Biology at True Resolution

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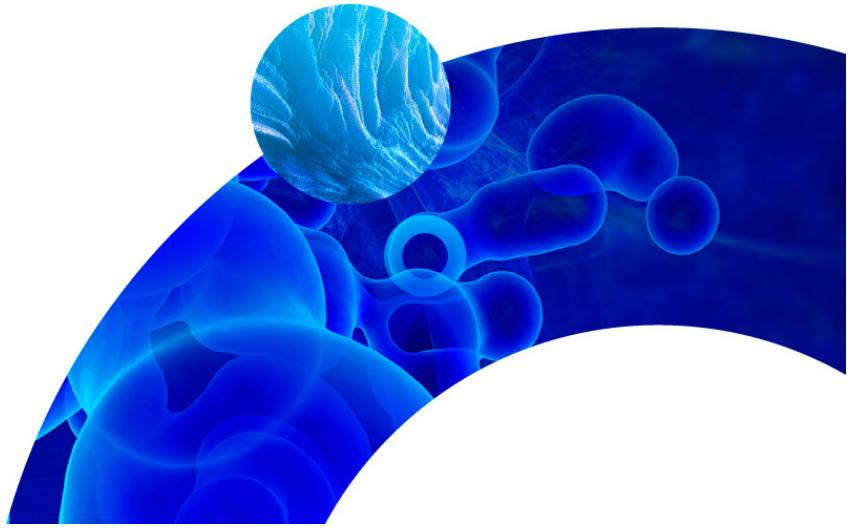


Biology at true resolution

10x Genomics mission

Accelerate the mastery of biology to advance human health

A comprehensive view of biological systems at needed resolution and scale

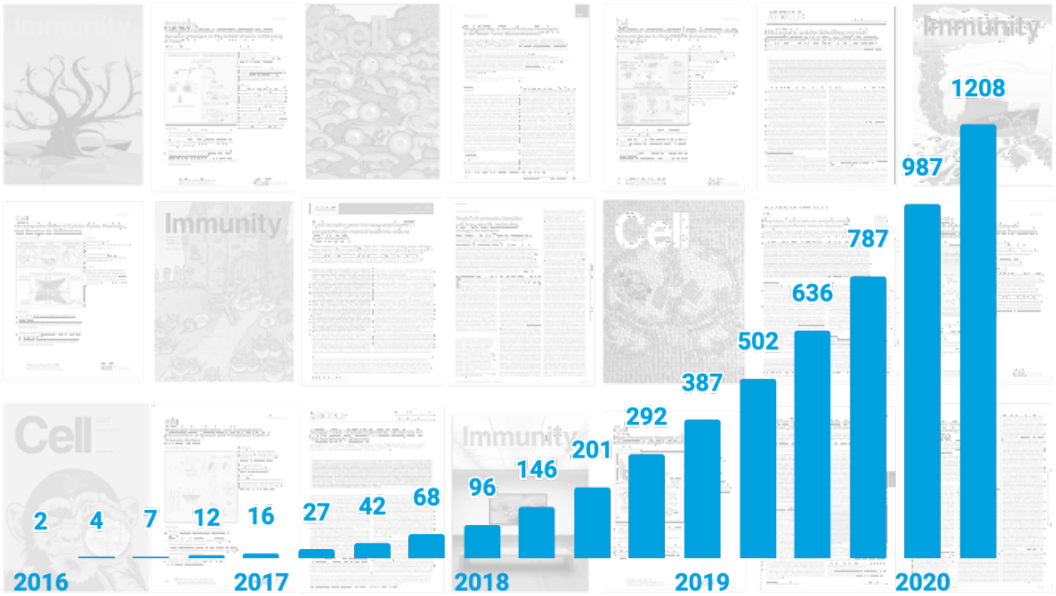
Measurement, understanding and mastery of the Immune System

Functional Genomics

10X GENOMICS

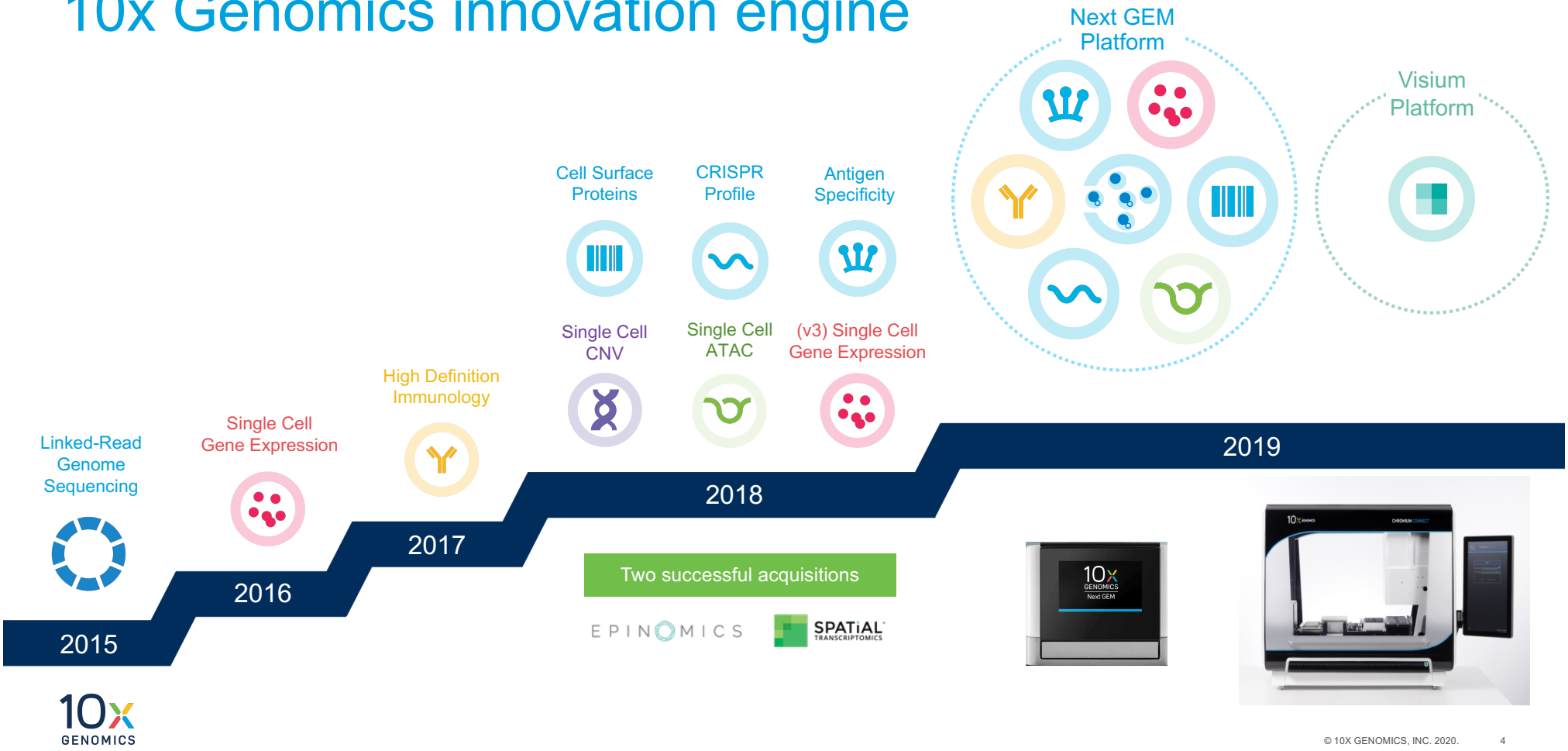
Biology at True Resolution

10x Genomics publications continue to scale



1,200+ publications

10x Genomics innovation engine



Solving Problems With Continued Innovation

10x Genomics provides complete solutions

Instruments

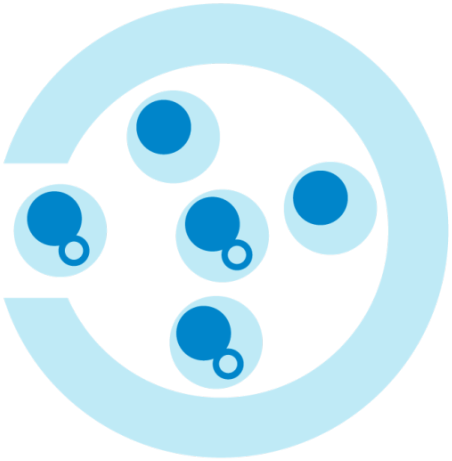
Consumables

Software

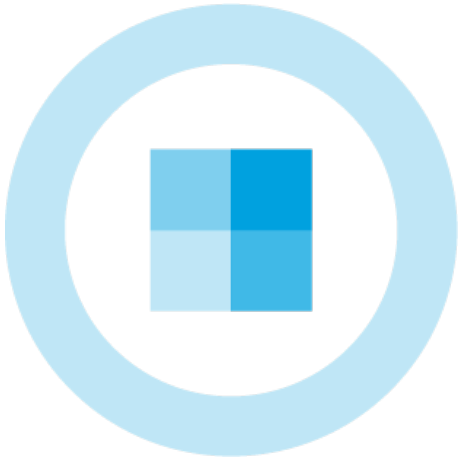
10x GENOMICS

Agenda

Chromium Platform

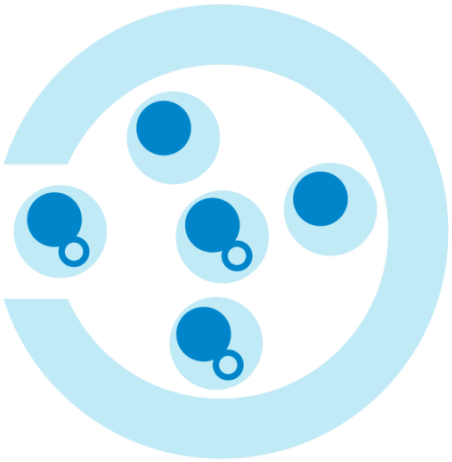


Visium Platform



Advances in Single Cell Genomics

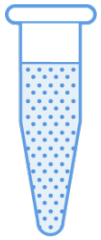
Chromium Platform



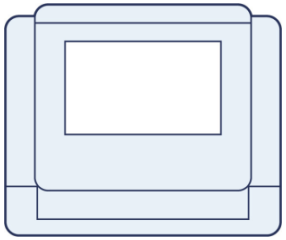
Visium Platform

Chromium Single Cell Solutions

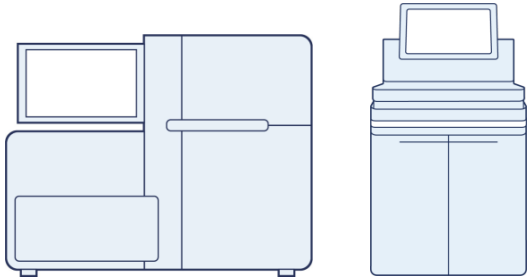
A transformative and easily integrated technology



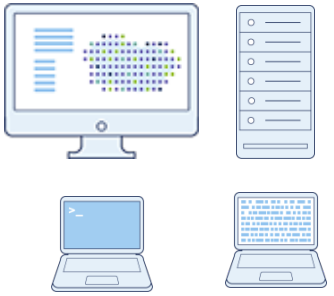
Flexible input
Single cell suspensions of 100s to 1000s of cells



Flexible throughput
Automated barcoding, then library construction



Single cell sequencing
Use existing short-read technologies



Turnkey analysis
Robust, secure, maintained, open-source software

10X GENOMICS

10x Genomics Single Cell Solutions

Single Cell Gene Expression

Single Cell Immune Profiling

Single Cell ATAC

- Flexible cell input: capture 100s to 1,000s of cells per channel
- Recover up to 65% of cells loaded
- Compatible with whole cells or nuclei* across range of cell sizes
- Enabled with Feature Barcoding technology (Gene Expression & Immune Profiling)

