

Spatial mapping of the hepatocellular carcinoma landscape identifies unique intratumoural perivascular-immune neighbourhoods

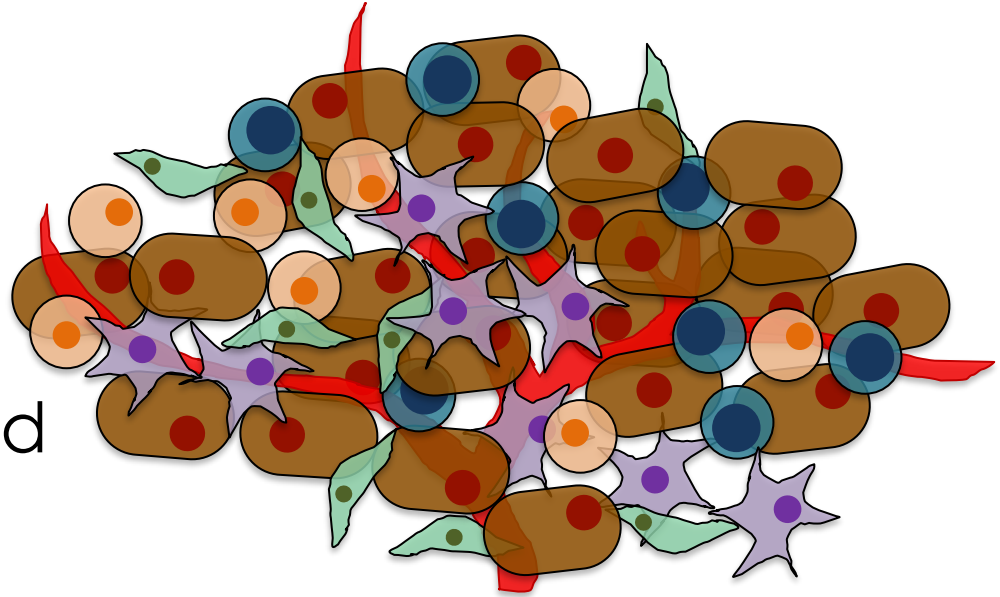
Felix Marsh-Wakefield, Cositha Santhakumar, Angela L Ferguson, Joo Shin, Ken Liu, Geoffrey McCaughan, Umaimainthan Palendira

Hepatocellular carcinoma (HCC)

- Most common primary liver cancer
- Sixth most common cancer worldwide, third most common cause of cancer death
 - Sung *et al.*, 2020 (*CA Cancer J Clin*)
- In 2021, mortality rates in Australia >80%, double that of the preceding two decades
 - Australian Institute of Health and Welfare, *Cancer in Australia 2021*

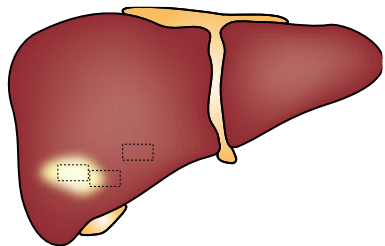
Tumour microenvironment

- Consists of cancer, immune, and stromal cells
- Associated with patient aetiologies and outcomes
- **More work needed to understand role in HCC**



Sample collection

16 HCC patients
Liver resections



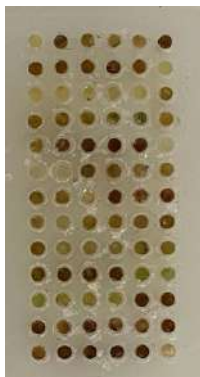
Non-tumour



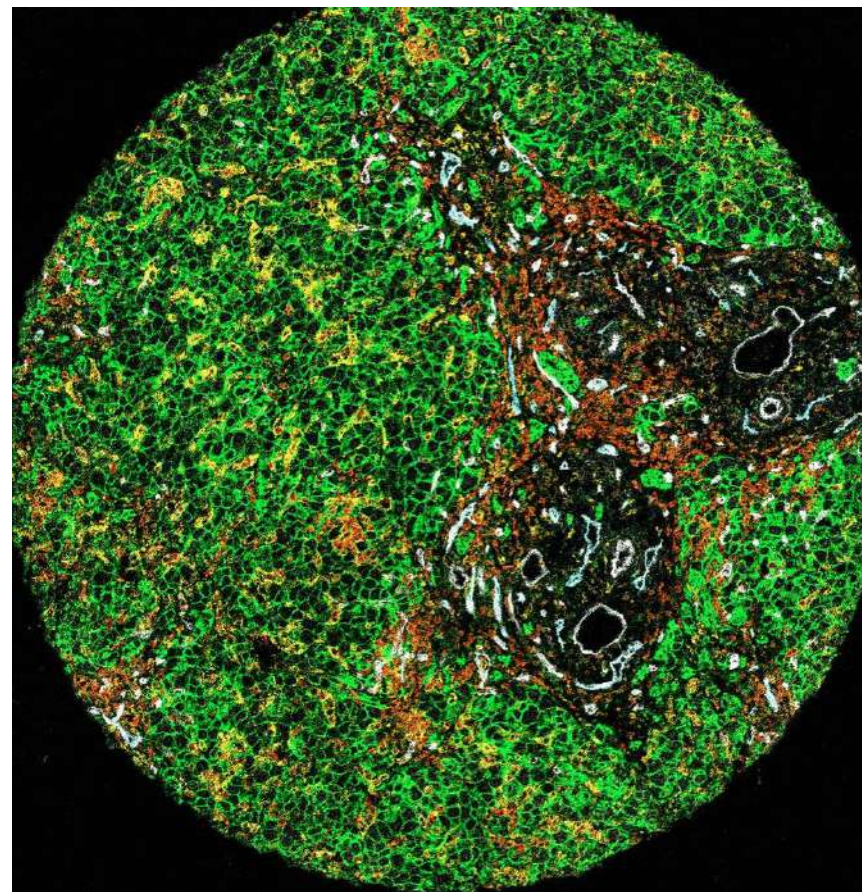
Interface



Tumour

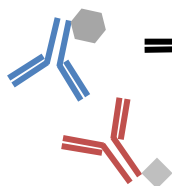


1mm circles

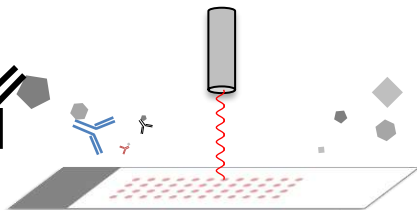


Imaging mass cytometry

Antibody staining



Tissue ablation



Mass spectrometry



Imaging mass cytometry panel

Hepatocytes

CK8/18

E-cadherin

HepPar1

Structural markers

α SMA

CD34

podoplanin

vimentin

CD3

CD4

CD8a

CD11b

CD11c

CD14

CD16

CD20

CD45

Immune cell markers

CD45RO

CD56

CD57

CD66a

CD68

CD69

CD86

CD127

CD206

CD209

CD303

Foxp3

FXIIIa

Granzyme B

HLA-DR

IgA

Ki67

MPO

NaKATPase

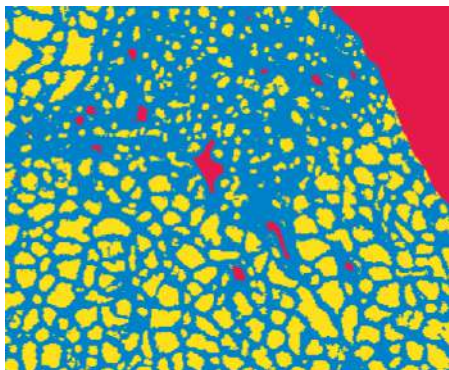
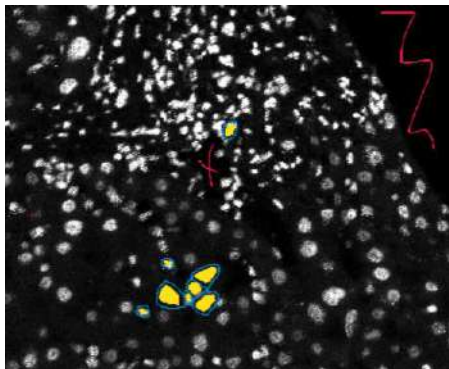
PD-L1

