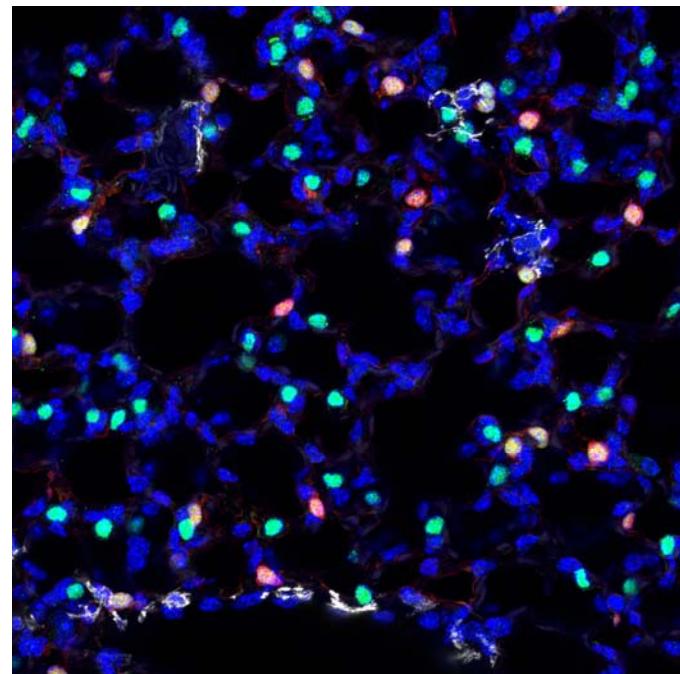
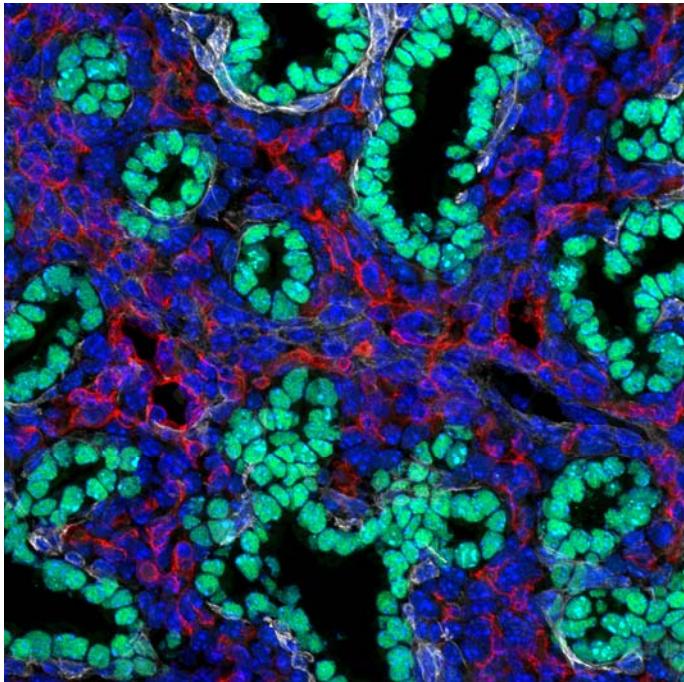


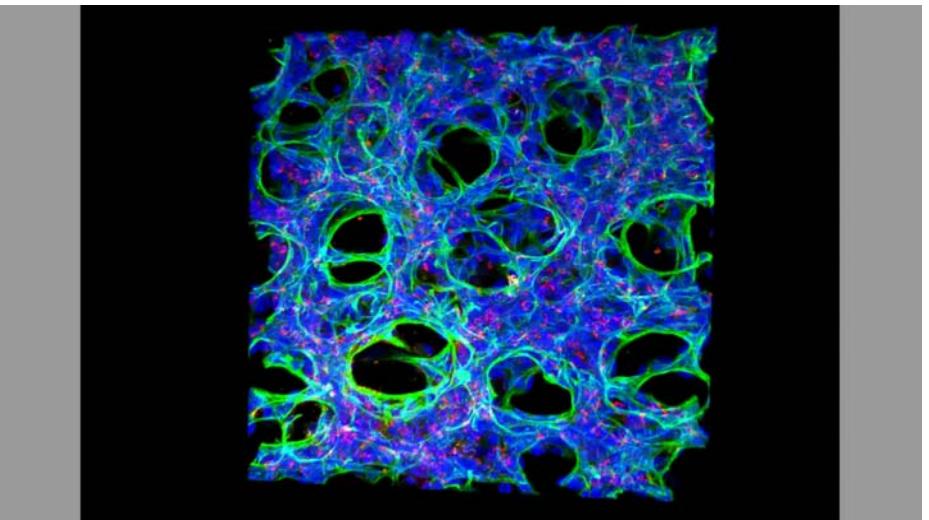
SanDiego 2017:Rare Pediatric Lung Disease

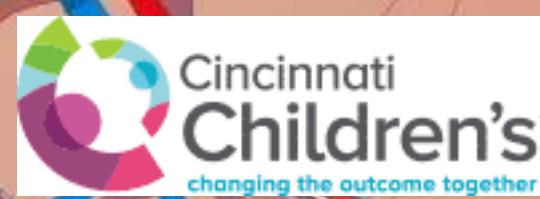
Single Cell Expression Analysis to Understand Interstitial Pulmonary Diseases



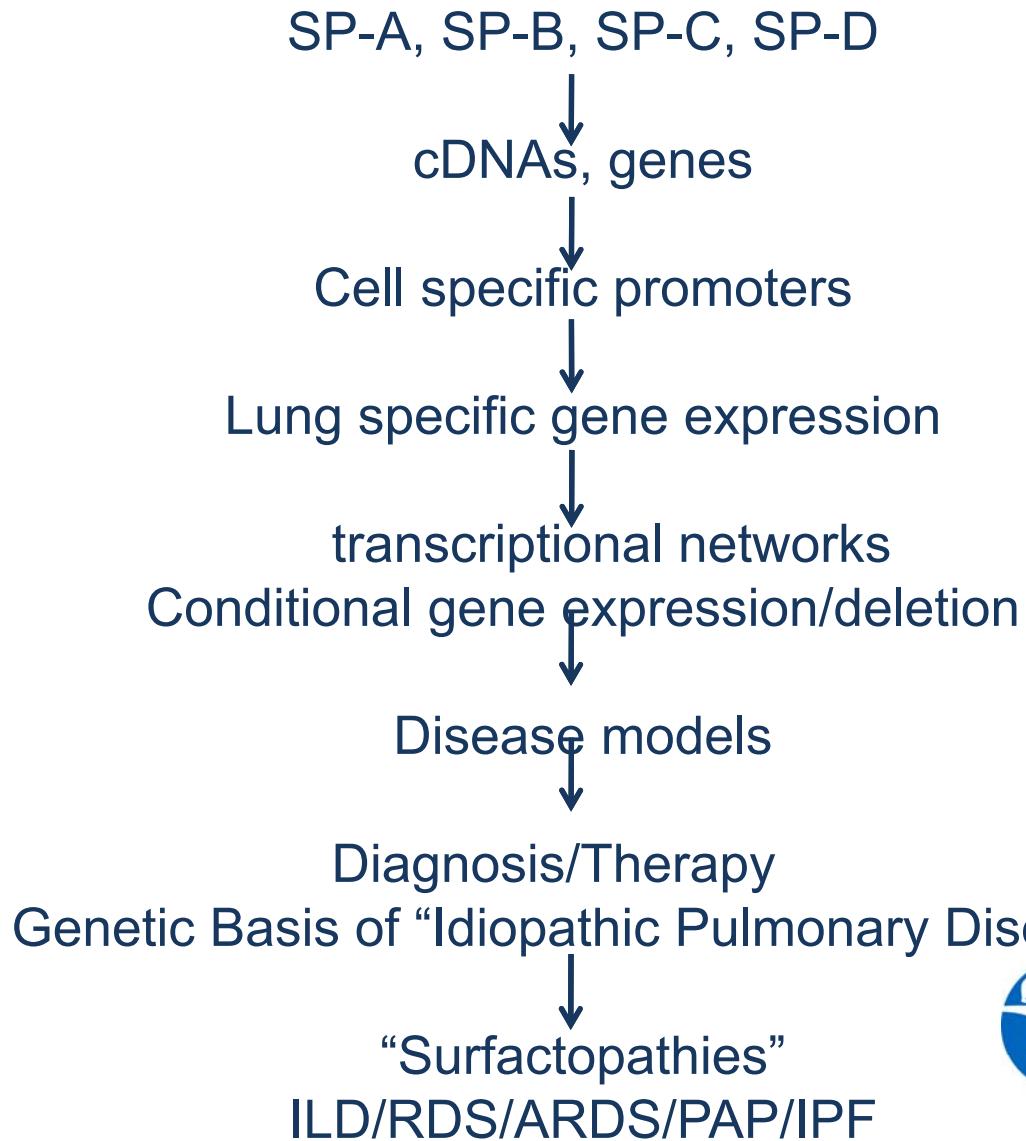
Jeff Whitsett: Cincinnati Children's Hospital Medical Center

jeff.whitsett@cchmc.org



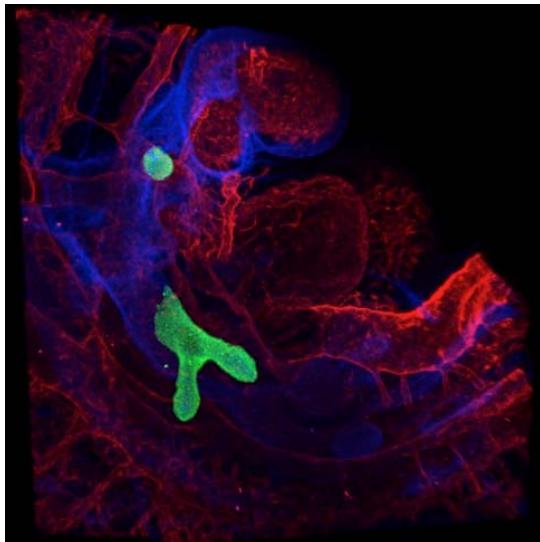


Molecular Tools to Explore Lung Biology

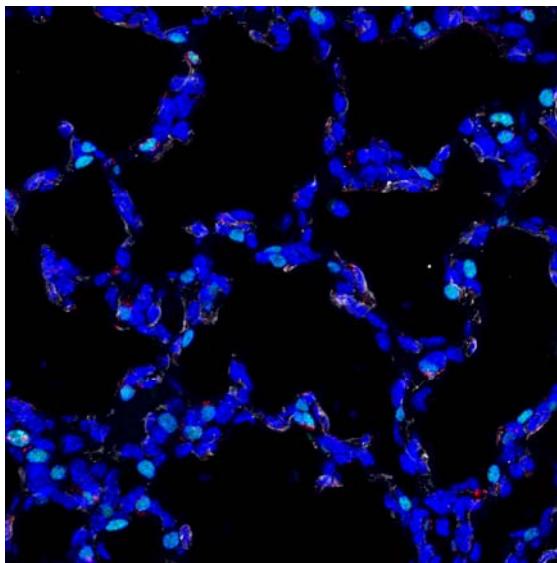


'Maturation' of the Alveolar Epithelium

Lung Buds



PND7



FOXA2, SOX17

E10

NKX2-1

Proximal Progenitors

SOX2

HOPX/AGER/AQP5

Alveoli

Endoderm

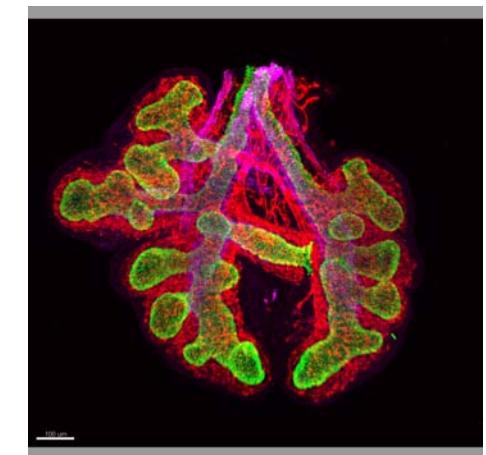
Foregut

Respiratory
epithelium

Alveolar
Type I

Alveolar
Type II

Branching Morphogenesis



Peripheral Progenitors
SOX9, NKX2-1

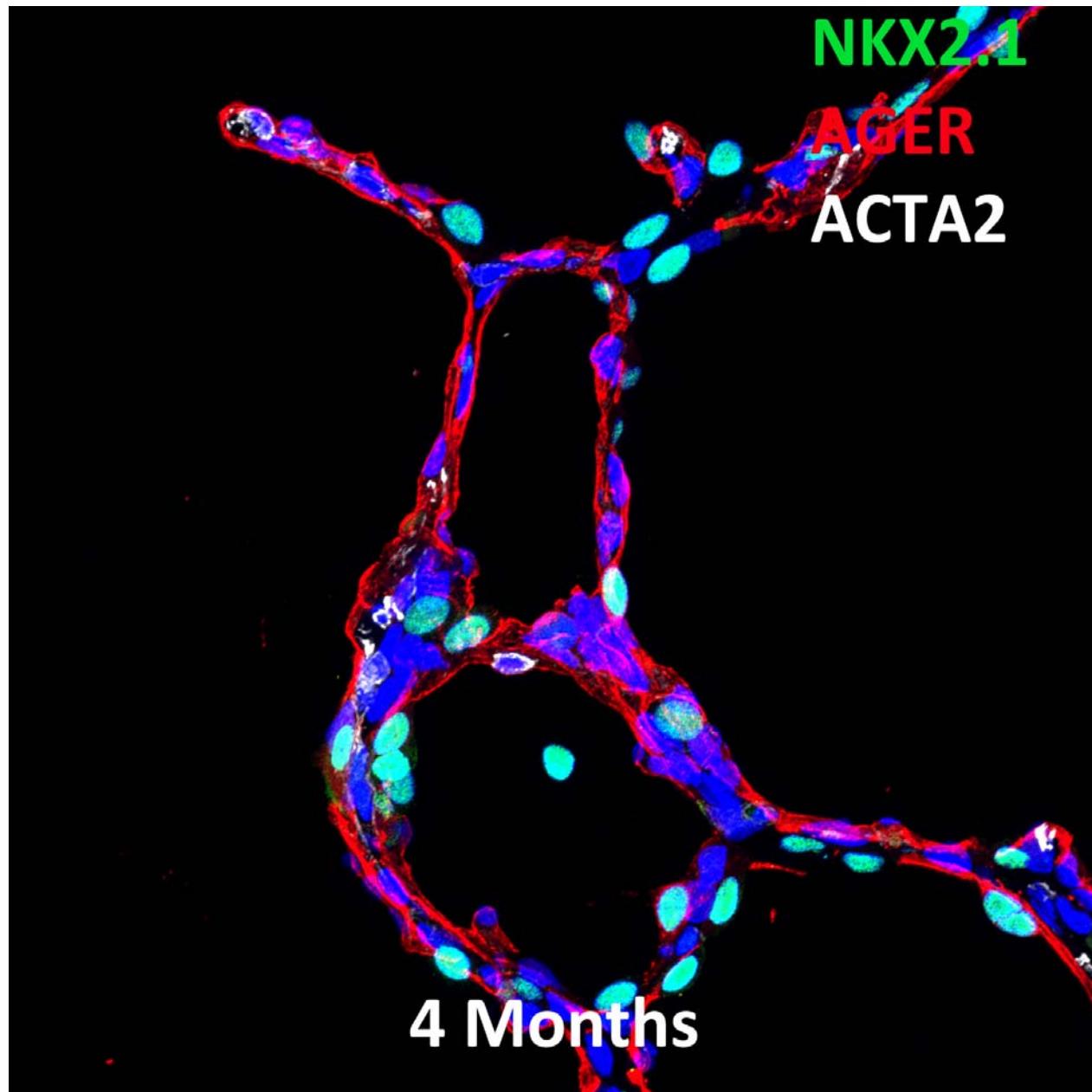


Alveolar Surfactant

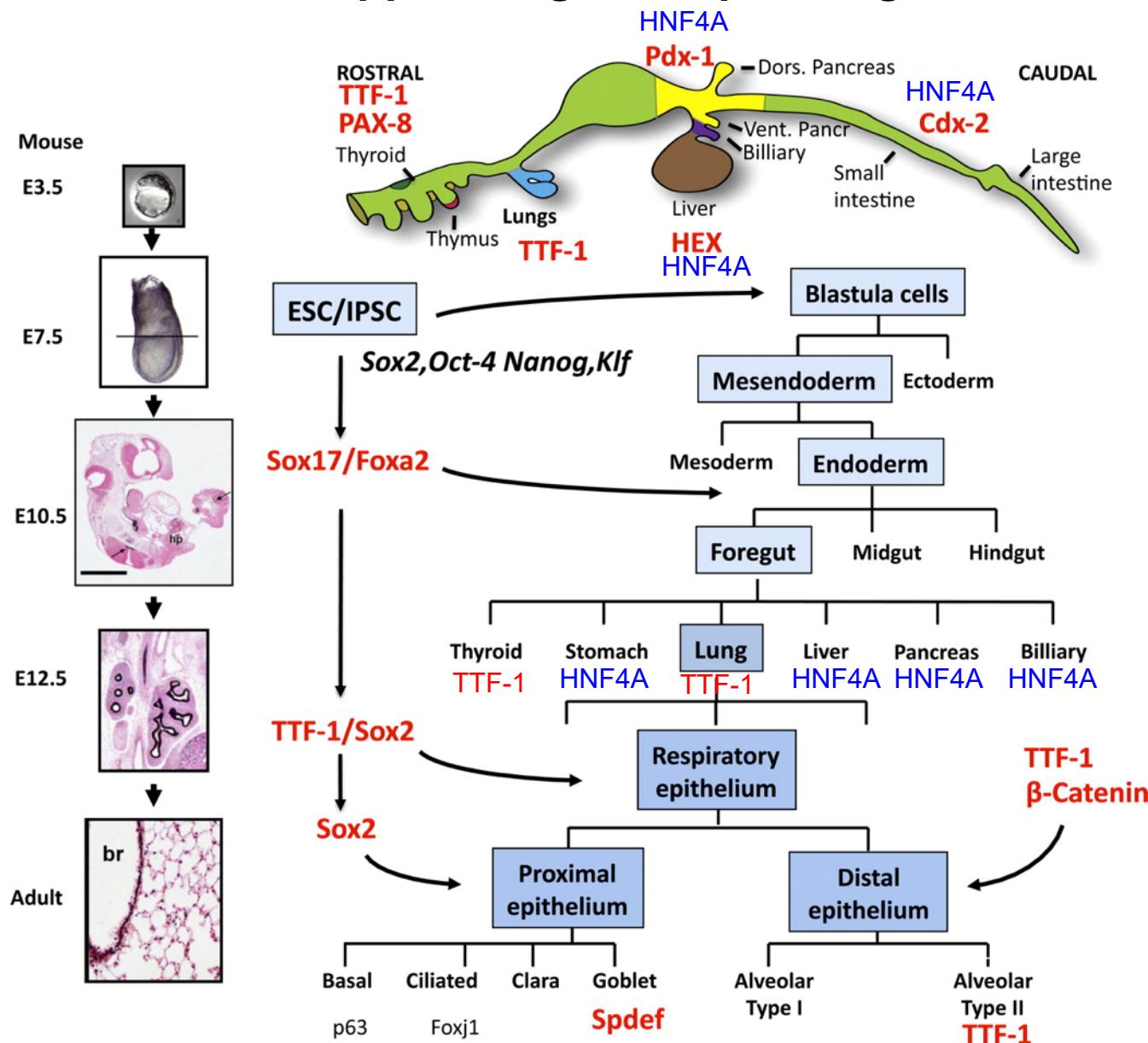
SFTPA/B/C/D

ABCA3, GPR116, NAPSA

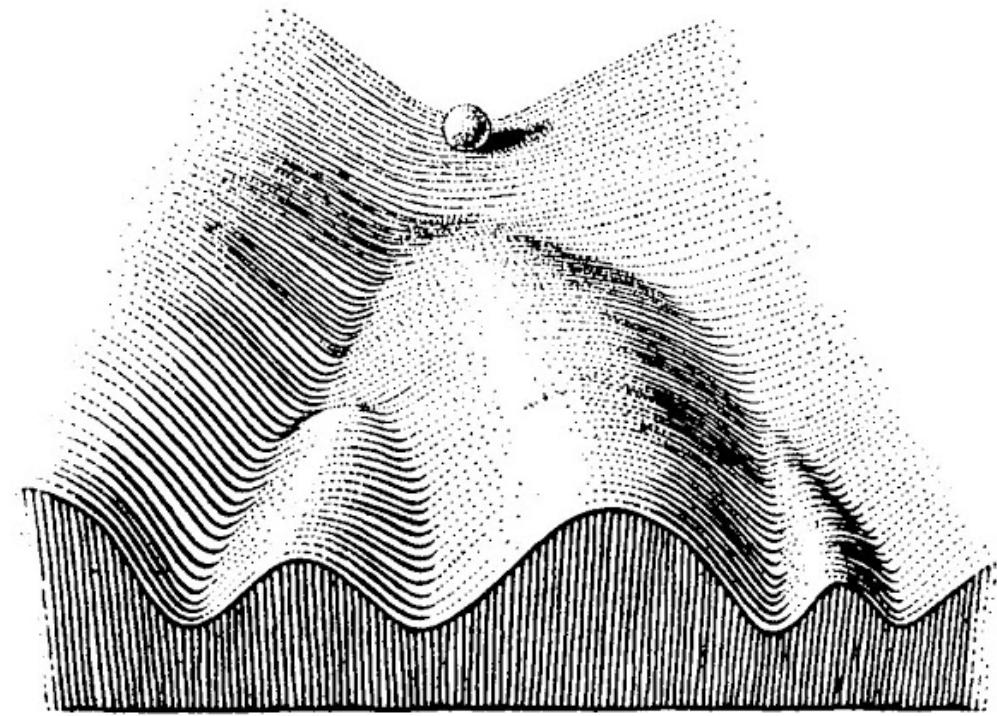
*Alveolar AT1 [**AGER**],AT2[NKX2-1] and Myofibroblasts [ACTA2] in Human Lung*



