

Novel Single Cell Multiome Approaches for Precision Medicine

Petro Leka / Dr. Andreas Schmidt

21.10.2022



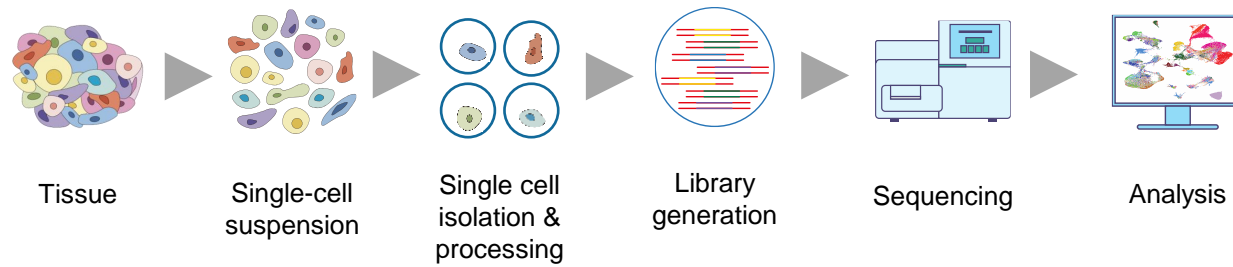


Our company

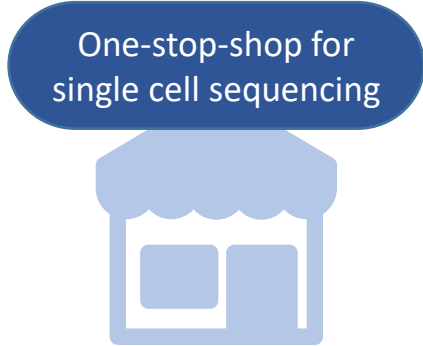




Kits, instruments and software for single-cell analysis



Outsourced services in our global service centers ★





Why single cell sequencing

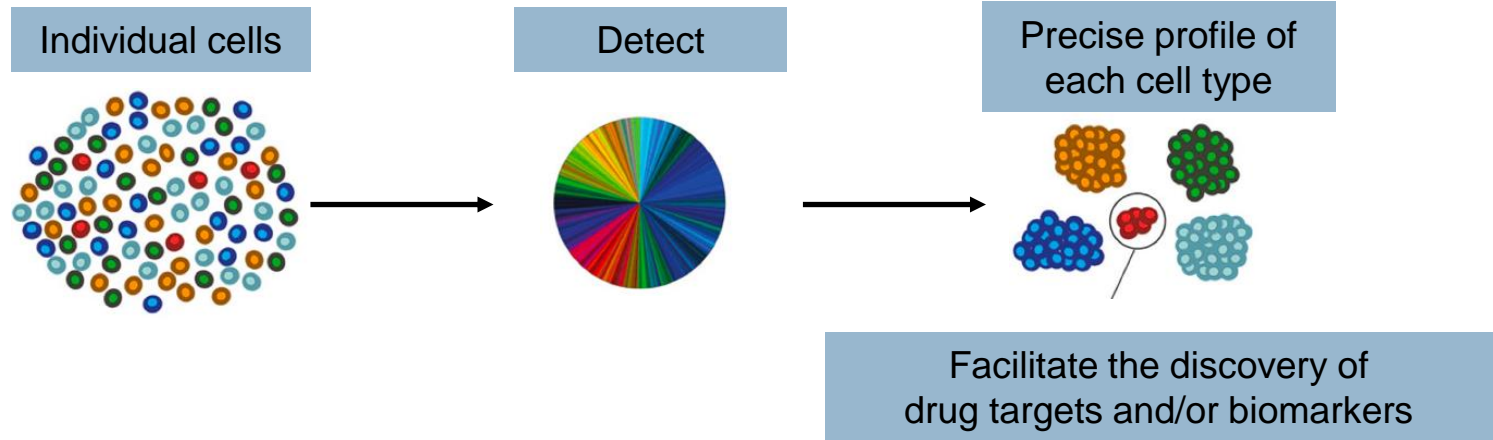
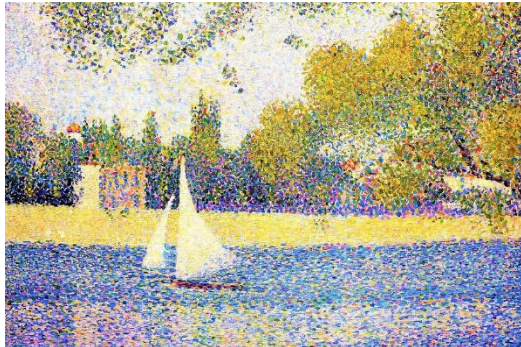


