

Building **OsteoCAR**, a Comprehensive Cross-Species Single-Cell Atlas of Osteosarcoma

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The Ohio State University

FACTOR 2025

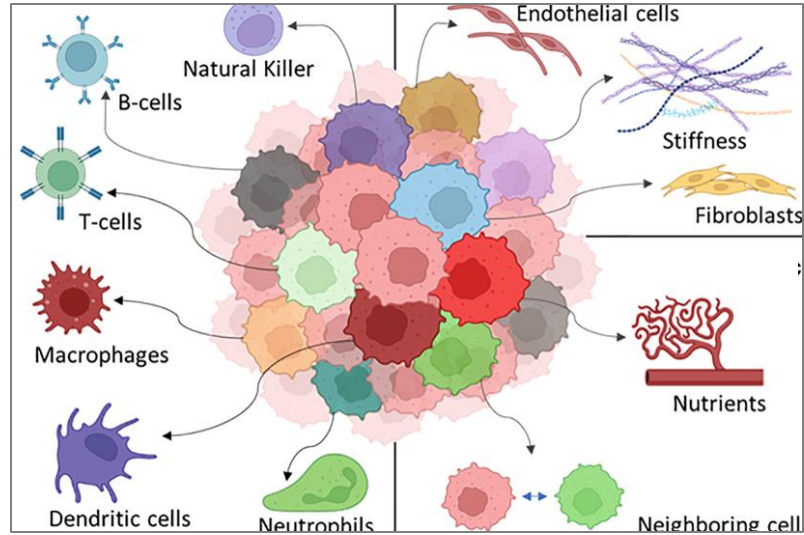


THE OHIO STATE UNIVERSITY



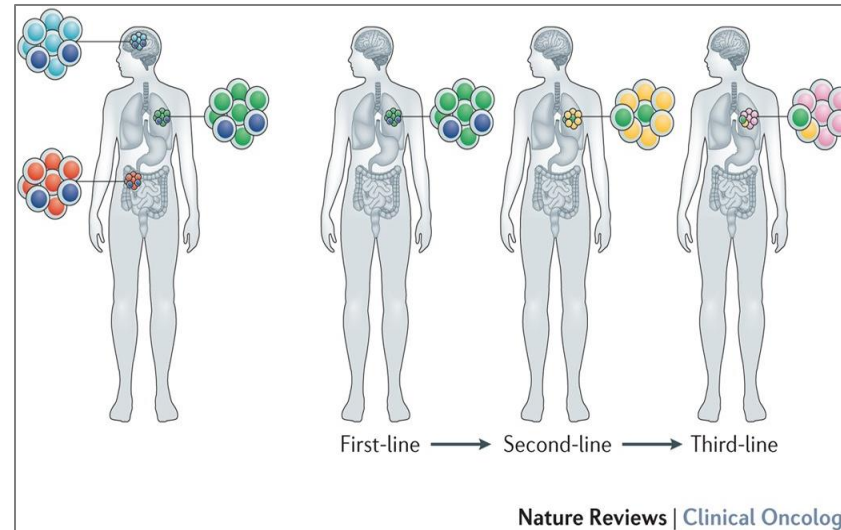
NATIONWIDE CHILDREN'S
When your child needs a hospital, everything matters.™

Tumors Comprise Diverse Cells that Adapt and Function Cooperatively



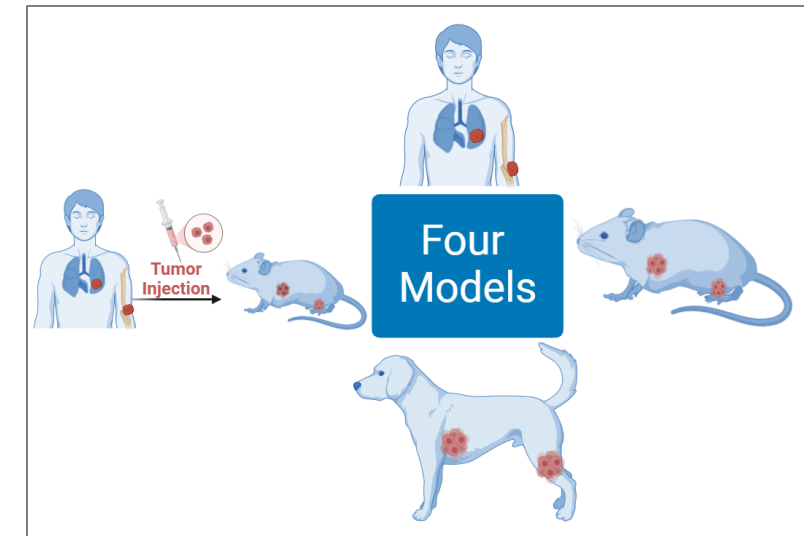
Intra-tumoral heterogeneity

DOI: [10.1038/nrclinonc.2017.166](https://doi.org/10.1038/nrclinonc.2017.166)



