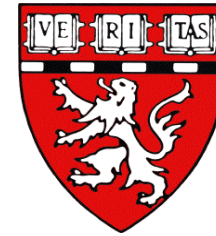




BRIGHAM AND
WOMEN'S HOSPITAL
| The Lung Center |



Lung Research Center Symposium

Non-Small Cell Lung Cancer: Large Scale Single Cell Sequencing of Lung Libraries for Tumor Comparison

By: Ahmed Sadek, MD

Mentor: Raphael Bueno, MD

*Disclosures: Funded by Roche/Genentech

Why Single-Cell?

Bulk RNA Sequencing

- Genetic expression profile is averaged among the entire sample
- Lacks details of intra-sample heterogeneity and microenvironment

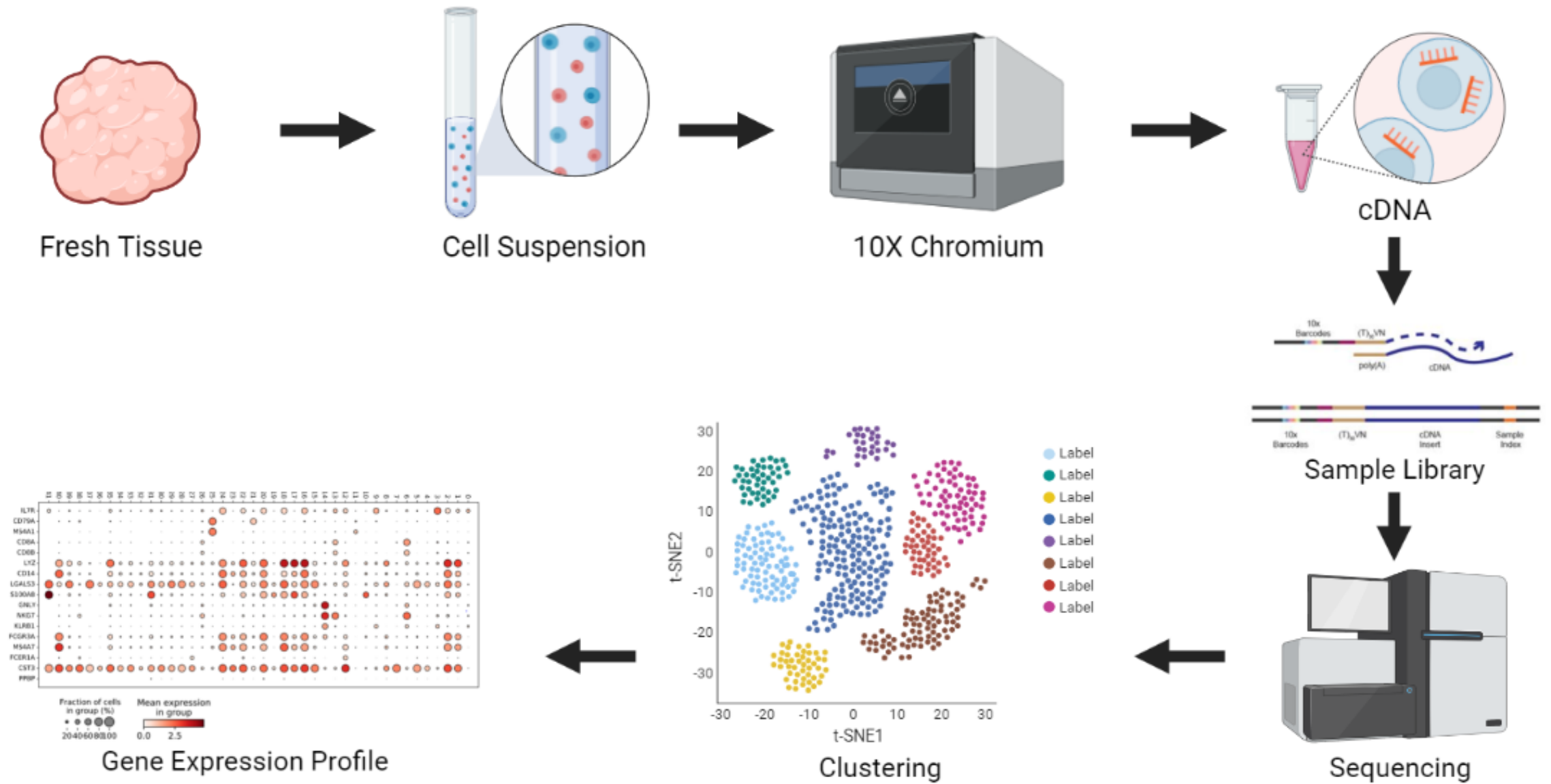


Single-Cell Sequencing

- Ability to identify cell types and their transcriptional profiles
- Differential gene expression between individual immune, tumor, and stromal cells

