## Breakout Session 6:

# The NHBLI LungMAP Cloud Ecosystem: Connecting Diverse Digital and Lung Biology Resources

Dr. Nathan Salomonis
*Associate Professor, Cincinnati Children's Hospital Medical Center*

LungMAP
Molecular Atlas of Lung Development Program

NIH National Heart, Lung, and Blood Institute

# The NHBLI LungMAP Cloud Ecosystem: Connecting Diverse Digital and Biology Resources

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# Grand Challenges in Lung Biology

LungMAP Molecular Atlas of Lung Development Program

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- Regeneration and repair
- Role of stem cells
- Developmental hierarchies
- Mechanisms of disease
- Genetics and infection

***Addressing these questions challenges require:***

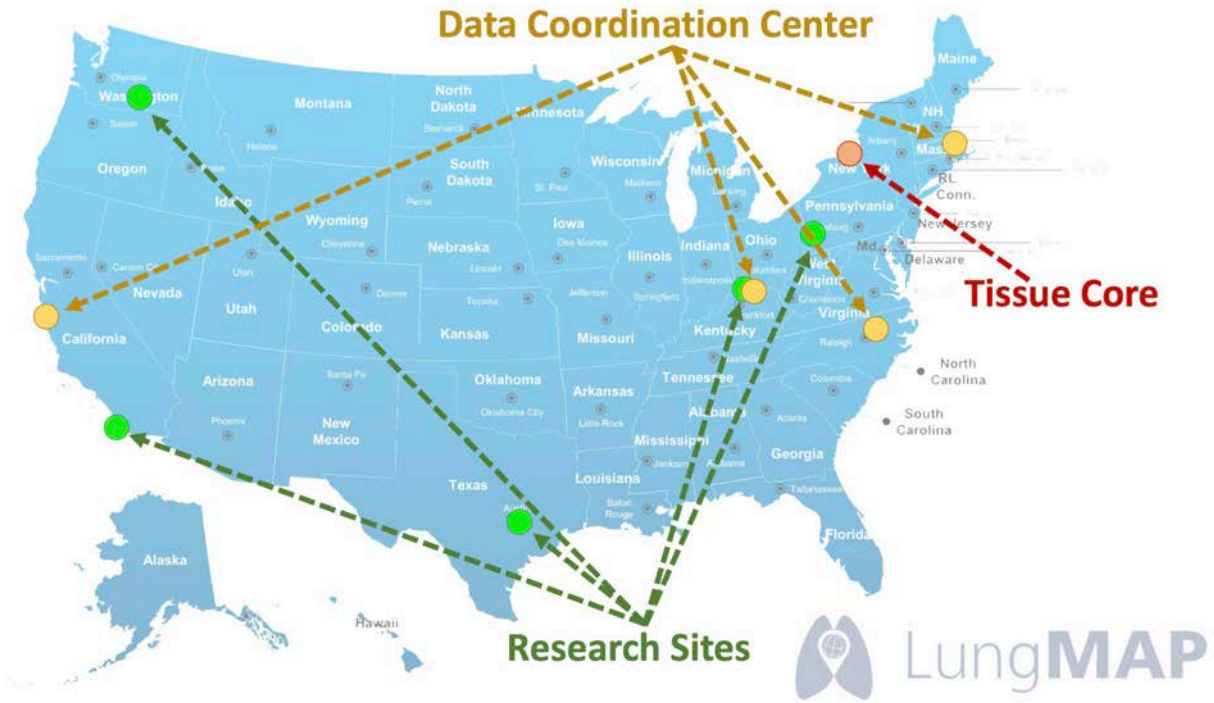
- Team science approaches with diverse experts
- New tools and techniques to construct systems models
- Integrated atlas level initiatives

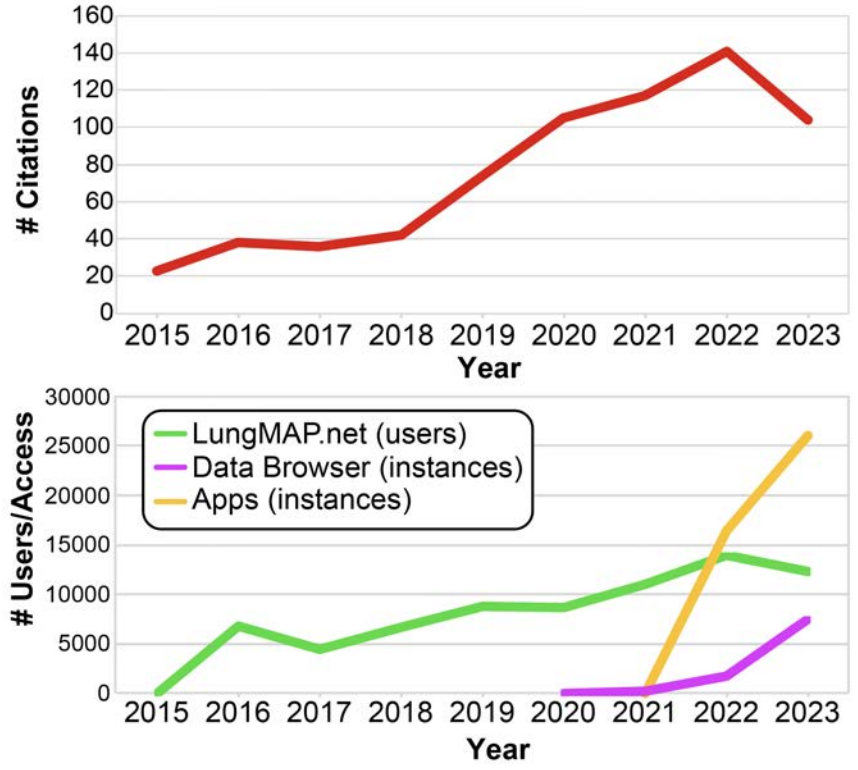
# The LungMAP Consortium

LungMAP Molecular Atlas of Lung Development Program

NIH National Heart, Lung, and Blood Institute

- NHBLI consortia spanning 6 research centers over the last 10 years
- Human Tissue Core at the University of Rochester (Gloria Pryhuber)
- Data Coordination Center: CCHMC, Broad, UCSC, RTI
- *Entering Phase 3 in 2023 to create accessible atlases of lung disease*