TTF-1/NKX2-1 keeps lung integrity by activating lung specific genes and suppressing liver specific genes

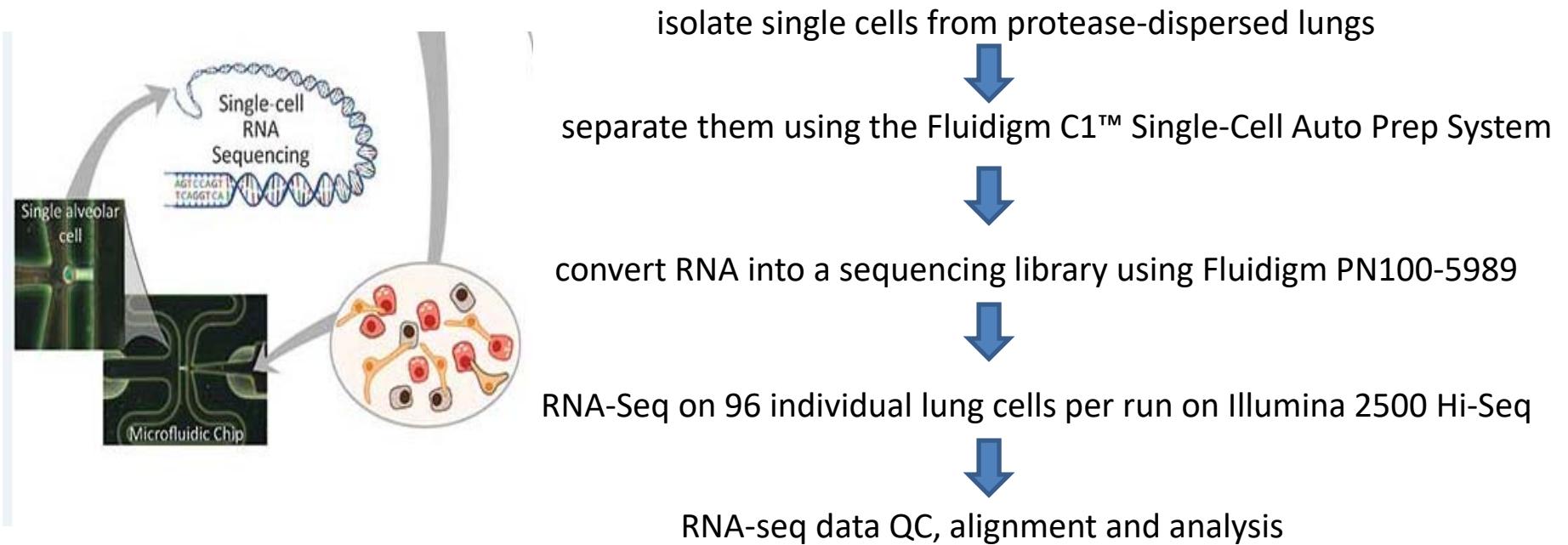
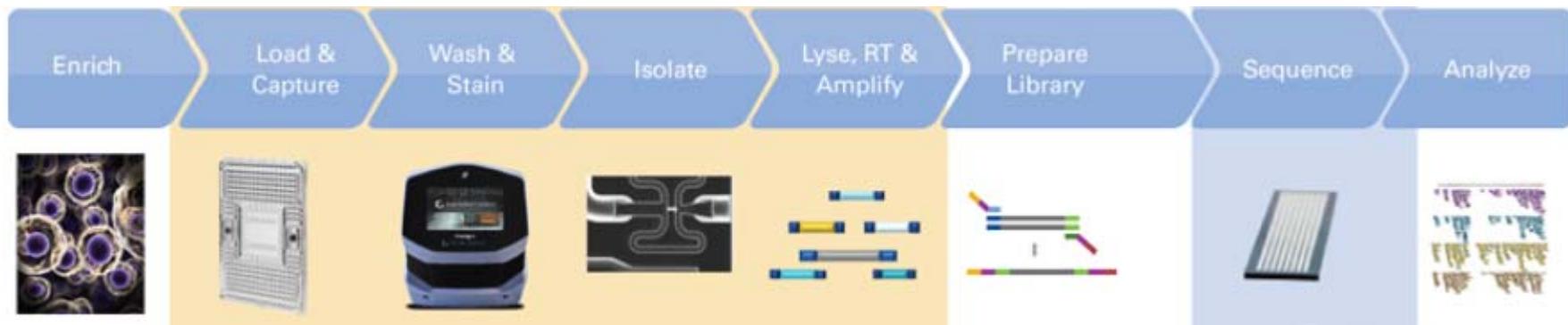


Modified from Whitsett et al., Am J Respir Crit Care Med 2011



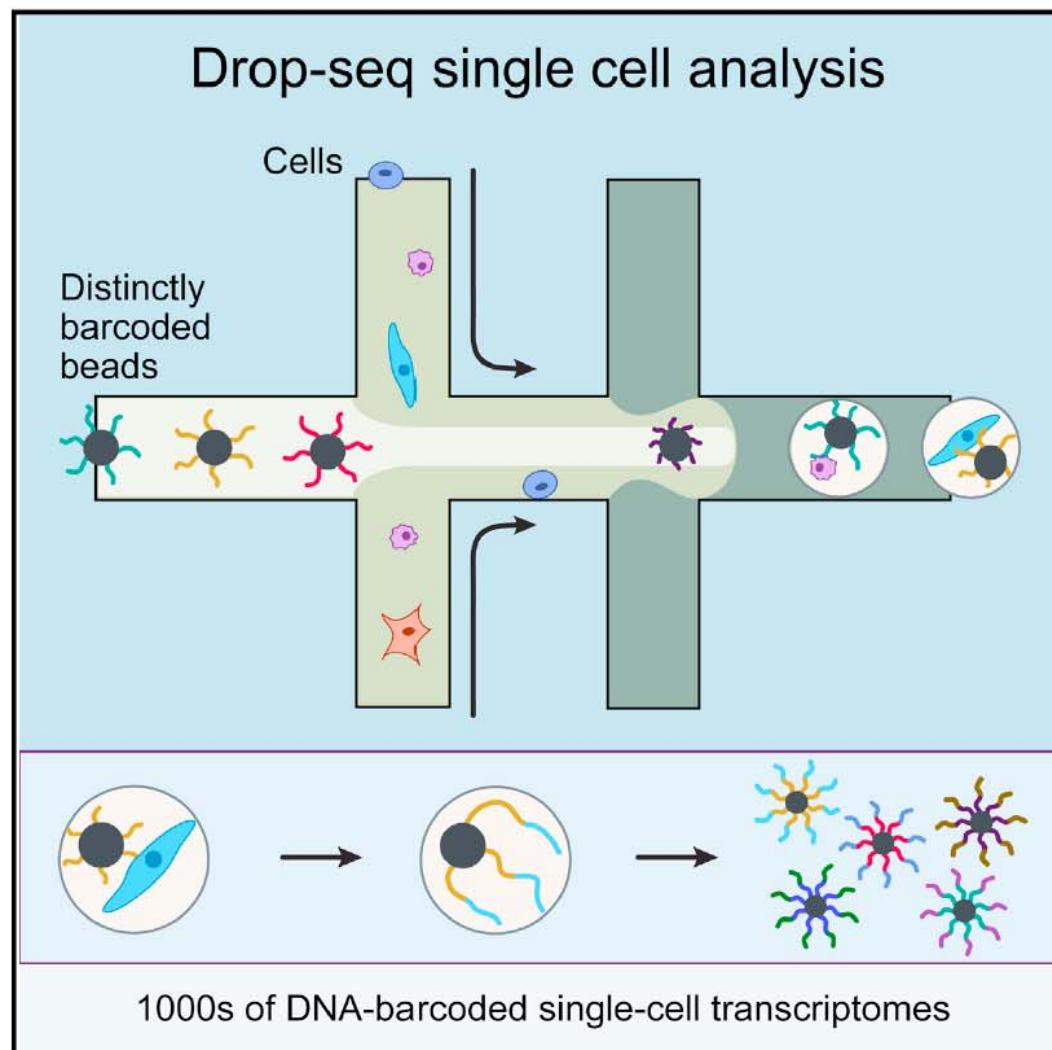
The Epigenetic Landscape - Waddington 1957

Single Cell RNA-Seq



Highly Parallel Genome-wide Expression Profiling of Individual Cells Using Nanoliter Droplets

Graphical Abstract



Authors

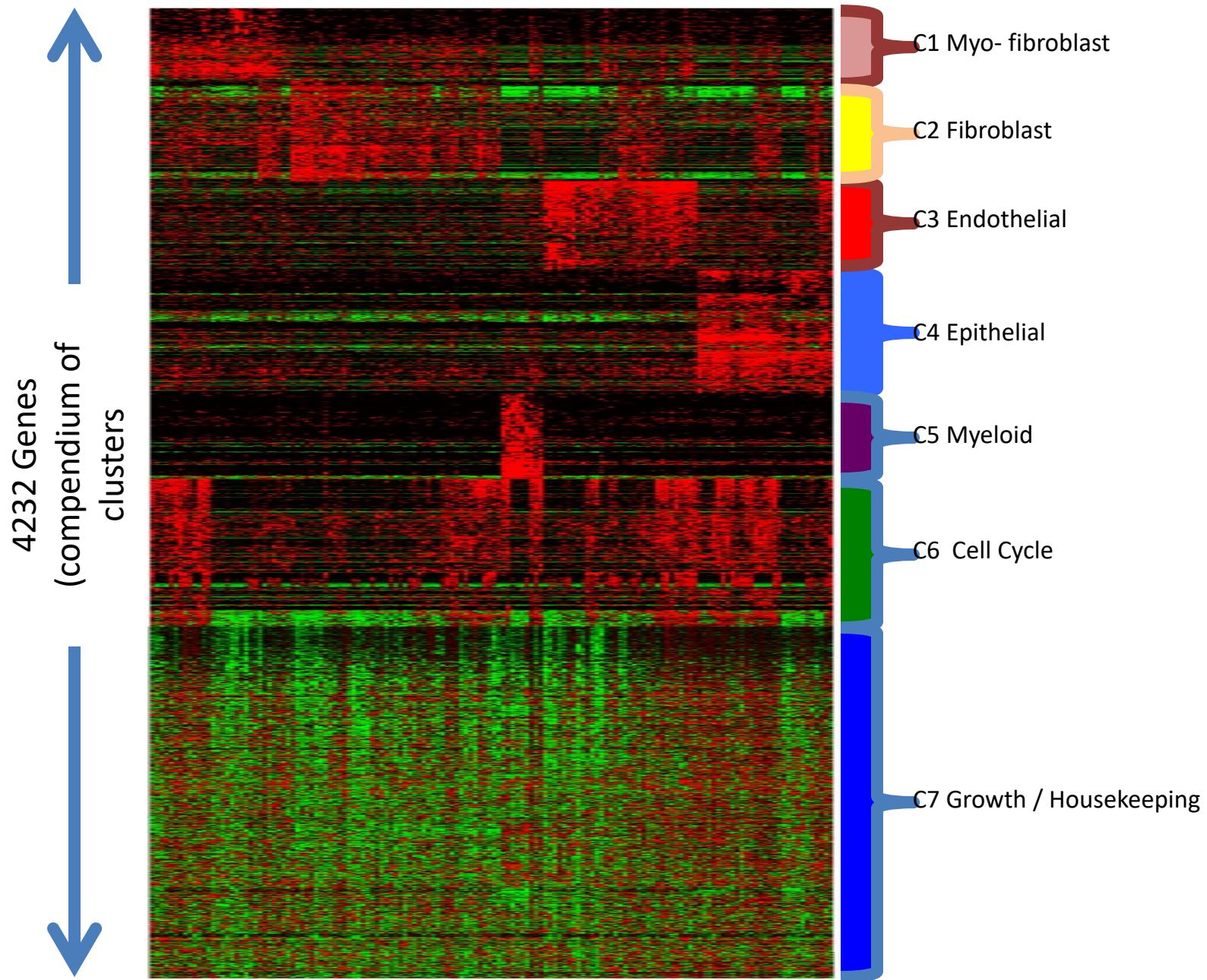
Evan Z. Macosko, Anindita Basu, ..., Aviv Regev, Steven A. McCarroll

Correspondence

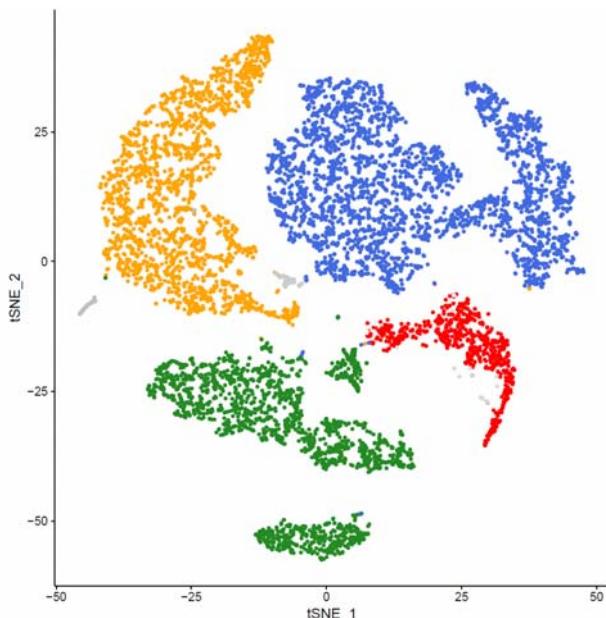
emacosko@genetics.med.harvard.edu
(E.Z.M.),
mccarroll@genetics.med.harvard.edu
(S.A.M.)

In Brief

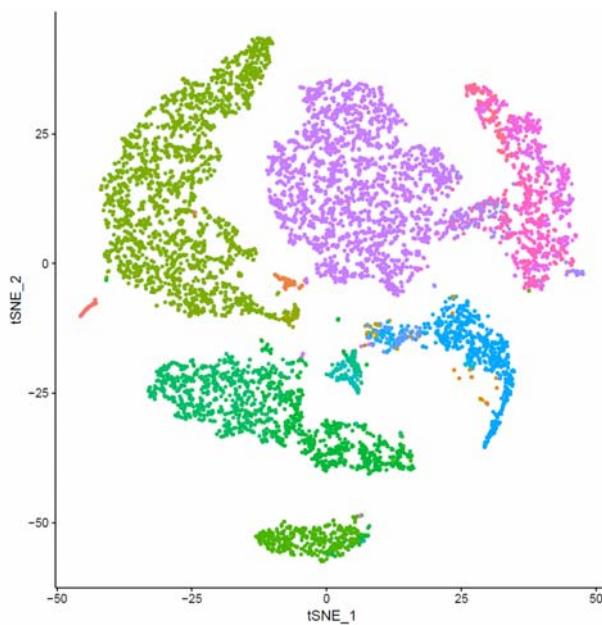
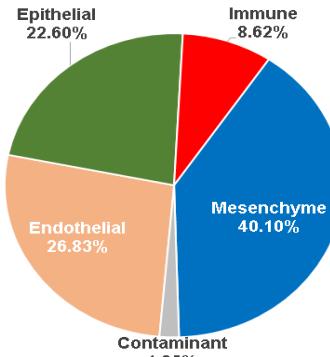
Capturing single cells along with sets of uniquely barcoded primer beads together in tiny droplets enables large-scale, highly parallel single-cell transcriptomics. Applying this analysis to cells in mouse retinal tissue revealed transcriptionally distinct cell populations along with molecular markers of each type.



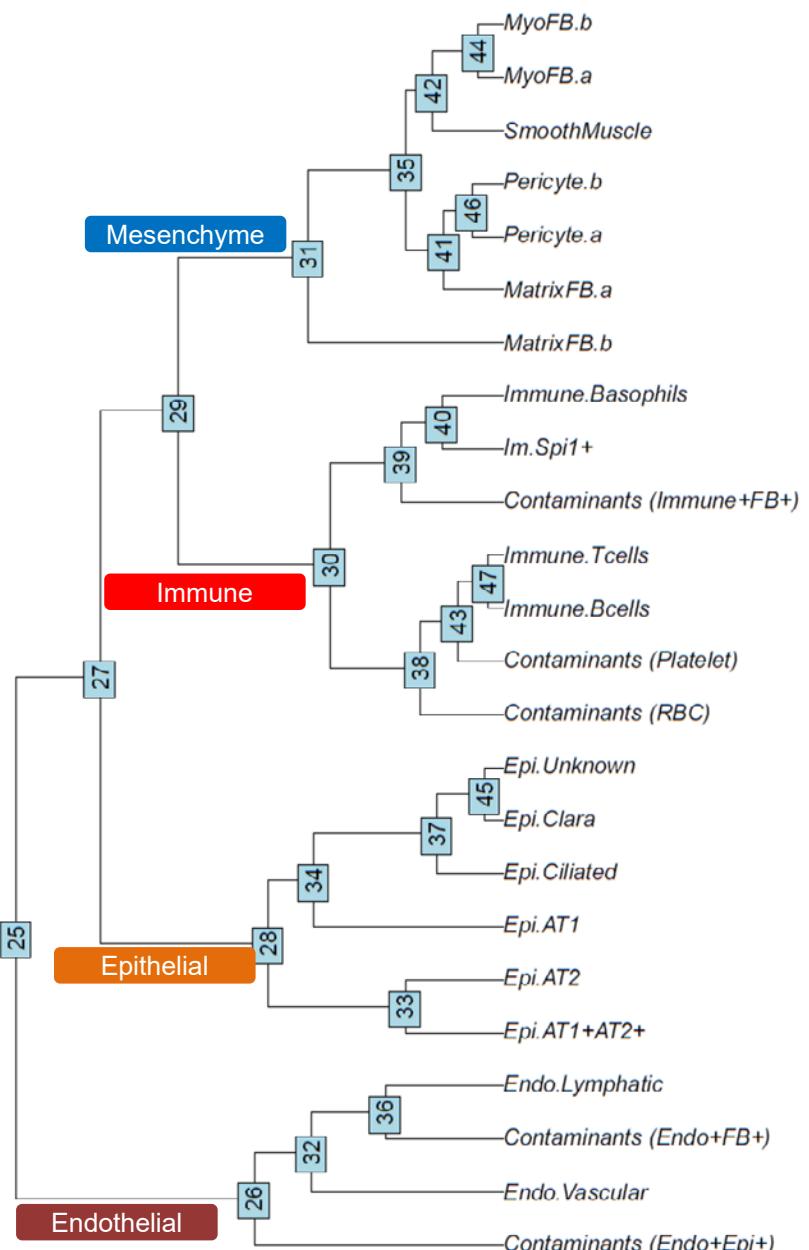
Mouse P1 Cell Types Identification



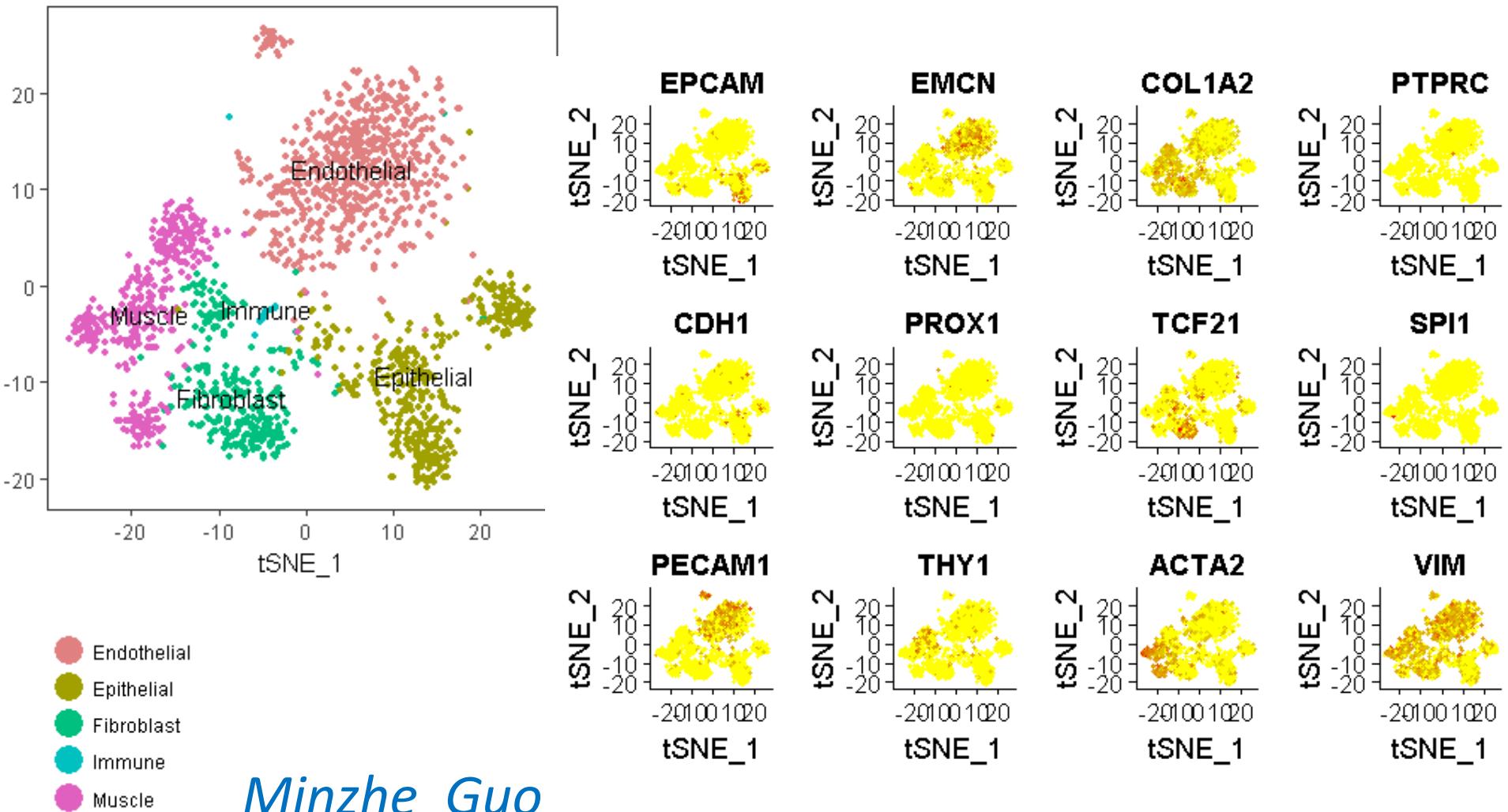
- Major cell type**
- Endothelial n=2147
 - Epithelial n=1809
 - Immune n=690
 - Mesenchyme n=3209
 - Contaminants (Endo+Epi+) n=42
 - Contaminants (Endo+FB+) n=49
 - Contaminants (Immune+FB+) n=20
 - Contaminants (Platelet) n=5
 - Contaminants (RBC) n=32