PD-L2

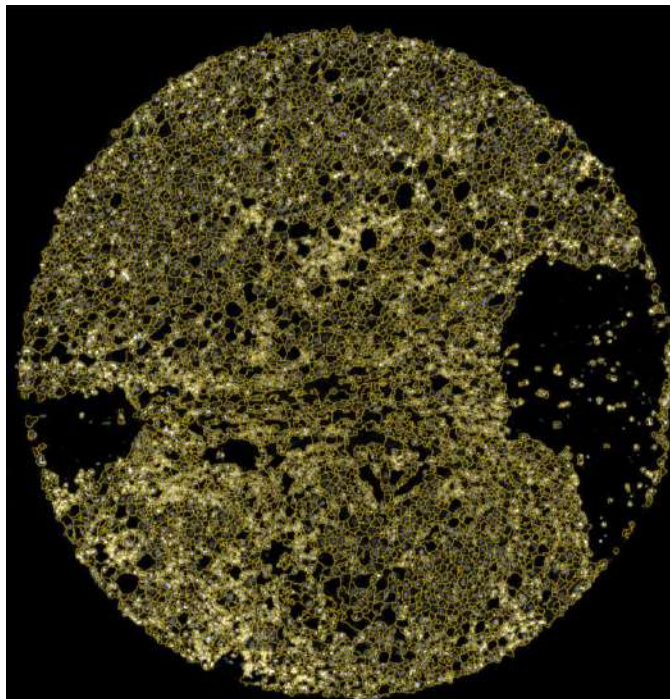
SirPa

T-bet

Training

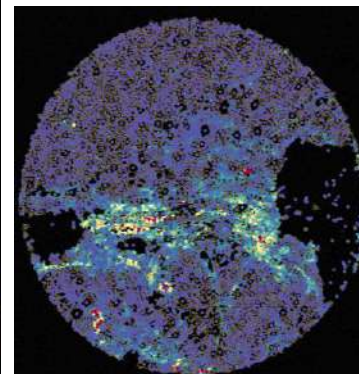


Cell segmentation



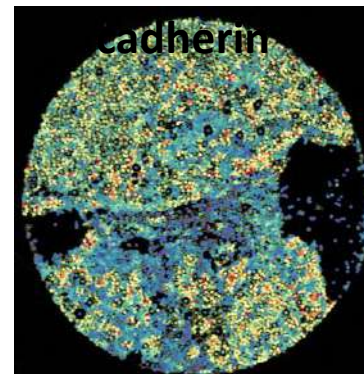
Marker quantification

α SMA

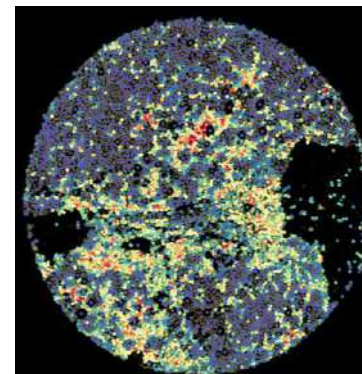


E-

cadherin



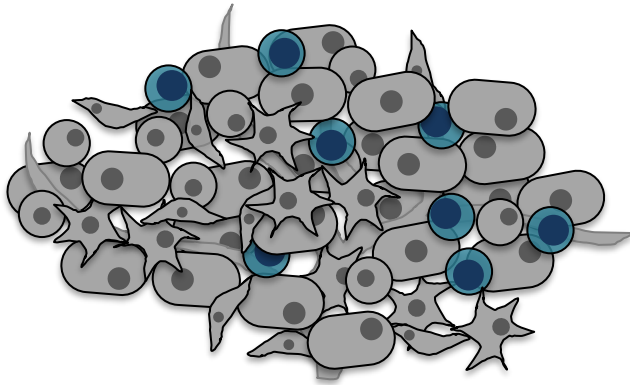
CD45



'ilastik' software, Berg *et al.*, 2019 (*Nat Methods*)

Quantify spatial data

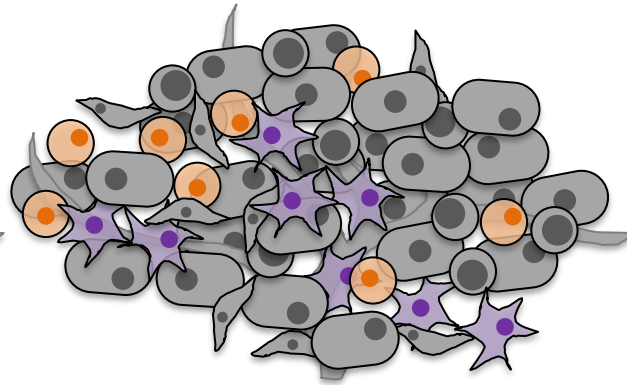
Cell densities



Cells per mm^2



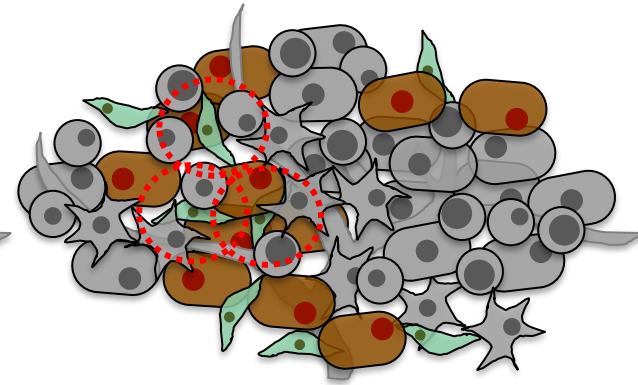
Distance between cells



Distance between



Neighbouring cells



Interaction between



Done using 'Spectre' in R
Ashhurst, Marsh-Wakefield, Putri *et al.*, 2022 (*Cytometry A*)

Are there differences in neighbourhood interactions between liver regions?

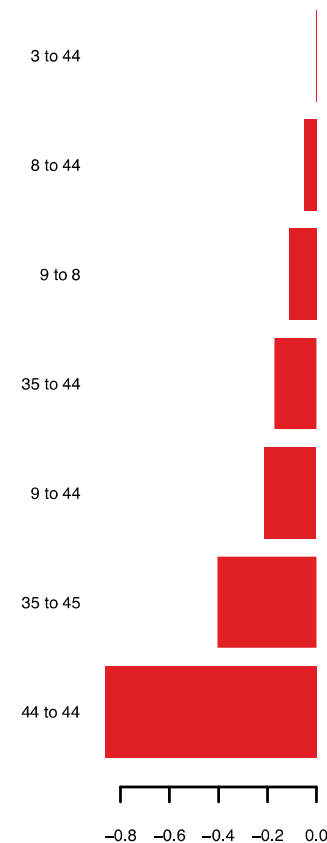
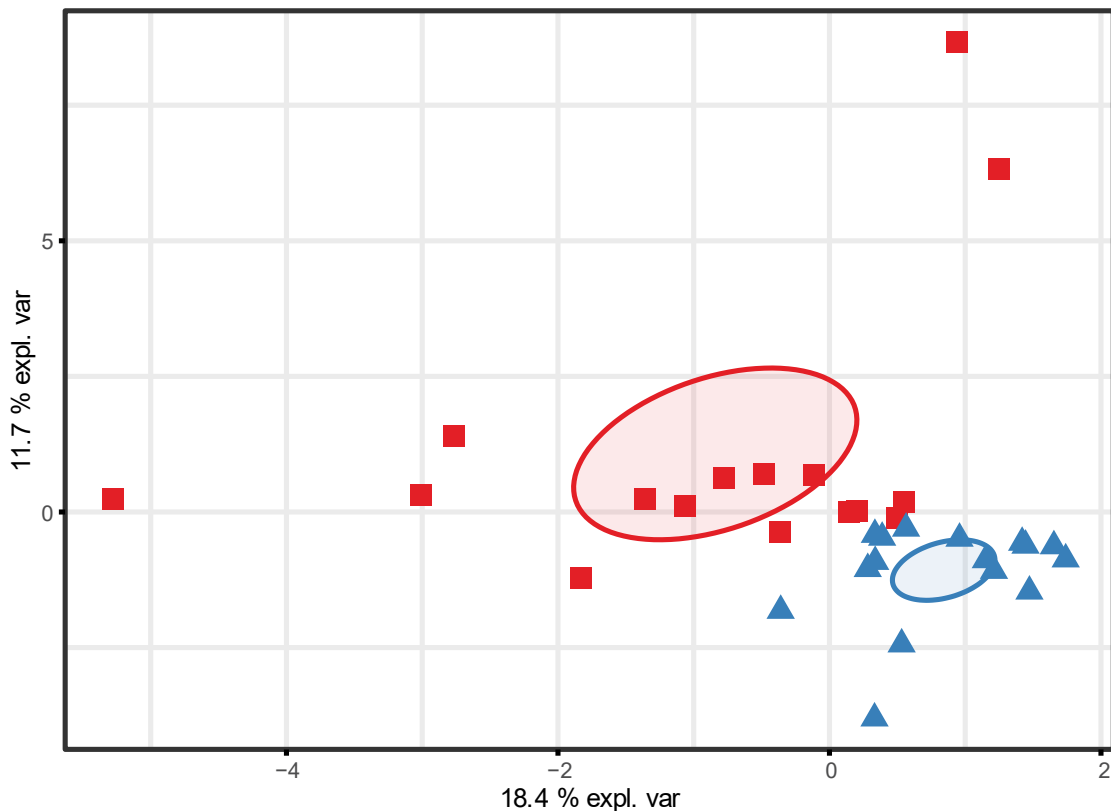
Linear dimensionality reduction