10x GENOMICS

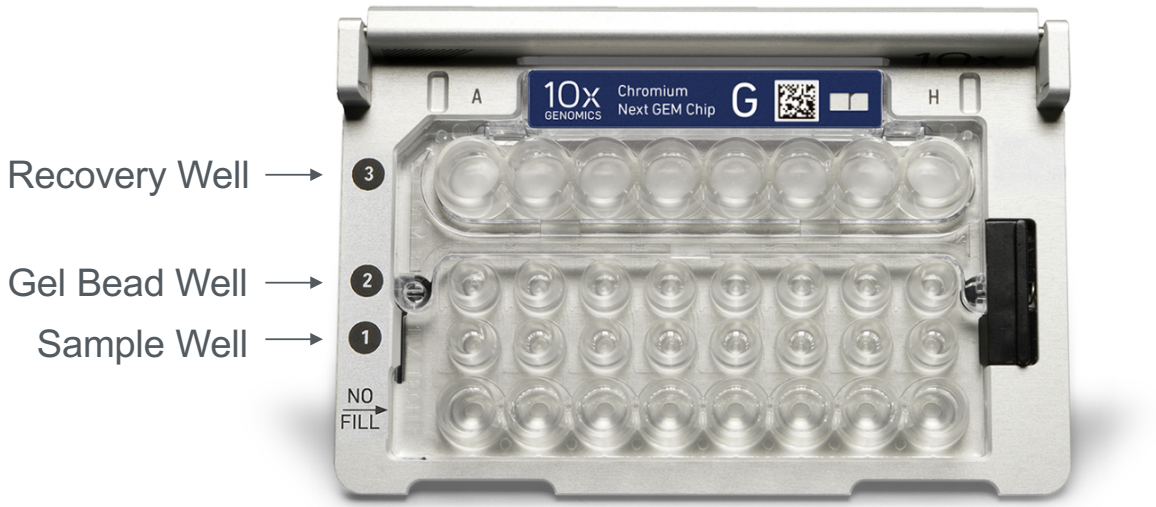
*Single Cell ATAC-seq input is compatible with nuclei only