- Cell Type**
- Endo.Lymphatic
 - Endo.Vascular
 - Epi.AT1
 - Epi.AT1+AT2+
 - Epi.AT2
 - Epi.Ciliated
 - Epi.Clara
 - Epi.Unknown
 - Immune.Basophils
 - Immune.Bcells
 - Immune.Macrophages
 - Immune.Tcells
 - MatrixFB.a
 - MatrixFB.b
 - MyoFB.a
 - MyoFB.b
 - Pericyte.a
 - Pericyte.b
 - SmoothMuscle
 - Contaminants (Endo+Epi+)
 - Contaminants (Endo+FB+)
 - Contaminants (Immune+FB+)
 - Contaminants (Platelet)
 - Contaminants (RBC)
- 19 Subtypes



Human Infant-DAY1 Drop-seq: Major Cell Types and Marker Expression (HTC)

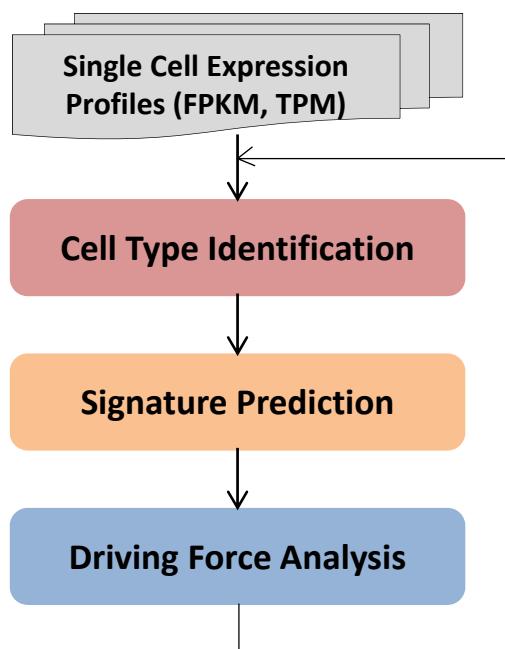


Minzhe Guo

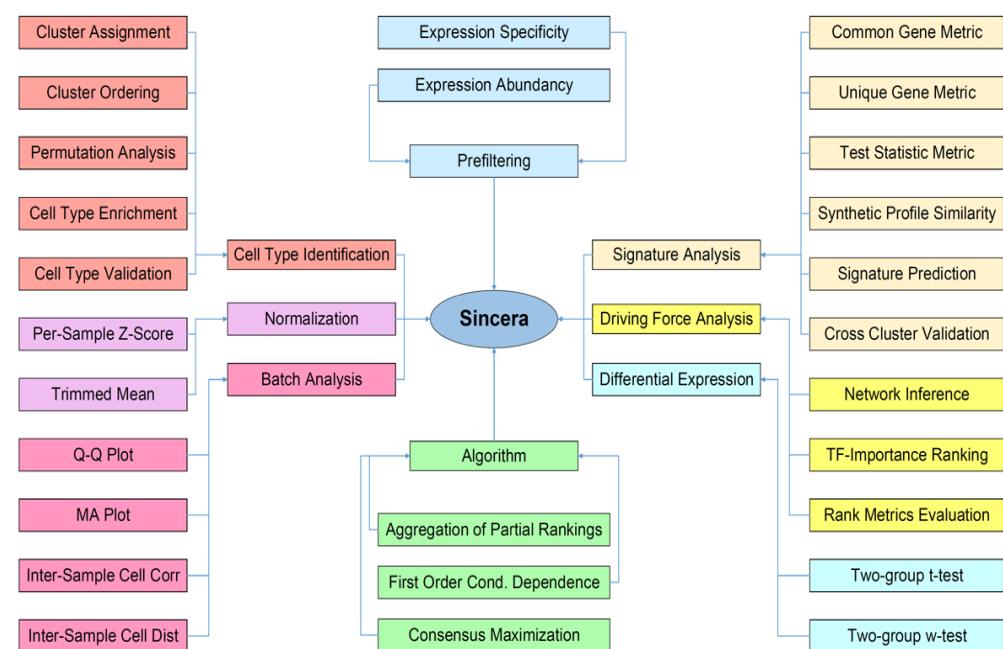
CCHMC/U of Rochester

Sincera: a computational pipeline for SIngle CELl Rna-seq profiling Analysis

Main Analysis Components



Program Structure of Sincera

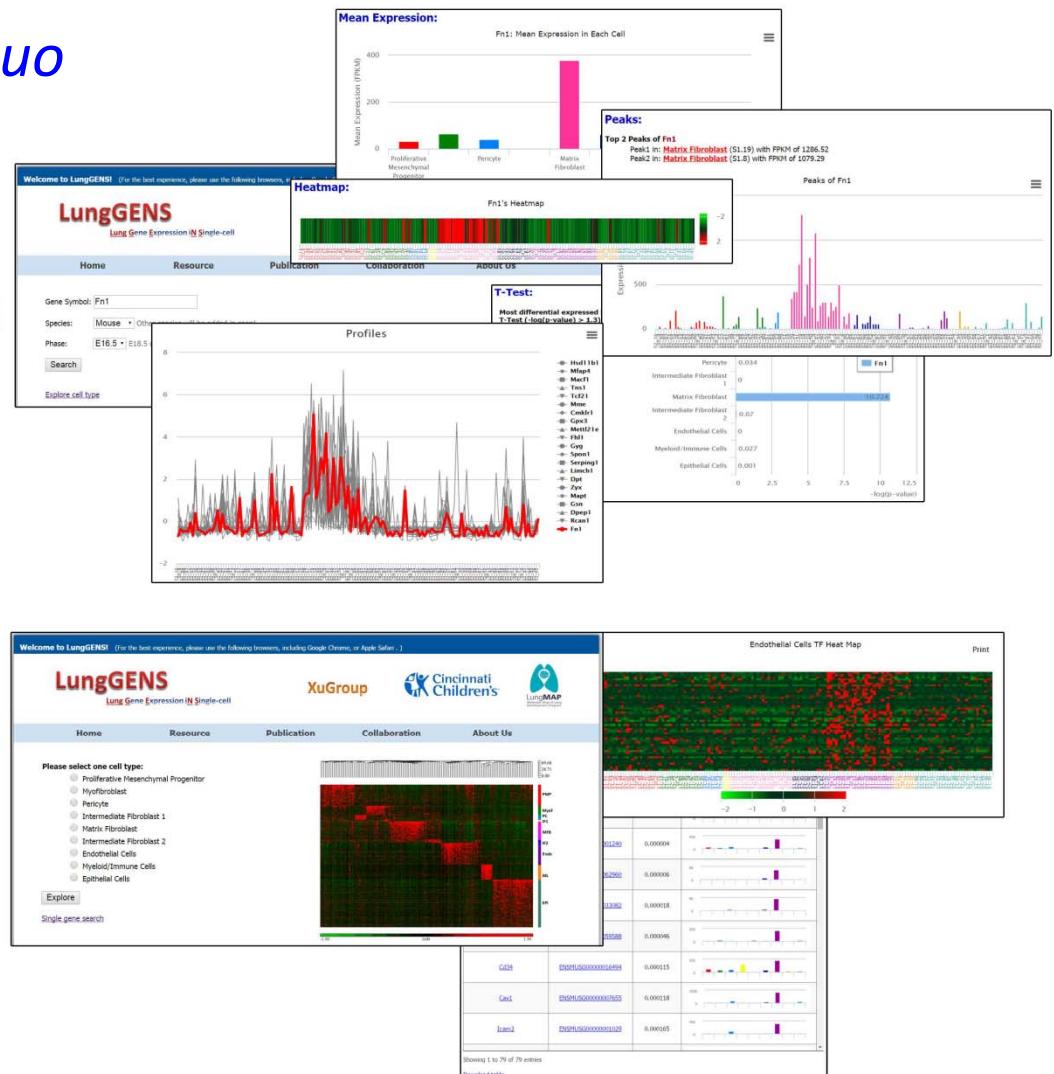
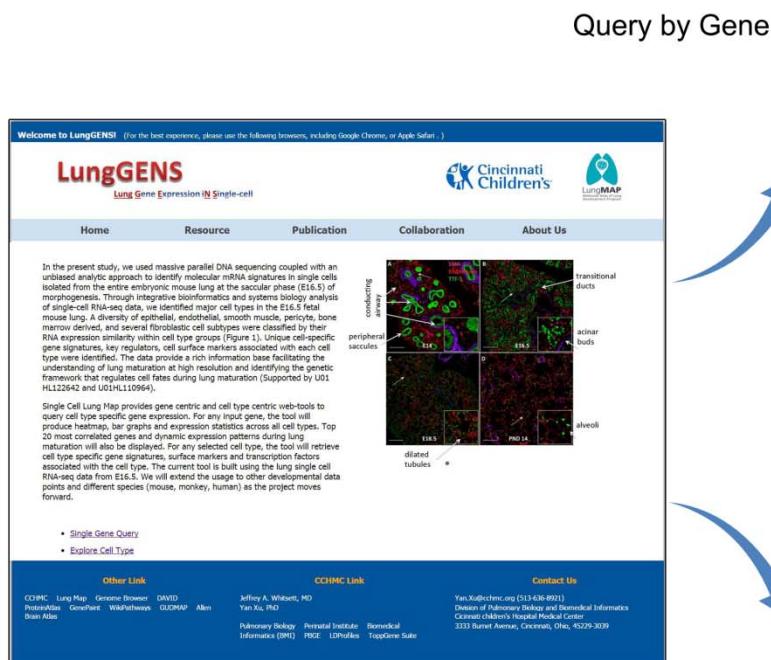


<https://research.cchmc.org/pbge/sincera.html>

Screenshot of LungGENS

(<https://research.cchmc.org/pbge/lunggens/default.html>)

Yan Xu, Yina Du, Mizhe Guo



CCHMC

LGEA Web Portal

Lung Gene Expression Analysis Web Portal



LGEA Web Portal

LungGENS

Lung Image

Collaboration

News

LGEA Tools

We previously developed "LungGENS", a web site for mapping single cell gene expression in the developing lung. Initial phases of the webtool were built based on single cell RNA-seq data from normal fetal mouse lung at E16.5. Web statistics indicated that "LungGENS" is well received and visited by research investigators worldwide. With the continued support from the "LungMAP" consortium, transcriptome data derived from different technique platforms, species and lung development stages are quickly expanding. We now extend the scope and contents of the LungGENS database to accommodate heterogeneous data structures and types. We present "LGEA web portal" (Lung Gene Expression Analysis web portal), an extended version of LungGENS web portal for analyses of lung gene expression patterns and mapping cell types in the developmental lung from single cells, sorted cell populations and whole tissue developmental studies.

LGEA implements a number of new features and analytical methods. It allows the analysis of 1) single cell transcriptomes using [LungGENS](#); 2) sorted lung cell populations using [LungSortedCells](#); 3) Lung Developmental Time Course analysis using [LungDTC](#) and 4) Lung Disease analysis [LungDisease](#).

News and updates:

- [Introduction of LungMAP -- Dr.Jeffrey Whitsett](#)
- [5-8-2017: LGEA added in mouse P7 scRNA-seq dataset, and Human iPSC-derived NKO2-1 lung scRNA-seq dataset, from Kotton Lab.](#)
- [4-22-2017: Dr.Whitsett and Dr.Xu's new published chapter: *Transcriptional Networks-Control of Lung Maturation*.](#)
- [4-22-2017: Check out our 3 new sections: "LungEpigenetics", "LungImage" and "LGEA-ToolBox".](#)
- [4-10-2017: LGEA web portal has just been published by *Thorax* \(PubMed\)](#)
- [6-9-2016: Check out this new book "Fetal and Neonatal Lung Development: Clinical Correlates and Technologies for the Future \(Lung Growth, Development, and Disease\)" \(1st Edition by Alan Jobe \(Editor\), Jeffrey Whitsett \(Editor\), Steven Abram \(Editor\)\). \[Amazon\]](#)

Current version and under development

**If you are experiencing problems displaying LGEA pages, please refresh the page or clear the browser cache.

LungGENS

LungGENS - species

- Mouse (scRNA-seq, drop-seq) (E16.5, E18.5, P1, P7, P28) [\[more\]](#)
- Monkey (Day 98 TGA) [\[more\]](#)

LungGENS - query

- Query by single gene [\[more\]](#)
- Query by cell type [\[more\]](#)
- Query by gene list [\[more\]](#)

LungSortedCells

Human

- Human Sorted (Immune, Endothelial, Mesenchymal and Epithelial Cells) [\[more\]](#)

Mouse

- Mouse AT2 (P1, P7, P28) [\[more\]](#)
- Mouse Pdgfra+ Fibroblast (E16.5, E18.5, P1, P7, P28) [\[more\]](#)
- Mouse Sorted (Immune, Endothelial and Epithelial Cells) [\[more\]](#)

LungSortedCells-query

- Query by gene list [\[more\]](#)

LungDTC

MicroArray

- LDProfiles [\[more\]](#)
- MGI: developmental time course [\[more\]](#)

RNA-seq

- Mouse Lung (E16.5, E18.5, P1, P7, P14 and P28) [\[more\]](#)
- Rhesus Macaque Lung (GA102, GA130, GA150) [\[more\]](#)

LungDisease

scRNA-seq Analysis

- Human IPF (540 normal and disease cells) [\[more\]](#)
- Human iPSC-derived NKX2-1+ lung (Kotton Lab normal and CF) [\[more\]](#)

Sorted RNA-seq

- Human IPF (Human A549 cells) [\[more\]](#)

LungEpigenetics

ENCODE

- Mouse histone PTM chip-seq data [\[more\]](#)

LungMAP research center

- TBA

LungImage

Confocal Imaging

- Mouse C57BL6 lung (E16.5, E18.5, P1, P3, P7, P10...) [\[more\]](#)
- Human Lung (Fetal and Adult) [\[more\]](#)

H&E Staining

- Human Lung (Fetal and Adult) [\[more\]](#)

Query by cell type

- TBA

LGEA-ToolBox

Database query tool

- Signature comparison [\[more\]](#)
- Gene at glance [\[more\]](#)
- LDProfiles [\[more\]](#)

Research tools

- SINCERA [\[more\]](#)
- SLICE [\[more\]](#)

Other resource

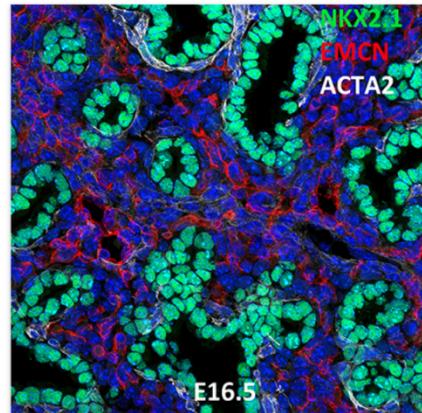
- Tool list [\[more\]](#)

<https://research.cchmc.org/pbge/lunggens/mainportal.html>

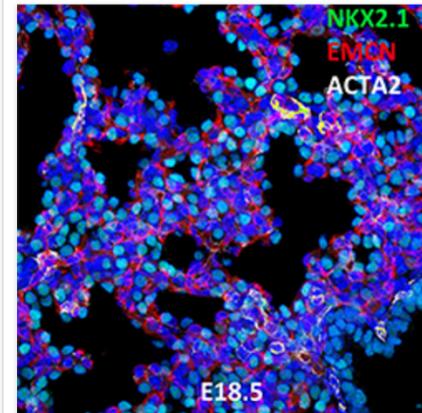
<https://www.lungmap.net/>

"LGEA "and "Breath":Atlas of Mouse Lung Cell Types During Development

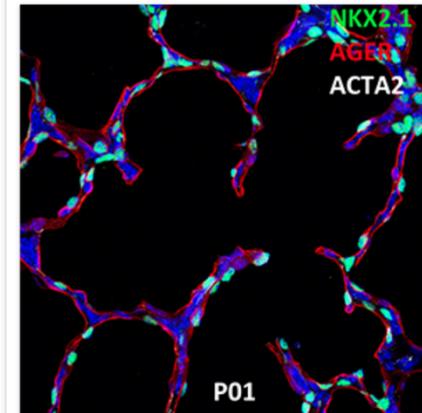
C57BL/6



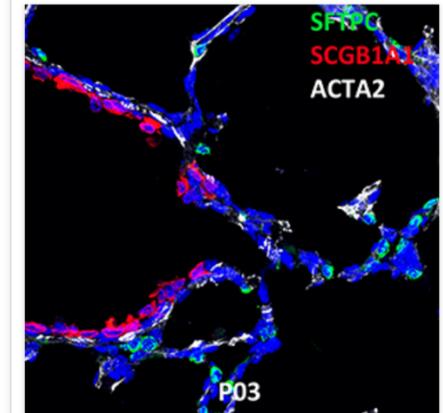
E16.5 C57BL6 Confocal Imaging



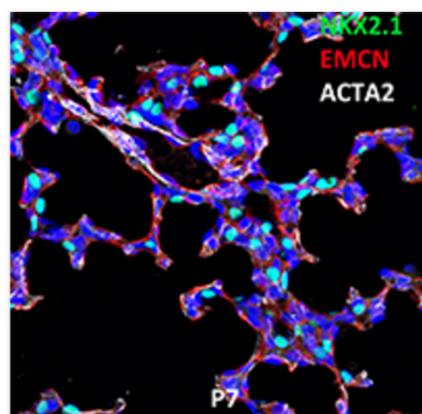
E18.5 C57BL6 Confocal Imaging



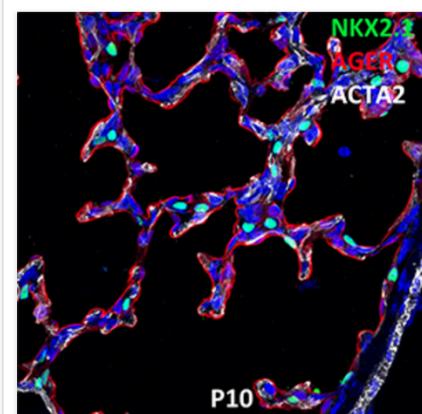
Postnatal Day 1 C57BL6 Confocal Imaging



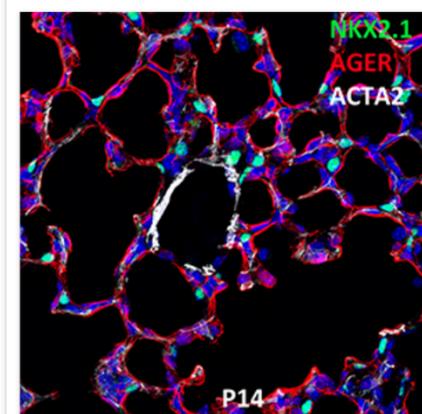
Post Natal Day 3 C57BL6 Confocal Imaging