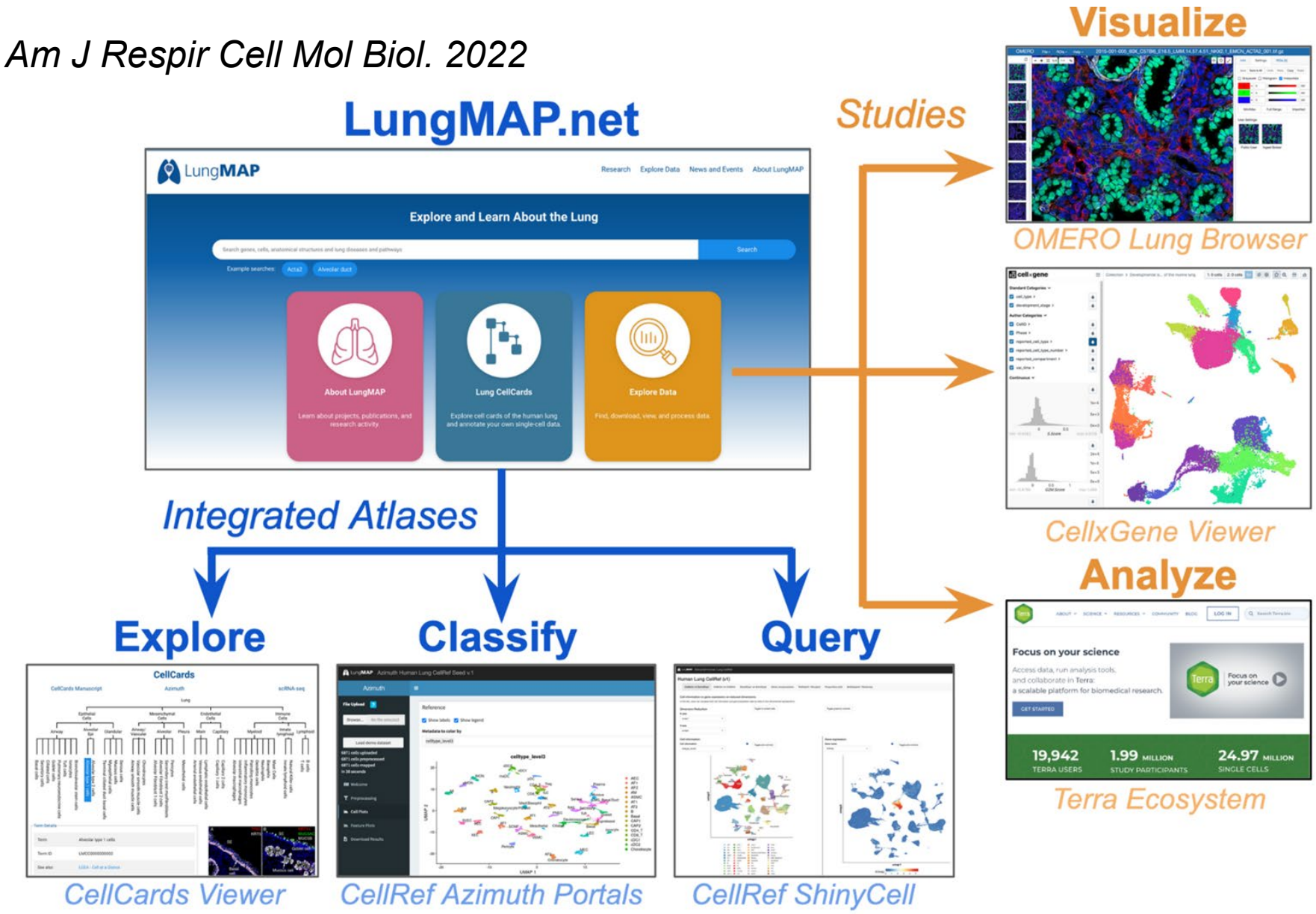



# LungMAP Knowledgebase

LungMAP Molecular Atlas of Lung Development Program

NIH National Heart, Lung, and Blood Institute

*Gaddis et al. Am J Respir Cell Mol Biol. 2022*



# LungMAP.net Ecosystem

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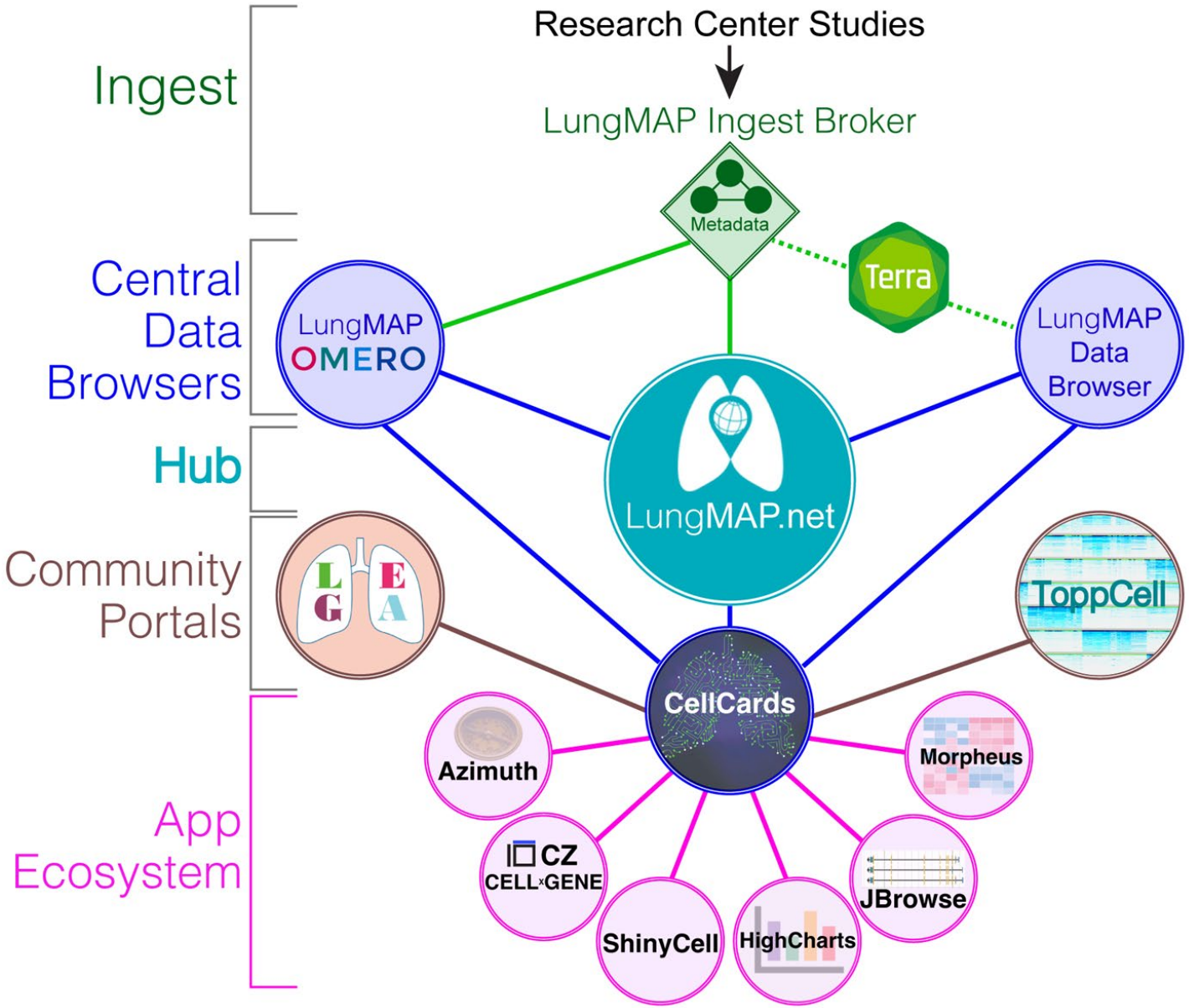


- Redesigned website
- CellCards and App focused
- Driving towards maximal interactivity (within/between)
- Pushing data and analysis to the cloud.

*Gaddis et al. Am J Respir Cell Mol Biol. 2022*

# What are the Products of LungMAP?

LungMAP
Molecular Atlas of Lung Development Program

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- **Insights**: New cell-states, regulatory models
- **Tissues**: Biopsies, whole lung
- **Data**: Omics, imaging
- **Protocols**: Experimental, analytical
- **Tools**: Organoids, omics, informatics