Chromium Single Cell Solutions

Efficient and scalable cell capture

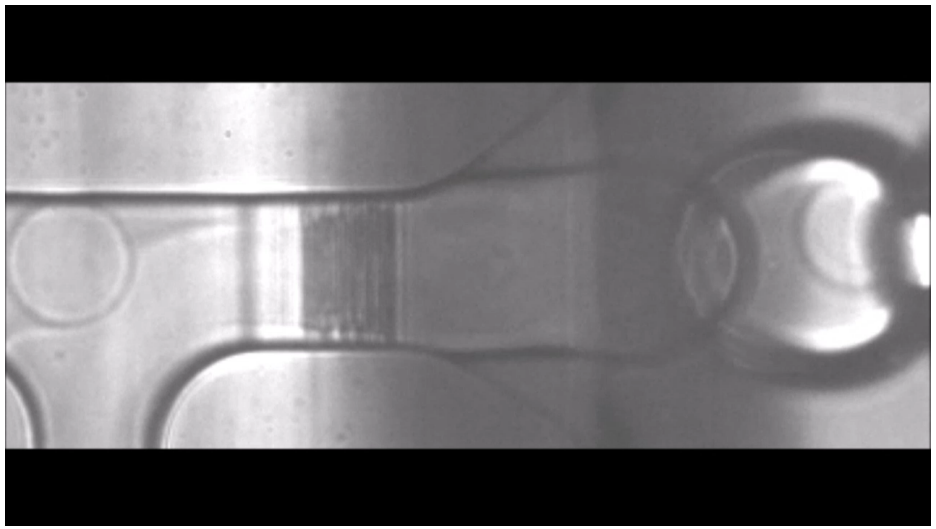
Easy loading

Single-use microfluidics chip



Chromium Single Cell Solutions

Efficient and scalable cell capture



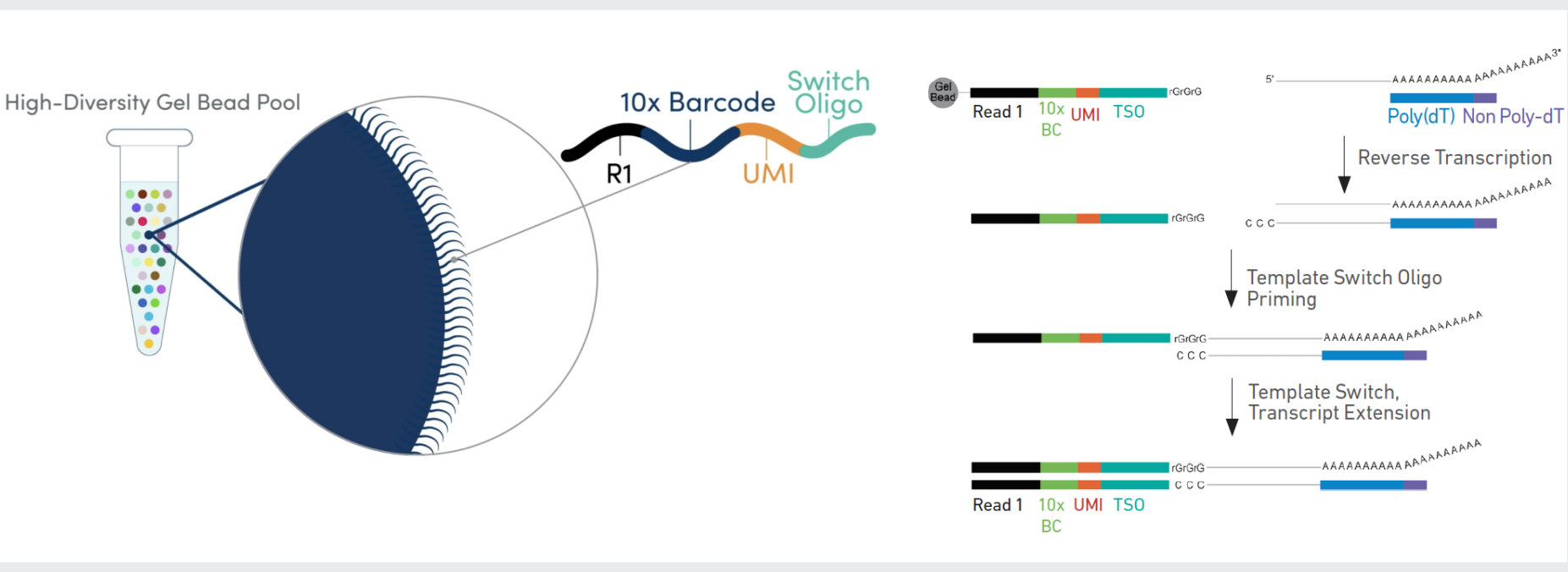
10x GENOMICS

Single Cell Immune Profiling

10X GENOMICS

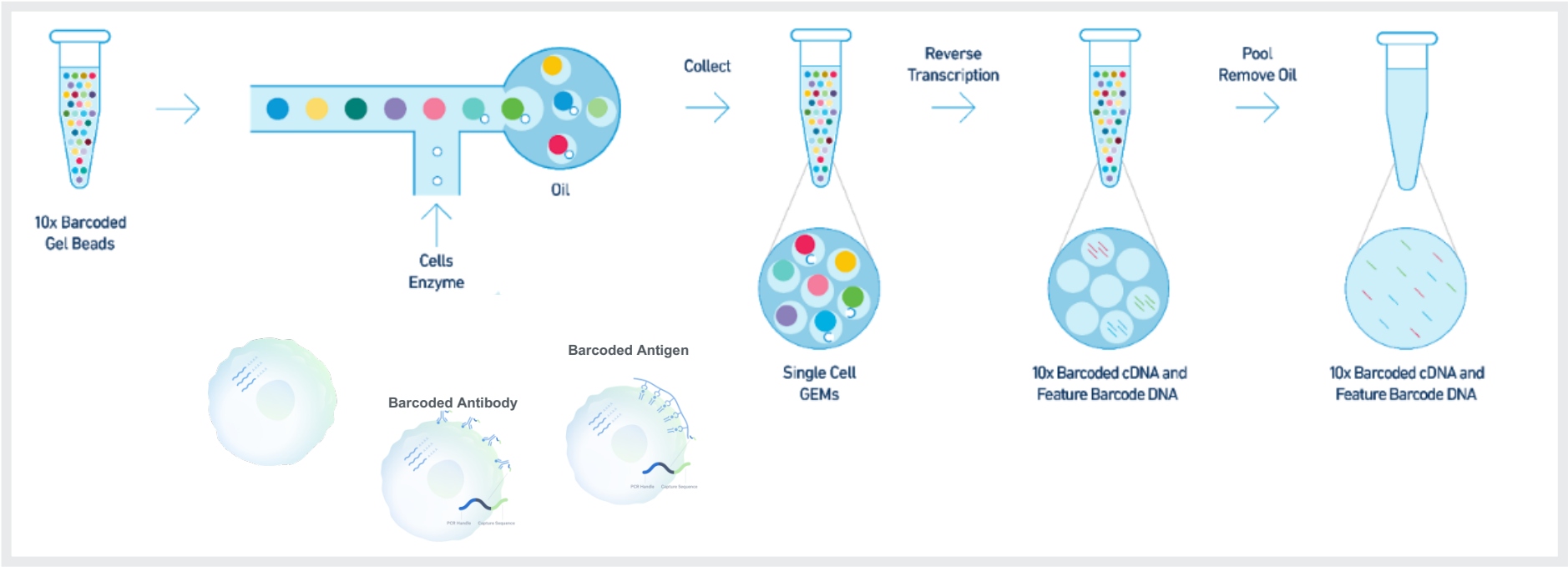
10x Genomics single cell technology

Barcoding single cell transcriptomes and other readouts

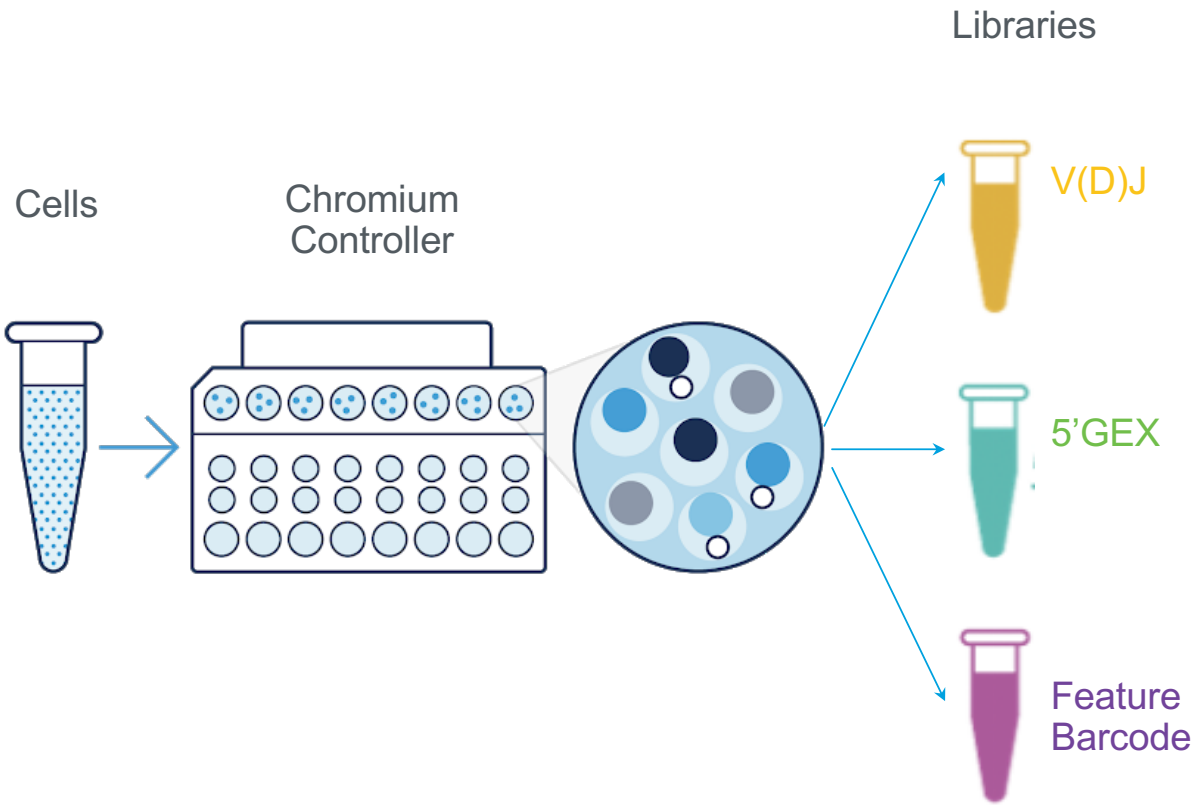


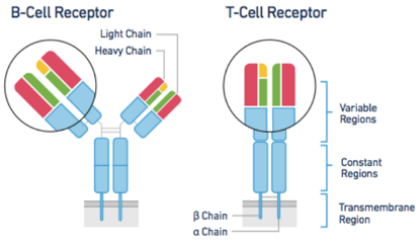
10x Genomics core technology for molecular barcoding and partitioning

Millions of parallel reactions



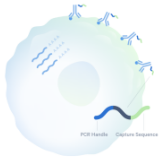
Single cell immune profiling library output



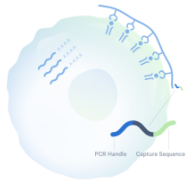


Full length paired chains

Whole Transcriptome Profiling
(or)
Targeted Gene Profiling



Surface protein profiling



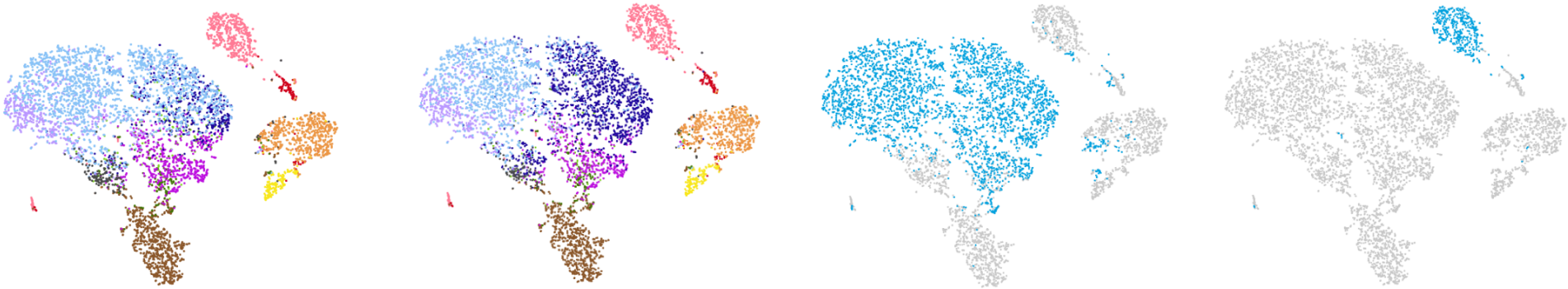
Antigen Specificity

10X GENOMICS

Multiomic profiling provides true resolution

Combined gene expression, cell surface protein and TCR / Ig clonotyping
for every single cell

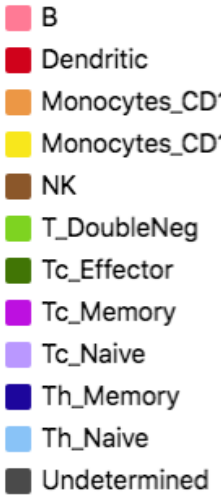
Targeted gene expression + **Cell surface protein** + **TCR clonotypes** + **Ig clonotypes**



10X GENOMICS

Intersection of cellular phenotyping with paired TCR repertoire profiling

TCR clonotypes can be assigned on a per cell basis



Cell type annotation based on Gene expression **and** the cell surface antibody profile

Cells with TCR clonotypes identified

TCR sequences are full length and paired

>clonotype2_consensus_1_alpha
AGATCAGAAGAGGAGGCTTCTCACCCTGCAGCAGGGACCTGTGA
GCATGGCATGCCCTGGCTTCCTGTGGGCACTTGTGATCTCCACCT
GTCTTGAATTTAGCATGGCTCAGACAGTCACTCAGTCTCAACCAG
AGATGTCTGTGCAGGAGGCAGAGACCGTGACCCTGAGCTGCACA
TATGACACCAGTGAGAGTGATTATTATTTATTCTGGTACAAGCAG
CCTCCCAGCAGGCAGATGATTCTCGTTATTCGCCAAGAAGCTTAT
AAGCAACAGAATGCAACAGAGAATCGTTTCTCTGTGAACTTCCAG
AAAGCAGCCAAATCCTTCAGTCTCAAGATCTCAGACTCACAGCTG
GGGGATGCCGCGATGTATTTCTGTGCTTATAGGAGCGTGTATTCA
GGAGGAGGTGCTGACGGACTCACCTTTGGCAAAGGGACTCATCT
AATCATCCAGCCCTATATCCAGAACCCTGACCCTGCCGTGTACCA
GCTGAGAGACT

>clonotype2_consensus_1_beta
AGTGACACTGATCTGGTAAAGCCCTCATCCTGTCCTGACCCTGCC
ATGGGCACCAGTCTCCTATGCTGGGTGGTCCTGGGTTTCCTAGGG
ACAGATCACACAGGTGCTGGAGTCTCCCAGTCTCCCAGGTACAAA
GTCACAAAGAGGGGACAGGATGTAGCTCTCAGGTGTGATCCAAT
TTCGGGTCATGTATCCCTTTATTGGTACCGACAGGCCCTGGGGCA
GGGCCCAGAGTTTCTGACTTACTTCAATTATGAAGCCCAACAAGA
CAAATCAGGGCTGCCCAATGATCGGTTCTCTGCAGAGAGGCCTGA
GGGATCCATCTCCACTCTGACGATCCAGCGCACAGAGCAGCGGG
ACTCGGCCATGTATCGCTGTGCCAGCAGCTTAGCGGGACAGGGG
GCACCAAGAGACCCAGTACTTCGGGCCAGGCACGCGGCTCCTGG
TGCTCGAGGACCTGAAAAACGTGTTCCCACCCGAGGTCGCTGTGT
TTGAGCCATCAGAAGCAGAGATCTCCCACACCCAAAAGGCCACA
CTGGTGTGCCTGGCCACAGGCTTCTACCCCGACCACGTGGAGCTG
AGCTGGTGGGTGAATGGGAAGGAGGTGCACAGTGGGGTCAGCAC
AGACCCGCAGCCCCTCAAGGAGCAGCCCGCCCTCAATGACTCCA
GATACTGCCTG

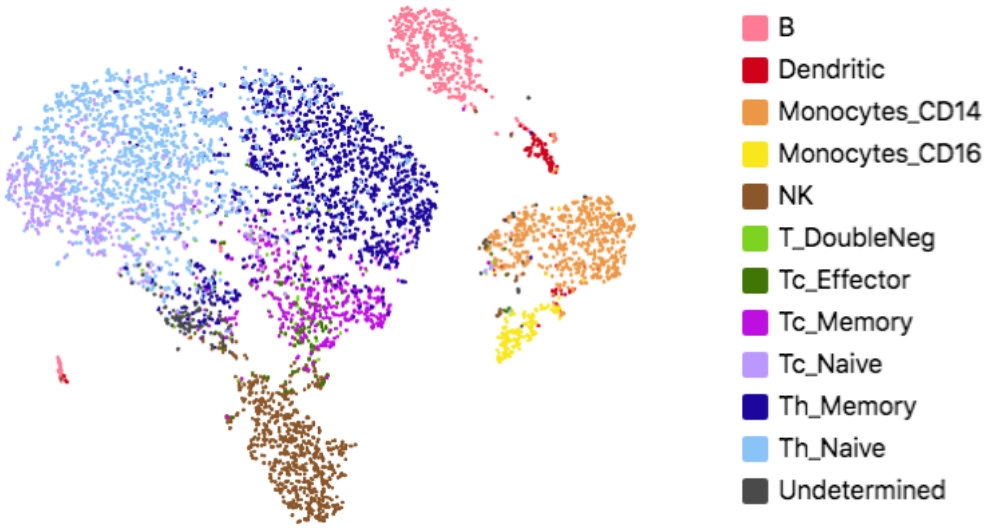
	V	D	J	C	#
α	TRAV27		TRAJ36	TRAC	3
β	TRBV12-3	TRBD1	TRBJ2-3	TRBC2	
α	TRAV21		TRAJ17	TRAC	2
β	TRBV6-3	TRBD1	TRBJ2-1	TRBC2	
α	TRAV12-3		TRAJ24	TRAC	2
β	TRBV15	TRBD1	TRBJ2-2	TRBC2	
α	TRAV17		TRAJ29	TRAC	2
β	TRBV14		TRBJ2-7	TRBC2	
α	TRAV8-2		TRAJ23	TRAC	2
β	TRBV12-3	TRBD1	TRBJ1-3	TRBC1	
α	TRAV8-1		TRAJ27	TRAC	2
β	TRBV12-3	TRBD2	TRBJ1-1	TRBC1	
α	TRAV38-2...		TRAJ17	TRAC	2
α	TRAV8-2		TRAJ8	TRAC	2
β	TRBV25-1		TRBJ1-1	TRBC1	
α	TRAV12-1		TRAJ48	TRAC	2
β	TRBV7-2	TRBD2	TRBJ2-7	TRBC2	
α	TRAV38-2...		TRAJ53	TRAC	2
β	TRBV6-6	TRBD2	TRBJ2-4	TRBC2	
α	TRAV2		TRAJ8	TRAC	2
β	TRBV4-3	TRBD1	TRBJ1-2	TRBC1	

Filter: Cluster

Cluster: Identity: Th_Memory

Intersection of cellular phenotyping with paired Ig repertoire profiling

B cell compartment mapped to Ig clonotypes



Cell type annotation based on Gene expression **and** the cell surface antibody profile

Cells with Ig clonotypes identified

Paired, full length Ig sequences

Paired, full length Ig sequences for B cell compartment

>clonotype1_consensus_1_H
TGGGGACCCAAAAACCACACCCCTCCTTGGGAGAATCCCCTAGATTACAGCTC
CTCACCATGGACTGGACCTGGAGCATCCTTTTCTTGGTGGCAGCAGCAACAGG
TGCCCACTCCCAGGTTCAGCTGGTGCAGTCTGGAGCTGAGGTGAAGAAGCCT
GGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGTTACACCTTTACCAGCTC
CATCTCTGGTATTACCTGGGTGCGACAGGCCCCTGGACAAGGGCTTGAGTGGA
TGGGATGGGTCAGCGGTGACAATGGTGACACAAAGTATGCACAGAAGTTCCAG
GGCAGAGTCACCATGACCACAGACACATCCACGAGTACAGGCTACATGGAGCT
GAGGAGCCTGAGATCTGACGACACGGCCGTGTATTACTGTTCGAGAGACGTCA
GTCCCCACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAGCACCCACCAA
GGCTCCGGATGTGTTCCCCATCATATCAGGGTGCAGACACCCAAAGGATAACA
GCCCTGTGGTCCTGGCATGCTTGATAACTGGGTACCACCCAACGTCCGTGACT
GTCACCTGGTACATGGGGACACAGAGCCAGCCCCAGAGAACCTTCCCTGAGAT
ACAAAGACGGGACAGCTACTACATGACAAGCAGCCAGCTCTCCACCCCCCTCC
AGCAGTGGCGCCAAGGCGAGTACAAATGCGTGGTCCAGCA

