

Clinical Biomarkers and Therapy Candidates via Spatial Analysis

Alex Xu

Spatial Biology Congress



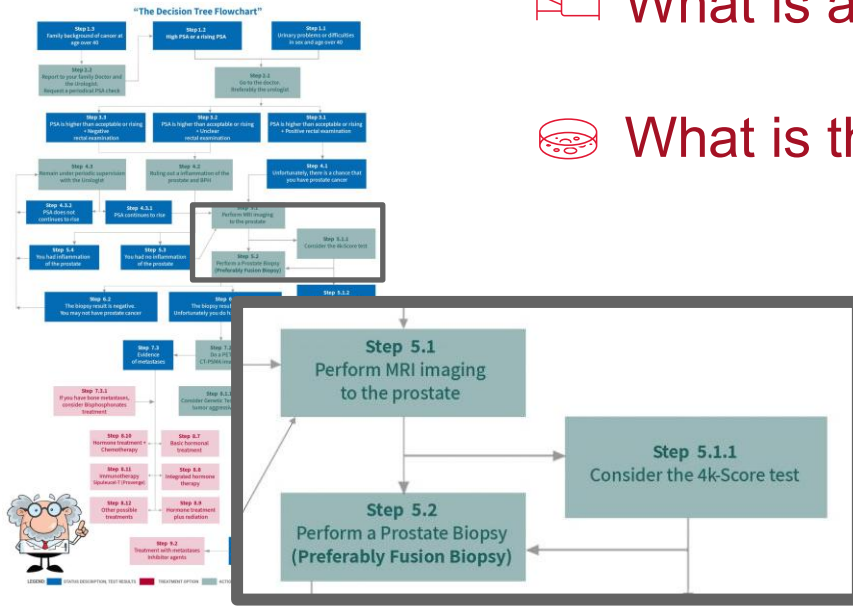
Clinical Decision Making and Motivations



What is a patient's diagnosis (risk)?



What is the molecular basis for the disease?



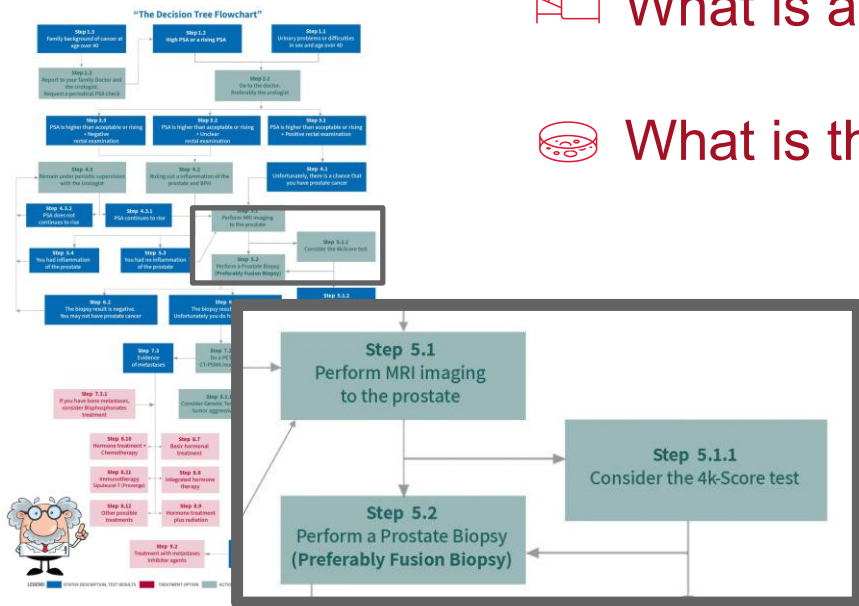
Clinical Decision Making and Motivations



What is a patient's diagnosis (risk)?



What is the molecular basis for the disease?



Is there a concise measurement that captures risk or biology?



Empirical

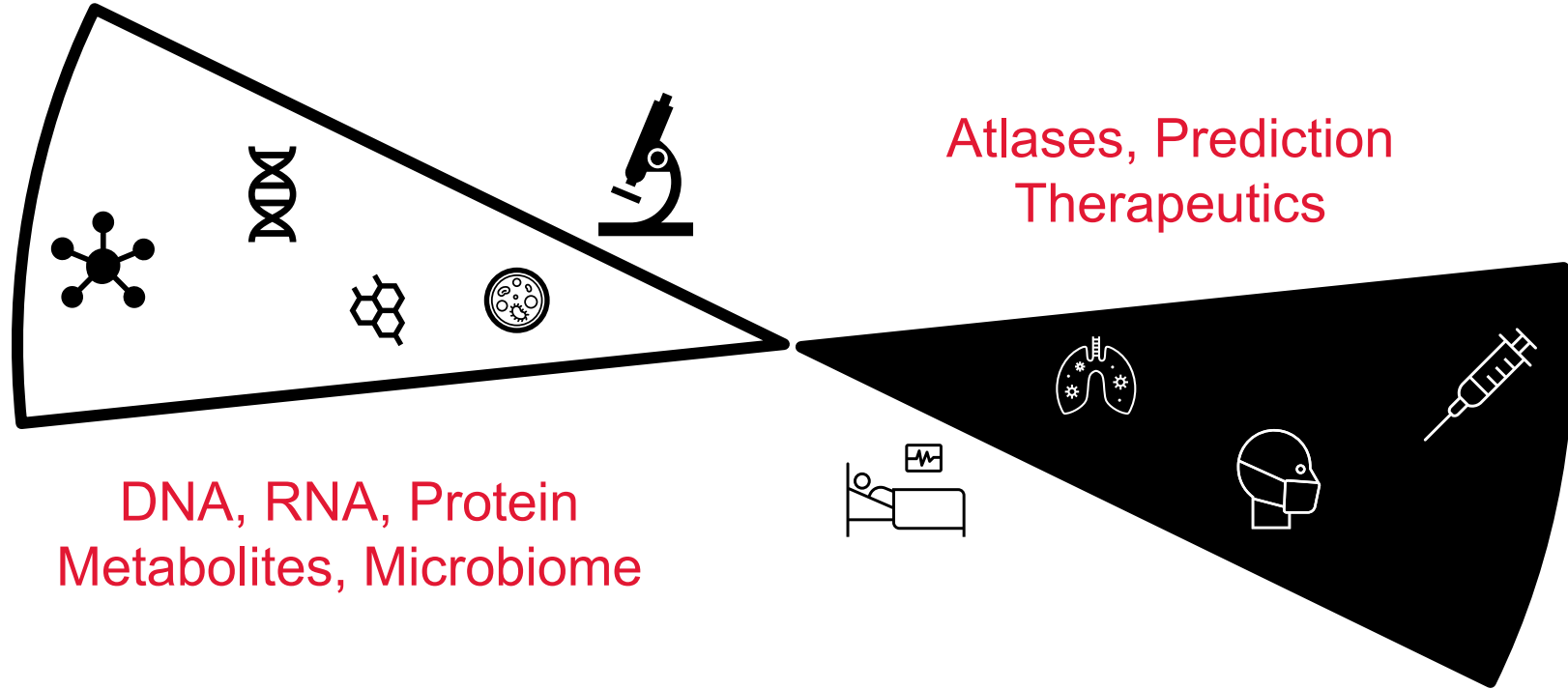


Hypothesis-Driven

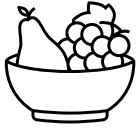
a.k.a. a Biomarker?



Spatial Biology Methods and Applications



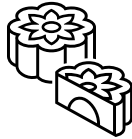
A Simple Analogy for Biomarkers



Do I want to eat this fruit?

A Simple Analogy for Biomarkers

Smoothie-salad-fruit cake analogy



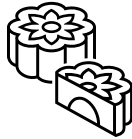
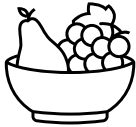
Bulk mixed fruits
Single mixed fruits
Spatial mixed fruits

Do I want to eat this fruit?



A Simple Analogy for Biomarkers

Smoothie-salad-fruit cake analogy



Bulk mixed fruits
Single mixed fruits
Spatial mixed fruits

Do I want to eat this fruit?

Goopy cake analogy



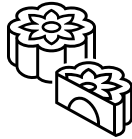
Pineapple-y cherries?
Cake-y cherries?

How does spatial change
the flavor of fruit?



A Simple Analogy for Biomarkers

Smoothie-salad-fruit cake analogy



Bulk mixed fruits
Single mixed fruits
Spatial mixed fruits

Do I want to eat this fruit?

Goosey cake analogy



Unpublished data



Pineapple-y cherries?
Cake-y cherries?


How does spatial change
the flavor of fruit?

Acknowledgment

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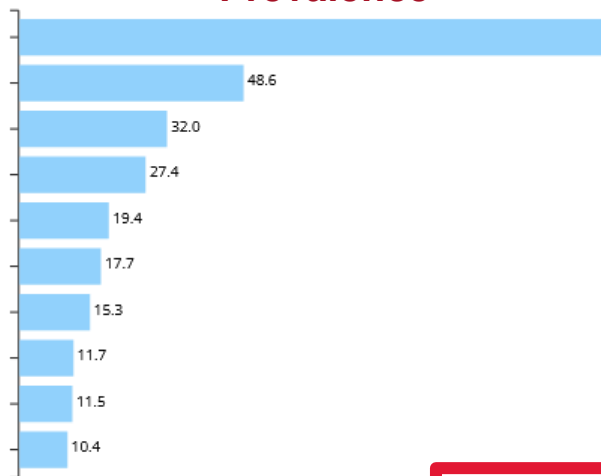
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Ovarian Cancer Burden and Severity

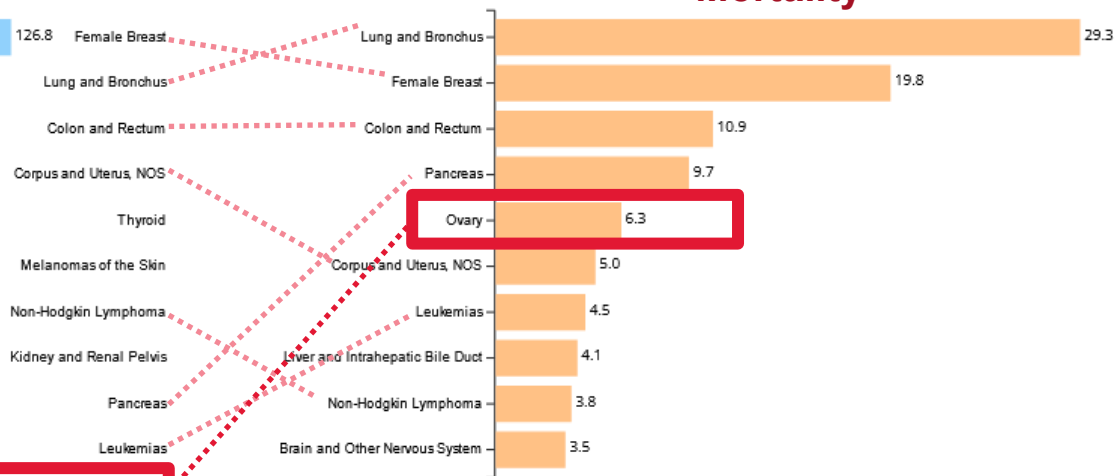
Ovarian cancer is a leading cause of cancer death in women

Prevalence



~10 Ovary

Mortality



Late Diagnosis

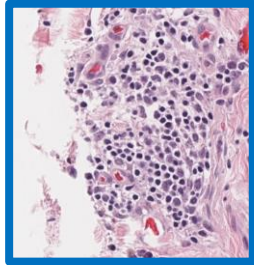
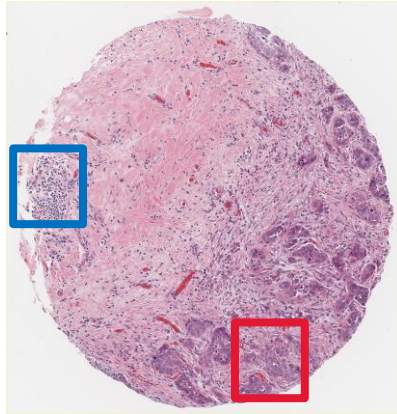
Tumor Tissue Composition is Linked to Outcomes

Tumor, stroma, and immune cells

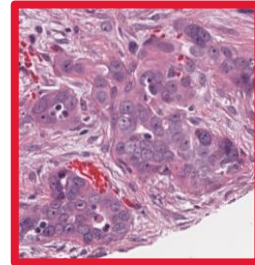


Tumor Tissue Composition is Linked to Outcomes

Tumor, stroma, and immune cells



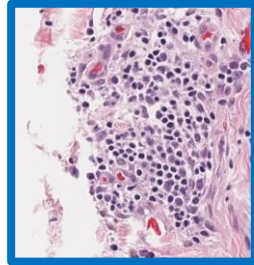
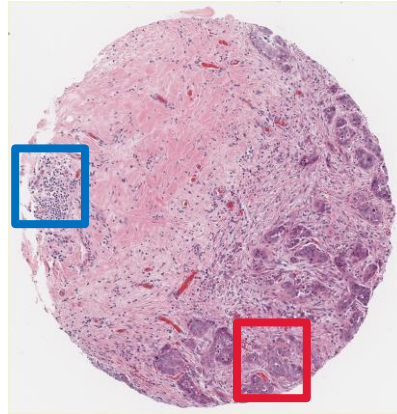
Immune Cells