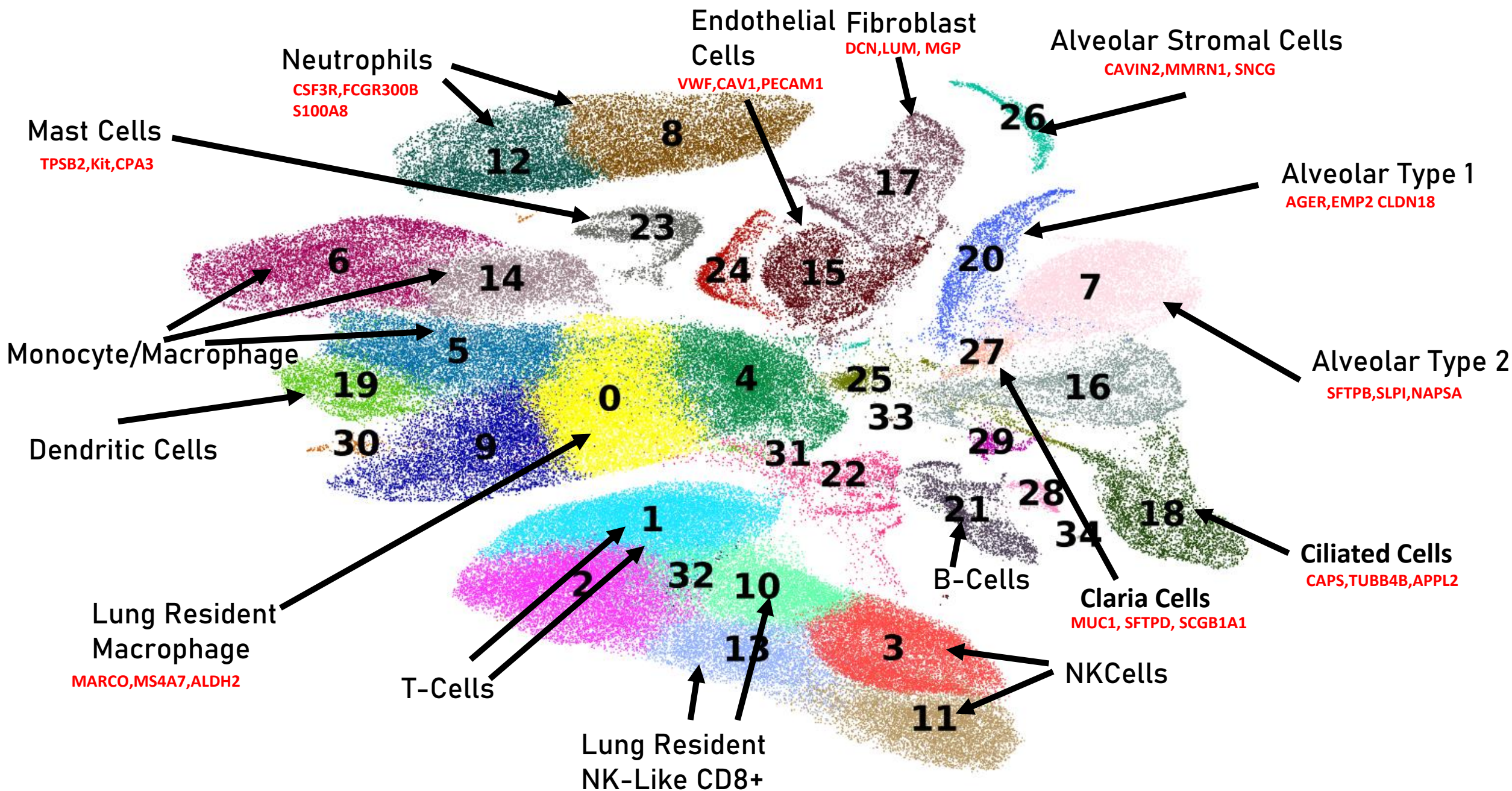


Work Flow



Normal Lung Library Overview

Category	Statistic
Total Patient Libraries	52
Total Paired Reads	
Total Transcriptome Bases (Insert Bases only)	
Total Bases Sequenced (Insert + Barcodes Bases)	
Median Median UMI Per Cell	
Total Cells	179,932



Significance and Future Directions

- The largest collection of sequenced cells from normal lung parenchyma
- Comparison with single-cell transcriptomes from tumor tissue
- Characterize molecular pathways of NSCLC
- Identify prognostic and therapeutic targets for therapy

Acknowledgements

Bueno Lab

Raphael Bueno MD

Matthew Brian Couger, PhD

Assunta De Rienzo, PhD

William Richards, PhD

Corinne Gustafson, PhD

David Severson, DPhil*

Samuel Freyaldenhoven, MD*

Juuso Paajanen, MD*

Vivian Wang, MD*

Benjamin Wadowski, MD*

Mary Dao*

Molly Likes*



HARVARD
MEDICAL SCHOOL

BRIGHAM HEALTH



**BRIGHAM AND
WOMEN'S HOSPITAL**

Division of Thoracic Surgery

Julianne Barlow

Simona Innocenti

Tina Sidopoulos

Eugene Kim

Sarah Lobo

Sam Weinhouse

Kimberly Vermilya

Roche

Genentech