



# 21<sup>st</sup> century disease models

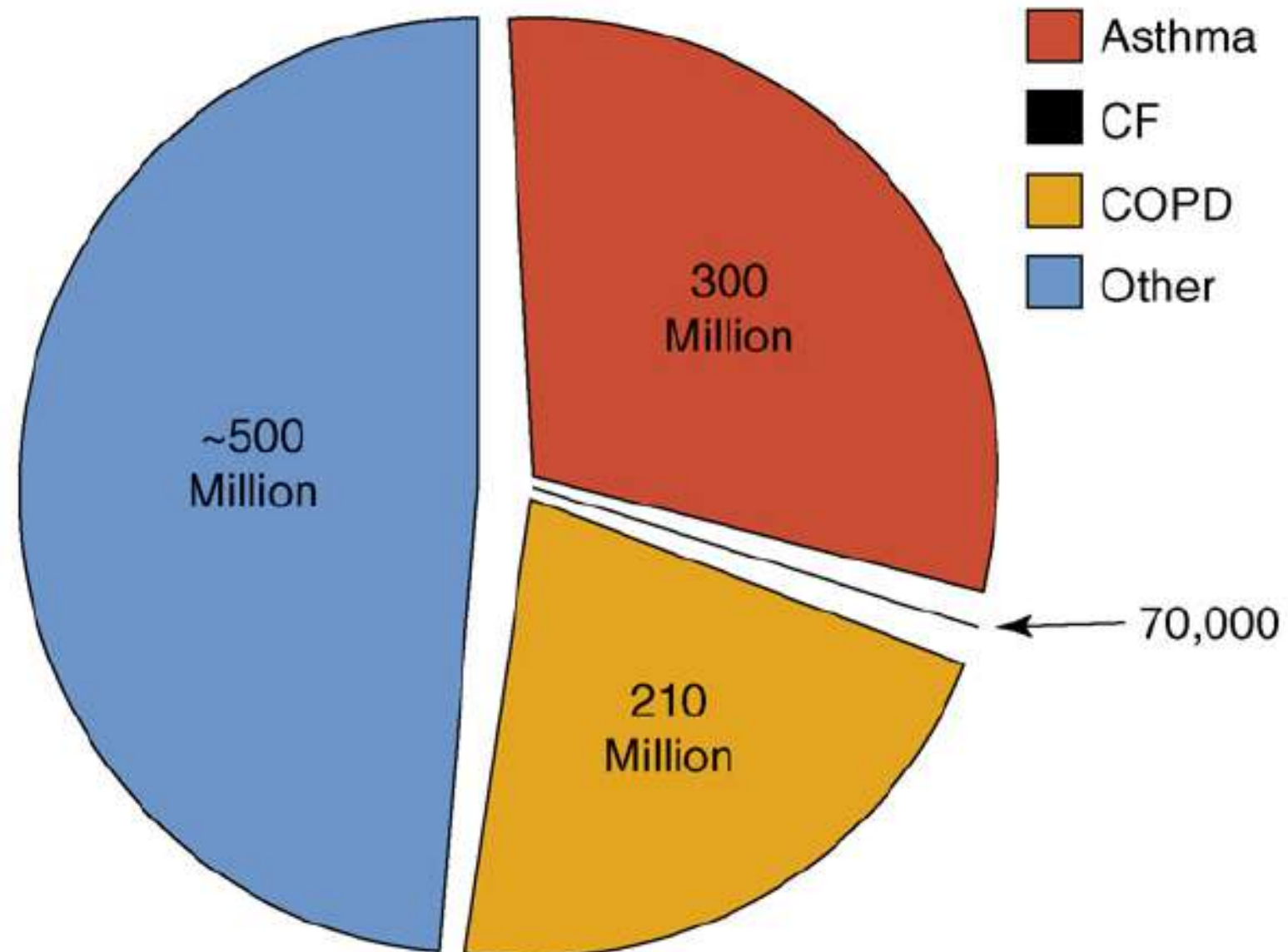
## Case study: COPD and severe asthma

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# Worldwide prevalence of inflammatory lung diseases