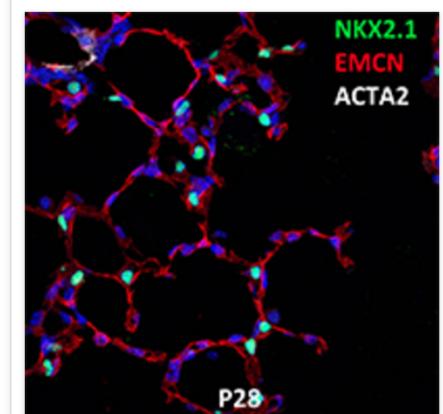
Postnatal Day 7 C57BL6 Confocal Imaging



Postnatal Day 10 C57BL6 Confocal Imaging

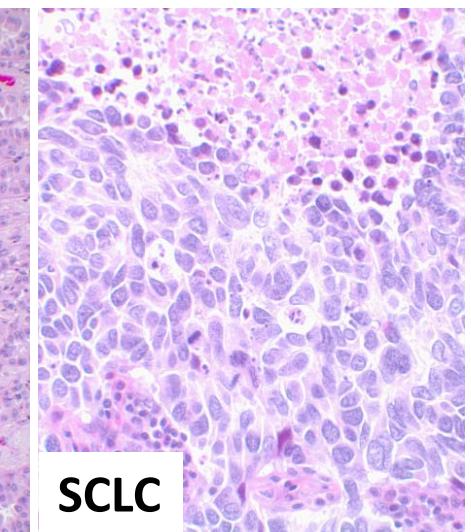
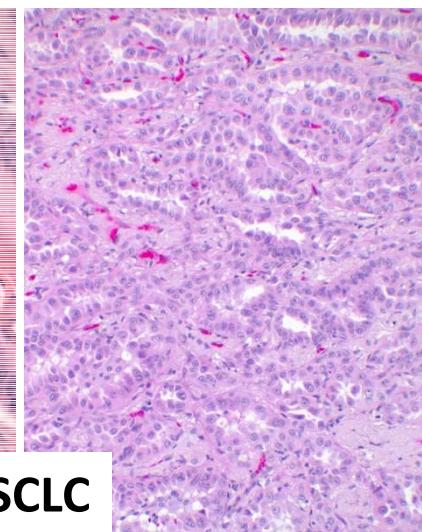
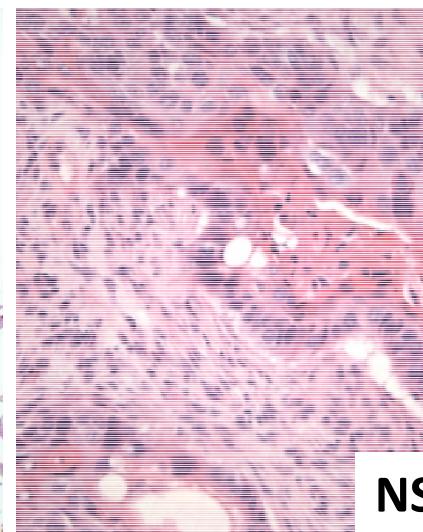
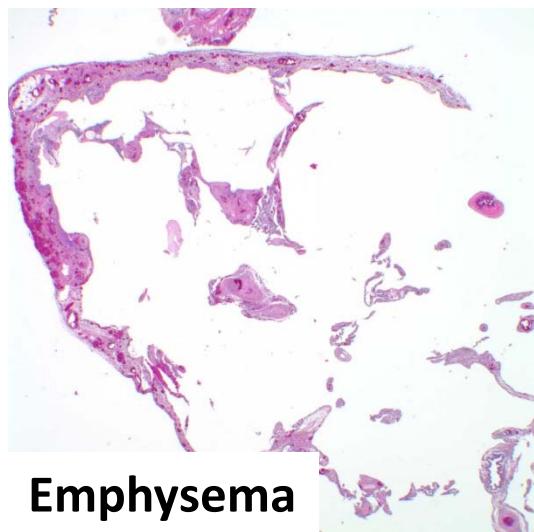
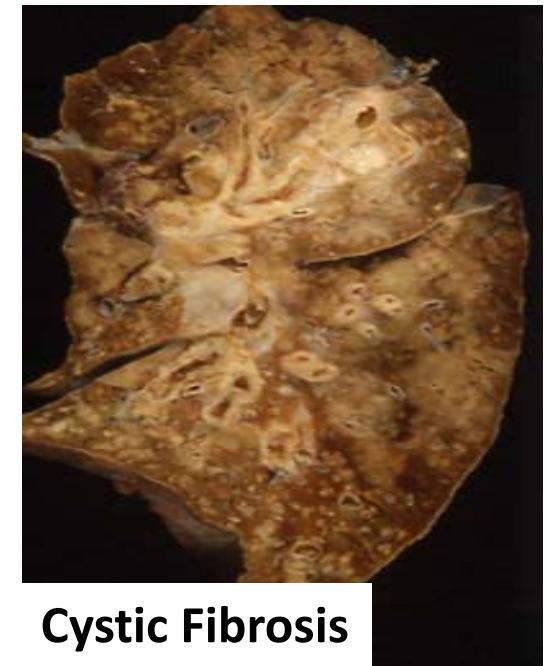
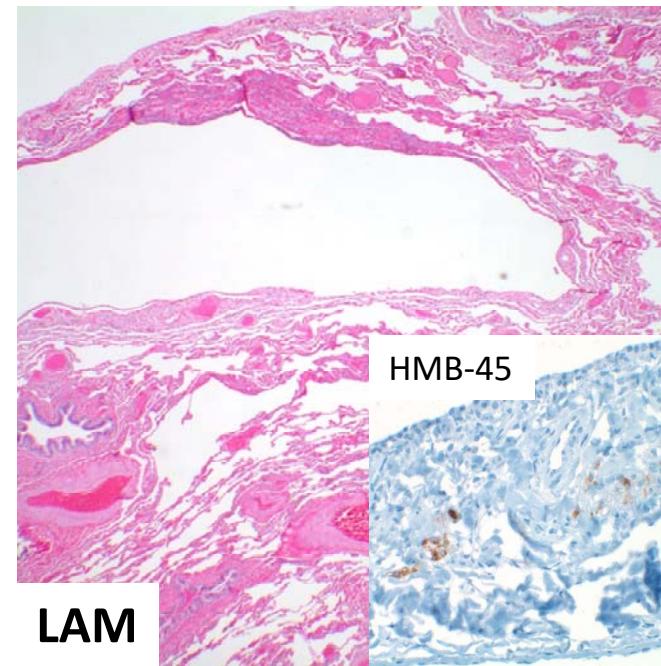
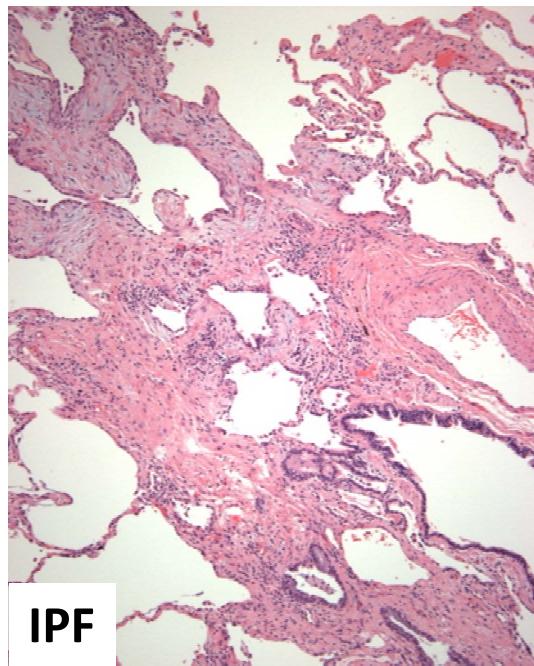


Postnatal Day 14 C57BL6 Confocal Imaging



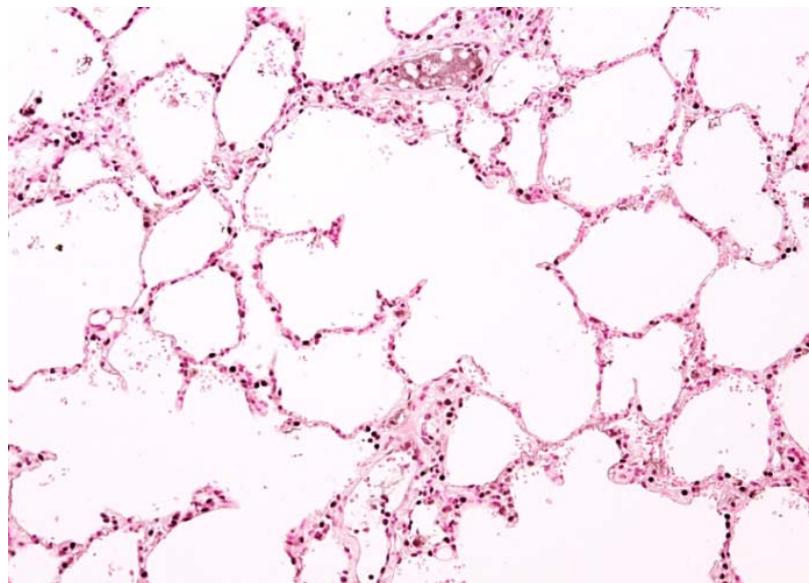
Postnatal Day 28 C57BL6 Confocal Imaging

Challenge of Chronic Pulmonary Diseases

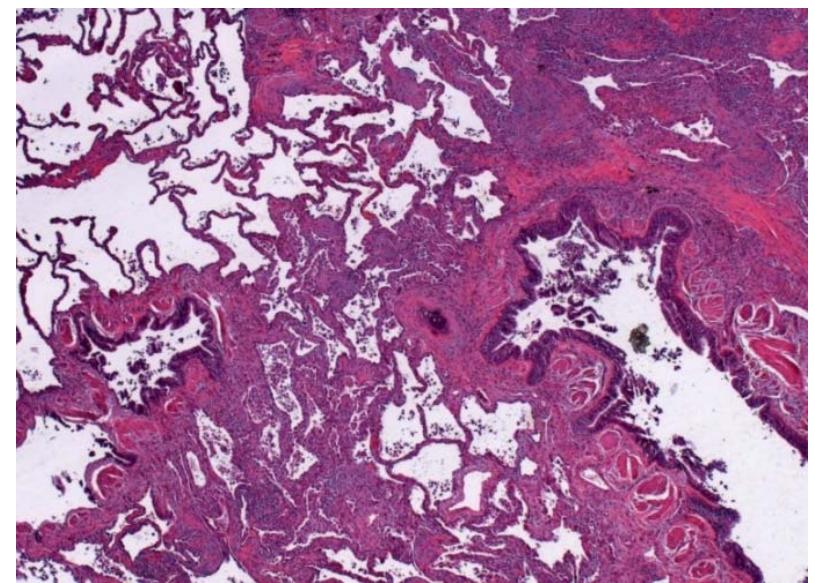


Idiopathic Pulmonary Fibrosis

- Normal

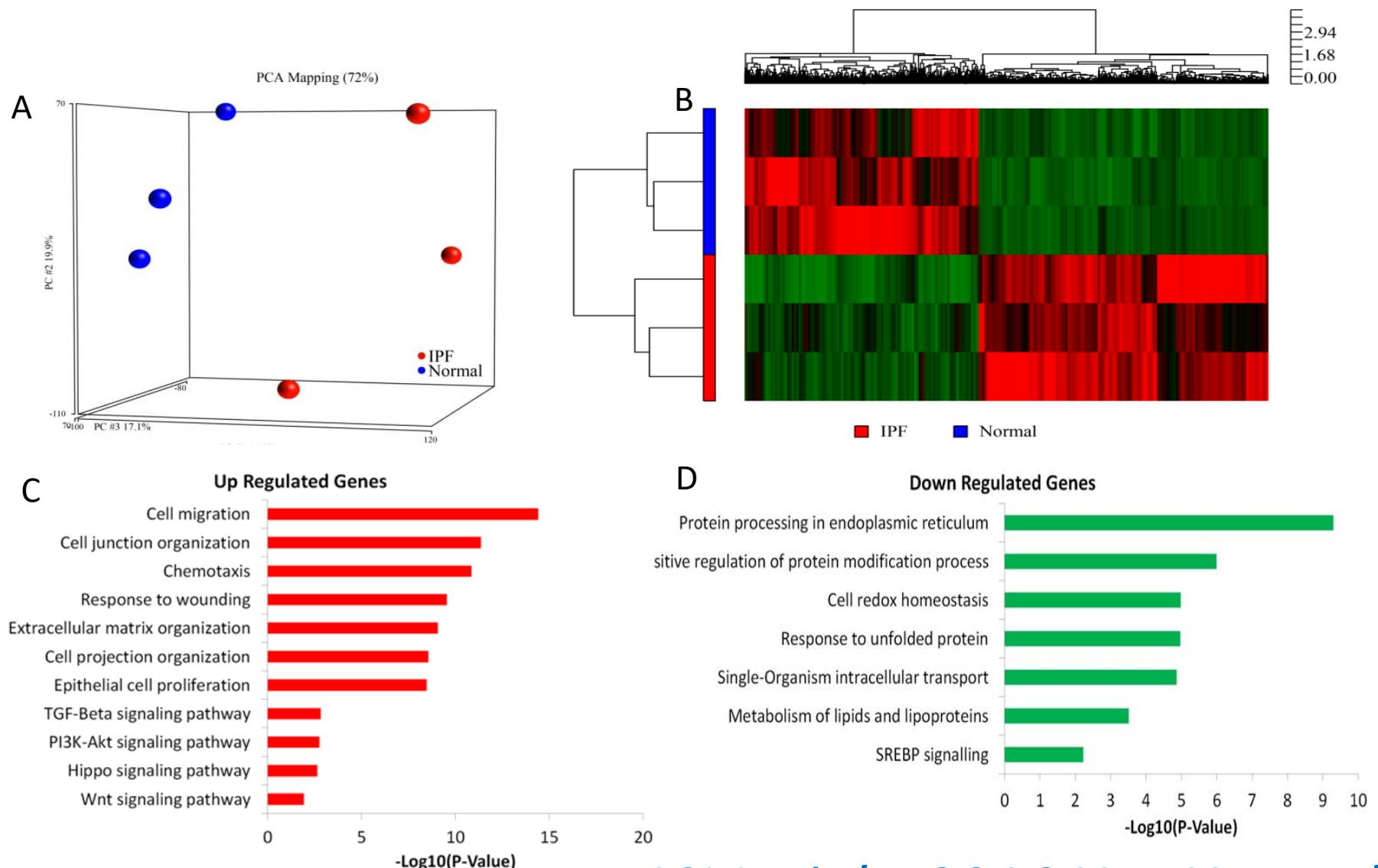


IPF



Barry Stripp-Cedar Sinai

Gene Expression in Human IPF :Sorted Epithelial Cells

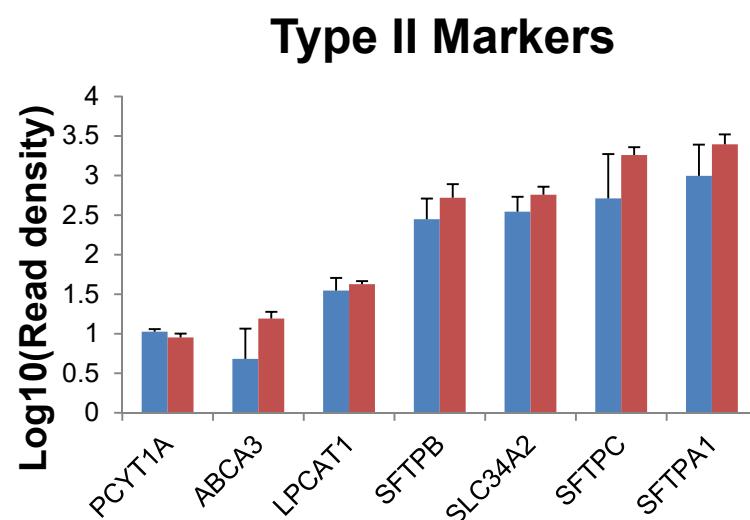


JCI Insight 2016: Yan Xu et al

Expression of Proximal Epithelial Markers in IPF Type 2 Cells

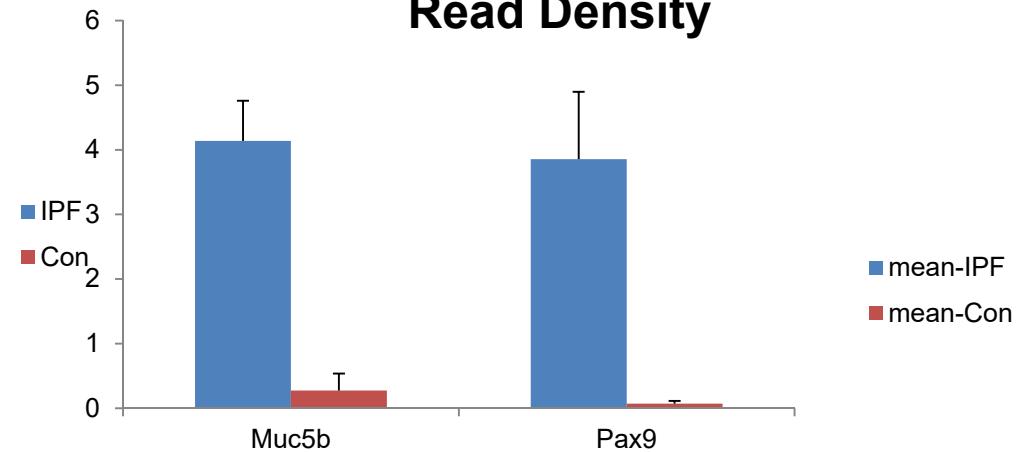
Loss of Normal Epithelial Cell Identity

SFTPA1, SFTPB, SFTPC, PCYT1A,
ABCA3, SLC34A1, LPCAT1



Muc5b Pax9

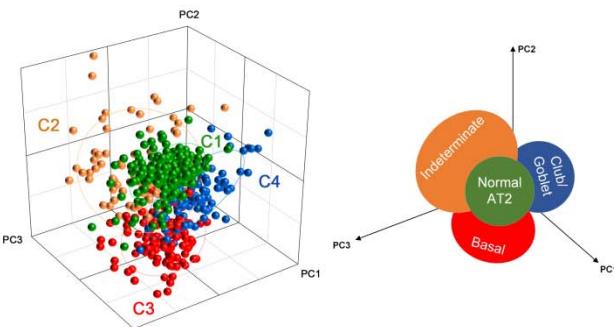
Read Density



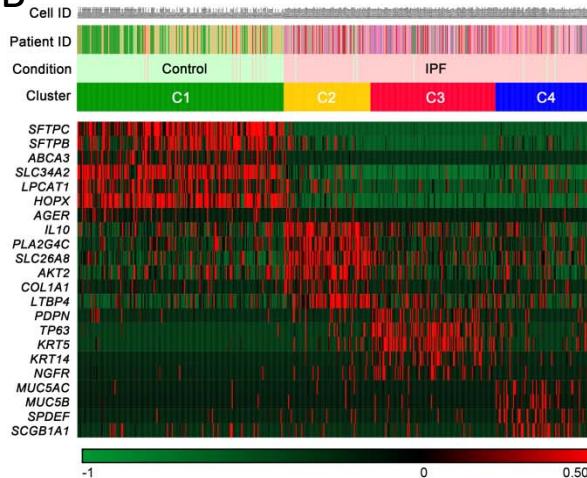
Single Cell RNA Expression Patterns in IPF

