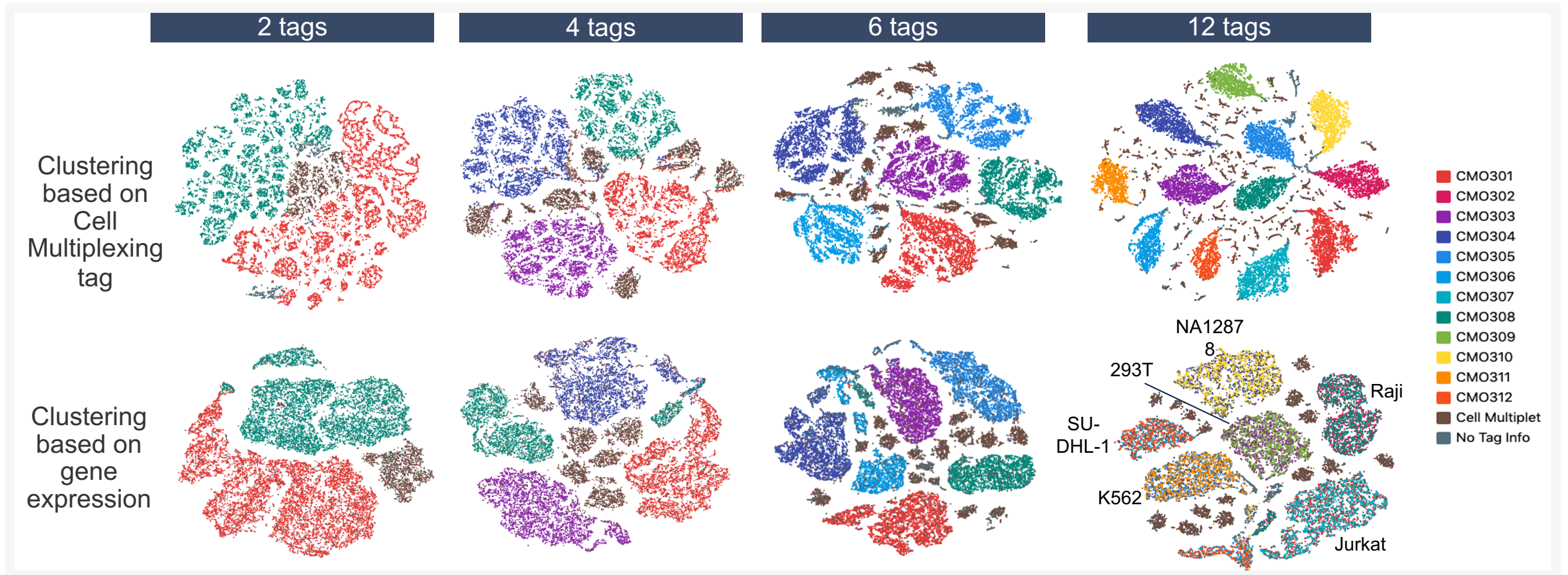
Highly similar to existing Feature Barcode workflows





# Cell multiplexing demonstration

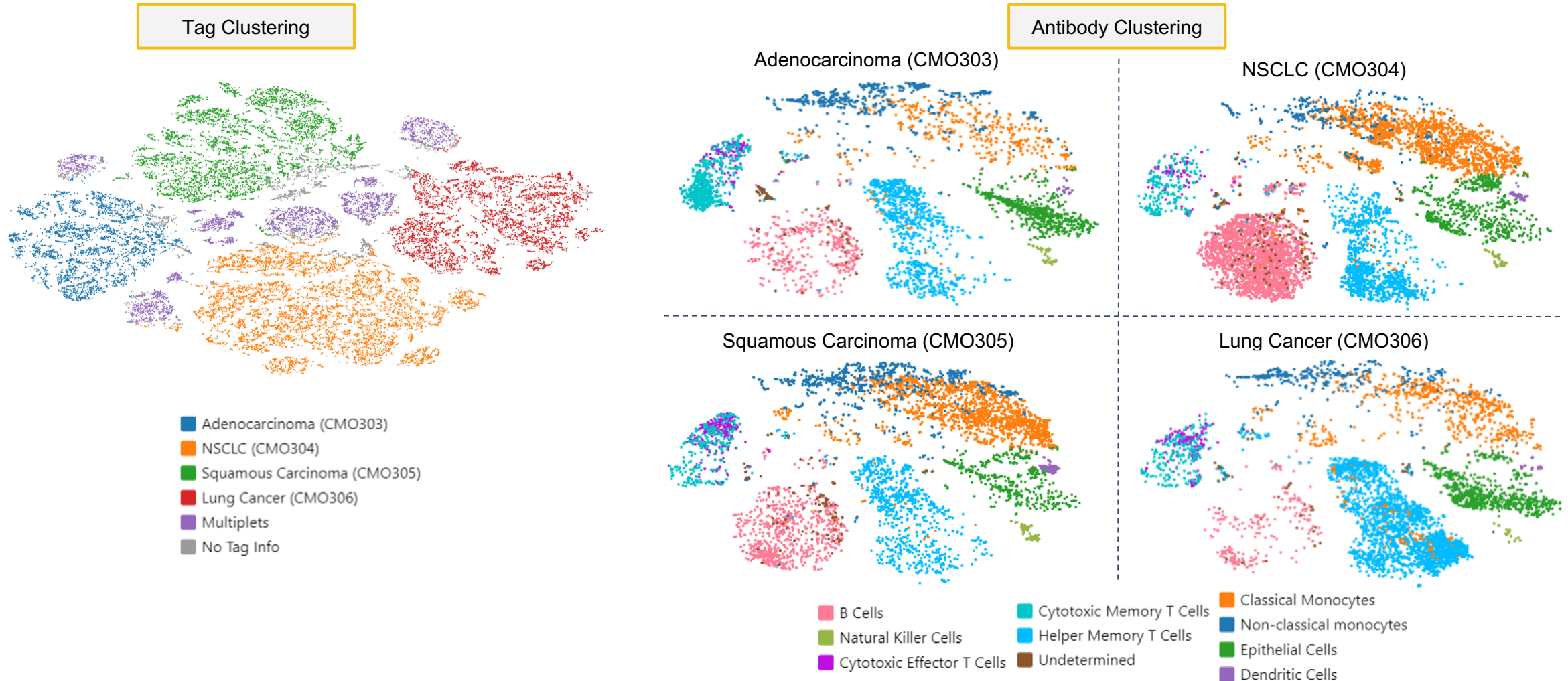
12 CMO tags with 6 human cell lines





# Compare differences in sample composition with multiomic data

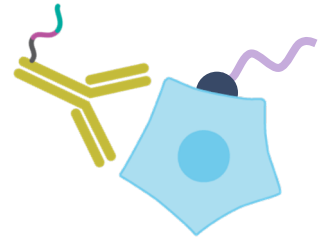
3' CellPlex enables multiplexing with multiomic workflows



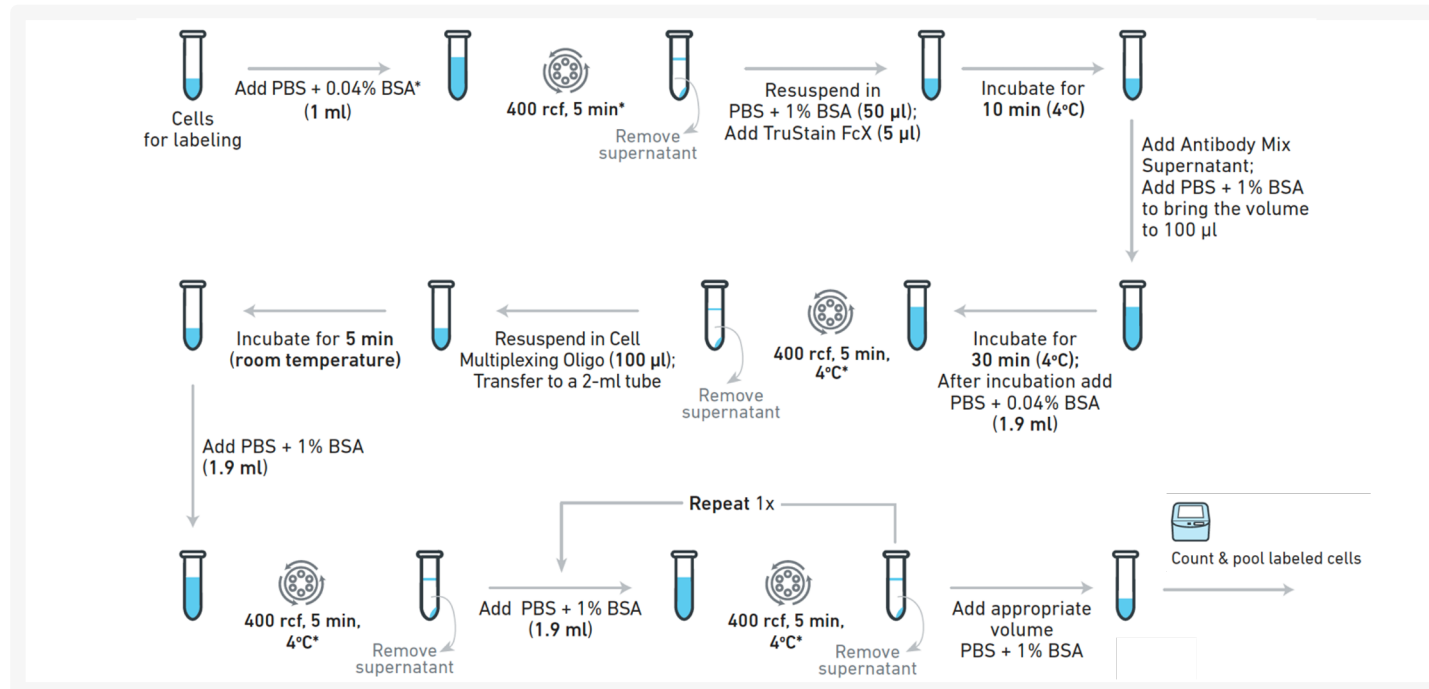


# Demonstrated protocol for CMO labeling

## Labeling cells with CMO & antibodies



- Label cells with oligo-conjugated antibodies for 30 min
- Label cells in CMO for 5 min
- Wash to remove unbound antibodies and CMO



