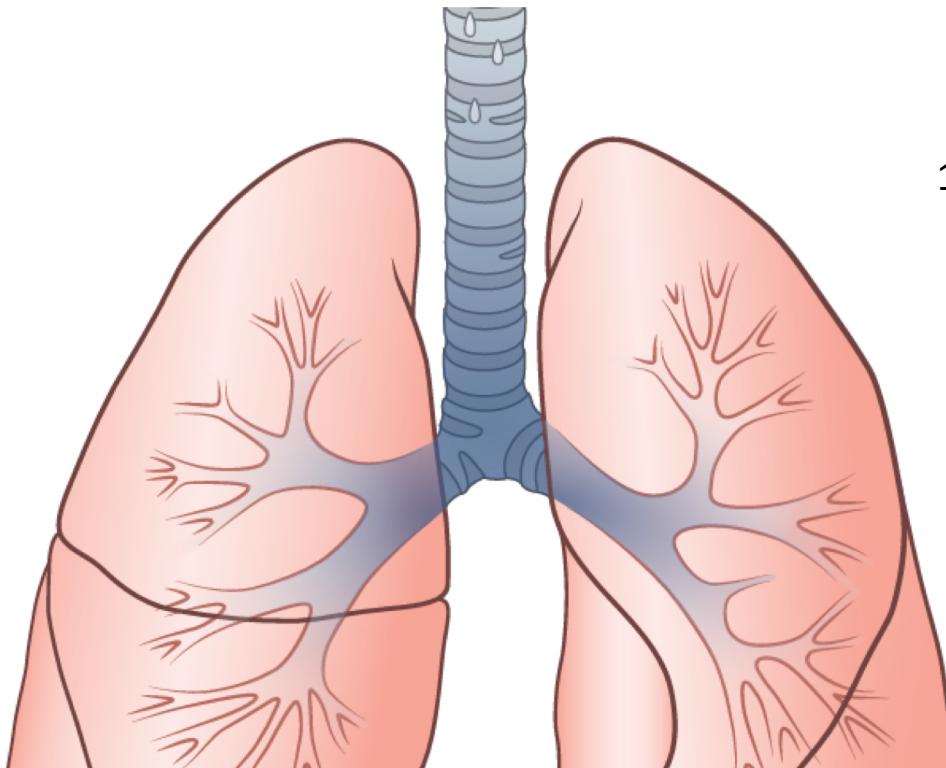


# Lung Cancer



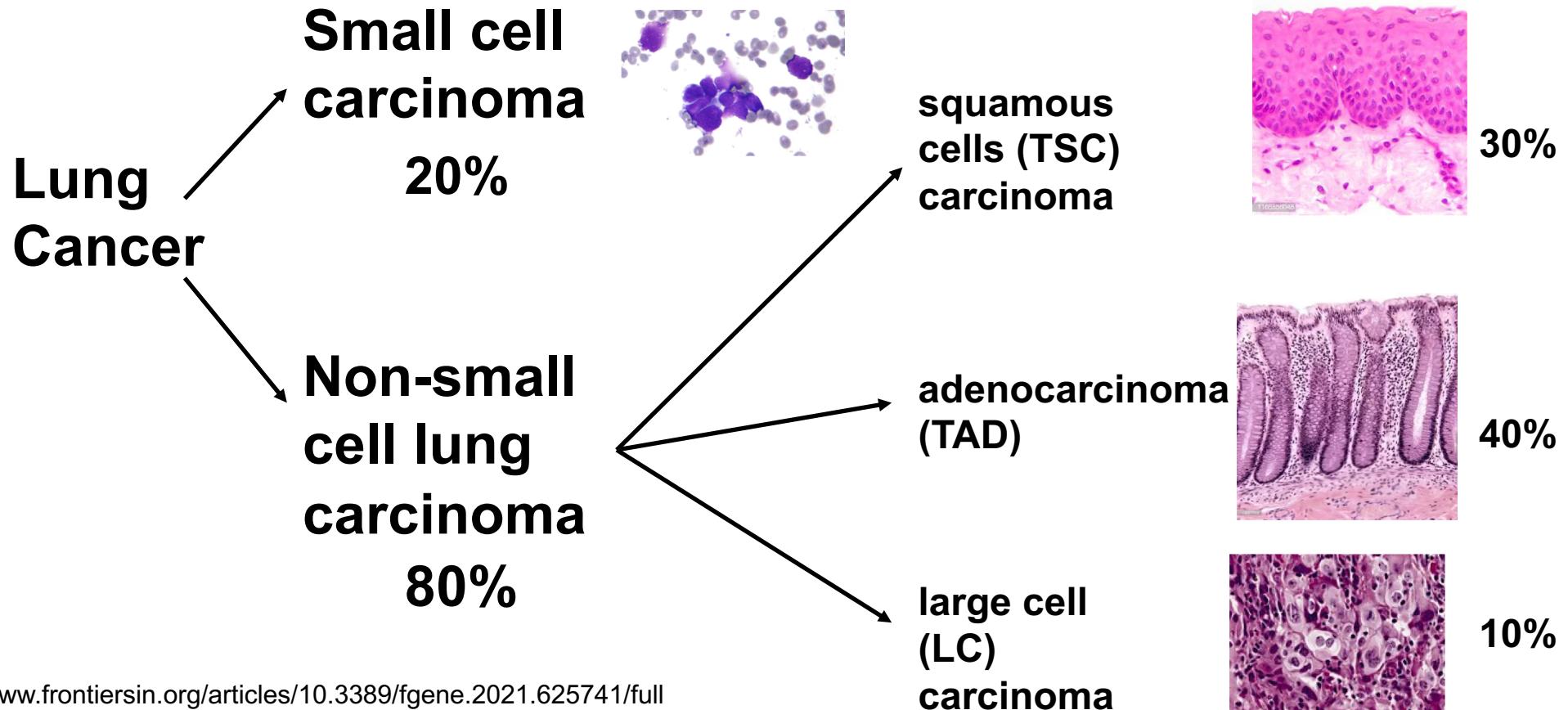
1.59 million deaths  
(2012)

1.76 million  
deaths (2018)

## Why?

- Few therapeutic options
  - Resistance
  - Heterogeneity

# Types of lung cancer



Received 24 May 2019, Revised 30 August 2019, Accepted 6 December 2019, Available online 13 January 2020.

