Lung at a Glance: an integrative web toolset of lung ontology, imaging and single cell omics

Yina Du¹, Weichen Ouyang¹, Joseph A Kitzmiller¹, Minzhe Guo¹, Shuyang Zhao¹, Jeffrey A Whitsett^{1,3} and Yan Xu^{1,2,3}

¹The Perinatal Institute and Section of Neonatology, Perinatal and Pulmonary Biology, Cincinnati Children's Hospital Medical Center, Cincinnati, OH, 45229, USA.

²Division of Biomedical Informatics, Cincinnati Children's Hospital Medical Center, Cincinnati, OH, 45229, USA.

³Department of Pediatrics, University of Cincinnati School of Medicine, Cincinnati, OH, 45229, USA.

Corresponding author

Yan Xu

Divisions of Pulmonary Biology, Perinatal Institute and Biomedical Informatics, Cincinnati Children's Hospital Medical Center, 3333 Burnet Avenue, MLC7029, Cincinnati, OH, USA, 45229-3039; Email: Yan.Xu@cchmc.org; Fax: (+01) 513-803-096 Tel: (+01) 513-636-8921

Author contributions

Y.X., Y.D. and M.G. conceived and designed the web application; Y.D. developed the database and web application of LGEA web portal; W.O. developed the web application of LGEA lung Ontology; Y.D. and W.O. developed “Lung-at-a-glance” toolsets; J.A.K. and J.A.W. designed and developed the web application of Lung Image; M.G., Y.D., S.Y. and Y.X. contributed to

data analysis and interpretation; Y.D., J.A.W. and Y.X. wrote the manuscript. All authors contributed to the manuscript editing and approved the final manuscript.

Funding

This work is supported by US National Institutes of Health (NIH) grants U01HL122642 (LungMAP 1), U01HL148856 (LungMAP 2), U01HL134745, and P30 DK117467.

Running title: Web tool for lung data integration & visualization

Descriptor number: 3.2, 3.3

Word count: 1248

ABSTRACT

Recent advances in single-cell omics and high-resolution imaging have provided unanticipated data resources for the elucidation of genes underlying the complex biological processes critical for organ formation and function. However, processing and integrating large amounts of single-cell omics and imaging data presents a major challenge for most researchers. There is a critical need for ready-to-use computational tools for data/knowledge integration and visualization. Here we present “Lung-at-a-glance”, an easy-to-use web toolset for visualizing and interoperating complex omics and imaging data, providing an interactive web interface to bridge lung anatomic ontology classifications to lung histology and immunofluorescence confocal images, and cell-type-specific gene expression. “Lung-at-a-glance” contains three interactive components: 1) “Region at a glance”, 2) “Cell at a glance” and 3) “Gene at a glance”. “Lung-at-a-glance” and other newly developed web tools for lung-related data query, integration and visualization are publicly available on LGEA web portal v3 <https://research.cchmc.org/pbge/lunggens/mainportal.html>.

Keywords: Pulmonary development; Pulmonary diseases; Web application; LungMAP; LGEA

Abstract word count: 145

INTRODUCTION

LGEA web portal offers user-friendly and comprehensive web-based query functions on extensive bulk, sorted, single-cell transcriptomic and image data from human and mouse lung at different stages of development (1, 2). LGEA web portal has been used by researchers from more than 130 institutes from 52 different countries and has been cited by more than 120 scientific publications. With the continuing support from the LungMAP consortium, we extended the scope of the LGEA web portal database to include proteomics and epigenetic data from lung developmental and lung disease studies. To facilitate utilization and integration of these data resources, we developed “Lung-at-a-glance” to serve as an interactive bridge to connect lung anatomic ontology, histology and lung gene/protein expression data with easy-to-use web interfaces. A number of other newly developed bioinformatics tools for users to query, compare and integrate diverse lung omics datasets are also made available on LGEA new release.

METHODS

Modern JavaScript-based charting libraries (<https://www.highcharts.com>), CSS framework of Bootstrap (<https://getbootstrap.com>) and W3.CSS (<https://www.w3schools.com/w3css>) are integrated for web design and data visualization. The new features are implemented into the existing LGEA web architecture to improve its stability and modularity, including separation of front-end and back-end, and continuous integration and delivery. Oracle database management system 12c (<https://www.oracle.com/database>) is used for central data storage and maintenance.