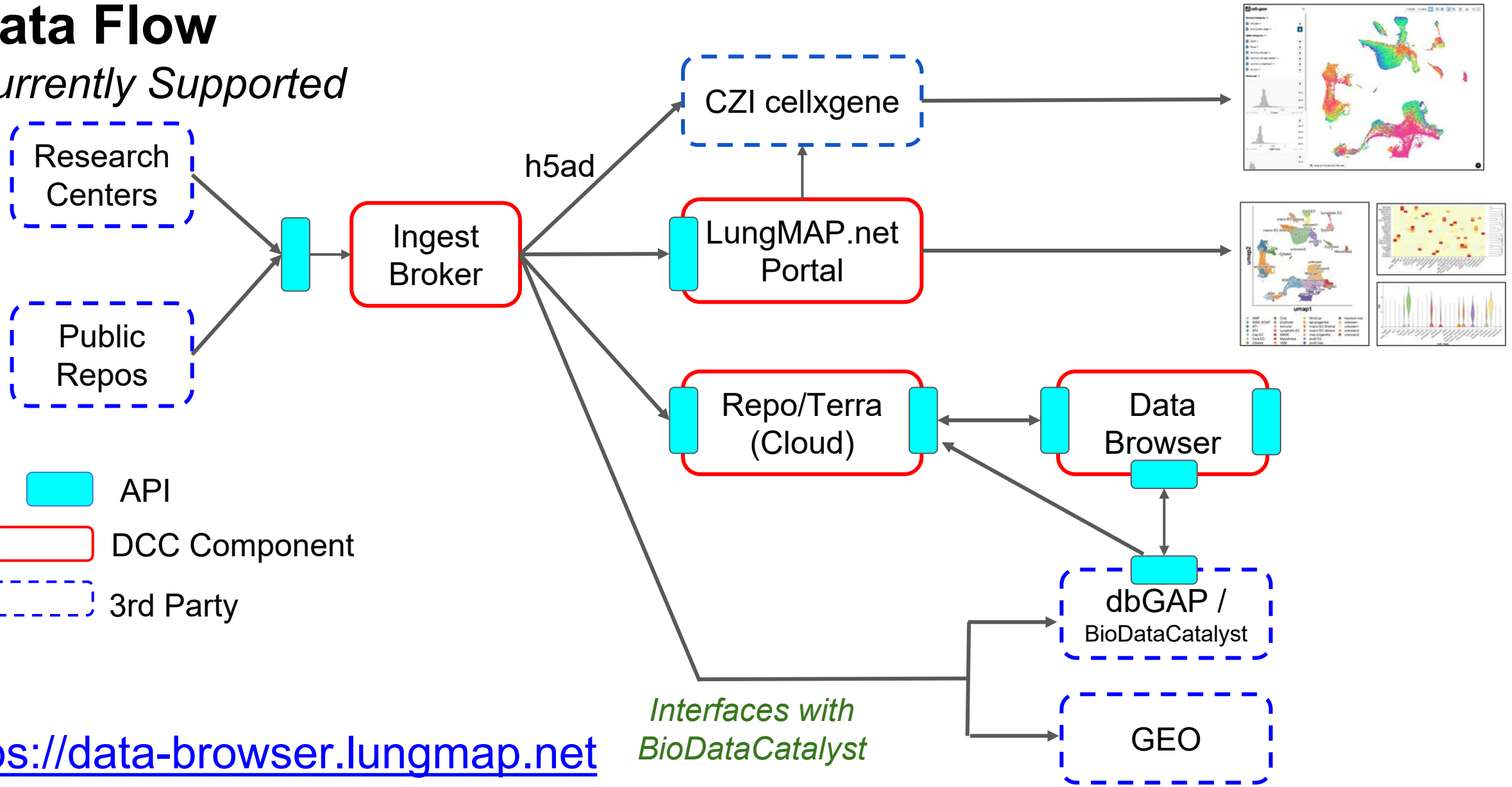
# LungMAP Data Flow

LungMAP Molecular Atlas of Lung Development Program

NIH National Heart, Lung, and Blood Institute

## Data Flow

*Currently Supported*




https://data-browser.lungmap.net

# LungMAP.net Website

LungMAP
Molecular Atlas of Lung Development Program

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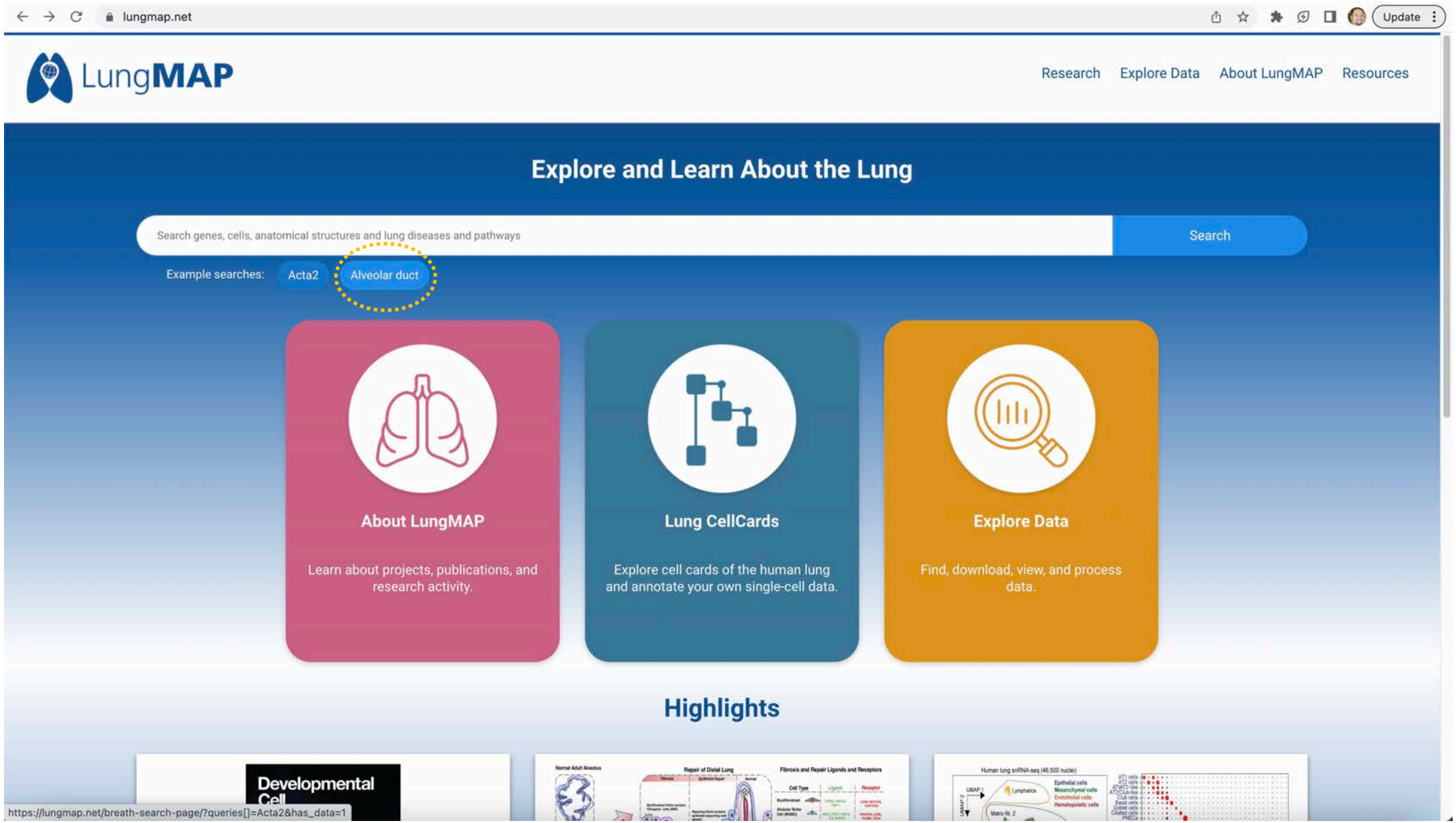

# Tissues

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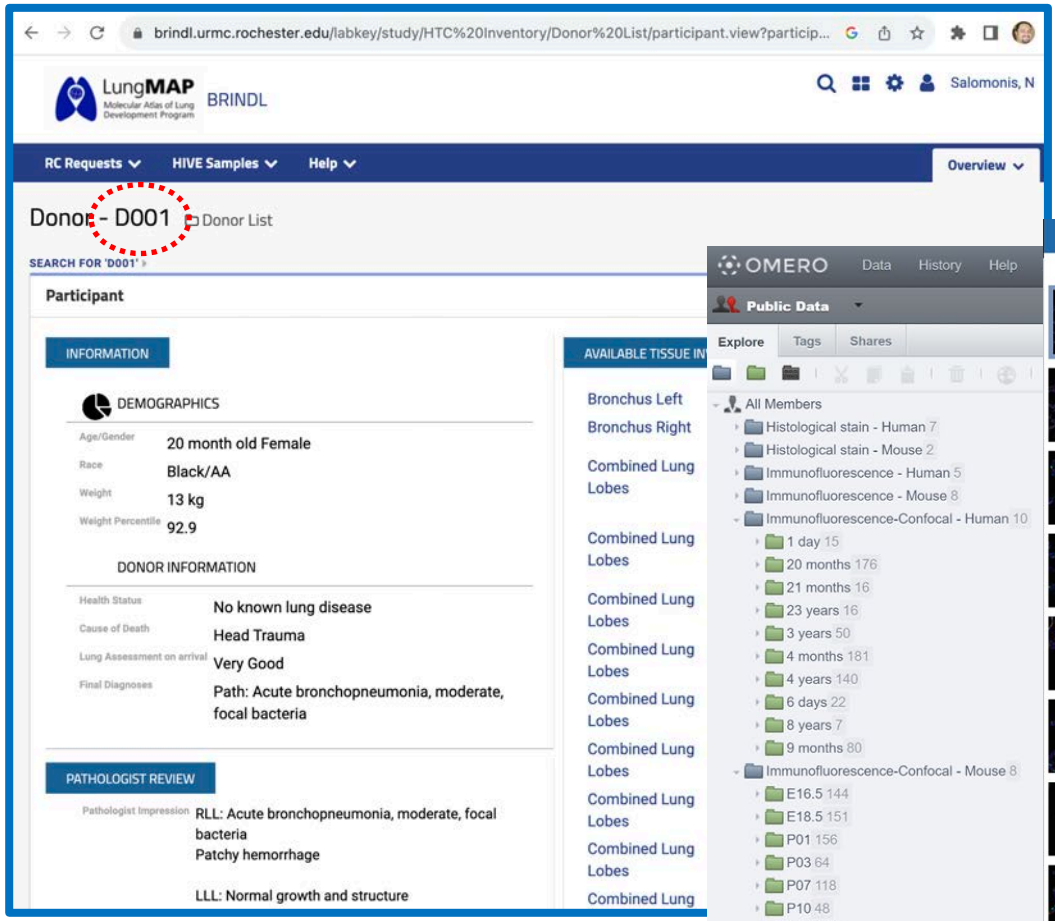
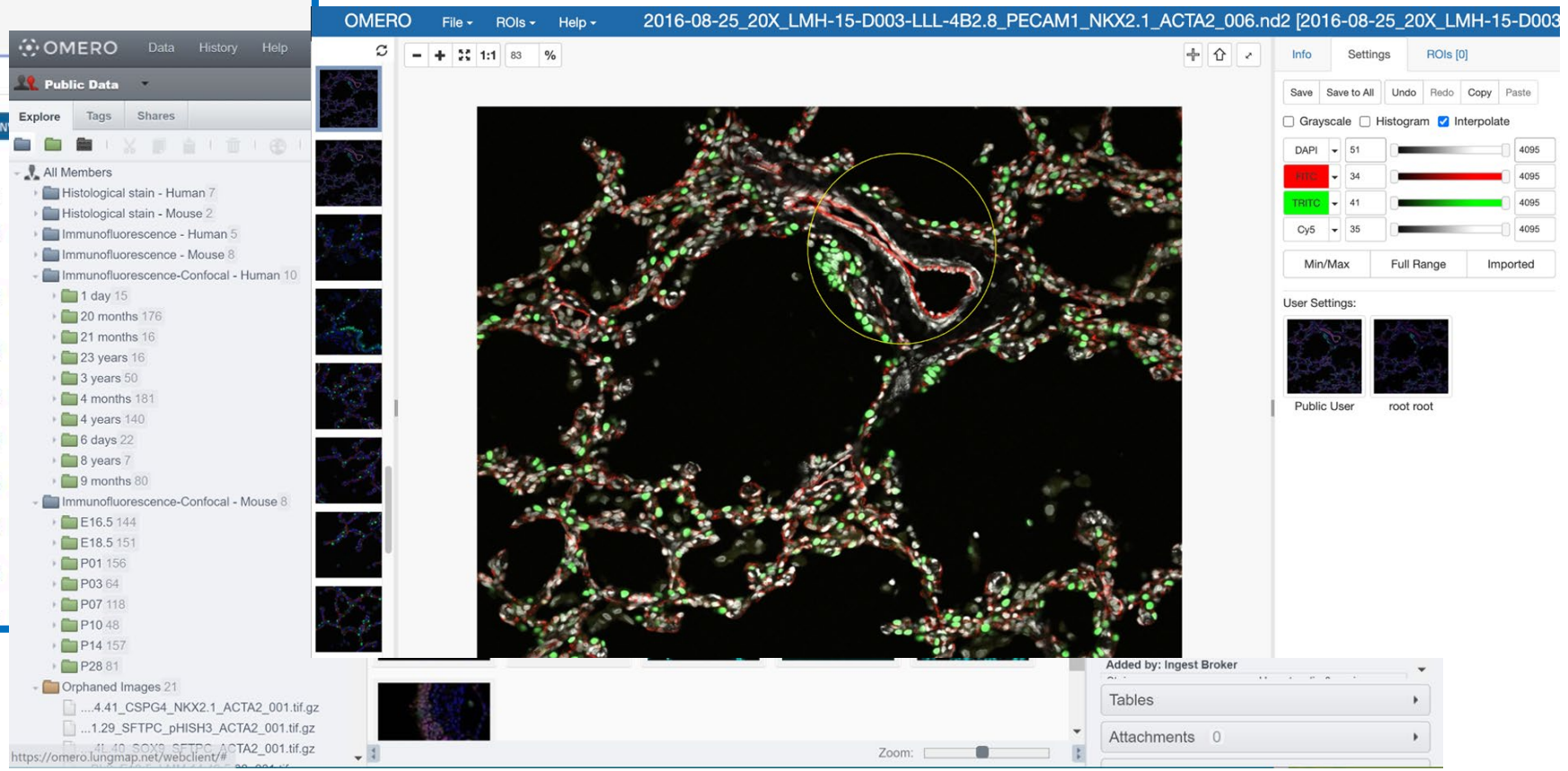
## BRINDL Tissue Repository