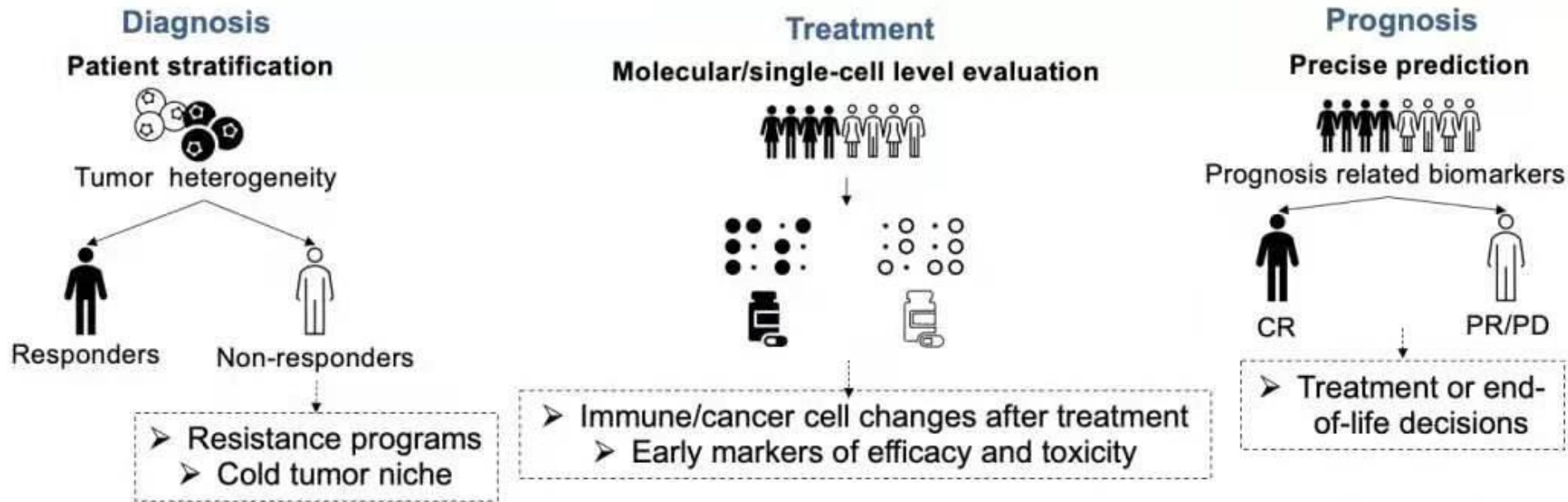


Bulk Sequencing



Single-Cell Sequencing

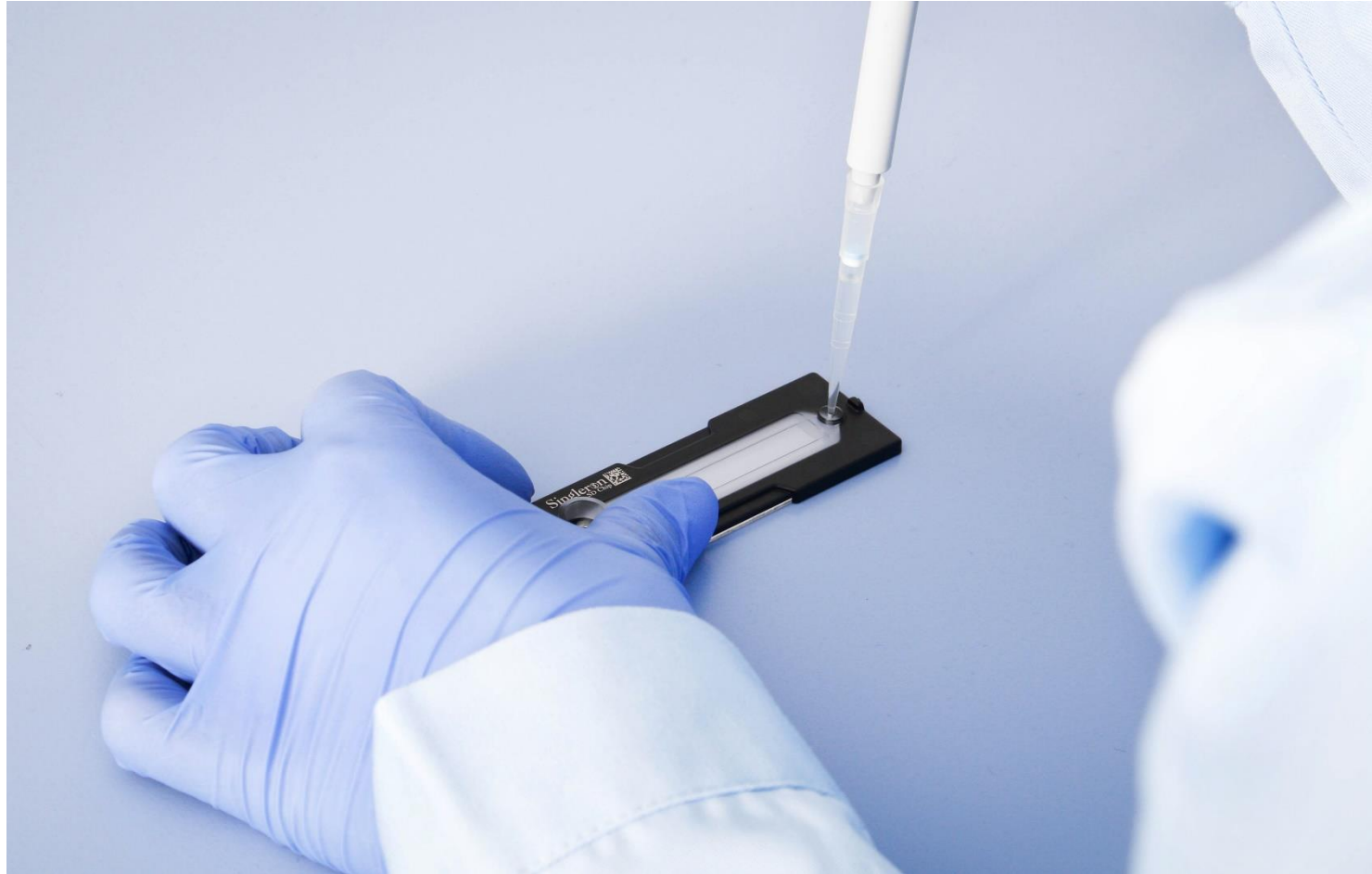


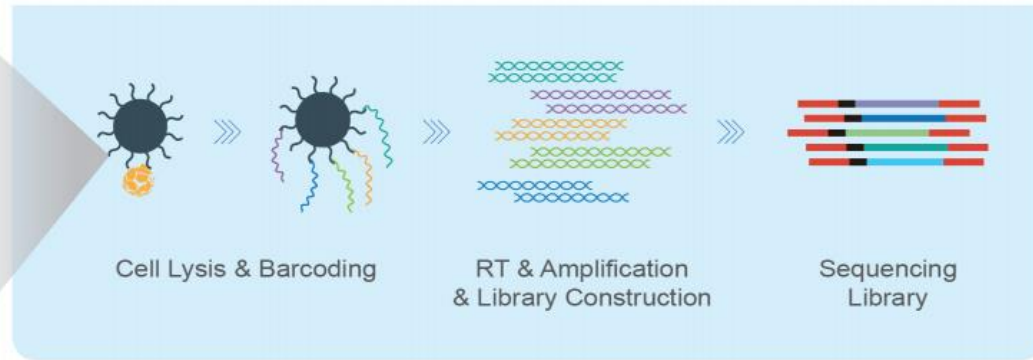
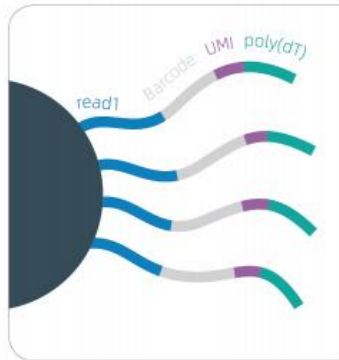
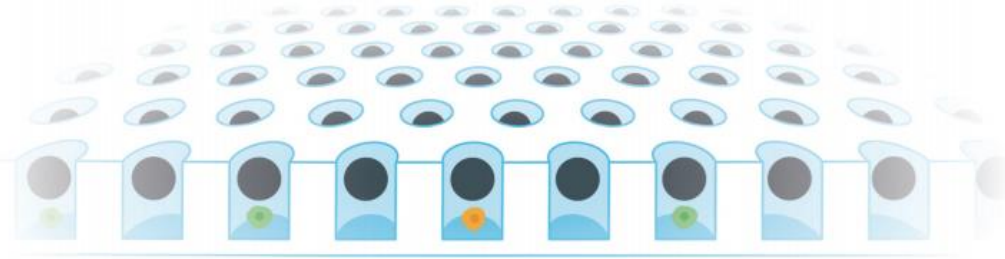




Singleron's Technology





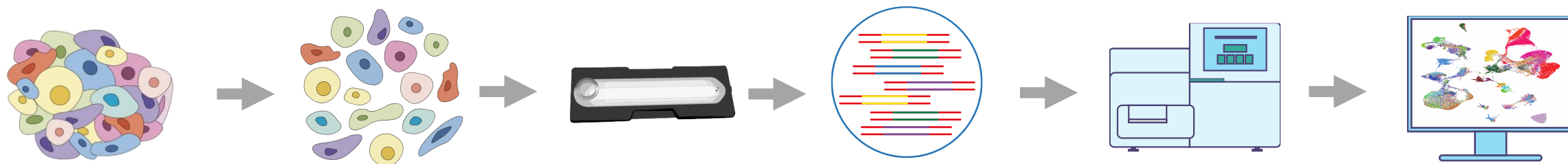


Standard Chip
Up To 10,000 Cells

High Density Chip
Up To 30,000 Cells

Standard SCOPE Chip
40µm Wells

Large-well chips
100µm Wells



Tissue

Single-Cell
Suspension

Cell Partitioning
Cell Lysis
mRNA Capture

cDNA Generation
Library Construction

Sequencing

Bioinformatic
Analysis

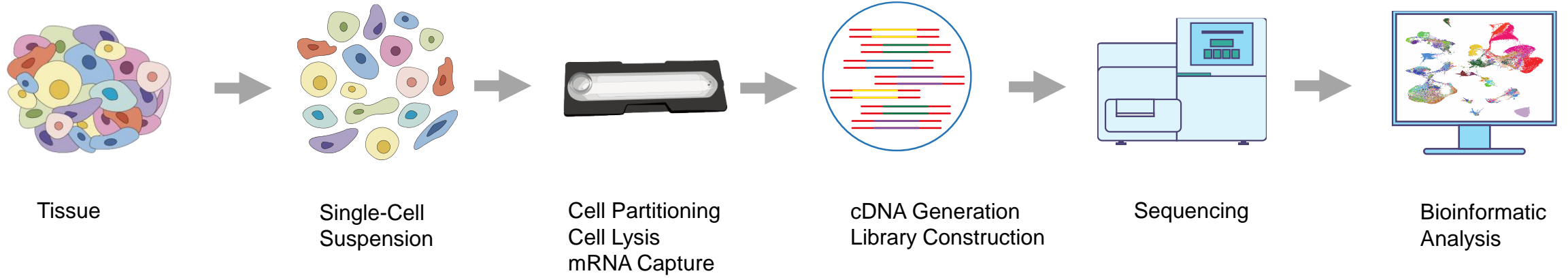
sCelliVE®
PythoN®
CLindeX®

GEXSCOPE® Products
FocuSCOPE®
sCircle™
DynaSCOPE®

Compatible With
Standard Illumina
Sequencing

Telescope®
SynEcoSys®

Services Available For All Steps Of The Pipeline

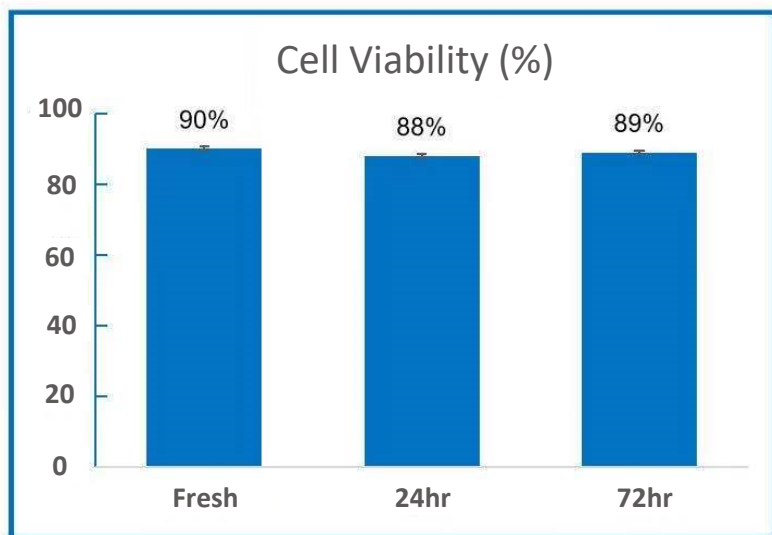


sCelliVE[®]
PythoN[®]
CLindeX[®]



