Comprehensive in situ immune phenotyping with the CosMx™ high plex protein assay

Case Study

Tiên Phan-Everson
Scientist
Research and Development
NanoString Technologies

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Results

CosMx successfully profiles 68* targets in **888k cells** in an ascending colon stage IIA Adenocarcinoma using the Human I/O 64-plex protein assay and enables proteomic profiling of tissue micro-environment at **subcellular resolution**.

Conclusions

Spatial proteomics analyses highlighted the differences in immunological environments between the two tumor lobes. Heterogeneity within a single patient suggested that tailored immunotherapy approaches would benefit patient outcome.

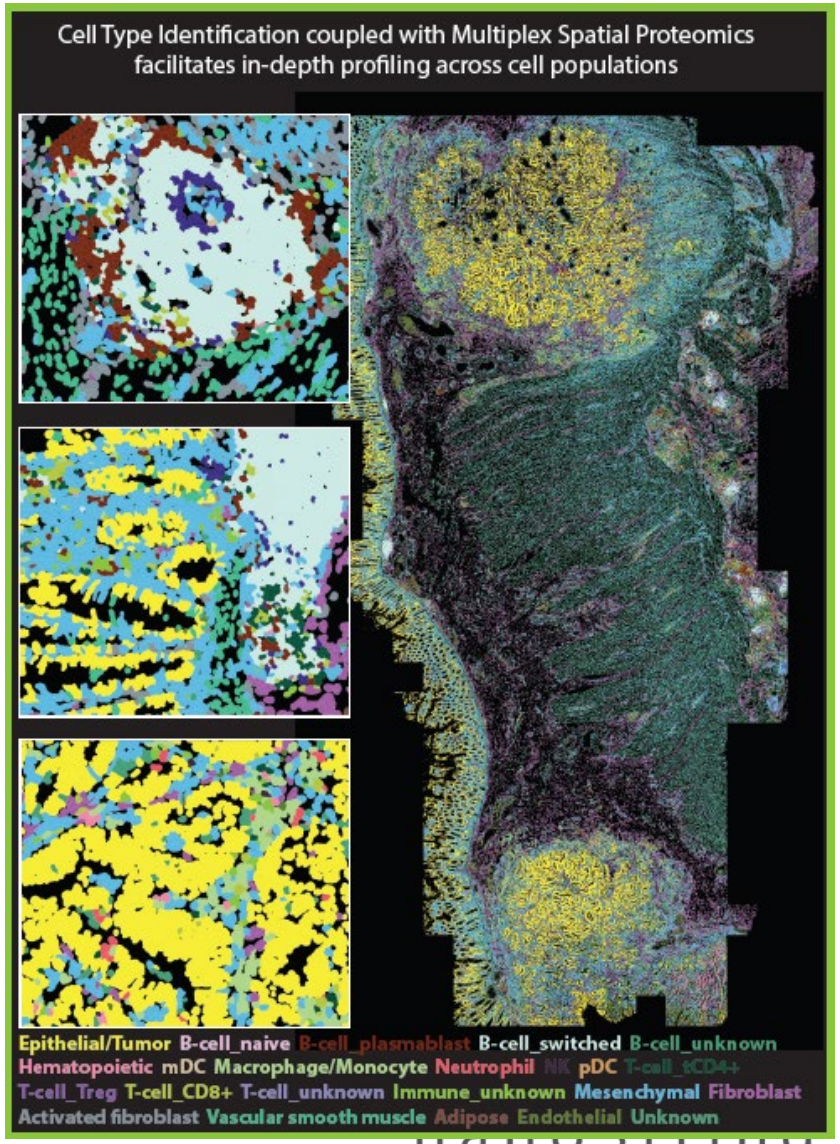
Why CosMx?

The CosMx human IO protein panel consists of 64 immuno-oncology focused targets and 4 segmentation markers. All 68 targets have been **validated with both pathology review and quantitative analyses**.

Machine learning-based image analysis software enables **accurate cell segmentation and phenotyping**.

A **cloud-based informatics system** empowers researchers with high-performance on-demand resources for data analysis, visualization, and management.

*with cell segmentation markers



How do immune cell populations differ within distinct Human colon adenocarcinoma macro- and microenvironments?

Background

- The spatial interactions between the immune system and tumor cells greatly influence antitumoral immunity, patient prognosis, and therapeutic efficacy. However, few methods exist to query large numbers of immune biomarkers at subcellular spatial resolution.

Research question

- Can the CosMx Human I/O 64-plex protein assay provide data sufficient for immune cell profiling and tumor microenvironment characterization?