# An Integrated Gene Expression Landscape Profiling Approach to Identify Lung Tumor Endothelial Cell Heterogeneity and Angiogenic Candidates

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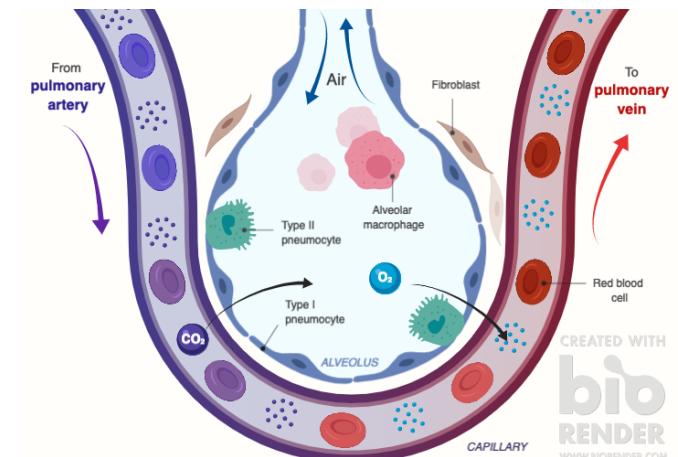
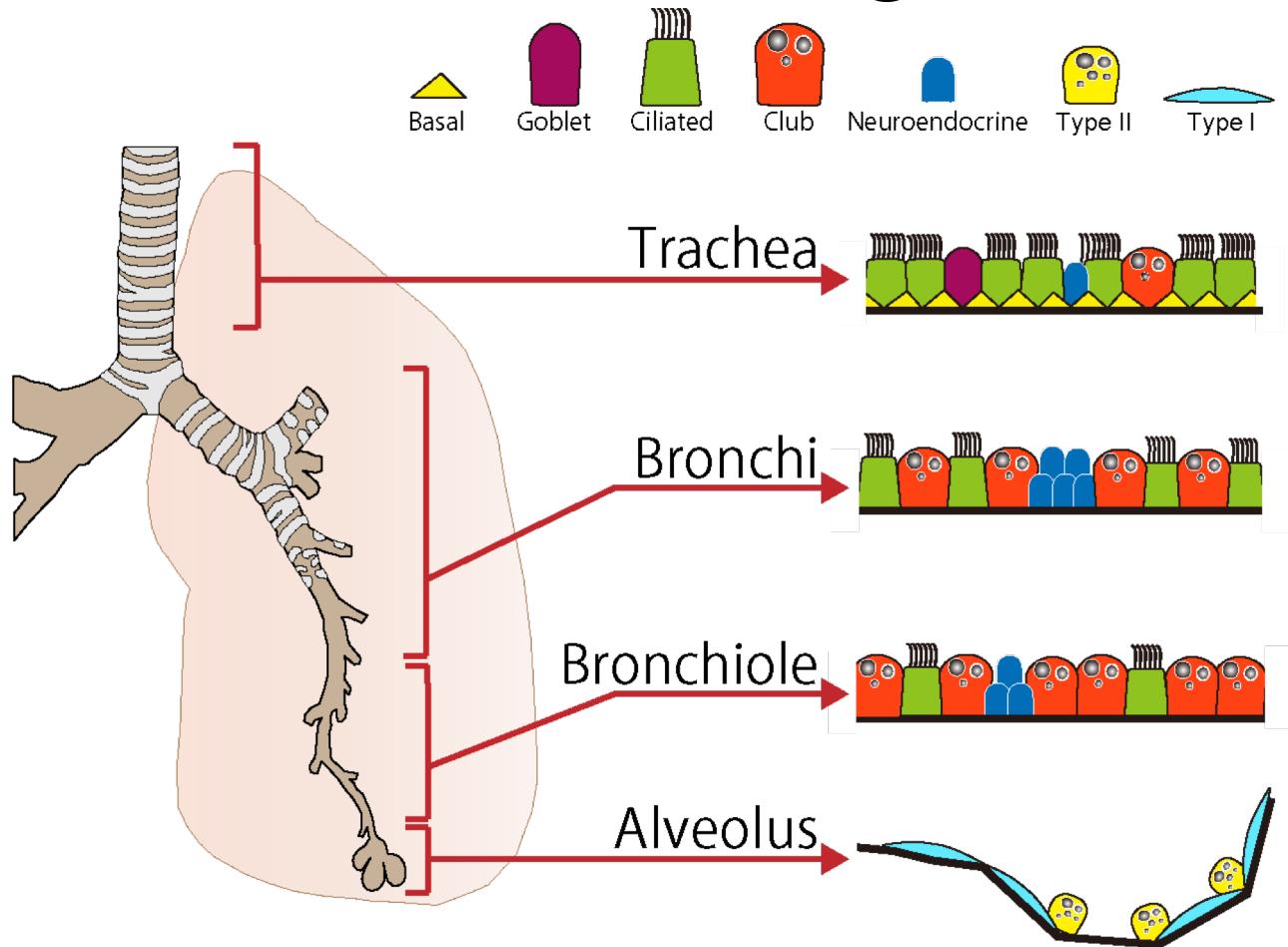
<sup>6</sup>Translational Cell & Tissue Research, Department of Imaging & Pathology, KU Leuven, Leuven 3000, Belgium