CG000391

## Cell Multiplexing Oligo Labeling for Single Cell RNA Sequencing Protocols

**DEMONSTRATED PROTOCOL**

CG000391 - Rev A

### Cell Multiplexing Oligo Labeling for Single Cell RNA Sequencing Protocols with Feature Barcode technology

**Overview**

The 10x Genomics 3' CellPlex Kit provides a species agnostic sample multiplexing solution through the use of a set of 12 Feature Barcode oligonucleotides each conjugated to a lipid. These Cell Multiplexing Oligos can be used to label individual cells or nuclei samples and the labeled cells can be pooled together prior to loading onto a 10x Genomics chip. The Feature Barcode molecules can be directly captured by oligonucleotides present on the Gel Beads inside a GEM during GEM-RT, subsequently amplified and used to generate Cell Multiplexing libraries.

This protocol provides guidance for:

- Labeling cells/nuclei with CellPlex reagents (See Page 2-3, Cell Multiplexing Oligo Labeling for use with Single Cell RNA sequencing protocols with Feature Barcode technology for Cell Multiplexing CG000391 and Single Cell RNA sequencing protocols with Feature Barcode technology for CRISPR Screening & Cell Multiplexing CG000391).
- Labeling cells with antibody-oligonucleotide conjugates and CellPlex reagents (See Page 4-5, Cell Surface Protein & Cell Multiplexing Oligo Labeling for use with Single Cell RNA sequencing protocols with Feature Barcode technology for Cell Surface Protein & Cell Multiplexing CG000391).

This protocol was demonstrated using primary cells including peripheral blood mononuclear cells (PBMCs), dissociated tumor cells and dissociated brain tissue, cell lines including Jurkat, Raji, A20 and EL4 as well as cell lines that have been transduced with CRISPR machinery including K562, A549, SK-N-SH and U2OS. Modifications to this protocol may be required when working with other cell types (e.g. centrifugation speed and time). For additional information on preparation of specific sample types, consult the 10x Genomics Demonstrated Protocols available on the 10x Genomics support website.

**Additional Guidance**

Consult Demonstrated Protocol: Cell Preparation Guide (Document CG000393) for Tips & Best Practices on handling cells and Technical Note Guidelines on Accurate Target Cell Counts (Document CG000391) for determining accurate cell counts.

Cells carry potentially hazardous pathogens. Follow material supplier recommendations and local laboratory procedures and regulations for the safe handling, storage and disposal of biological materials.

**Preparation - Buffers**

Buffer	Reagents
Wash & Resuspension Buffer for Cells*	PBS + 1% BSA for PBMCs, cell lines, and dissociated tumor cells NAAG-1 + 1% BSA for dissociated brain tissues
Wash & Resuspension Buffer for Nuclei*	PBS + 1% BSA + Nuclei Isolation Buffer
Additional Buffers	PBS + 0.04% BSA (maintain at room temperature) *Wash & resuspension buffers depend upon the sample type. Use the buffer appropriate for the sample.

**Specific Reagents & Consumables**

Vendor	Item	Part Number
10x Genomics	3' CellPlex Kit Set A	1000001
Thermo Fisher Scientific	UltraPure Beadman Serum Albumin (BSA, 500 mg/ml)	AM6514
	Trypan Blue Stain (0.4%)	T10282
	Coulter's FFL Automated Cell Counter	AMAGM1000
	Coulter's FFL Automated Cell Counting Chamber Slides	C10228
Corning	Phosphate-Buffered Saline, TX	21-040-CV
	without Calcium and Magnesium	
Millipore Sigma	Bovine Serum Albumin in DPBS (1250)	A1595
	Substituted to Thermo Fisher product	
	Propagator Phase Indicator	33309001
Brands	NAAG-1	NAAG-1
	Neurotransmitter medium	100
Boehringer	Human TruStain FcX (Fc Receptor Binding Inhibitor)	422901
	StatTag™ Antibody Oligonucleotide	-
	(StatTag™ ID)	

**10x GENOMICS**

Demonstrated Protocol - Cell Multiplexing Oligo Labeling for Single Cell RNA Sequencing Protocols - Rev A



# Comparing standard and HT single cell assays

## Assay-level specifications with sample multiplexing

Sensitivity, mapping rates, gene length distributions, library quality, etc. are similar

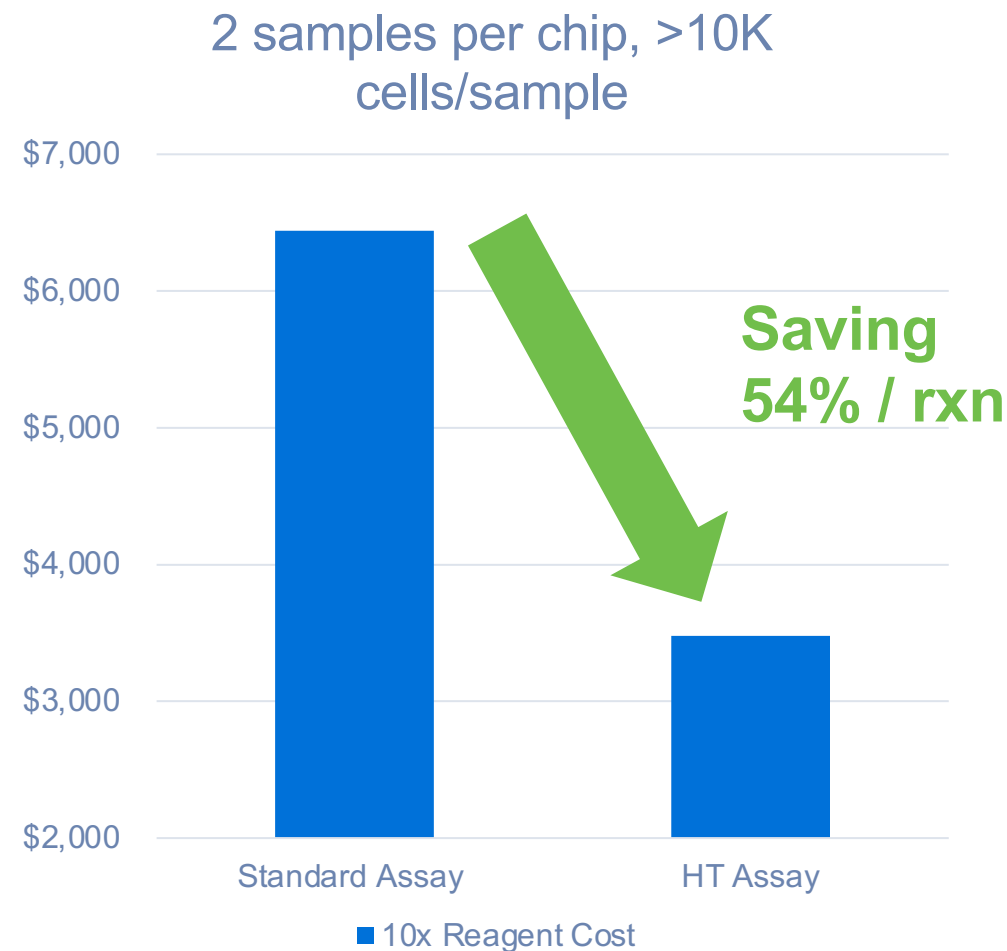
	Standard assay		HT assay	
Supported Dynamic Range (per sample input well)	500 – 30,000		2,000 – 60,000*	
Singlets per sample input	~500 - 17,700		~1,980 - 45,600	
Optimal Cell Stock Concentration (cells/μL)	1,300 - 1,600			
Cell Multiplet Rate per 1,000 cells	~0.8%		~0.4%	
Cell Recovery Efficiency	Up to 65%			
Number of GEMs per recovery well	~100k		~200K	
Number of reactions per kit	4 rxn	16 rxn	8 rxn	48 rxn
Number of chips per kit	2	6	1	5

***\*Up to 960,000 cells/chip***



# Break-even point between HT and Standard Assays

- Start saving approximately in 10x reagents cost when either scenario occurs:
  - Scenario #1 (see graph)
    - Running 2 samples/chip and
    - >10,000 cells sample
  - Scenario #2
    - Running 4 samples/chip and
    - Any number of cells/sample
- Plus, 2X cells compared to ST
- These scenarios do not require combining samples with CellPlex