- Principal component analysis (**PCA**) reduces dimensions by summarising **overall variance**
 - All variability influence (human, experiment, etc.)
- Sparse partial least squares-discriminant analysis (**sPLS-DA**) reduces dimensions by summarising **differences between groups**
 - Need to know which groups to compare

Regions differ in neighbourhood interactions

■ Tumour ▲ Non-Tumour

Contribution on comp 1



Sparse partial least squares-discriminant analysis (sPLS-DA)

Cluster 44

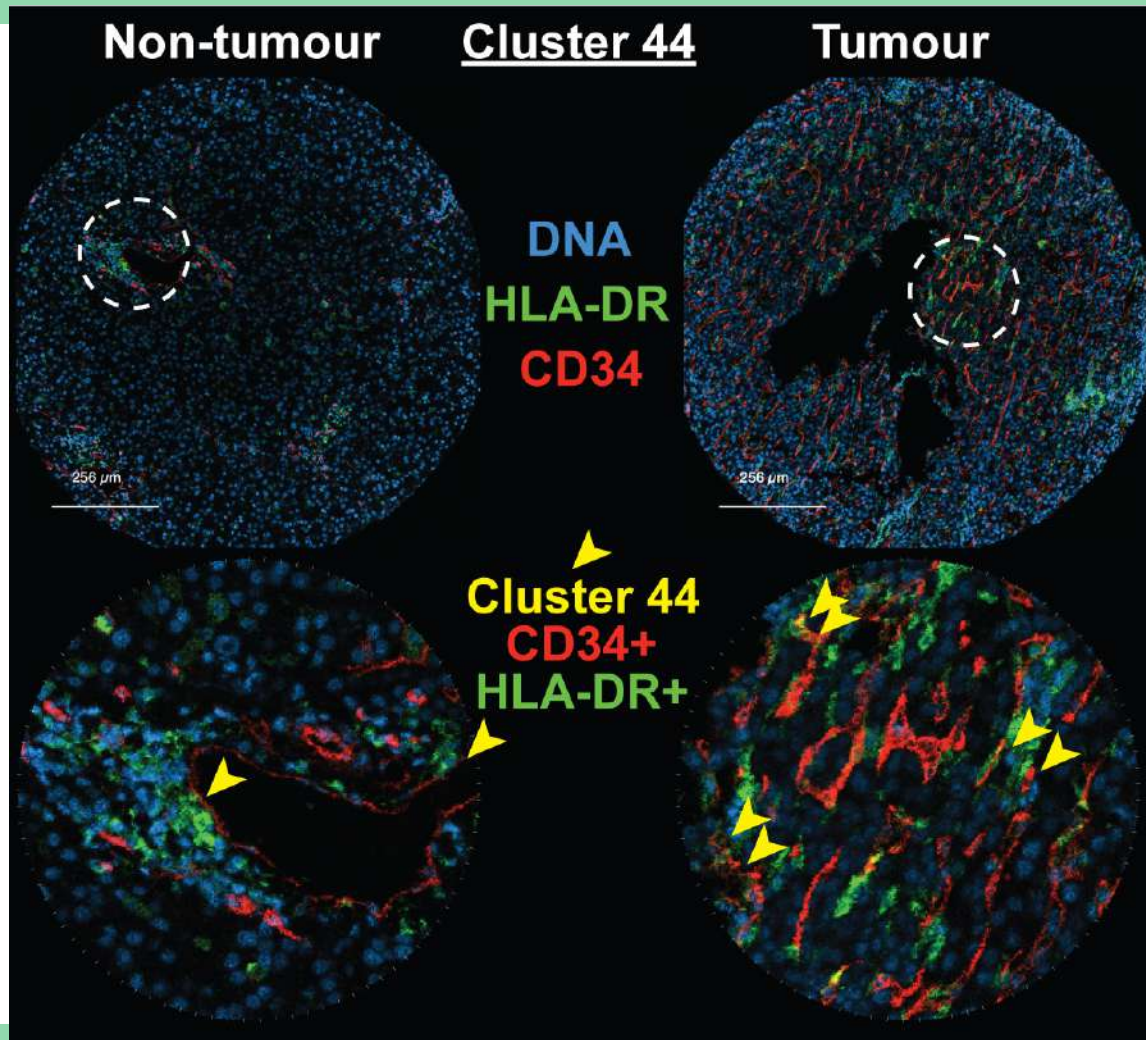
CD34+ macrophage?

- CD69_FITC.150Nd
- CD8a.146Nd
- CD11c.142Nd
- CD20.141Pr
- granzymeB.171Yb
- PDL2.159Tb
- PDL1_Cy3.152Sm
- Foxp3_biotin.143Nd
- HLADR.174Yb
- SirPa.164Dy
- CD206.172Yb
- CD14.160Gd
- CD86.156Gd
- CD68.153Eu
- CD16.148Nd
- CD303.175Lu
- IgA.162Dy
- CD3.170Er
- CD45RO.149Sm
- Tbet.158Gd
- CD4.173Yb
- FXIIIa.161Dy
- CD34.155Gd
- CD66a.167Er
- MPO.144Nd
- CD11b.163Dy
- Ki67.168Er