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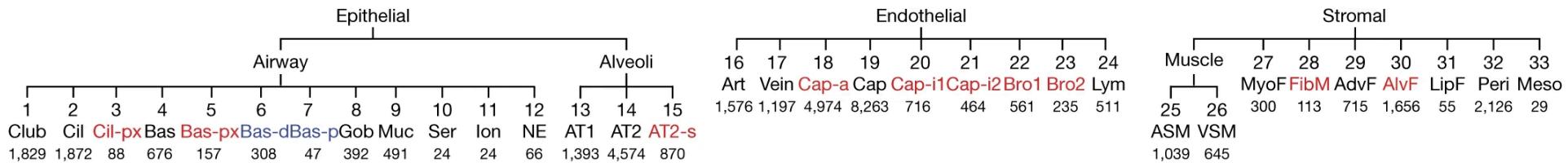
# Lung structure



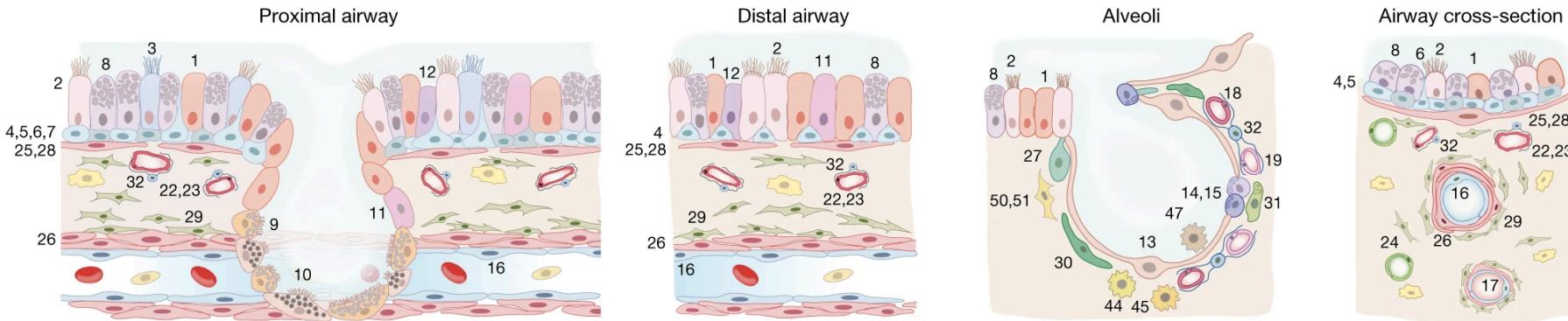
# Lung structure

A molecular cell atlas of the human lung from single-cell RNA sequencing

a



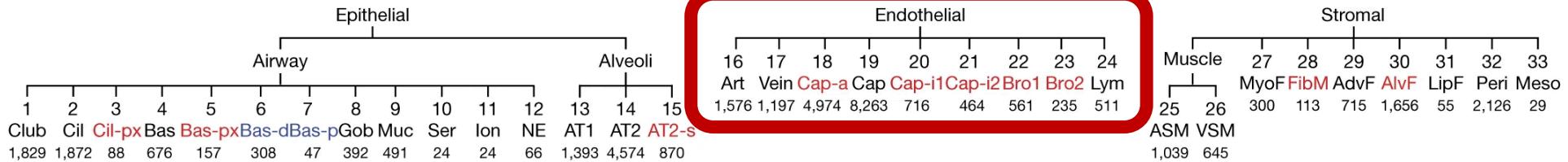
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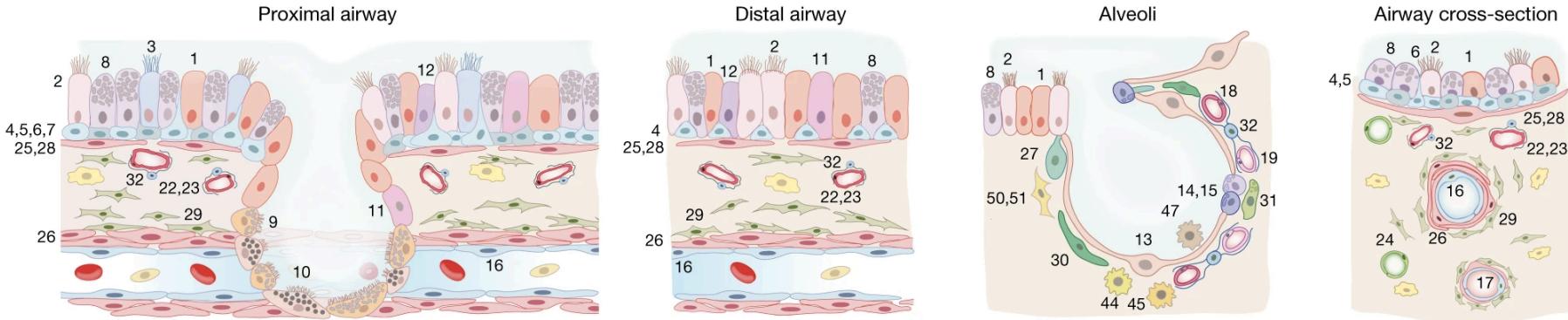
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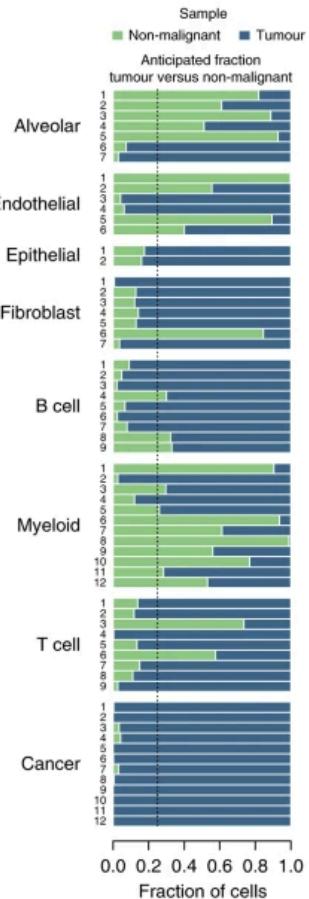