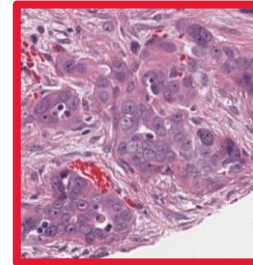
Tumor +
Fibroblasts

Tumor Tissue Composition is Linked to Outcomes

Tumor, stroma, and immune cells

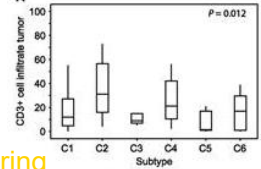


Immune Cells

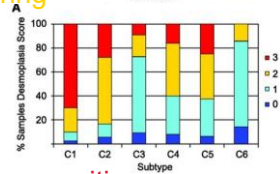


Tumor +
Fibroblasts

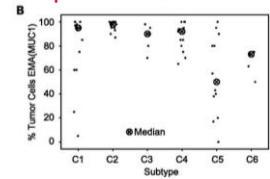
Immune infiltrate



Stromal scoring

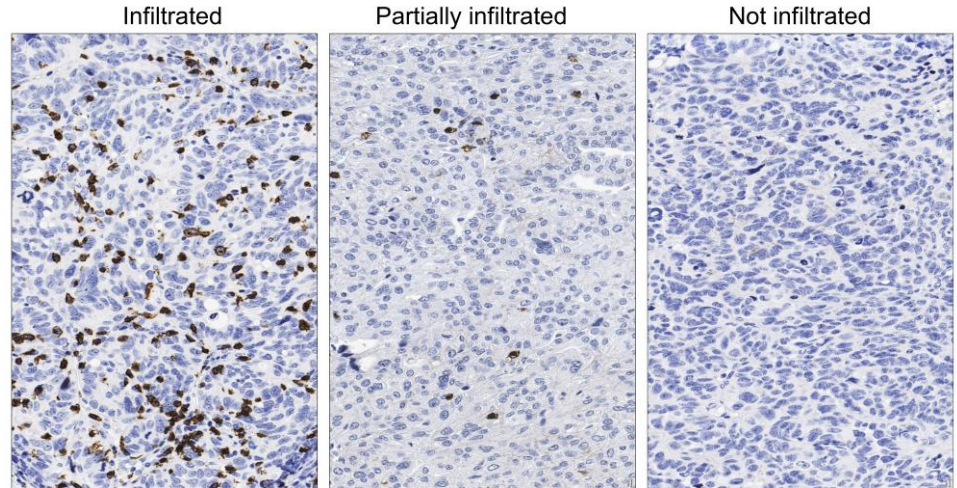
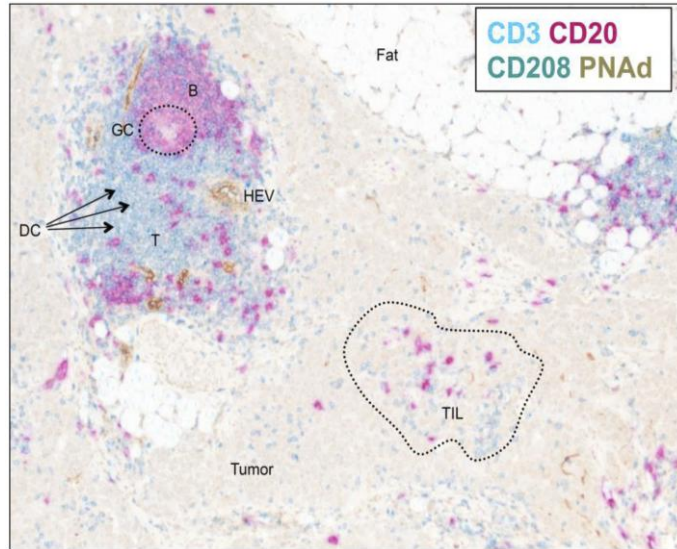


Tumor cell composition

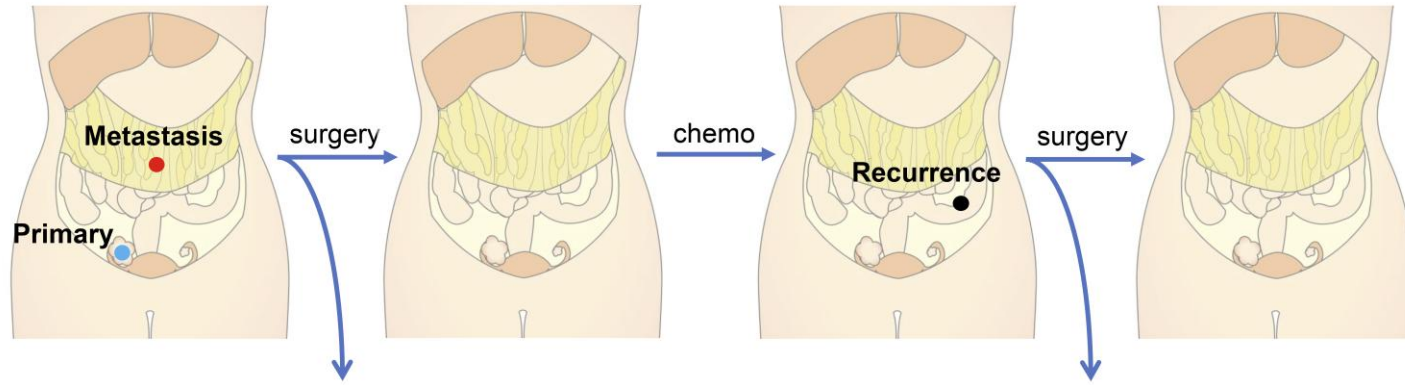


Measuring the Tumor Microenvironment is Imprecise

Clinical descriptors are semi-quantitative

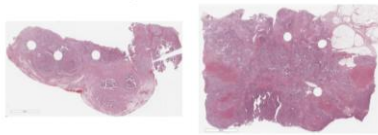


Recurrent Ovarian Cancer Cohort



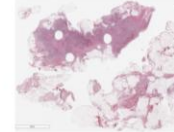
N = 42

● Primary ● Metastasis



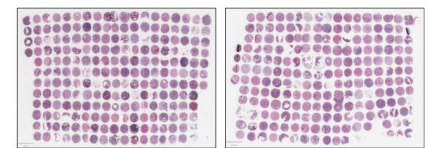
chemonaive

● Recurrence

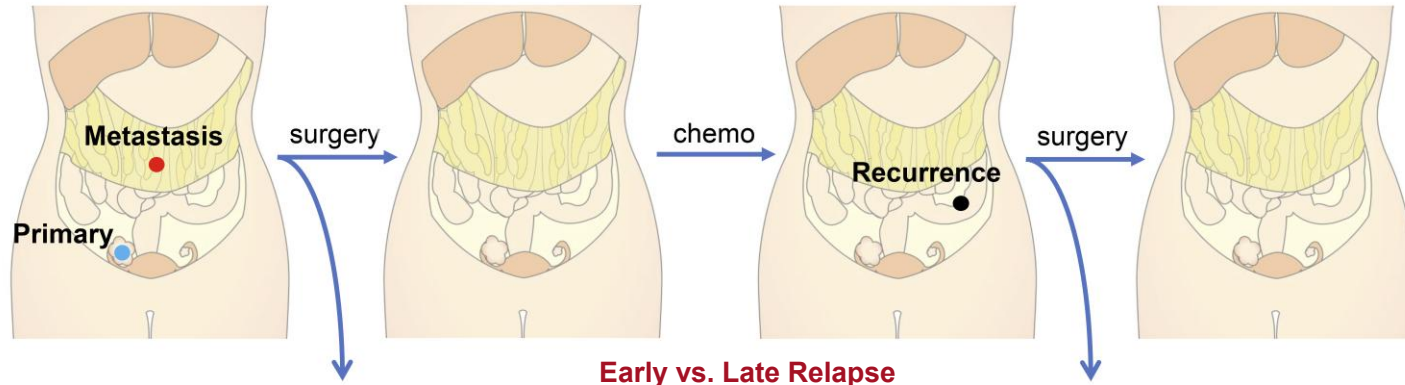


post-chemo

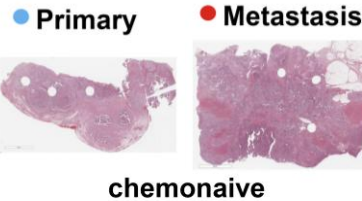
Tissue Microarray



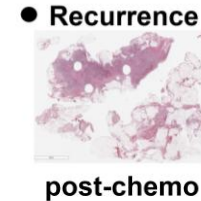
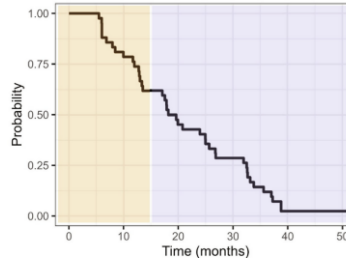
Recurrent Ovarian Cancer Cohort



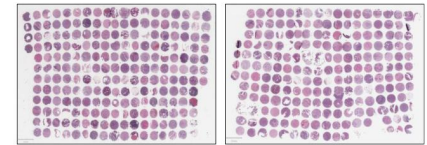
N = 42



Early vs. Late Relapse

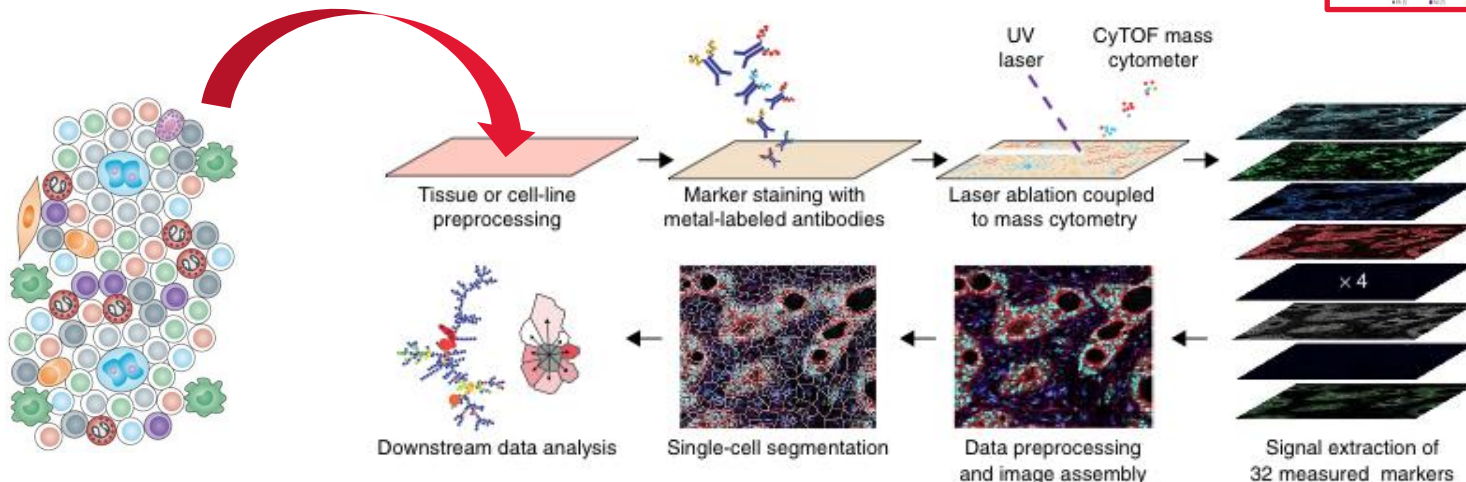
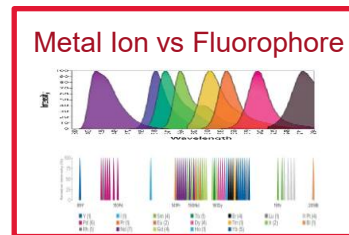


Tissue Microarray



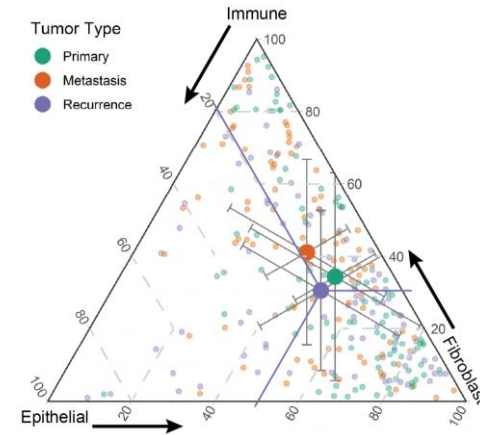
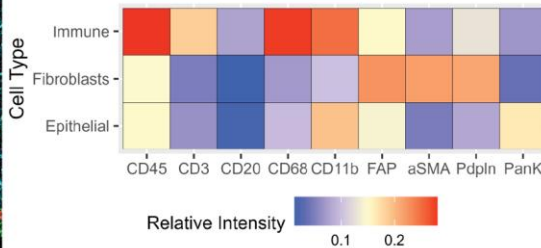
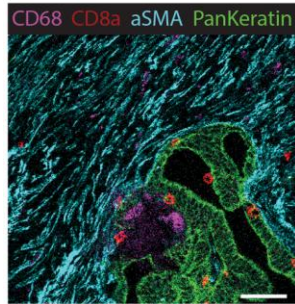
Highly Multiplexed Spatial Analysis of TME

Imaging Mass Cytometry profiles ~40 proteins at 1 μm resolution



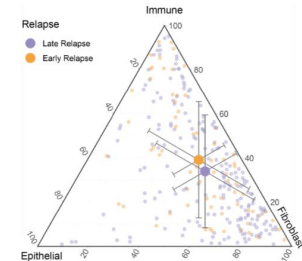
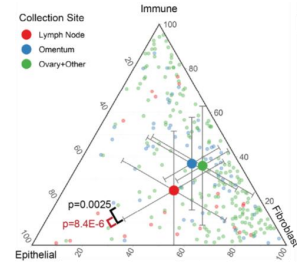
Tumor Heterogeneity

Tumor + Stroma + Immune Composition



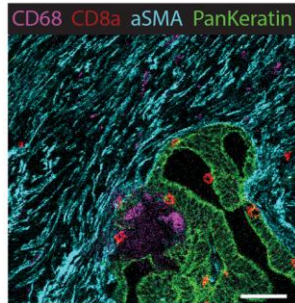
No significant differences

Observed more immune in recurrence

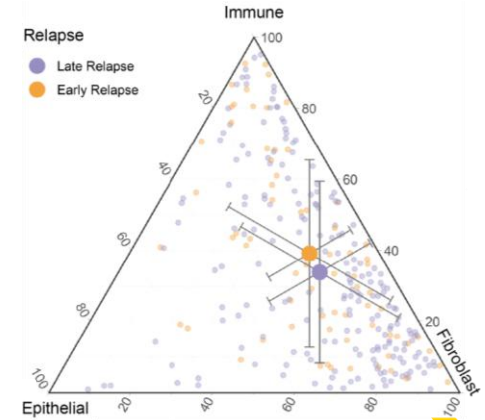
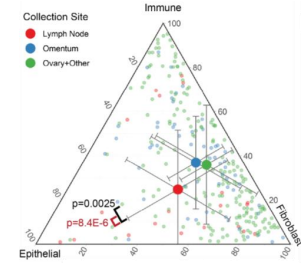
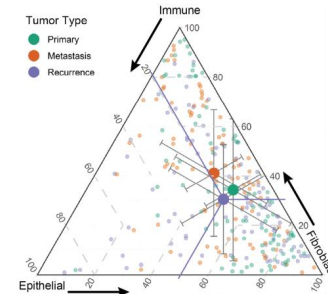
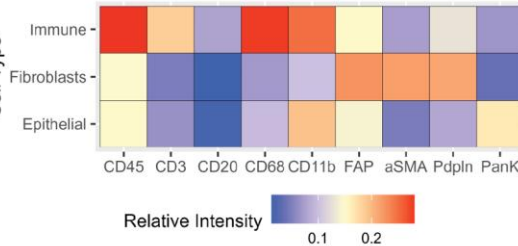