>clonotype1_consensus_1_K
GCCCCTCCAGGCCACGACCAGCTGTTTGGATTTTATAAACGGGCCGTTTGCAT
TGTGAACTGAGCTACAACAGGCAGGCAGGGGCAGCAAGATGGTGTTGCAGAC
CCAGGTCTTCATTTCTCTGTTGCTCTGGATCTCTGGTGCCTACGGGGACATCGT
GATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC
ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAATAAGGAGTAC
TTAGCTTGGTACCAGCAGAAACCAGGACAGTCCCCTAAGCTGCTCATTTACTGG
GCATCCACCCGGGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTG
GGACAGATTTCACTCTCACCATCAGCGGCCTGCAGGCTGAAGATGTGGCAGTT
TATTACTGTCAGCAATATTCTAGTACTCCGTACACTTTTGGCCAGGGGACCAAG
CTGGAGATCAAACGAACTGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCT
GATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTGCTGAATAACTTC
TATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATCGGG
TAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAGCACCTACAGC
CTCAGCAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAA

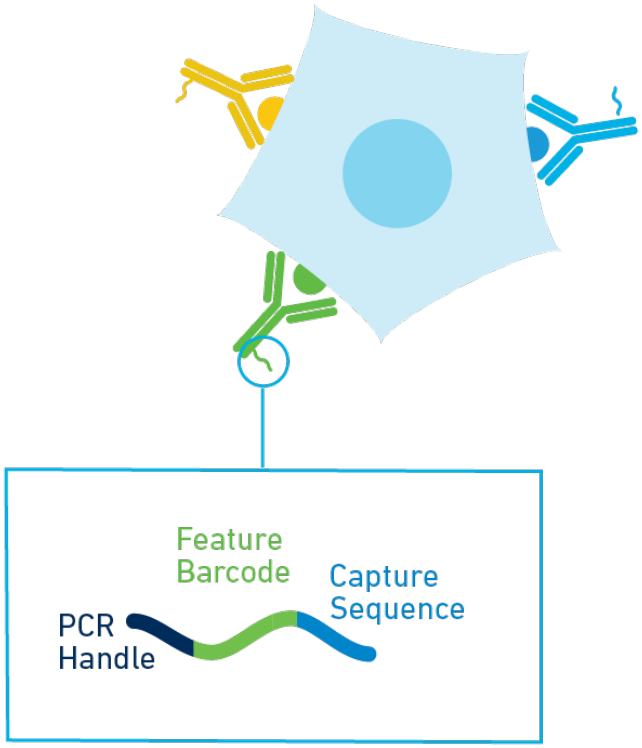
	V	D	J	C	#
H	IGHV1-18	IGHD2-2	IGHJ4	IGHD	
κ	IGKV1-9		IGKJ1	IGKC	4
κ	IGKV4-1		IGKJ2	IGKC	
H	IGHV3-72	IGHD3-9	IGHJ4	IGHM	
κ	IGKV1-16		IGKJ4	IGKC	2
H	IGHV3-43	IGHD6-13	IGHJ4	IGHM	
λ	IGLV2-14		IGLJ2	IGLC2	2
H	IGHV4-39	IGHD3-10	IGHJ4	IGHM	
H	IGHV5-51	IGHD2-8	IGHJ6	IGHM	
λ	IGLV1-44		IGLJ3	IGLC2	
λ	IGLV3-19		IGLJ2	IGLC2	
H	IGHV3-11	IGHD1-1	IGHJ4	IGHM	
λ	IGLV1-51		IGLJ2	IGLC2	
H	IGHV3-30	IGHD3-22	IGHJ6	IGHM	
λ	IGLV3-1		IGLJ2	IGLC2	
H	IGHV3-33	IGHD6-6	IGHJ6	IGHA1	
λ	IGLV2-14		IGLJ3	IGLC3	
H	IGHV2-5	IGHD6-19	IGHJ4	IGHG2	
H	IGHV3-72	IGHD6-19	IGHJ4	IGHG2	

Filter Cluster

Cluster Identity: B

Single Cell Immune Profiling

Feature Barcoding Technology: Cell Surface Protein



BioLegend®
Enabling Legendary Discovery™

- **TotalSeq™- C** Oligo Conjugated Antibodies specific for the Chromium Single Cell Immune Profiling Solution with Feature Barcoding Technology
- Menu focus on antibodies for immune profiling in human, custom also available
- Enables highly multiplexed, simulations profiling of cell surface proteins
- For more info: https://www.biolegend.com/totalseq

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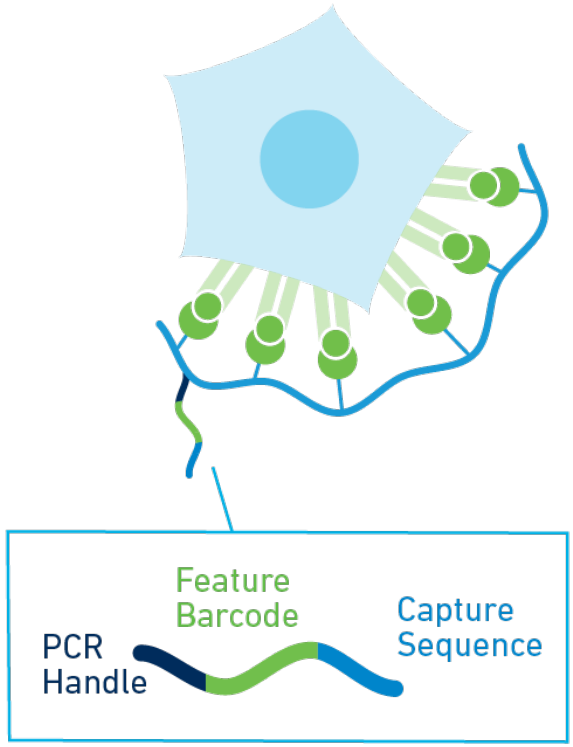
Single Cell Immune Profiling

Feature Barcoding Technology: Antigen Mapping



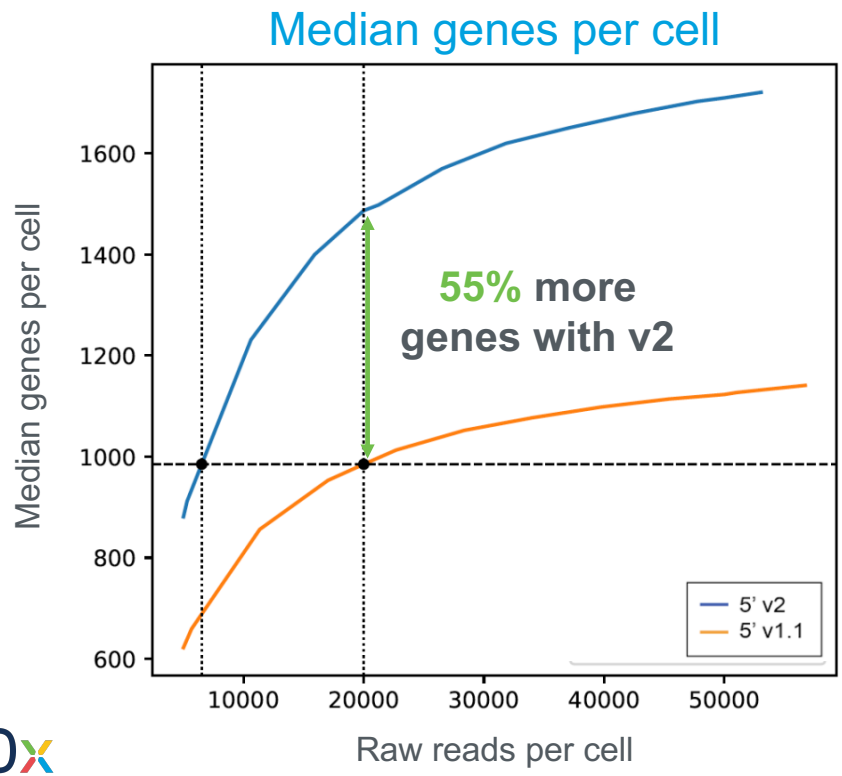
IMMUDEX
PRECISION IMMUNE MONITORING

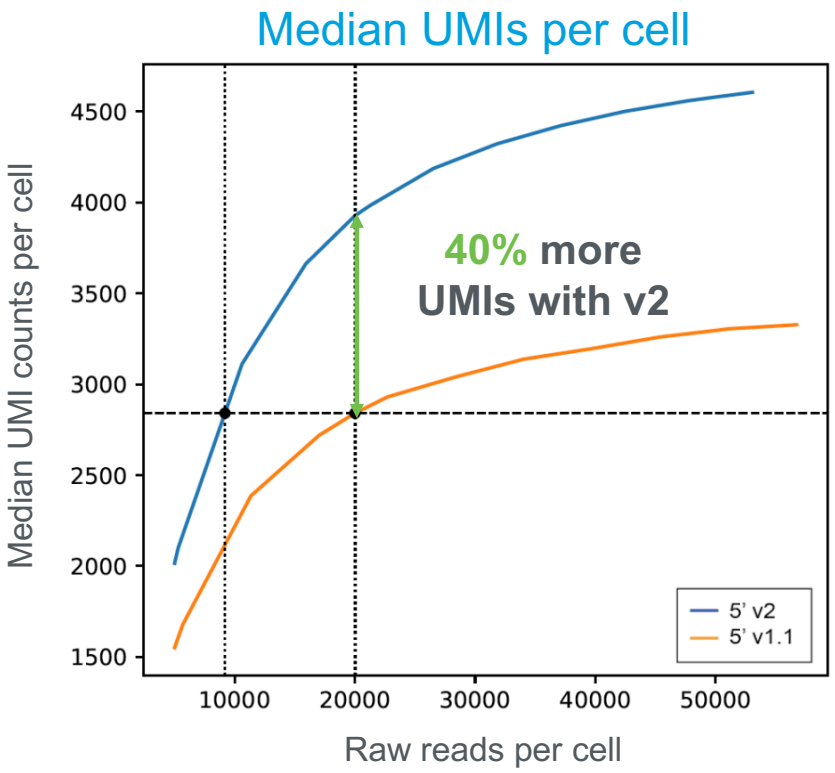
- **dCODE™ Dextramer®** Oligo Conjugated Dextramers specific for the Chromium Single Cell Immune Profiling Solution with Feature Barcoding Technology
- Menu focus on conventional T cells (MHC I + MHC II)
- Enables highly multiplexed TCR pMHC antigen specificity
- For more info: http://www.immudex.com/products/dcode-dextramer.aspx