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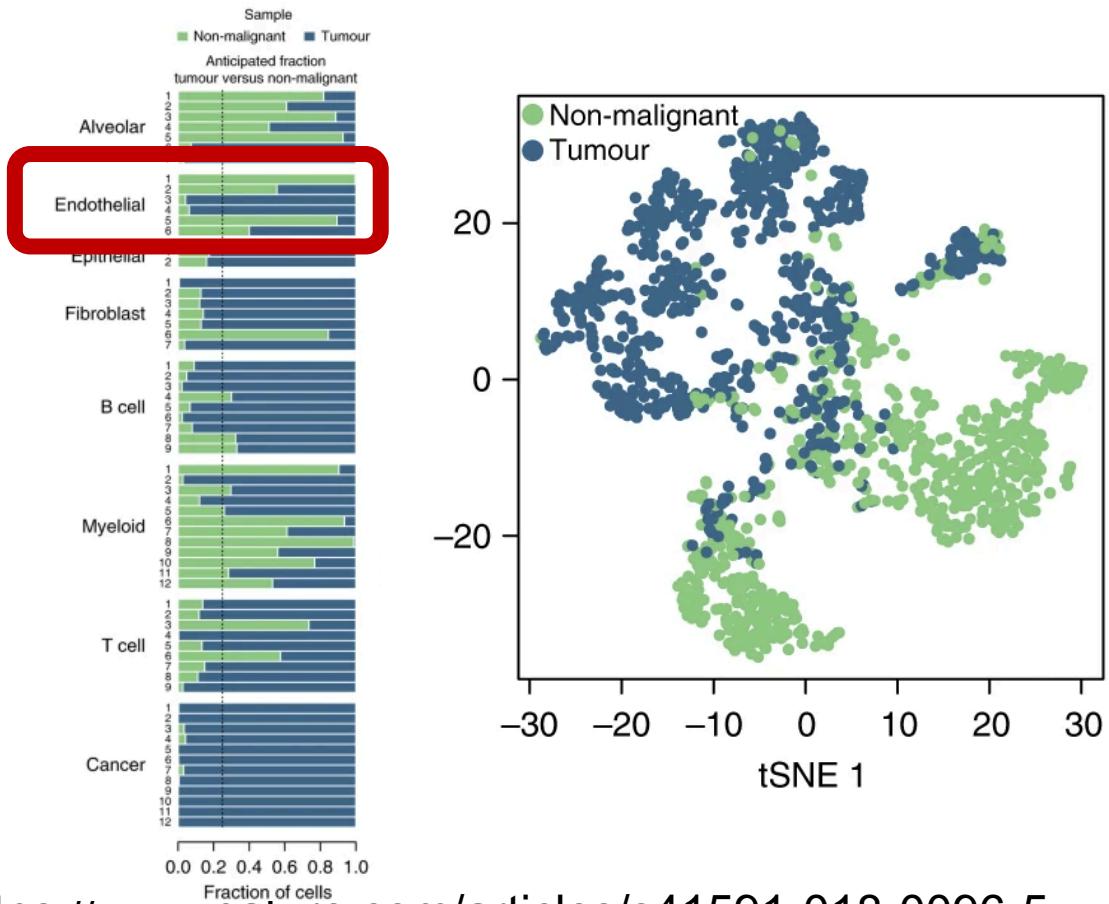