# Maximizing multiomic insights with Single Cell HT

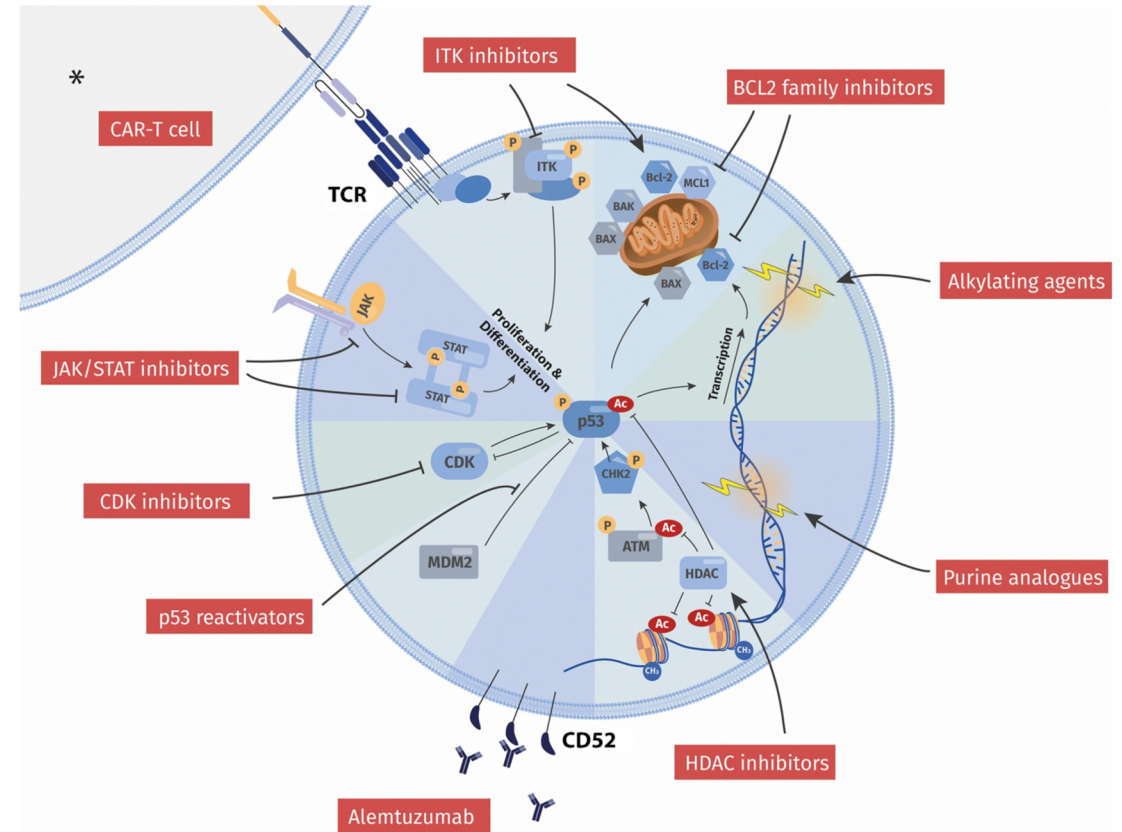
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Highlighting Chromium Next GEM Single Cell 5' HT v2



# Why study T-PLL?

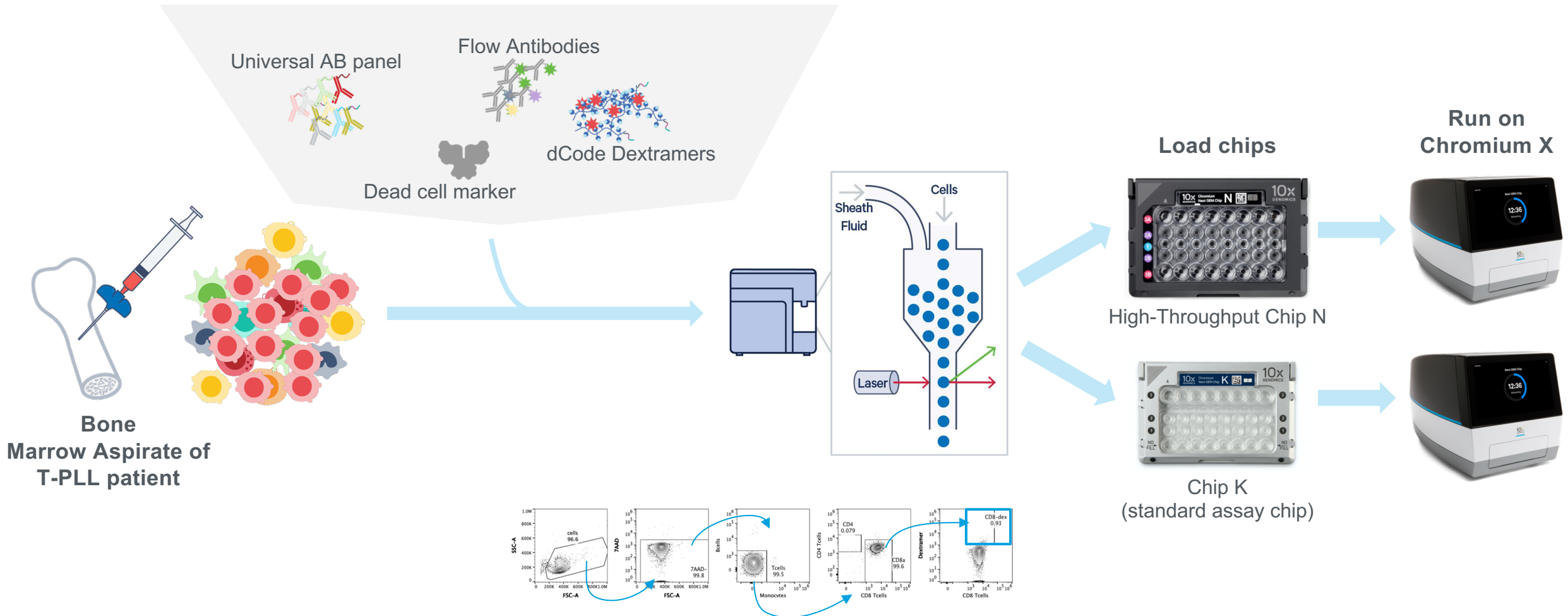
- T-cell prolymphocytic leukemia (T-PLL) is a rare and aggressive cancer that is characterized by the out of control growth of mature T-cells
- Only 10-20% of patients treated with standard treatments reach long-term remission
- Median survival after diagnosis is < 3 years
- Novel strategies are needed in order to improve clinical outcomes



Braun, T., von Jan, J., Wahnschaffe, L. *et al.* Advances and Perspectives in the Treatment of T-PLL. *Curr Hematol Malig Rep* 15, 113–124 (2020).



# Using Single Cell Immune Profiling with Feature Barcode technology to detect TCR-antigen specificity





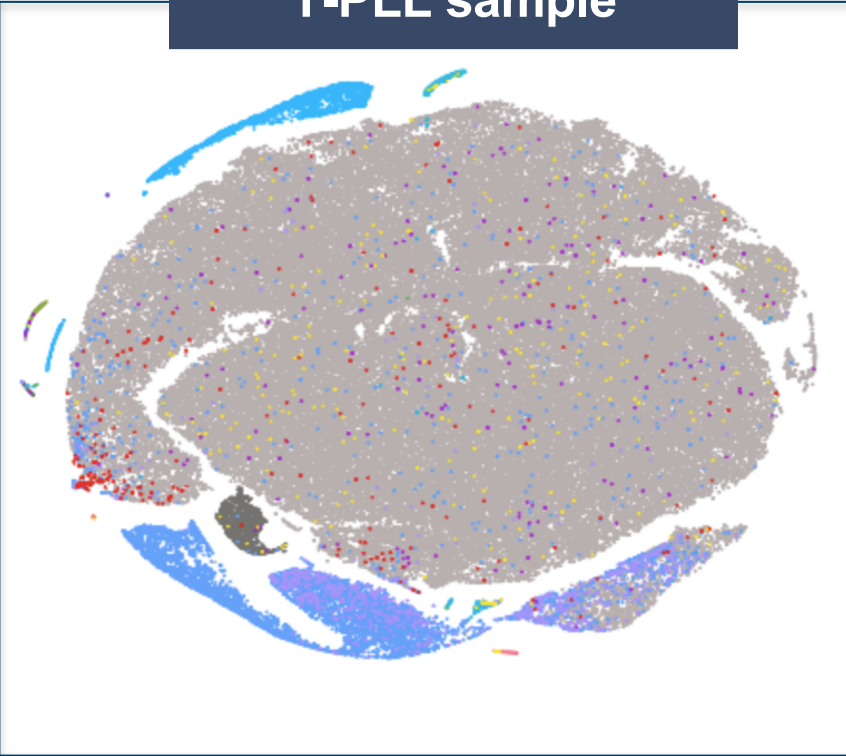
# Patients with T-PLL suffer from uncontrolled T cell growth

Healthy Bone Marrow



- ✓ B Memory (262)
- ✓ B Naive (1715)
- ✓ Dendritic classic (405)
- ✓ Dendritic plasmacytoid (72)
- ✓ Doublets (2321)
- ✓ HSC (25)
- ✓ MAIT (253)
- ✓ Monocytes CD14 (2491)
- ✓ Monocytes CD16 (1090)
- ✓ NK Cytotoxic (2330)
- ✓ NK Immunoregulatory (407)
- ✓ T gamma-delta (160)
- ✓ Tc Effector (1002)
- ✓ Tc Memory (1013)
- ✓ Tc Naive (1067)
- ✓ Th Effector (571)
- ✓ Th Memory (7490)
- ✓ Th Naive (3108)
- ✓ CMP (11)
- ✓ GMP (7)
- ✓ MEP (27)
- ✓ MLP (18)
- ✓ MPP (5)