10X GENOMICS

Huge gains in gene expression sensitivity in v2

1,000 Human PBMCs

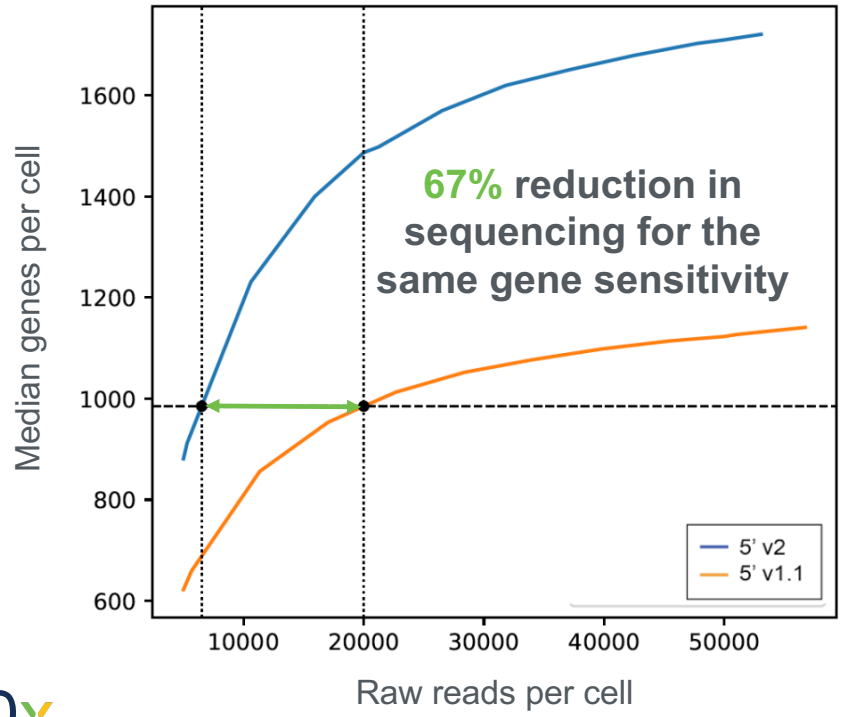




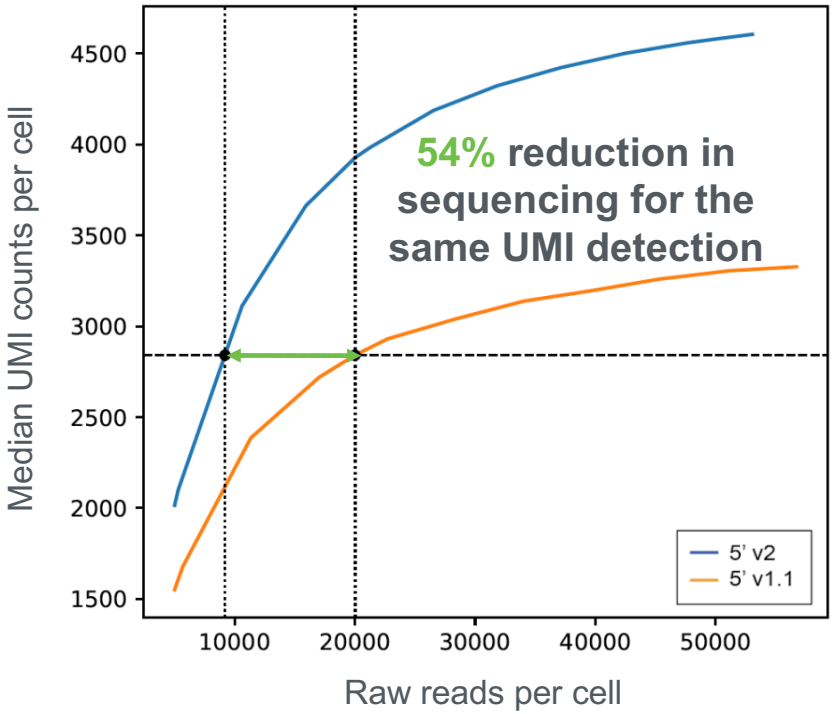
...allows for reduced sequencing depths

1,000 Human PBMCs

Median genes per cell



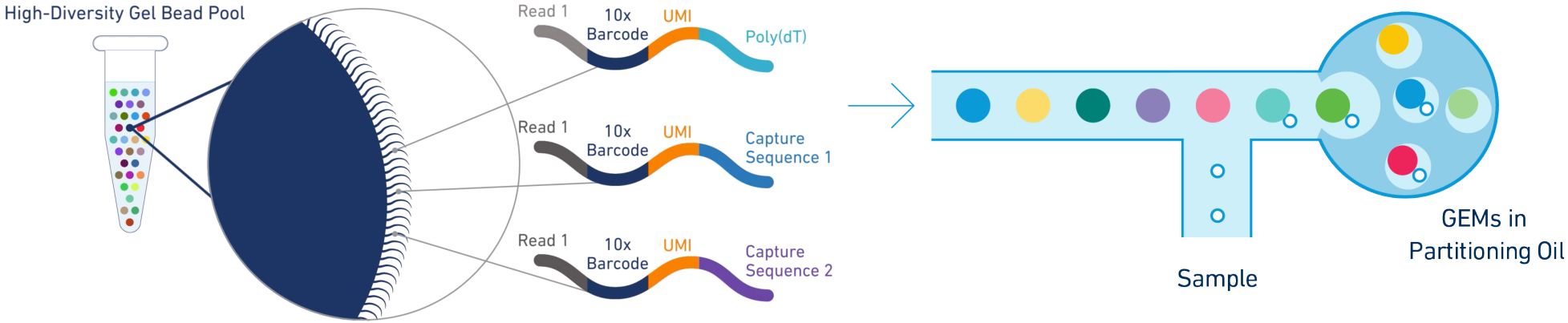
Median UMIs per cell



Single Cell Gene Expression

10X GENOMICS

How it works

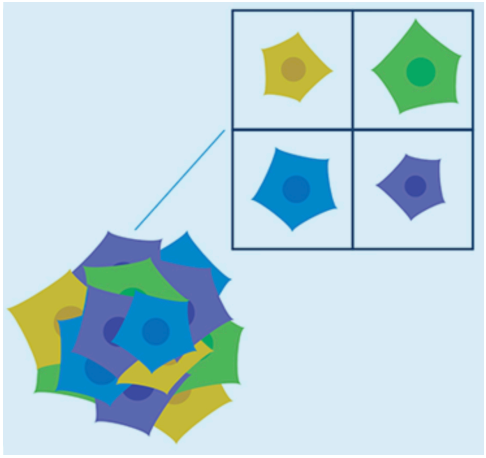


10x Barcode = Cell ID

GEMs = Gel beads in EMulsions

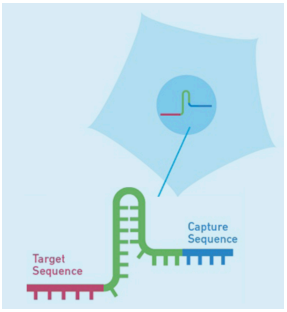
Multimodal measurements from the same cell

Feature Barcoding technology

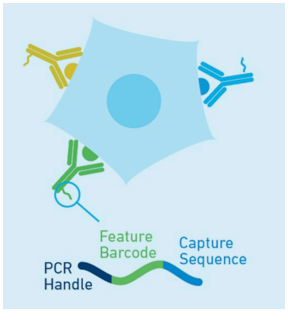


Gene Expression

+



CRISPR Screening



Cell Surface Protein

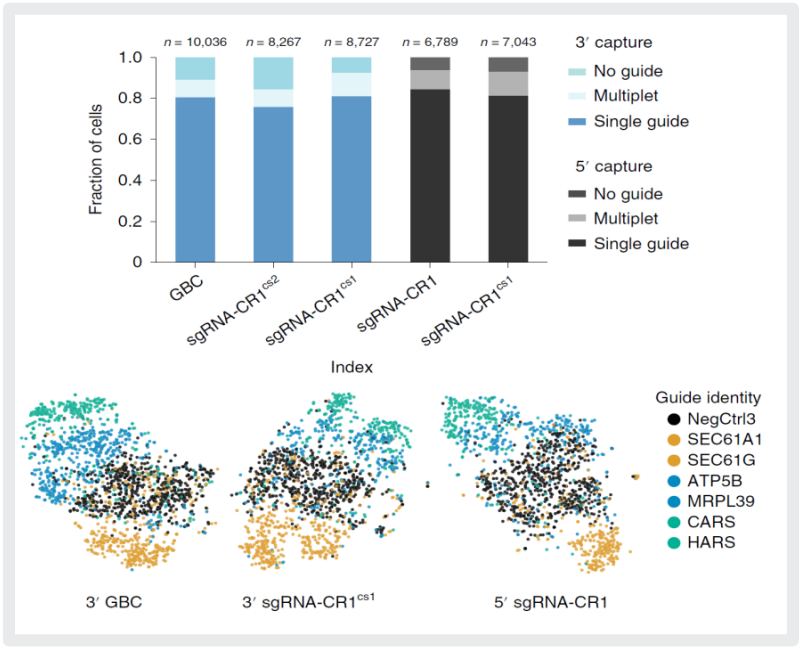
10x GENOMICS

Combinatorial single-cell CRISPR screens by direct guide RNA capture and targeted sequencing

nature biotechnology

Direct guide RNA capture improves efficacy of pooled CRISPR interference screens

- Presentation of direct capture of guide RNAs for pooled single cell CRISPR screens using 10x Genomics Chromuim Single Cell Gene Expression 3'RNA and 5'RNA solutions.
- Greater versatility demonstrated by direct priming of guide RNAs versus indirect identification by index transcipts (Perturb-Seq)
- The authors demonstrated the utility of the direct capture approach for high-throughput investigation of interactions between the cellular processes involved in cholesterol biogenesis and DNA repair.
- Targeted gene expression panels based on hybridization-based capture approach enabled the cost-effective analysis of focused panel of genes at single cell resolution.



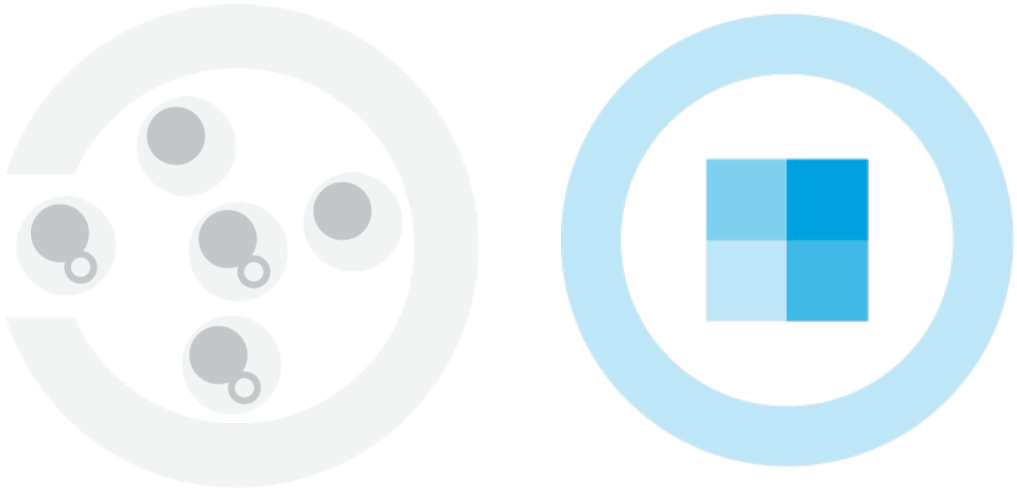
Replogle et al 2020, nature biotechnology, https://doi.org/10.1038/s41587-020-0470-y

