



Mass General Brigham

The use of single-nucleus RNA-sequencing in malignant pleural mesothelioma: a pilot study

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Background

Malignant pleural mesothelioma

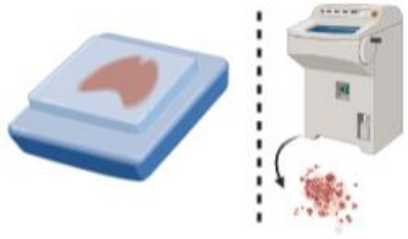
- Cancer of the mesothelial cells
- Approximately 3000 annual cases in US
- Primary etiology is asbestos
- Three major histology
 - Epithelioid
 - Sarcomatoid
 - Biphasic

Single nucleus RNA-sequencing

-  Sequencing at a single-cell level -> high throughput data
-  Allows the use of archived frozen specimens
-  Can be used on difficult to dissociate cell types
-  Nuclei isolation needs to be optimized by tissue type
-  Gene detection rate is lower compared to sc-RNA-seq



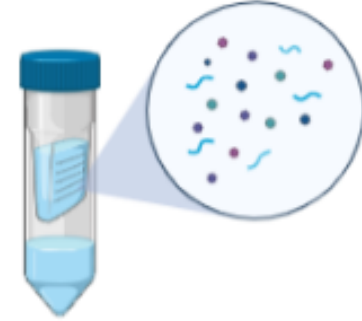
Methods



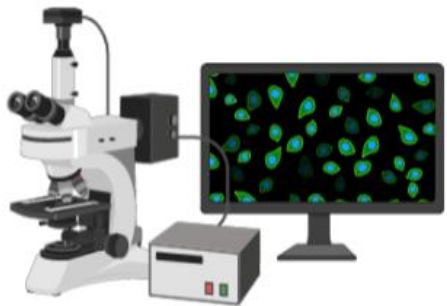