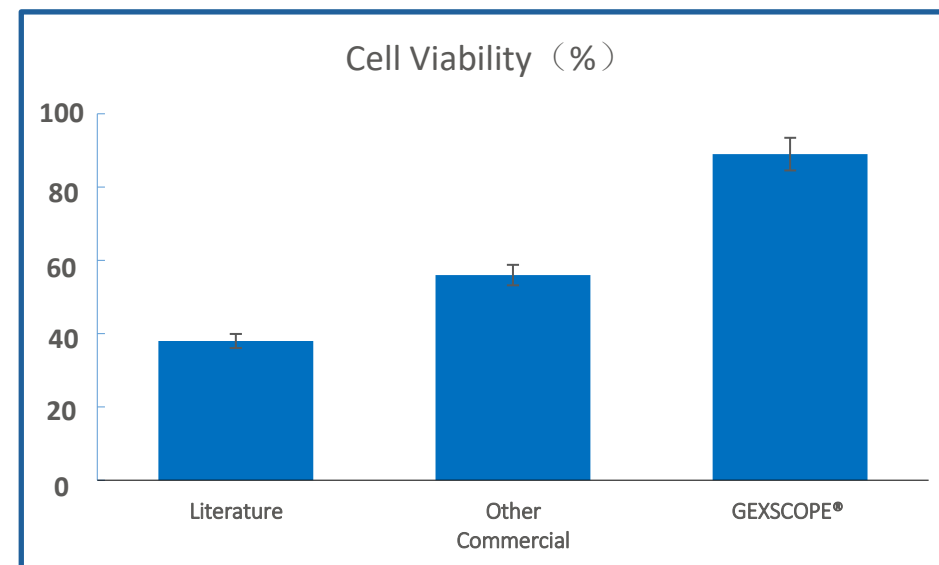
sCellLiVE® Tissue Preservation Buffer

- Can effectively preserve the tissue for **72 hours at 4 °C**.
- No chemical fixatives



sCellLiVE® Tissue Dissociation Master Mix

- Can dissociate different types of tissues with high efficiency **typically in 15-20 minutes**.
- Option for automation





From fresh solid tissue to single cell suspension

sCellLive[®] Tissue
Dissociation Solution



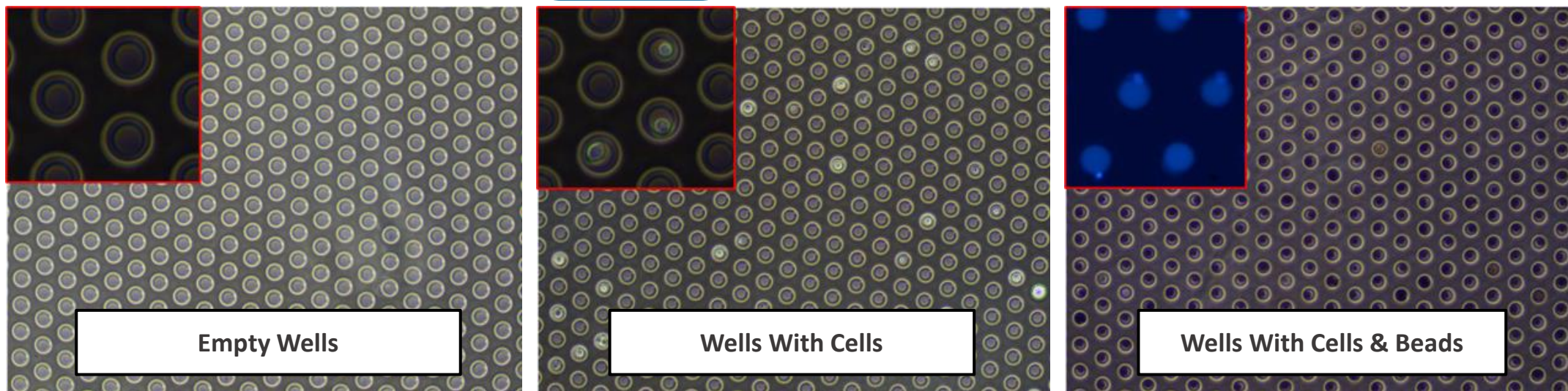
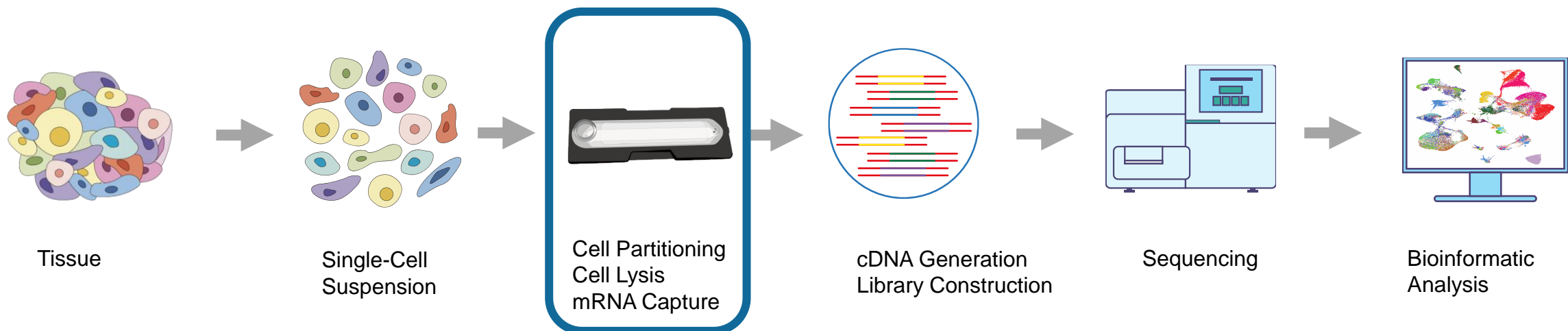
PythoN[®] Automated Tissue
Dissociation System



PythoN[®]
Dissociation Unit



- High viability, high yield
- 15min standard run time
- Broad range of tissue types
- 10mg-4000mg tissue input
- Suitable for biopsies and small samples
- 8 channels
- Both preset and customizable programs



No Need For Specialized Equipment – Use A P200

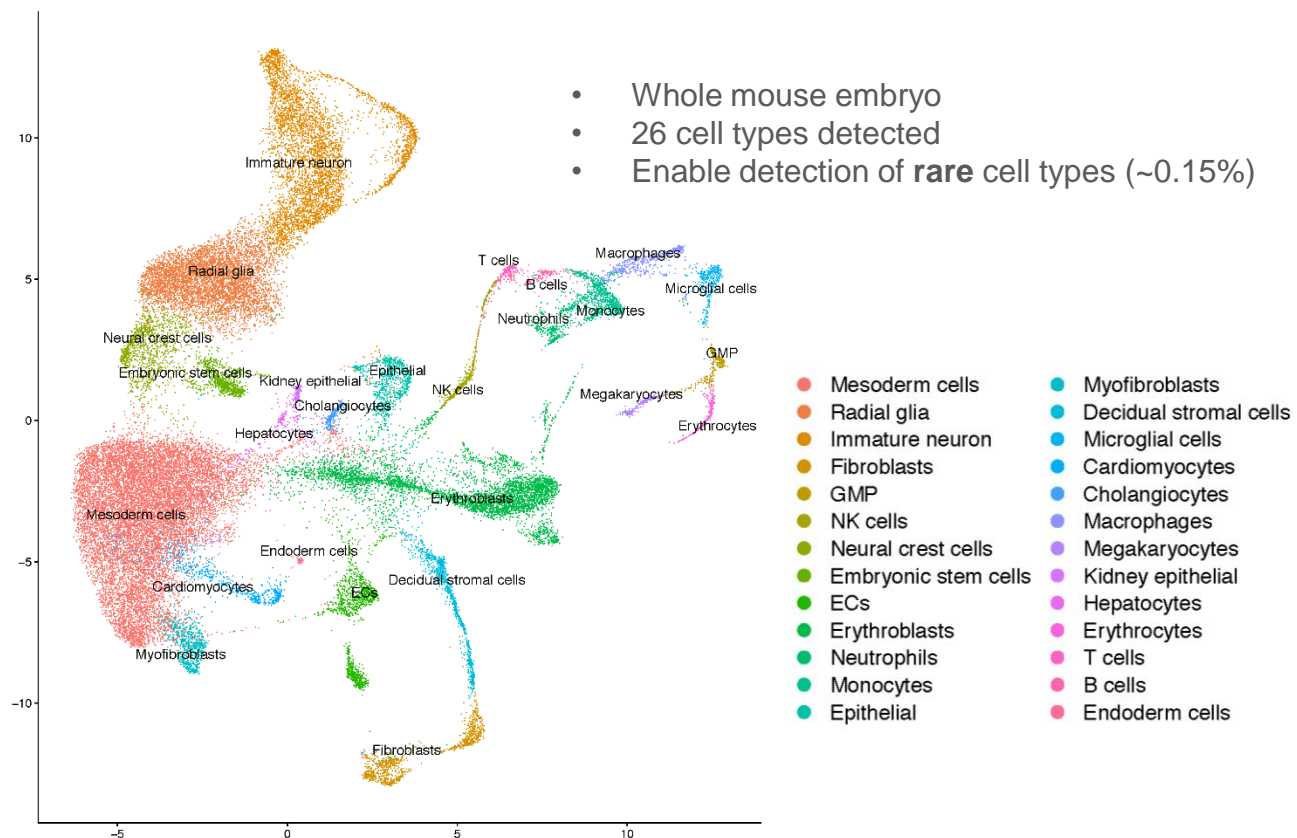
View Cell Loading With Any Standard Microscope