A

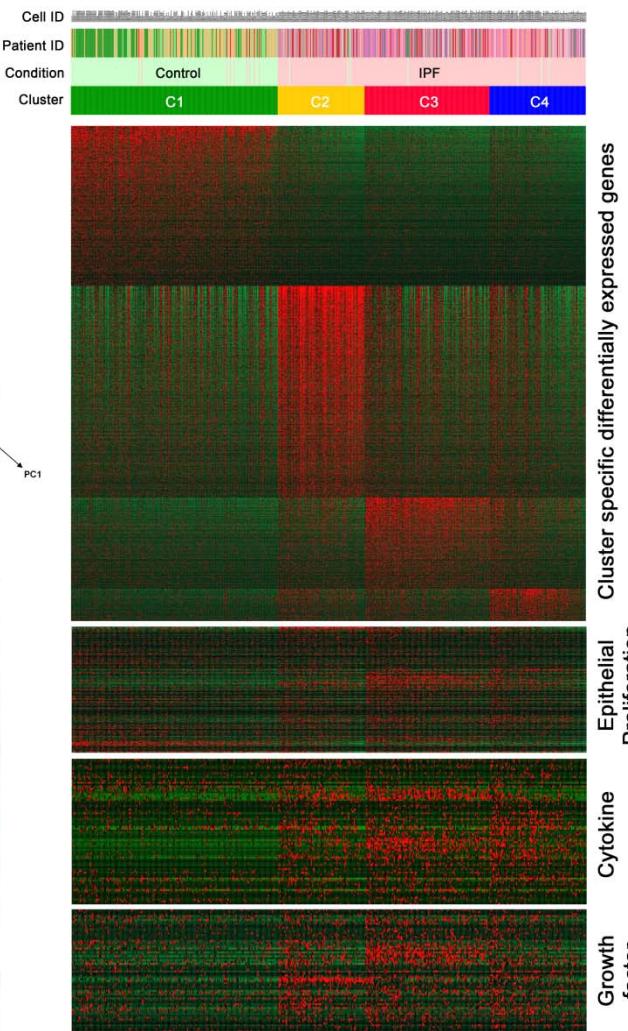
Cluster	Condition	Patient ID
C1	Control	CC002 IPF003
C2	IPF	CC006 IPF009
C3		CC019 IPF010
C4		IL006 IPF012
		IPF002



B



C



D

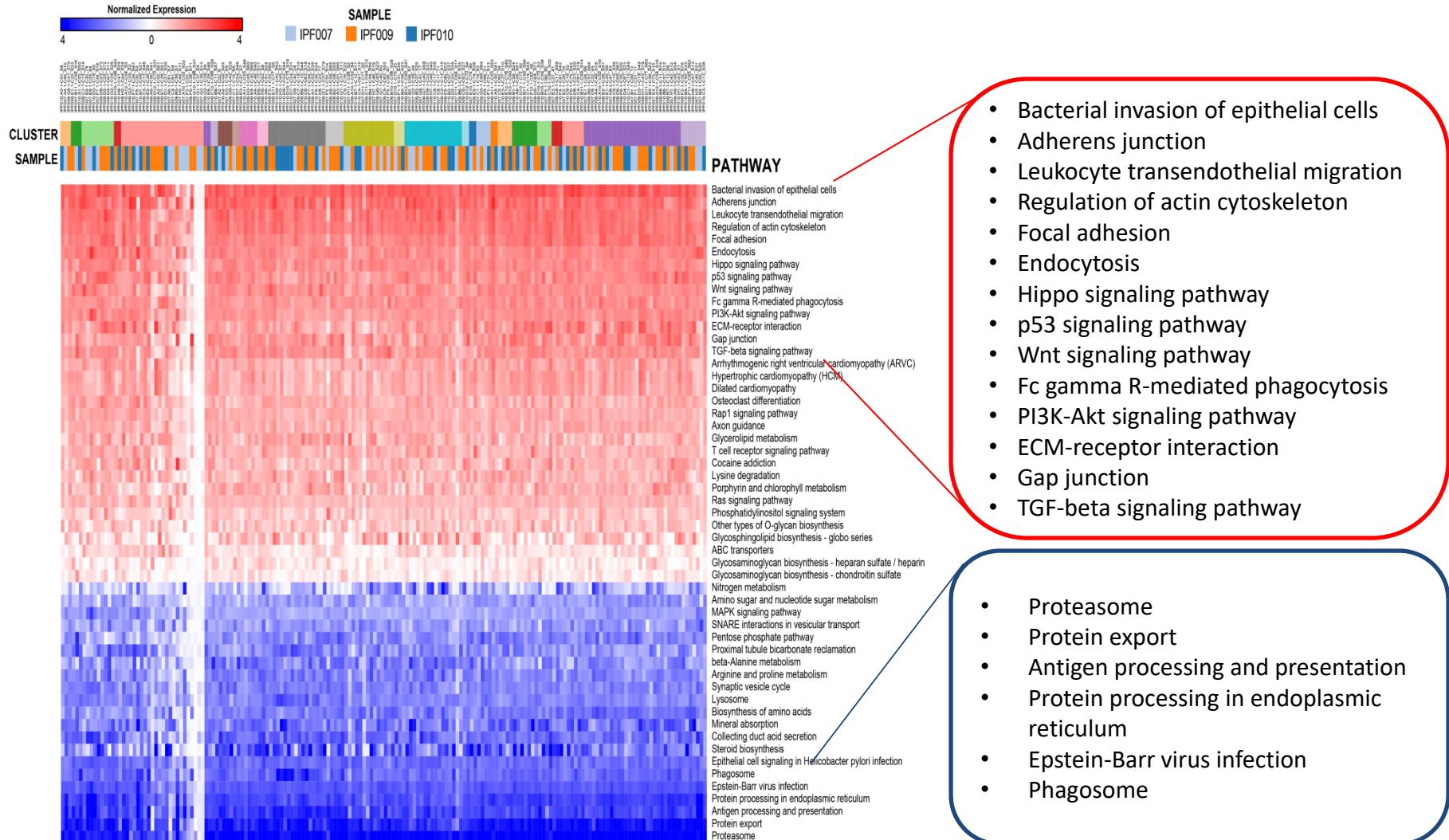
C1	
Functional terms	P-value
GO:0009636	response to toxic substance/detoxification
GO:0055114	oxidation-reduction process
GO:006629	lipid metabolic process
GO:006869	lipid transport
GO:0043129	surfactant homeostasis
GO:0042599	lamellar body
Transcription Factor Binding Site	V\$CEBP_Q2_01
Transcription Factor Binding Site	V\$GATA6_01

C2	
Functional terms	P-value
GO:0006820	anion transport
GO:0043409	negative regulation of MAPK cascade
GO:0043547	positive regulation of GTPase activity
GO:0050709	negative regulation of protein secretion
GO:0042098	T cell proliferation
GO:0045936	negative regulation of phosphate metabolic process
GO:0006954	inflammatory response
GO:0006869	lipid transport
GO:0019752	carboxylic acid metabolic process

C3	
Functional terms	P-value
GO:0031581	hemidesmosome assembly
GO:0034330	cell junction organization
GO:0016477	cell migration
GO:0042060	wound healing
GO:0005604	basement membrane
Pathway	Laminin interactions
Pathway	PI3K-Akt signaling pathway
Transcription Factor Binding Site	CATTGTYY_VSSOX9_B1

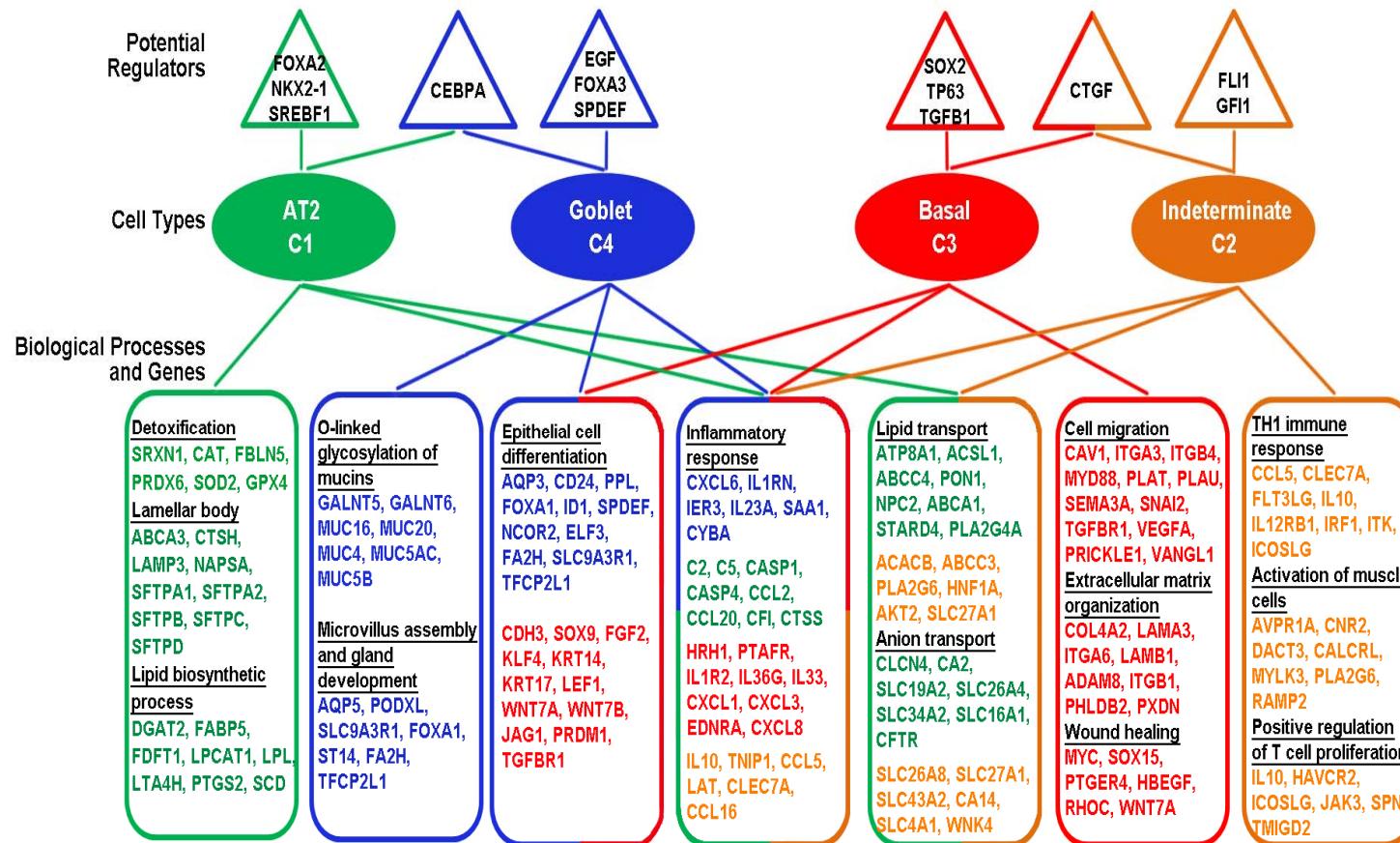
C4	
Functional terms	P-value
GO:0009617	response to bacterium
GO:0009100	glycoprotein metabolic process
GO:0030855	epithelial cell differentiation
GO:0070085	glycosylation
GO:0005902	microvillus
GO:0005794	Golgi apparatus
MP:0000511	abnormal intestinal mucosa morphology
MSigDB M5885	Ensemble of genes encoding ECM-associated proteins including ECM-affiliated proteins, ECM regulators and secreted factors