## OMERO Image Viewer



# Cross-Consortia Cell-Type Curation

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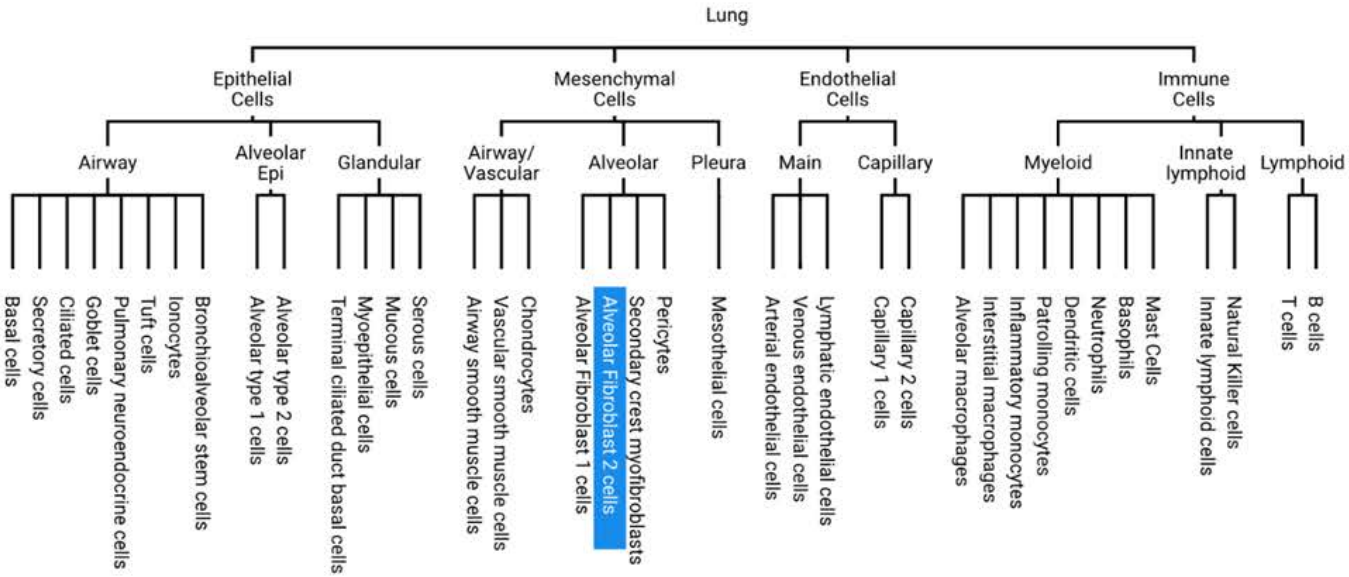
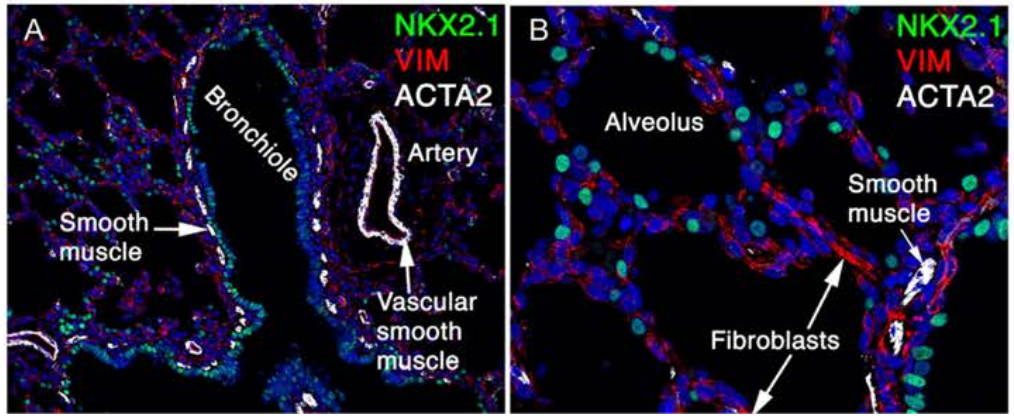
## CellCards

CellCards Reference | CellRef scRNA-seq | CellRef ATAC-seq | CellRef Azimuth




Term Details

| | |
|---|---|
| Term | Alveolar Fibroblast 2 cells |
| Term ID | LMCC0000000026 |
| See also | LGEA - Cell at a Glance |
| Related synonyms | Type-2 associated stromal cell (TASC)(Chung, et al., 2018) \| Type-2 associated stromal cell (TASC)(Chung, et al., 2018) \| Adventitial fibroblast (Travaglini, et al., 2020) \| Adventitial fibroblast (Travaglini, et al., 2020) \| Matrix fibroblast 2 \| MANC (Zepp, et al., 2017) (Park, et al., 2019) (Torday, et al., 2016) \| MANC (Zepp, et al., 2017) (Park, et al., 2019) (Torday, et al., 2016) \| Mesenchymal alveolar niche cell |