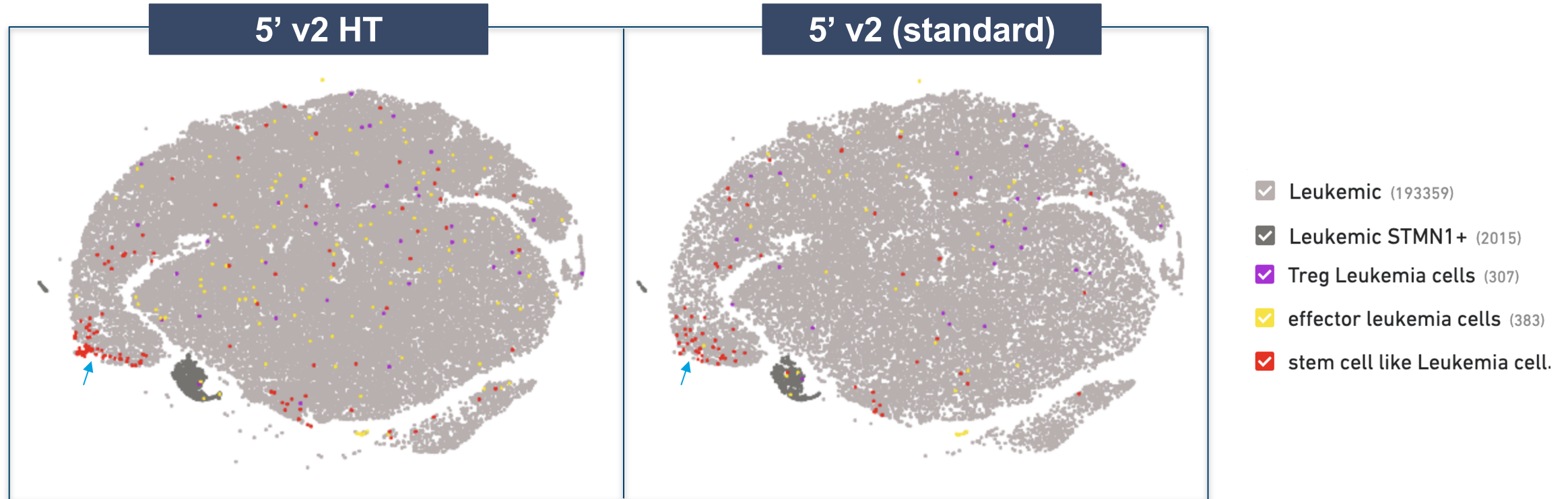
T-PLL sample



- ✓ B (167)
- ✓ Dendritic (69)
- ✓ Leukemic (193359)
- ✓ Leukemic STMN1+ (2015)
- ✓ Monocytes\_CD14 (245)
- ✓ Monocytes\_CD16 (66)
- ✓ NK (332)
- ✓ RBC (22)
- ✓ T\_DoubleNeg (106)
- ✓ Tc\_Effector (1040)
- ✓ Tc\_Memory (3284)
- ✓ Tc\_Naive (32)
- ✓ Th\_Memory (10271)
- ✓ Th\_Naive (1417)
- ✓ Treg Leukemia cells (307)
- ✓ effector leukemia cells (383)
- ✓ stem cell like Leukemia cell.



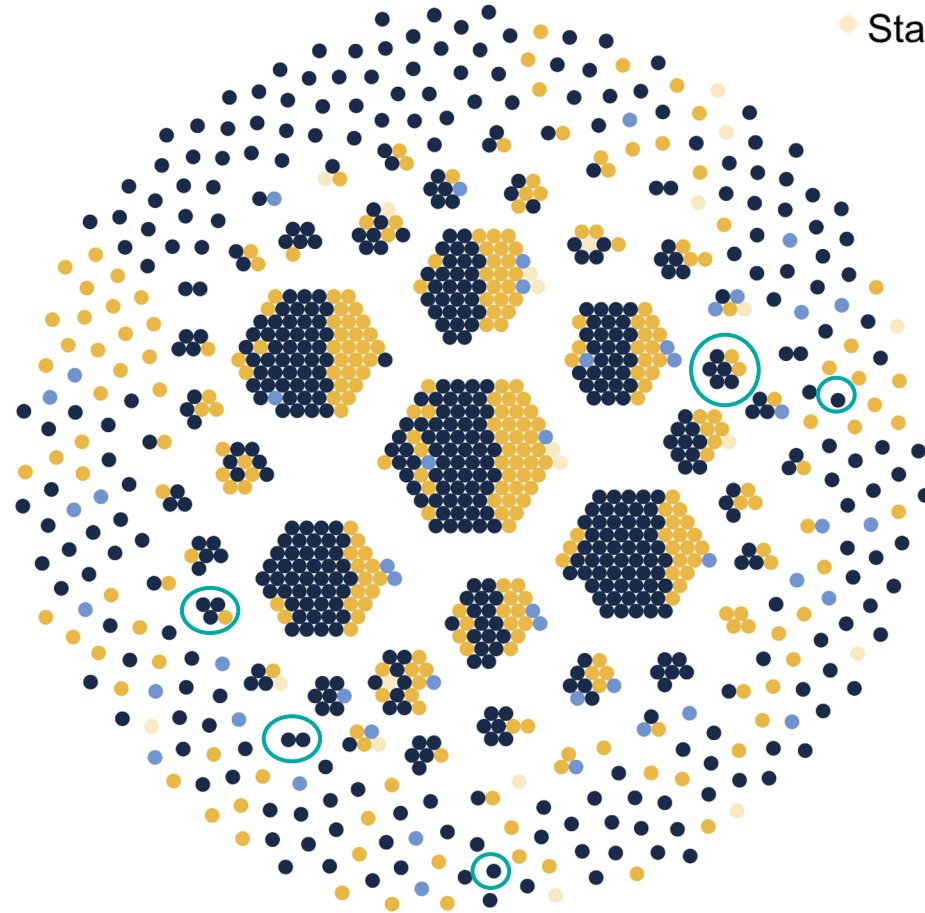
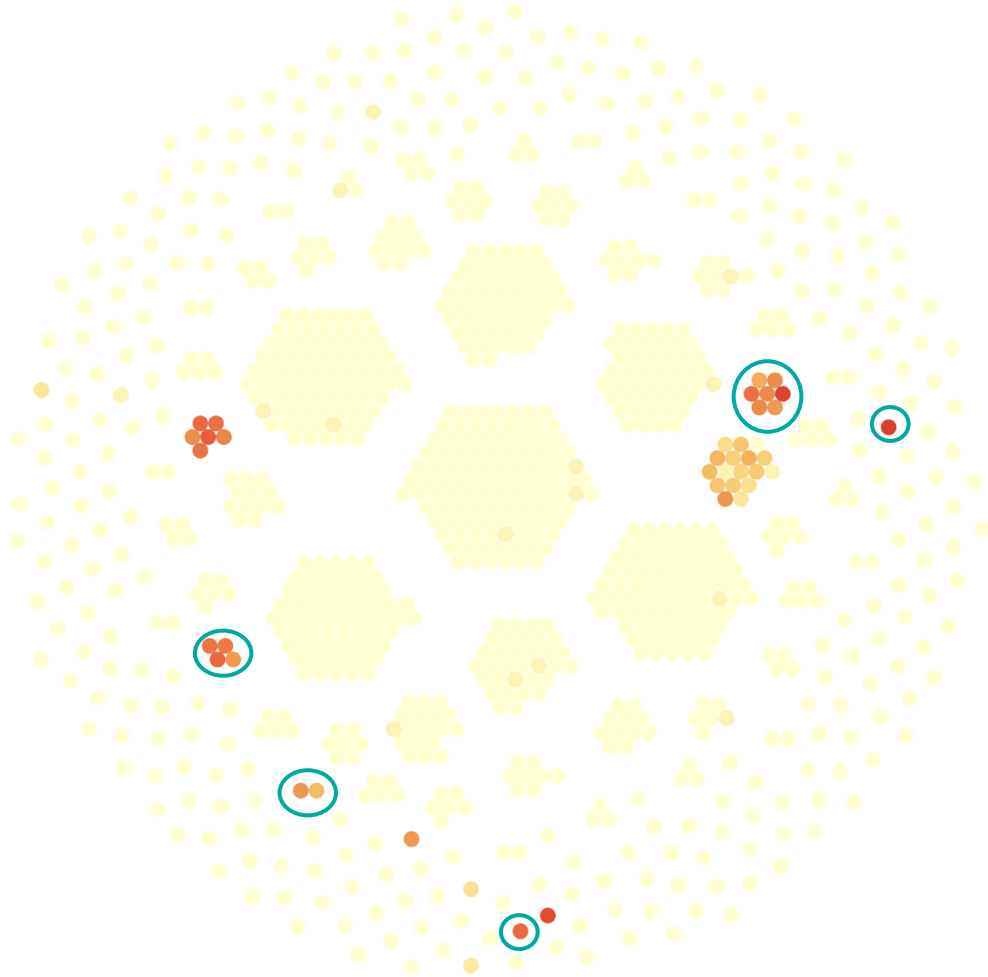
# Better detection of minor leukemia clones in HT