UCSC Genome Browser (<https://genome.ucsc.edu>) is embedded into web application to provide an interactive visualization of epigenetic data.

RESULTS

“Lung-at-a-glance”, a featured toolset in LGEA

“Lung-at-a-glance” consists of three interactive components: “Region-at-a-glance”, “Cell-at-a-glance”, and “Gene-at-a-glance”; all designed to provide data access with a single-click on the icons located on the top of “Lung-at-a-glance” homepage (https://research.cchmc.org/pbge/lunggens/tools/lung_at_a_glance.html). The “at-a-glance” toolset is designed to serve as an interactive bridge to connect lung anatomic ontology, histology and immunofluorescence confocal images in Lung Image gallery (<https://research.cchmc.org/lungimage/>) and lung gene expression data in the LGEA web portal. The toolset provides a collection of comprehensive interrelated data and knowledge resources with a user friendly intuitive and interactive web-interface for data analysis, integration and visualization (**Figure 1**). The anatomic ontology for human and mouse lung was developed by NHLBI LungMAP Consortium, Ontology Subcommittee using Web Ontology Language (OWL 2). The ontology contains ~ 300 terms for fetal and postnatal lung structures, tissues, and cells which were identified for each species (3). We converted the abstract version of anatomic ontology terms into searchable, clickable and expandable web tree structures, we further incorporated the ontology tree as an interactive component into LGEA. Investigators can navigate the hierarchical structure of the anatomical tree or use the search box to directly locate regions or cells of interest.

“Region-at-a-glance” allows users to search a specific lung region using the interactive tree navigation or click one of the annotated lung regions, e.g., “Proximal airway”, “Submucosal gland”, “Bronchiole”, “Terminal Bronchiole”, and “Alveoli” on the H&E staining lung image. Users can explore cells within selected regions using interactive mouse-hover features which are embedded in the anatomical ontology tree, images and diagrams (**Figure 1A**). “Cell-at-a-glance” can be activated by clicking the cell name or image on the “Cell-at-a-glance” page or by clicking a cell of interest in selected regional diagrams on the “Region-at-a-glance” page. With the same interactive web page design pattern, “Cell-at-a-glance” offers a collection of information related to the queried cell type including cell definition, cell type specific positive and negative markers, transcription factors, ligand-receptors predicted by our group (https://github.com/xu-lab/LGEA_Cell_Signature), and hyperlinks to all LGEA web portal datasets and immunofluorescence confocal images related to the chosen cell type. Approximately 40 cell types are available for study in the current “Cell-at-a-glance” (**Figure 1B**). “Gene-at-a-glance” allows users to query a gene of interest and obtain its expression patterns (including protein expression levels if available) and statistics in all LGEA datasets in a 2-D heatmap linking developmental times and cell types (**Figure 1C**). Hyperlinks to external knowledge-bases and immunofluorescence confocal images of relevant cell markers are provided in the “Gene-at-a-glance” page (**Figure 1C**). The three components of “Lung-at-a-glance” are interconnected offering users a one-stop bioinformatics-tool for lung research. For example, investigators can start their search at specific anatomic regions, explore a particular cell type within the region, and identify cell specific markers, ligands-receptors and transcription factors expressed in the cell type of interest across lung developmental stages.

Diverse datasets and web functionality

In addition to “Lung-at-a-glance”, the LGEA new release represents a significant update of the previous version, expanding to ten functional query panels from three panels in the previous version (1, 2). The analytic tools and functionalities of current LGEA web portal are briefly introduced below (**Figure 2**).

- The “LungGENS”, “LungSortedCells”, “LungDTC” supports ‘Query by single gene’, ‘Query by gene list’ and ‘Query by cell type’ function on single-cell, sorted-cell and whole lung developmental time course data collected from mouse lung tissues from embryonic day 16.5 to postnatal day 28 (eight time points) and human lung samples from neonate, infant, child and adult at various ages.
- The “LungDisease” panel allows investigators to search altered gene expression patterns, disease related signatures and lung disease related images including idiopathic pulmonary fibrosis(4), lymphangioleiomyomatosis (5), cystic fibrosis, bronchopulmonary dysplasia (BPD), primary alveolar microlithiasis, asthma, ABCA3 mutations, TBX4 deletion and lung growth disorder.
- The “LungEpigenetics” panel contains ChIP-seq data during mouse lung development downloaded from ENCODE (<https://www.encodeproject.org/>). Developmental stages and specific histone modifications associated with the gene of interest are viewed on the embedded UCSC Genome Browser with selected tracks enabled.
- “LungProteomics” provides protein centered query functions based on proteomic data generated at Pacific Northwest National Laboratory (PNNL) in the LungMAP project. Correlations between protein and mRNA expression profiles, and an overview of

expression levels of the queried protein/gene expression across all data sets in the LGEA database can be visualized.