High



Low



VEGFA+ macrophages

Patient 21

Patient 19

Patient 18

Patient 17

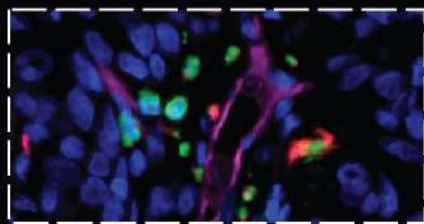
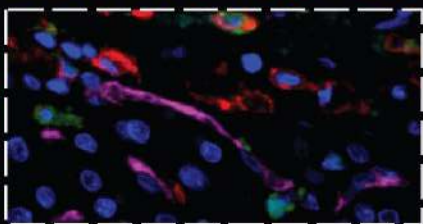
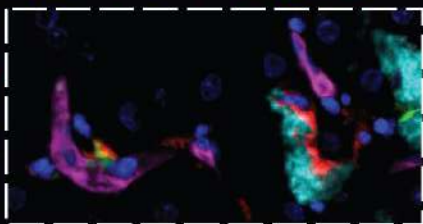
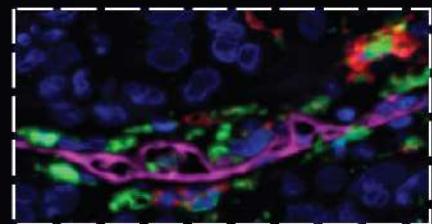
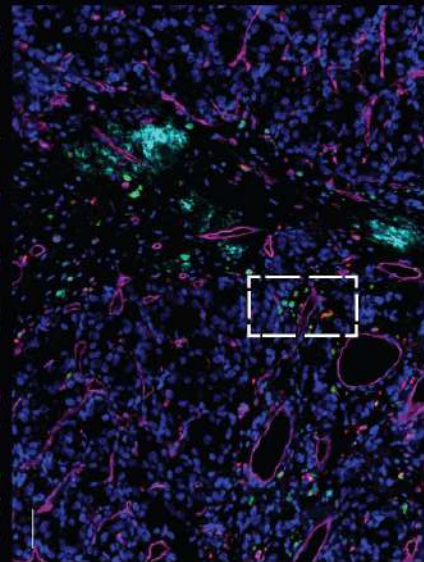
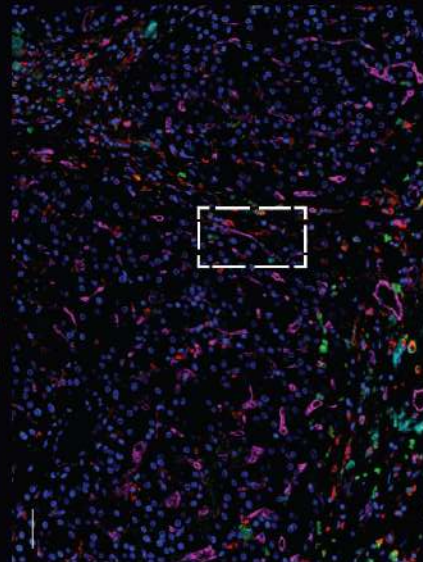
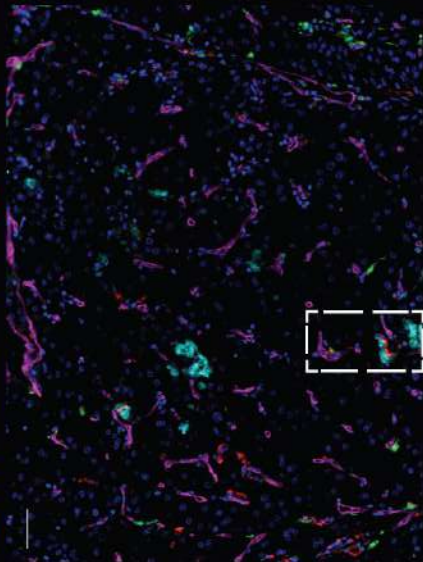
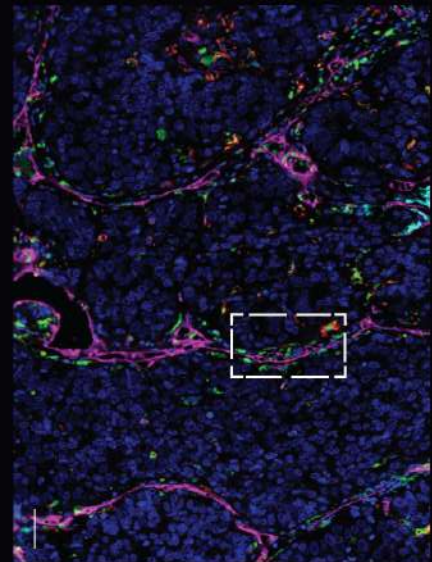
DAPI

CD34

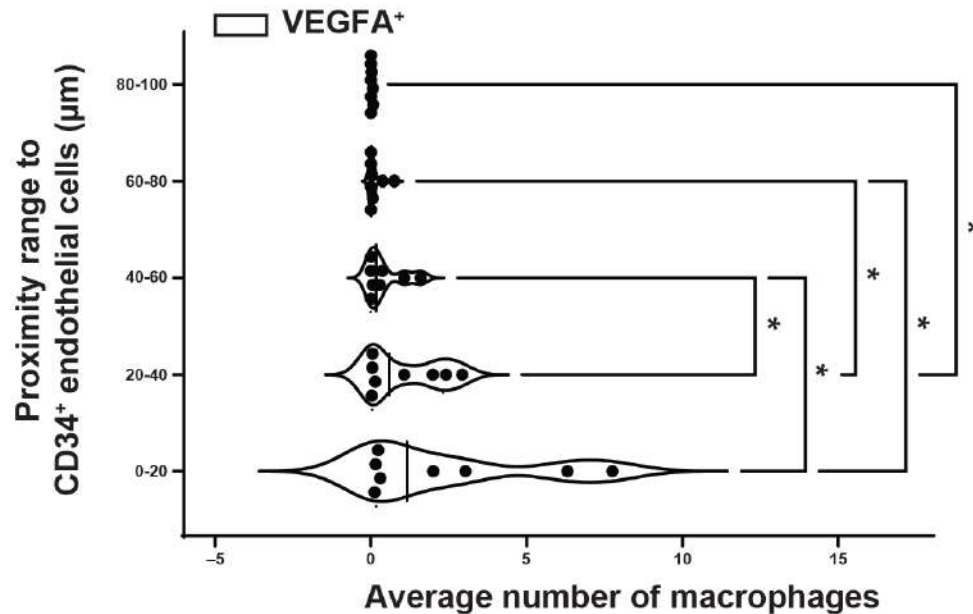
FXIIIa

HLA-DR

VEGFA



Macrophages reside closely to CD34+ endothelial cells



**Is there any communication
between these cells?**

**Use scRNAseq to identify (potential)
ligand-receptor communication**

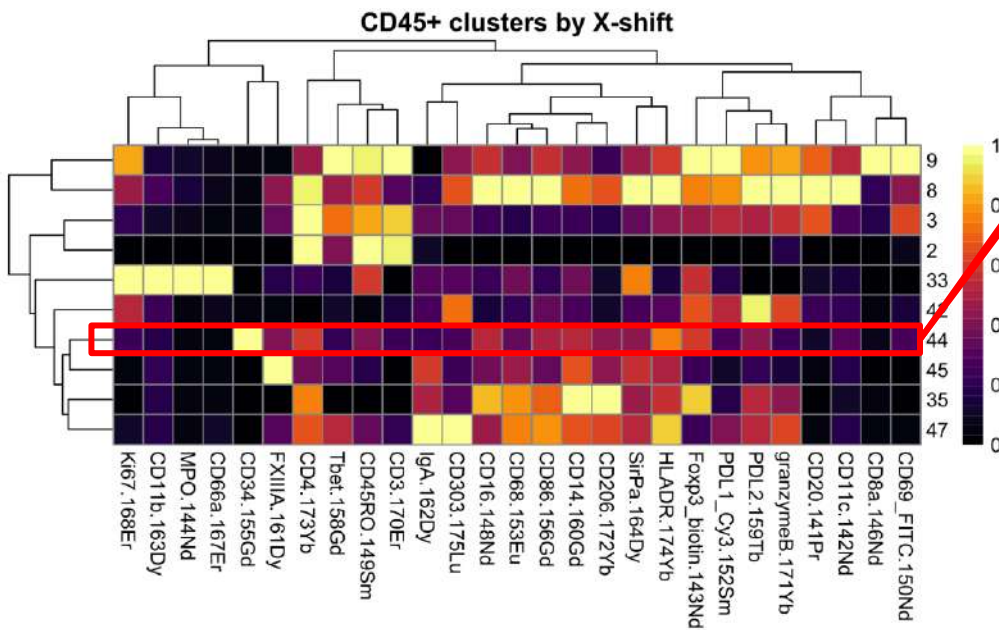
A single-cell atlas of the multicellular ecosystem of primary and metastatic hepatocellular carcinoma

[Yiming Lu](#),^{#1} [Aiqing Yang](#),^{#1} [Cheng Quan](#),^{#1} [Yingwei Pan](#),^{#2} [Haoyun Zhang](#),² [Yuanfeng Li](#),¹ [Chengming Gao](#),¹ [Hao Lu](#),¹ [Xueting Wang](#),^{1,3} [Pengbo Cao](#),¹ [Hongxia Chen](#),¹ [Shichun Lu](#),² and [Gangqiao Zhou](#)^{✉1,4}