# Higher cell throughput from the HT assay enables detection of rare TCR clonotypes

- HT, sorted
- HT, unsorted
- Standard, sorted
- Standard, unsorted

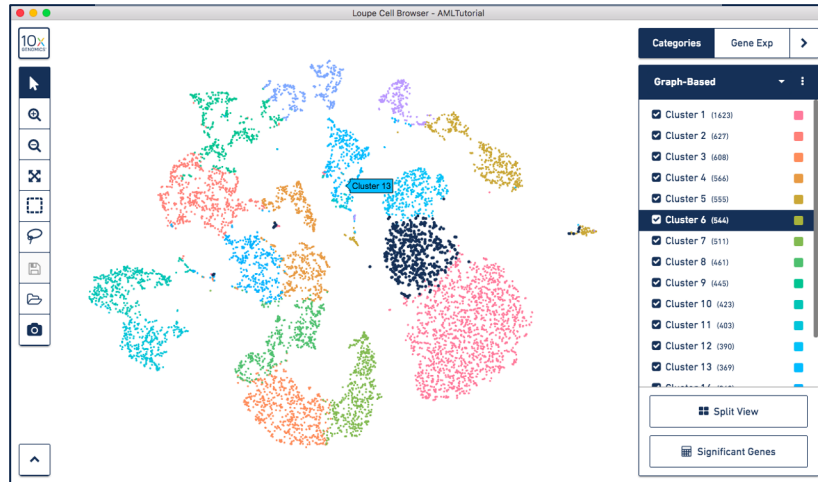


Circled cells/clonotypes are only identified (or are more confidently assigned as expanded and specific) in the HT data

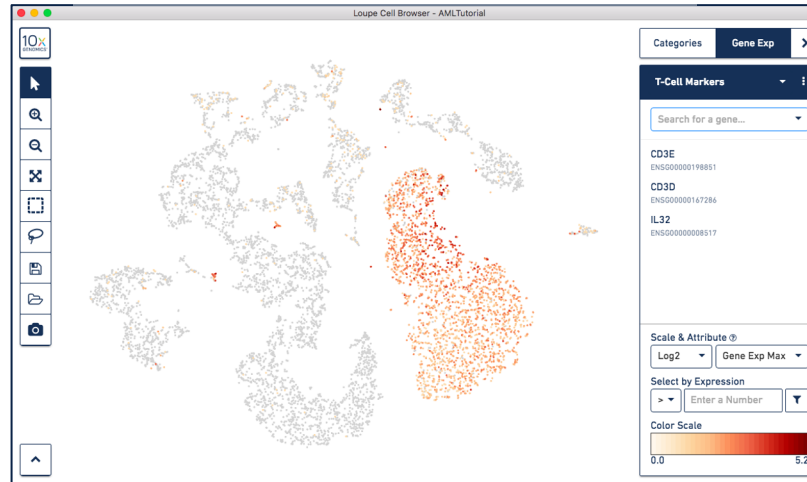


# Loupe Browser – analysis for everyone

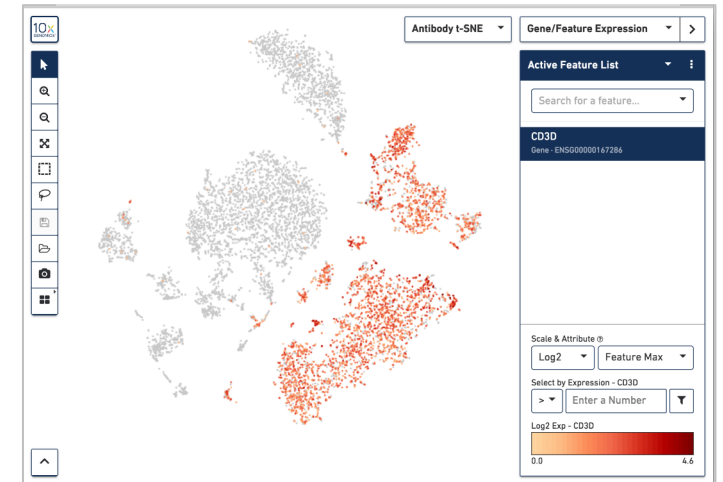
Precomputed GEX clusters



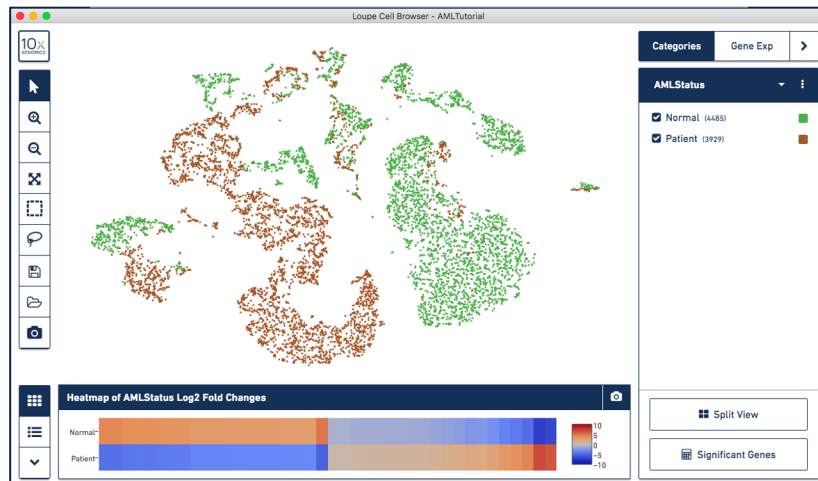
Gene expression level



Protein expression level



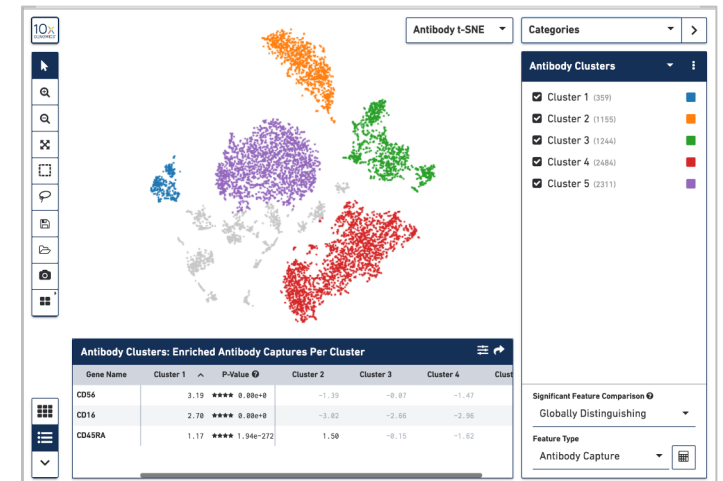
Experimental conditions



CRISPR guide Clusters



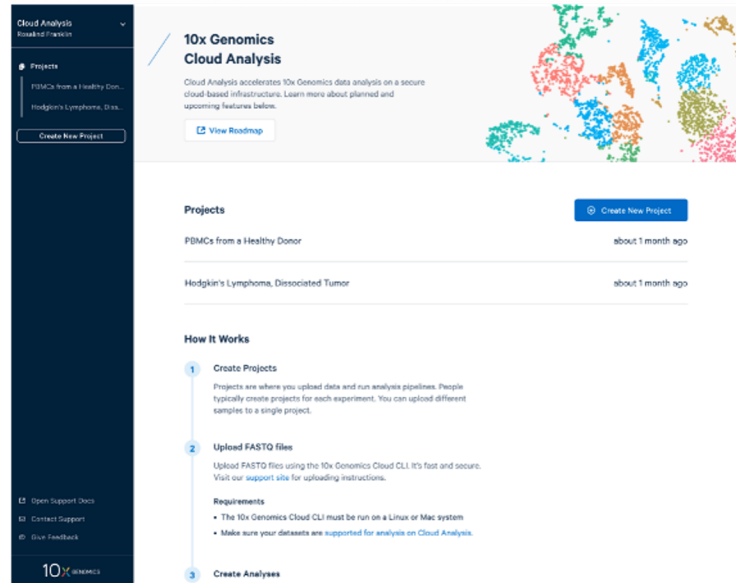
Precomputed protein clusters





# 10x Genomics Cloud Analysis

Accelerate your data analysis



- Quickly get started analyzing 10x data
- Standard set of analysis per sample at no additional cost<sup>1</sup>
- Scale your data analysis

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<sup>1</sup>See [10x Genomics Cloud Terms of Use](#) for restrictions and details