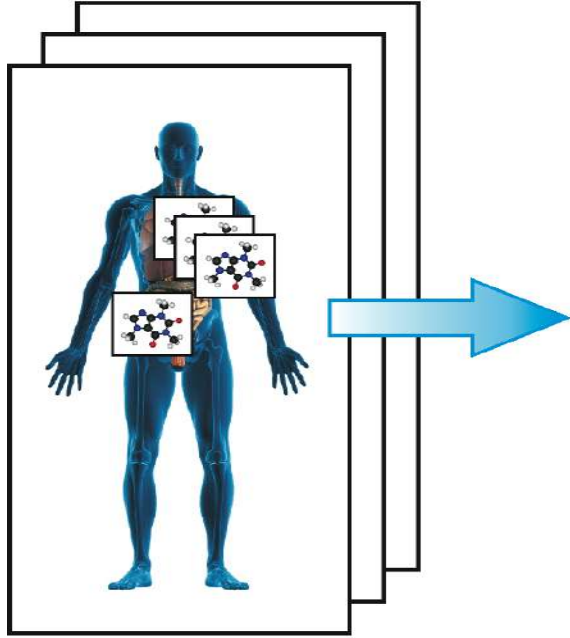


## Severe asthma and COPD: the problem

- Current treatments are insufficient
- All disease is not the same –
  - heterogenous diseases with distinct phenotypes



## Patient recruitment



U-BIOPRED project:  
Hypothesis  
generation

# Consensus clustering on clinical features

Smoking (cluster 2) vs non-smoking (cluster 3) of airflow obstruction

- *Pathway analysis of cell transcriptomics*

Regulation of actin cytoskeleton (*ITGB1, FN1, ACTN2*)

Fibronectin matrix formation (*ITGB1, FN1*)

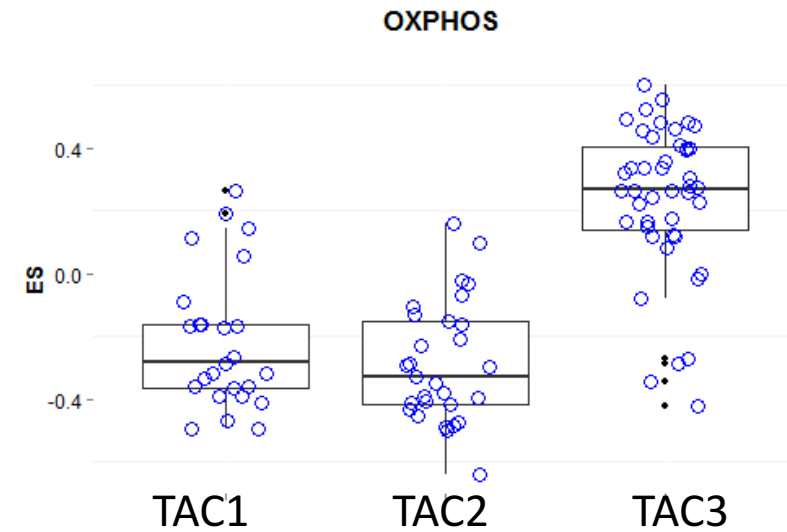
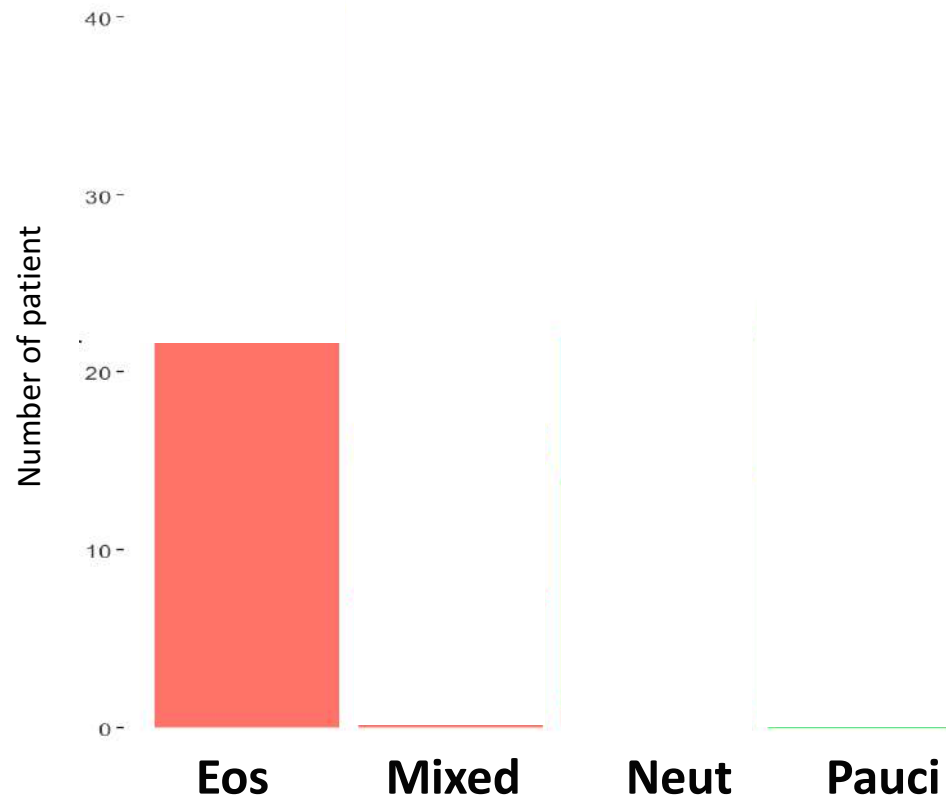
- *Differentially-expressed proteins in supernatants*