Tumor Heterogeneity

Tumor + Stroma + Immune Composition



Cell Type

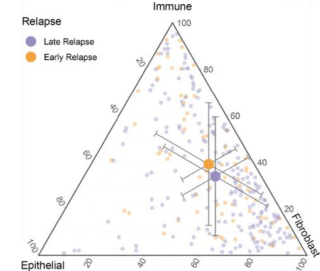
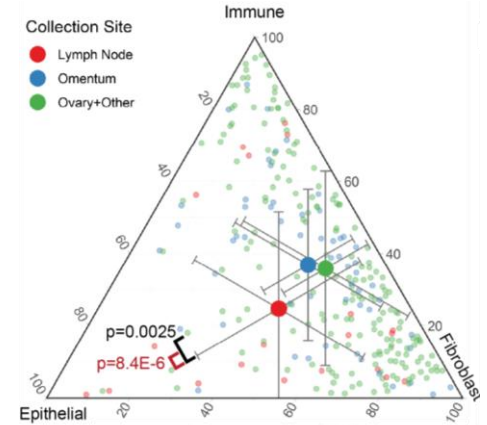
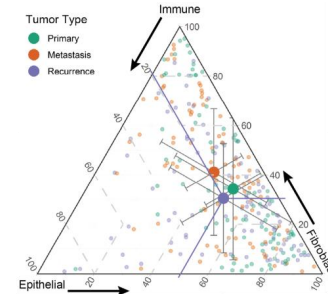
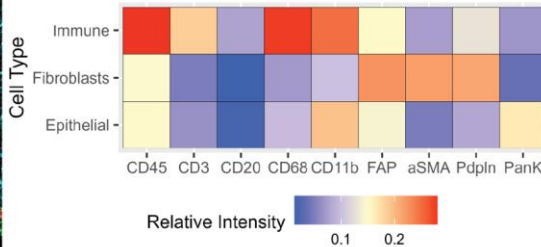
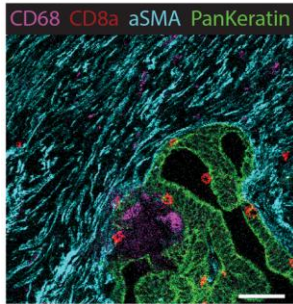


No significant differences

Observed less tumor in early relapse

Tumor Heterogeneity

Tumor + Stroma + Immune Composition

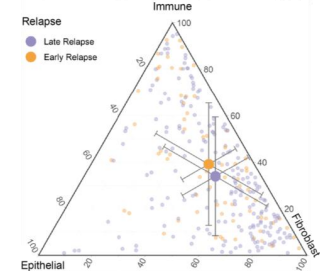
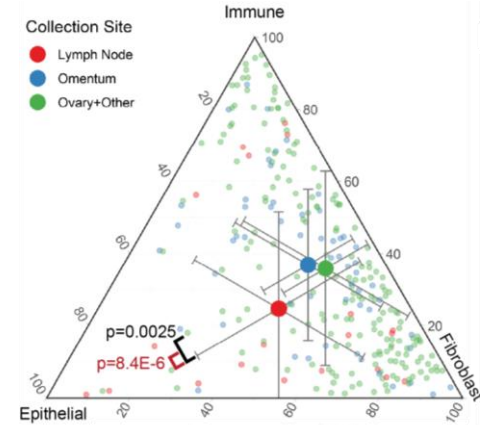
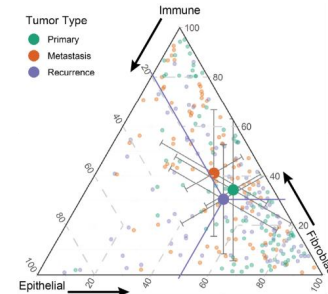


Lymph node metastasis/recurrence



Tumor Heterogeneity

Tumor + Stroma + Immune Composition



Lymph node metastasis/recurrence



Tumor Heterogeneity

Tumor + Stroma + Immune Composition

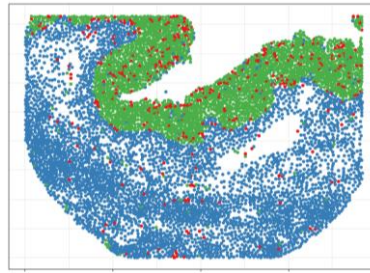
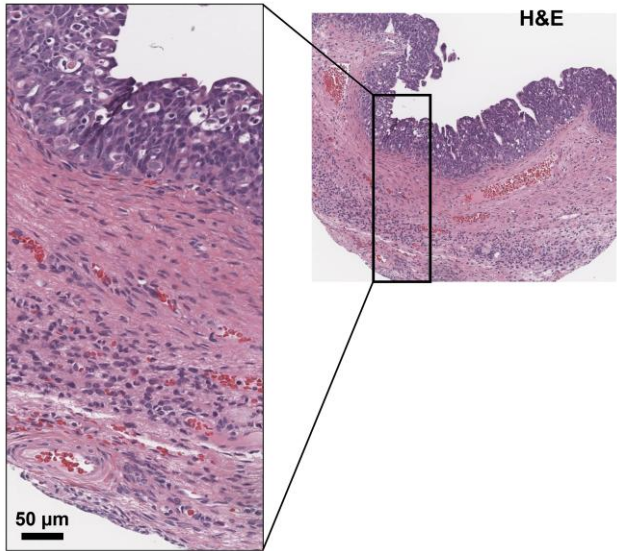


Spatial vs bulk

Immune/Stroma/Tumor Distributions

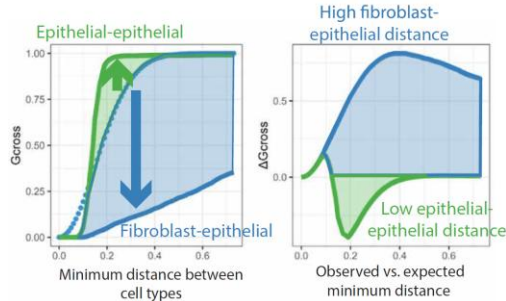
Describe the TME

Quantifying cell-cell contacts – bulk Gcross

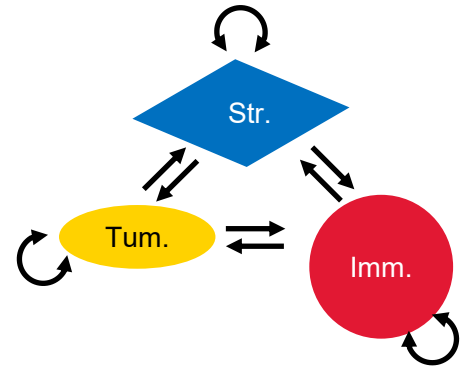


Cell Type

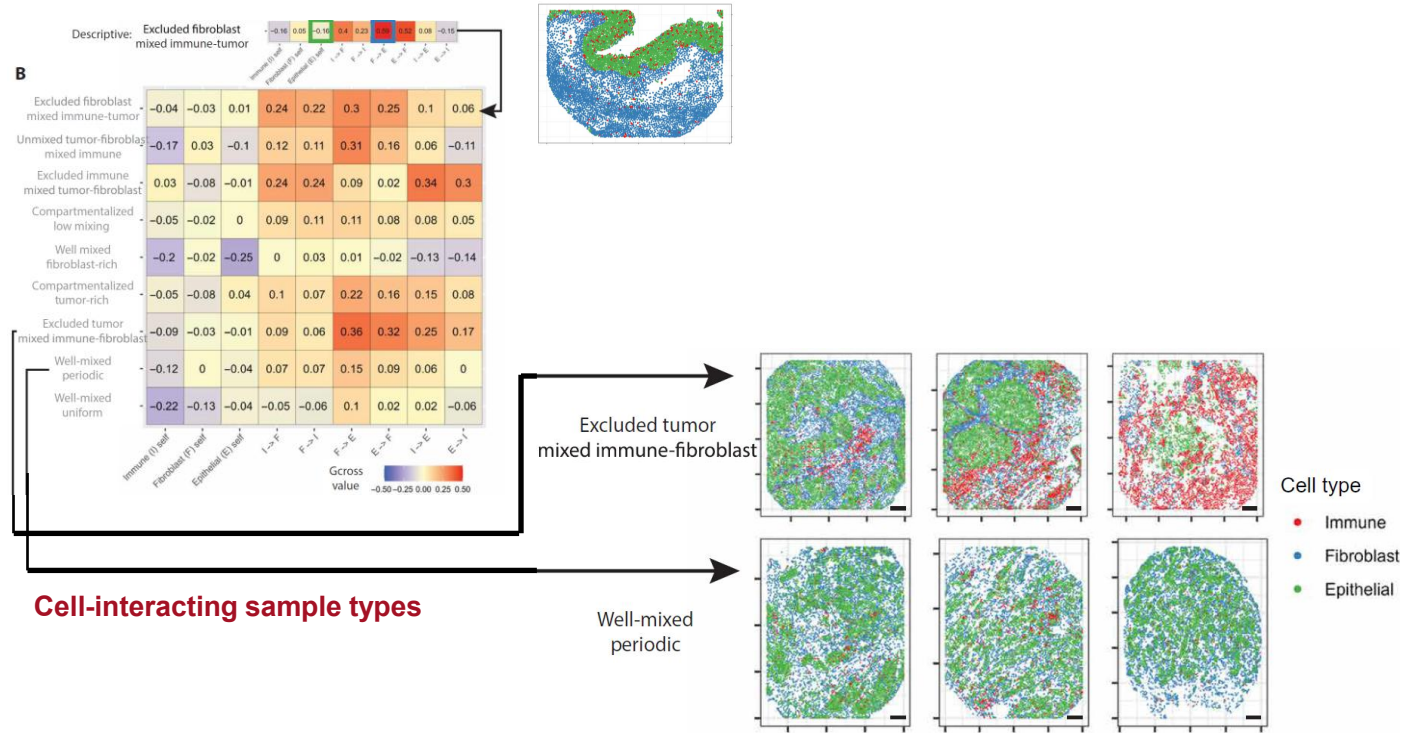
- Immune
- Fibroblasts
- Epithelial



For each sample:
Interaction score
between cell types



Distribution Carries More Information



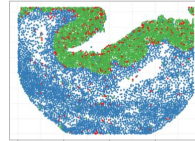
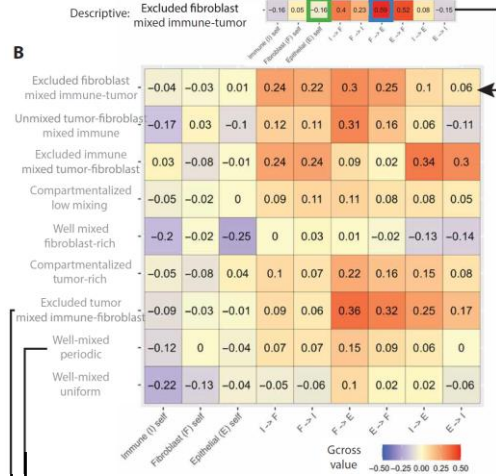
Distribution Carries More Information

Cell-proportion sample types

Fibroblast hi	9.91	30.5	59.59	6.31	2.75	4.74	5.16	3.16	25.02	2.49	14.42	3.35	5.14	1.21	1.21
Tumor-mid	10.72	7.08	42.2	8.05	3.44	5.5	1.71	9.88	91.5	5.35	7.16	5.13	1.82	1.35	1.26
Fibroblast hi	10.72	7.08	42.2	8.05	3.44	5.5	1.71	9.88	91.5	5.35	7.16	5.13	1.82	1.35	1.26
Triple positive	24.2	62.11	13.89	0.5	4.76	12.87	7.59	1.34	1.53	1.65	1.18	4.83	0.86	0.12	0.12
Tumor-hi	45.58	36.76	27.64	6.37	15.08	20.38	6.73	3.9	11.99	3.12	2.26	4.52	0.71	0.19	0.19
Immune-hi	9.98	76.9	18.11	0.32	0.6	2.37	2.01	1.29	1.08	3.04	1.54	5.37	2.63	9.2	9.2
Tumor-hi	3.5	49.87	4.83	3.24	0.32	2.13	1.08	0.33	1.98	0.85	0.86	1.5	0.36	0.94	0.94
Fibroblast hi	13.51	14.96	72.52	2.46	3.86	4.96	1.91	13.68	13.78	12.14	1.84	27.91	0.51	0.2	0.2
Tumor-hi	12.33	78.15	9.53	0.07	2.36	6.68	3.07	0.94	2.49	1.36	0.5	1.84	0.68	0.13	0.13
Tumor-hi	7.13	40.12	33.76	0.08	1.14	5.3	2.67	3.52	7.25	4.36	3.86	7.81	3.69	0.71	0.71
Fibroblast-mid	12.26	42.96	44.78	0.19	1.53	8.35	2.24	3.02	6.11	6.76	7.34	10.69	6.64	1.44	1.44
Fibroblast-mid	12.26	42.96	44.78	0.19	1.53	8.35	2.24	3.02	6.11	6.76	7.34	10.69	6.64	1.44	1.44

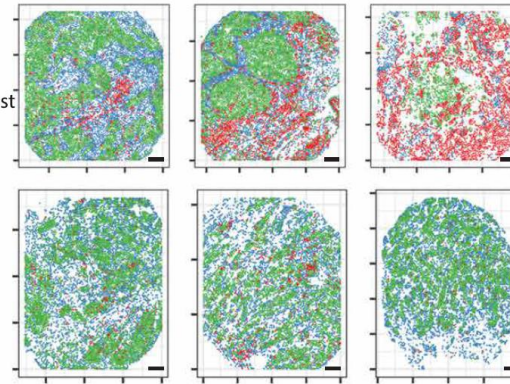
Cell type

- Immune
- Fibroblast
- Epithelial



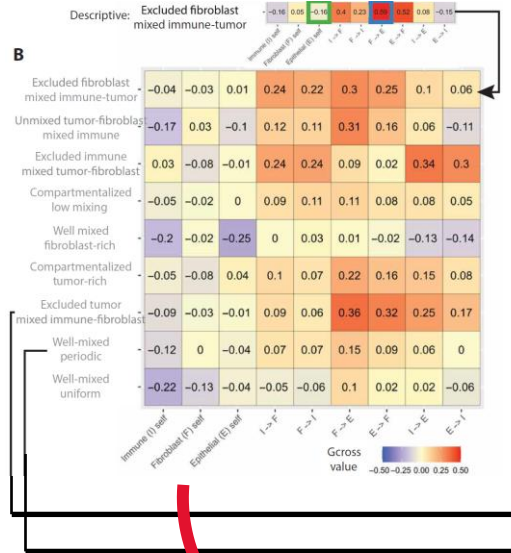
Excluded tumor mixed immune-fibroblast

Well-mixed periodic

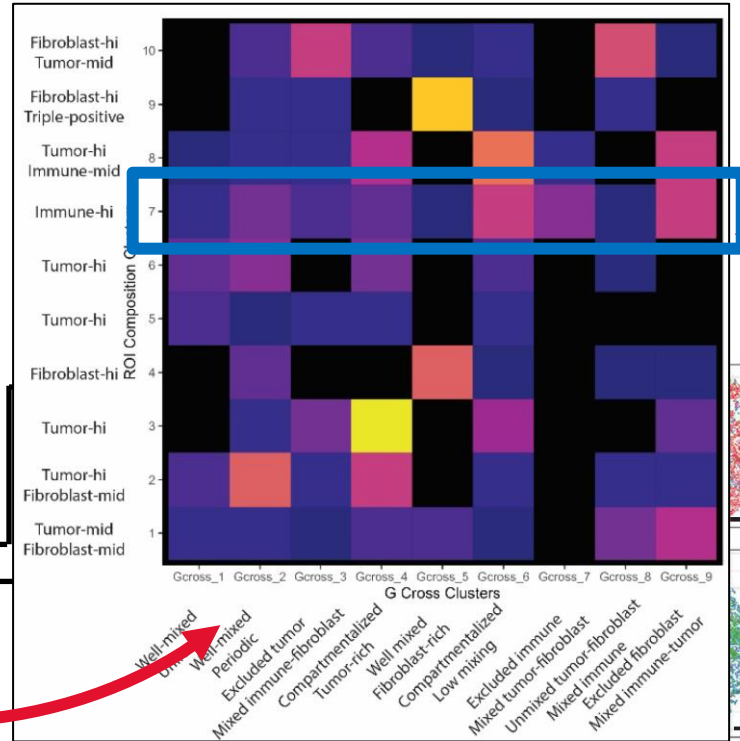


Cell-interacting sample types

Distribution Carries More Information



Cell-interacting sample types



Cell-proportion sample types

Fibroblast-hi	0.91	0.05	0.09	0.31	2.79	4.74	5.16	3.16	25.02	2.49	14.42	0.05	0.14	1.21	1.21
Tumor-mid	10.72	7.08	42.2	0.05	3.44	5.9	1.71	9.88	91.5	5.35	7.16	5.13	1.82	1.35	1.26
Fibroblast-hi	24.2	62.11	13.69	0.3	4.76	12.87	7.59	1.34	1.53	1.65	1.18	0.83	0.86	0.12	0.12
Triple-positive	45.58	26.76	27.64	0.37	15.06	20.38	8.73	3.9	11.99	3.12	2.26	4.52	0.71	0.19	0.16
Tumor-hi	4.98	76.9	18.11	0.02	0.6	2.37	2.01	1.29	1.08	3.04	1.54	5.37	2.63	9.2	3.2
Immune-hi	3.5	49.87	4.83	3.94	0.32	2.13	1.08	0.33	1.95	0.85	0.86	1.5	0.36	0.94	0.94
Tumor-hi	13.51	14.96	72.02	2.69	2.86	4.96	1.91	13.68	13.78	12.14	1.84	27.91	0.51	0.2	0.2
Fibroblast-hi	12.33	78.15	9.53	0.07	2.96	6.68	3.07	0.94	2.49	1.36	0.5	1.84	0.68	0.13	0.13
Tumor-hi	7.13	40.12	33.76	0.08	1.14	9.3	2.67	3.52	7.25	4.98	3.86	7.81	3.02	0.71	0.71
Fibroblast-mid	12.26	42.96	44.78	0.19	1.53	8.35	2.24	3.02	6.11	6.76	7.34	10.69	6.64	1.44	1.44
Fibroblast-mid															