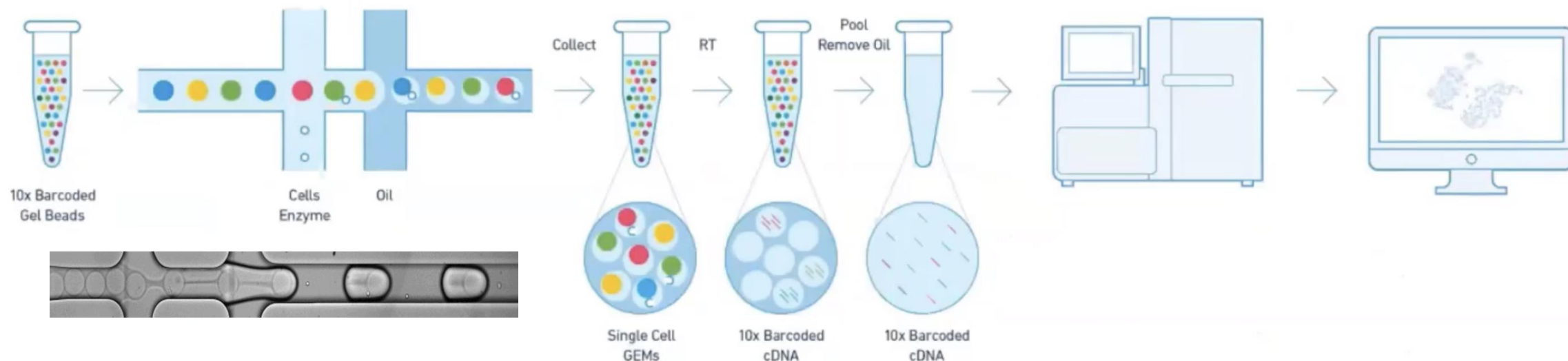
Site-specific and Temporal heterogeneity

DOI: [10.3389/fonc.2023.1164535](https://doi.org/10.3389/fonc.2023.1164535)



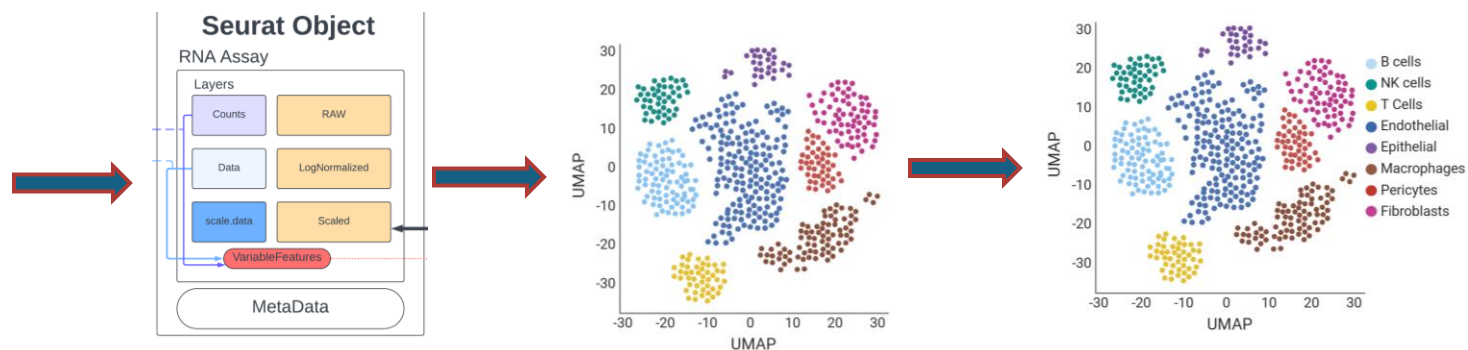
Inter-species heterogeneity

scRNAseq has Become a Powerful Tool for Studying Biology

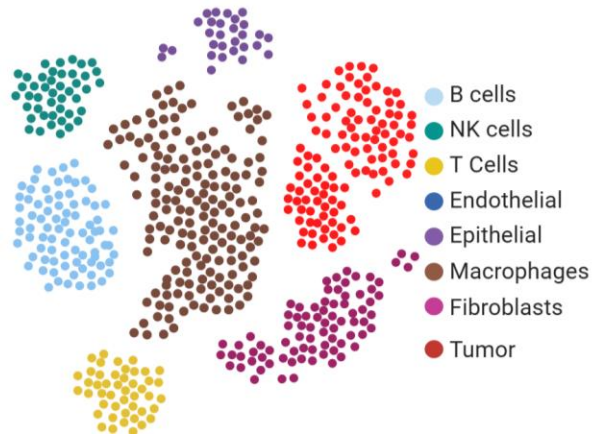


	Cell1	Cell2	...	CellN
Gene1	3	2	.	13
Gene2	2	3	.	1
Gene3	1	14	.	18
...
...
...
GeneM	25	0	.	0