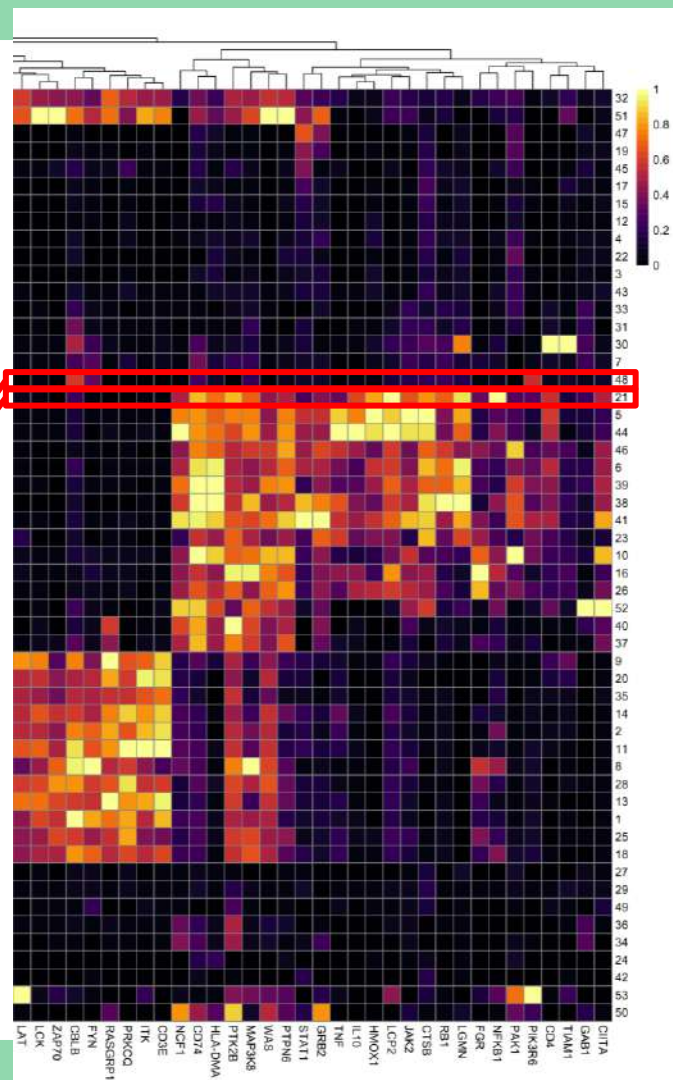
- >70,000 cells from 10 HCC patients
 - Sites include **non-tumour**, **tumour**, metastatic lymph node, and portal vein thrombus

Compare phenotypes between IMC and scRNAseq

IMC clusters

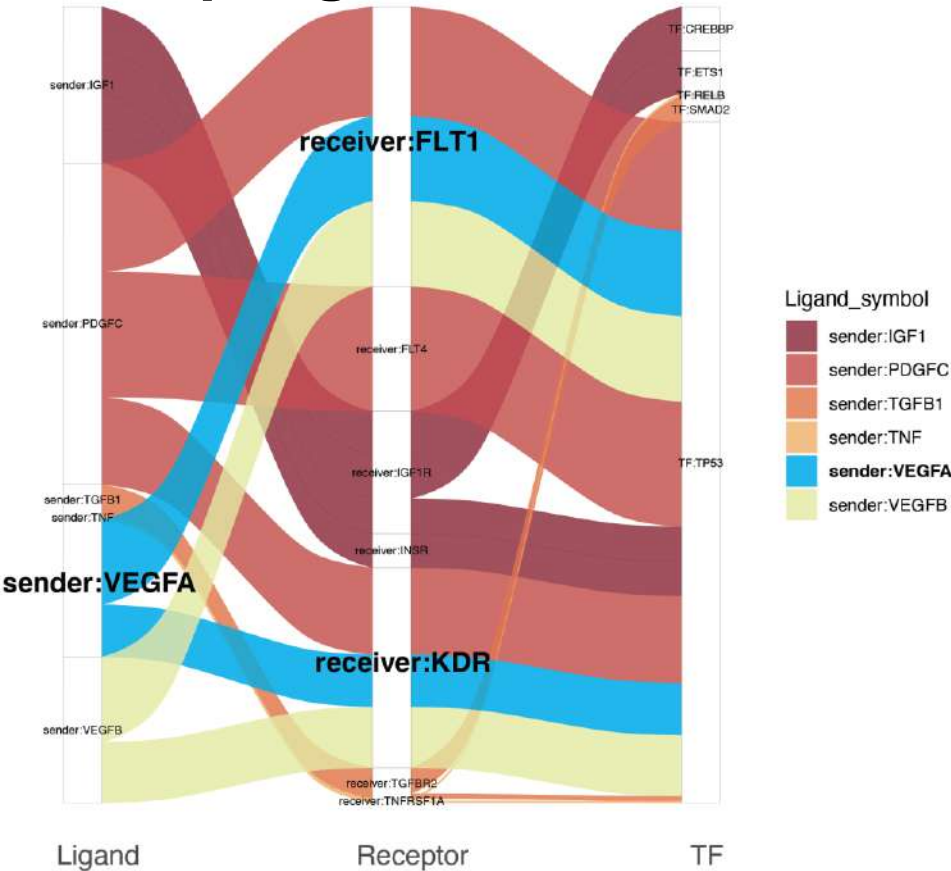


scRNAseq clusters



Macrophage-endothelial cell communication

Macrophage Endothelial



- Macrophages within tumour may communicate with endothelial cells

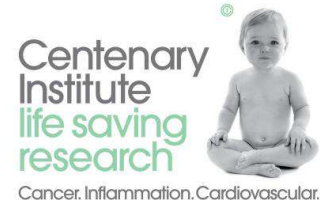
Lu *et al.*, 2022

Nature Communications

‘CellCall’ R package

Zhang *et al.*, 2021

Nucleic Acids Research



Public spatial transcriptomic data

nanoString

PRODUCTS RESEARCH FOCUS SUPPORT & RESOURCES COMPANY

CosMx SMI Human Liver FFPE Dataset

REQUEST MORE INFORMATION

LIVER DATA SUMMARY

INTERACTIVE VISUALIZATIONS

DOWNLOAD DATA

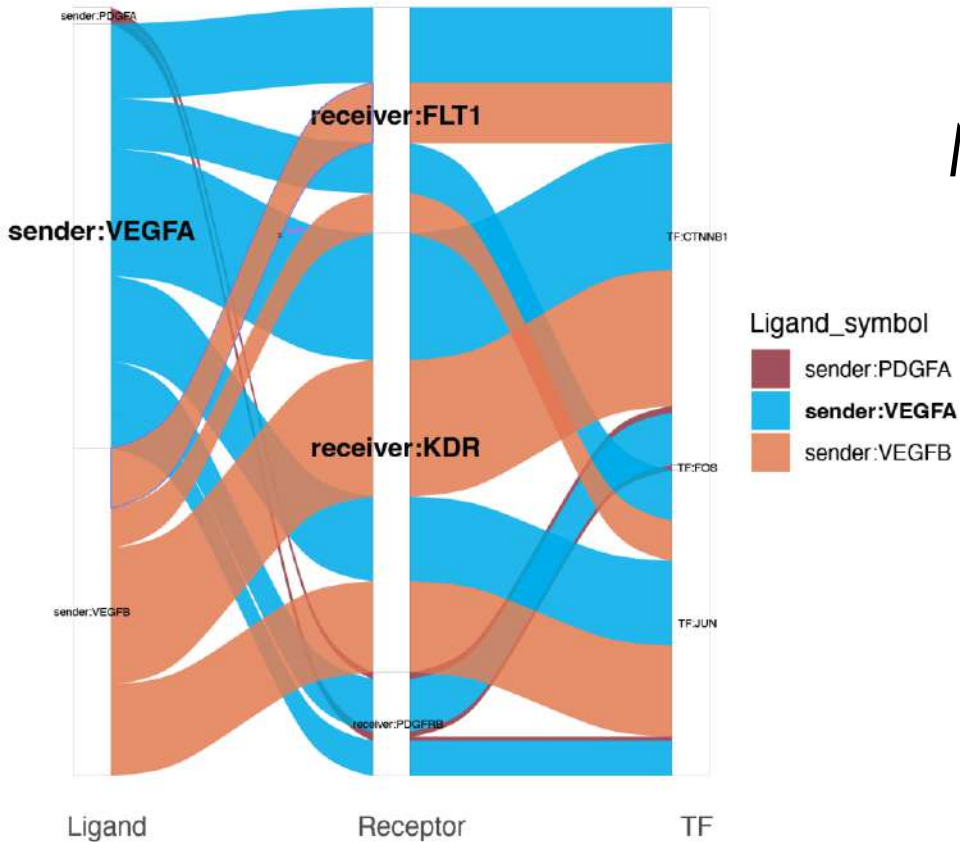
Home » Products » CosMx Spatial Molecular Imager » CosMx SMI Human Liver RNA...