# JBrowse - Epigenomic Data Browser

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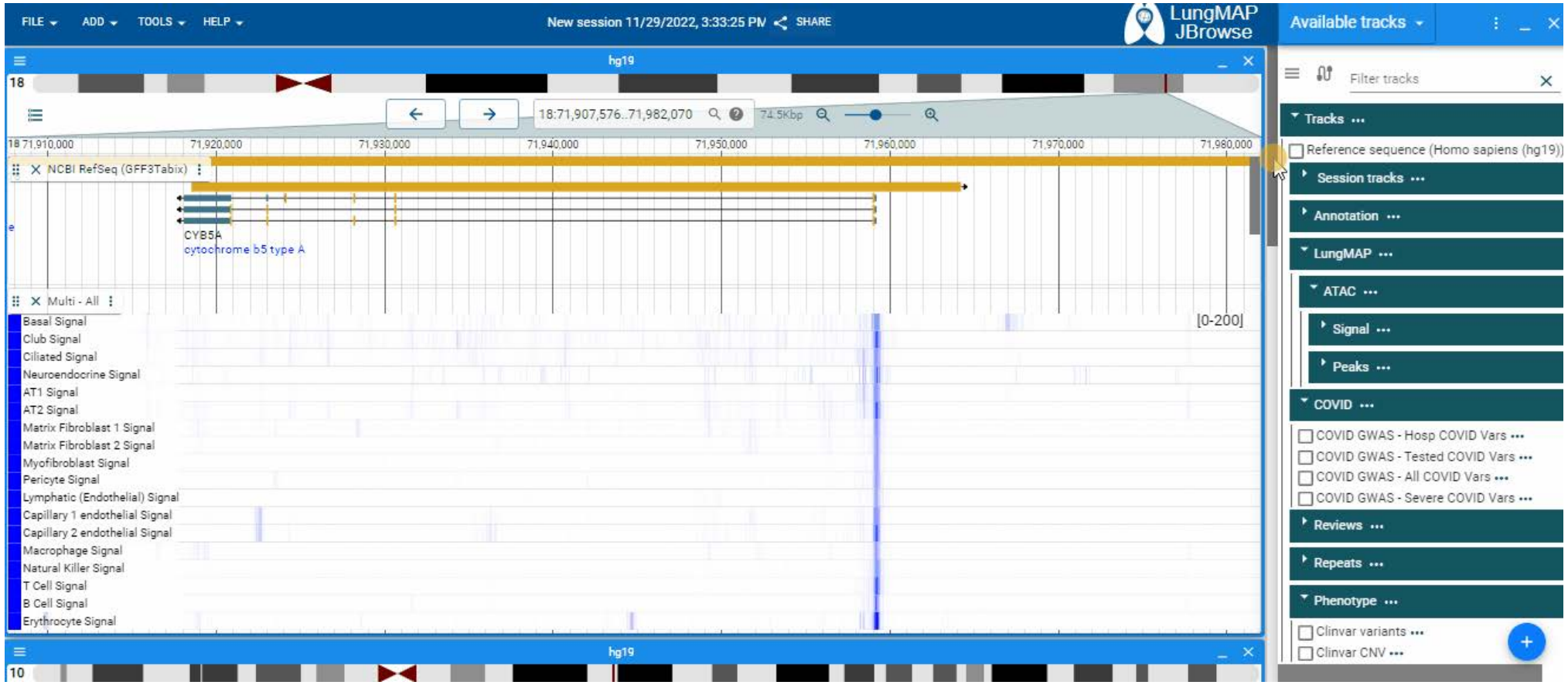
- View pre-loaded, UCSC Track Hub, or bring-your-own-track
- View and compare multiple loci (including species*)



# LungMAP App Ecosystem

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## Human CellCards Multi-Study CellRef 1.0 Atlas

Minzhe Guo (CCHMC) | Geremy Clair (PNNL) | Joshua N. Adkins (PNNL) | Gloria Pryhuber (HTC/URMC) | Ravi Misra (HTC/URMC) | Bruce Aronow (CCHMC) | Timothy L. Tickle (Broad) | Nathan Salomonis (CCHMC) | Xin Sun (UCSD) | Edward E. Morrisey (UPenn) | Jeffrey A. Whitsett (CCHMC) | Yan Xu (CCHMC)

How to explore data (tutorial)

**Description**

The "LungMAP Human Lung CellRef" atlas incorporates 48 well-defined lung cell types (CellCards) catalogued from diverse anatomic locations and stages of lung maturation. This atlas spans sc/snRNA-seq of 505,256 lung cells from 148 normal human lung samples from 104 donors from parenchyma, trachea, bonchi, bronchus SMG and small airway. This study includes 21 new lung samples. An accompanying R-shiny app (Azimuth) enables fast supervised annotation of user-provided single-cell RNA-Seq datasets (see below).

**LungMAP ID:** LMEX0000004396

**Organism:** Human

**Stages:** Adult | Child | Adolescent

**Assay type:** Single-cell RNA-seq

**Technology:** 10x Genomics

**Reference:** Guo, et al. (2022)

**Exploratory Tools** Samples Downloads

| ShinyCell | CellCards | Azimuth | JBrowse | LGEA | CELLxGENE | MORPHEUS Interactive Heatmap Browser | Chart View | Omics Data Browser |
|---|---|---|---|---|---|---|---|---|
| (Tutorial) | (Tutorial) | (Tutorial) | | (Tutorial) | (Tutorial) | (Tutorial) | (Tutorial) | (Tutorial) |

# LungMAP App Ecosystem

LungMAP Molecular Atlas of Lung Development Program

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## Visualize Data

Filter by: Species | Age Range | Sample Type | Researcher | Technology

Single-Cell RNA-seq (32) | RNA-seq (10) | mRNA (1) | microRNA (3) | Proteomics (10) | Metabolomics (1) | Lipidomics (4) | Methylation (5) | 2D Imaging (3919 sets)

Search:

| Dataset | Species | Stage | Cells | Explore |
|---|---|---|---|---|
| Human CellCards Multi-Study CellRef 1.0 Atlas | Homo sapiens | Adult \| Child \| Adolescent | 505256 | |
| Mouse CellCards Multi-Study CellRef 1.0 Atlas | Mus musculus | E16.5-E17.5 \| E17.5-E19.5 \| P0-P3 \| P4-P36 | 95658 | |
| Single cell transcriptomic signatures of normal human newborn, child and adult lungs | Homo sapiens | Neonate \| Child \| Adult | 46500 | |
| Single cell transcriptomic profiling identifies molecular phenotypes of newborn human lung cells | Homo sapiens | Neonate | 5499 | |
| Systematic identification of 58 lung cell populations in bronchi and parenchyma from 3 normal lungs | Homo sapiens | Adult | 65662 | |
| A molecular single-cell lung atlas of lethal COVID-19 | Homo sapiens | Adult | 116314 | |
| Single-cell RNA-seq reveals ectopic and aberrant lung-resident cell populations in idiopathic pulmonary fibrosis | Homo sapiens | Adult | 312928 | |
| Single-cell RNA-seq of 13 normal, LPS-exposed, or anti-inflammatory treated third trimester Rhesus macaque lungs | Macaca mulatta | Saccular | 120042 | |

# Interactive Visualization & Analysis

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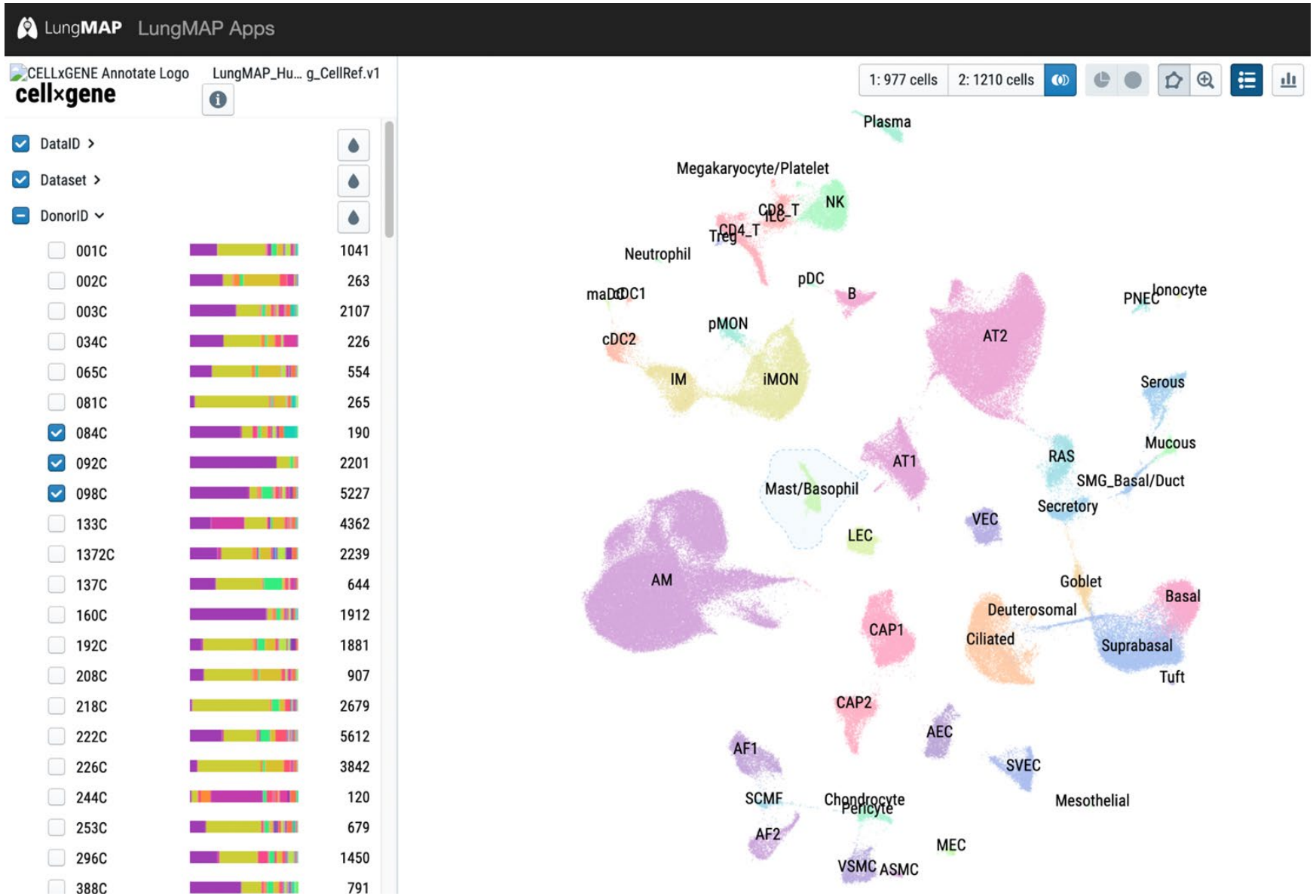