Raw count matrix



Aims and Significance



1. Build a tool to streamline data analysis

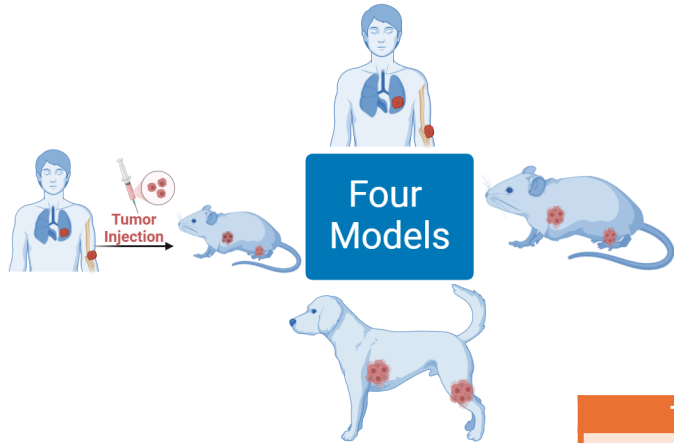


2. Facilitate collaboration



3. Allow exploration

Assembling a Comprehensive Dataset for Atlas



Type	Sub-Type	No. of Samples	Data Sources	No. of Cells	Methods
Human Patient	Primary	25	GEO, SJ	152,770	SC, SN
	Metastatic	36	GEO, NCH, NCI, SJ	221,271	SC, SN
Dog Patient	Primary	17	CSU, TU, UoM	110,827	SC
	Metastatic	16	CSU, TU	78,323	SC, SN
Human Xenograft	Primary	12	NCH, SJ	72,265	SC, SN
	Metastatic	12	NCH, SJ	59,207	SC, SN
Syngeneic Mouse	Primary	3	NCH, SJ	16,579	SC
	Metastatic	8	NCH	64,199	SC, SN
TOTAL	ALL	129	ALL	775,441	ALL

Data Sources: Gene Expression Omnibus (GEO), St. Jude Children's Research Hospital (SJ), Nationwide Children's Hospital (NCH), National Cancer Institute (NCI), Colorado State University (CSU), Tufts University (TU), University of Minnesota (UoM).

Methods: Single Cell (SC), Single Nucleus (SN)

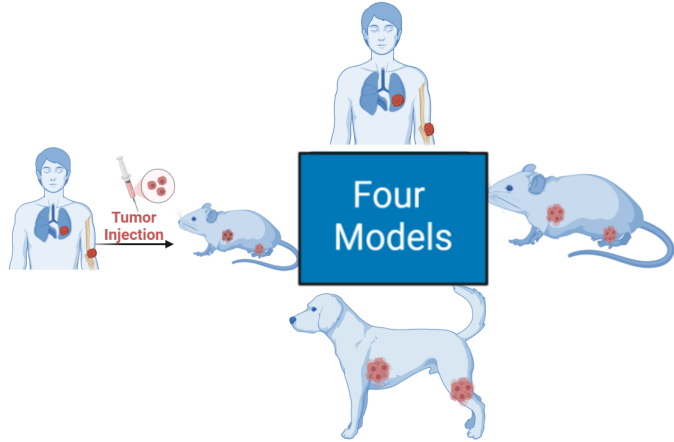
Note: Over **1,000,000** cells, including the samples used for tumor cell identification and reference validation.



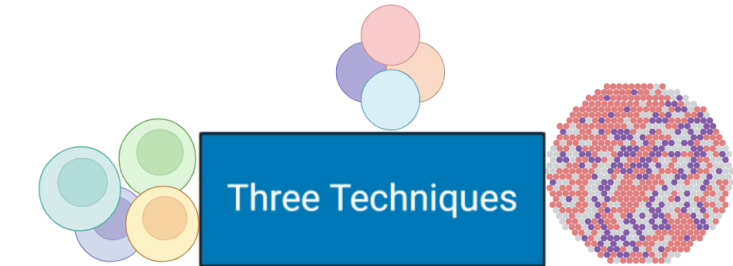
About
100
Samples

About
1,000,000
Cells

Presenting **Osteo-CAR** (**O**steosarcoma **C**ell-type **A**nnotation **R**eference)



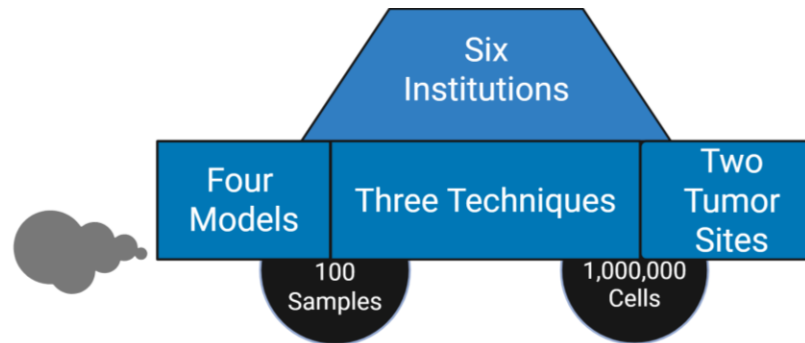
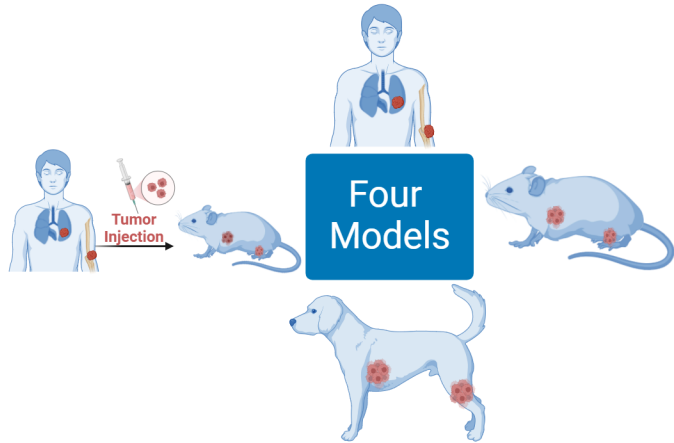
About
100
Samples