Cell type

- Immune
- Fibroblast
- Epithelial

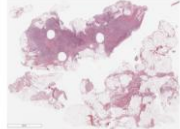
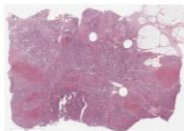
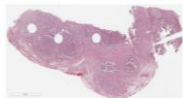
No significant associations with early relapse



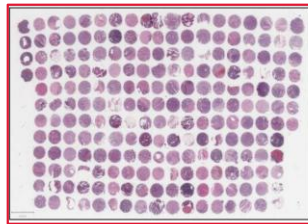
Tumor Microarrays are Curated

Representative Regions Selected

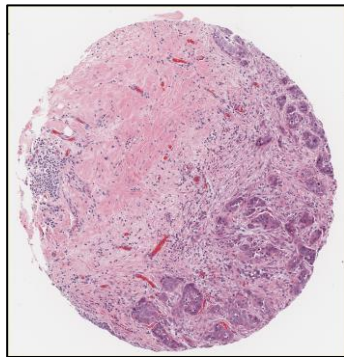
● Primary ● Metastasis ● Recurrence



Representative Regions



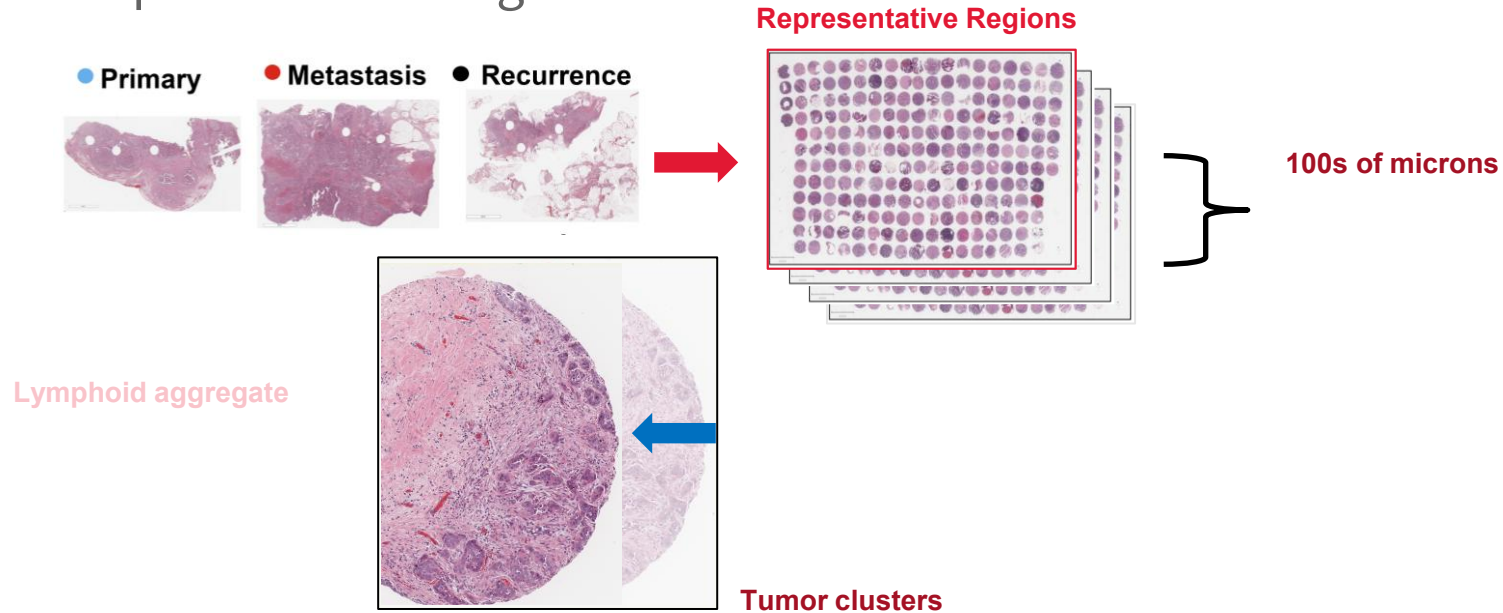
Lymphoid aggregate



Tumor clusters

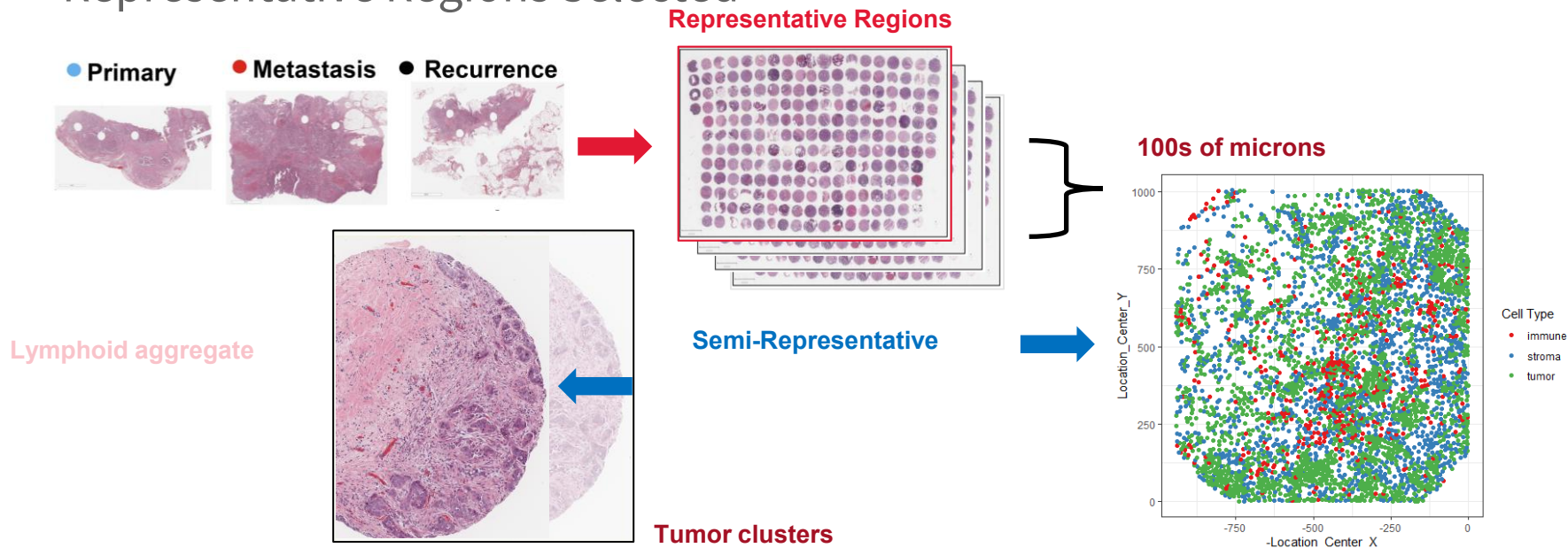
Tumor Microarrays are Curated

Representative Regions Selected



Tumor Microarrays are Curated but not Static

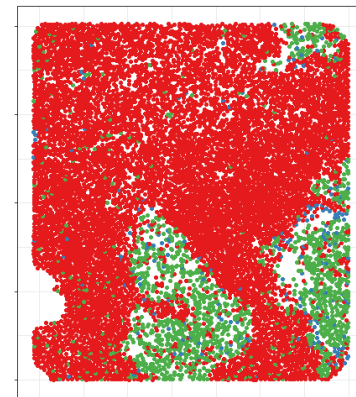
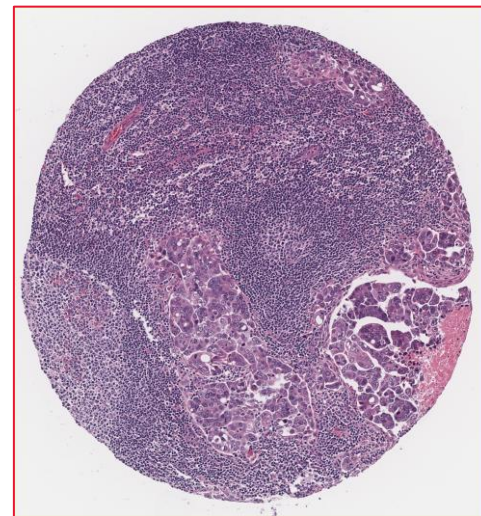
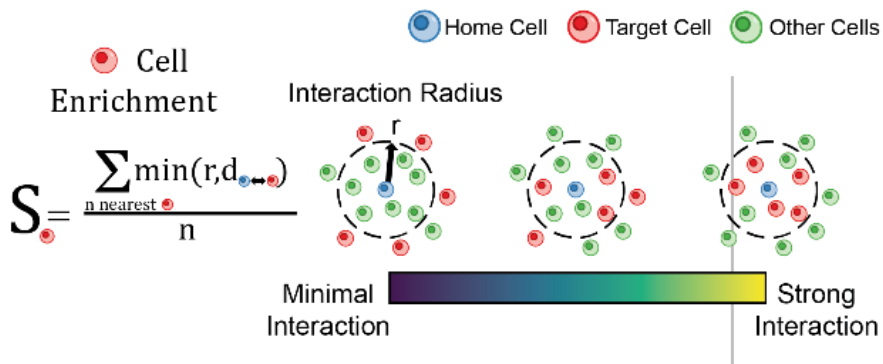
Representative Regions Selected



Cell-Type Specific Spatial Enrichments

Describe the TME

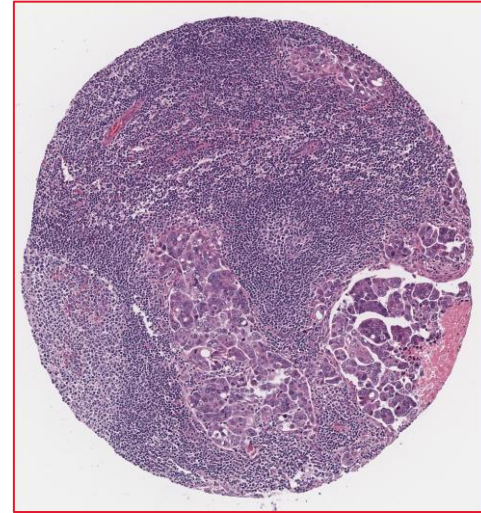
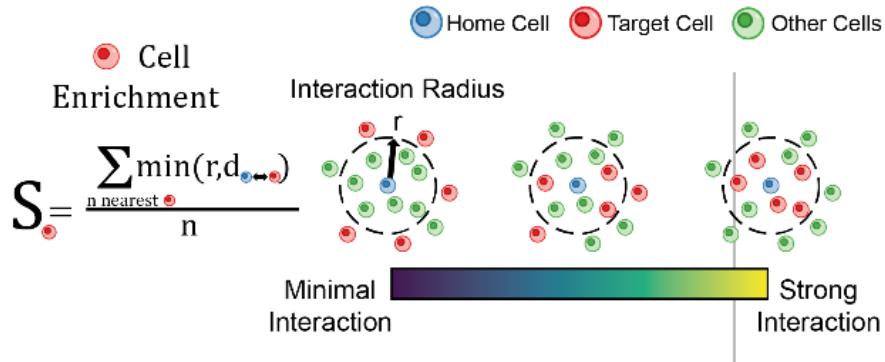
Spatial enrichment score \rightarrow local microenvironment



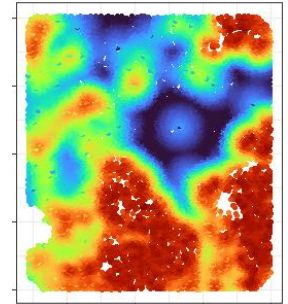
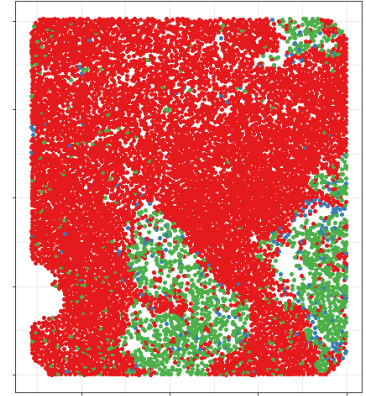
Immune-surrounded tumor