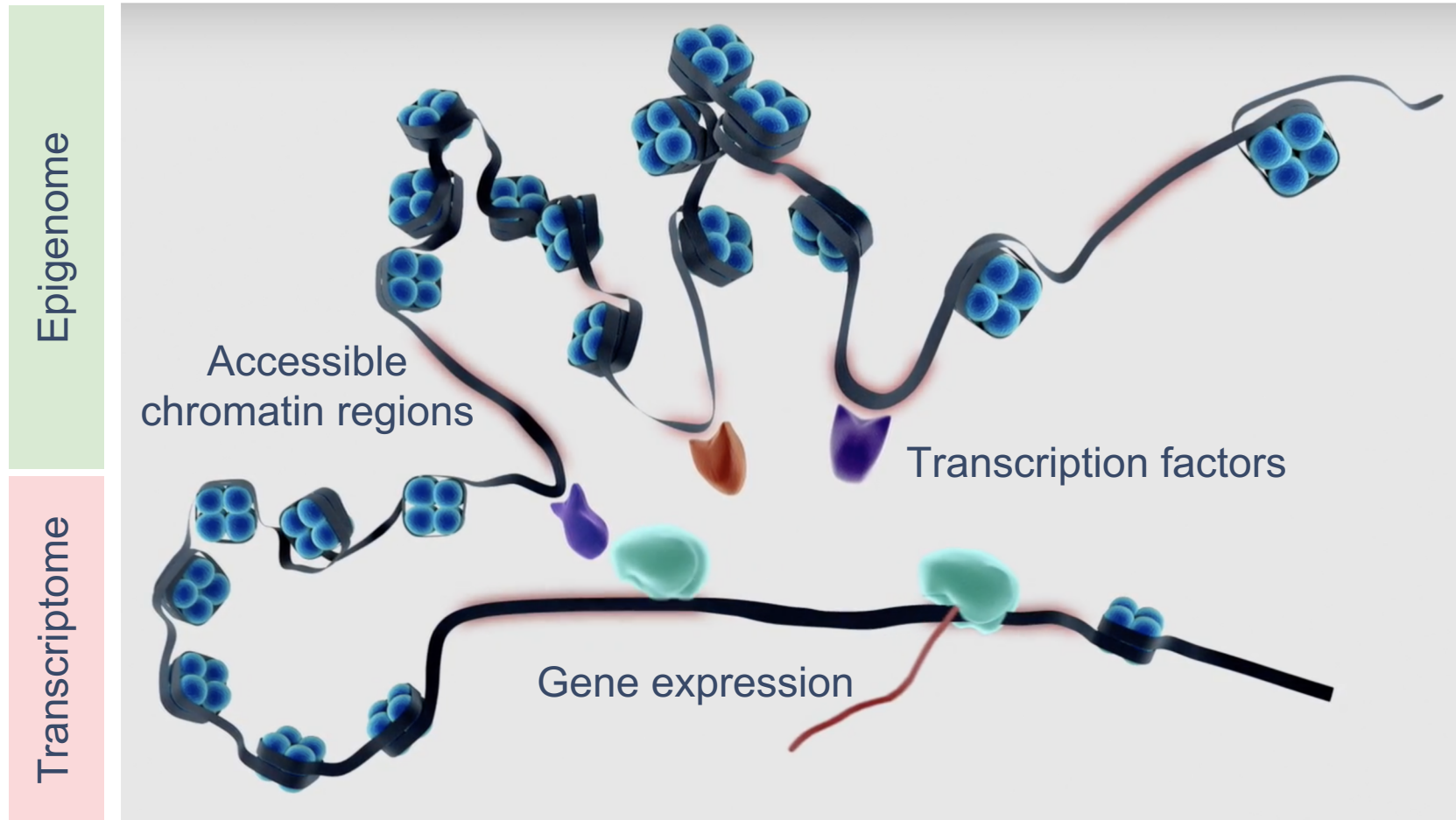


# Single Cell Multiome ATAC + Gene Expression

---

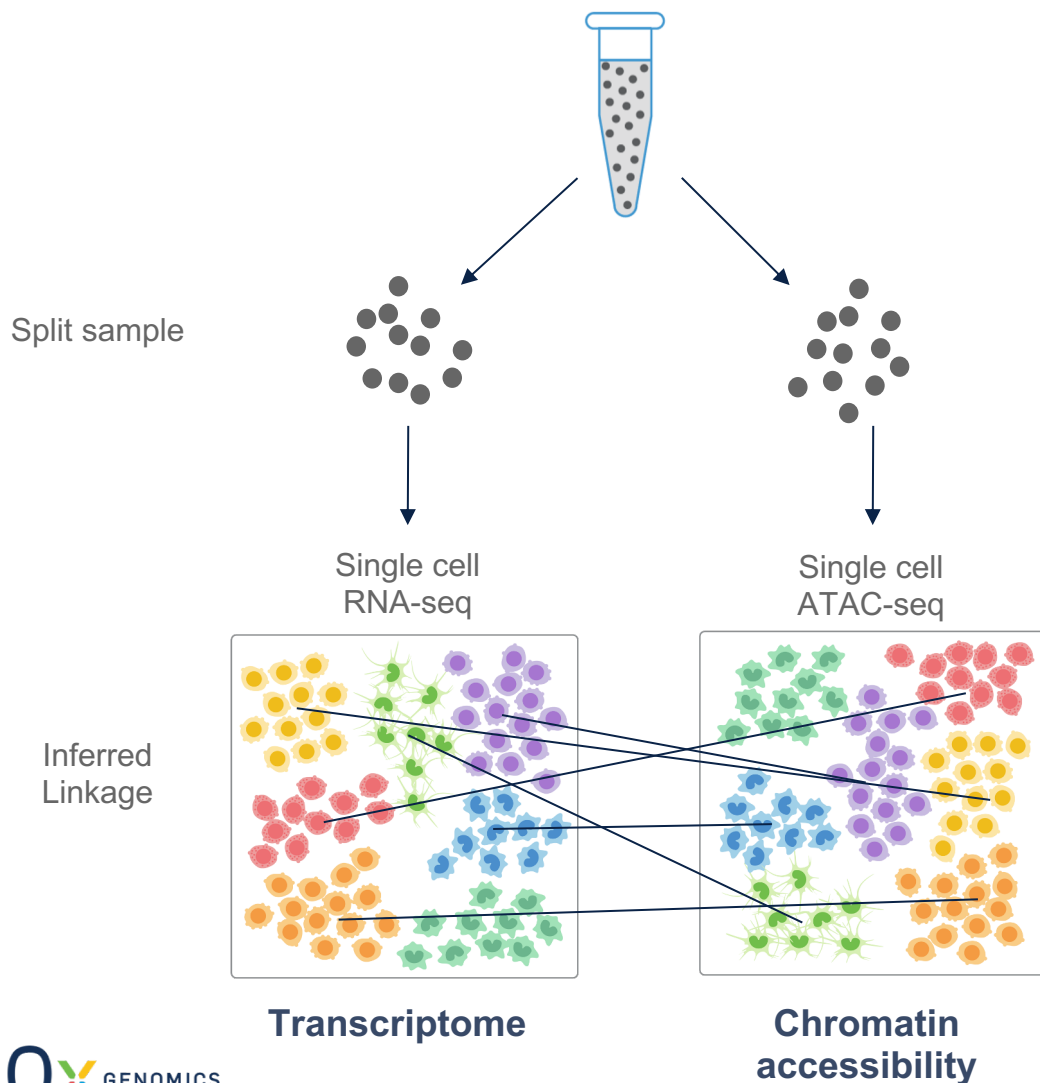


# Interplay between epigenetic programs and gene expression





# Computational approaches to integrate single cell transcriptomic and epigenomic data



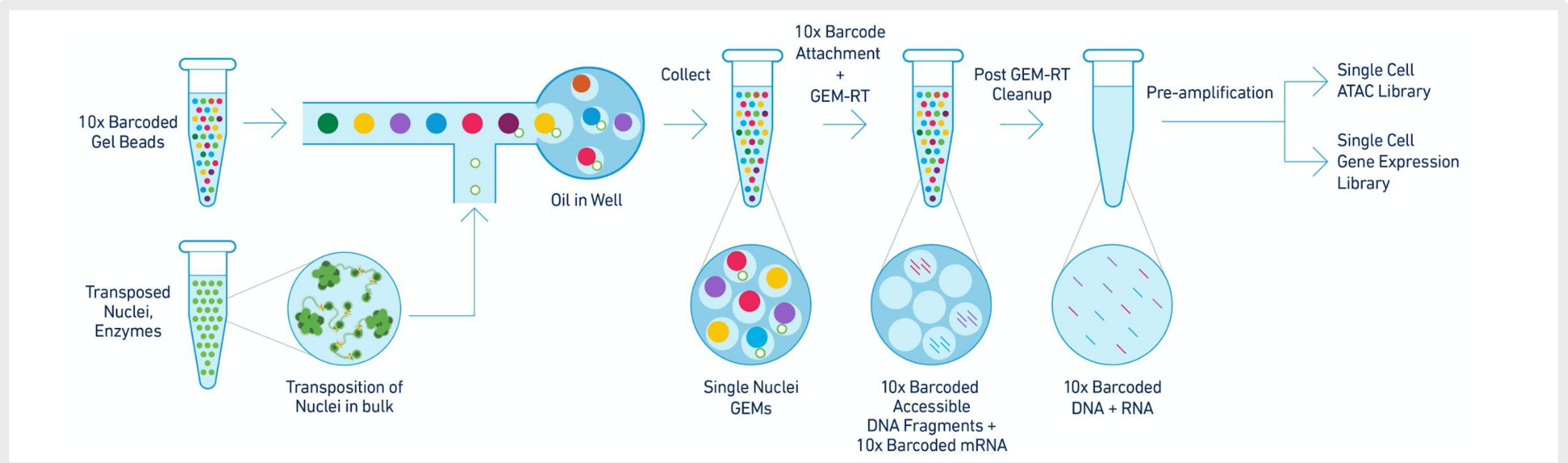
## Potential downsides:

- Chromatin accessibility is assumed to be positively correlated with gene expression
- Chromatin changes can precede gene expression (lineage priming)
- Open chromatin peaks not associated with promoters is discarded (rich in cell type information)

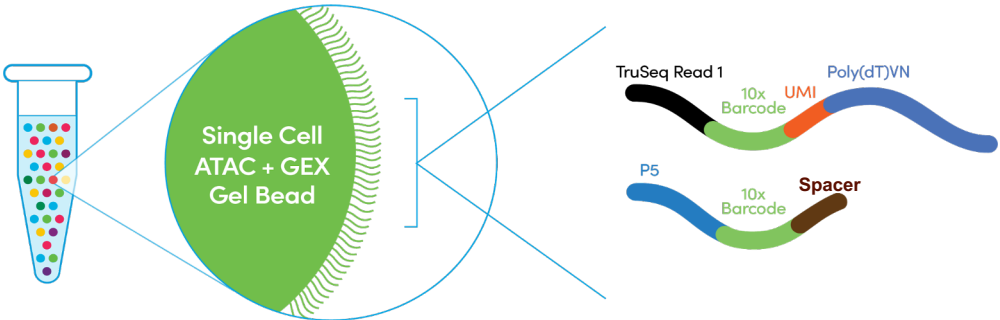
*Cell types may be misassigned  
Rare cells may be difficult to link*