High Density Microfluidic Chip

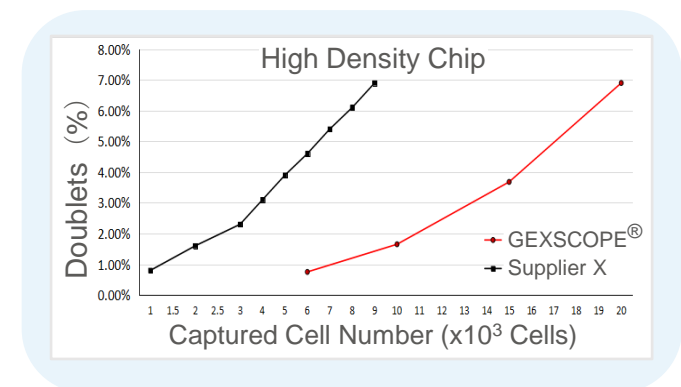
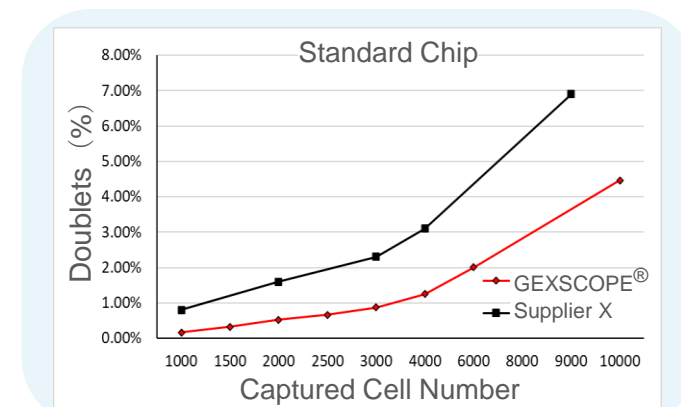
Can capture up to 30,000 cells on one chip

Detect rare cell types (<1%)



Low Doublet Rate

Microwell system has a lower doublet rate than microfluidics-based systems

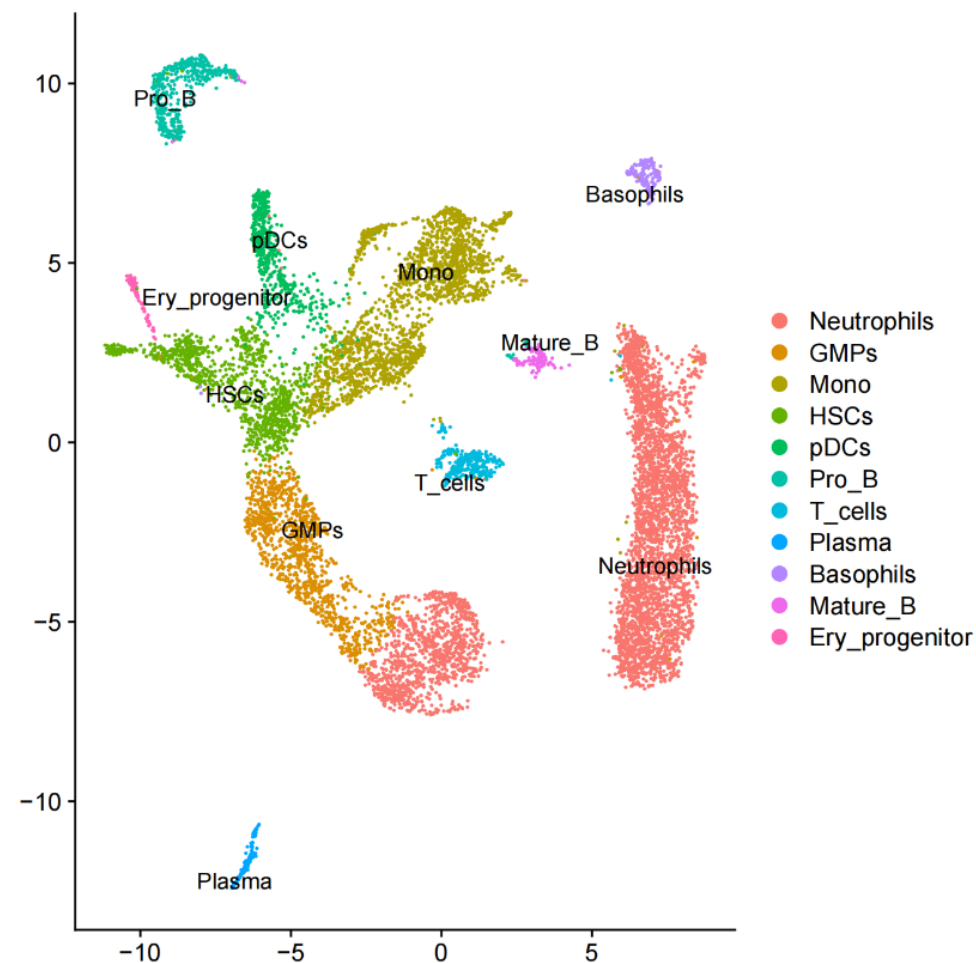


Capture Sensitive Cell Populations

In bone marrow samples, neutrophils account for >33% of captured cell types.



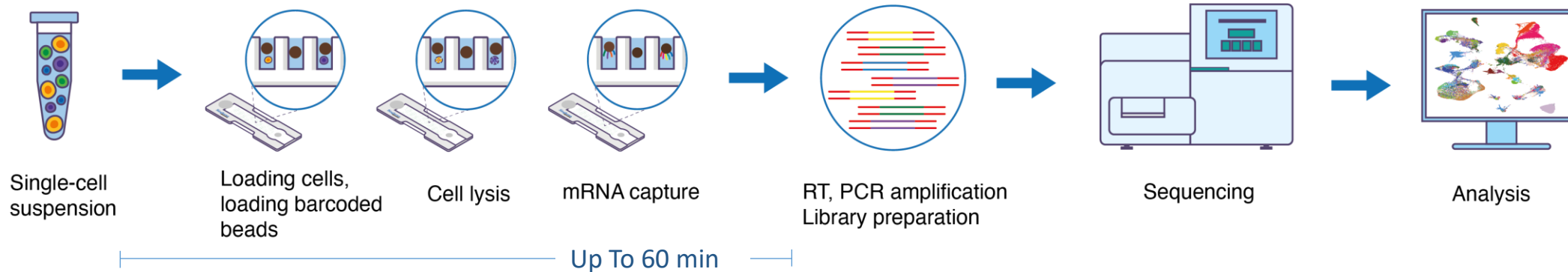
Bone Marrow (Mouse)