DATA SUMMARY		
Tissue type	FFPE human normal liver	FFPE human hepatocellular carcinoma
Panel	Human Universal Cell Characterization Panel 1000 plex	Human Universal Cell Characterization Panel 1000 plex
Total scan area	76 mm ²	100 mm ²
Total cells	340,517	464,126
% Cells passed QC	97.8%	99.3%
Total transcripts detected	198,546,375	533,910,466
Mean total transcripts/cell	583	1150
Mean total transcripts/um ³	0.67	1.41
Mean negatives/target/cell	0.04	0.07
Mean FalseCode/target/cell	0.008	0.008

<https://nanosttring.com/products/cosmx-spatial-molecular-imager/human-liver-rna-ffpe-dataset/>

Same communication occurs spatially

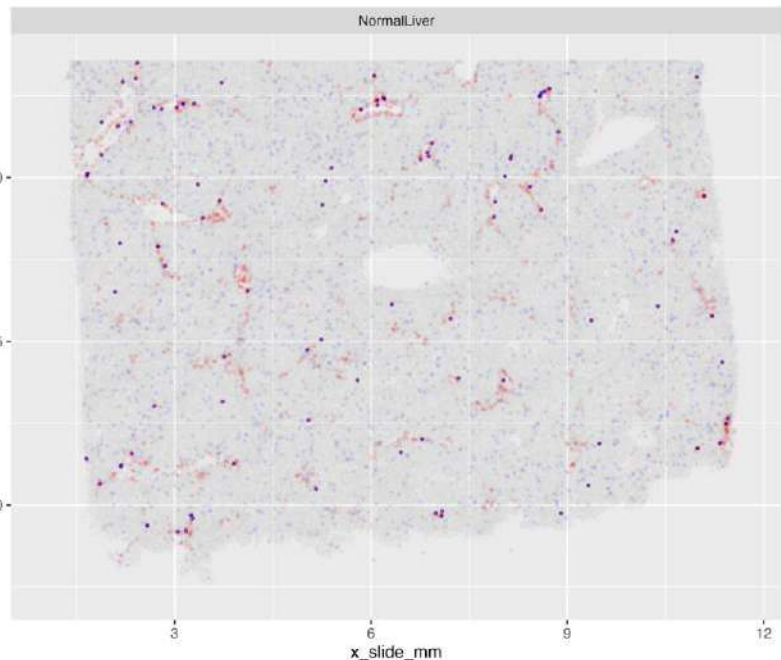
Macrophage Endothelial



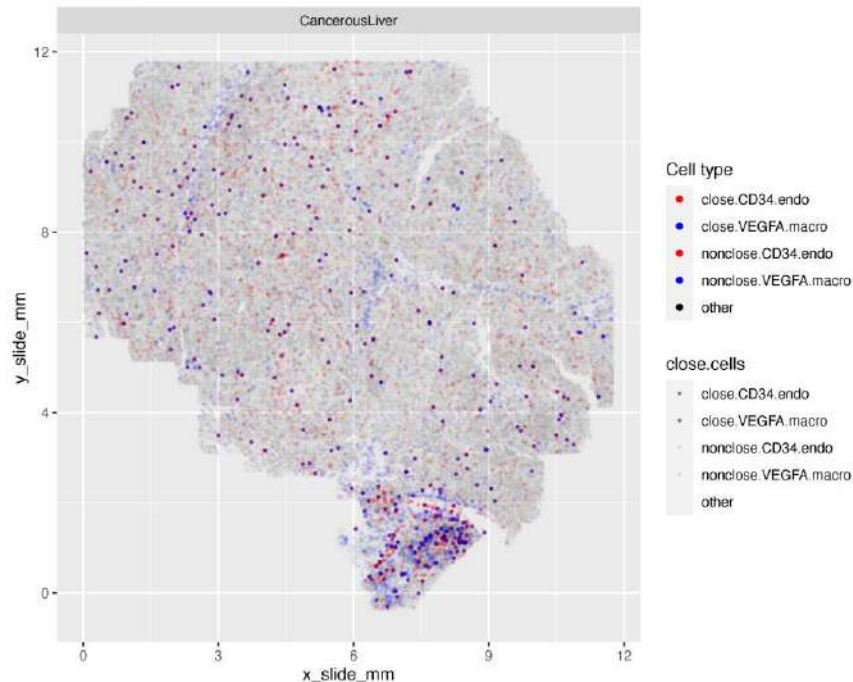
Macrophage-endothelial
cell communication by
VEGFA

Close ($\leq 20\mu\text{m}$) cell interactions

Normal liver



HCC liver



Subset density (cells/mm ²)	Normal	HCC
VEGFA ⁺ macrophages	26.34	36.27
Close VEGFA ⁺ macrophages	1.26	3.65
CD34 ⁺ endothelial cells	26.75	46.61
Close CD34 ⁺ endothelial cells	1.51	4.04

Subset proportions	Normal	HCC
Close VEGFA ⁺ macrophages (% VEGFA ⁺ macrophages)	4.80%	10.1%
Close CD34 ⁺ endothelial cells (% CD34 ⁺ endothelial cells)	5.66%	8.67%

Average number within 20 μm	Normal	HCC
Macrophage to endothelial cell	0.060	0.132
Endothelial cell to macrophage	0.055	0.088

Anti-VEGFA treatment in HCC

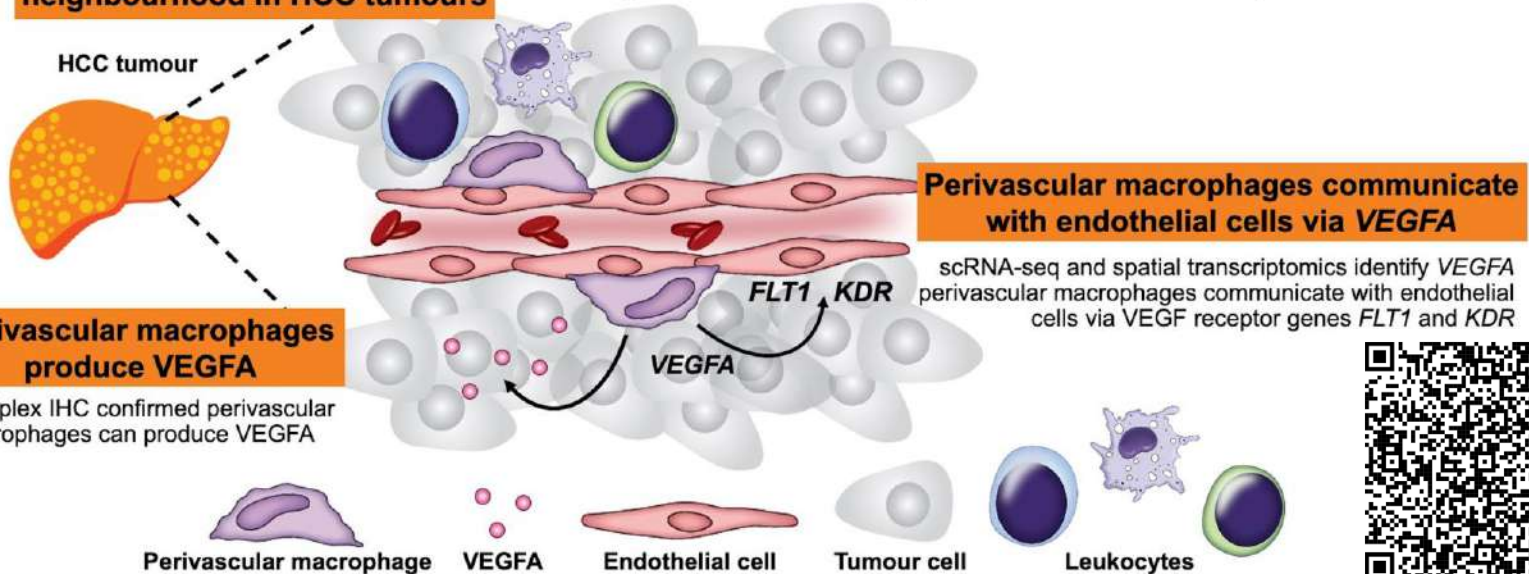
- HCC patients treated with combination atezolizumab (anti-PD-L1) and bevacizumab (anti-VEGF-A) have better overall survival
 - Finn *et al.*, 2020, *New England Journal of Medicine*
- Depleting *Vegfa* in macrophages results in reduced vascular permeability in breast cancer mouse model
 - Harney *et al.*, 2015, *Cancer Discovery*

More information

Spatial Mapping of the Hepatocellular Carcinoma Landscape Identifies Unique Intratumoural Perivascular-immune Neighbourhoods