Cell-Type Specific Spatial Enrichments Describe the TME

Spatial enrichment score \rightarrow local microenvironment

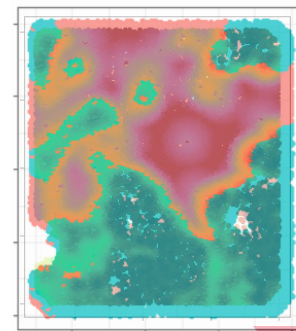
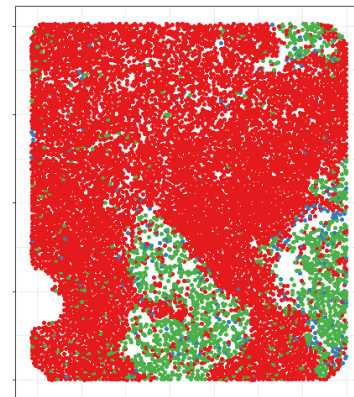
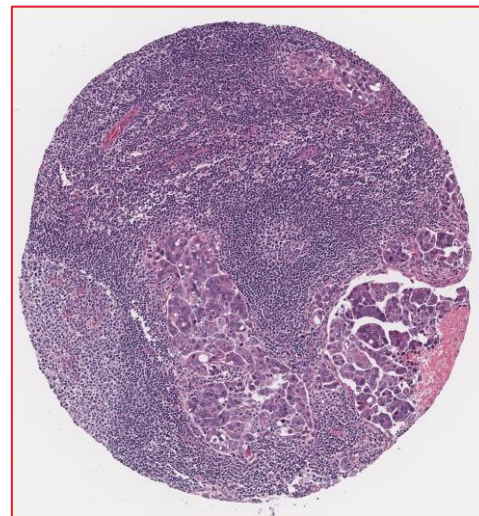
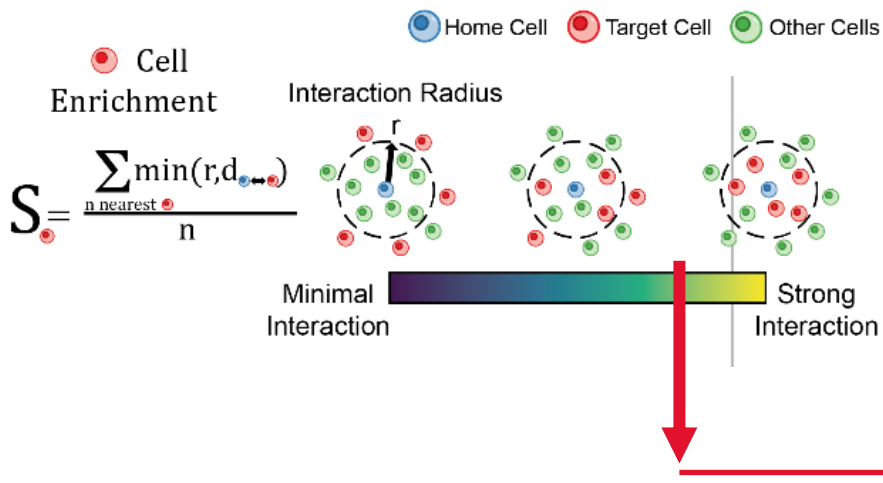


Tumor enrichment



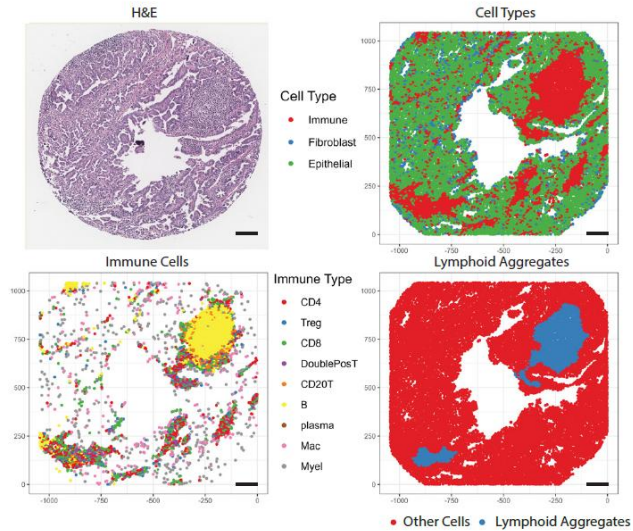
Cell-Type Specific Spatial Enrichments Describe the TME

Spatial enrichment score \rightarrow local microenvironment



Spatial Enrichment Analysis

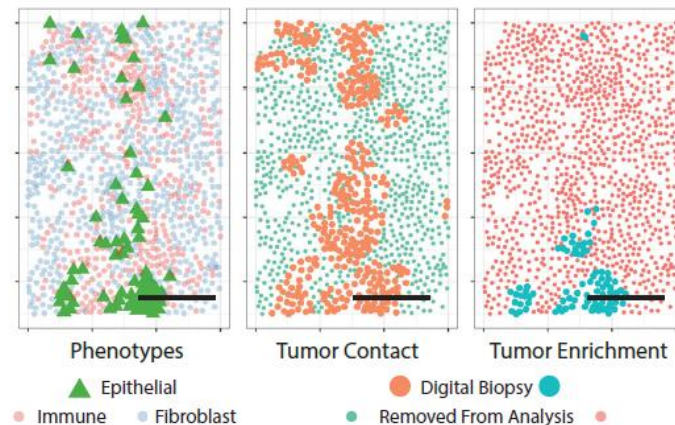
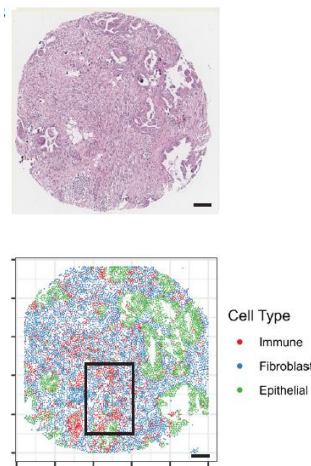
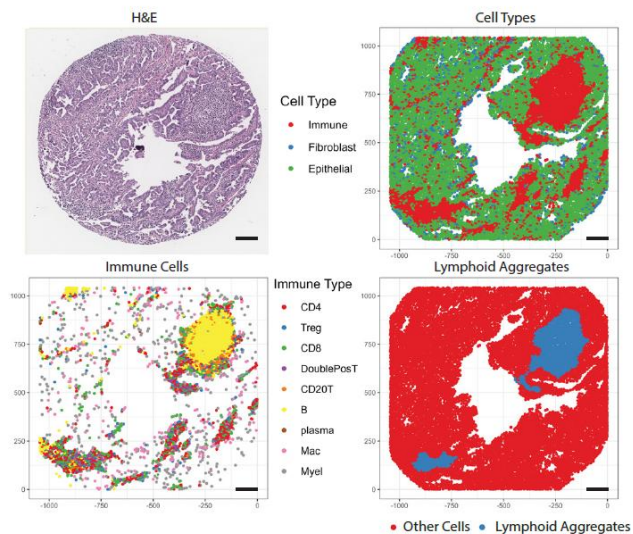
Lymphoid Aggregates



Spatial Enrichment Analysis

Lymphoid Aggregates

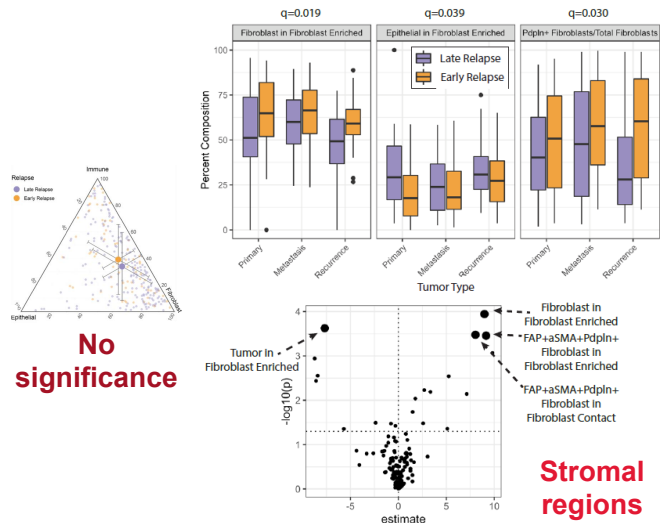
Context-specific niches (Digital biopsy)



Spatial Predictors of Early Relapse

Statistical Associations between early/late relapsers

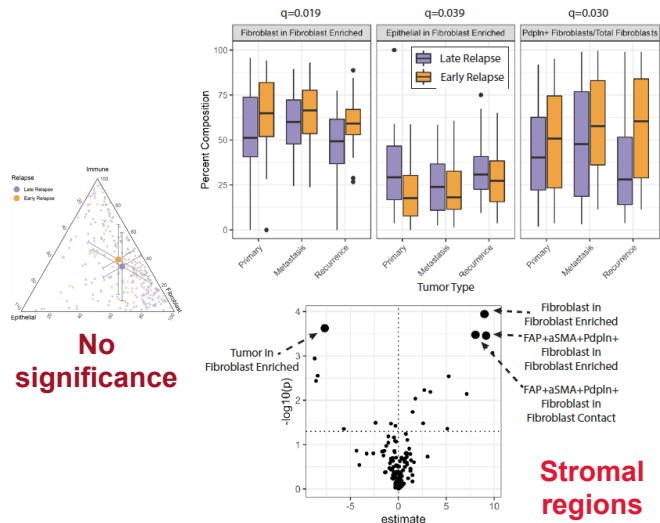
Spatially-restricted cell proportions



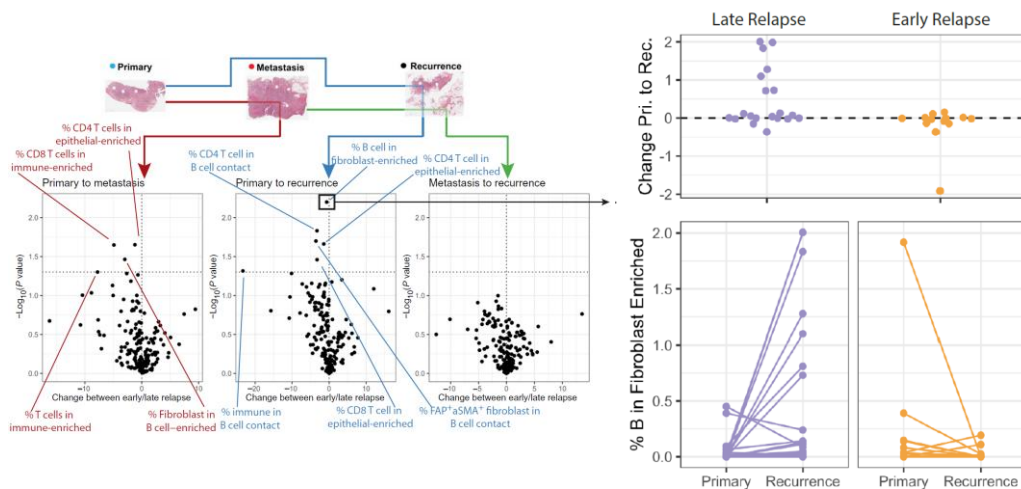
Spatial Predictors of Early Relapse

Statistical Associations between early/late relapsers

Spatially-restricted cell proportions



Spatio-temporal associations with early relapse

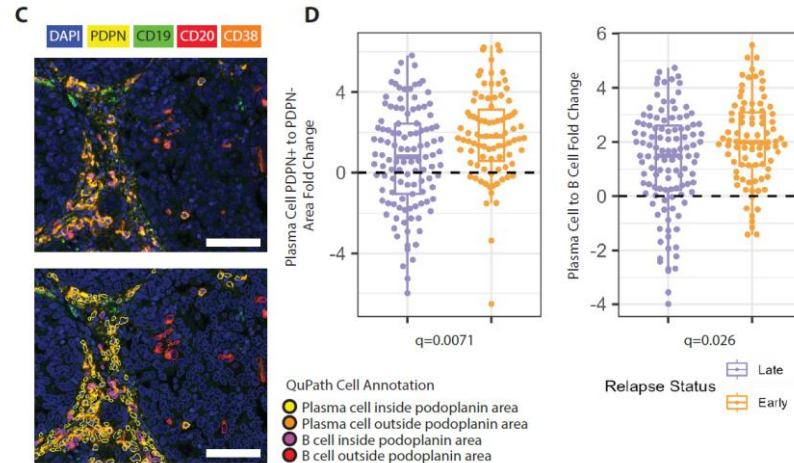
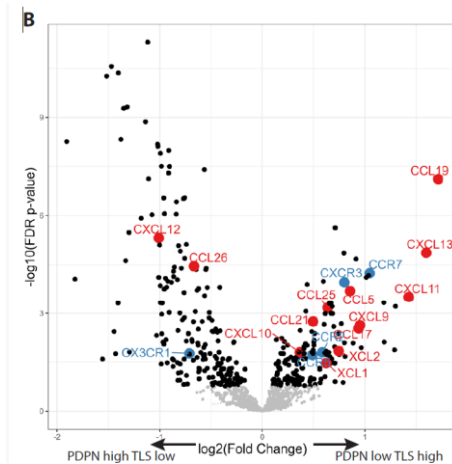


Follow ups

Alternative omics follow up to spatially significant B cell changes

Visium gene expression

Multiplex IF

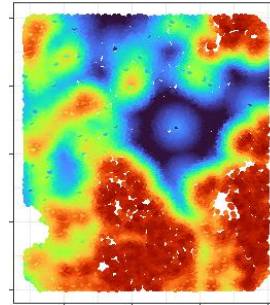
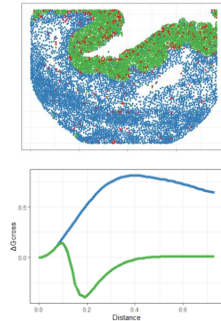
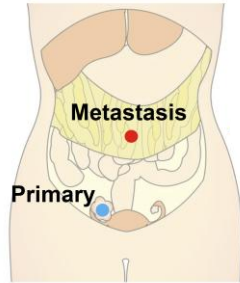


Conclusions

42 patients with matched samples over tumor progression

Qualitative eye-test vs quantitative

Digitally isolating specific sample regions reveals significant patterns



Other things:

- Predictors of early relapse
- IMC/H&E Concordance
- Unifying hypothesis for B/plasma cells