Matrix[®] - Highly Reproducible & Automated Single-Cell Processor



Manual

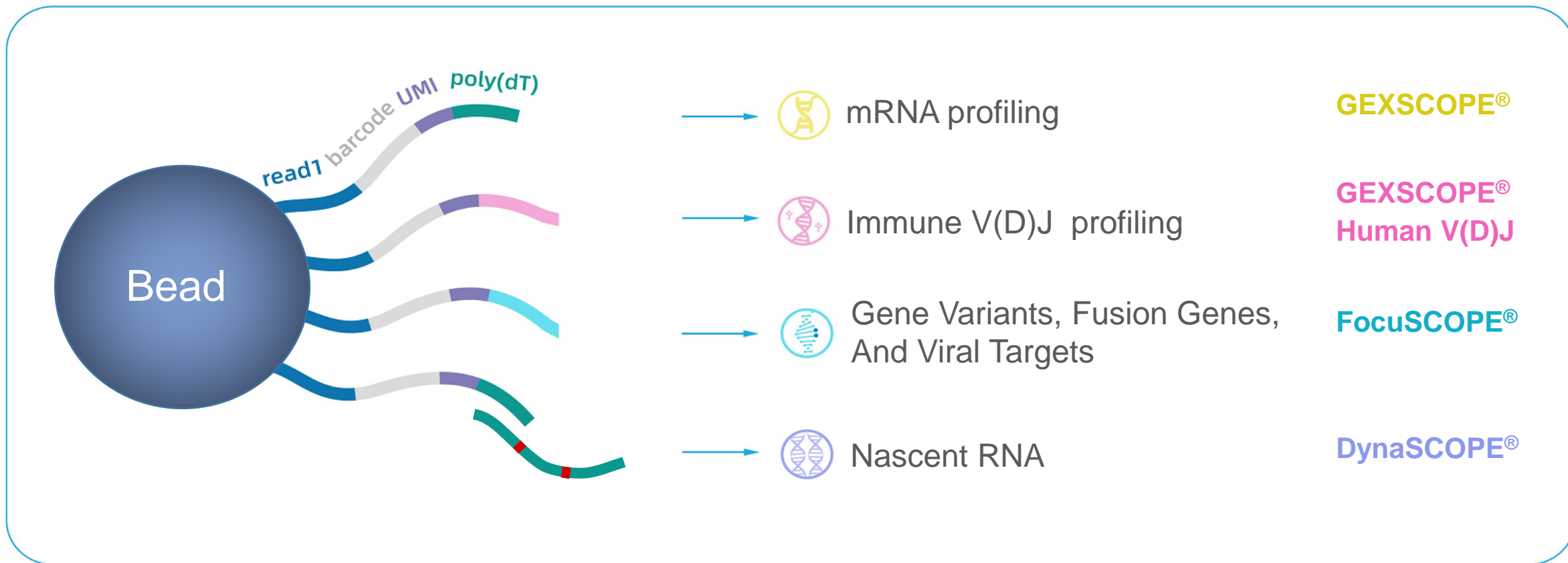


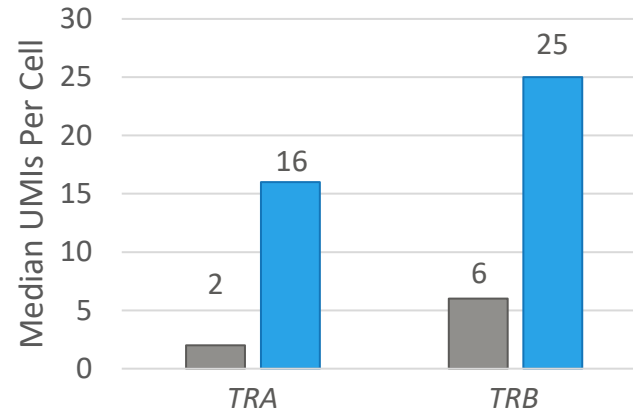
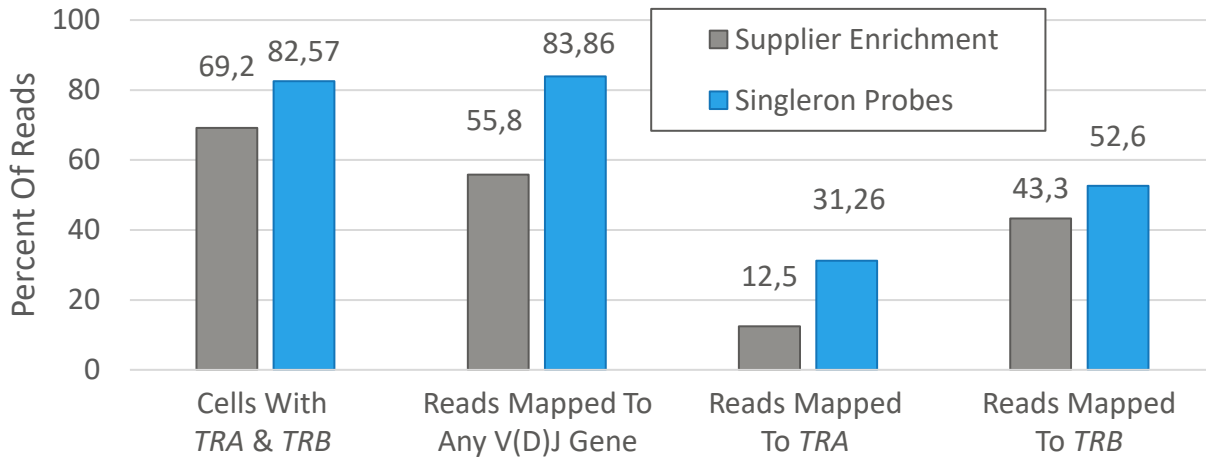
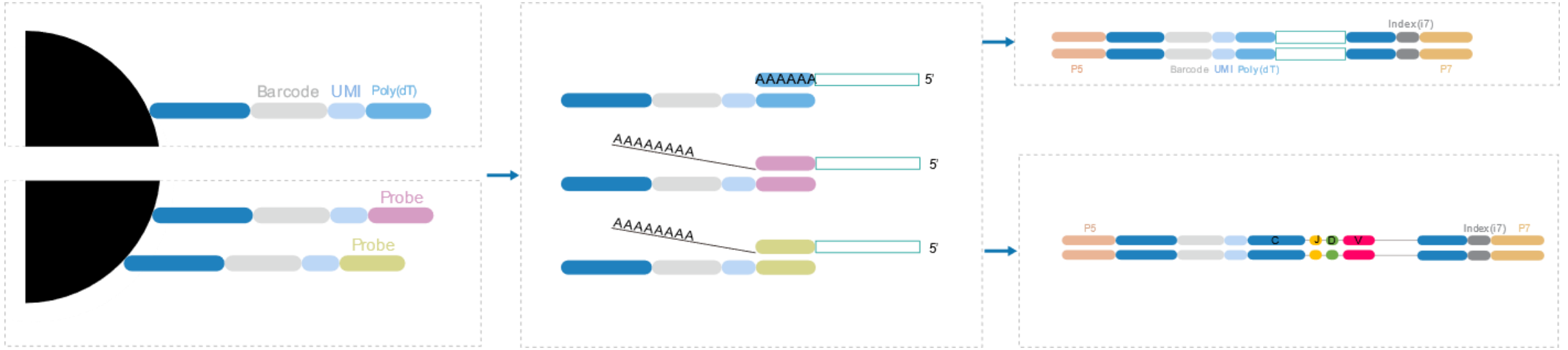
Automated



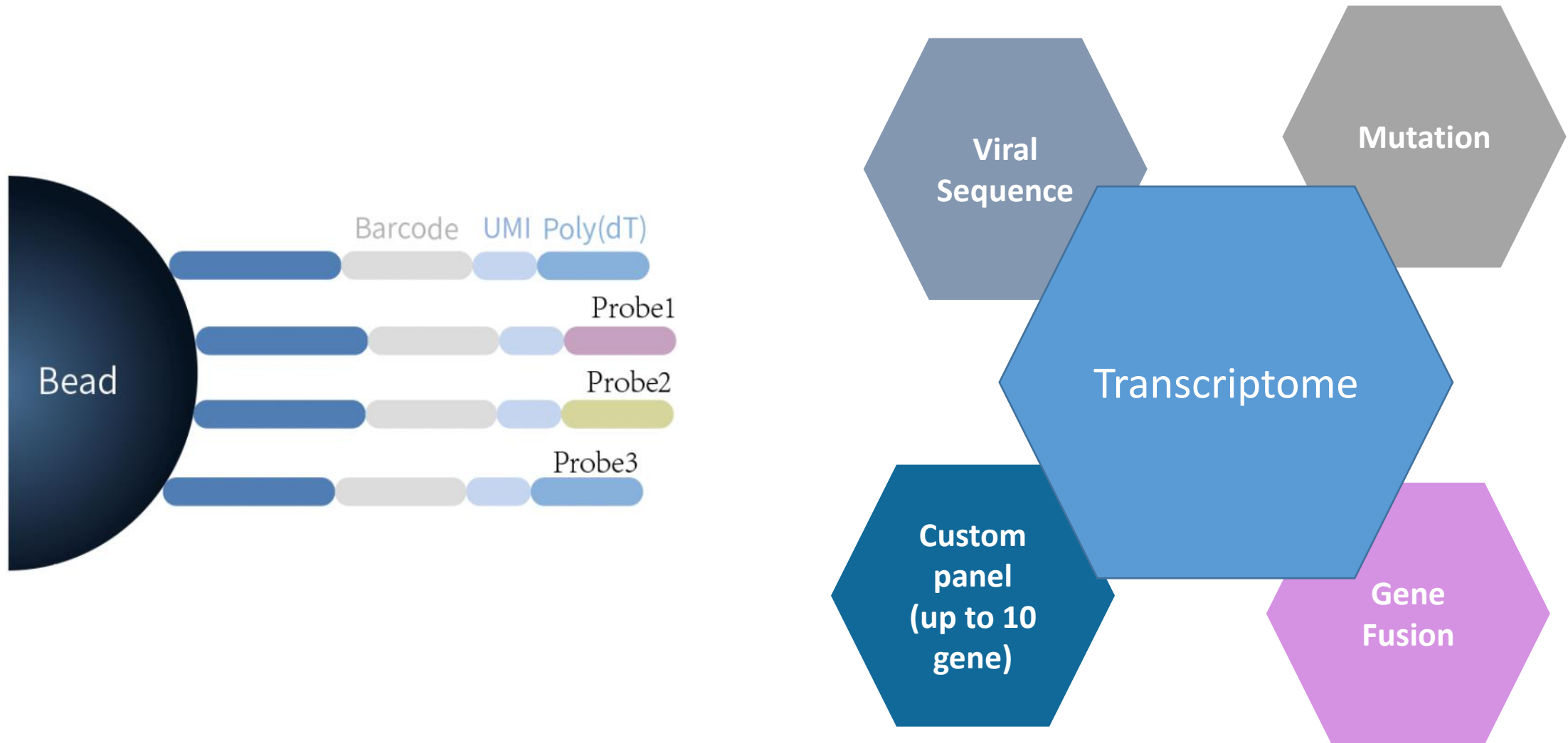
Automated operation:

- Reduced manual labor
- Shorter operation procedure
- High stability and reproducibility



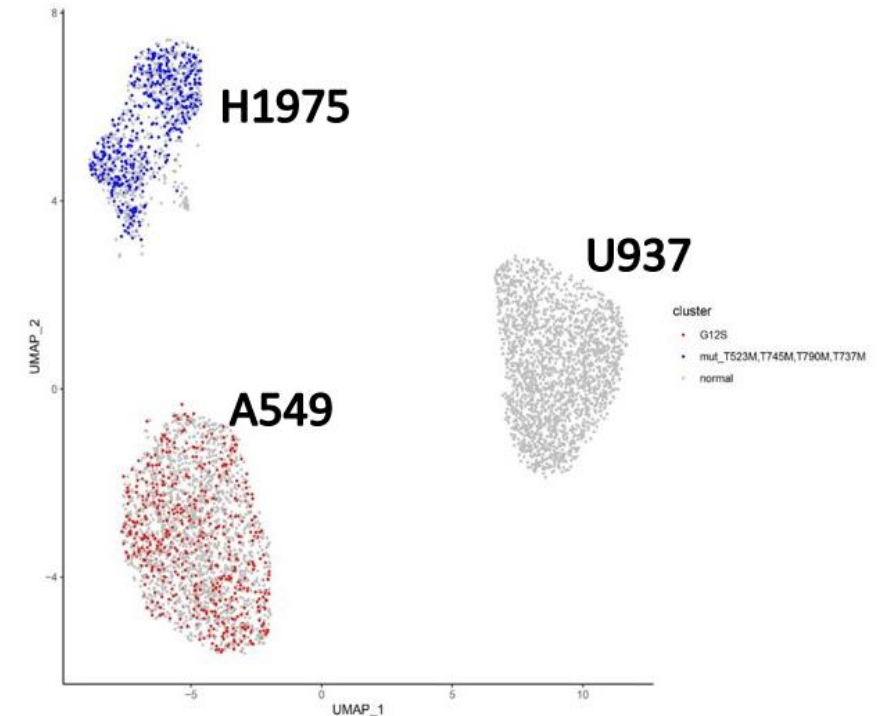


- Designated TCR/BCR Probes For Increased Specificity
- Higher Capture Efficiency