Study design

- Characterize tumor heterogeneity and immune cell populations in macro- and microenvironments of distinct tumor areas of Human ascending colon stage IIA adenocarcinoma using the CosMx Human I/O 64-plex protein assay and integrated CosMx bioinformatics pipeline

Study Details	
Research area:	Stage IIA adenocarcinoma
Organism and tissue:	Human Colon
Sample type:	FFPE
Instrument:	CosMx™ SMI
Analyte:	Protein
Assay:	Human I/O 64-plex
Conference, Year:	SITC, 2022

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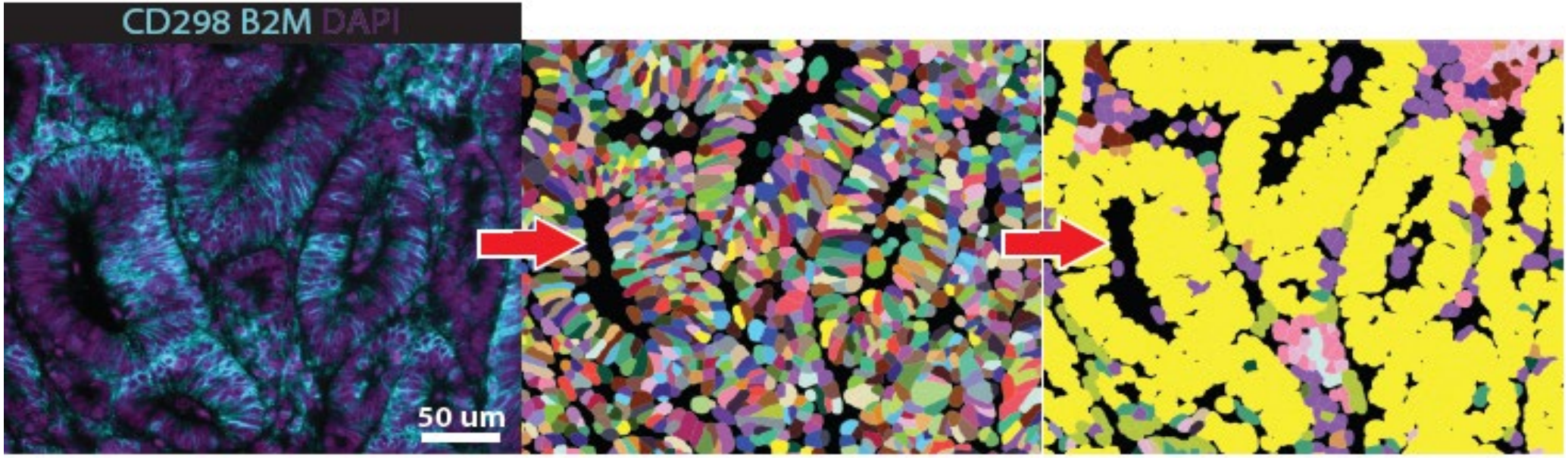
Human I/O 64-plex protein assay successfully profiles 888k cells in an ascending colon stage IIA Adenocarcinoma sample using machine-learning-based cell segmentation and cell typing