LYN: src non-receptor lyn tyrosine kinase

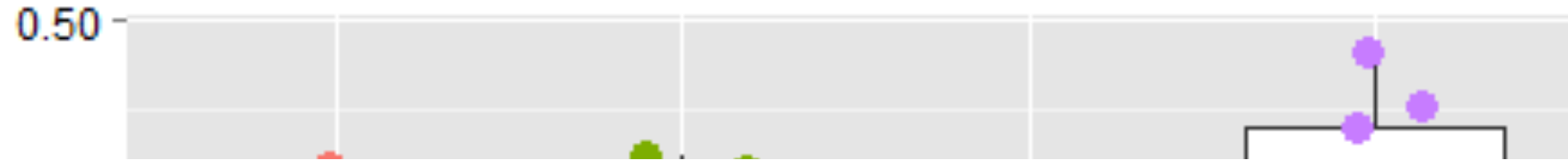
FUT5: Fucosyltransferase 5

# Relationship between sputum inflammatory pattern and the 3 transcriptomic modules

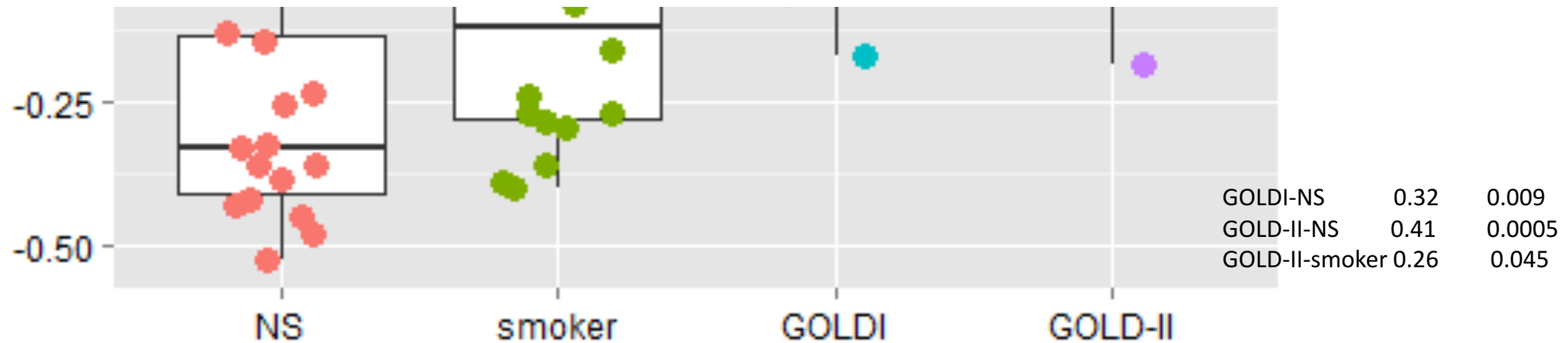
Linked to OXPHOS and ageing and specific macrophage subtypes