10X GENOMICS

Advances in Spatial Genomics

Chromium Platform

Visium Platform



Gain a Complete View of Biology with Single Cell and Spatial Analysis

Complementarity of single cell and spatial methods from 10x Genomics

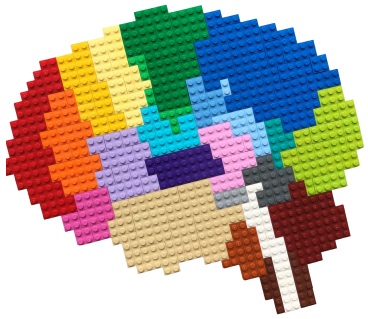
Bulk RNA-seq

- Get a general idea about gene expression but lacks cellular or spatial resolution

Single Cell RNA-seq

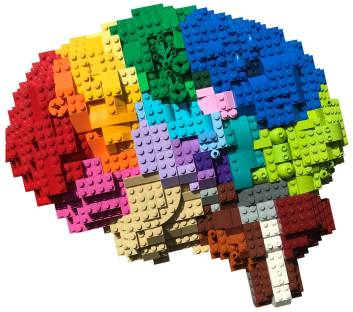
- Identify distinct cell types and their gene expression profiles

Spatial Transcriptomics



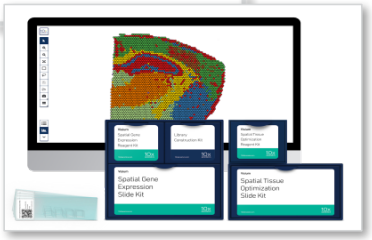
- Visualize gene expression profiles with tissue context

Functional Tissue



- Single cell plus spatial analysis provides the spatial organization of distinct cell types and their gene expression profiles

Chromium Single Cell Gene Expression Products



Visium Spatial Gene Expression Products

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Images and concept courtesy of Bo Xia, NYU School of Medicine

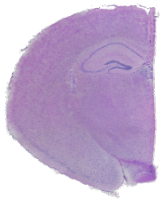
Visium Platform: Rich Spatial Characterization

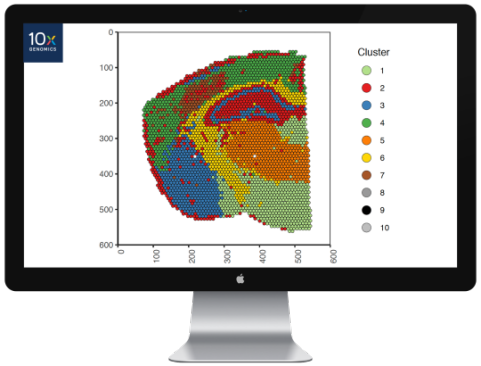
Sample

Visium consumables

Next generation sequencer

Analysis and visualization software





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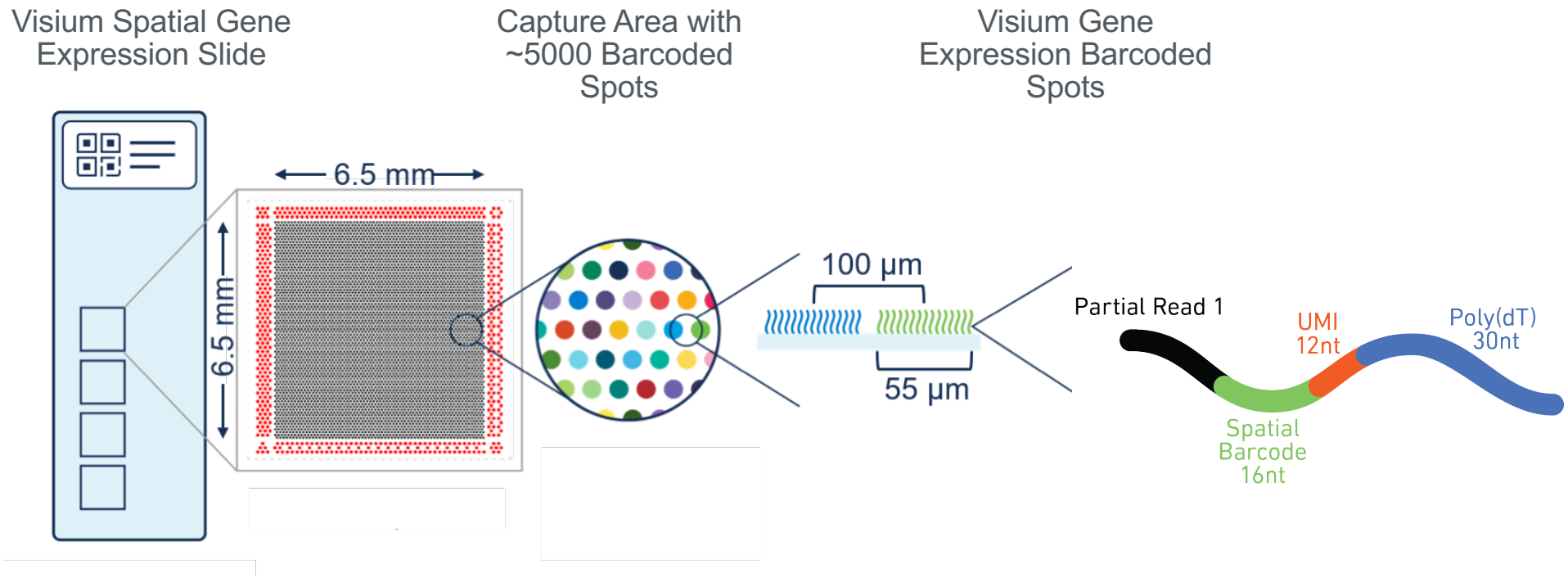
Unbiased gene expression at high spatial resolution

Utilizing poly-A capture and unique spatial barcodes



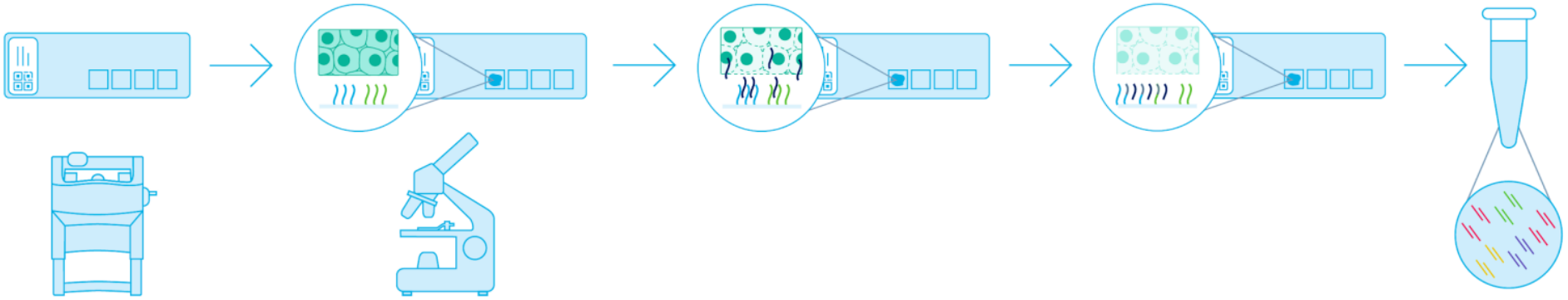
Visium Sample & Library Prep Workflow

Sample Prep
Cryosectioned tissue slice

Stain and Visualize
H&E stain and image

Capture RNA
Permeabilize cells, capture mRNA

Library Prep
Digest tissue and collect labeled molecules



< 1 Day (many available stopping points)

From sectioned tissue to sequence-ready libraries

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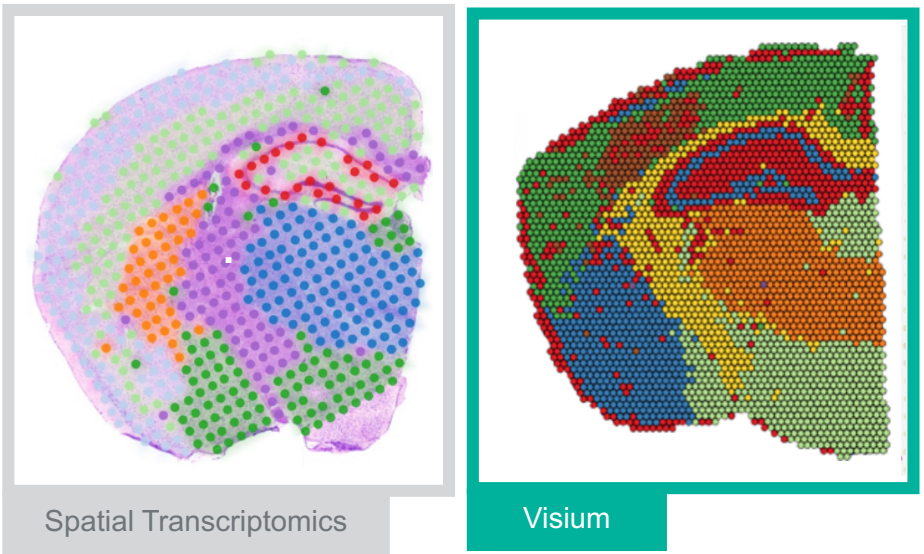
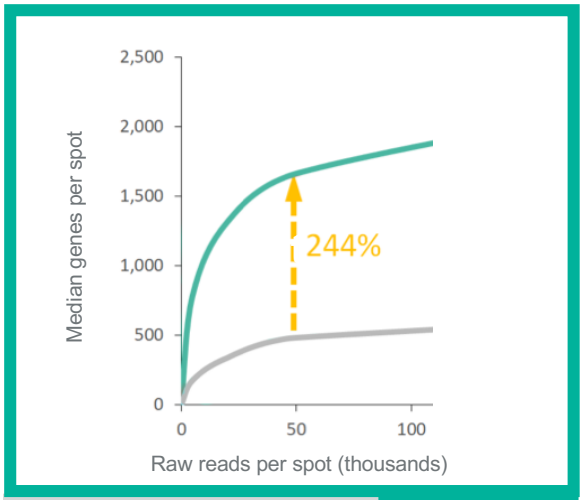
Visium Improvements

Increased resolution



Spatial Transcriptomics | Visium

Increased sensitivity



Spatial Transcriptomics | Visium

Shortened workflow

Spatial Transcriptomics — 3 DAYS

Visium — 1 DAY

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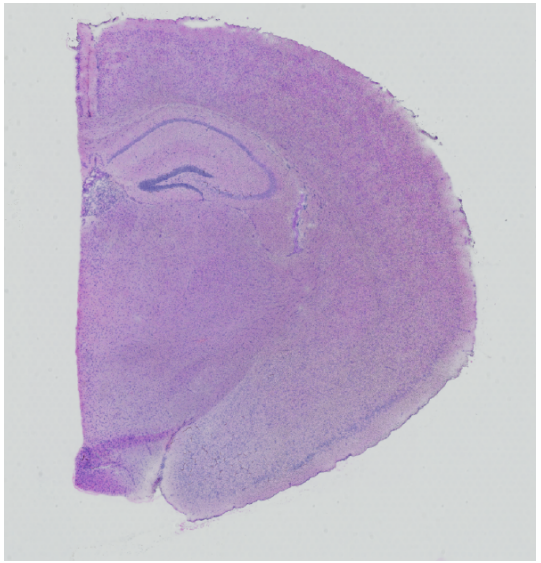
Visium Spatial Gene Expression

Mouse Brain



H&E Tissue Section

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Image or Gene Expression Driven Analysis of Spatial Data