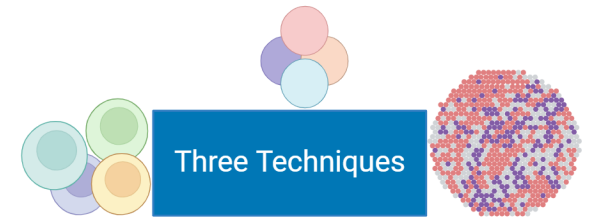
About
1,000,000
Cells



Presenting Osteo-CAR



About
100
Samples

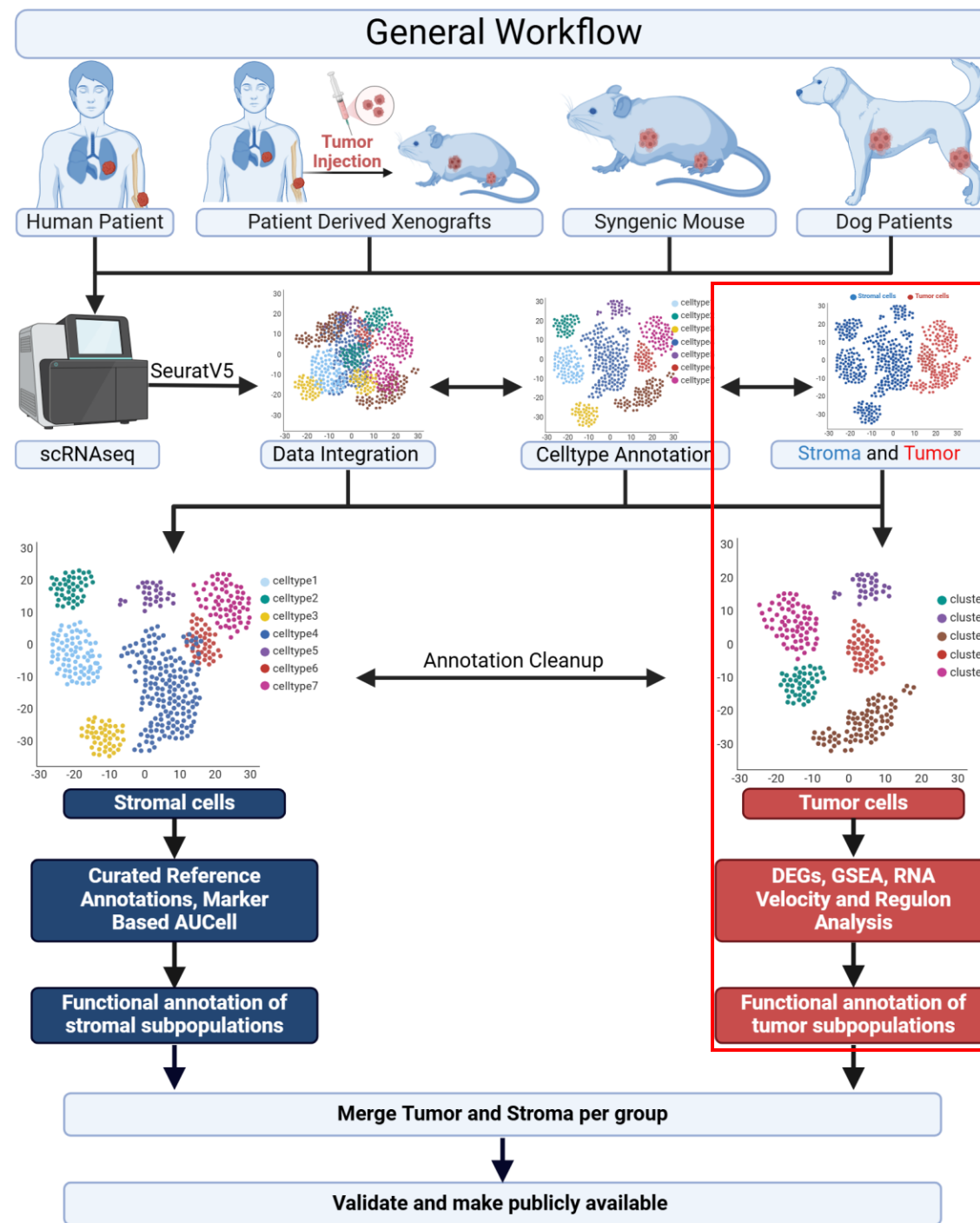


About
1,000,000
Cells



Data Analysis and Cell Type Annotation Pipeline

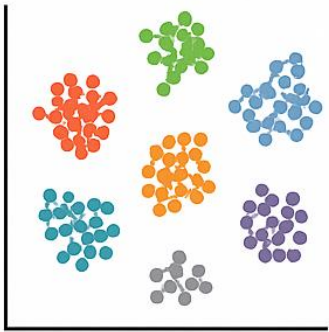
For simplification, this talk will focus on human patient data