TAC3 cluster also enriched in COPD patients



TAC1 enrichment predicts ICS responders in GLUCOLD patients



# Summary of Transcriptome Modules in asthma from sputum analysis

Specific genes characterise each TM and subgroup

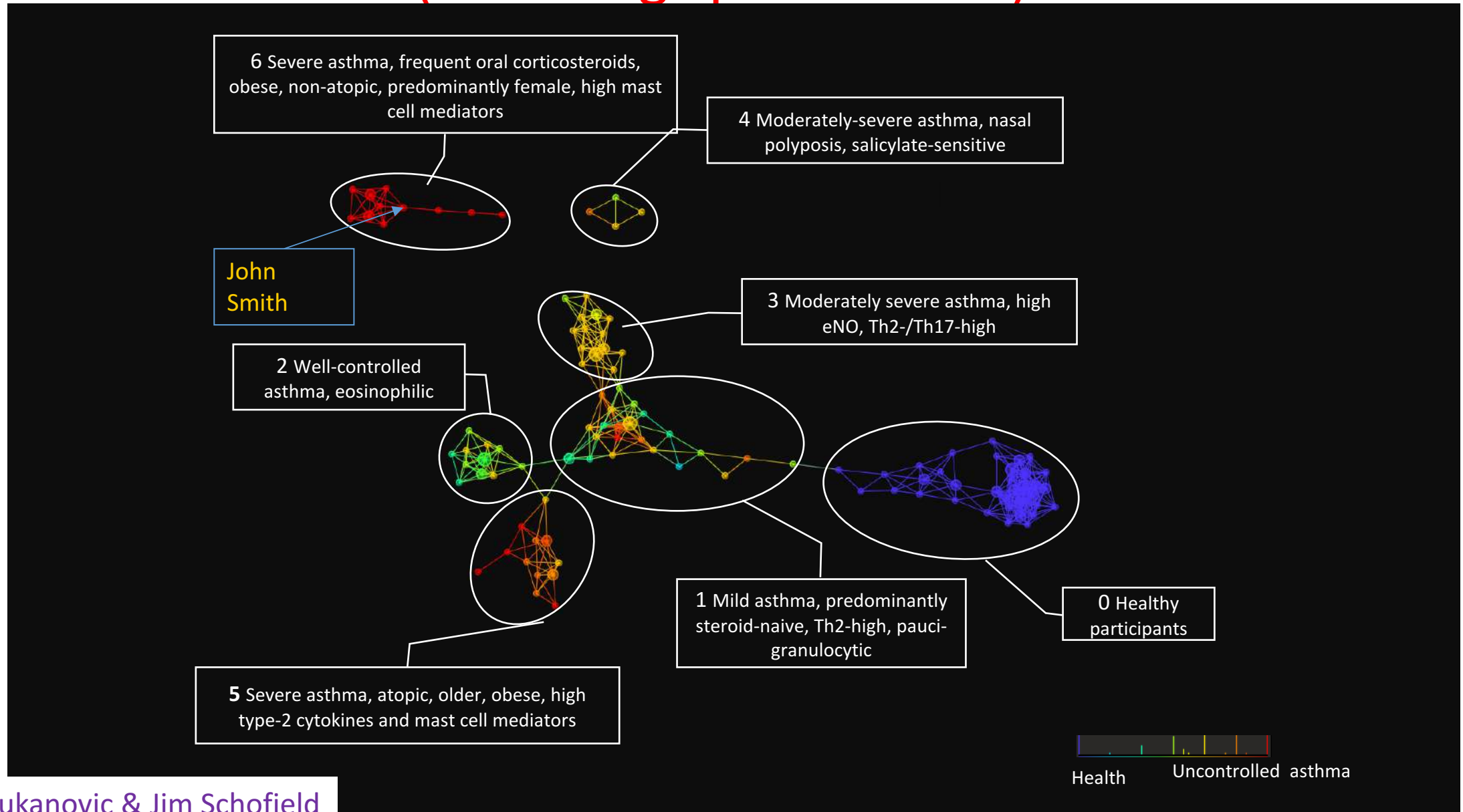
TM clustering in sputum used to define blood biomarkers  
(*IL5RA*, *VEGFA*; *GCG*, *PLA2G2A*; *CD55*, *TGFB1*, *CD22*)

Biomarker tests for molecularly targeted therapies are the key to unlocking precision medicine