- “LGEA-ProjectBased” is designed to introduce and share high impact lung related projects from internal and external research groups.
- The LGEA-ToolBox includes a number of new bioinformatics tools, including “signature comparison”, “gene list query”, and “gene list analysis” to facilitate comparison and integration of datasets to meet the ever-increasing needs of the research community. Users can compare different datasets in LGEA database or enter their gene list of interest to compare cell type specific signature genes provided by LGEA.

DISCUSSION

Recent advances in single-cell omics have provided increasing insights into the pathogenesis of human disease, including those affecting the lung (6-10). The density of omics data relevant to lung biology is increasing exponentially, providing information that, with suitable integrative analysis, may provide important insights into the processes underlying lung function. The LGEA web portal is designed for intuitive and practical interrogation use of comprehensive “omics” data obtained during normal lung morphogenesis and from lung diseases by research investigators with varying computational training. LGEA new release provides improved interactive, graphical web interfaces for search, visualization, and secondary analyses, in which output can be readily interpreted and downloaded. Featured toolset of “Lung-at-a-glance” offers end-to-end web functions to access and search lung anatomic ontology terms, and to explore the corresponding structure and morphology of tissue regions, cells, and marker gene expression

patterns in all datasets in the LGEA database. To our knowledge, this is the first web application connecting anatomic ontology terms to structure and histology images and to single cell expression data. These tools and enriched data resources can be used to enhance hypothesis generation and scientific discovery. The LGEA web portal database will be continually updated with more omics data generated in LungMAP 2 and new query functions will be developed to further enhance data and knowledge interrogation. Data are made available and synchronized at the LungMAP website (<https://www.lungmap.net/>).

ACKNOWLEDGEMENTS

The authors acknowledge the support of Dr. Sara Lin (Program Director) and all members of LungMAP research Consortium.

DECLARATION OF INTERESTS

The authors declare that there are no conflicts of interest.

DATA AVAILABILITY

LGEA web portal v3 are freely available for non-commercial use at <http://research.cchmc.org/pbge/lunggens/mainportal.html> and data is readily integrated with omics data and lung image data from other research centers at “BREATH” database and display on the LungMAP website (<https://www.lungmap.net/>).

REFERENCES

1. Du Y, Guo M, Whitsett JA, Xu Y. 'LungGENS': a web-based tool for mapping single-cell gene expression in the developing lung. *Thorax* 2015; 70: 1092-1094.