Inconsistent Results from Conventional Tumor Cell Identification Methods Led to the Development of Custom Method(s)

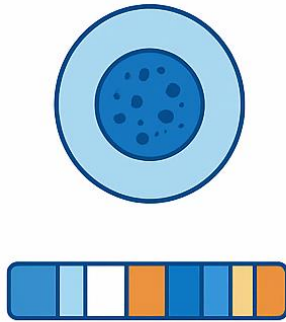
Conventional methods

scATOMIC



single cell Annotation
of TumOur Micro-
environments In pan-
Cancer settings

SCEVAN



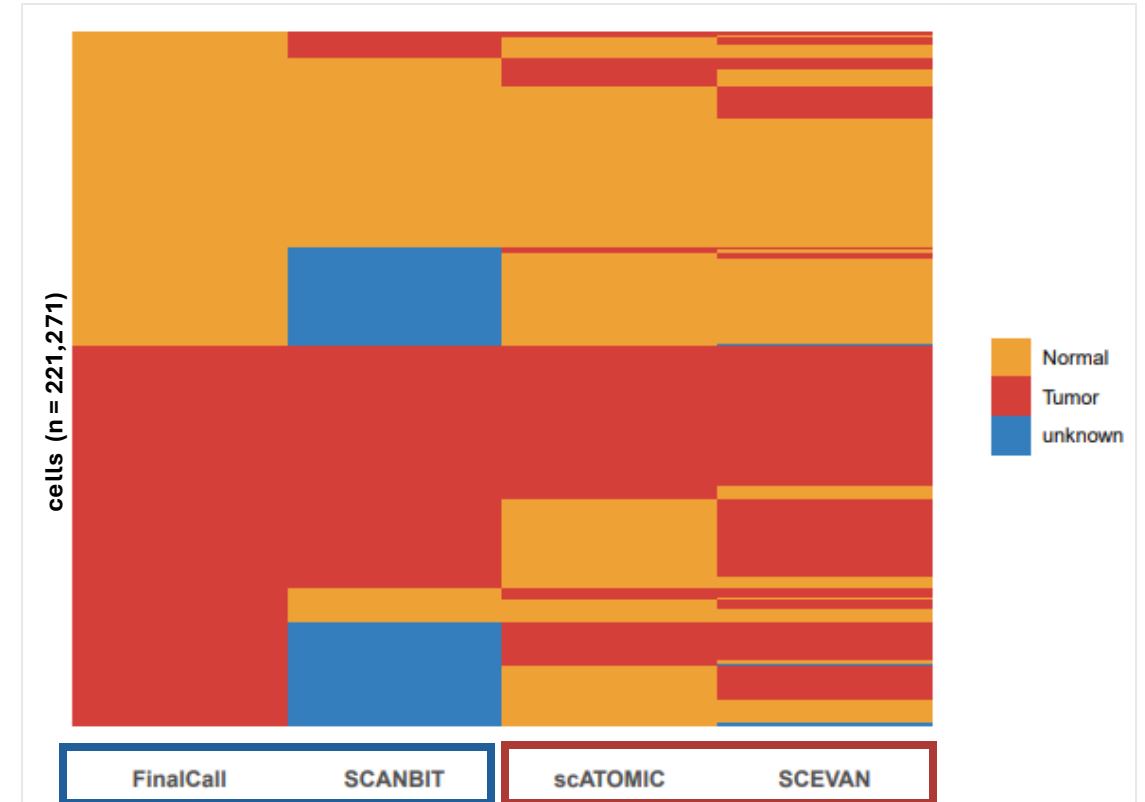
Single CELL
Variational
ANeuploidy
analysis