Enrichment of KEGG Pathway in IPF SC



Normal AT2 Cells

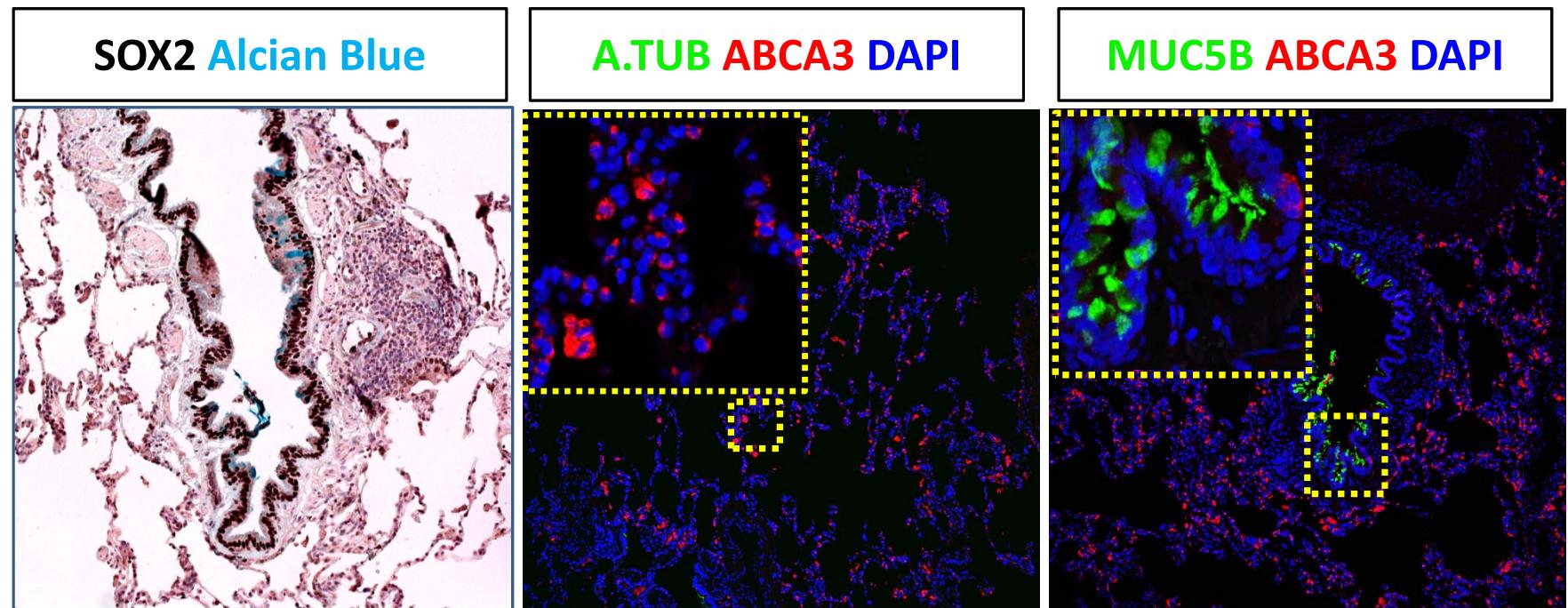
IPF Epithelial Cells



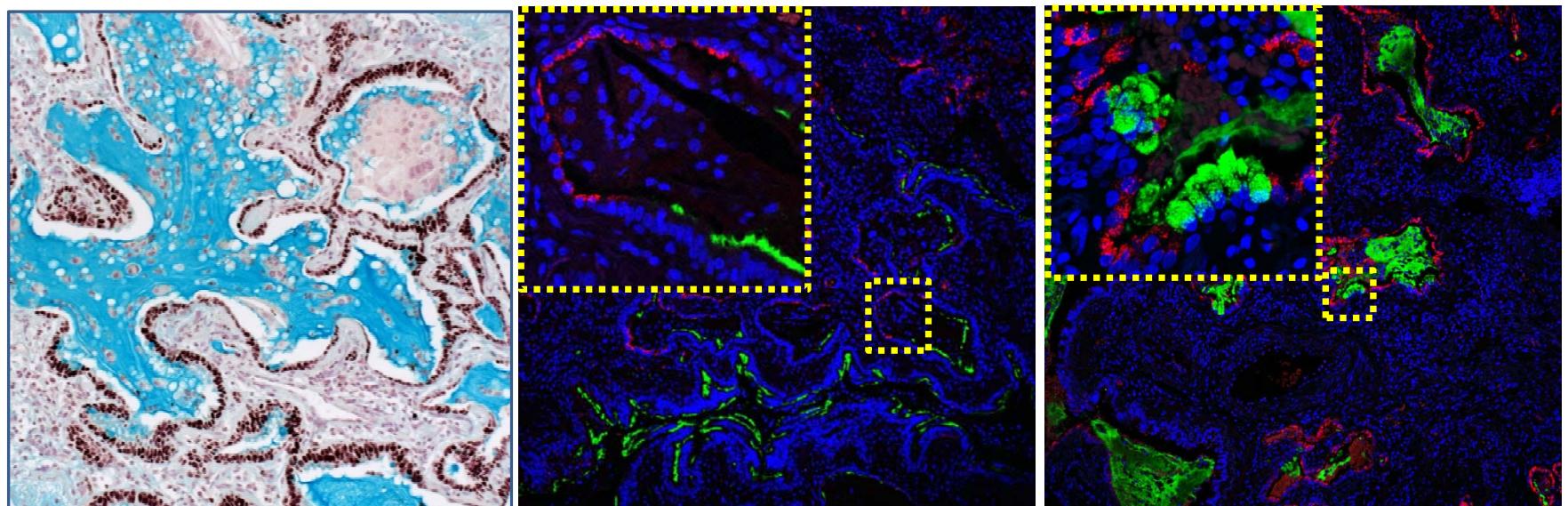
Loss of Alveolar Cell Identity in IPF

“Proximalization” of the peripheral lung in IPF

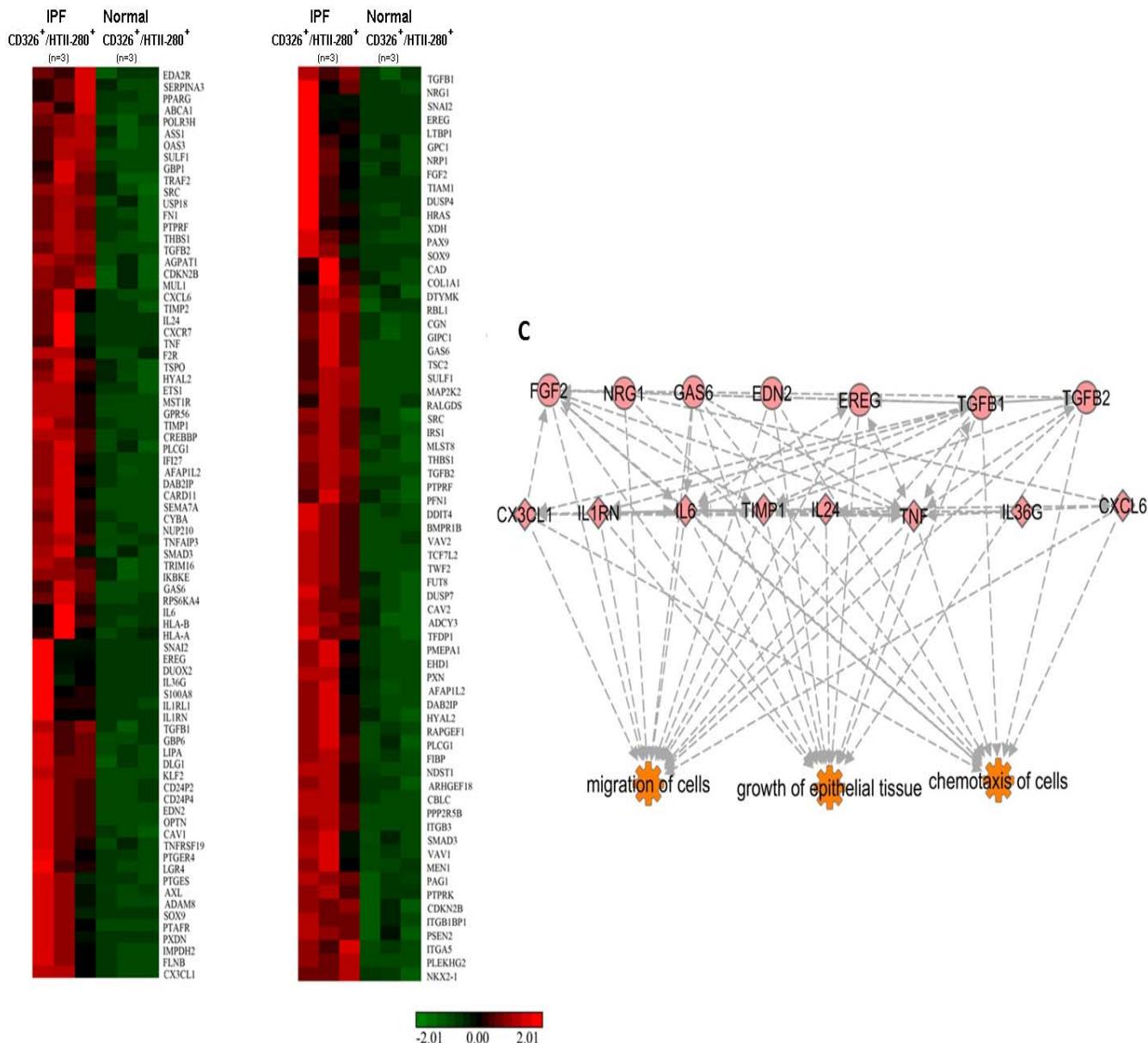
DONOR



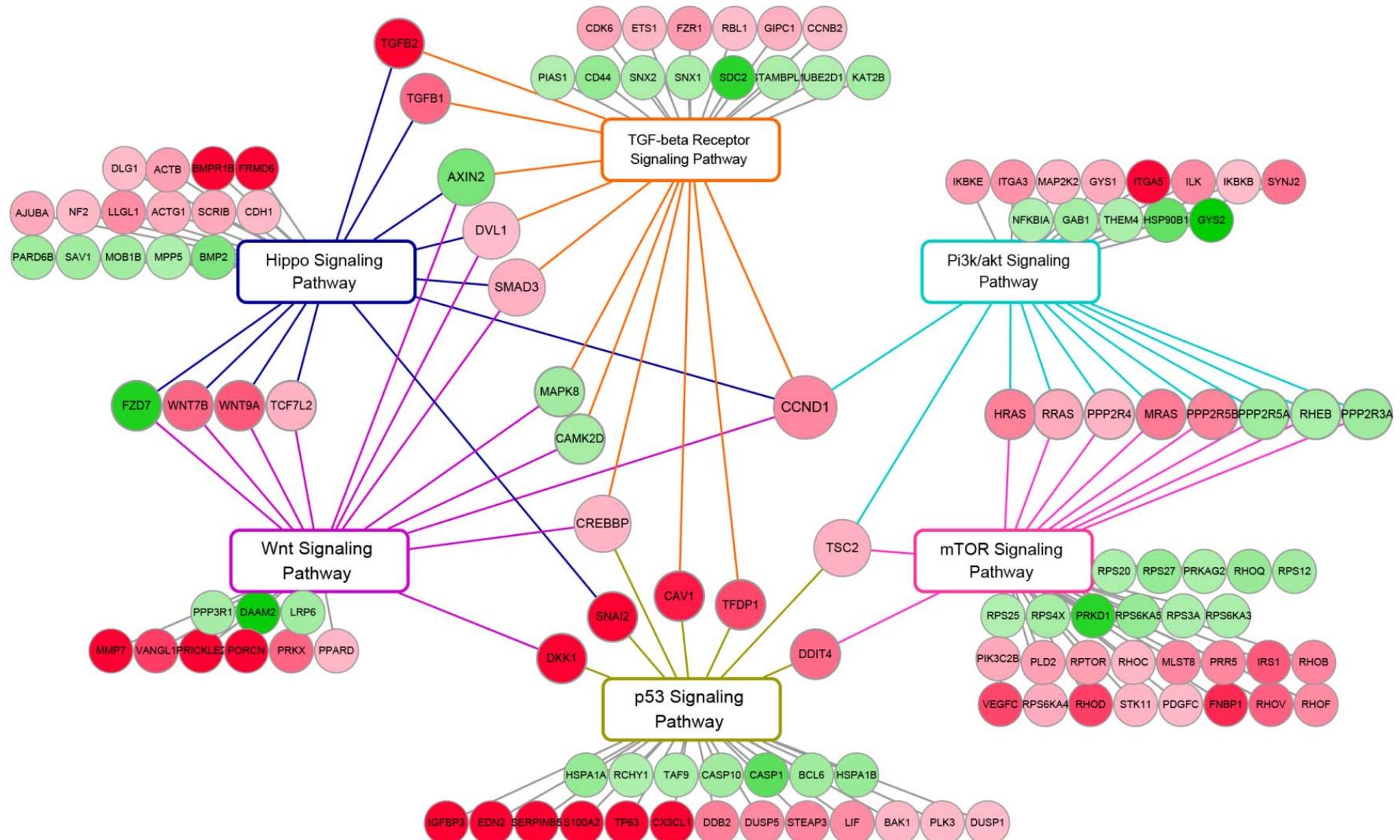
IPF

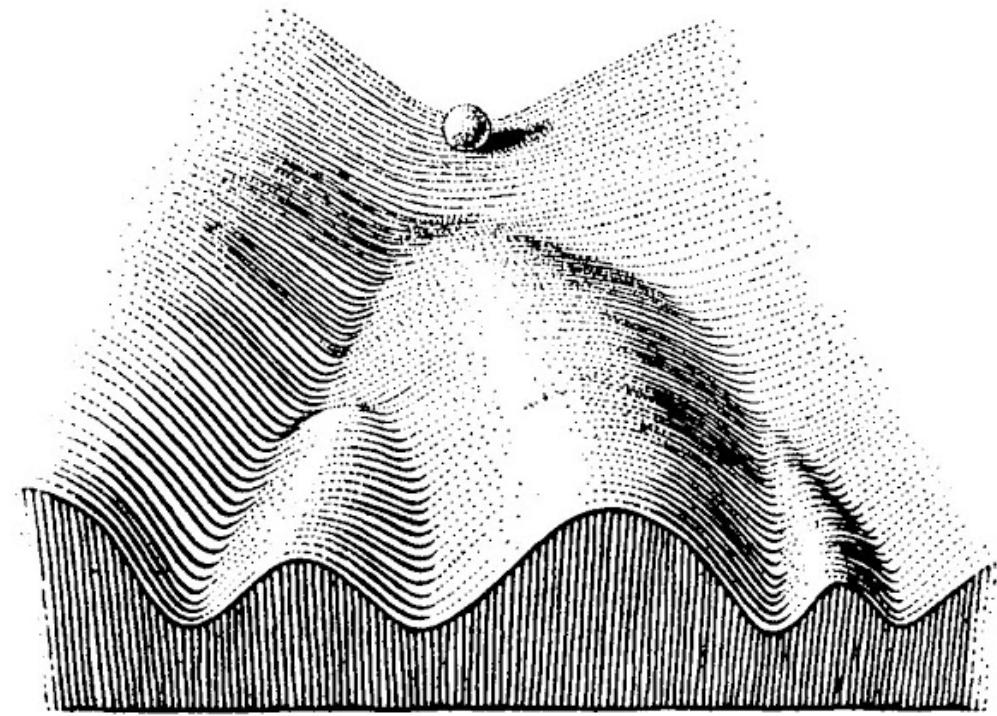


Activation of Cytokine and Growth Factor Signaling in IPF



Prediction of Abnormal Cell Signaling Driving IPF





The Epigenetic Landscape - Waddington 1957

Monogenic Diseases of Surfactant Homeostasis

ABCA3: Surfactant lipid transport in AT2 cells

SFTPB: Intra cellular packaging and function of surfactant

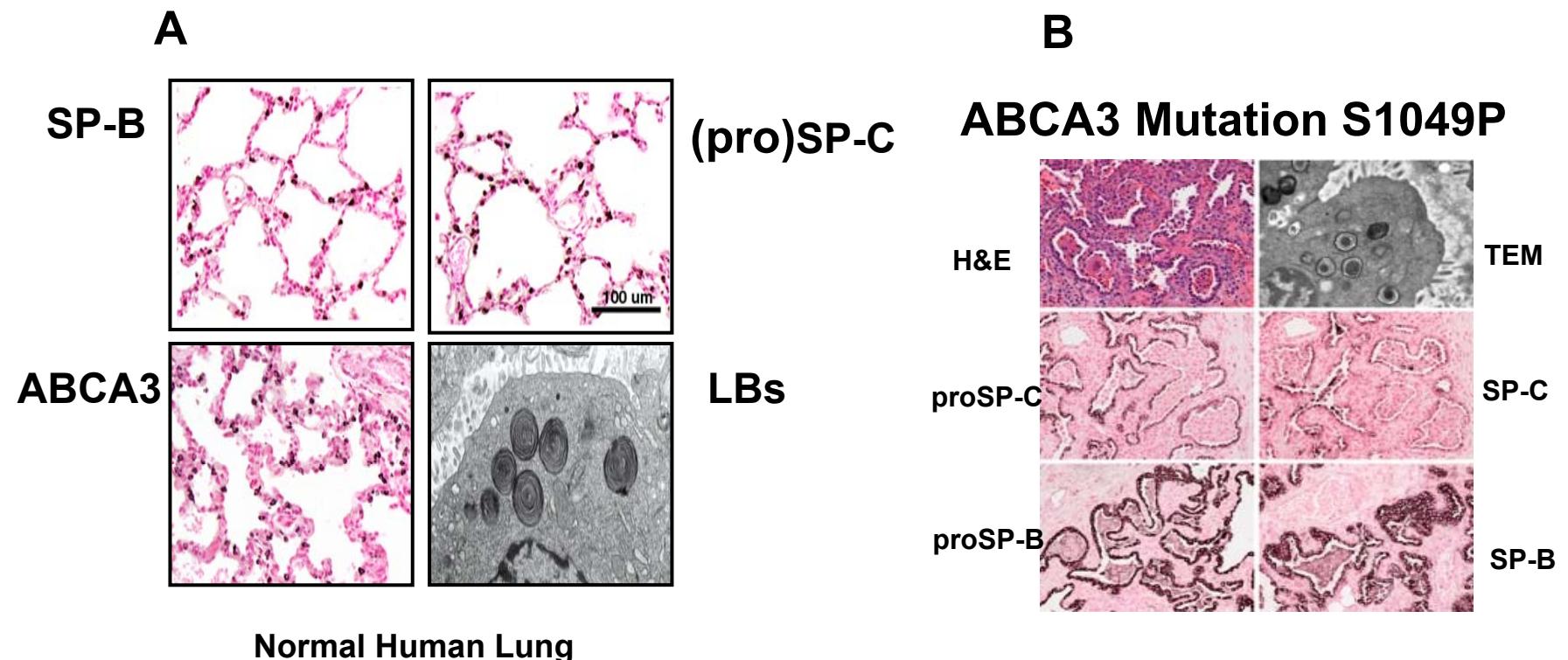
SFTPC: Surfactant function / host defense

SFTPA: Host defense, surfactant structure

NKX2-1: AT2 cell differentiation and function

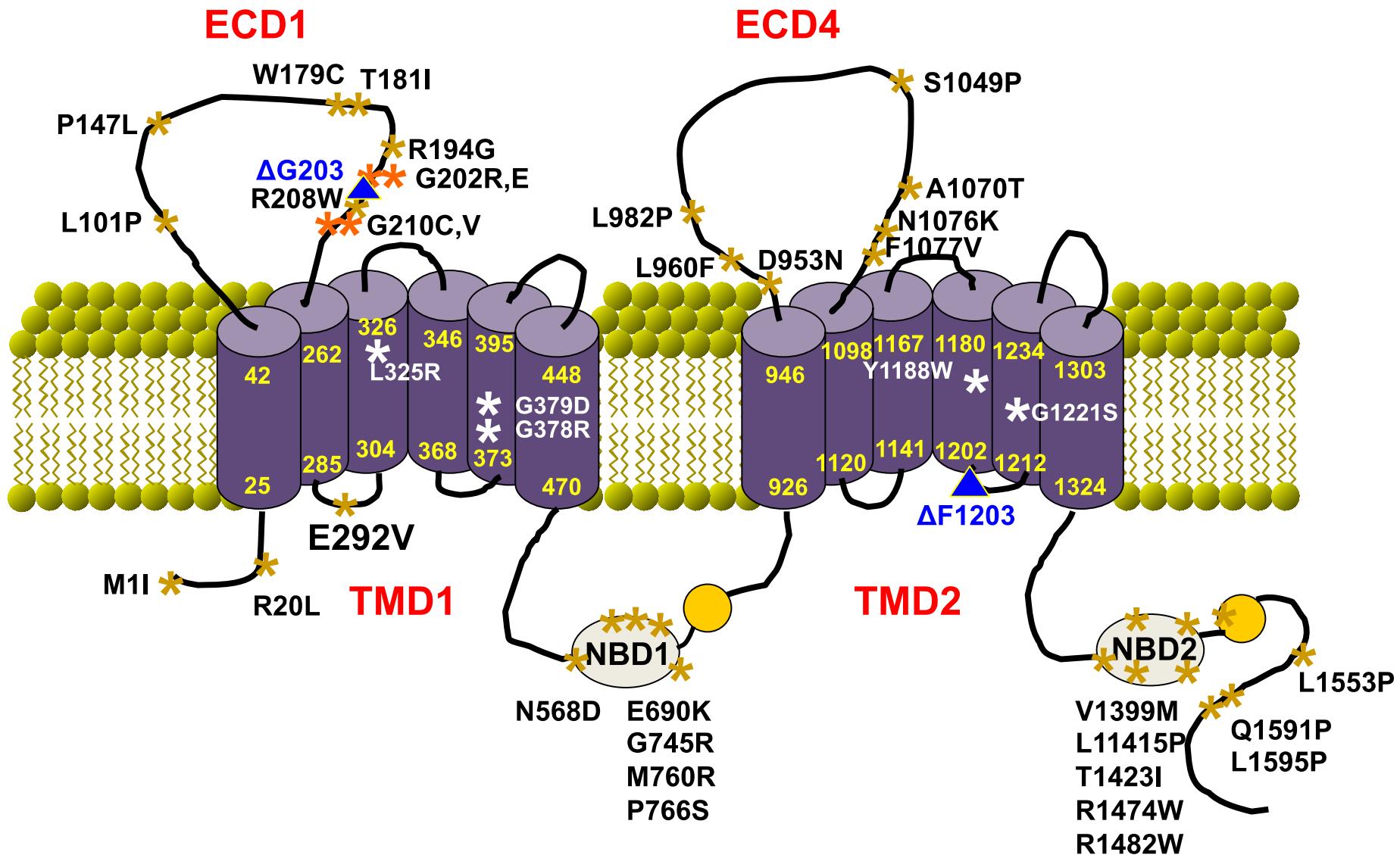
GMCSFa/b Receptors:Hereditary PAP/Macrophage

Histopathology of ABCA3 Deficiency



Partial Map of ABCA3 Mutations

Larry Nogee – Johns Hopkins

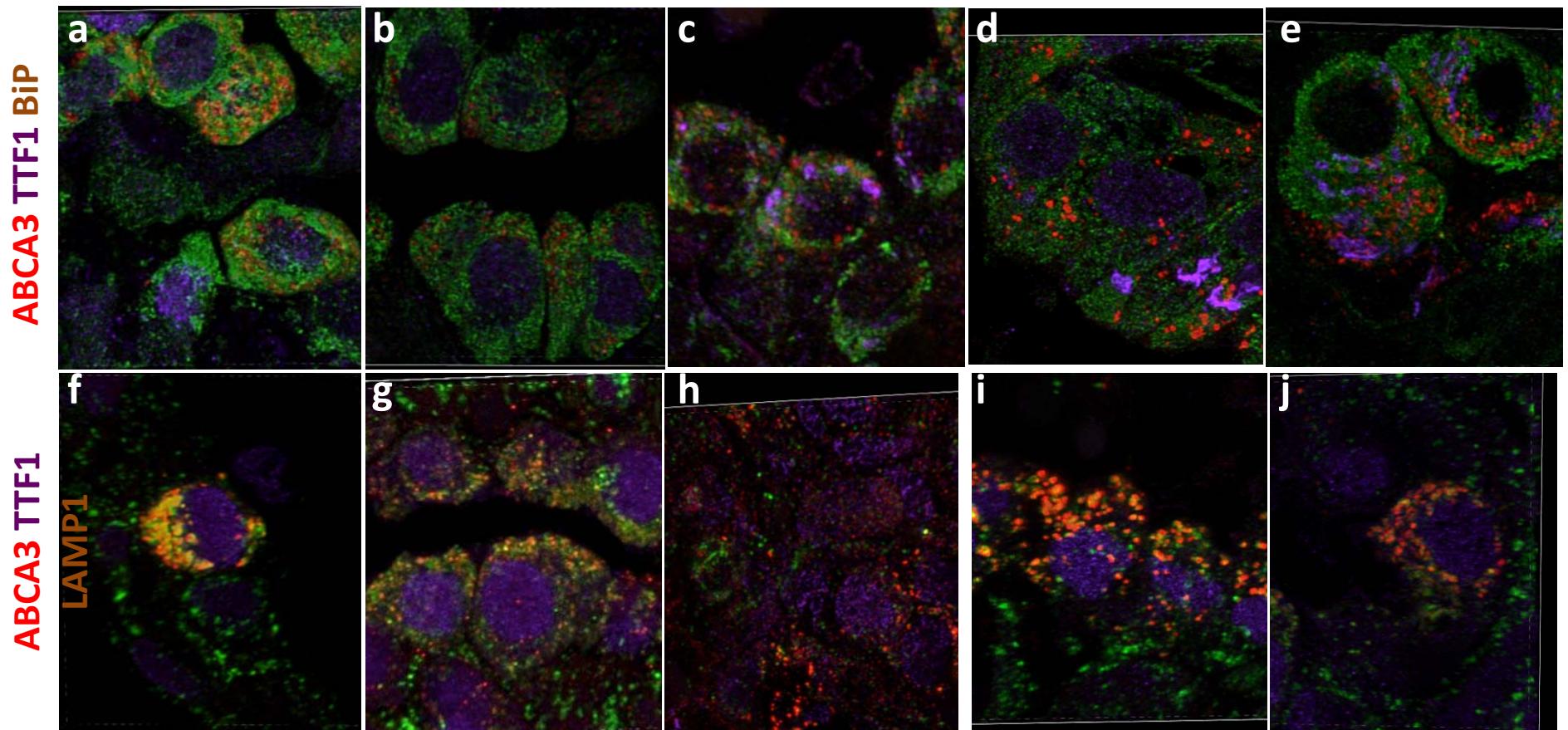


Current Classification of ABCA3 Mutations

Clinical Phenotype	Type I Mutations Impaired Processing / Trafficking	Type II Mutations Impaired ATP Hydrolysis / Lipid Transport
	Localized to ER	Localized to LB-like vesicles
NRF (11)	L101P (1,2,6) L982P (2) W1142X (2) L1553P (2) Gly1518Val*1 (2) Q215K (9,10)	R43L (6,8) R295C (severely impaired)(5) N568D (1,2,4) E690K (severely impaired) (4) T1114M (severely impaired) (4) G1221S (1, 2) L1580P (2)
chILD (11)	R280C (partial) (6) Q1591P (2)	E292V (moderately impaired) (4,9,10) D253H (7) T1173R (7)

NRF, Neonatal Respiratory Failure; chILD, Children's Interstitial Lung Disease

Subcellular Localization of ABCA3 Mutant Proteins



Expression of ABCA3 in human lungs. Confocal images were acquired by oversampling in x, y and z, deconvolved by landweber 3D. Control (**a** and **f**) and ABCA3 mutants S1049P/S1049 (**b** and **g**), Q1591P/Q1131R (**c** and **h**), W1142X/W1142X (**d** and **i**), and L982P/G1221S (**e** and **j**) stained with ABCA3 (red), TTF1 (purple) and the ER marker GRP78 (BiP) (green **top row panels a-e**) or lysosome marker LAMP1 (green **bottom row panels f-j**).

Progenitor Cell Translational Consortium -

Towards Correction of Monogenic Pulmonary Disorders

Collaborative Multi-PI Program

Jeff Whitsett – CCHMC

Ed Morrissey – University of Pennsylvania

Darrell Kotton – Boston University

F. Session Cole & Jennifer Wambach – Washington University

Larry Nogee – The Johns Hopkins University

Charles Ansong – Pacific Northwest National Laboratory



Towards Pathogenesis and Treatment of Monogenic Disorders of Surfactant Homeostasis

Model Human Surfactant Disorders: Mice, IPSC's, Organoids

Identify AT2 cell progenitors

Phenotype human/mouse AT2 s, IPSC's, Progenitors

Target and Deliver: RNA's, c DNA's, Gene editing tools to AT2 cell progenitors.