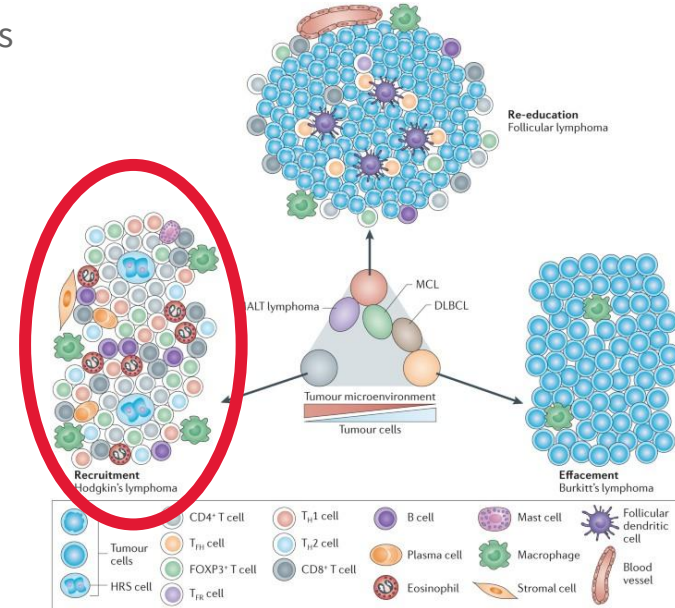


Xu et al., Science Advances, 2024

The Hodgkins Lymphoma (HL) Tumor Microenvironment (TME) is immune-rich

Immune-rich tumor microenvironments (TME) of B-cell Lymphomas

Hodgkin's: Rare CD30+ tumor cells



Nature Reviews | Cancer

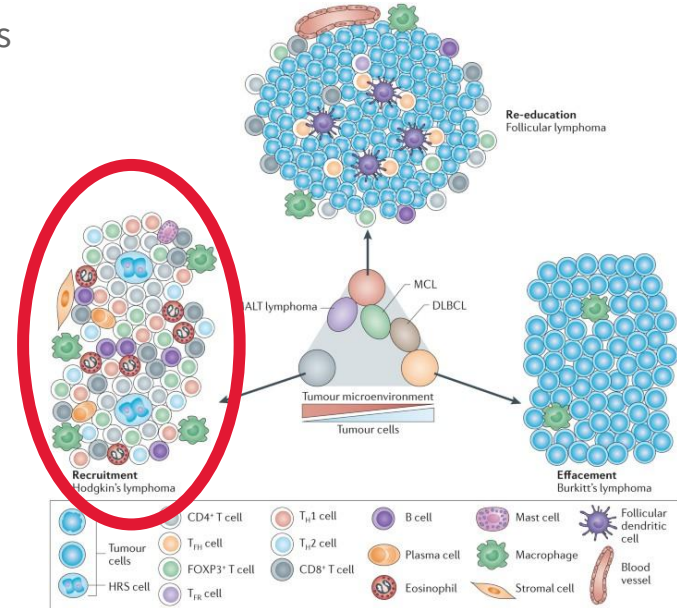
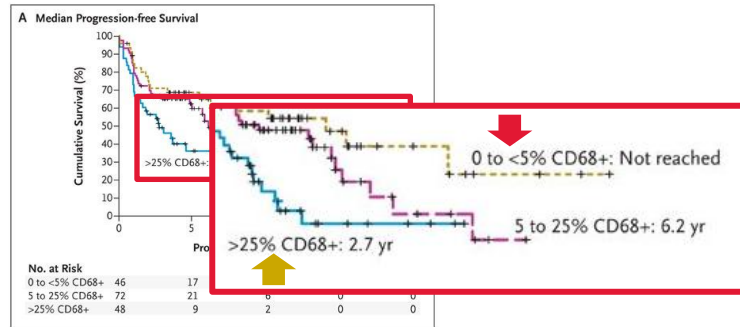
TME Elements are associated with clinical outcomes

Immune-rich tumor microenvironments (TME) of B-cell Lymphomas

Hodgkin's: Rare CD30+ tumor cells

Stratifying patients for prognosis, outcomes

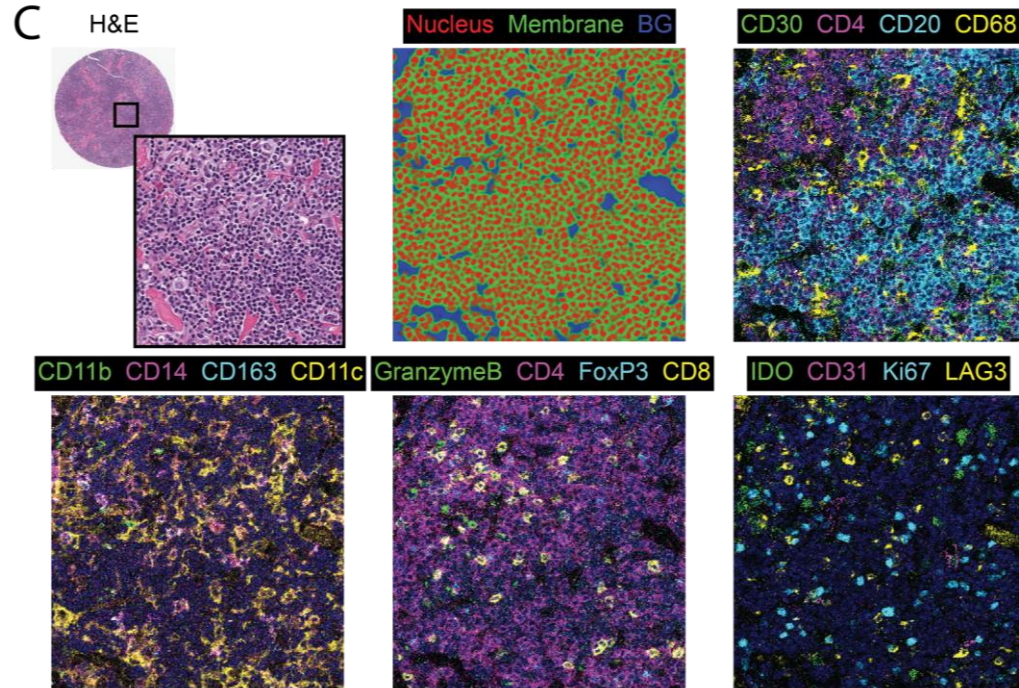
HL: CD68+ macrophages, etc.



Nature Reviews | Cancer

HL TME is densely populated with immune cells

Segmentation
Sparse tumor cells (CD30)
Myeloid/Lymphoid infiltrate

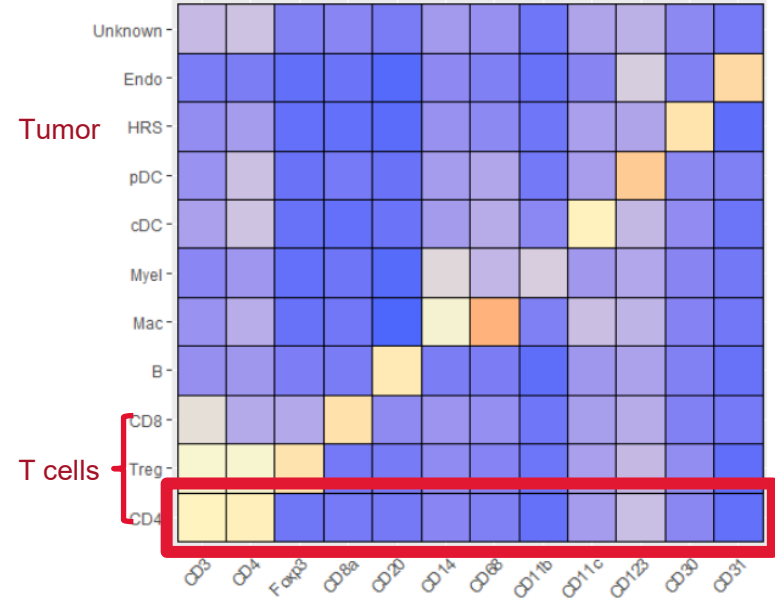
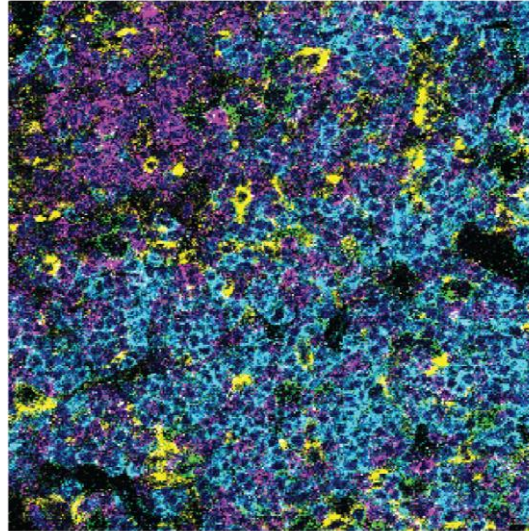


Phenotyping identifies 10 major cell types

Sparse tumor cells (CD30), immune rich – T cells (CD4, CD8), Macrophages (CD68)

10 major phenotypes

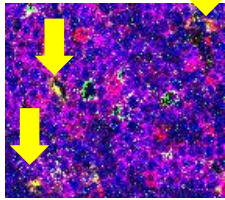
CD30 CD4 CD20 CD68



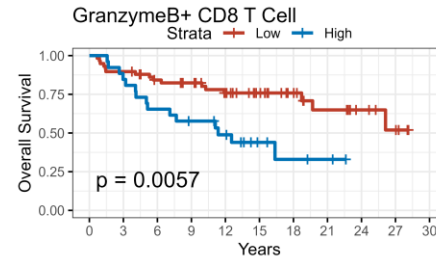
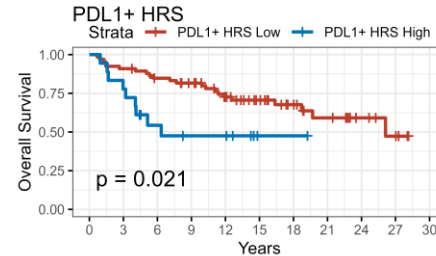
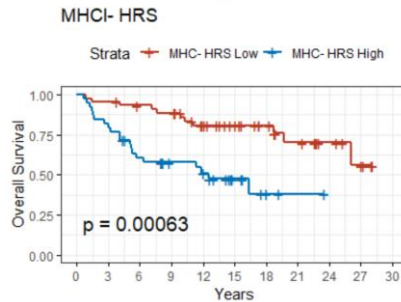
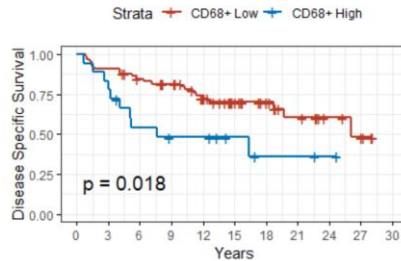
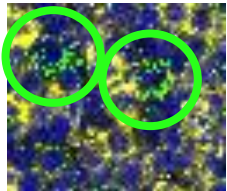
Biomarkers of Hodgkin's Lymphoma

IMC-derived biomarkers in Diagnostic Samples

%CD68 Macrophage CD68+ Macrophage



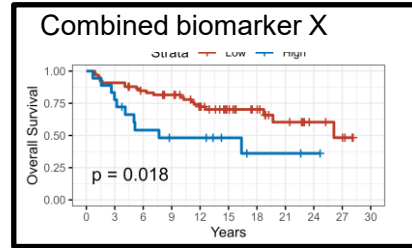
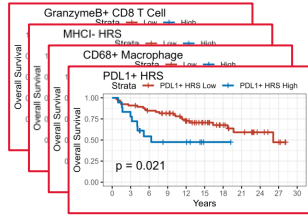
HRS tumor
<MHC1 than
neighbors



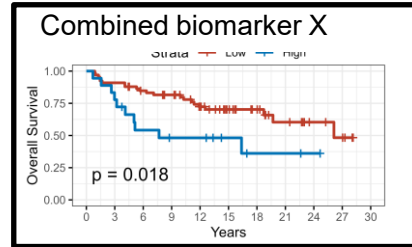
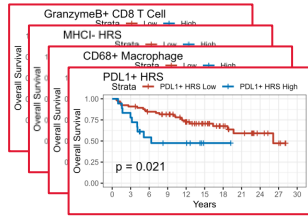
Spatial Biomarkers as a
Universal Metric



Translating IMC to actionable biomarkers

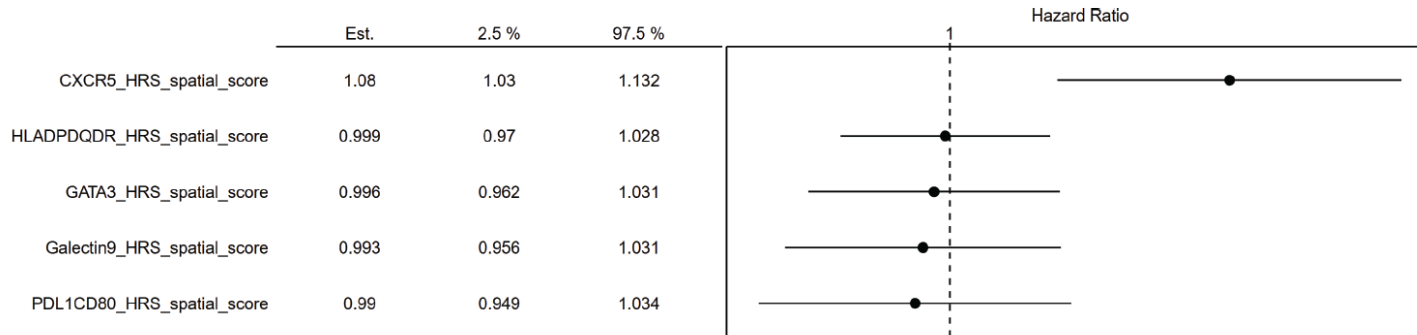


Translating IMC to actionable biomarkers



Dimensional reduction of IMC terms identifies significant predictors (LASSO)

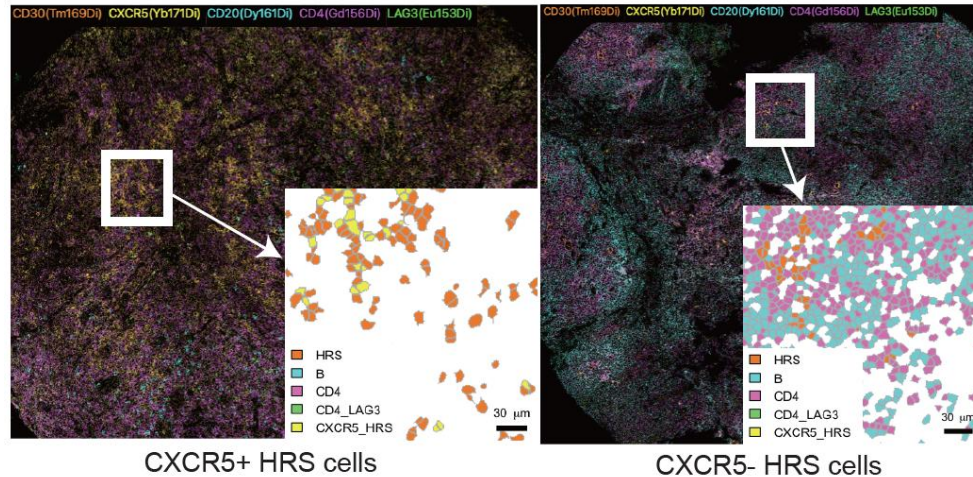
Establish a score for each patient based on spatial metrics and a high/low cutoff (XGBoost)