# How it works



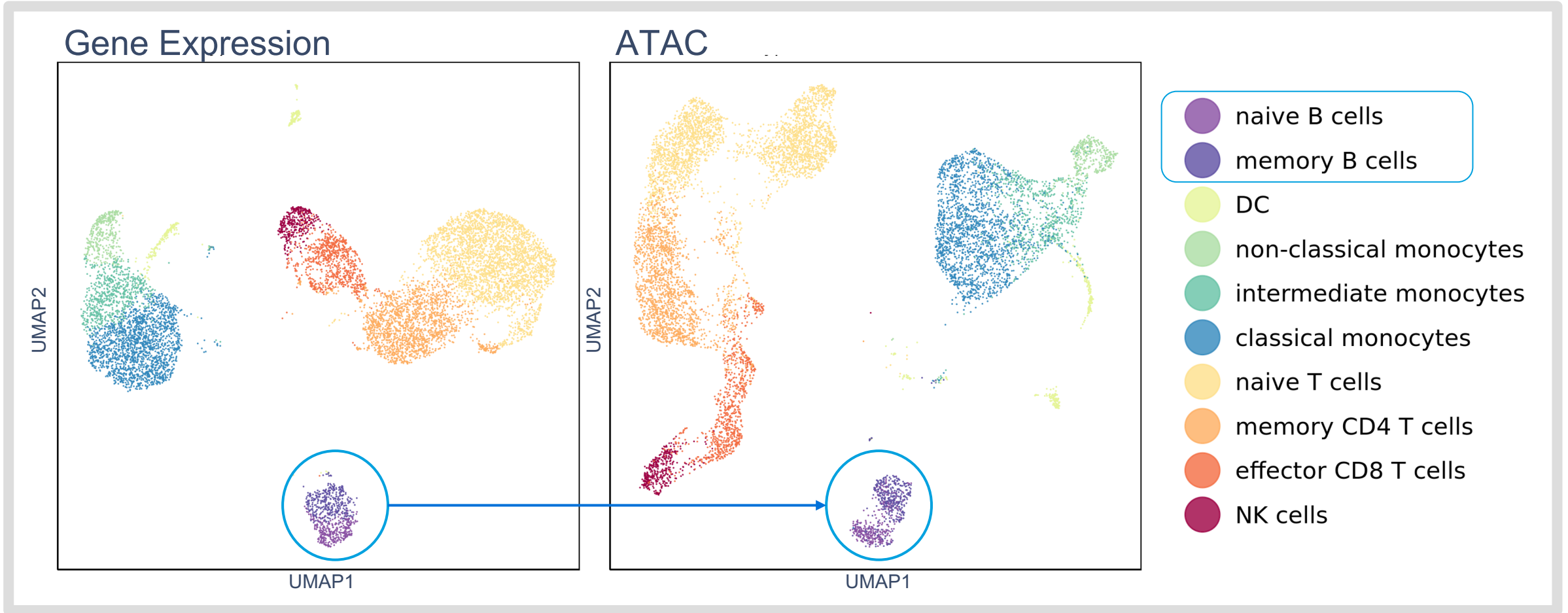
Multiome  
ATAC + GEX  
Gel Beads



Redesigned gel beads combine oligos for capturing 3' ends of mRNA & ATAC fragments

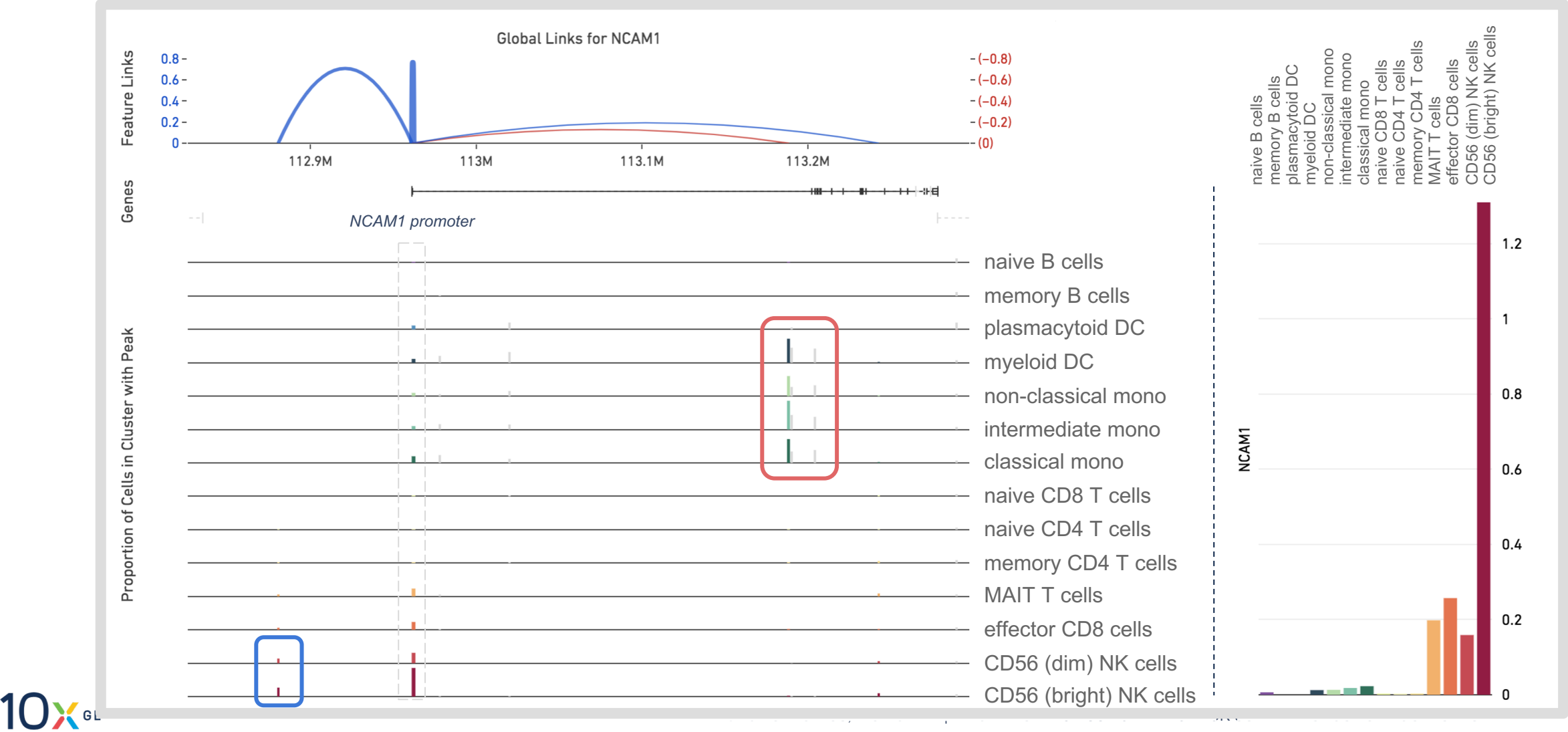


# Better separate PBMC populations on ATAC space





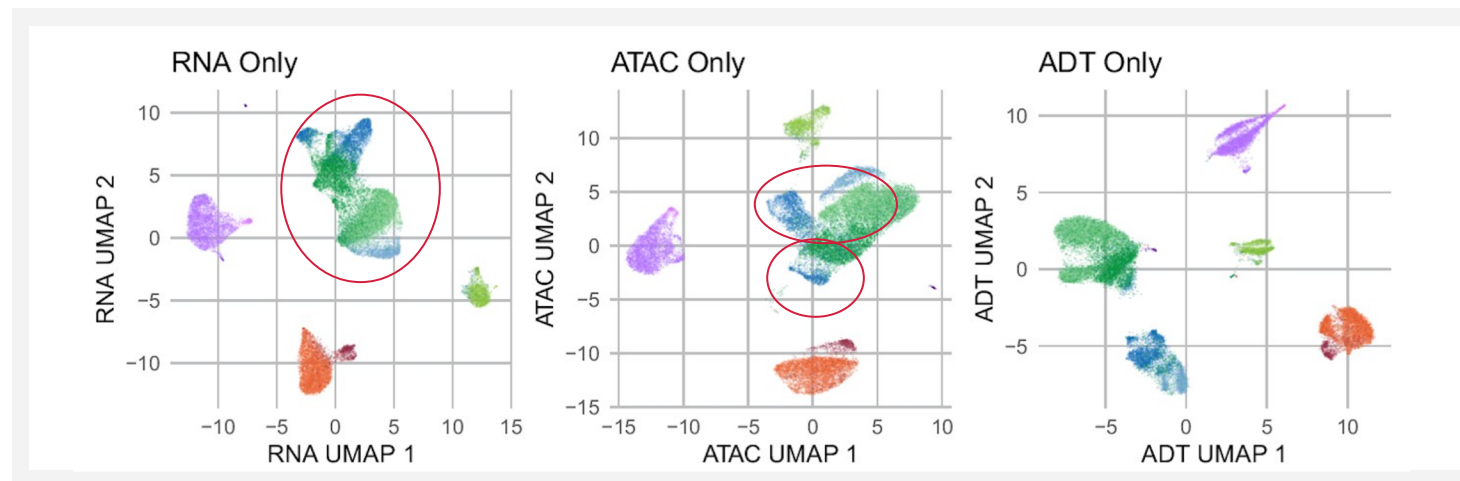
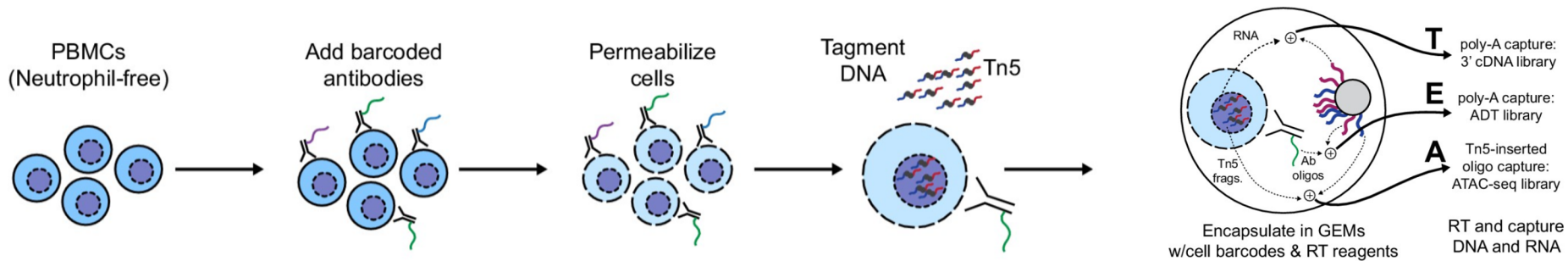
# Identify putative regulatory elements linked to a gene of interest