2. Du Y, Kitzmiller JA, Sridharan A, Perl AK, Bridges JP, Misra RS, Pryhuber GS, Mariani TJ, Bhattacharya S, Guo M, Potter SS, Dexheimer P, Aronow B, Jobe AH, Whitsett JA, Xu Y. Lung Gene Expression Analysis (LGEA): an integrative web portal for comprehensive gene expression data analysis in lung development. *Thorax* 2017; 72: 481-484.
3. Pan H, Deutsch GH, Wert SE, Ontology S, Consortium NMAoLDP. Comprehensive anatomic ontologies for lung development: A comparison of alveolar formation and maturation within mouse and human lung. *J Biomed Semantics* 2019; 10: 18.
4. Xu Y, Mizuno T, Sridharan A, Du Y, Guo M, Tang J, Wikenheiser-Brokamp KA, Perl AT, Funari VA, Gokey JJ, Stripp BR, Whitsett JA. Single-cell RNA sequencing identifies diverse roles of epithelial cells in idiopathic pulmonary fibrosis. *JCI Insight* 2016; 1: e90558.
5. Guo M, Yu JJ, Perl AK, Wikenheiser-Brokamp KA, Riccetti M, Zhang EY, Sudha P, Adam M, Potter A, Koprass EJ, Giannikou K, Potter SS, Sherman S, Hammes SR, Kwiatkowski DJ, Whitsett JA, McCormack FX, Xu Y. Identification of the lymphangioliomyomatosis cell and its uterine origin. *bioRxiv* 2019.
6. Goldfarbmuren KC, Jackson ND, Sajuthi SP, Dyjack N, Li KS, Rios CL, Plender EG, Montgomery MT, Everman JL, Bratcher PE, Vladar EK, Seibold MA. Dissecting the cellular specificity of smoking effects and reconstructing lineages in the human airway epithelium. *Nat Commun* 2020; 11: 2485.
7. Reyfman PA, Walter JM, Joshi N, Anekalla KR, McQuattie-Pimentel AC, Chiu S, Fernandez R, Akbarpour M, Chen CI, Ren Z, Verma R, Abdala-Valencia H, Nam K, Chi M, Han S, Gonzalez-Gonzalez FJ, Soberanes S, Watanabe S, Williams KJN, Flozak AS, Nicholson TT, Morgan VK, Winter DR, Hinchcliff M, Hrusch CL, Guzy RD, Bonham CA, Sperling AI, Bag R, Hamanaka RB, Mutlu GM, Yeldandi AV, Marshall SA, Shilatfard A, Amaral LAN, Perlman H, Sznajder JI, Argento AC, Gillespie CT, Dematte J, Jain M, Singer BD, Ridge KM, Lam AP, Bharat A, Bhorade SM, Gottardi CJ, Budinger GRS, Misharin AV. Single-Cell Transcriptomic Analysis of Human Lung Provides Insights into the Pathobiology of Pulmonary Fibrosis. *Am J Respir Crit Care Med* 2019; 199: 1517-1536.
8. Schiller HB, Montoro DT, Simon LM, Rawlins EL, Meyer KB, Strunz M, Vieira Braga FA, Timens W, Koppelman GH, Budinger GRS, Burgess JK, Waghay A, van den Berge M, Theis FJ, Regev A, Kaminski N, Rajagopal J, Teichmann SA, Misharin AV, Nawijn MC. The Human Lung Cell Atlas: A High-Resolution Reference Map of the Human Lung in Health and Disease. *Am J Respir Cell Mol Biol* 2019; 61: 31-41.
9. Vieira Braga FA, Kar G, Berg M, Carpaij OA, Polanski K, Simon LM, Brouwer S, Gomes T, Hesse L, Jiang J, Fasouli ES, Efremova M, Vento-Tormo R, Talavera-Lopez C, Jonker MR, Affleck K, Palit S, Strzelecka PM, Firth HV, Mahbubani KT, Cvejic A, Meyer KB, Saeb-Parsy K, Luinge M, Brandsma CA, Timens W, Angelidis I, Strunz M, Koppelman GH, van Oosterhout AJ, Schiller HB, Theis FJ, van den Berge M, Nawijn MC, Teichmann SA. A cellular census of human lungs identifies novel cell states in health and in asthma. *Nat Med* 2019; 25: 1153-1163.
10. Raredon MSB, Adams TS, Suhail Y, Schupp JC, Poli S, Neumark N, Leiby KL, Greaney AM, Yuan Y, Horien C, Linderman G, Engler AJ, Boffa DJ, Kluger Y, Rosas IO, Levchenko A, Kaminski N, Niklason LE. Single-cell connectomic analysis of adult mammalian lungs. *Sci Adv* 2019; 5: eaaw3851.

FIGURE LEGENDS

Figure 1. “Lung-at-a-glance” consists of three interactive and interconnected components: “Region at a glance”, “Cell at a glance”, and “Gene at a glance”.

(A) “Region at a glance” allows users to search a specific lung region using the interactive ontology tree navigation or clicking the boxes in the lung image to explore cells reside in the selected region.

(B) “Cell at a glance” offers a collection of information of queried cell type, including cell definition, cell type specific positive and negative markers, transcription factors, ligand-receptors, and hyperlinks which are mapped to the chosen cell type in all datasets in LGEA web portal and immunofluorescence confocal images of the chosen cell type.

(C) “Gene at a glance” allows users to query a gene of interest to obtain associated gene information including hyperlinks to external knowledge base, to expression patterns in LGEA datasets, and to immunofluorescence confocal images. A two-dimensional heatmap by developmental times and cell types was used to summarize expression patterns and statistics of queried gene in all datasets available in LGEA databases.

Figure 2. LGEA web portal home page.

The new release of LGEA web portal provides query and analytic tools including “LungGENS”, “LungSortedCells”, “LungDTC”, “LungDiseases”, “LungEpigenetics”, “LungImage”, “LungProteomics”, “LungOntology”, “LGEA-ProjectBased” and “LGEA-ToolBox”. Newly developed feature toolset “Lung-at-a-glance” is highlighted on top of the home page.