Start with the Gene Expression Data or Image data of the Same Section

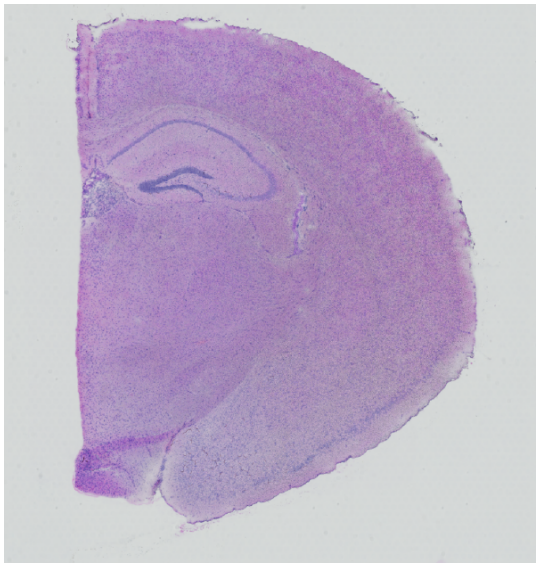
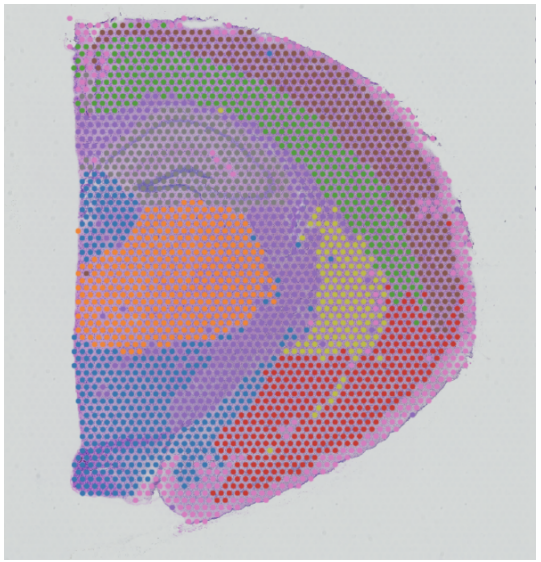
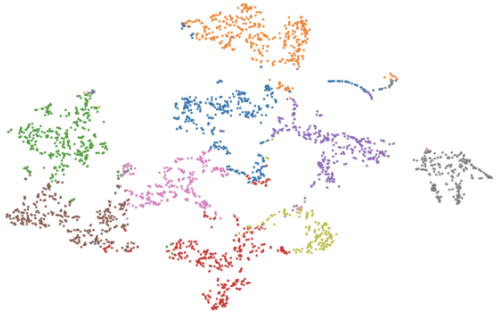


Image Data



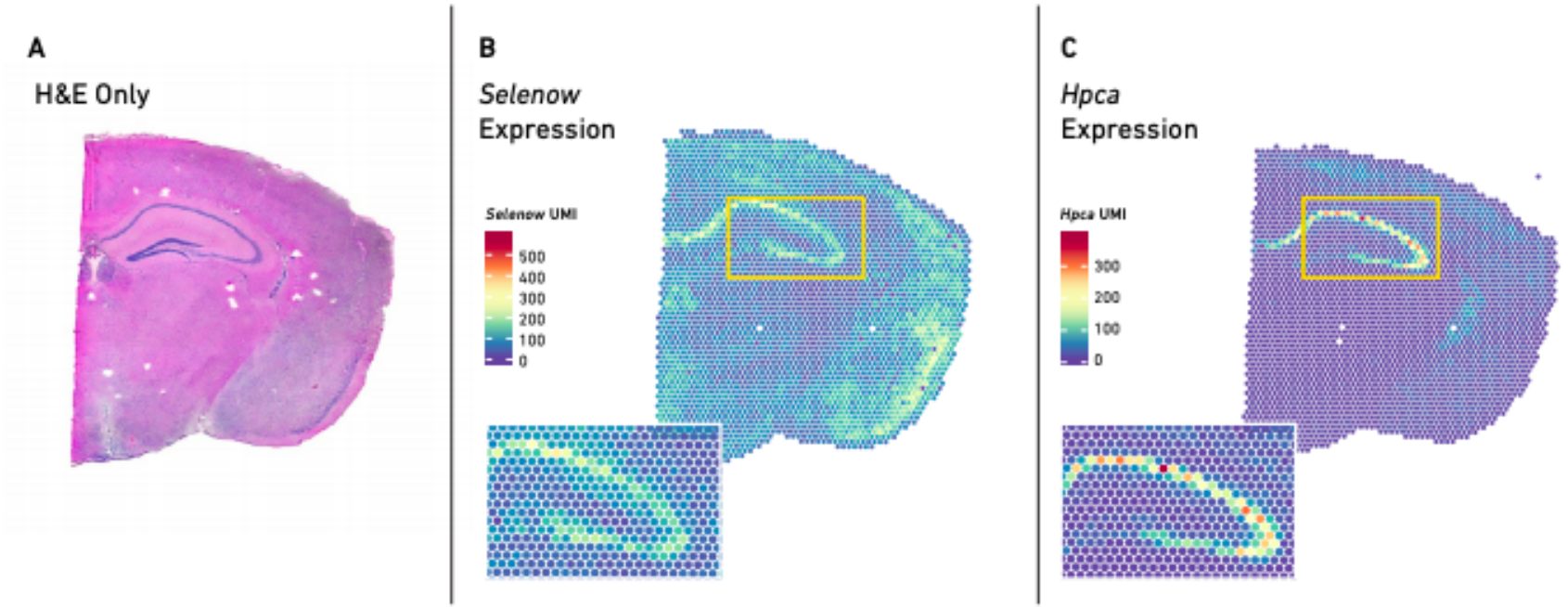
Gene Expression Clustering



Gene Expression Data (t-SNE)

Spatially Resolved Expression in the Mouse Brain

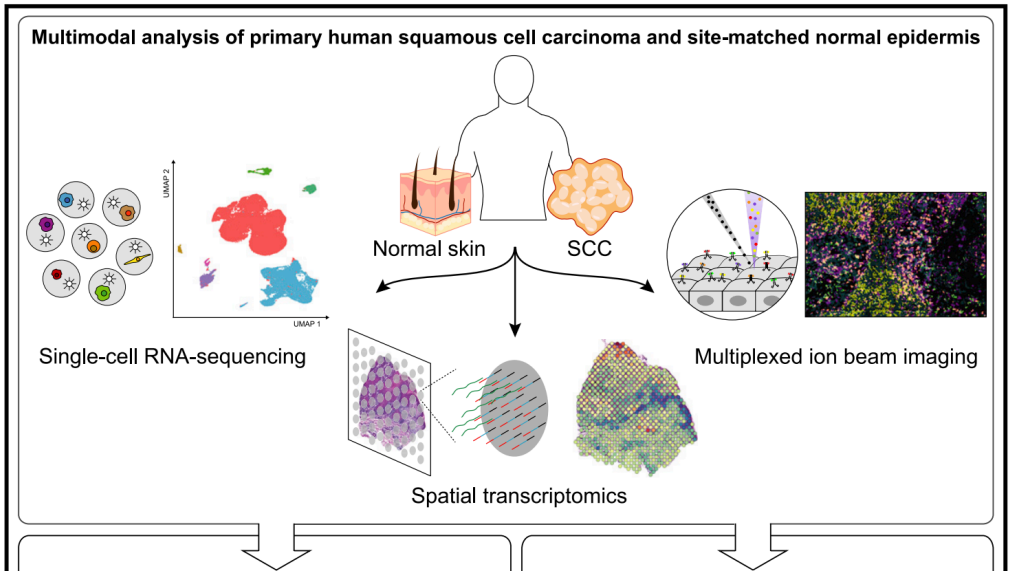
Hippocampal Gene Expression Coincides with Known Gene Expression Patterns



Multimodal Analysis of Composition and Spatial Architecture in Human Squamous Cell Carcinoma

CellPress

Graphical Abstract



Authors

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khavari@stanford.edu

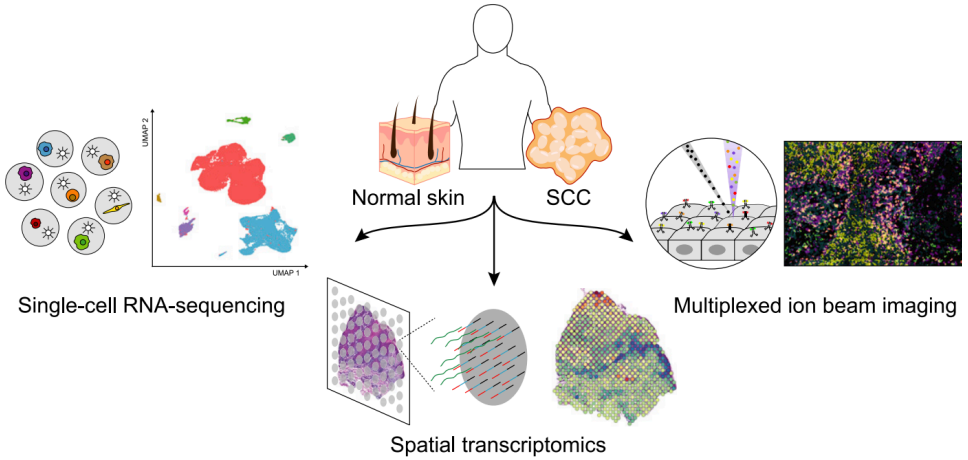
In Brief

Integration of high-dimensional multi-omics approaches to characterize human cutaneous squamous cell carcinoma identifies a tumor-specific keratinocyte

10X GENOMICS https://doi.org/10.1016/j.cell.2020.05.039

Integration of Single Cell and Spatial Gene Expression

Ji *et al*., 2020, Cell

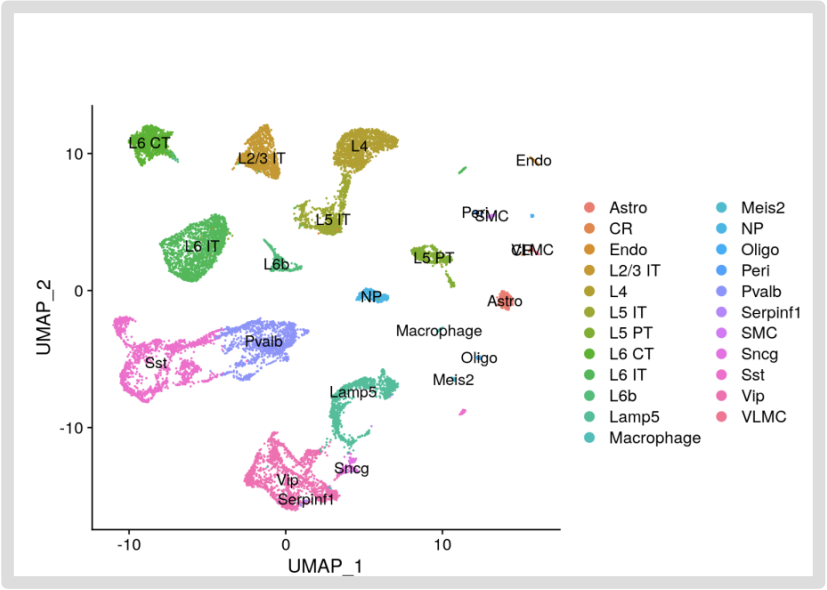


- Profiling of 10 human skin SCCs and matched normal skin via scRNA-seq, ST, and MIBI
- Tumor-specific keratinocytes (TSKs) reside within a fibrovascular niche at leading edges of tumor tissue
- Distinct ligand-receptor and spatial niche associations for tumor and stromal cells
- Subpopulation essential tumorigenic gene networks defined by *in vivo* CRISPR screening