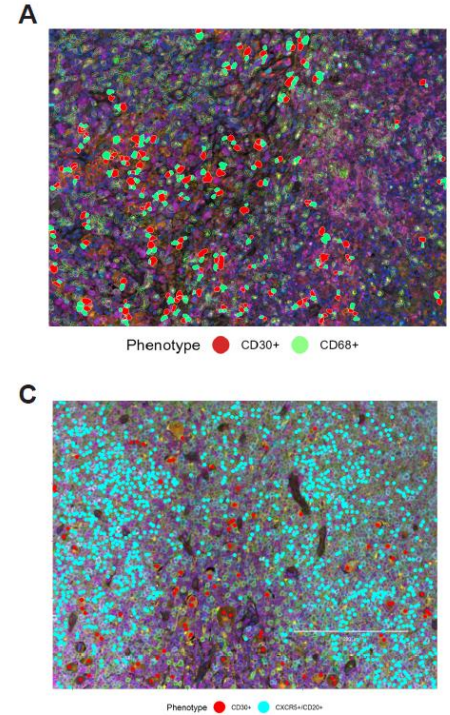
Multi-color IF of reduced IMC panel

6 marker IF vs 35 marker IMC
>1.6M combinations

IMC

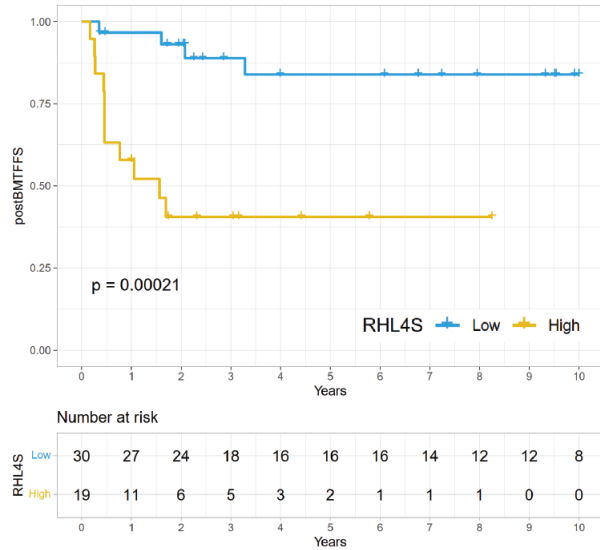


IF

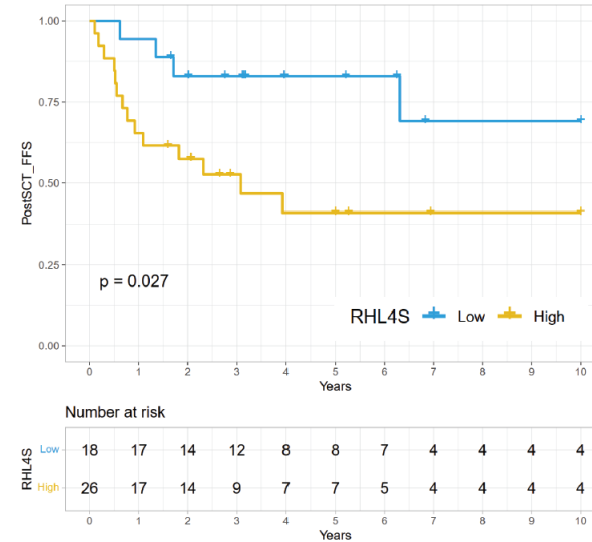


Multi-color IF of reduced IMC panel

Survival in IMC Cohort w/ IMC

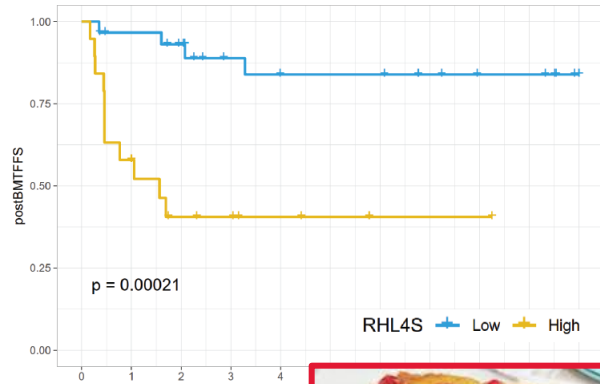


Survival in Validation Cohort w/ mIF



Multi-color IF of reduced IMC panel

Survival in IMC Cohort w/ IMC



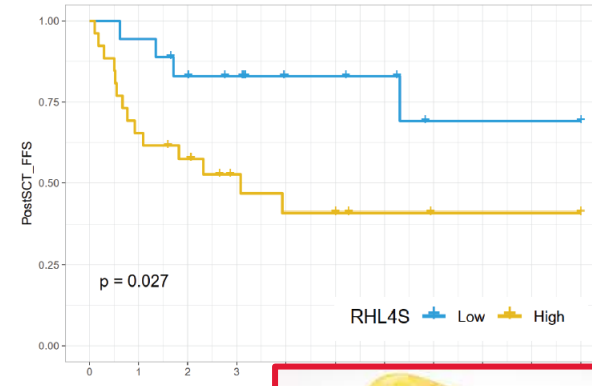
Number at risk

RHL4S Low	30	27	24	18	16
RHL4S High	19	11	6	5	3
	0	1	2	3	4



Research-Scale

Survival in Validation Cohort w/ mIF



Number at risk

RHL4S Low	18	17	14	12
RHL4S High	26	17	14	9
	0	1	2	3



Clinical-Scale

Conclusions

95 longitudinal Hodgkin's lymphoma patient samples

The gooey cake fruit – a localized spatial pattern metric predicts outcomes

Translating IMC biomarkers into an mIF assay



Aoki*, Jiang*, Xu* et al., JCO 2024

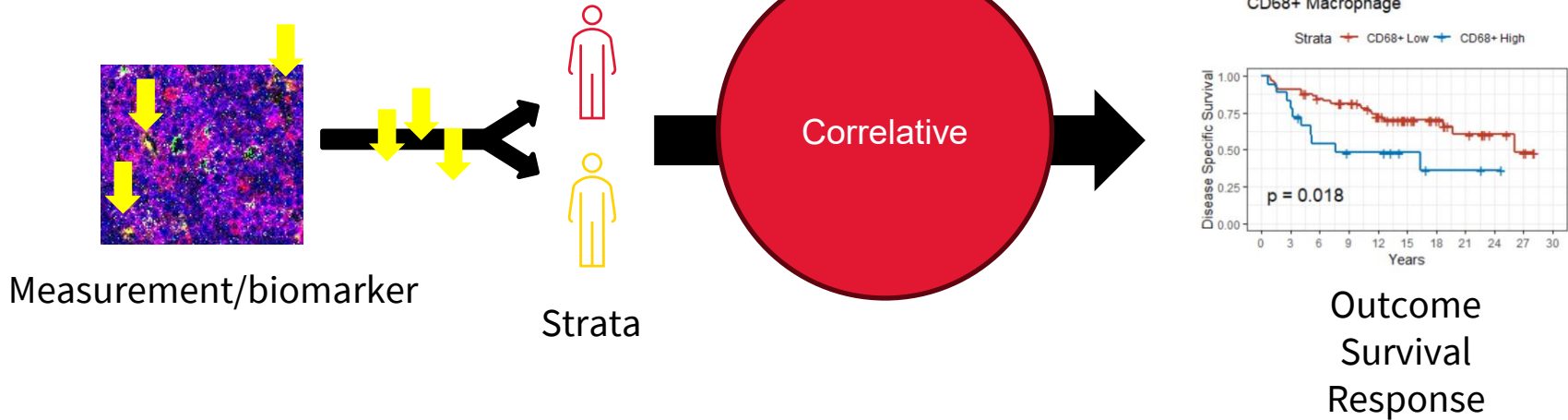
Other things:

- Deep phenotyping
- Spatial clusters/niches
- Temporal changes per patient
- Spatial/protein biomarker search
- Propose biomarker candidates



