

# Fully integrated end-to-end spatial biology workflow

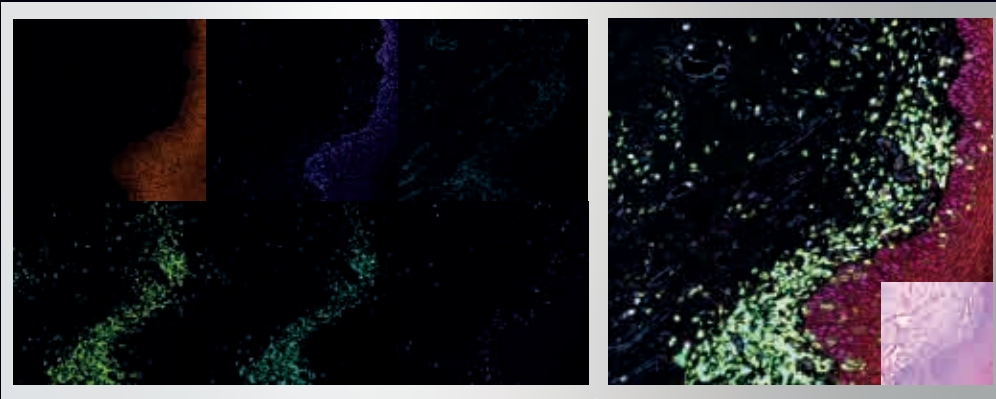
Tissue preparation - staining - analysis - reporting



Step

## 1 Panel Development

- Selection from a large catalog of optimized antibodies for custom panel development
- Validation of additional antibodies against your biomarker of interest



Optimization of individual antibody panel staining.  
Top row: Pan-cytokeratin (orange), PCNA (purple), PD-L1 (cyan). Bottom row: CD45 (green), CD3 (teal), CD8a (magenta)

Combined antibody panel with hematoxylin & eosin stain for comparison (inset)

Step

## 2 Staining & Image Generation

- Access to our Akoya Phenomager® HT & Lunaphore COMET™
- Ability to stain up to 40 plex

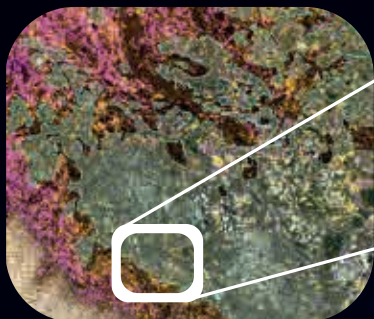
Step

## 3 Image Management

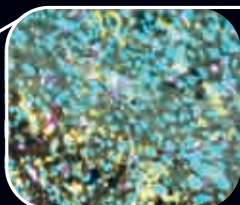
- Image transfer via Pathcore's cloud-based image viewing system

# Step 4 Image Segmentation, Phenotyping & QC

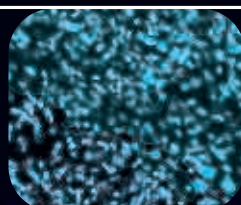
- Identification of tissue regions based on presence of specific biomarkers
- Defining cellular boundaries, identities, and measuring spatial relationships



Tumor Nest Regions (cyan) are identified by tissue classifiers trained on cytokeratin (white), amongst CD8 T cells (magenta) and CD68 macrophages (yellow)



Magnified region showing tumor boundary (red), DAPI nuclei (cyan) CD8 (magenta) and CD68 (yellow)



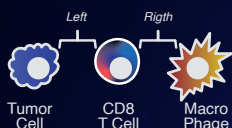
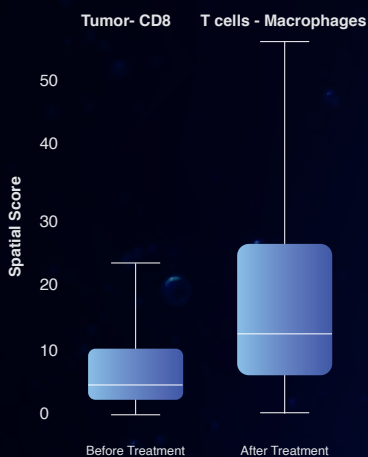
Cell & Nuclear boundaries are identified using deep learning based computer vision algorithms (DAPI in cyan)



Cells are phenotyped based on the presence of combinations of biomarkers, and distance relationships are measured (white lines)

# Step 5 Post-processing & Statistical Analysis

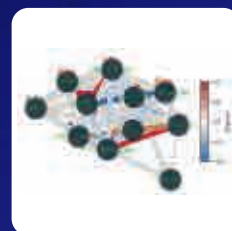
- Characterization of cellular neighborhoods and distance relationships
- Reporting of significant changes between treatment groups



The SpatialScore describes the ratio of distances between CD8 T cells and Macrophages to the distance between CD8 T cells and tumor cells, revealing immune cell interactions altered between before-treatment and on-treatment samples.



A Spatial Interaction Heatmap reveals the frequency and significance of cellular co-occurrence patterns, where any significant deviation from random cellular interactions are displayed on a color scale representing the scaled abundance of interactions.



A Spatial Interaction Network graph, which highlights significant interactions between cell phenotypes in the tumor microenvironment.

# START YOUR PROJECT TODAY

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