Novel method

SCAN-BIT



Single Cell Altered
Nucleotide-Based
Inference of
Tumor

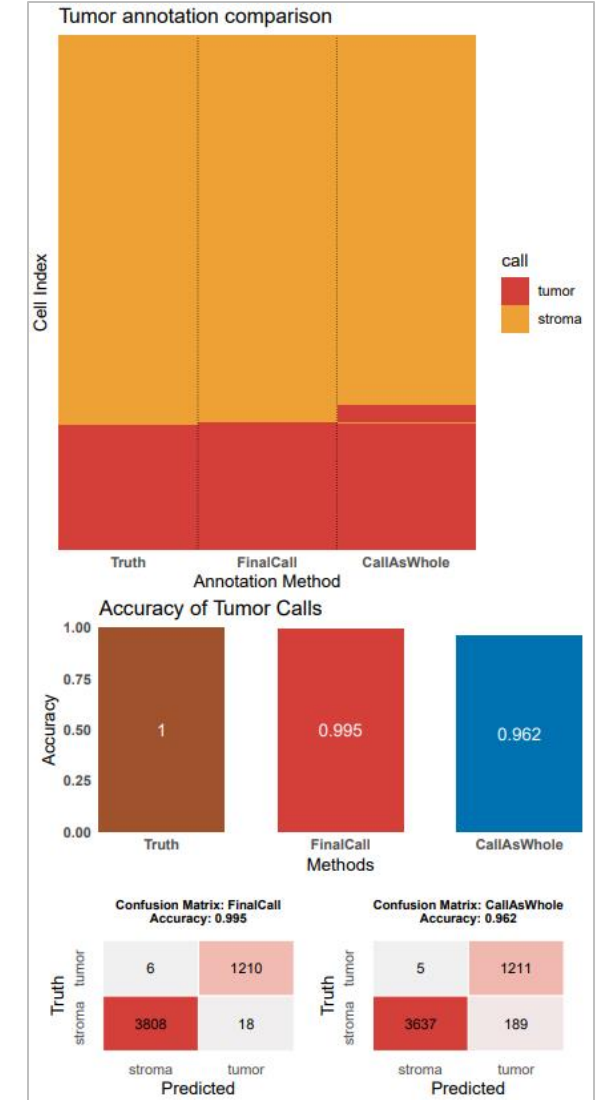
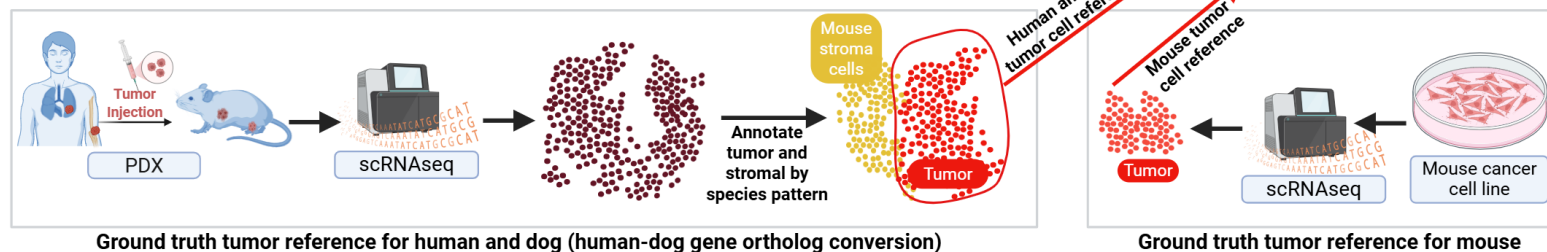
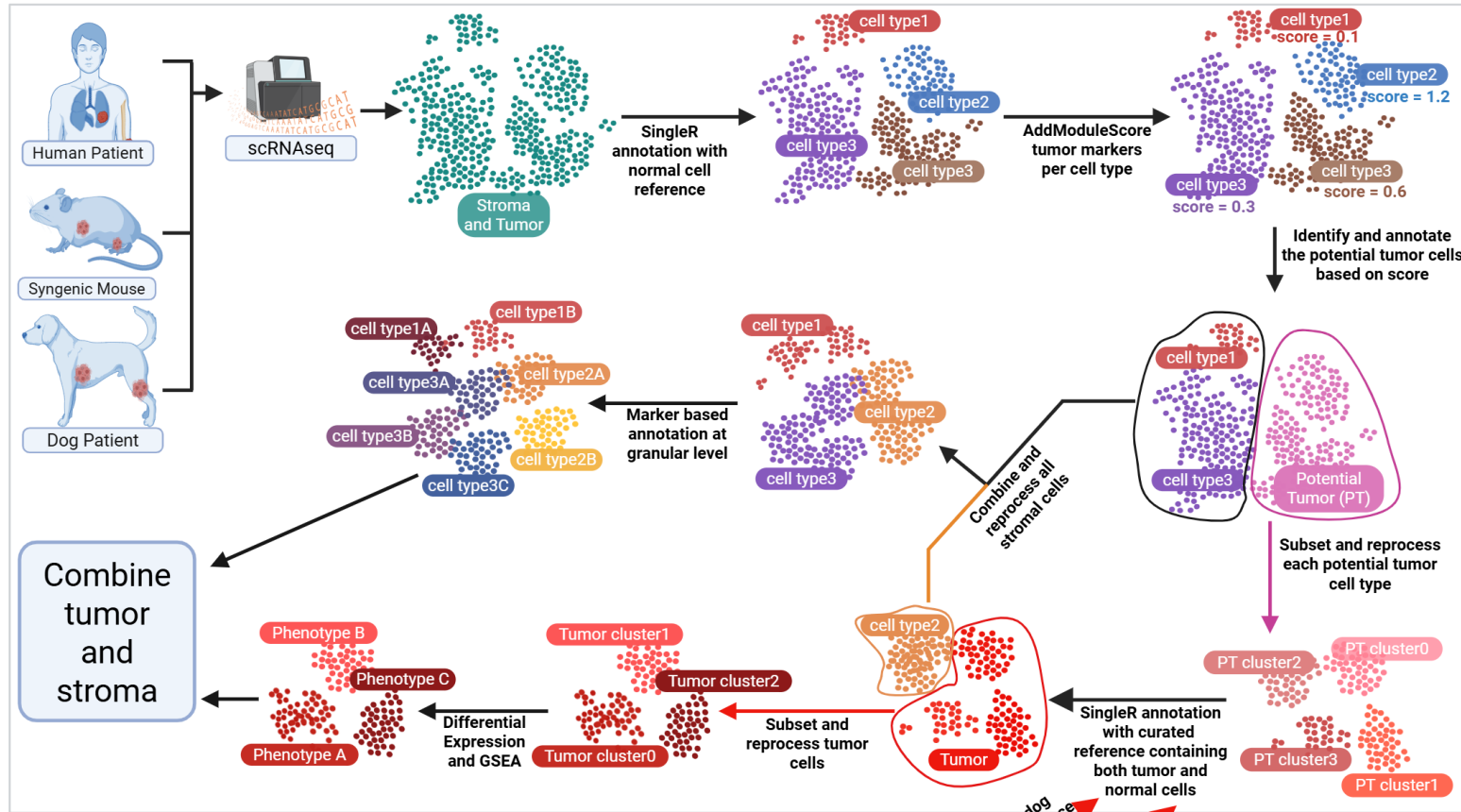