# TDA analysis of 22 clinico-pathological clusters in asthma (including sputum cells)



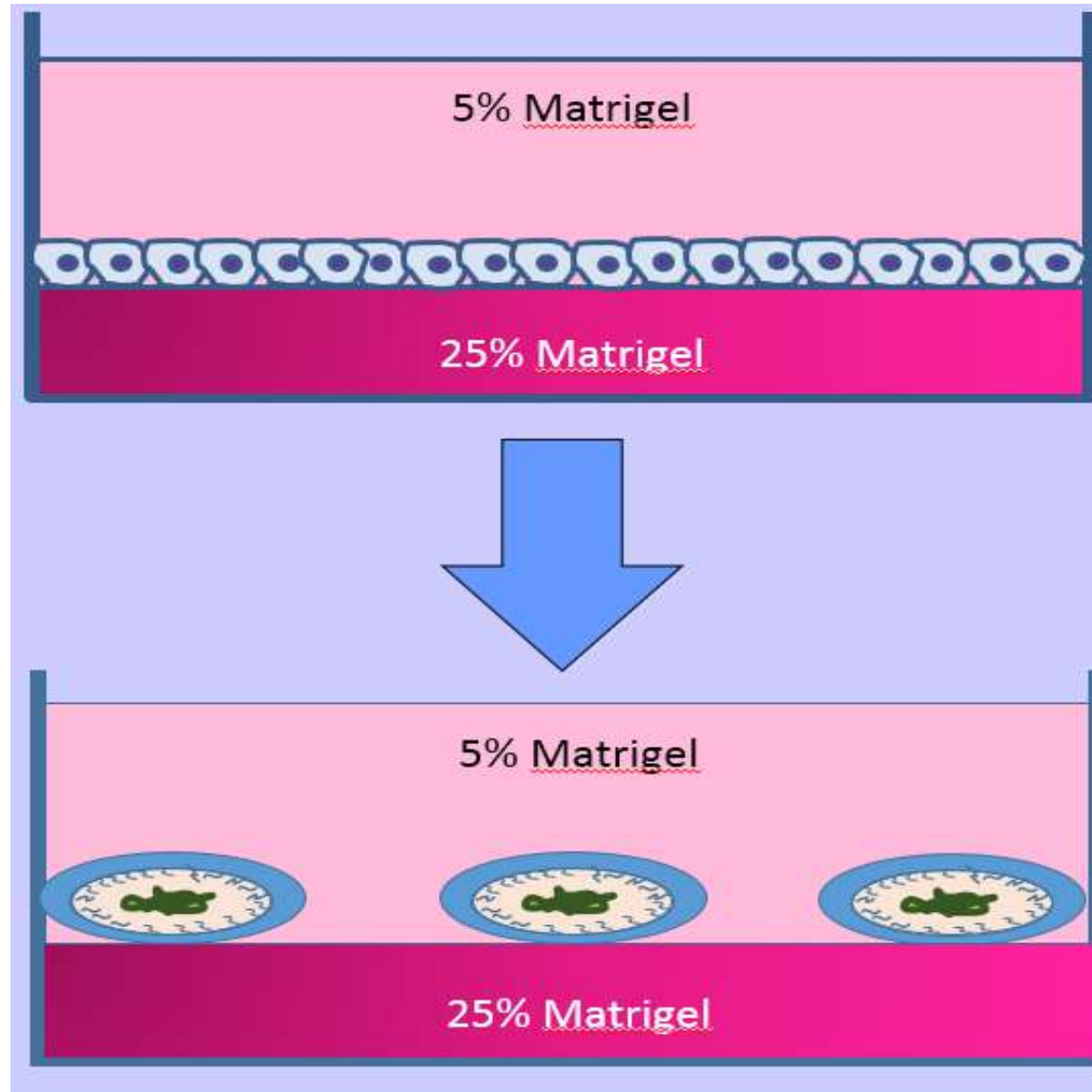
**Transcriptomic analysis of lung tissue from cigarette smoke induced emphysema murine models  
and human COPD show shared and distinct pathways**

Jeong H. Yun<sup>1,2</sup>, Jarrett Morrow<sup>1</sup>, Caroline A.Owen<sup>2,3</sup>, Weiliang Qiu<sup>1</sup>, Kimberly Glass<sup>1</sup>, Taotao Lao<sup>1</sup>,  
Zhiqiang Jiang<sup>1</sup>, Mark A. Perrella<sup>2,4</sup>, Edwin K. Silverman<sup>1,2</sup>, Xiaobo Zhou<sup>1,2\*</sup>, Craig P. Hersh<sup>1,2\*</sup>

\*contributed equally

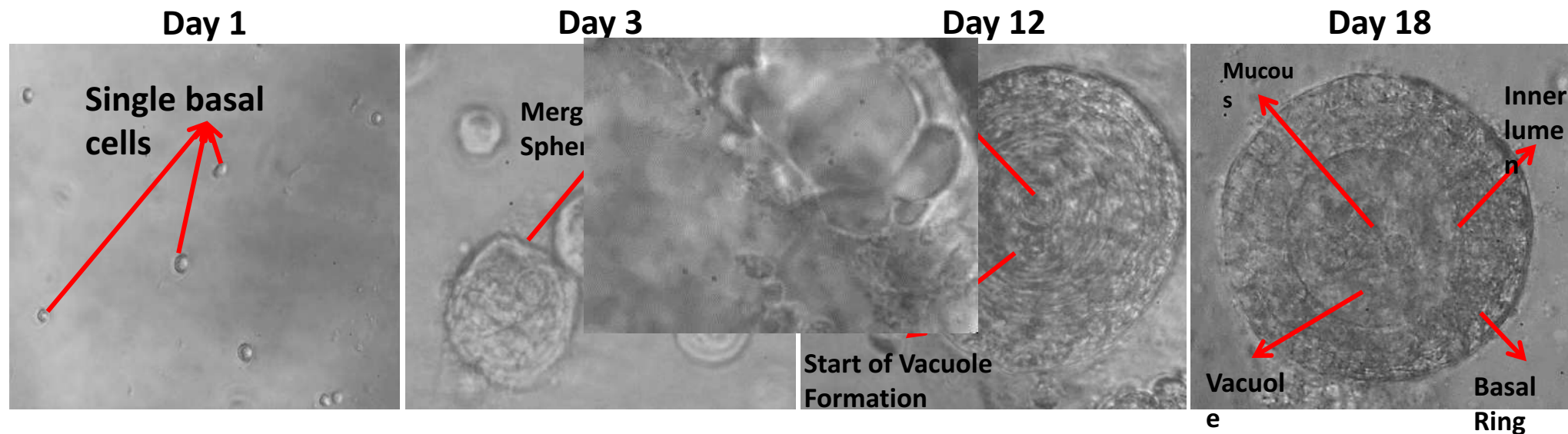
AJRCMB Articles in Press. Published on 01-March-2017 as 10.1165/rcmb.2016-0328OC