# Why endothelial cells?

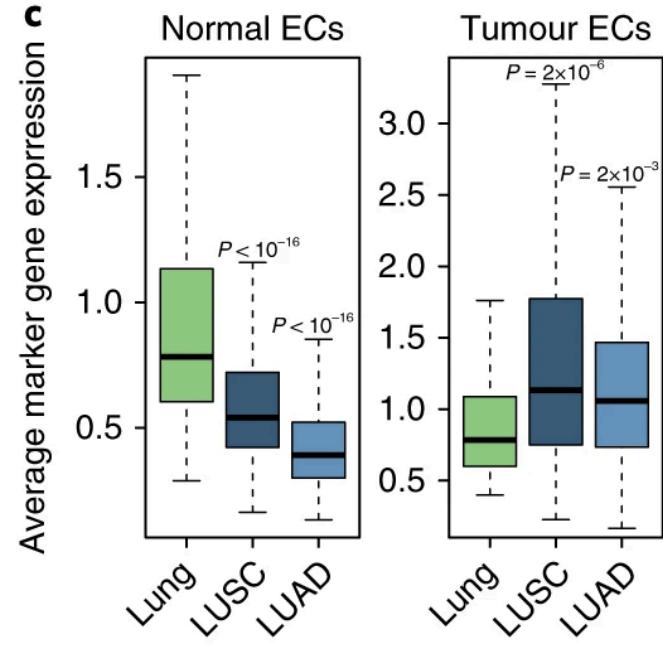
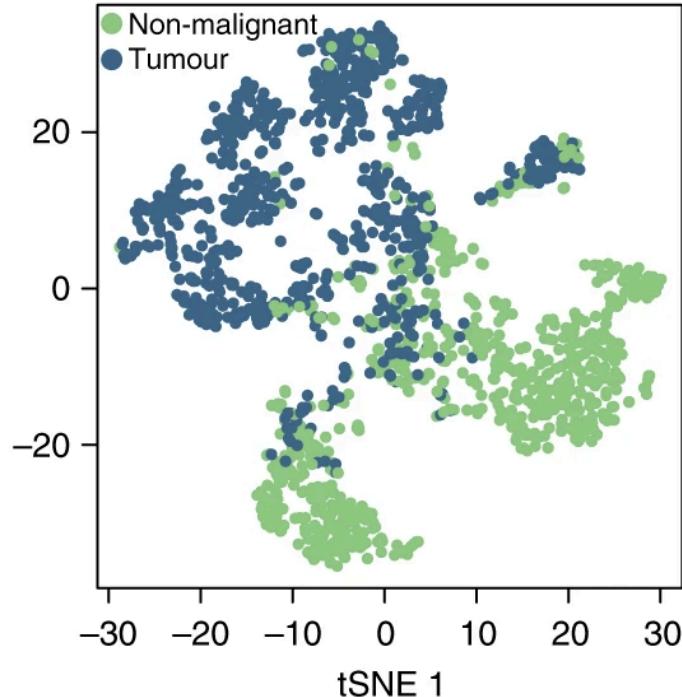
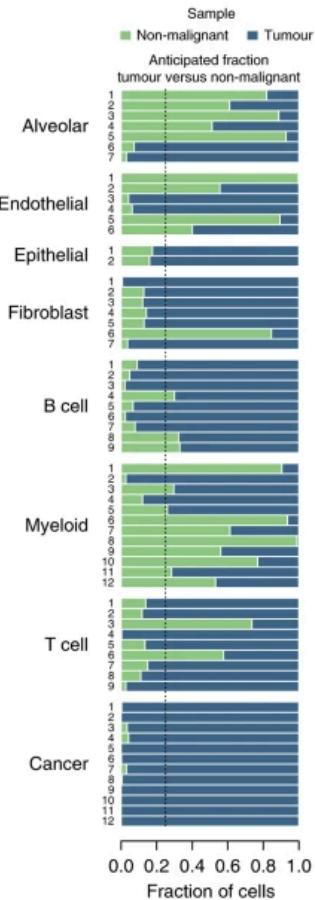
# Endothelial cells in lung tumors



# Endothelial cells in lung tumors



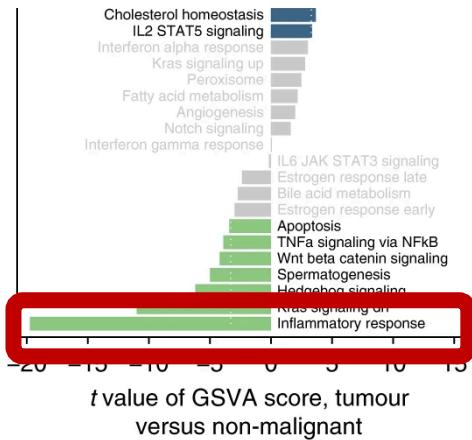
# Endothelial cells in lung tumors



Lung squamous carcinoma (LUSC)

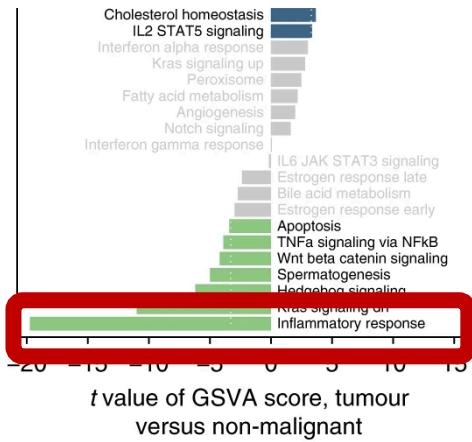
Lung adenocarcinoma (LUAD)

# Endothelial cells in lung tumors



The most significantly downregulated pathway was involved in inflammatory responses