Pathogenesis of ABCA3 related disease:

Molecular pathways: Modeling ABCA3 mutations

Proteomics, Lipidomics, Transcriptomics

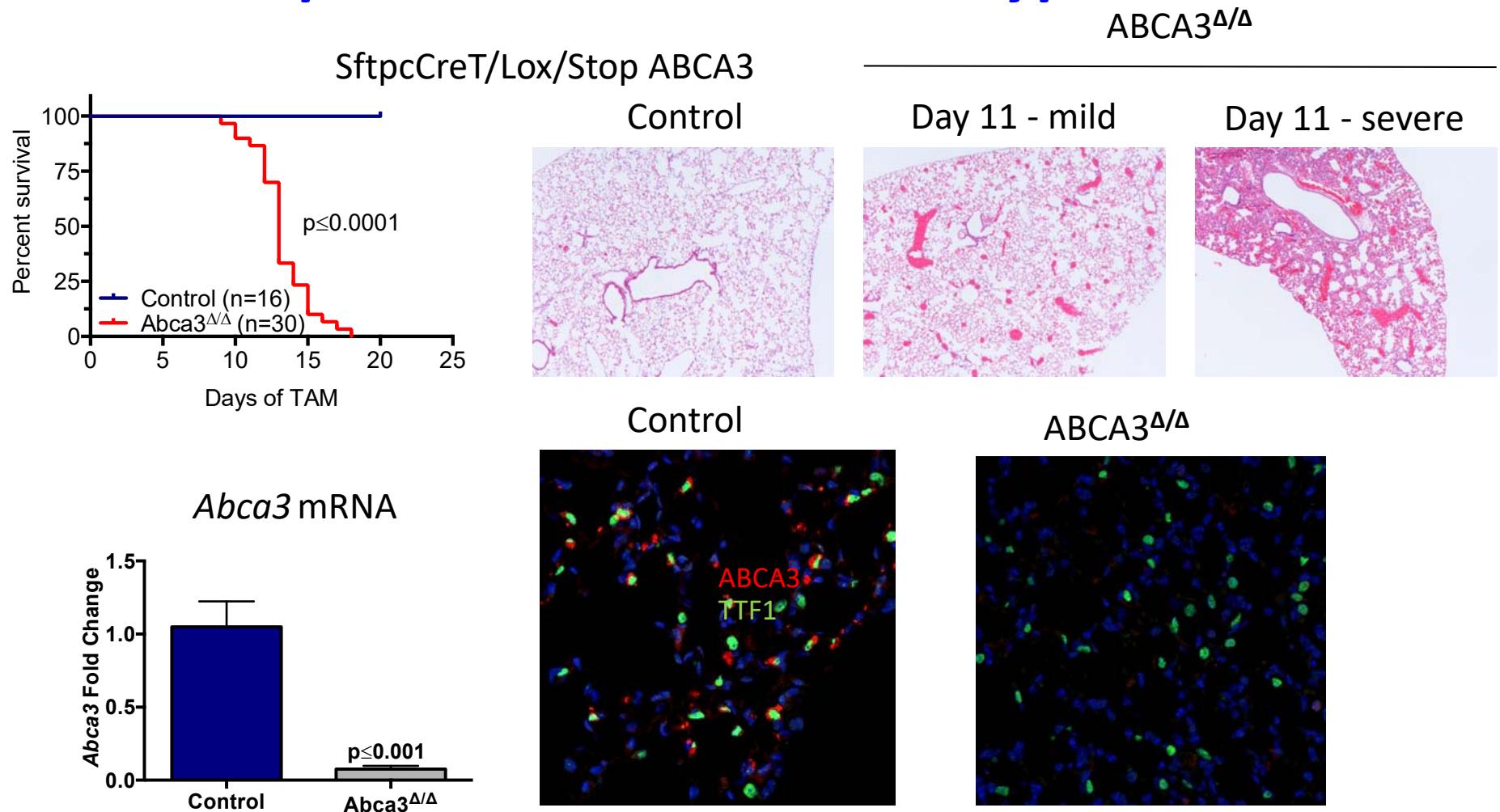
Mechanisms of tissue remodeling and lung dysfunction

Correction of ABCA3 disease: Replacement Editing

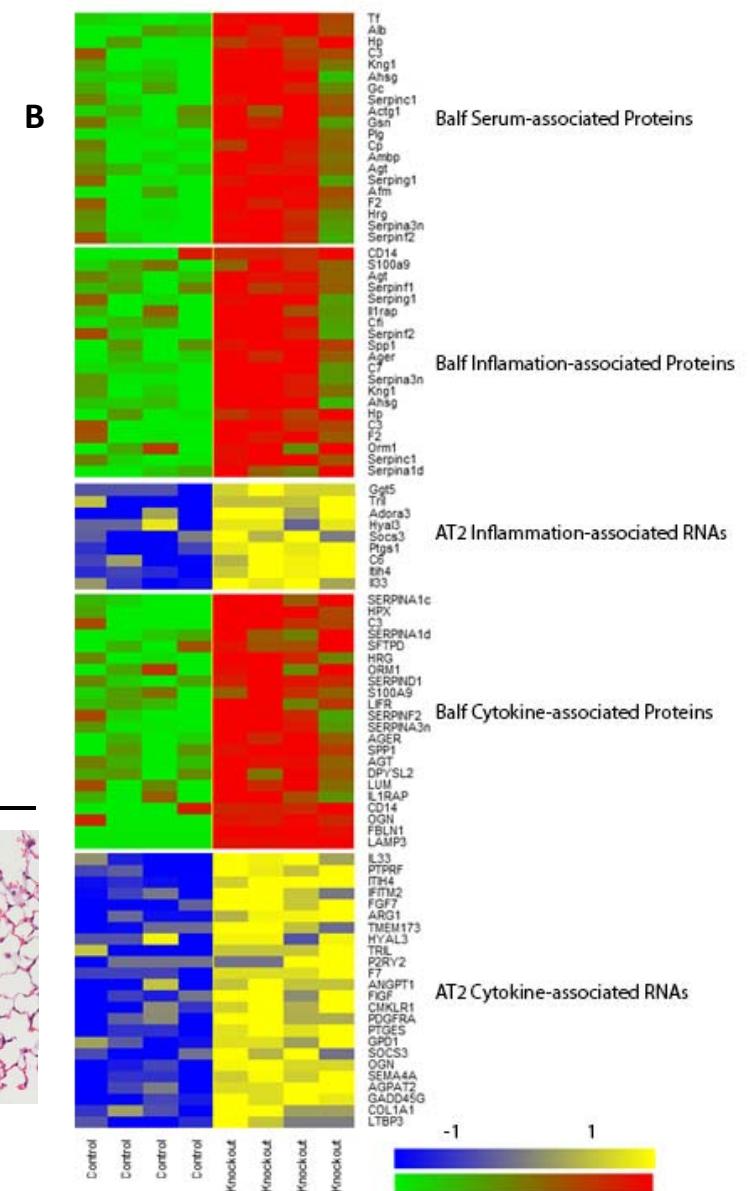
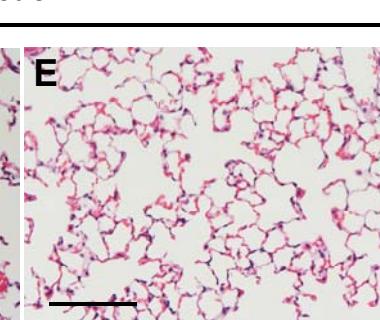
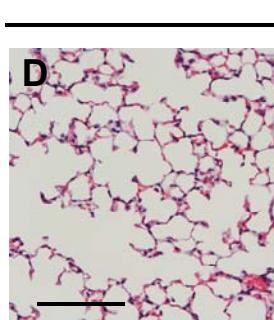
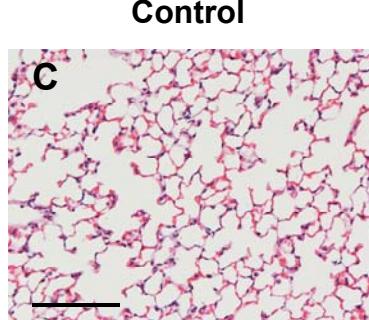
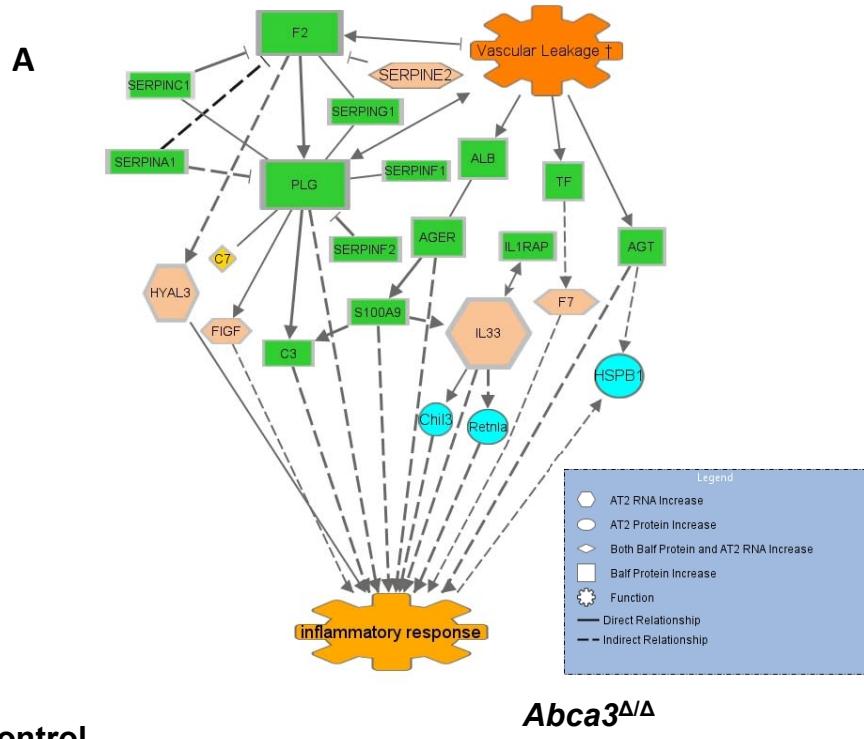


Disease Modeling in Transgenic Mice:

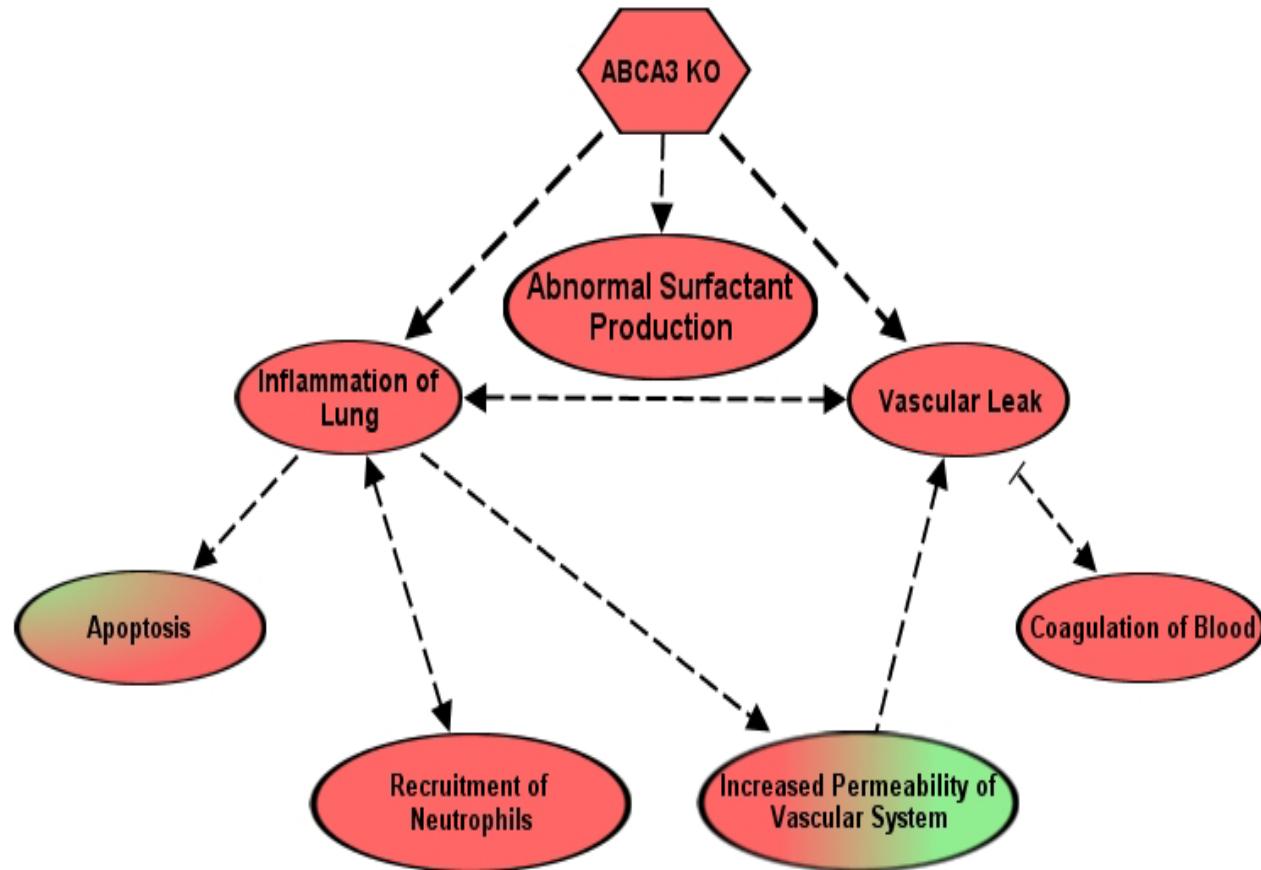
Conditional ABCA3 Deletion in Type II Cells Recapitulates Disease Phenotype in Mice



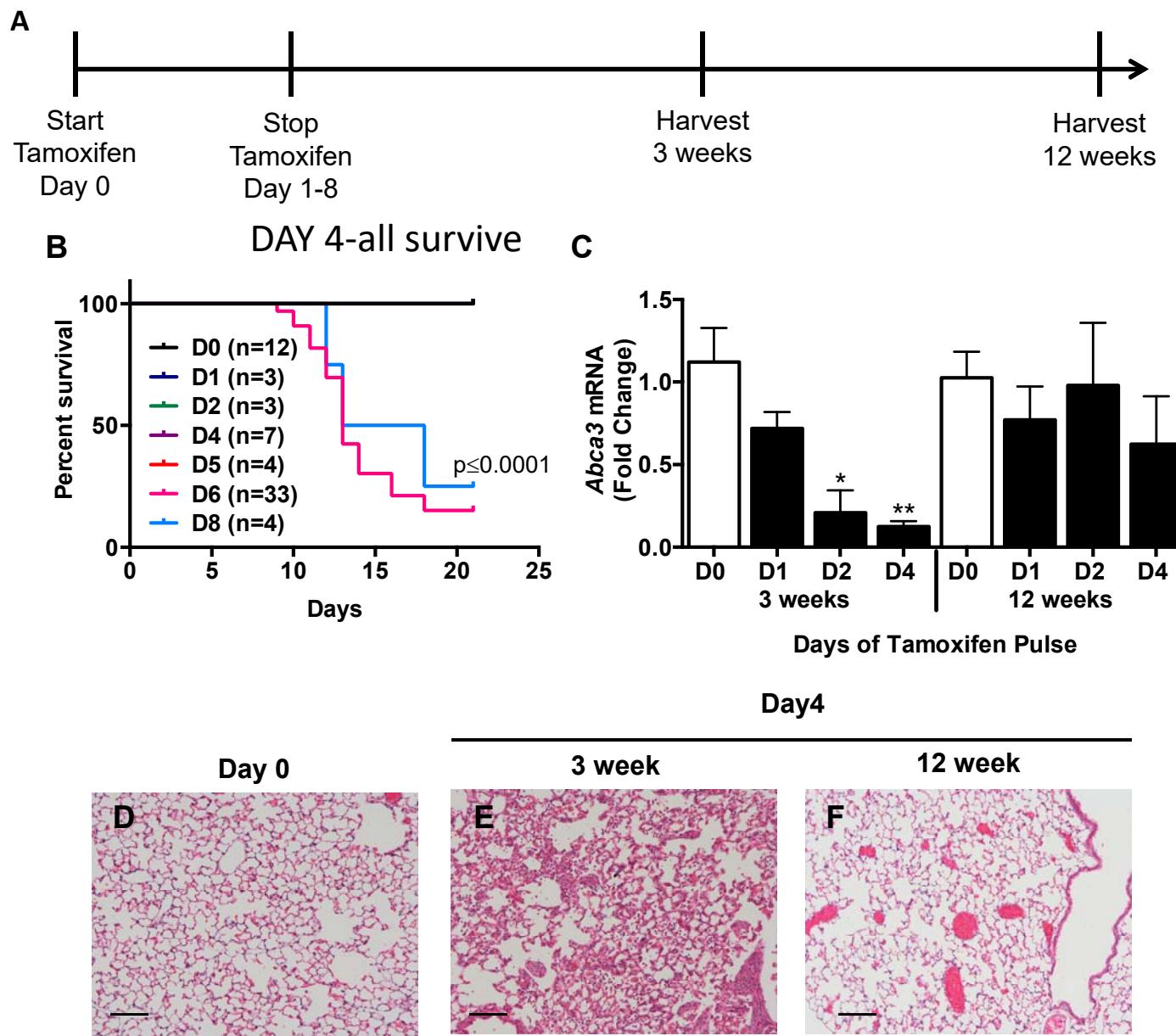
Deletion of ABCA3 initiates inflammation and capillary leak



Pathogenesis of Respiratory Failure in ABCA3 Deficiency

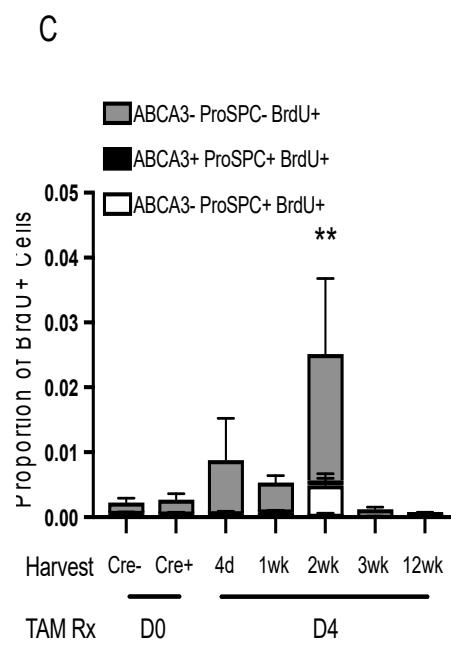
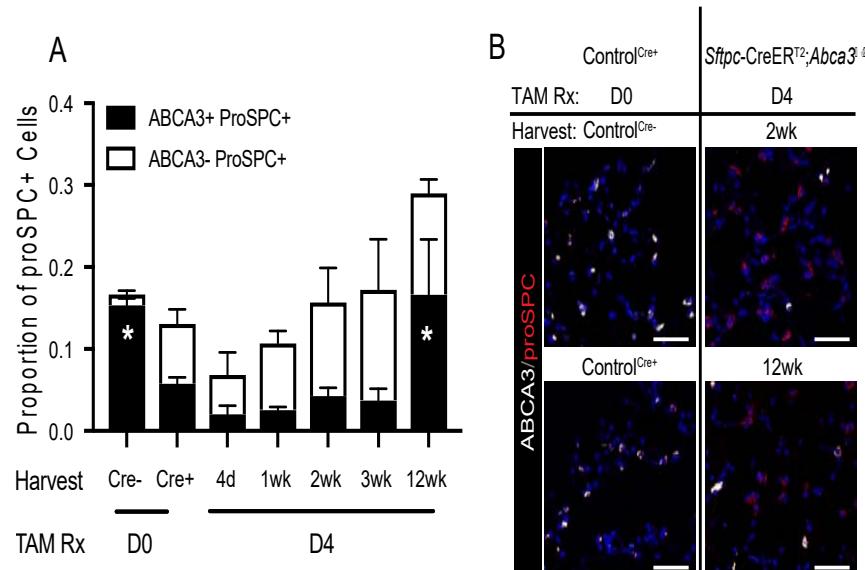