# Schematic of Bronchosphere Culture



Plus stiffening agent

# NHBE Bronchosphere Development



**Basal Cells**

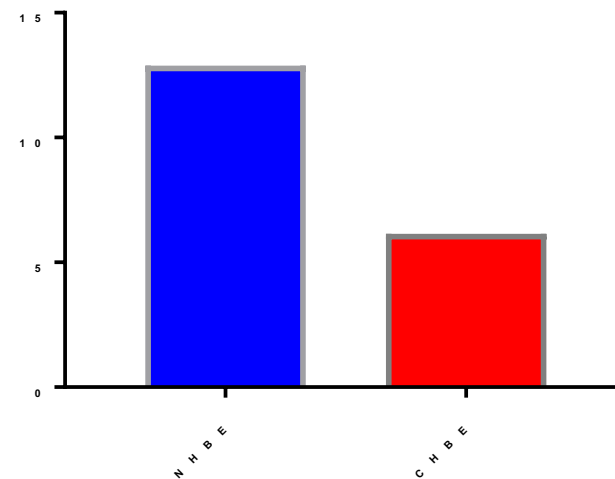
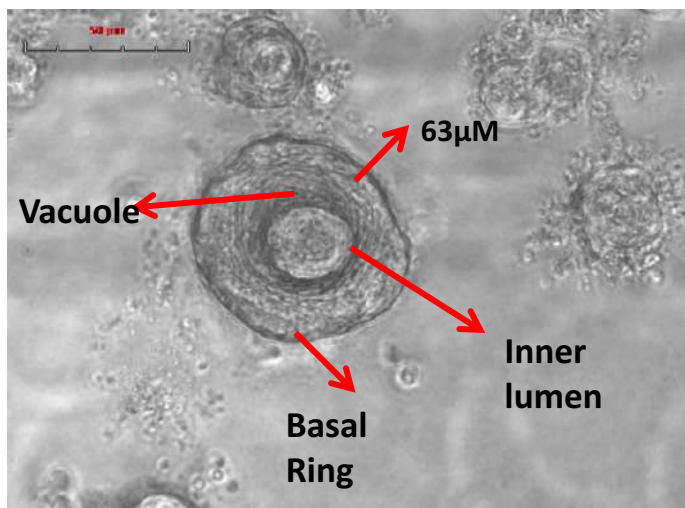
**Spheroids**

**Intermediate Spheroid**

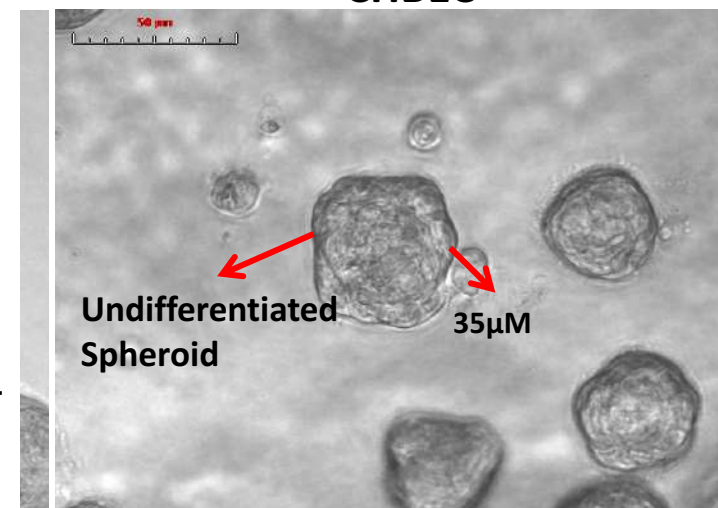
**Bronchosphere**

Basal cell marker positive (P63<sup>+</sup>, NFGFR<sup>+</sup> and ITGA6<sup>+</sup>)