Cell segmentation cocktail: PanCK, CD3, CD45, DAPI

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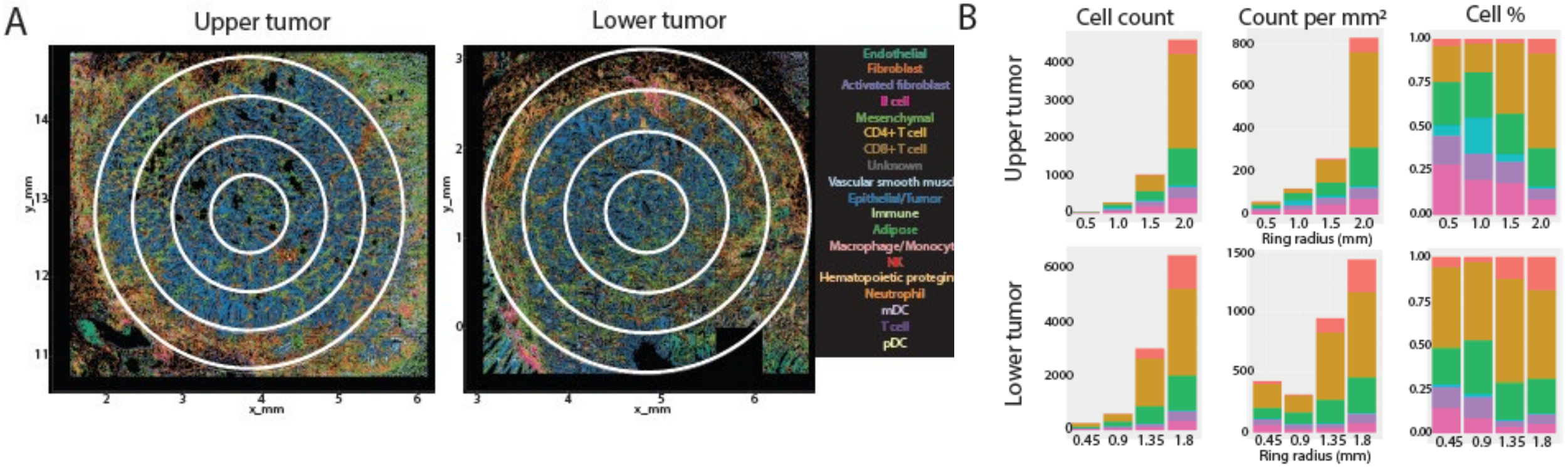
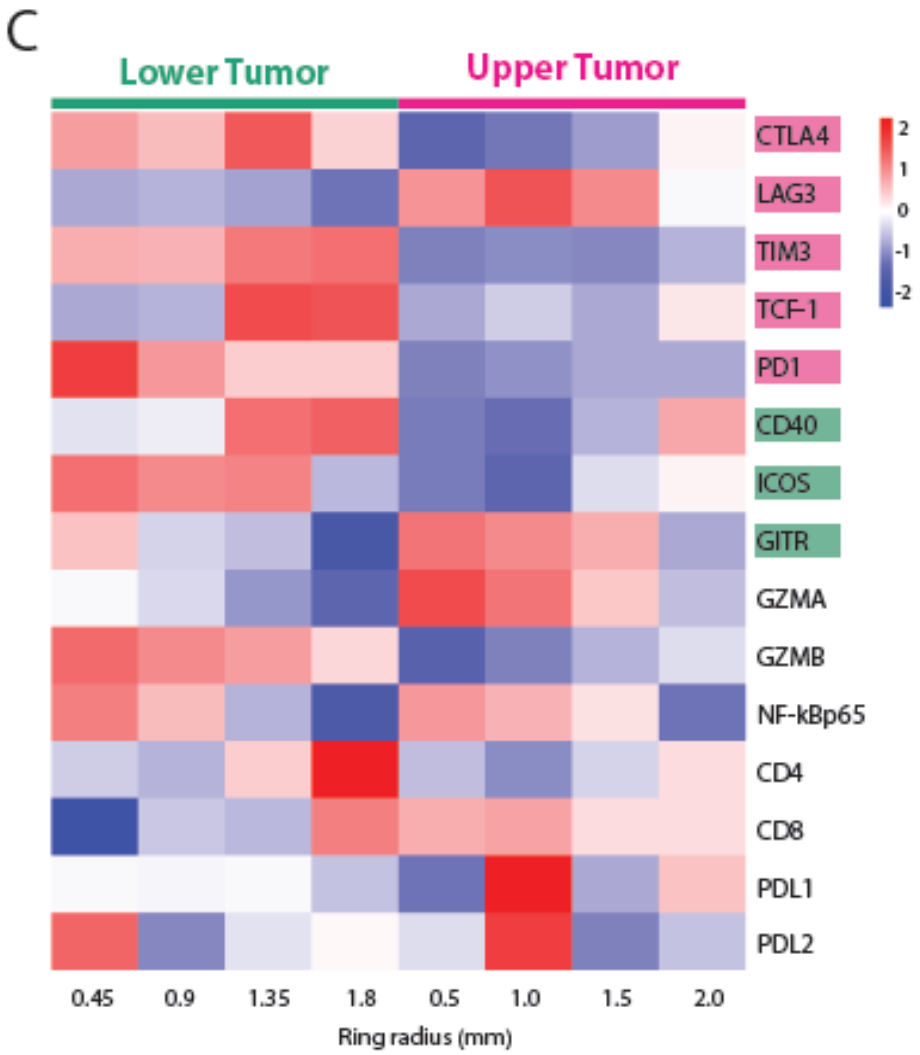
Characterization of the spatial organization and composition of immune cell infiltrate