Remarkable Regeneration of the Peripheral Lung from ABCA3 Sufficient Cells

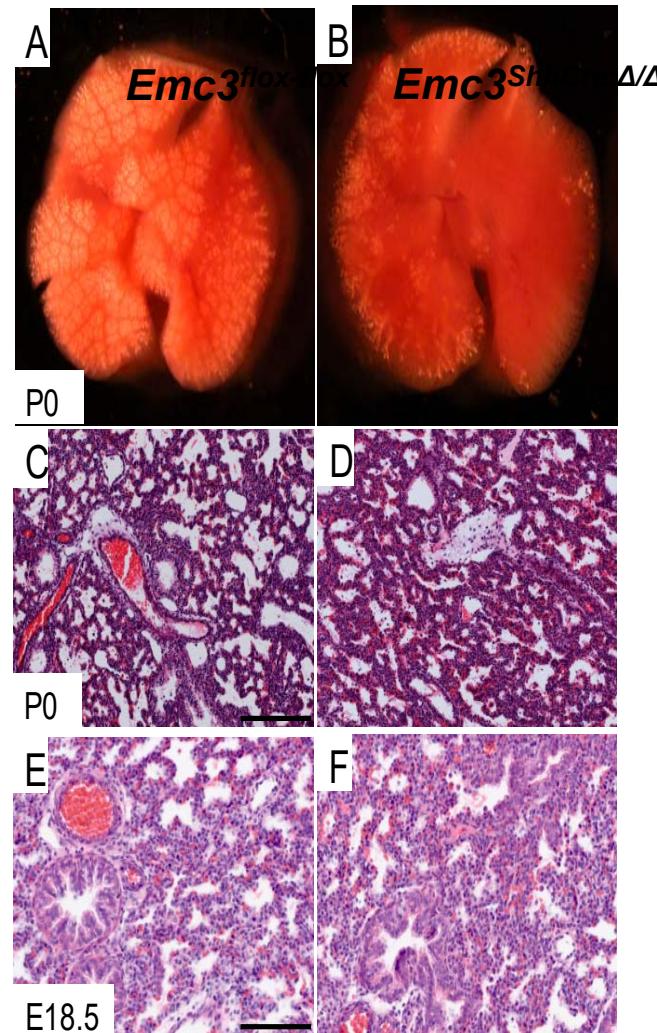


Complete

Alveolar Repair after Deletion of ABCA3

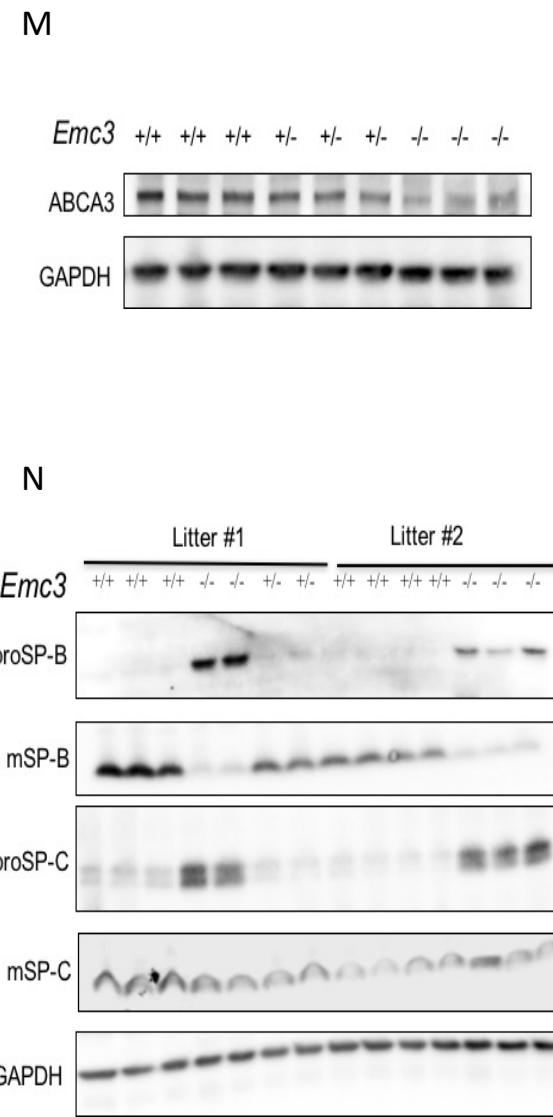
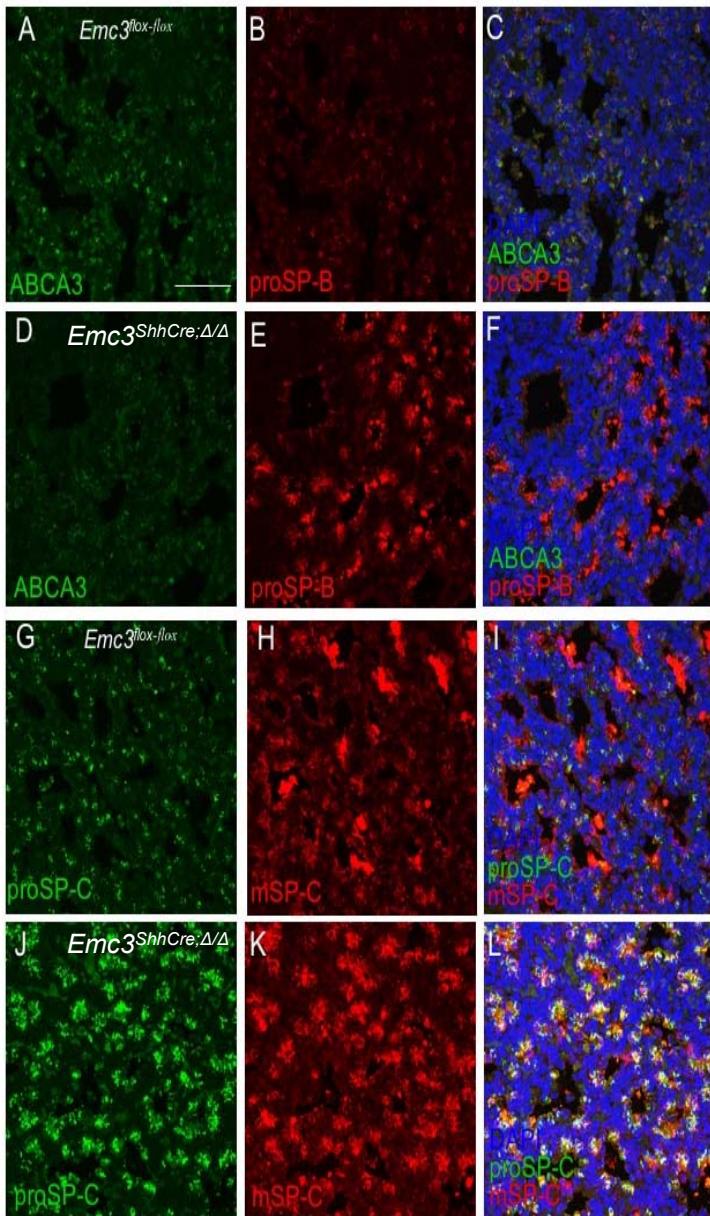


Cellular Mechanisms Controlling ABCA3/SP-B/SP-C Trafficking and Processing

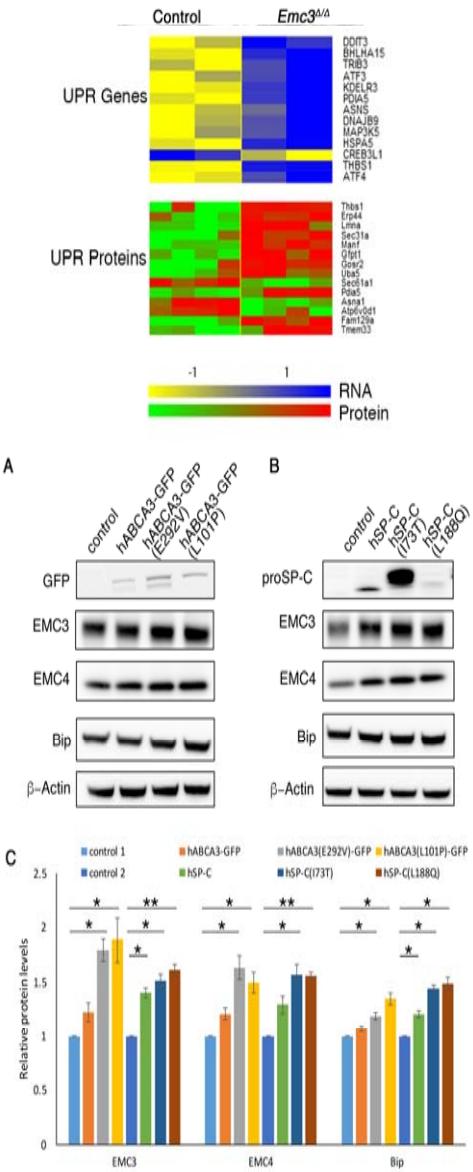
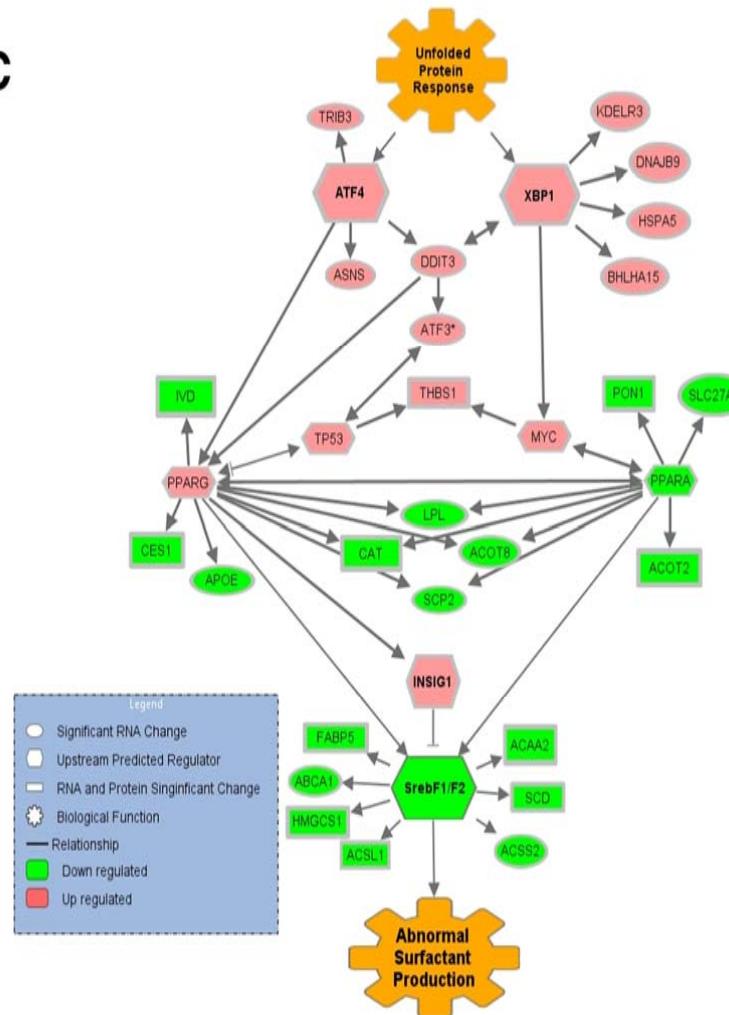
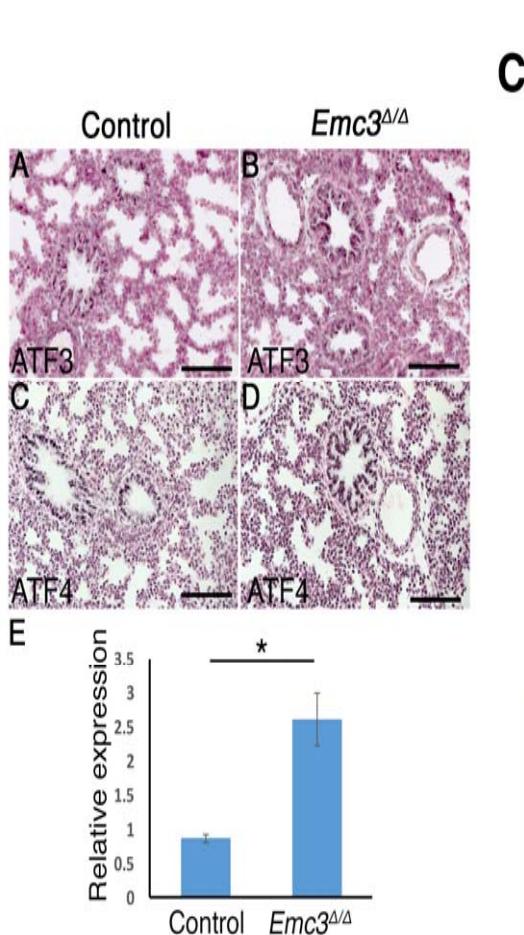


Respiratory Failure in EMC3 Deficient Mice

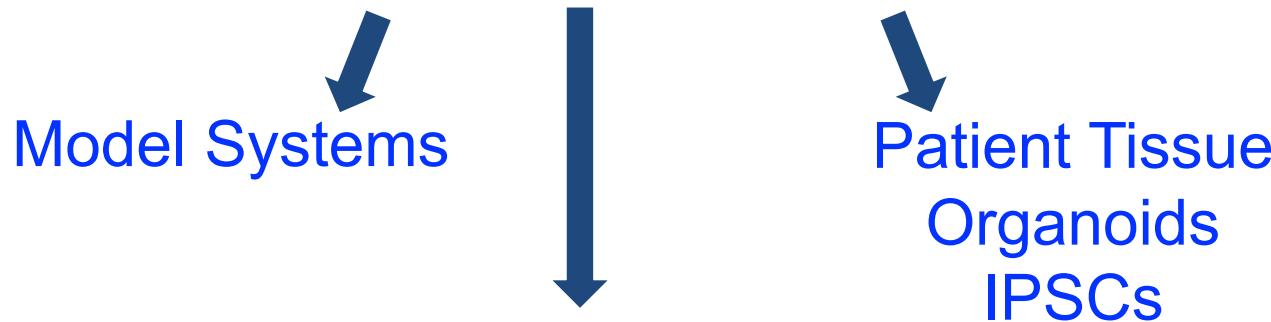
Decreased ABCA3 and Abnormal Surfactant Protein Processing in Emc3^{ShhCre;Δ/Δ}Mice



Role of EMC3 in UPR Modeled by Integration of RNA Sequencing and Proteomics



Genetic Basis of Disease



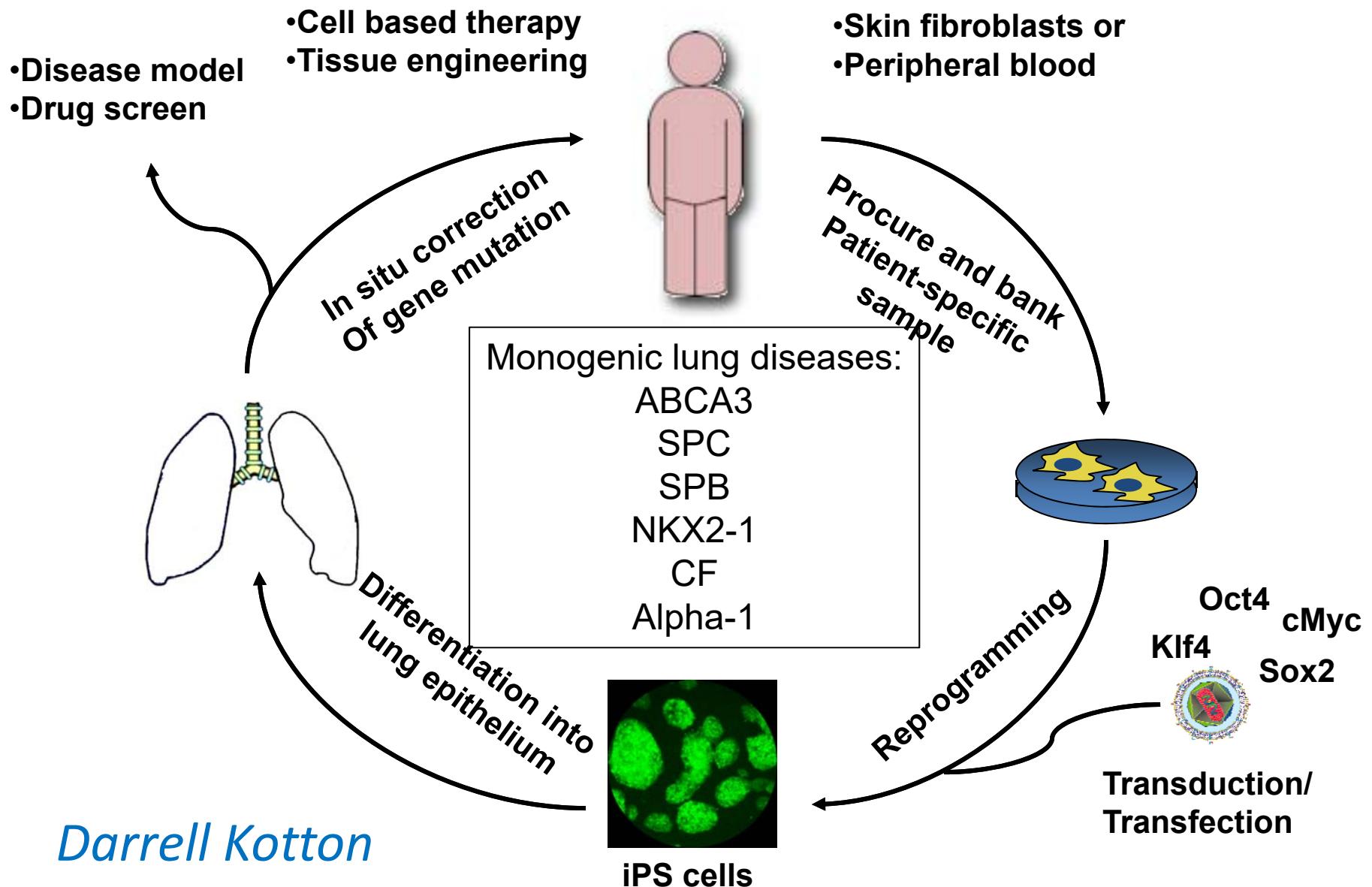
Advancing Technologies

“Systems Biology”

Mechanisms of Disease Pathogenesis

DX and RX

iPSCs to Model Disorders of Surfactant Homeostasis



SFTPC^{tdTomato}
NKX2.1^{GFP}

Darrel Kotton, Jeff Whitsett, Anusha Sridharan

Vectors for Gene Transfer to the Respiratory Epithelium

AAV9/2 and AAV6/2: Single RNA's, Cas9, SP-C/SP-B

BOCA virus: ABCA3 ~ 5Kb

Lenti: ABCA3 and mutants

SNIMs: Stabilized, Modified RNA's: Cas9 sg RNA's

Can We Correct Monogenic Disorders of Surfactant Homeostasis?



Lung MAP and “Single Cell-NexGen Sequencing to Identify Mechanisms Mediating Lung Formation Prior to Birth”

Pulmonary Biology

Yan Xu ,Yina Du

Anusha Sridharan

Joseph Kitzmiller

Minzhe Guo /XiaoFang Tang/Xinhua Lin

Anna-K Perl



Developmental Biology

Steven Potter

Eric Brunskill

Matthew Kofron

DNA Core CCHMC

Imaging Core CCHMC

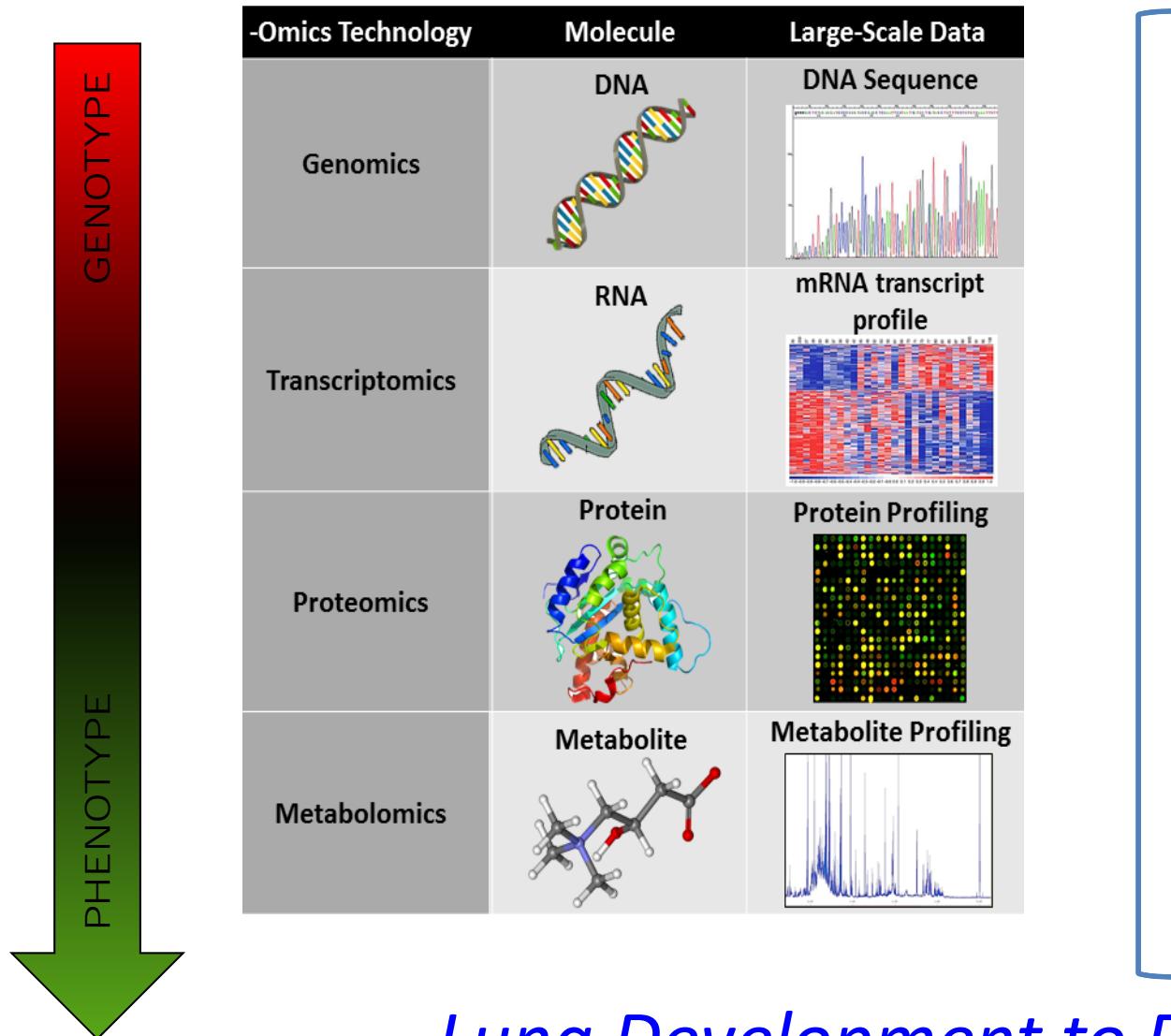
Division of Bioinformatics

Bruce Aronow

Phillip Dexheimer

LungMap“omics”: Mouse and Human Lung

Data Integration Access and Display



Lung Development to Disease

Thanks! LungMAP

Coordinating Center

Duke

Scott Palmer
Cliburn Chan
Laura Johnson
Jerry Kirchner
Carol Bova Hill



National Heart, Lung,
and Blood Institute

Research Centers

CCHMC

Jeff Whitsett
Steve Potter
Bruce Aronow
Yan Xu

PNNL

Richard Corley
Charles Ansong

UAB

Namasivayam
Ambalavanan
N Kaminski
J Hagood

USC

David Warburton
Wei Shi
Scott Fraser
Rex Moats

URMC – Tissue Procurement

Gloria Pryhuber
Ravi Misra

Progenitor Cell Translational Consortium:NHLBI