# Interactive Visualization & Analysis

LungMAP Molecular Atlas of Lung Development Program

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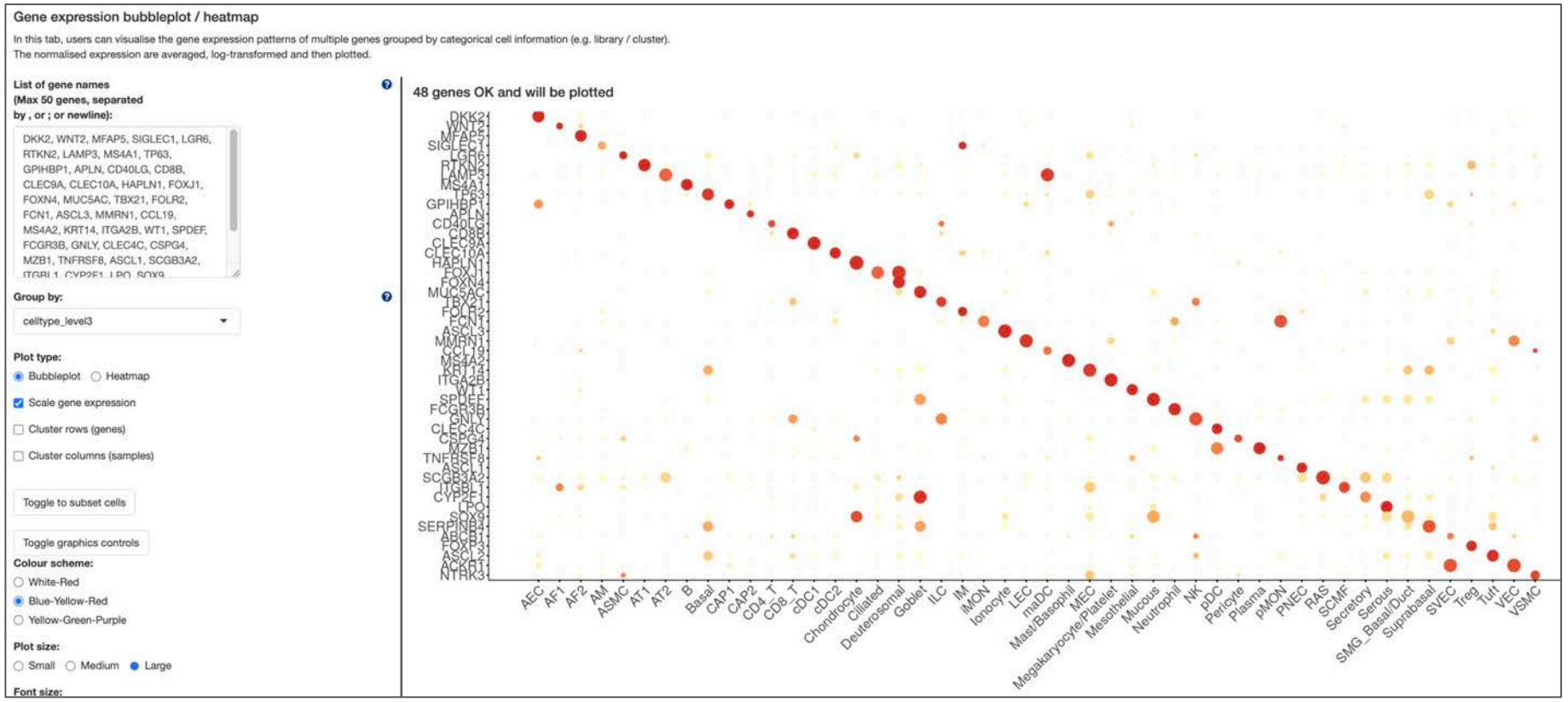
# Interactive Visualization & Analysis

LungMAP Molecular Atlas of Lung Development Program

NIH National Heart, Lung, and Blood Institute



# Interactive Visualization & Analysis

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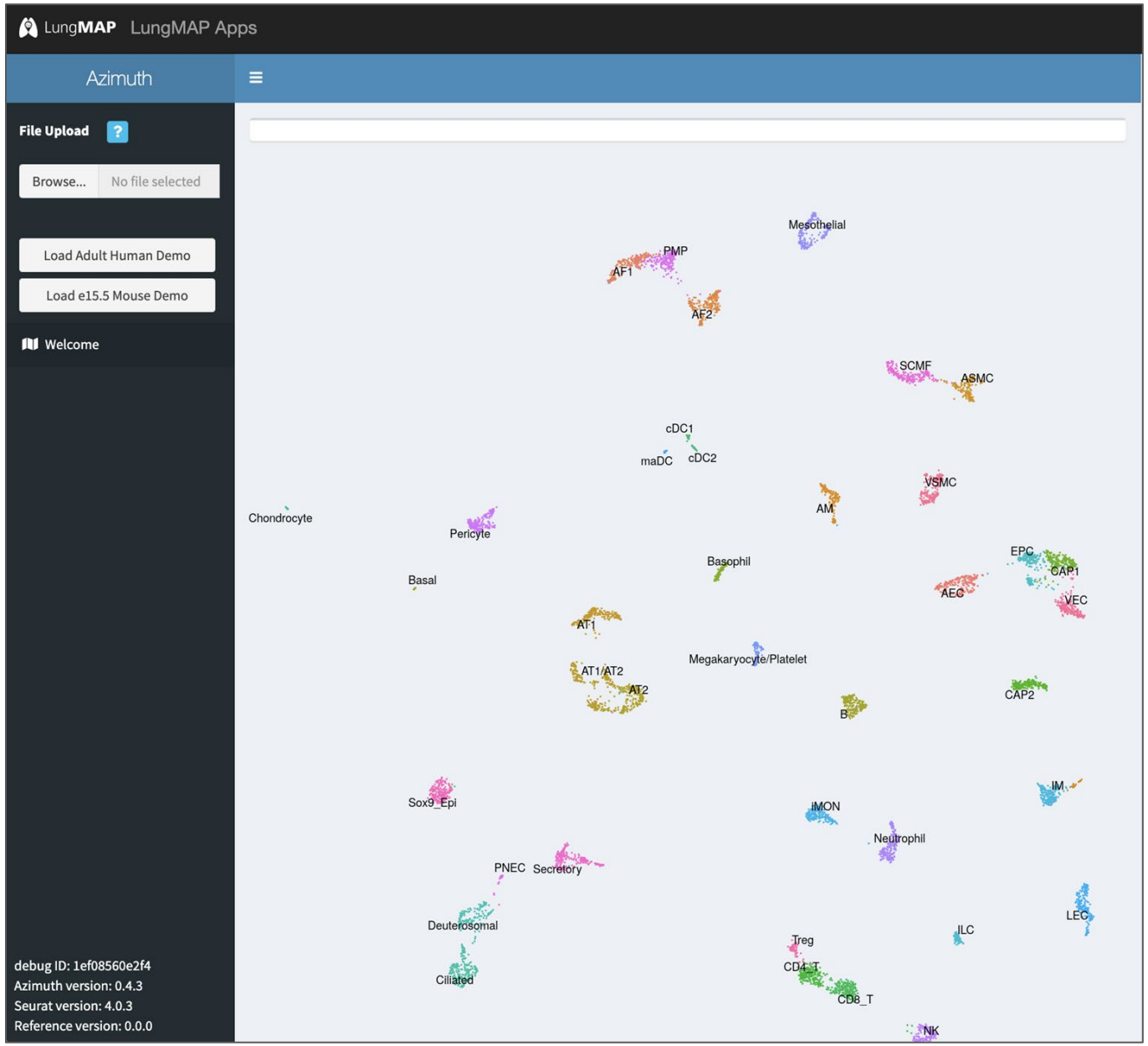