Unique perivascular neighbourhood in HCC tumours

Imaging mass cytometry identified a unique perivascular neighbourhood consisting of perivascular macrophages, endothelial cells, and leukocytes



Ongoing analyses

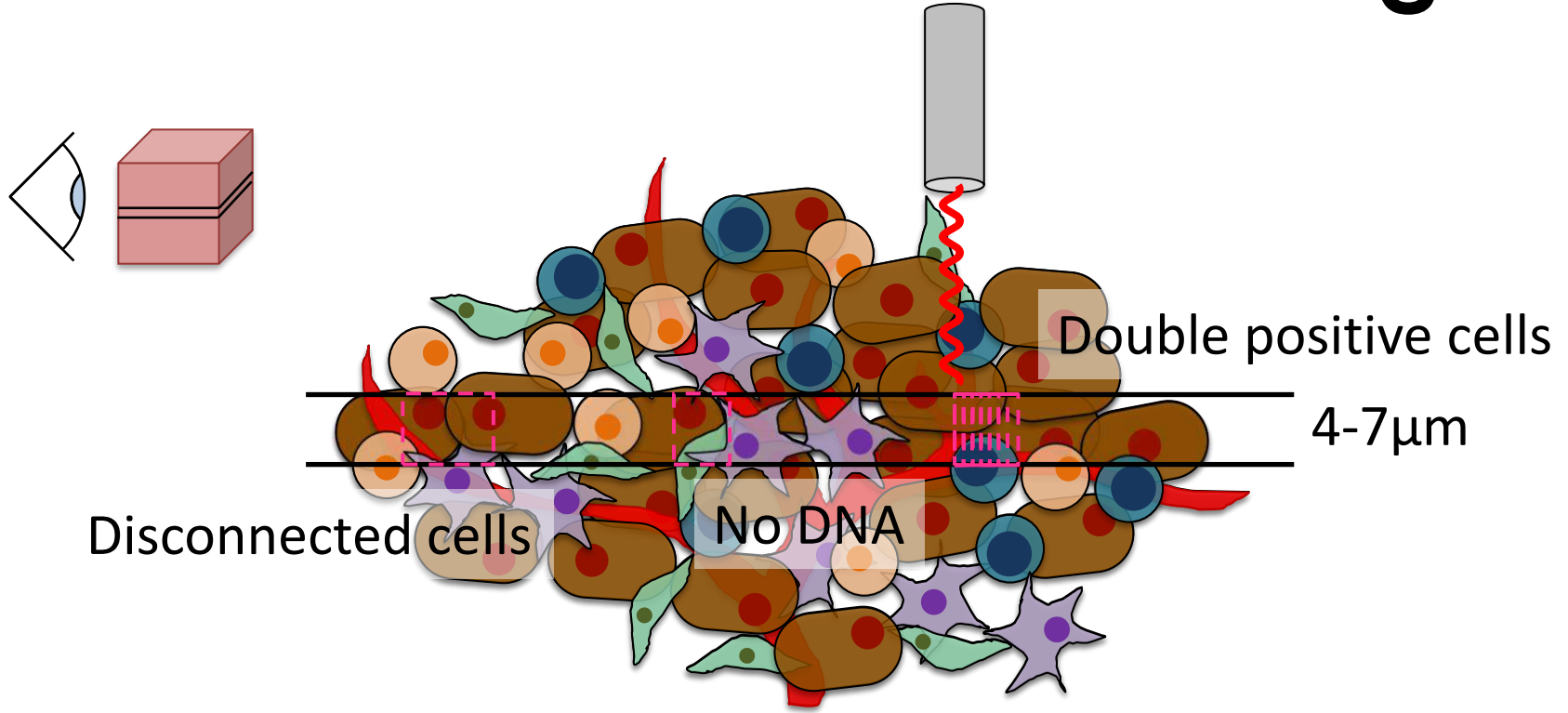
- Compare differences between aetiologies and tumour recurrence risk factors
- Non-immune cell interactions
 - Fibroblasts, hepatocytes...

α SMA	E-cadherin	Podoplanin
CD34	FXIIIa	T-bet
CK8/18	HepPar1	Vimentin
	NaKATPase	

More IMC!

- Additional 16 HCC patients (32 total)
 - 15 cirrhotic, 16 MVI
 - 8 HBV, 12 HCV, 6 MASH, 6 ALD, 3 unknown

Limitations of tissue staining

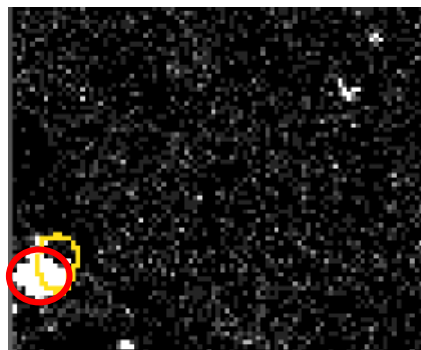


Overlapping markers

CD3



FXIII A



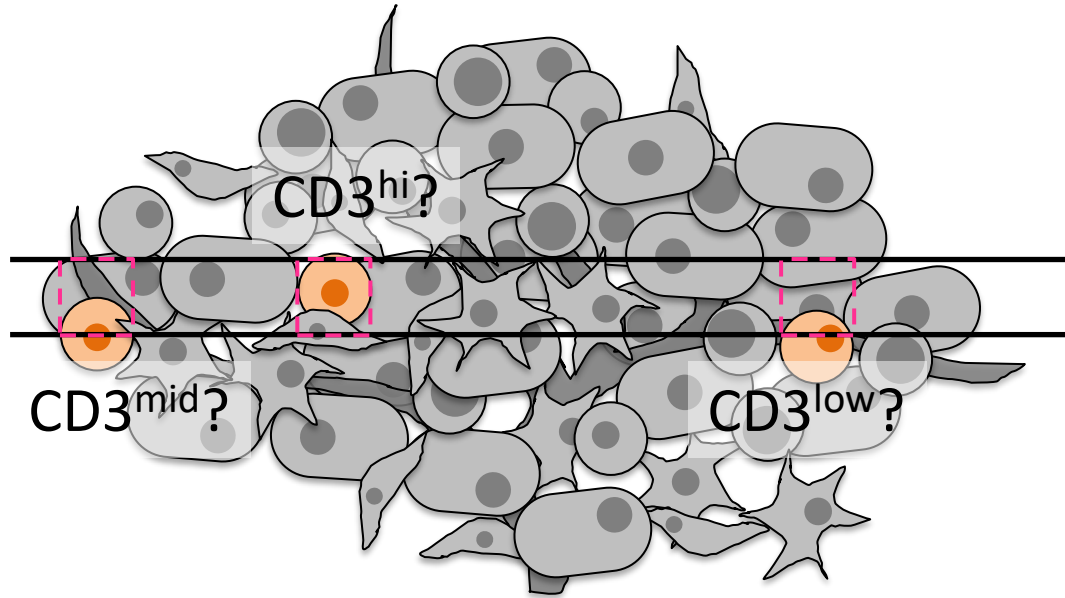
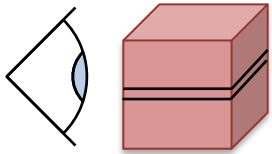
CD3+ macrophage?

FXIII A+ T cell?

Double positive cell?

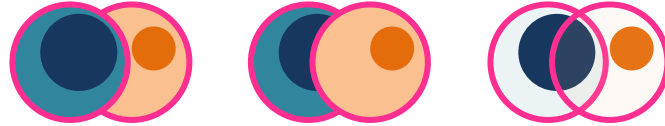
'ilastik' software, Berg *et al.*, 2019 (*Nat Methods*)

Sensitivity



A solution?