# Endothelial cells in lung tumors

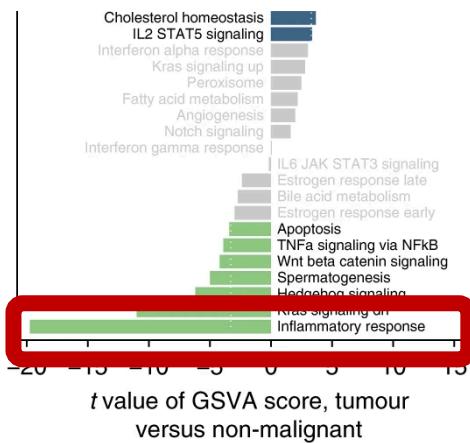


## Why / How ??

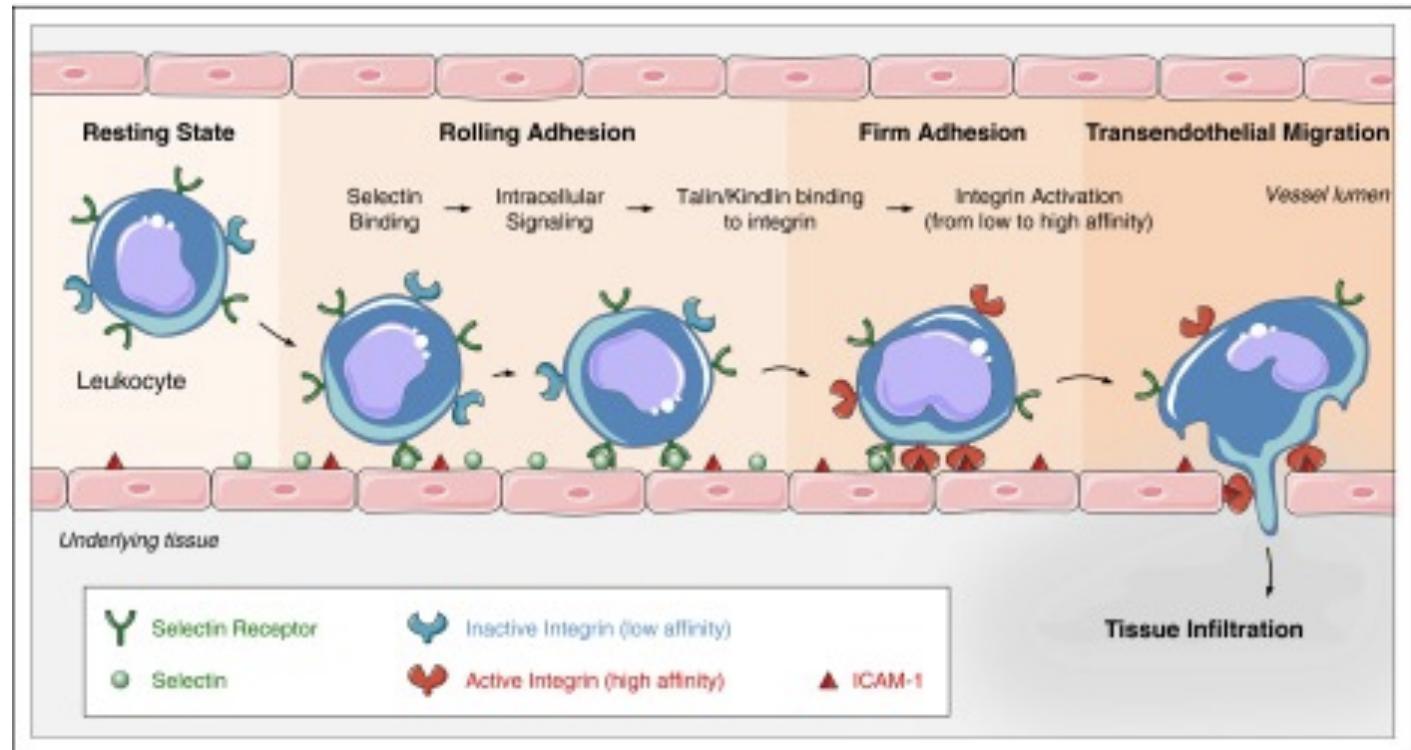
The most significantly downregulated pathway was involved in inflammatory responses

# Endothelial cells in lung tumors

## Immune cell homing



The most significantly downregulated pathway was involved in inflammatory responses



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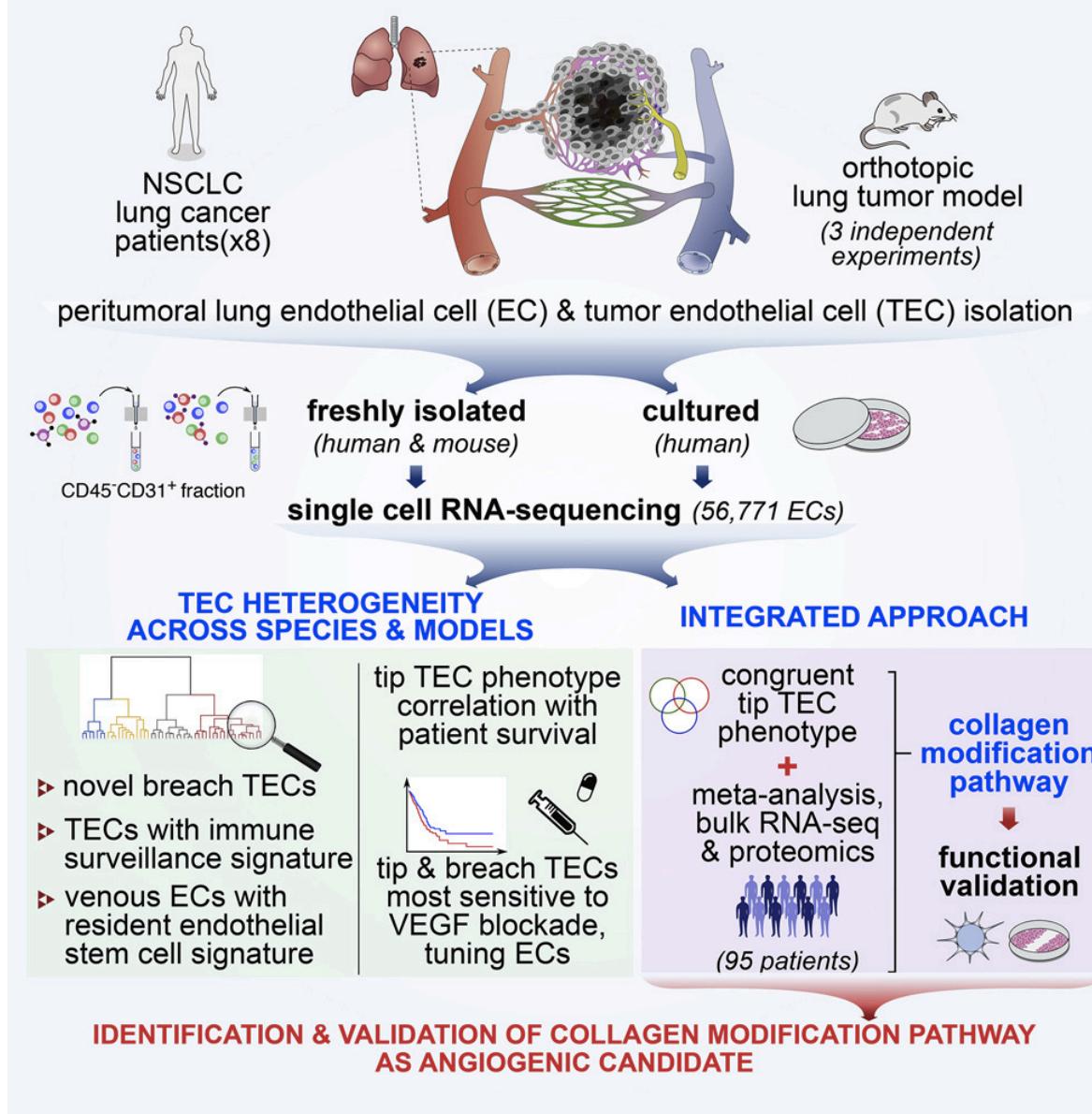
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non-small cell lung cancer (NSCLC)