Novel methods being
developed in the lab

Conventional
methods

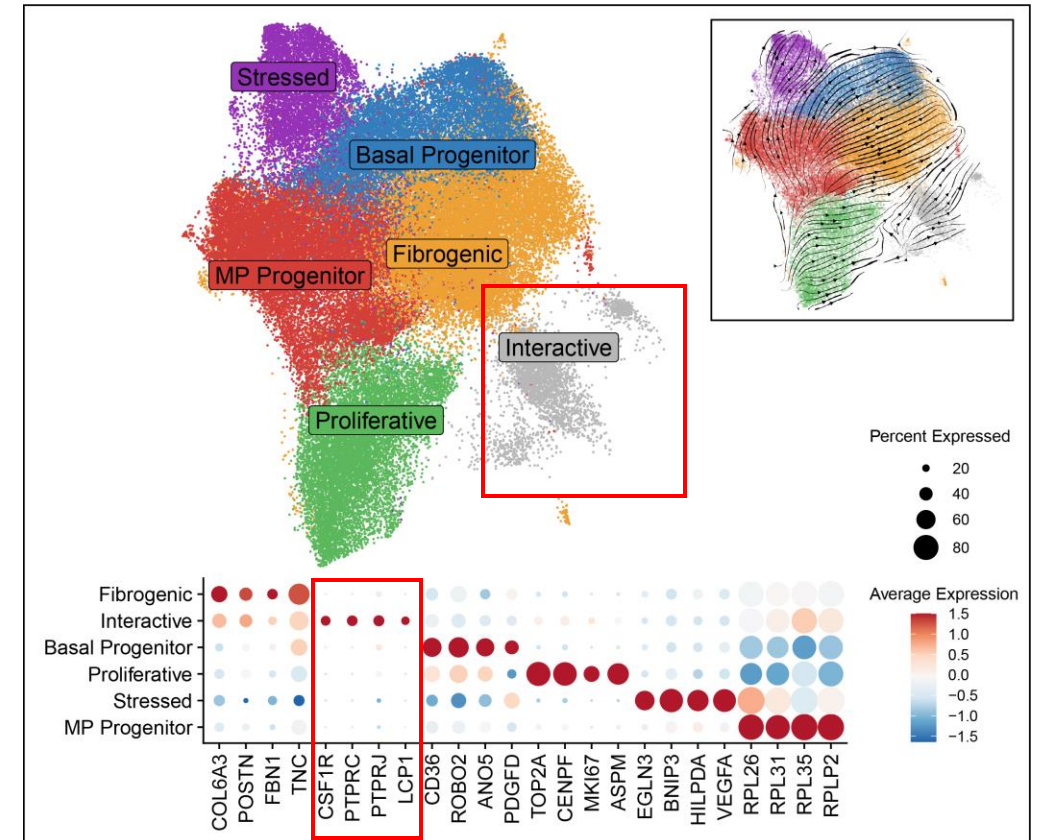


Our Custom Method of Identifying Tumor Cells Leverages the Cross-Species Data

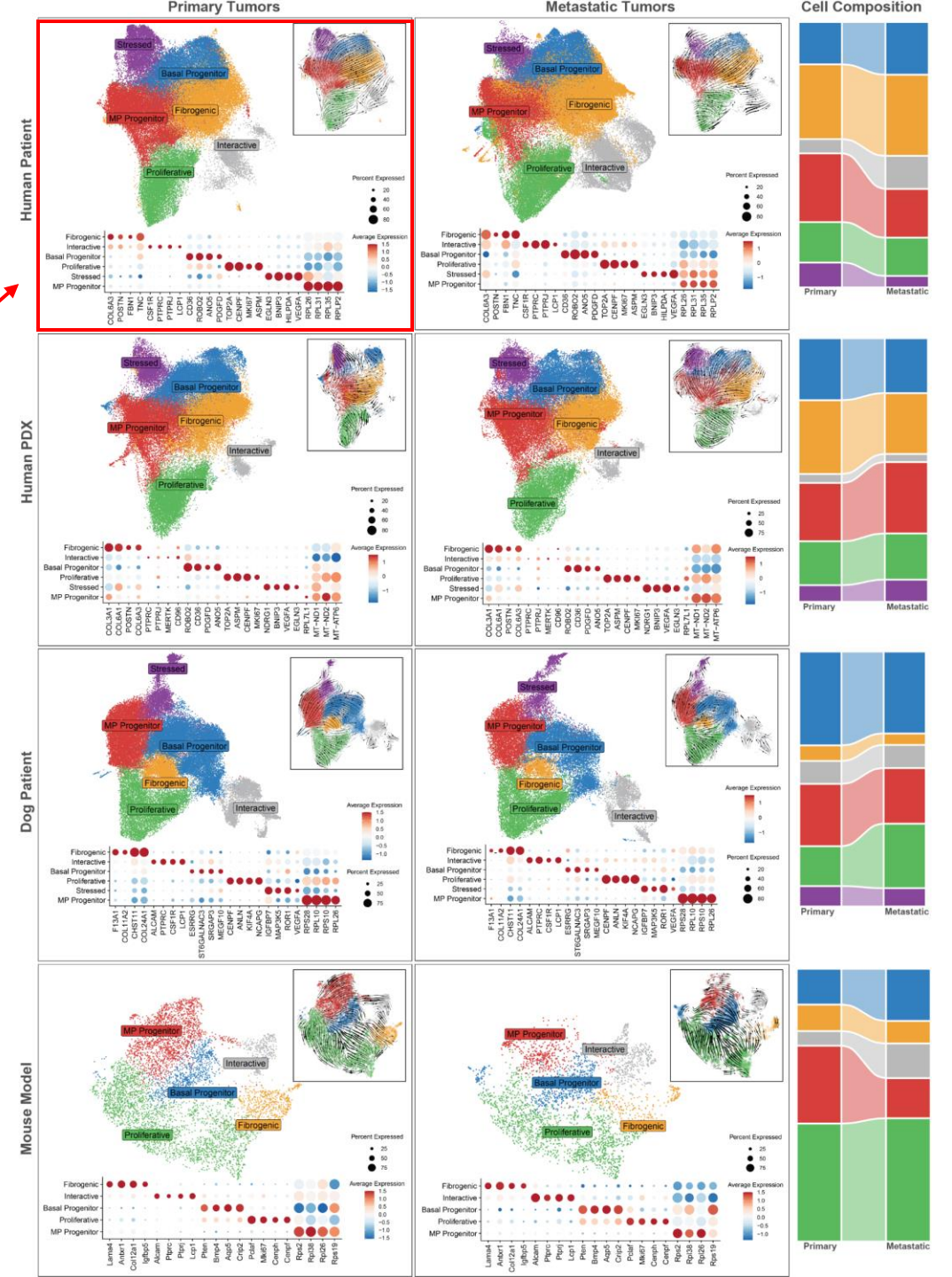
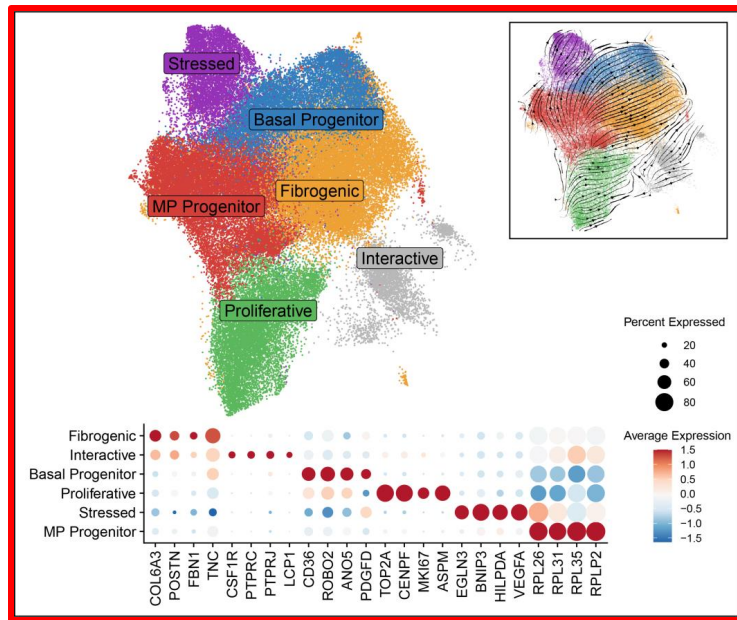


Tumor Subpopulations are Described by Specific Pathways

- **Proliferative**
 - Cell cycle pathways
- **Stressed**
 - Hypoxia and angiogenic pathways
- **Basal Progenitor**
 - Fewer pathways
- **Metabolically Primed (MP) Progenitor**
 - OxPhos and Metabolic pathways
- **Fibrogenic**
 - ECM and fibrotic pathways
- **Interactive**
 - Inflammatory and Immune-related pathways



Osteosarcoma Tumors Exhibit Conserved Cellular Heterogeneity Across Sites and Species



Acknowledgments

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- Roberts Lab
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 - Daniel Regan, DVM, PhD (CSU)
 - Heather Gardner, DVM, PhD (Tufts)
 - Jaime Modiano, DVM, PhD (UoM)
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Dr. Anand Patel



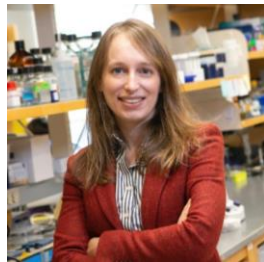
Dr. Troy McEachron



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Dr. Jaime Modiano



Dr. Heather Gardner