Gene at a glance

Cell at a glance

Gene at a glance

Gene information

Mouse info

Gene symbol: Foxj1

Gene ID: 15223

Full Name: forkhead box J1

Chromosome: 11

Gene type: protein-coding

Human info

Gene symbol: FOXJ1

Gene ID: 2302

Full Name: forkhead box J1

Chromosome: 17

Gene type: protein-coding

Links external resources

[LungMAP](#)
[NCBI](#)
[GeneCard](#)
[MGI](#)
[Ensembl](#)
[The Human Protein Atlas](#)
[HGNC](#)
[UCSC](#)
[UniProt](#)
[OMIM](#)

Links to LGEA datasets

Query foxj1 in datasets below:

LungGENS
[E16.5](#)
[E18.5](#)
[PND1](#)
[PND3](#)
[PND7](#)
[PND10](#)
[PND14](#)
[PND28](#)
[DP-E16.5](#)
[DP-PND1](#)
[DP-PND3](#)
[DP-PND7](#)
[DP-PND28](#)
[DP-PND1\(human\)](#)

LungSortedCells
[Human Day1](#)
[Human 20months](#)
[Human Neo-fo-Adult](#)
[Mouse p0lfalt;FB](#)
[Mouse E16.5](#)
[Mouse E18.5](#)
[Mouse PND1](#)
[Mouse PND7](#)
[Mouse PND14](#)
[Mouse PND28](#)

LungOTC
[\(mouse RNA-Seq\)](#)
[\(E16-PND28\)](#)
[\(Monkey RNA-Seq\)](#)
[\(GA105-GA150\)](#)

LungDroese
[Human ICF](#)
[cRNA-seq](#)
[Human AT2](#)
[VCF](#)
[RNA-seq](#)

LungEpigenetics
[PTM-chis-seq](#)
[\(Encode\)](#)

LungProteomics
[Human sorted 20moes](#)
[\(Mouse E16.5-PND28\)](#)

LungExternal
[Human \(PSC-derived lung primordial progenitors\)](#)
[\(Kotton\)](#)
[SCGB3A2+ airway epithelium](#)
[time course microarray](#)
[\(Kotton\)](#)

[SCGB3A2+ airway epithelium](#)
[single cell profiling](#)
[\(Kotton\)](#)
[SCGB3A2+ airway epithelium](#)
[single cell airway vs alveolar spheres](#)
[\(Kotton\)](#)

[Distinct mesenchymal lineages in mouse adult lung](#)
[\(Mortensen\)](#)
[CFTR-expressing ionocytes](#)
[DP](#)
[\(Rajagopal\)](#)

[CFTR-expressing ionocytes](#)
[pubseq](#)
[\(Rajagopal\)](#)
[CFTR-expressing ionocytes](#)
[C1](#)
[\(Rajagopal\)](#)

Links to Lung Image

Query by species: [Mouse\(C57BL/6\)](#) [Human](#) [Monkey](#)

Query by development:

[Mouse:Newborn](#)
[E16.5](#)
[E18.5](#)
[Mouse PND1](#)
[Mouse PND3](#)
[Mouse PND7](#)
[Mouse PND10](#)
[Mouse PND14](#)
[Mouse PND28](#)

Human:
[1 day](#)
[6 day](#)
[4 months](#)
[8 months](#)
[11 months](#)
[13 months](#)
[14 months](#)
[20 months](#)
[2 years](#)
[3 years](#)
[4 years](#)
[8 years](#)
[Adult 23 years](#)

Monkey:
[Fetal Monkey GD105](#)
[Fetal Monkey GD130](#)
[Fetal Monkey GD150](#)