- Paired samples

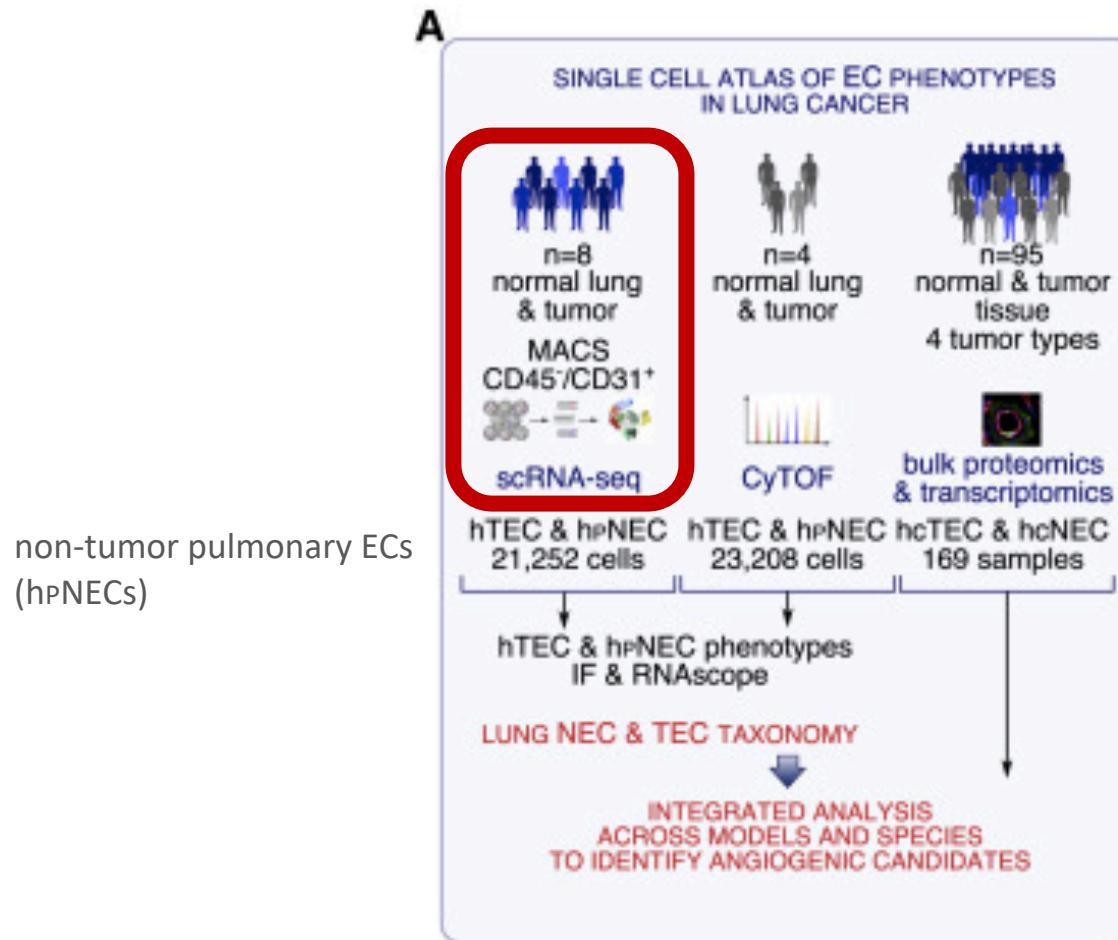


# Baseline characteristics of patients included in the study

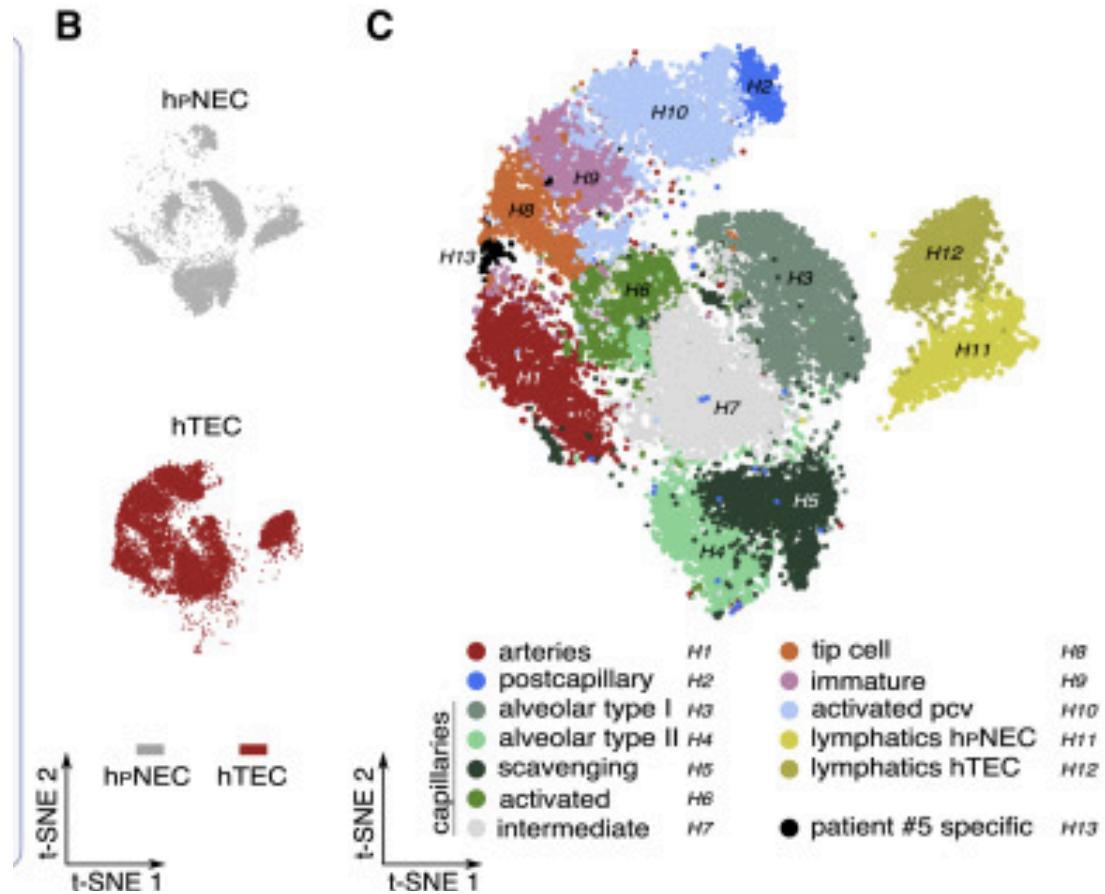
- Paired samples

human taxonomy construction (scRNA-seq)		Carcinoma type	Affected lobe	TNM	Tumor stage	Smoking status	Pack years*	COPD status	Gender	Age
	#1	squamous	left upper	pT2aN0M0	S-IB	active smoker	unknown	COPD stage I	m	60
	#2	squamous	left lower	pT2aN0	S-IB	former smoker	30	no COPD	m	75
	#3	squamous	left upper	pT3N0	S-IIB	former smoker	26	no COPD	m	69
	#4	squamous	right lower	pT3N0	S-IIB	active smoker	55	no COPD	m	74
	#5	large cell	right upper	pT4N0	S-IIIA	active smoker	40	no COPD	m	58
	#6	adeno	right upper	pT3N0	S-IIB	former smoker	18	COPD stage II	f	73
	#7	adeno	right upper	pT1cN0	S-IA3	never smoker	n/a	no COPD	f	71