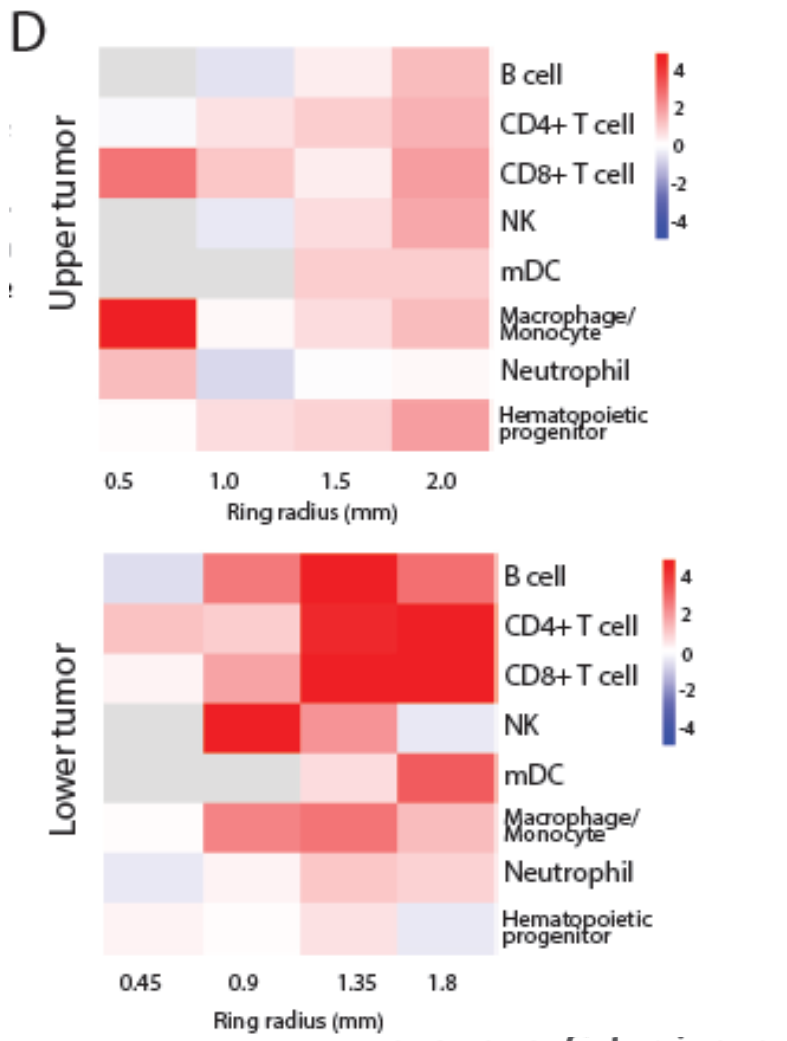
Immune cell population composition changes between the upper and lower tumor, and with increasing distance from the tumor center within each tumor.

Characterization of the spatial organization and composition of immune cell infiltrate



Markers of CD8 T cell exhaustion (pink) and activation (green) differ between the upper and lower tumor, also with respect to location within the tumor (C).

Cell proximity assessment indicates CD8 T cells in the lower tumor are more highly associated with other immune cells (D).