The figure illustrates a revised airway epithelial hierarchy. The main heatmap shows gene expression (Drop-Seq) across various cell types (Epithelial cells, Endothelial cells, Immune cells, Mesenchymal cells) and developmental stages (PND1, PND3, PND7, PND10, PND14, PND28, Day 1, 20moes, Neonate, Infant). The genes listed are AT1, AT2, AT10, AT12, AT13, AT14, AT15, AT16, AT17, AT18, AT19, AT20, AT21, AT22, AT23, AT24, AT25, AT26, AT27, AT28, AT29, AT30, AT31, AT32, AT33, AT34, AT35, AT36, AT37, AT38, AT39, AT40, AT41, AT42, AT43, AT44, AT45, AT46, AT47, AT48, AT49, AT50, AT51, AT52, AT53, AT54, AT55, AT56, AT57, AT58, AT59, AT60, AT61, AT62, AT63, AT64, AT65, AT66, AT67, AT68, AT69, AT70, AT71, AT72, AT73, AT74, AT75, AT76, AT77, AT78, AT79, AT80, AT81, AT82, AT83, AT84, AT85, AT86, AT87, AT88, AT89, AT90, AT91, AT92, AT93, AT94, AT95, AT96, AT97, AT98, AT99, AT100.

The detailed view of sorted cells shows the expression of various genes (Epi, Endo, Immune, Mes, Epi, Mesenchymal, Blospy) across different developmental stages (PND1, PND3, PND7, PND10, PND14, PND28, Day 1, 20moes, Neonate, Infant). The genes listed are Epi, Endo, Immune, Mes, Epi, Mesenchymal, Blospy.

Rajagopal Lab: A revised airway epithelial hierarchy includes CFTR-expressing ionocytes [PubMed]

Cell ontology in tree view

News and updates

Introduction of LungMAP -- Dr. Jeffrey Whitsett

11-4-2019: Dr. whitsett and Dr. Wert's manuscript : "Comprehensive Anatomic Ontologies for Lung Development: A Comparison of Alveolar Formation and Maturation within Mouse and Human Lung" has been published online. <PubMed>

7-9-2019: Check out our recent publication: Integration of Transcriptomic and Proteomic Data Identifies Biological Functions in Cell Populations From Human Infant Lung.

4-23-2019: New analyses of mouse sorted cells at PND1 and PND 14 are available in LungSortedCell Panel.

3-18-2019: ATS Webinar on the LungMAP PART 1 & PART 2.

New feature release: Lung at a glance

News panel

Lung at a glance

10 functional query panels

1 LungGENS

Mouse scRNA-seq

Mouse Fluidigm C1
(E16.5, E18.5, P1, P3, P7, P10, P14, P28)

Mouse Drop-seq
(E16.5, E18.5, P1, P3, P7, P10, P14, P28)

Human scRNA-seq

Human Drop-seq
Human 10x Genomics

2 LungSortedCells

Human

Major cell types (Immune, Endothelial, Mesenchymal and Epithelial Cells)

Airway (Basal, Bron-Epi/SMG)

Mouse

Major cell types (Immune, Endothelial, Mesenchymal and Epithelial Cells)

Airway (Basal, Bron-Epi/SMG)

LungSortedCells-query

Query by gene list

3 LungDTC

MicroArray

LDProfiles
MGI: developmental time course

RNA-seq

Mouse Lung
(E16, E18, P1, P3, P7, P14 and P28)

Rhesus Macaque Lung
(GA105, GA130, GA150)

4 LungDisease

scRNA-seq Analysis

Human IPF
(540 normal and disease cells)

Sorted RNA-seq

Human IPF
Human AT2 cells

LungImage-disease

LungImage

5 LungEpigenetics

ENCODE

Mouse histone PTM chip-seq data

CCHMC / LungMAP

TBA

6 LungImage

Confocal Imaging

Mouse C57BL6 lung
(E16.5, E18.5, P1, P3, P7, P10...)

Human Lung

(Postnatal and Adult)

H&E Staining

Human Lung

(Postnatal and Adult)

Query by gene

Marker list

7 LungProteomics

Mouse Lung

Mouse E16.5, E18.5, P7, P28

Human Lung

Human sorted 20 months

LungMAP site

TBA

8 LGEA-ToolBox

Database query tool

Signatures comparison

Gene at a glance

Gene list query

Gene list analysis

Lung at a glance

Research tools

SINCERA

SLICE

Other resource

9 LGEA-ProjectBased

CCHMC

Lung at birth
Integration of human protein and mRNA
GR signaling in lung maturation

External

Kotton's Lab
Krasnow's Lab
Morrissey's Lab
Rajagopal's Lab

10 LungOntology

Mouse

Anatomy

Cell type

Human

Anatomy

Cell type

LungGENS

LungSortedCells

LungDTC

LungDisease

LungEpigenetic

LungImage

LungProteomics

LungToolBox

LGEA-ProjectBased

LungOntology