	#8	adeno	right upper	pT3N0	S-IIB	former smoker	4	no COPD	f	58

# Data... a lot of data

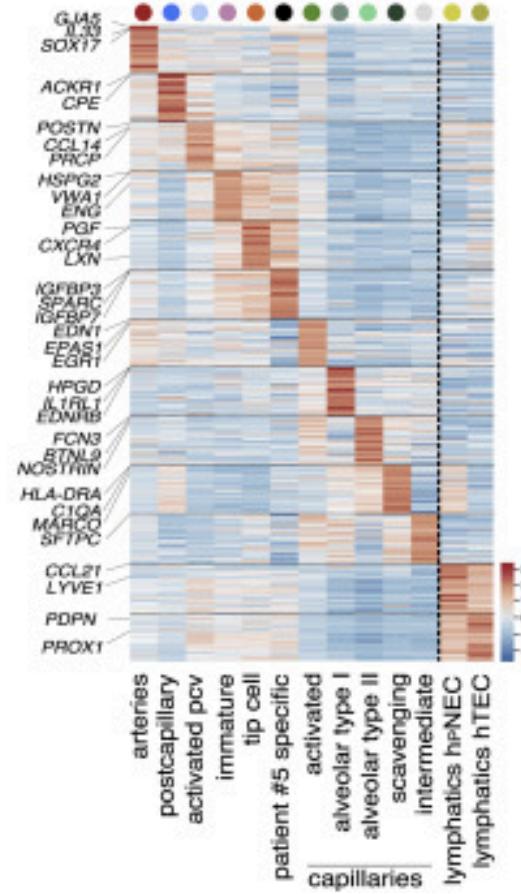


# scRNA-seq



# Top-ranking marker genes in different EC phenotypes

E



# Highlights

- They single-cell RNA-sequenced 56,771 endothelial cells (ECs) from human, mouse, and cultured lung tumor models.
- Tip ECs were resolved into migratory and basement-membrane remodeling phenotypes
- Capillary and venous ECs expressed immunoregulatory gene signatures
- Integrated analysis identified collagen modification as an angiogenic pathway

Goveia, J., Rohlenova, K., Taverna, F., Treps, L., Conradi, L. C., Pircher, A., ... & Carmeliet, P. (2020). An integrated gene expression landscape profiling approach to identify lung tumor endothelial cell heterogeneity and angiogenic candidates. *Cancer cell*, 37(1), 21-36.