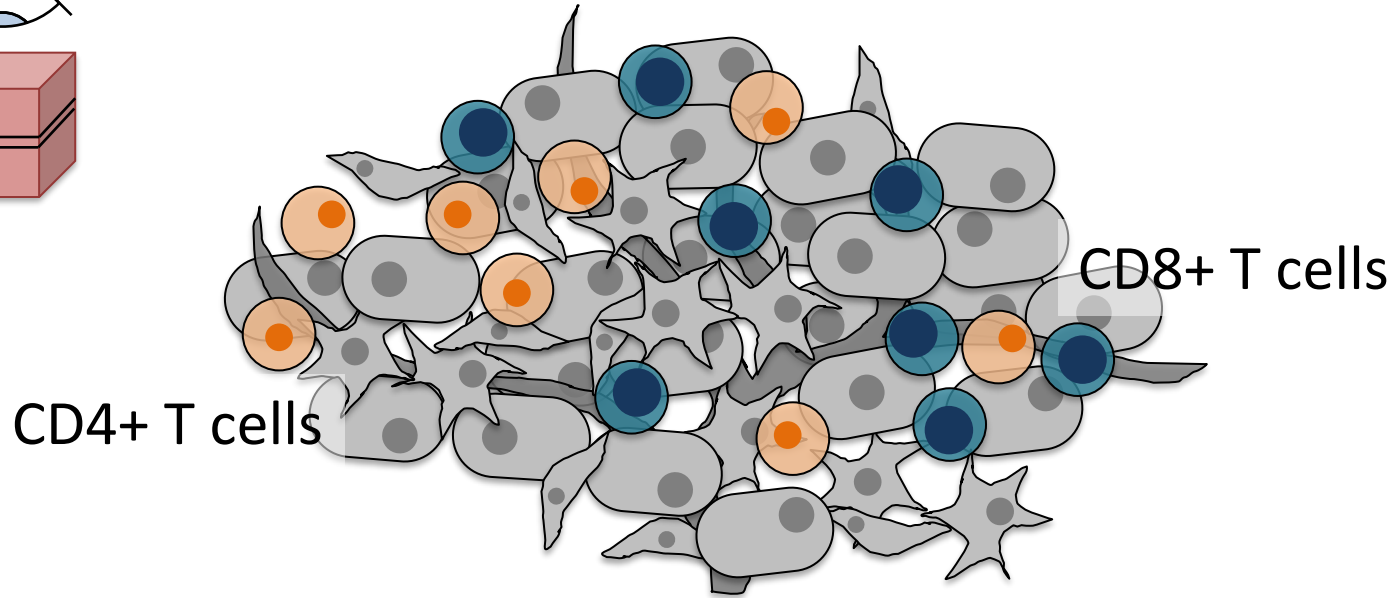
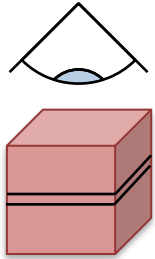
- Cell segmentation doesn't (generally) allow border overlap



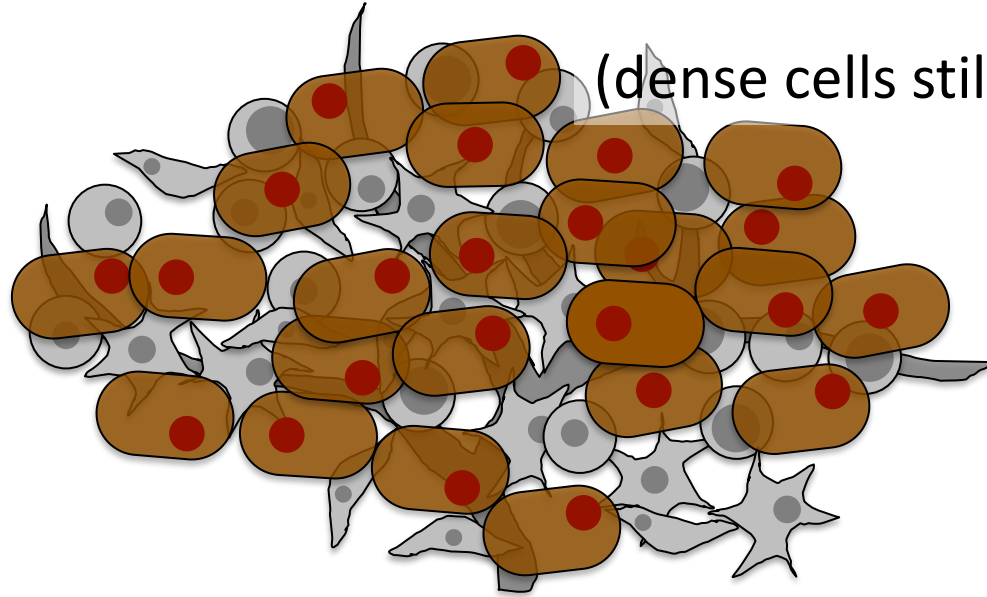
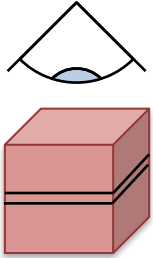
- It's definitive

- Protein expression is quantified within border
- Cell coordinates are (generally) based on cell centres
 - Distances are not based on borders

Segment cell types separately

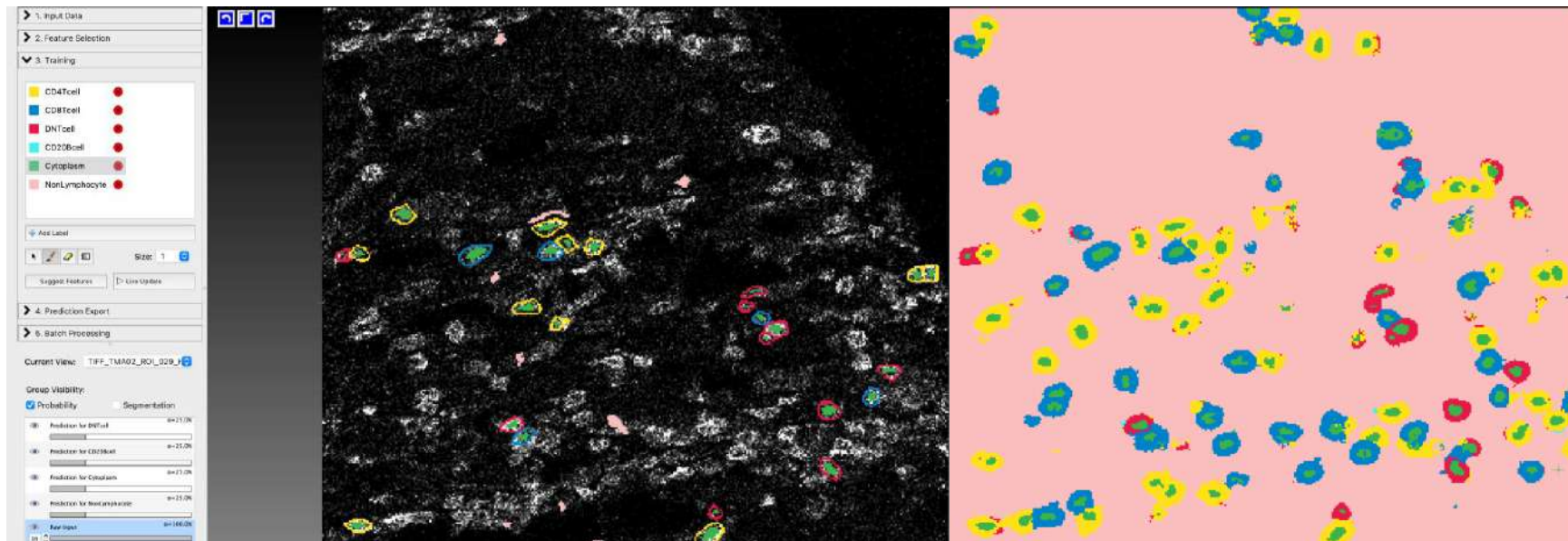


Segment cell types separately



(dense cells still an issue)

Lymphocyte segmentation



'ilastik' software, Berg et al., 2019 (*Nat Methods*)

Limitations

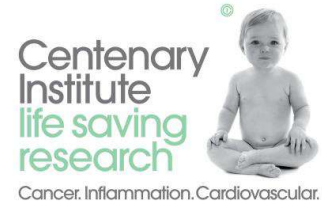
- It is possible cells are being counted twice
 - May also miss “unknown” cells
- Based on your data and input
- **Huge time sink...**
 - Lymphocytes
 - CD45+ non-lymphocytes
 - Stromal cells
 - Hepatocytes

What's the point!?

- Only need to do this once...
- Do your findings match the biology?
- Have others found the same thing?
- What other experiments can be done?

Special thanks to...

- Cosi Santhakumar
- Angela Ferguson
- Geoff McCaughan
- Mainthan Palendira
- Ken Liu
- Joo Shin
- Thomas Ashhurst
- Givanna Putri
- Joan Krefft bequest
- Sydney Cytometry
- ACS



f.marsh-wakefield@centenary.org.au