FocuSCOPE[®] Lung Cancer Druggable Mutation Panel

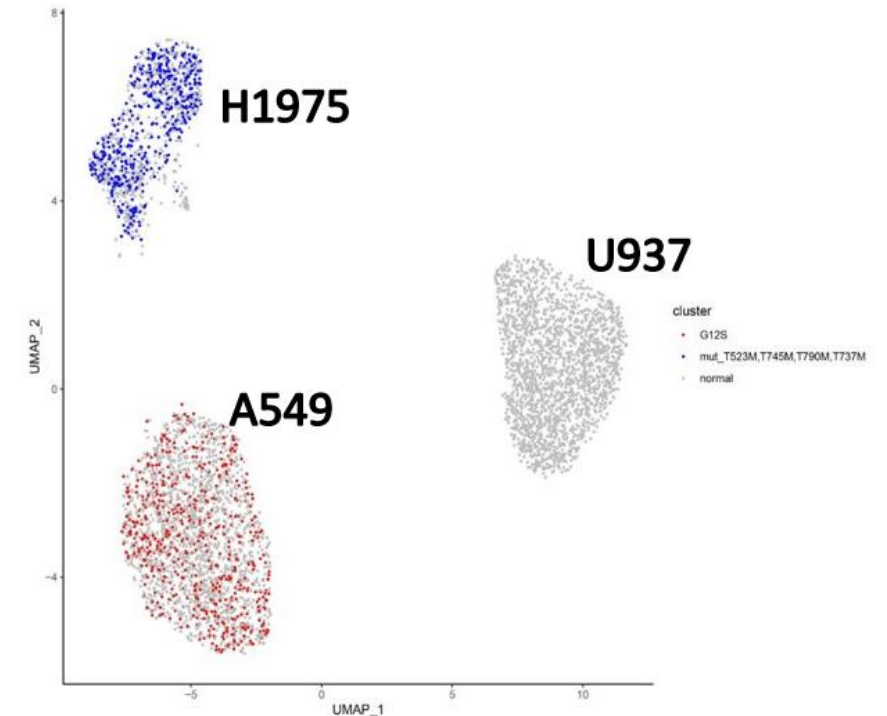
Gene	Exon	Drugs	Targeted Region
EGFR	18-21	Dacomitinib	Exon 19 deletion & Exon 21 L858R alteration
		Afatinib	Exon 19 deletion & Exon 21 L858R alteration
		Osimertinib	T790M
KRAS	2- 4	pan-KRAS inhibitor	G12,G13
		MRTX849	G12C
		TNO155	G12C
PIK3CA	10 and 21	Omipalisib	E542K, E545K, E546, M1004I
BRAF	11-15	Dabrafenib	V600E
		Trametinib	V600E
TP53	4, 6	APR-246	R175H, R248Q