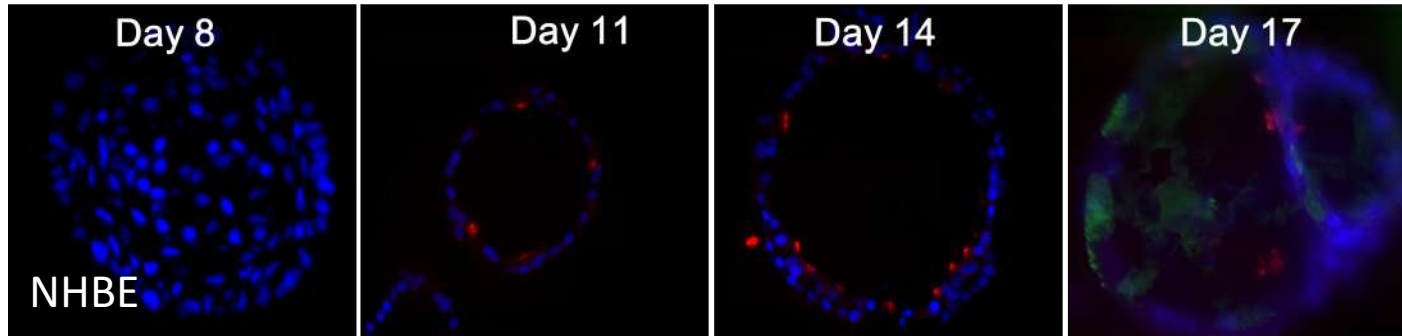
**NHBEC**



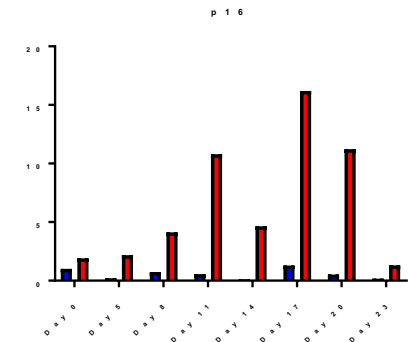
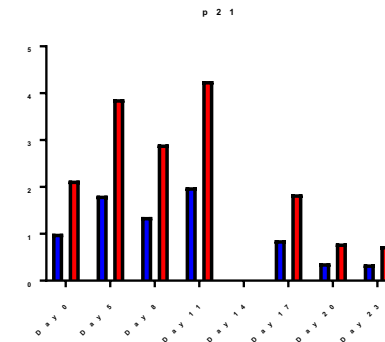
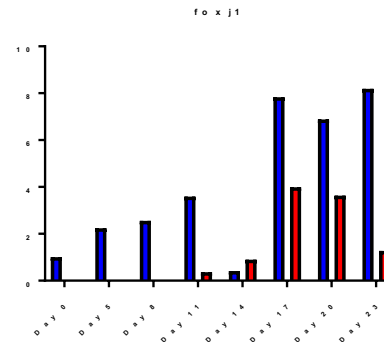
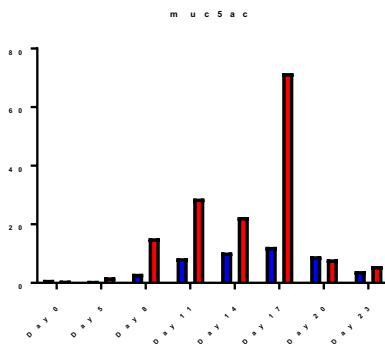
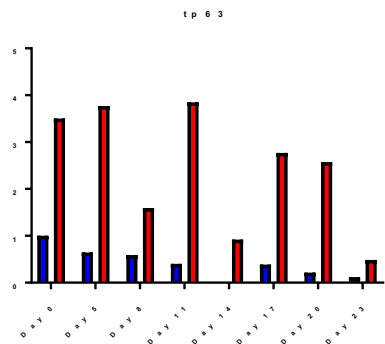
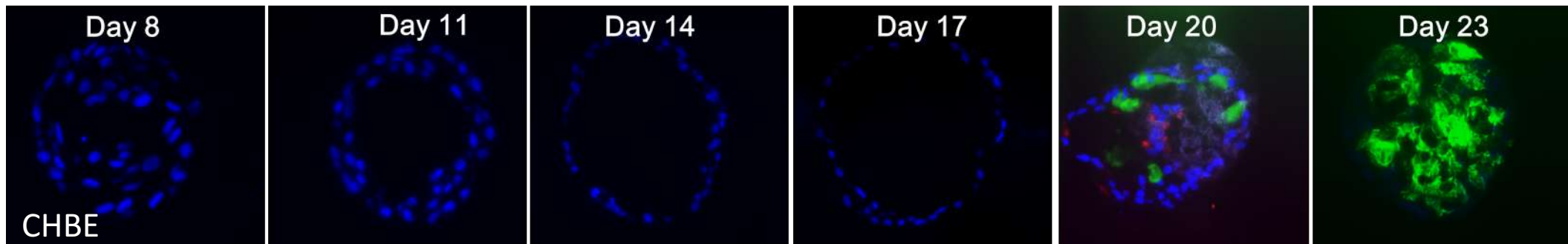
**CHBEC**