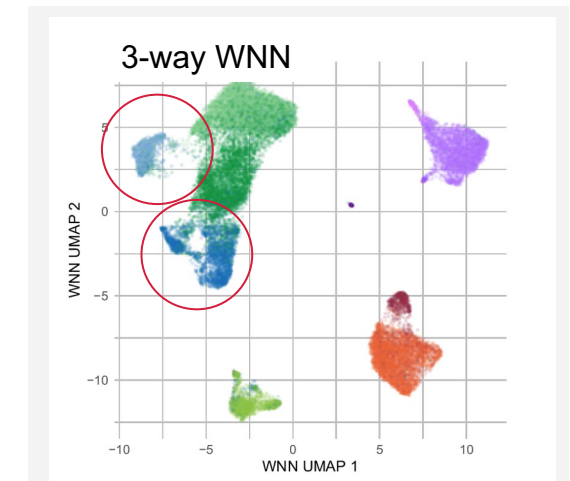
# Measuring additional modalities increases power to separate cell states

TEA-seq: Simultaneous detection of transcriptome, epitopes, and epigenome



Legend:

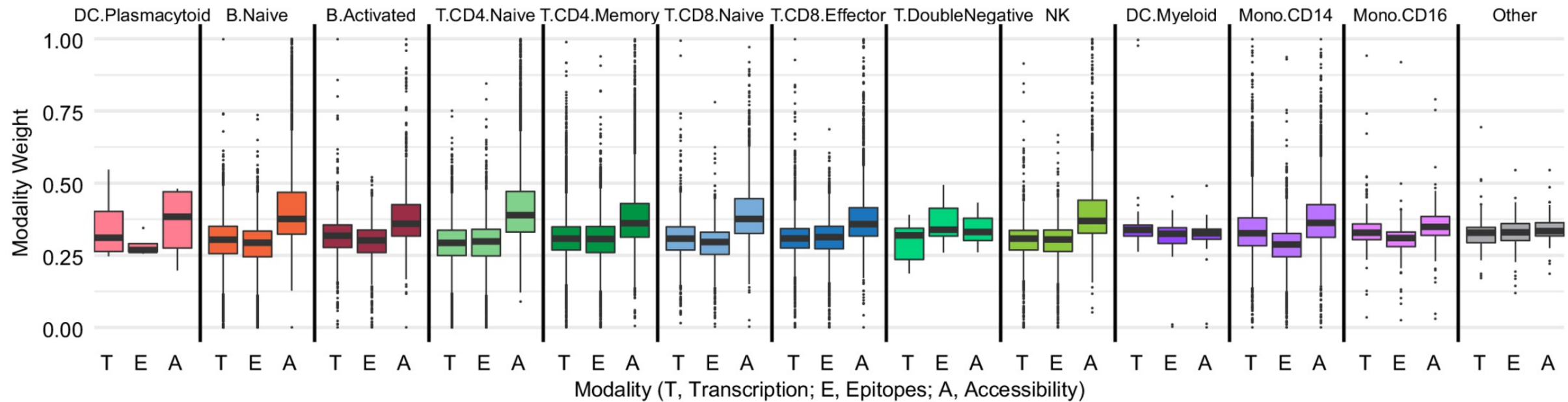
- B.Naive (orange)
- B.Activated (dark orange)
- T.CD4.Naive (light green)
- T.CD4.Memory (dark green)
- T.CD8.Naive (light blue)
- T.CD8.Effector (dark blue)
- T.DoubleNegative (medium green)
- NK (light green)
- Mono.CD14 (purple)
- Mono.CD16 (pink)
- DC.Myeloid (dark purple)
- DC.Plasmacytoid (red)



Improved resolution of CD4/CD8 T cell states when using RNA, ATAC, and protein data



# For many cell types, scATAC-seq largest contributor to improved cell state resolution





# Coming soon

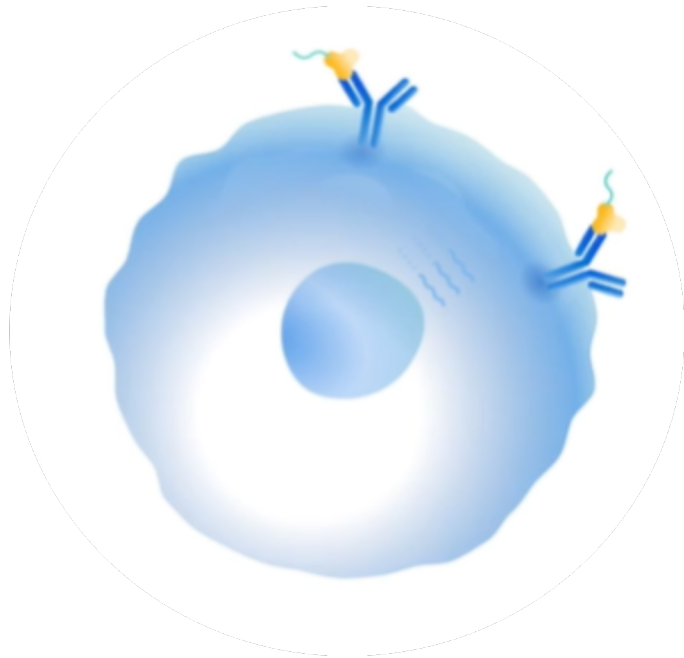
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# Antibody and T-cell Receptor Discovery at Massive Scale

## BEAM-Ab

Expected in 2H 2022



Single experiment on SARS-CoV-2 screened:

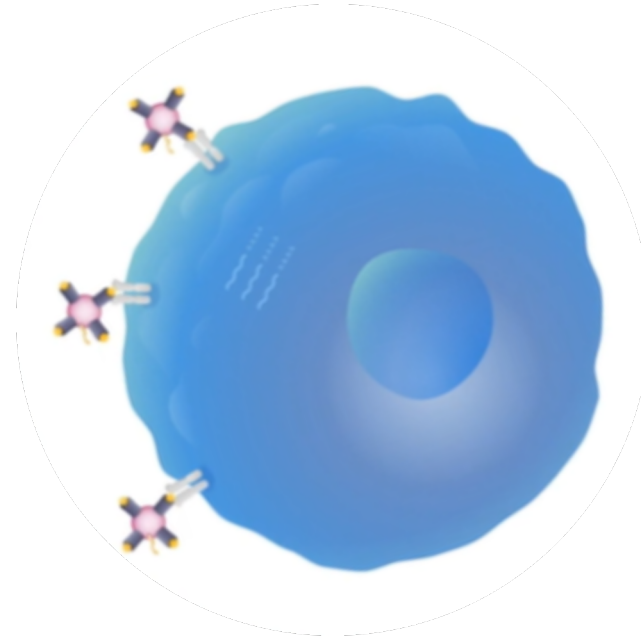
**4M+** B-cells in less than a week to yield

**55** human broadly neutralizing antibodies with pM affinity

**2** pan-coronavirus antibodies

## BEAM-T

Expected in 2H 2022



Find optimal T Cells for  
hyper-personalized cancer cell therapy



# 5' CRISPR

- Measure perturbation effects with multiomic readouts
- Increased flexibility for functional genomics studies
- Rapidly deploy existing Cas9 RNA libraries

Expected **Early 2022**





# Fixed RNA Profiling Kit

- Preserve biological states
- Flexible study designs
- New assay design for additional readouts in the future

Expected **Mid 2022**





# Chromium Nuclei Isolation Kits

- Standardize nuclei isolation
- Little to no optimization on most samples
- Built and optimized for 10x Genomics assays

Expected **Mid 2022**





# Xenium

## In Situ Platform

- Hundreds of gene targets
- Subcellular resolution
- Microscopy based read-out
- Fresh Frozen and FFPE
- Simultaneous RNA and proteins
- Throughput for larger cohorts

Expect **Late 2022**





# Thank you! Questions?

Your local 10x Team



**Eve-Marie Walter, Sales Executive**  
eve-marie.walter@10xgenomic.com



**Heather Eckart, Sales Associate**  
heather.eckart@10xgenomics.com



**Egon Ranghini, Science & Technology Advisor**  
egon.ranghini@10xgenomics.com



**Kara Pivarski, Field Application Scientist**  
kara.pivarski@10xgenomics.com



**Joseph Ipe, Sr. Field Application Scientist - Tissue Specialist**  
joseph.ipe@10xgenomics.com



**Leilani Marty Santos, Spatial Science & Technology Advisor**  
leilani.martysantos@10xgenomics.com