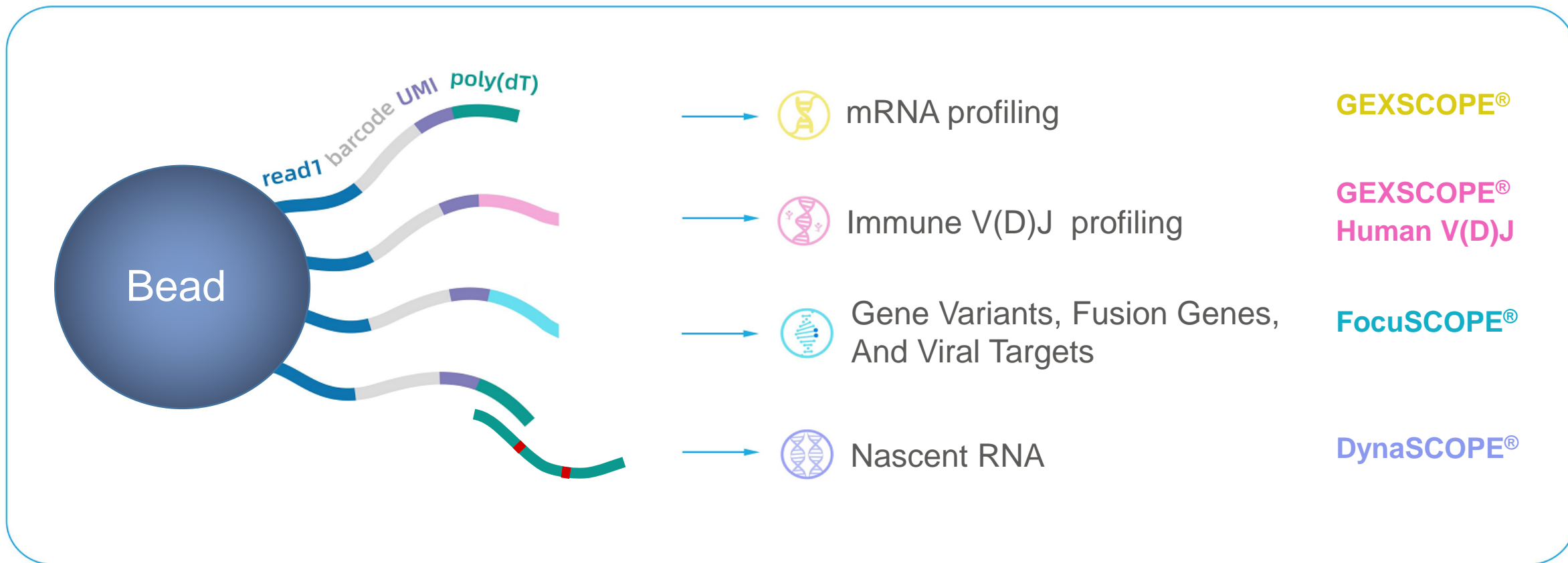
A549: KRAS G12S
H1975: EGFR T790M

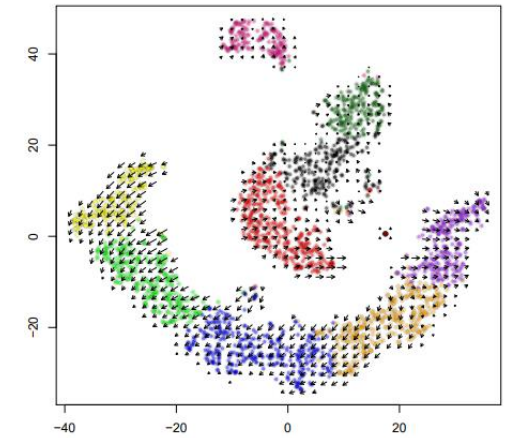
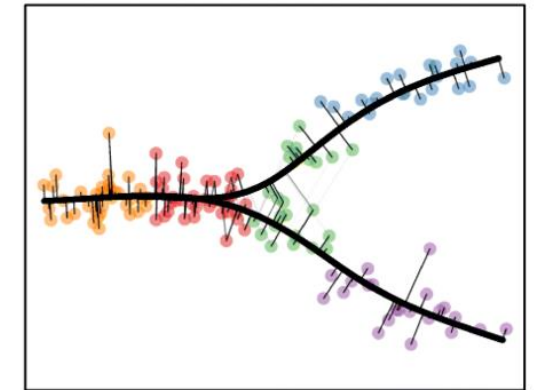
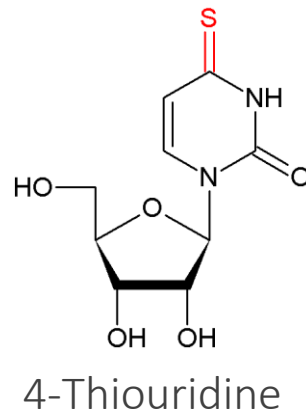
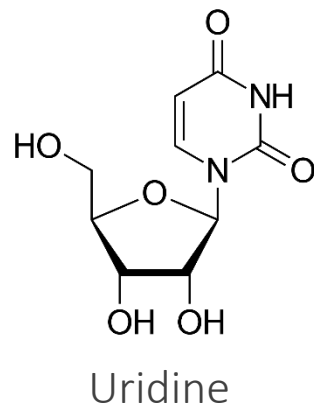
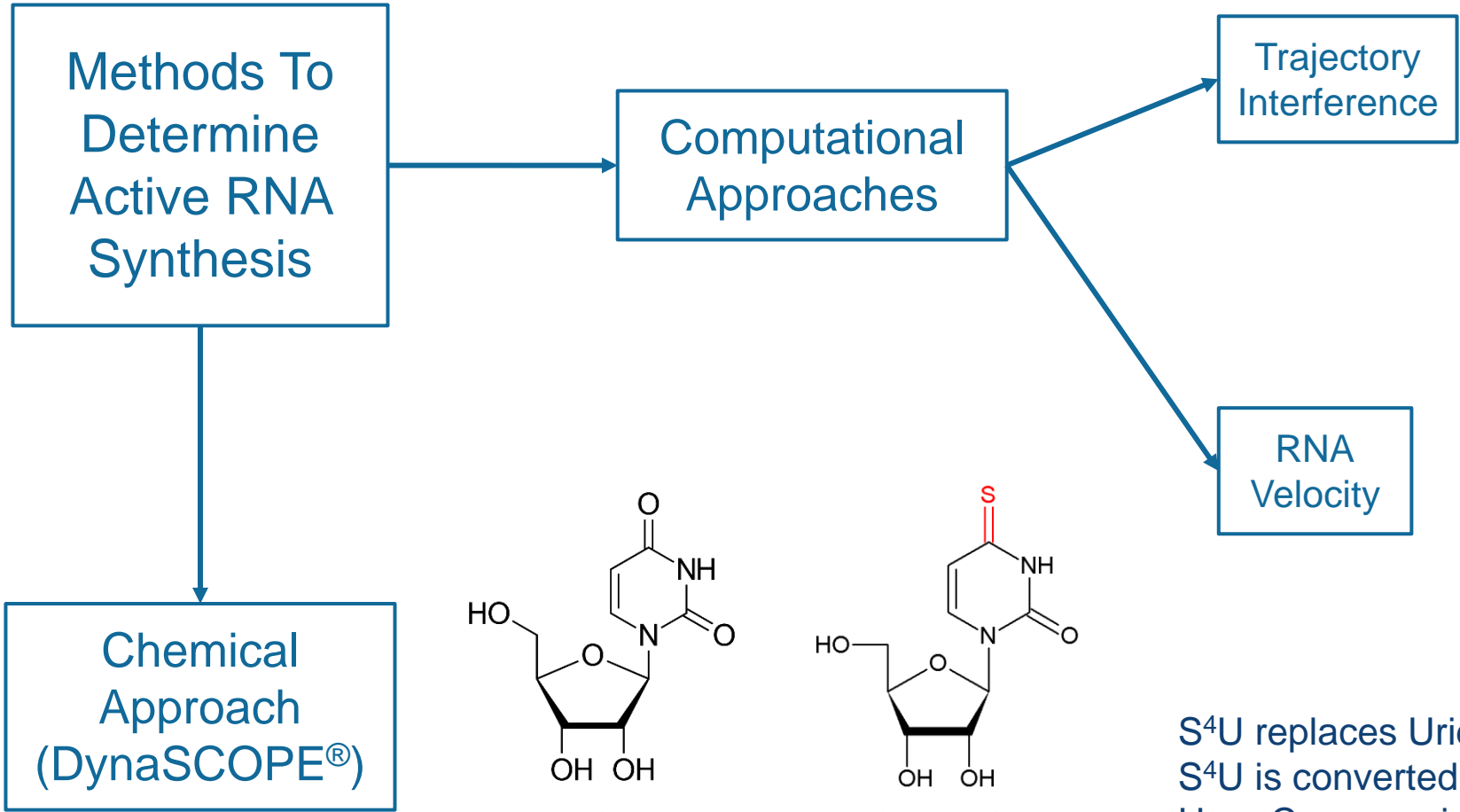
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		MRTX849	G12C
		TNO155	G12C
PIK3CA	10 and 21	Omipalisib	E542K, E545K, E546, M1004I
BRAF	11-15	Dabrafenib	V600E
		Trametinib	V600E
TP53	4, 6	APR-246	R175H, R248Q



A549: KRAS G12S
H1975: EGFR T790M





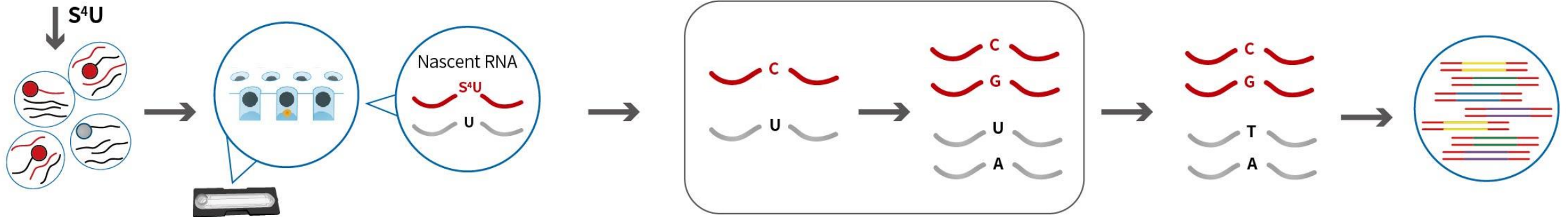
S⁴U replaces Uridine in newly synthesized RNA
 S⁴U is converted to a cytosine analogue *S⁴U
 U => C conversion in reverse transcription



1.) S⁴U Labeled Cells Or Dissociated Tissues

3.) Conversion Of S⁴U To A Cytosine Analogue

5.) Sequencing: Separation new and long-lived transcripts using bioinformatics



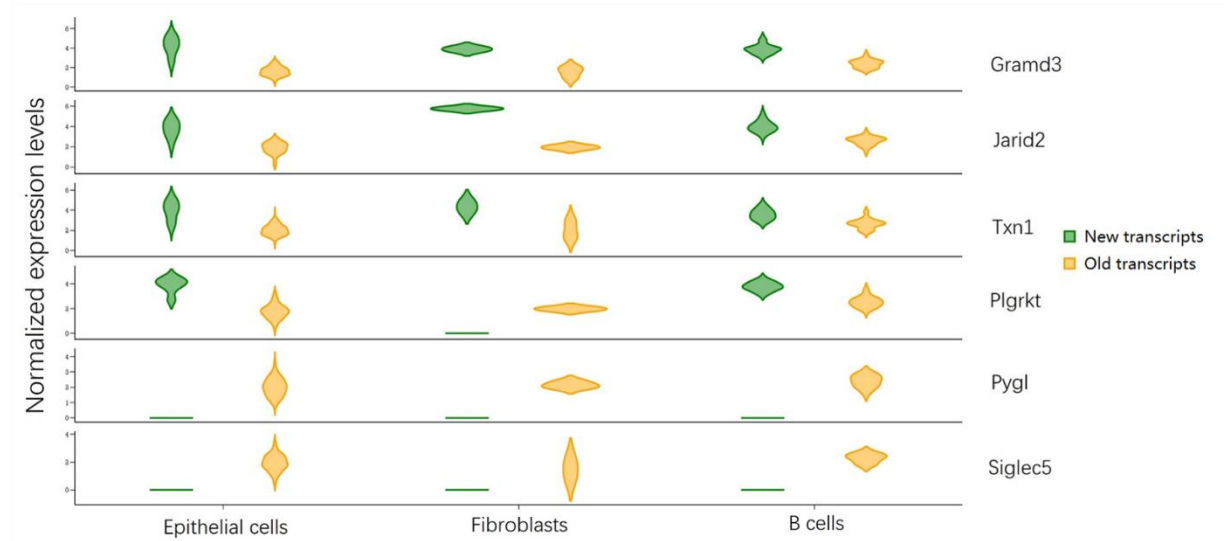
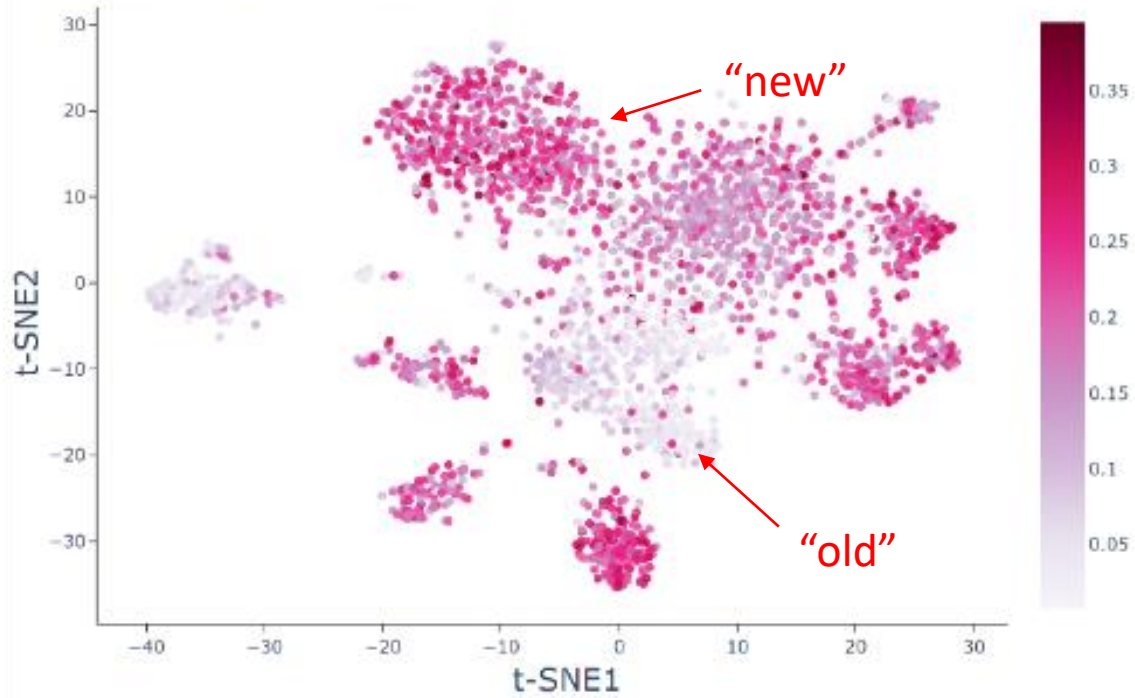
2.) Single Cell Lysis And Barcoding