# Interactive Visualization & Analysis

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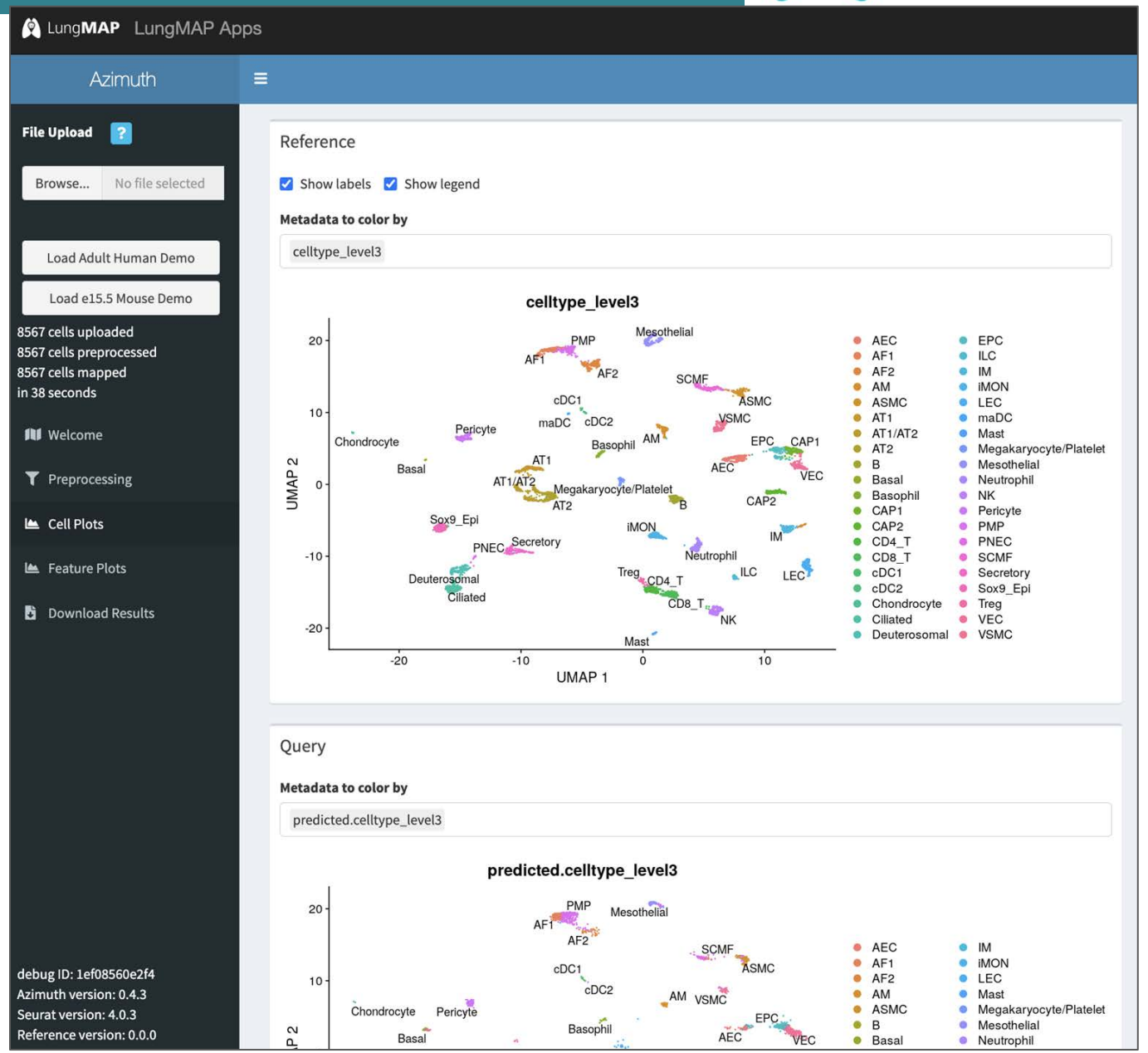

# Protocols

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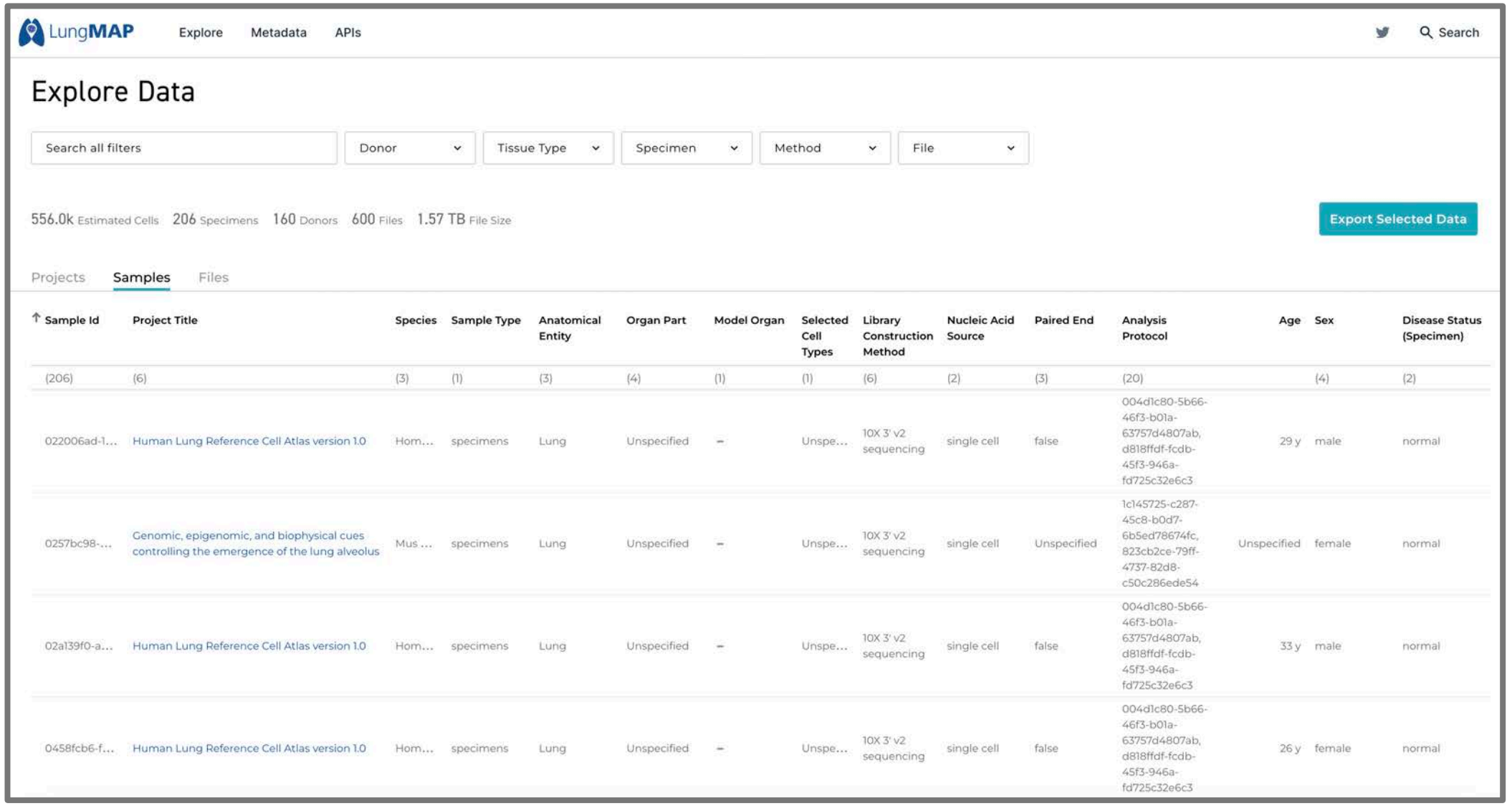
## #3 – LungMAP-HCA Data/Metadata Explorer