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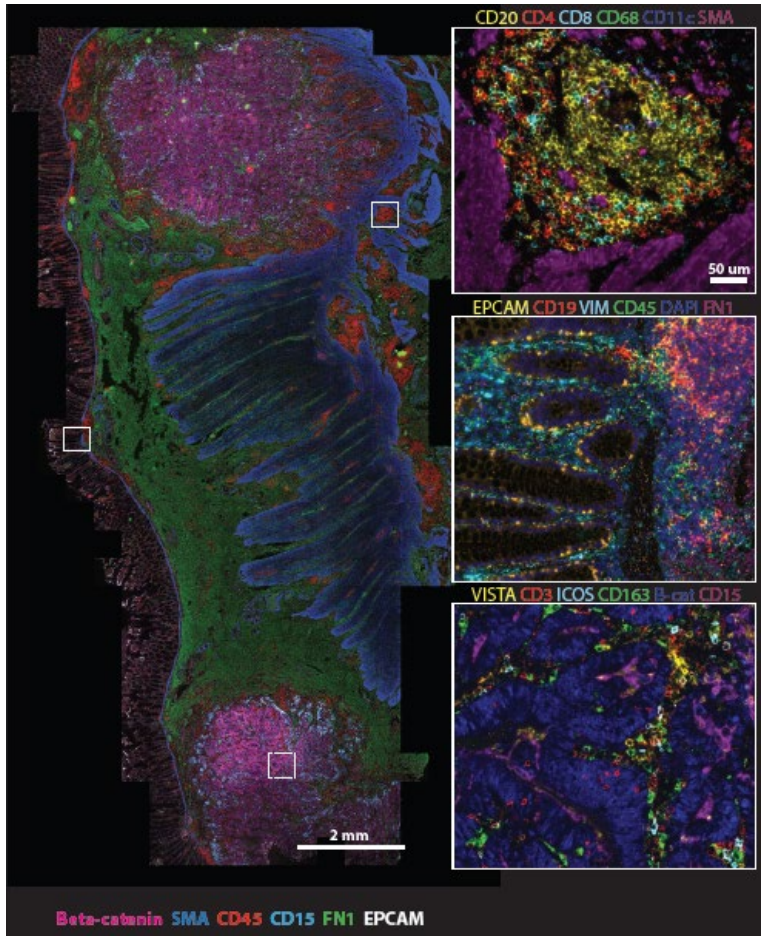
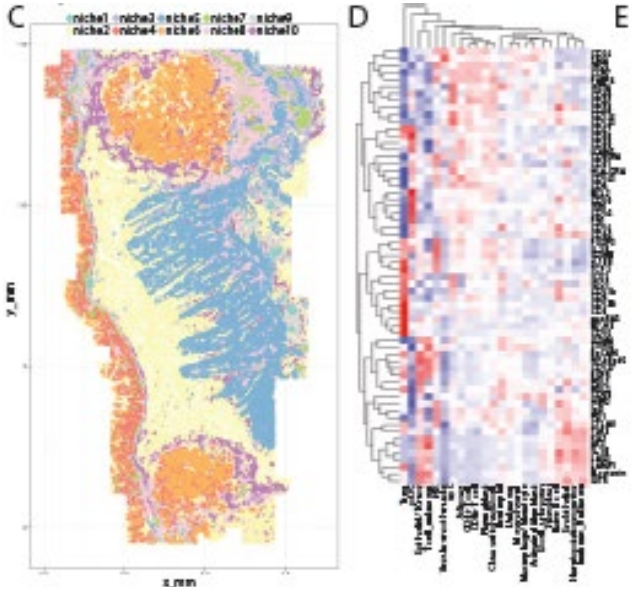
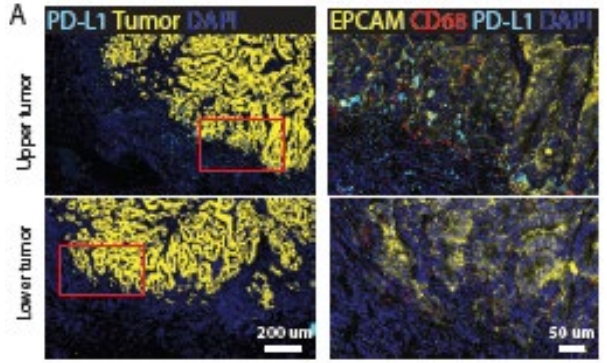
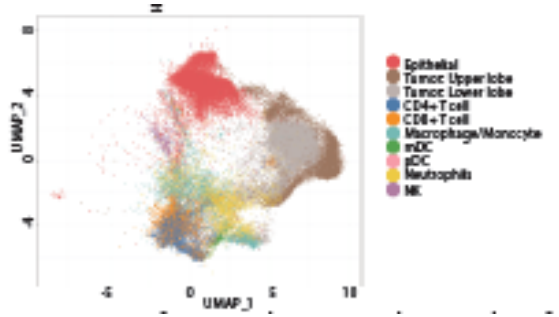
With one data set:

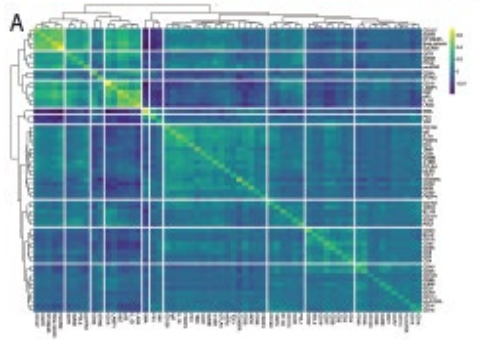
- Define tissue macro- and micro-environments
- Cell-type identification
- Identify spatially-dependent expression patters
- Characterize the spatial organization of immune infiltrates
- Examine cell type co-localization
- Discover relevant biomarkers

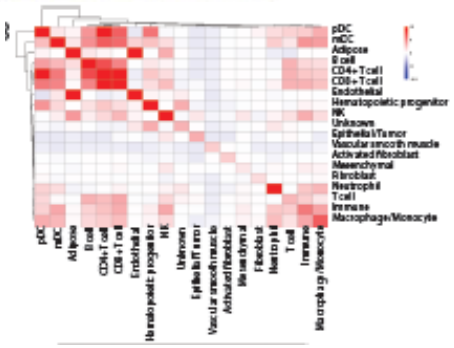












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