# Gene Expression During Bronchosphere Development



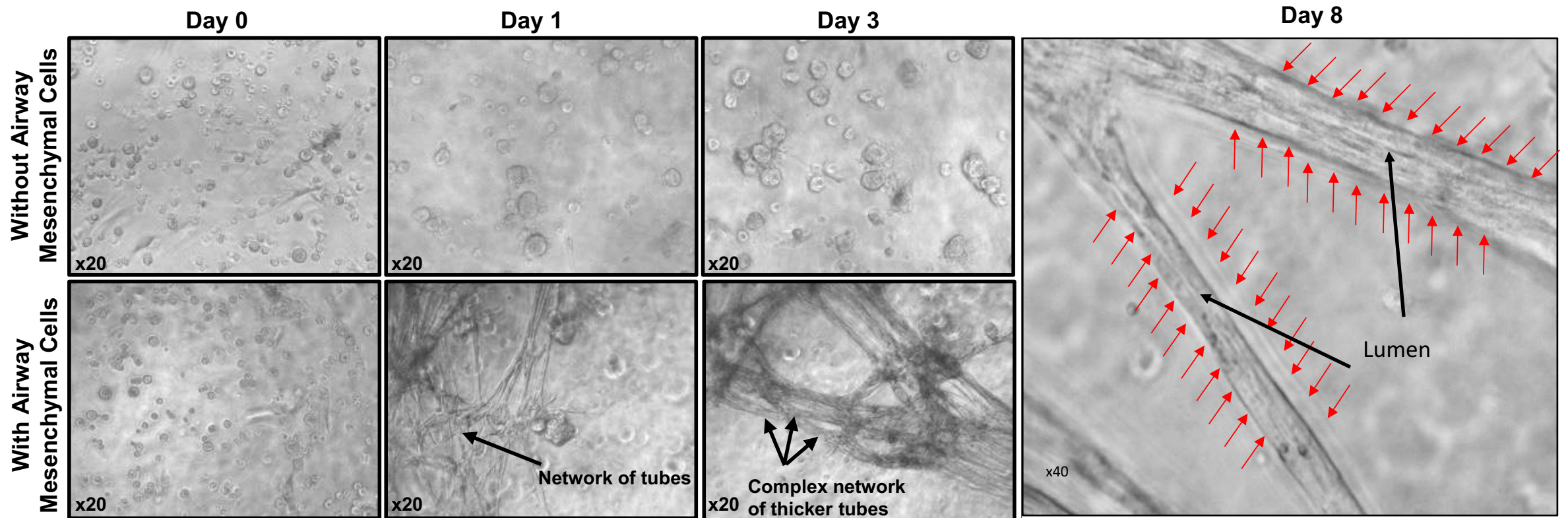
Representative staining of bronchosphere sections-  $\alpha$ -tubulin (cilia), goblet cell (MUC5AC and DAPI (nucleus) from day 2-17 (NHBE) and 8-23 (CHBE) to show luminal development. Bronchospheres replicate features of human airway lumen.





# Bronchotubules/organoid formation

ASM, fibroblasts or stem cells. Tubules contract with acetylcholine  
Stiffness essential as maintains structure – allows time to produce own matrix



# The future

- Precision medicine is a rapidly developing field in respiratory medicine
- Integration of large datasets over time can:
  - refine patient subsets,
  - indicate mechanisms to enable targeted therapy
- Analysis at the target site important for subphenotyping patients before examination of blood biomarkers
- Better models for mechanistic studies and PoC drug studies
- Need to translate to point of care

# With thanks to:

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## EFPIA Partners

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Amirall  
Amgen

## SME's

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Synairgen

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Lega Italiano Anti Fumo  
Netherlands Asthma Foundation