| Sample Id | Project Title | Species | Sample Type | Anatomical Entity | Organ Part | Model Organ | Selected Cell Types | Library Construction Method | Nucleic Acid Source | Paired End | Analysis Protocol | Age | Sex | Disease Status (Specimen) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| (206) | (6) | (3) | (1) | (3) | (4) | (1) | (1) | (6) | (2) | (3) | (20) | | (4) | (2) |
| 022006ad-1... | Human Lung Reference Cell Atlas version 1.0 | Hom... | specimens | Lung | Unspecified | – | Unspe... | 10X 3' v2 sequencing | single cell | false | 004d1c80-5b66-46f3-b01a-63757d4807ab, d818ffdf-fcdb-45f3-946a-fd725c32e6c3 | 29 y | male | normal |
| 0257bc98-... | Genomic, epigenomic, and biophysical cues controlling the emergence of the lung alveolus | Mus ... | specimens | Lung | Unspecified | – | Unspe... | 10X 3' v2 sequencing | single cell | Unspecified | 1c145725-c287-45c8-b0d7-6b5ed78674fc, 823cb2ce-79ff-4737-82d8-c50c286ede54 | Unspecified | female | normal |
| 02a139f0-a... | Human Lung Reference Cell Atlas version 1.0 | Hom... | specimens | Lung | Unspecified | – | Unspe... | 10X 3' v2 sequencing | single cell | false | 004d1c80-5b66-46f3-b01a-63757d4807ab, d818ffdf-fcdb-45f3-946a-fd725c32e6c3 | 33 y | male | normal |
| 0458fcb6-f... | Human Lung Reference Cell Atlas version 1.0 | Hom... | specimens | Lung | Unspecified | – | Unspe... | 10X 3' v2 sequencing | single cell | false | 004d1c80-5b66-46f3-b01a-63757d4807ab, d818ffdf-fcdb-45f3-946a-fd725c32e6c3 | 26 y | female | normal |

# Terra-powered Cloud Resources

LungMAP Molecular Atlas of Lung Development Program

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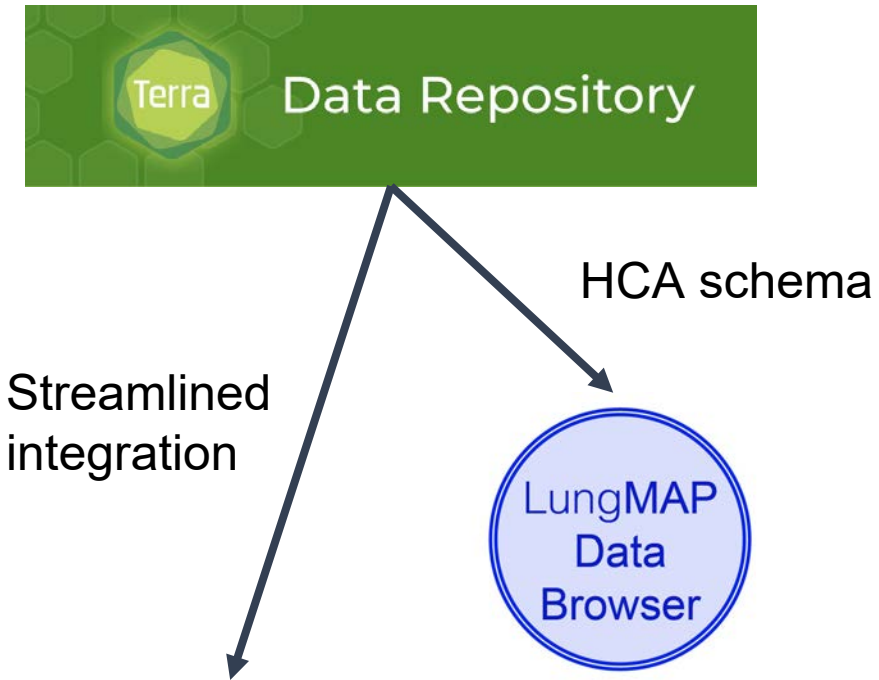
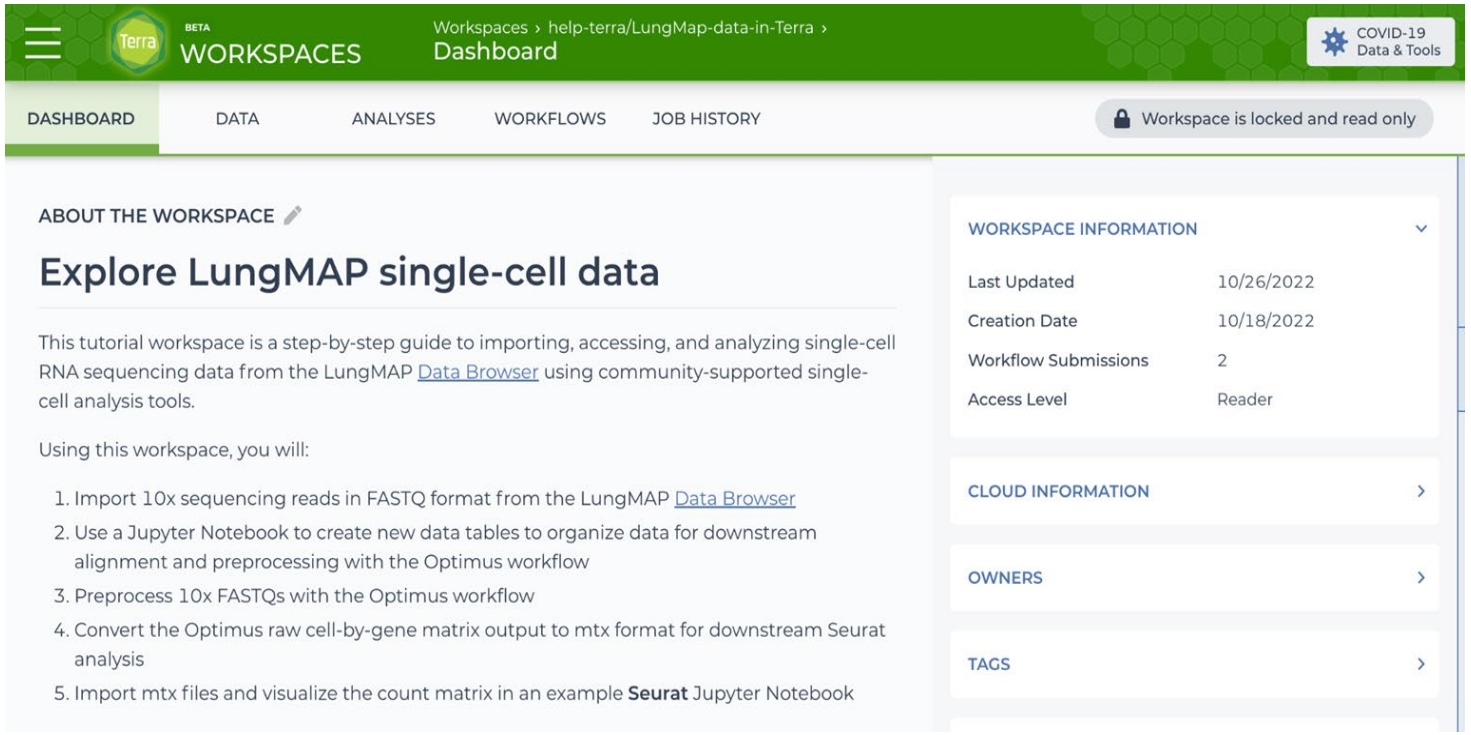
## **Open-access data repository** facilitating integration with NHLBI ecosystem




NIH National Heart, Lung, and Blood Institute | BioData CATALYST

## Cloud workspace for scalable analysis




Tutorials: https://lungmap.net/resources-2/tutorials/

- ➔ **Tutorial 5: Cloud-based omics data analysis with Terra**
- ➔ **Video 2: Exploring and Analyzing LungMAP Data in Terra**

Terra

# Next steps for LungMAP

LungMAP Molecular Atlas of Lung Development Program

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- **Exponential Growth**: Dozens of new atlases & interfaces
- **Creating atlases in the cloud**: Public + consortia + user
- **Leveraging AI**: User facing language models and disease gene regulatory network models.
- **Cost management**: Balancing growth, community needs and cloud versus on prem compute.

# Thank you!

LungMAP Molecular Atlas of Lung Development Program

NIH National Heart, Lung, and Blood Institute

## DCC Leadership

Bruce Aronow

Nathan Salomonis

Bing-Xing Huo

Timothy Tickle

Benedict Patten

*Surya Prasath*

Michal Kouril

Yan Xu

Jeff Whitsett

## DCC CCHMC

Eric Bardes

Scott Tabar

Joshua Fortriede

Kevin Burns

Liam Dolan

Benjamin Crooks

Kang Jin

Minzhe Guo

Dan Schnell

## DCC Broad Institute

Nate Calvanese

Kat Thayer

## ACC CCHMC

Stephanie Loos

Chelsea Yeary

## DCC UCSC

Trevor Heathorn

Hannes Schmidt

## RTI

Nathan Gaddis

*with assistance from CZI and the NIH Strides & dbGAP team*