① OCT-embedded frozen tissue dissection



② Chemical (CST) and mechanical lysis



③ Wash, filter and centrifuge



④ Quality control



⑤ 10x Chromium controller & library preparation



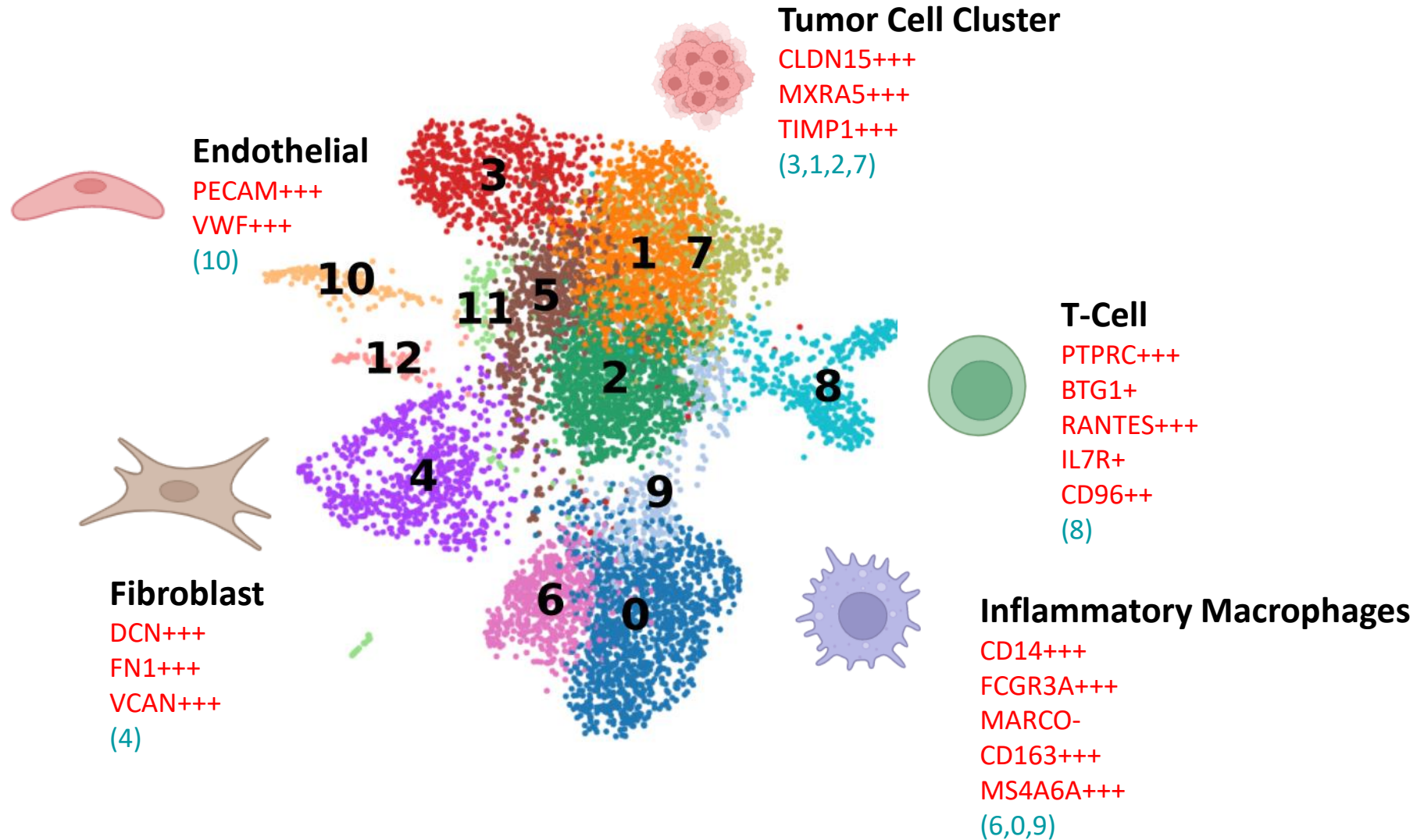
⑥ Sequencing & data analysis

Samples

	Total	Epithelioid	Biphasic	Sarcomatoid
Number of experiments	21	9	5	7
Good nuclei quality	14	5	4	5
10X	11	3	3	5
Successfully sequenced	8	2	3	3



UMAP of preliminary data

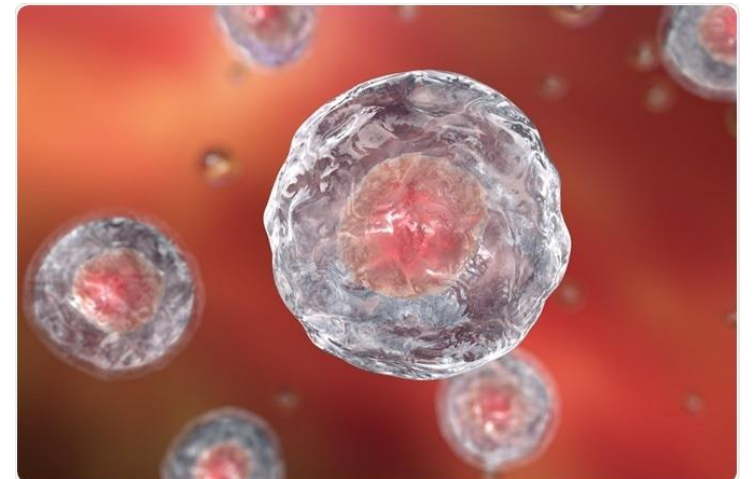


Conclusion and future plans

Validate sn-RNAseq relative gene expression by comparing to sc-RNAseq

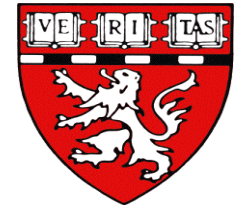
Characterize tumor microenvironment for:

- 1) Long-term survivals
- 2) Primary tumor and recurrence





Acknowledgements



Bueno lab

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