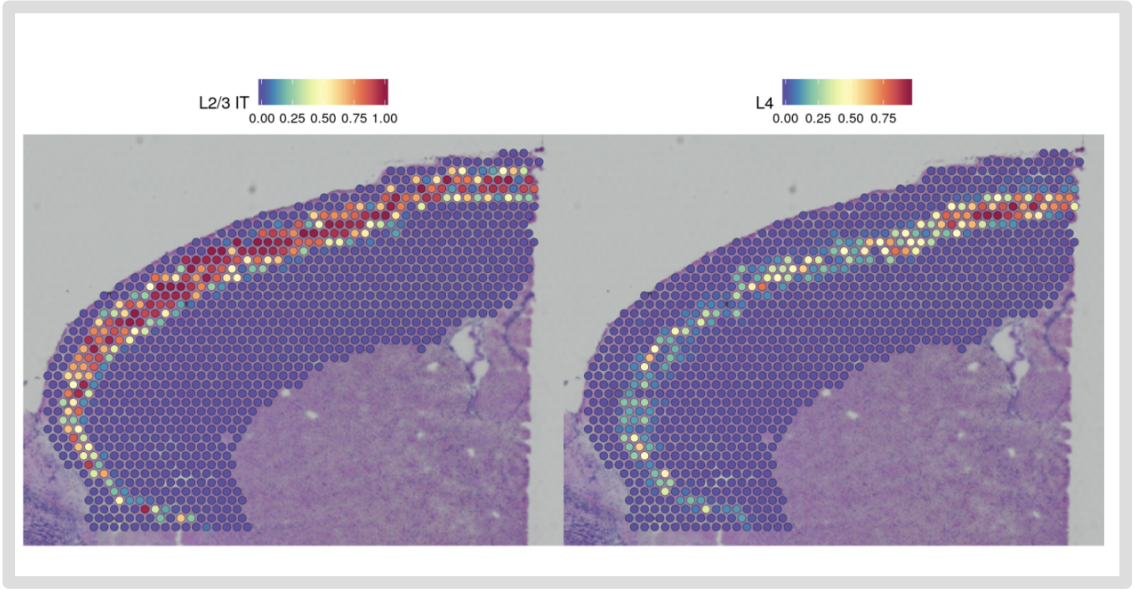
https://doi.org/10.1016/j.cell.2020.05.039

Spatial Analysis Tools: Single Cell Integration

Seurat Support for Spatial Analysis



Single Cell Neuron Annotations



Gene Signatures Mapped into Spatial GEX Clusters

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SEURAT R toolkit for single cell genomics

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Analysis, visualization, and integration of spatial datasets with Seurat

Compiled: 2020-01-03

Overview

This tutorial demonstrates how to use Seurat v3.2 to analyze spatially-resolved RNA-seq data. While the analytical pipelines are similar to the Seurat workflow for single-cell RNA-seq analysis, we introduce updated interaction and visualization tools, with a particular emphasis on the integration of spatial and molecular information. This tutorial will cover the following tasks, which we believe will be common for many spatial analyses:

- Normalization
- Dimensional reduction and clustering
- Detecting spatially-variable features
- Interactive visualization
- Integration with single-cell RN
- Working with multiple slices

For our first vignette, we anal
technology from 10x Genomics
additional data types in the ne
and MERFISH.

Installation

Seurat v3.2 is currently in a pre-release beta stage and is available for installation through Github.

```
devtools::install_github("satijalab/seurat", ref =
"spatial")
```

First, we load Seurat and the other packages necessary for this vignette.

```
library(Seurat)
library(SeuratData)
library(ggplot2)
library(cowplot)
library(dplyr)
```

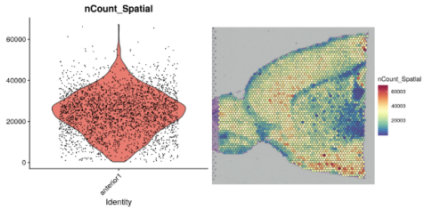
Dataset

Here, we will be using a recently released dataset of sagital mouse brain slices generated using the Visium v1 chemistry. There are two serial anterior sections, and two (matched) serial posterior sections.

You can download the data here, and load it into Seurat using the `Load10X_Spatial` function. This reads in the output of the spaceranger pipeline, and returns a Seurat object that contains both the spot-level expression data along with the associated image of the tissue slice. You can also use our SeuratData package for easy data access, as demonstrated below. After installing the dataset, you can type `?stxBrain` to learn more

heterogeneity here, which requires effective normalization.

```
plot1 <- VlnPlot(brain, features = "nCount_Spatial",
pt.size = 0.1) + NoLegend()
plot2 <- SpatialFeaturePlot(brain, features =
"nCount_Spatial") + theme(legend.position = "right")
plot_grid(plot1, plot2)
```



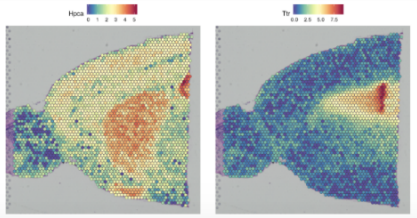
These plots demonstrate that the variance in molecular counts across spots is not just technical in nature, but also is dependent on the tissue anatomy. For example, regions of the tissue that are depleted for neurons (such as the cortical white matter), reproducibly exhibit lower molecular counts. As a result, standard approaches (such as the `LogNormalize` function), which force each data point to have the same underlying 'size' after normalization, can be problematic.

As an alternative, we recommend using sctransform (Hafemeister and Satija, In Press), which which builds regularized negative binomial models of gene expression in order to account for technical artifacts while preserving biological variance. For more details on sctransform, please see

Gene expression visualization

In Seurat v3.2, we have included new functionality to explore and interact with the inherently visual nature of spatial data. The `SpatialFeaturePlot` function in Seurat extends `FeaturePlot`, and can overlay molecular data on top of tissue histology. For example, in this data set of the mouse brain, the gene Hpca is a strong hippocampal marker and Ttr is a marker of the choroid plexus.

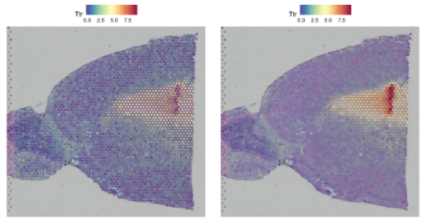
```
SpatialFeaturePlot(brain, features = c("Hpca", "Ttr"))
```



The default parameters in Serat emphasize the visualization of molecular

with lower expression

```
p1 <- SpatialFeaturePlot(brain, features = "Ttr",
pt.size.factor = 1)
p2 <- SpatialFeaturePlot(brain, features = "Ttr",
alpha = c(0.1, 1))
plot_grid(p1, p2)
```

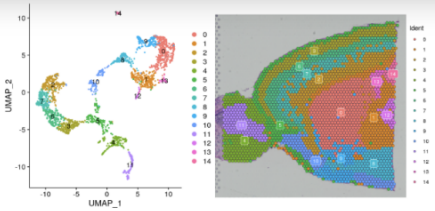


Dimensionality reduction, clustering, and visualization

We can then proceed to run dimensionality reduction and clustering on the RNA expression data, using the same workflow as we use for scRNA-seq analysis.

```
brain <- RunPCA(brain, assay = "SCT", verbose = FALSE)
brain <- FindNeighbors(brain, reduction = "pca", dims
= 1:30)
brain <- FindClusters(brain, verbose = FALSE)
brain <- RunUMAP(brain, reduction = "pca", dims =
```

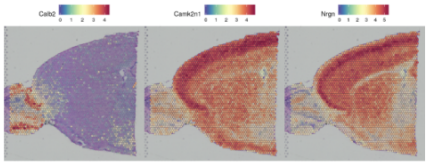
```
plot_grid(p1, p2)
```



As there are many colors, it can be challenging to visualize which voxel belongs to which cluster. We have a few strategies to help with this. Setting the `label` parameter places a colored box at the median of each cluster (see the plot above), and the `do.hover` parameter of `SpatialDimPlot` allows for an interactive viewing of the current spot identities.

```
# move your mouse
SpatialDimPlot(brain, do.hover = TRUE)
```

```
de_markers <- FindMarkers(brain, ident.1 = 4, ident.2
= 6)
SpatialFeaturePlot(object = brain, features =
rownames(de_markers)[1:3], alpha = c(0.1, 1), ncol =
3)
```



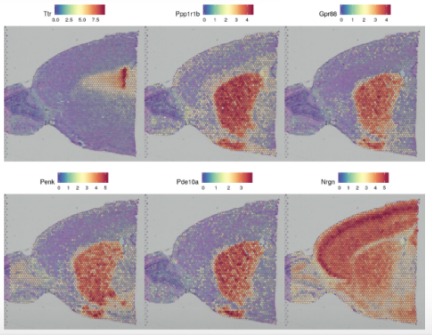
An alternative approach, implemented in `FindSpatiallyVariables`, is to search for features exhibiting spatial patterning in the absence of pre-annotation. The default method (`method = 'markvariogram'`), is inspired by the Trendsceek, which models spatial transcriptomics data as a mark point process and computes a 'variogram', which identifies genes whose expression level is dependent on their spatial location. More specifically, this process calculates gamma(r) values measuring the dependence between two spots a certain "r" distance apart. By default, we use an r-value of '5' in these analyes, and only compute these values for variable genes (where variation is calculated independently of spatial location) to save time.

We note that there are mulitple methods in the literature to accomplish this task, including SpatialDE, and Splotch. We encourage interested users to explore these methods, and hope to add support for them in the near future.

```
(brain, assay =
ain)[1:1000],
)
```

atures identified by this

```
eFeatures(brain,
selection.method = "markvariogram"), 6)
SpatialFeaturePlot(brain, features = top.features,
ncol = 3, alpha = c(0.1, 1))
```



https://satijalab.org/seurat/v3.1/spatial_vignette.html

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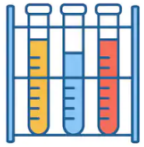
Support through your experimental workflow



Experimental Design

- Discussion with local Science & Technology Advisor (STA), Field Application Scientist (FAS)

Cell Ranger Data Processing

- Email 10x Support Team
- Software training from FAS
- Support site documentation and software tutorials

Data Visualization with Loupe Browser

- Email 10x Support Team
- Support site documentation and software tutorials

Data QC

- Data QC Technical Note
- Email 10x Support Team

Advanced Analysis and Results

- 10x customer publications
- 10x-pert & customer webinars
- Email 10x Support Team
- Open-source community tools
- 3rd party analysis services and products

support@10xgenomics.com

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Thank you!

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Compatible Tissues and Species with More to Come

https://support.10xgenomics.com/docs/Spatial_GEX_tissues

Human Tissue (Healthy/Diseased)
Brain, Cerebellum (Healthy)
Brain, Cerebral Cortex (Healthy, Glioblastoma Multiforme)
Breast (Healthy)
Breast (Invasive Ductal Carcinoma)
Breast (Invasive Lobular Carcinoma)
Breast (Triple Negative Breast Cancer)
Heart (Ventricle, Healthy, Myocardial Infarction)
Kidney (Healthy, Nephritis)
Large Intestine (Colorectal Cancer)
Lung (Healthy, Papillary Carcinoma)
Lymph node (Healthy, Inflamed)
Ovaries (Tumor)
Spinal Cord (Healthy)
Spleen (Healthy, Inflamed)

Mouse Tissue (Healthy/Diseased)
Brain (Healthy)
Brain, Embryonic (Healthy)
Eyes (Healthy)
Heart (Healthy)
Kidney (Healthy)
Large Intestine (Healthy)
Liver (Healthy)
Lungs (Healthy)
Ovary (Healthy)
Quadriceps (Healthy)
Small Intestine (Healthy)
Spleen (Healthy)
Stomach (Healthy)
Testes (Healthy)
Thyroid (Healthy)
Tongue (Healthy)

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