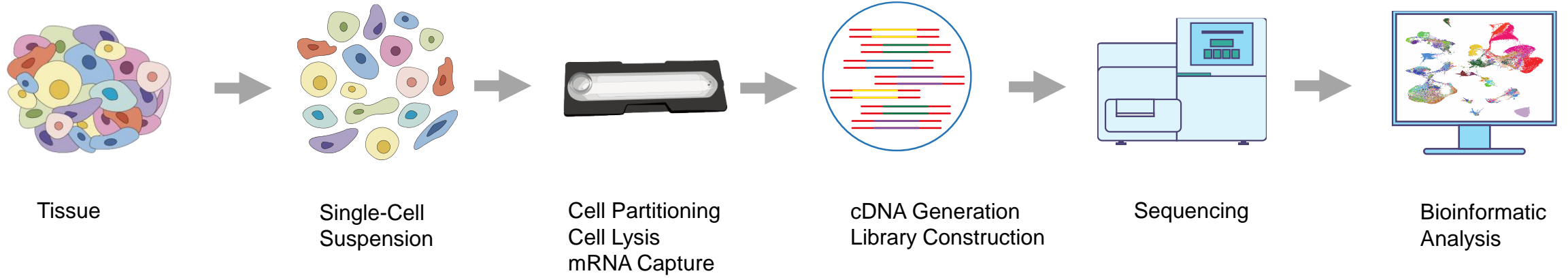
4.) Reverse Transcription

- New transcripts contain U => C substitutions
- Older transcripts are wild-type U



t-SNE plot colored by substitution rate





Telescope[®]
SynEcoSys[®]



CeleScope[®] Software

SynEcoSys[®] Database

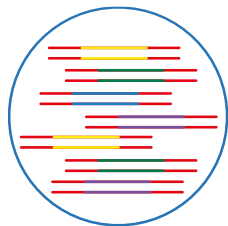
Raw data

Expression Matrix

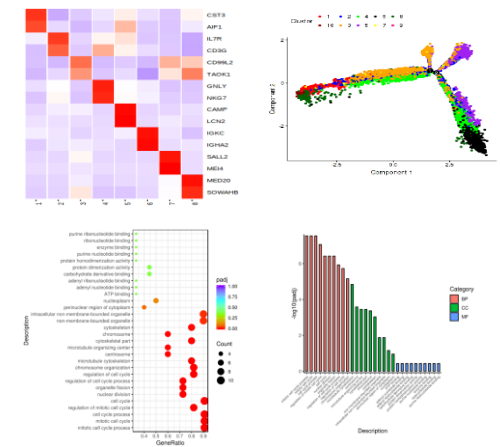
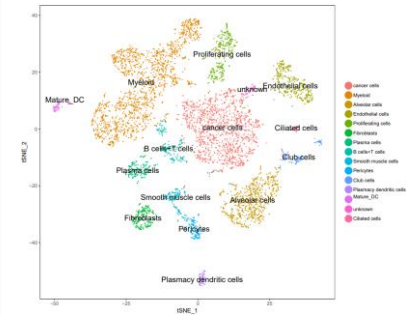
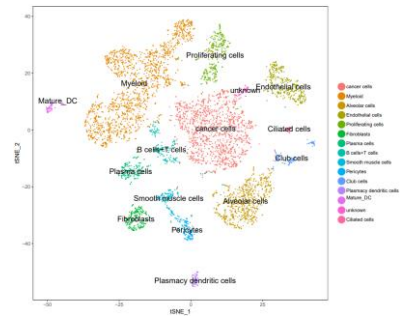
Data clustering

Cell Type Annotation

Secondary analysis



	Cell: 1	2	...	N
GENE 1	1	2		14
GENE 2	4	27		8
GENE 3	0	0		1
⋮	⋮	⋮		⋮
GENE M	6	2		0





Collection of public single cell sequencing data



Standardized
data collection
platform

Clinically
relevant
information

Easy to use data
visualization
tool



Comprehensive

- ✓ Sequencing data of 120,000,000+ single cells
- ✓ Automatic annotation of 2000+ cell types

Homo sapiens Mus musculus Rhesus macaque
 Hundreds of Tissues Thousands of cell types

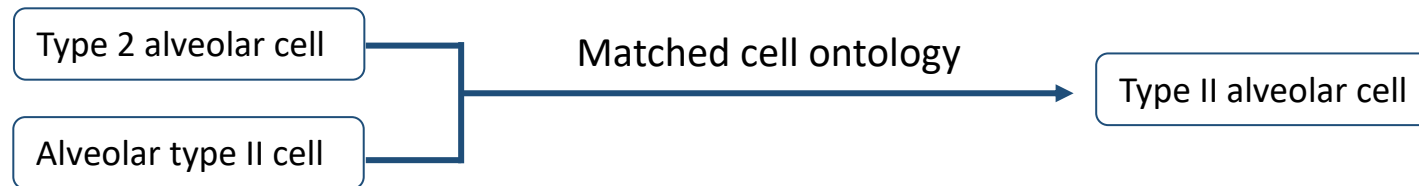
Accurate

- ✓ Accurate data annotations guarantee dataset qualities

Original published annotation vs SynEcoSys annotation
 DC vs pDC
 Lymphocytes vs NK & $\gamma\delta$ -T cells

Consistent

- ✓ Unifies terminologies of cell types





Your Data

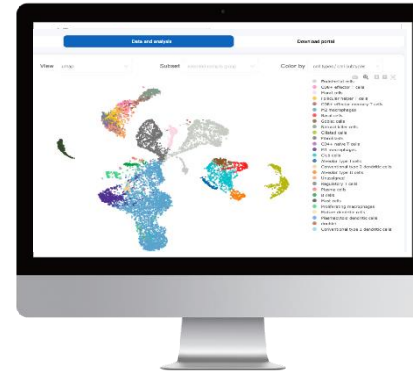
- ✓ Full expression matrix
- ✓ Sparse expression matrix



Automated pipeline

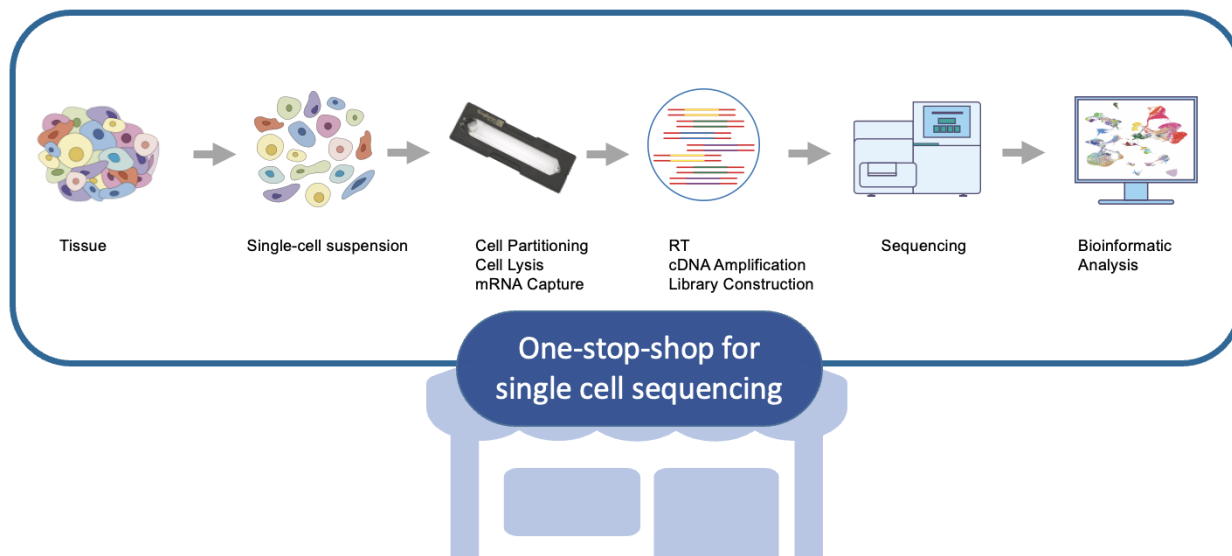
- Adjustable, replicable parameters
- ✓ Provided recommended defaults
- ✓ Customizable at your preference

Annotated and Visualized



- ✓ Accurate and precise annotation
- ✓ Customize labels at your preference





Transcriptome profiling

- single cell
- single nucleus
- yeast



Transcriptome + V(D)J profiling

- CDR3 profiling
- full-length TCR/BCR



Transcriptome + target sequences

- lung/ blood cancer
- EBV virus
- customized panels



Transcriptome with temporal resolution



SynEcoSys Database

Contact

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