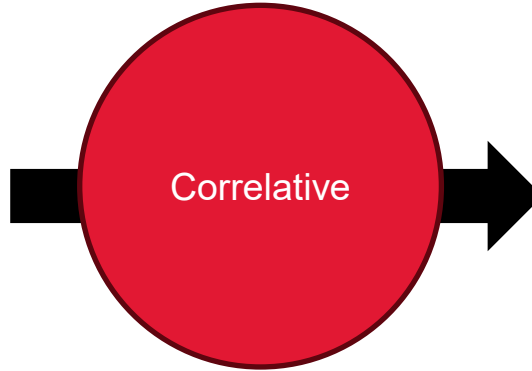
Spatial data for therapy

Prognostics vs predictions

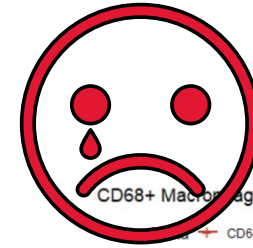


Spatial data for therapy

Pro

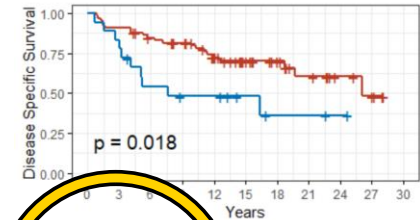


Measu

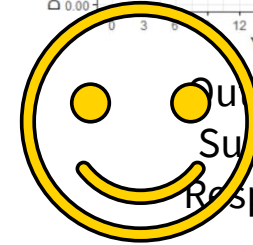


CD68+ Macrophage

CD68+ Low CD68+ High

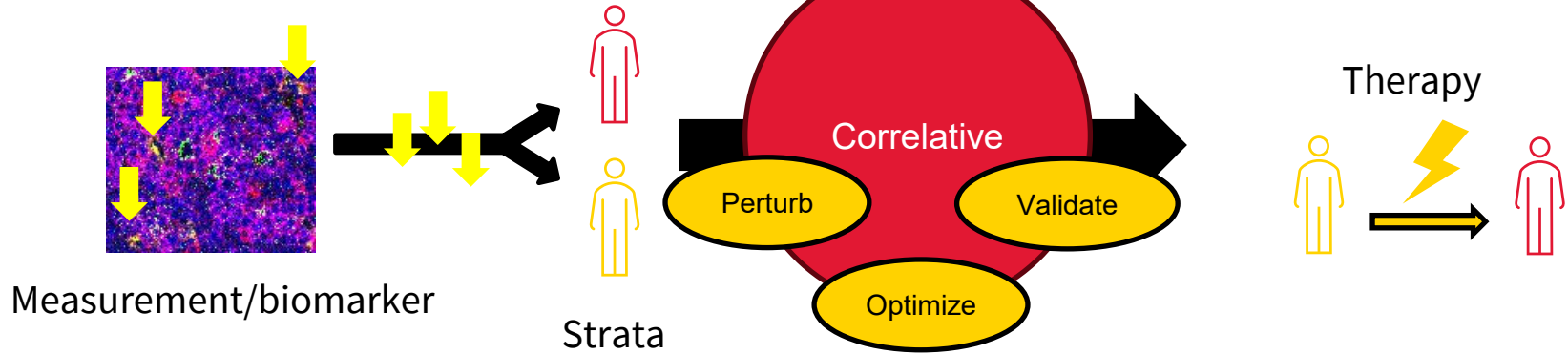


Outcome
Survival
Response

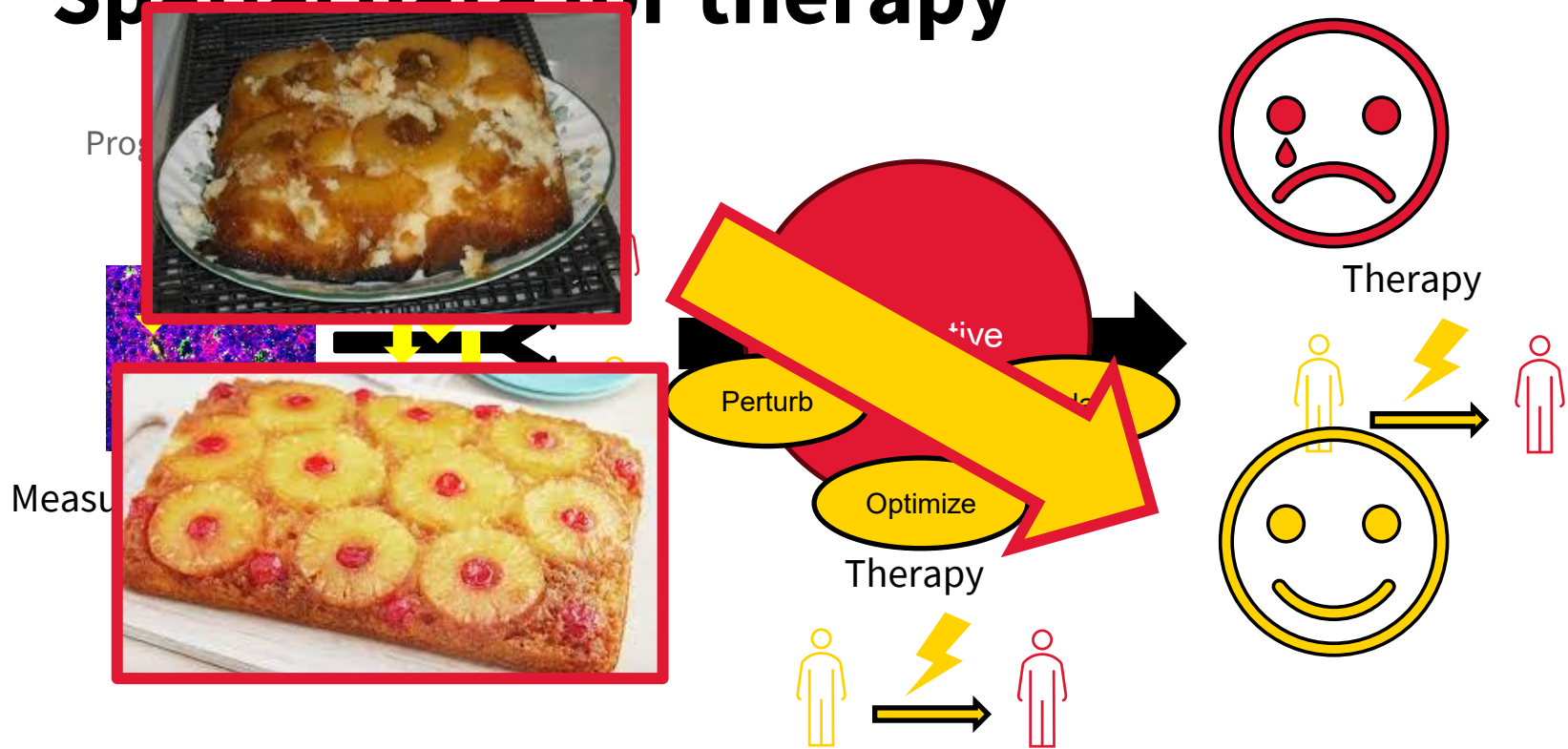


Spatial data for therapy

Prognostics vs **predictions**

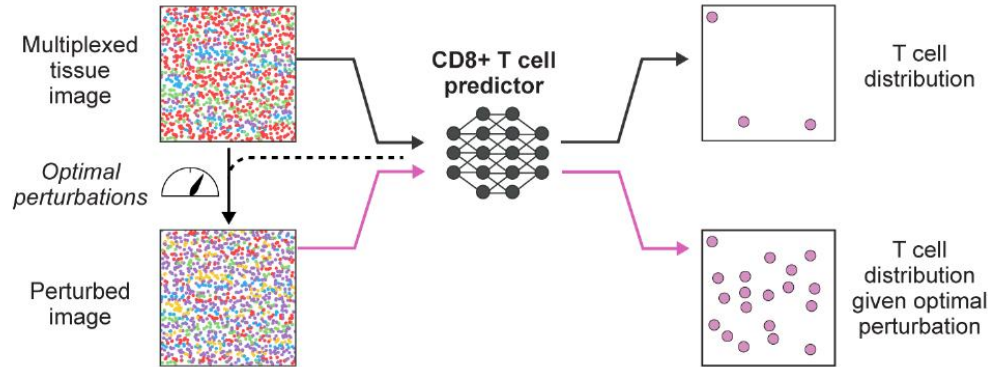


Spatial data for therapy

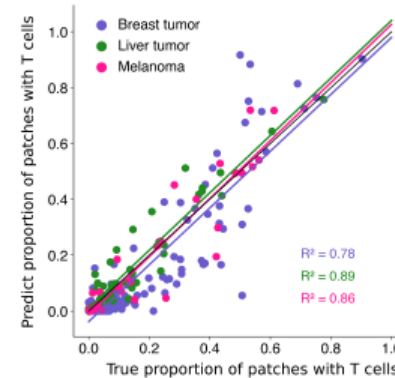


Prediction classifier for spatial features

Predict T cell infiltration in images



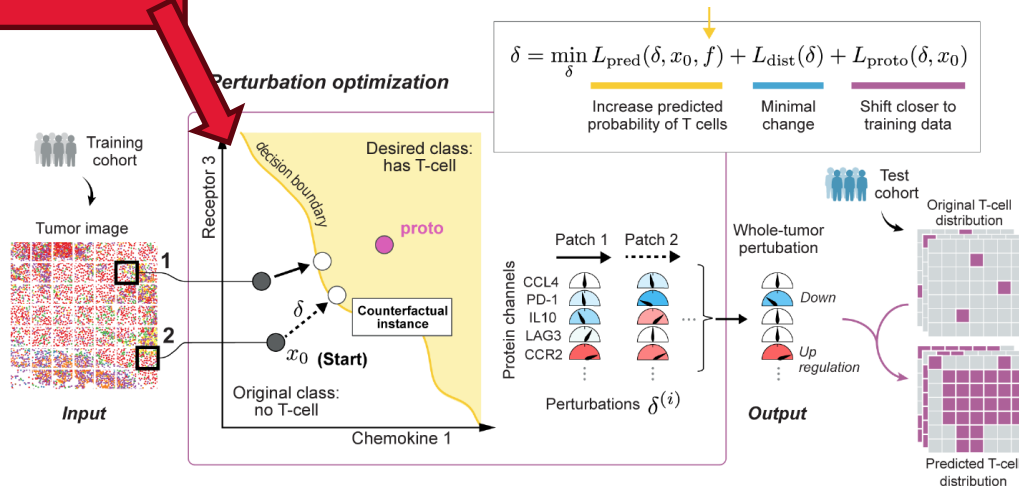
Accuracy



Perturbation testing

Predict perturbations constrained by real observations

In silico
perturbation

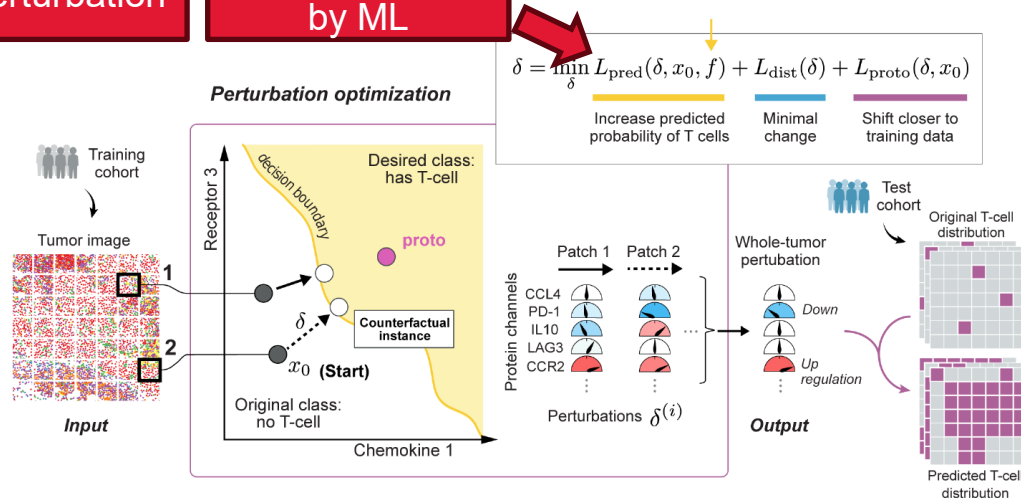


Perturbation optimization

Predict perturbations constrained by real observations

In silico
perturbation

Predictive
spatial features
by ML



Perturbation optimization

Predict perturbations constrained by real observations

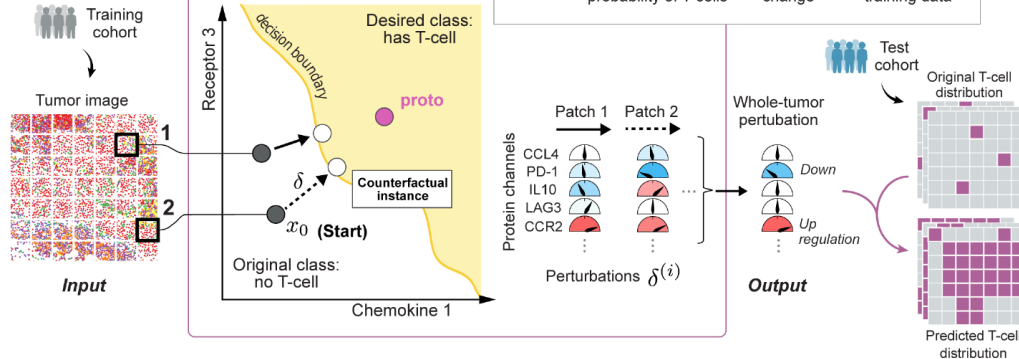
In silico
perturbation

Predictive
spatial features
by ML

Realistic
perturbation
size

$$\delta = \min_{\delta} L_{\text{pred}}(\delta, x_0, f) + L_{\text{dist}}(\delta) + L_{\text{proto}}(\delta, x_0)$$

Increase predicted probability of T cells Minimal change Shift closer to training data



Perturbation optimization

Predict perturbations constrained by real observations

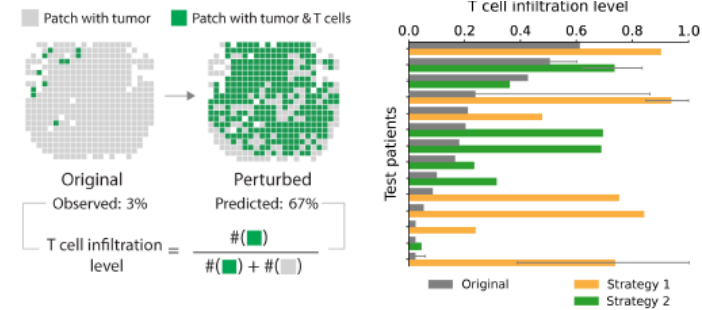
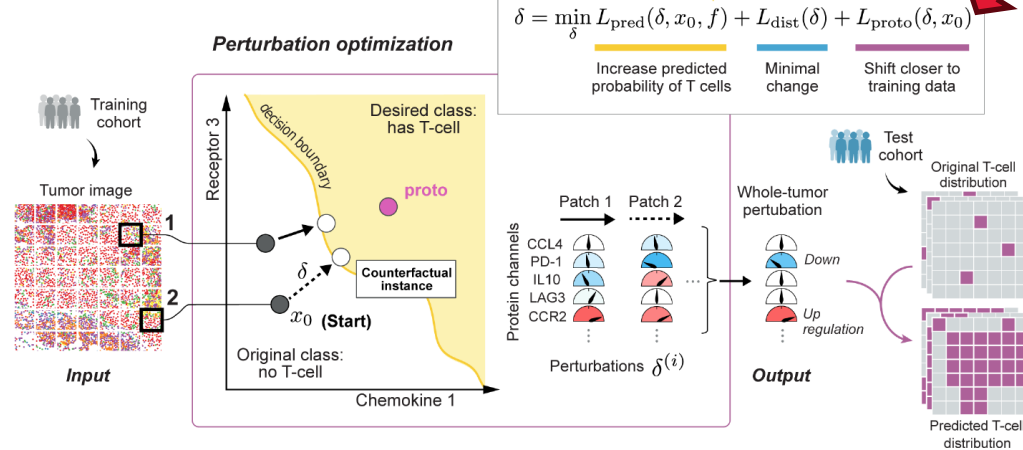
Increase T cell infiltration

In silico
perturbation

Predictive
spatial features
by ML

Realistic
perturbation
size

Realistic
perturbation
result



Melanoma Test Case

Multiplexed imaging mass cytometry of the chemokine milieu in melanoma characterizes features of the response to immunotherapy

TOBIAS HOCH ¹, DANIEL SCHULZ ², NILS ELING ³, JULIA MARTÍNEZ GÓMEZ ⁴, MITCHELL P. LEVESQUE ⁵ AND BERND BODENMILLER ¹ [Authors Info &](#)

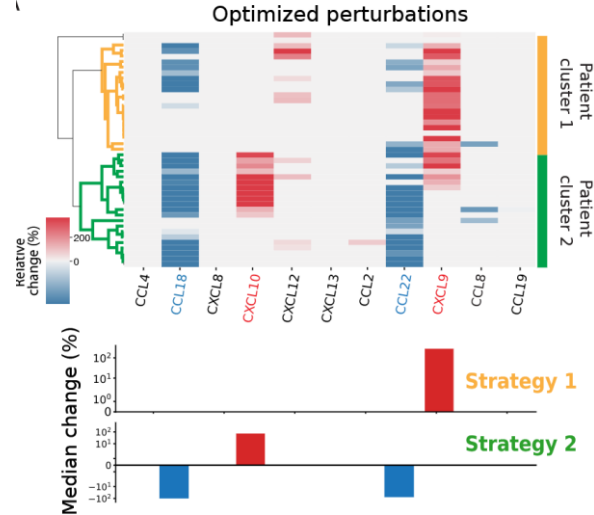
[Affiliations](#)

Melanoma + chemokine data set

Proposed perturbations

Per patient

Averaged over all patient patches



Melanoma Test Case

Multiplexed imaging mass cytometry of the chemokine milieu in melanoma characterizes features of the response to immunotherapy

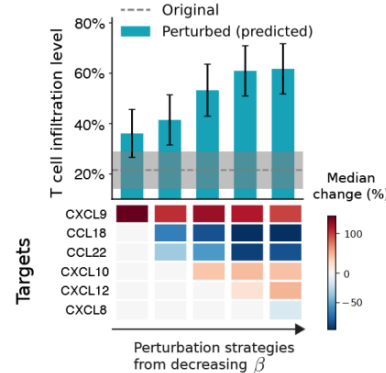
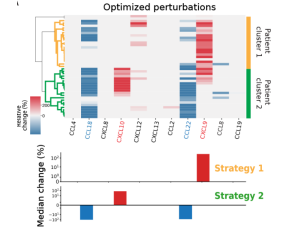
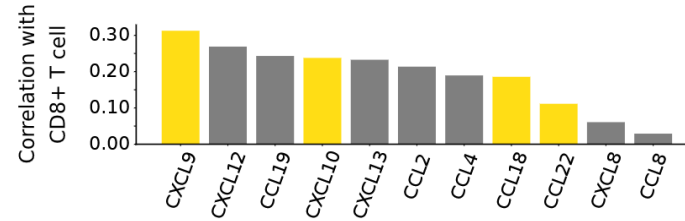
TOBIAS HOCH , DANIEL SCHULZ , NILS ELING , JULIA MARTÍNEZ GÓMEZ , MITCHELL P. LEVESQUE , AND BERND BODENMILLER  [Authors Info &](#)

[Affiliations](#)

Melanoma + chemokine data set

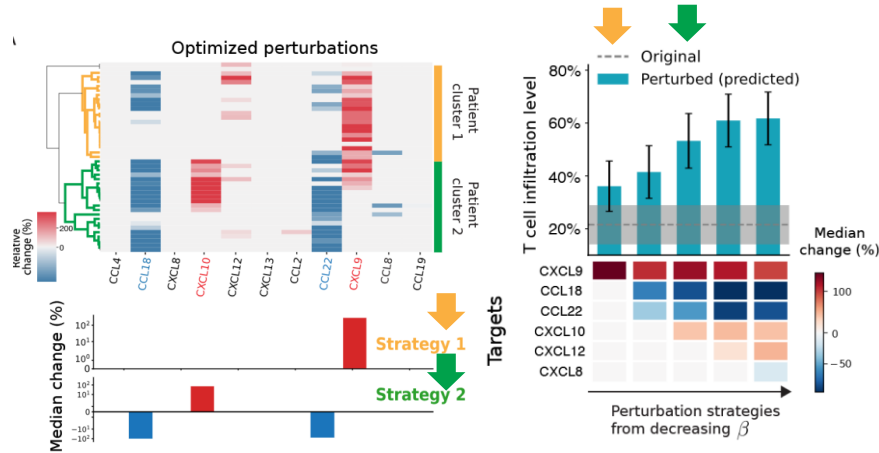
Not necessarily the most heavily correlated

Combinatorial candidates



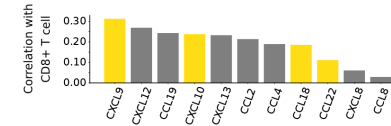
Melanoma Test Case

In vitro validation



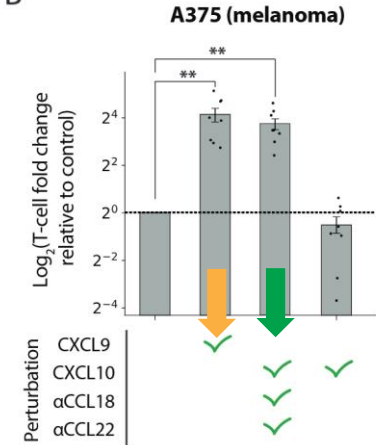
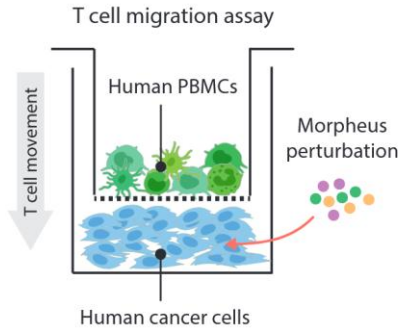
TOBIAS HOCH , DANIEL SCHULZ , NILS ELING , JULIA MARTÍNEZ GÓMEZ , MITCHELL P. LEVESQUE , AND BERND BODENMILLER [Authors Info &](#)

Affiliations



A

B



Conclusions

In silico testing of perturbations

Constrained by spatial library and observed tissue space

Single and combination therapy candidates based on spatial hypotheses

Wang, ... Xu, Thomson, **Nature Biomedical Engineering**, 2025



Conclusions

In silico testing of perturbations

Const

Single

Wang

More other things:

- Lymphoma Spatial Biomarkers
 - ... Xu et al, Blood Advances, 2022
 - ... Xu et al, Am. J. of Hematology, 2025
- CRC Cancer: Metastasis to Liver
 - ... Xu* et al, Cell Metabolism, 2023
 - ... You†, Xu†, Seki†, JCI, 2025
- HIV+ Immunocompromised DLBCL
 - Coelho, Roush, Xu et al, British Journal of Haematology, 2024
 - Roush, Coelho, Xu et al, JCI Insight, 2024



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PAUL G. ALLEN
FRONTIERS GROUP

Akil Merchant Lab

Alicia Gamboa

Sandra Orsulic Lab

Marcela Haro

Matthew Thomson Lab

Jerry Zitong Wang

Abdullah Farooq



Caltech



ITCR





Contact

alexmxu@umd.edu

