

# Analysis of melanoma and pancreatic ductal adenocarcinoma (PDAC) spatial transcriptomics data

5/4

Translational Science

Cancer  
Research

nature  
biotechnology

ARTICLES



<https://doi.org/10.1038/s41587-019-0392-8>

**Spatially Resolved Transcriptomics Enables Dissection of Genetic Heterogeneity in Stage III Cutaneous Malignant Melanoma** 

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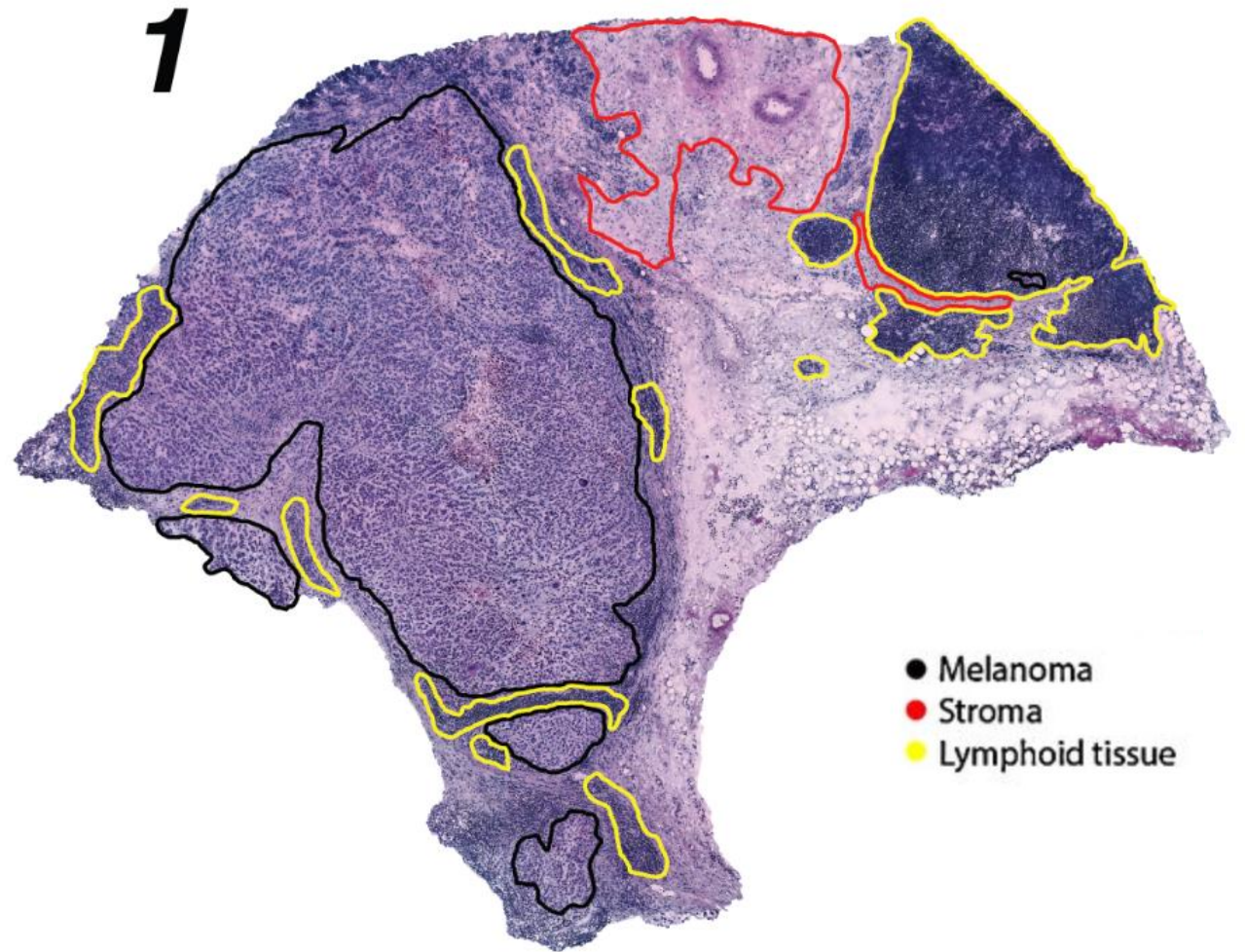


**Integrating microarray-based spatial transcriptomics and single-cell RNA-seq reveals tissue architecture in pancreatic ductal adenocarcinomas**

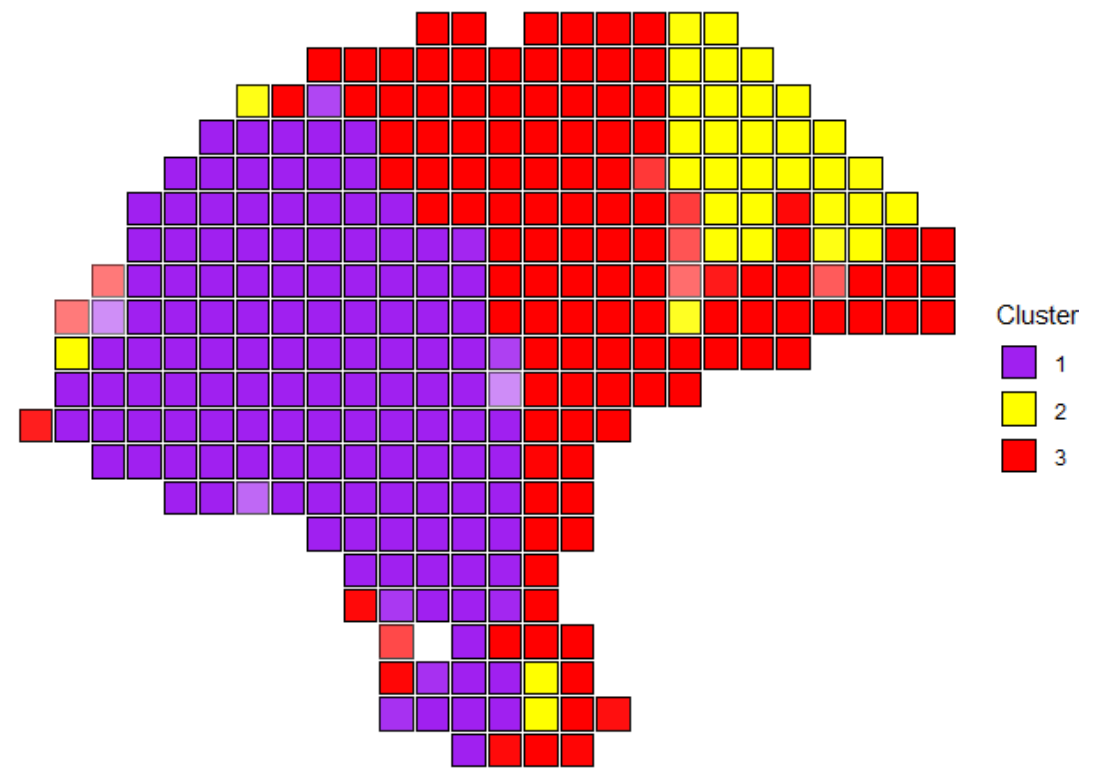
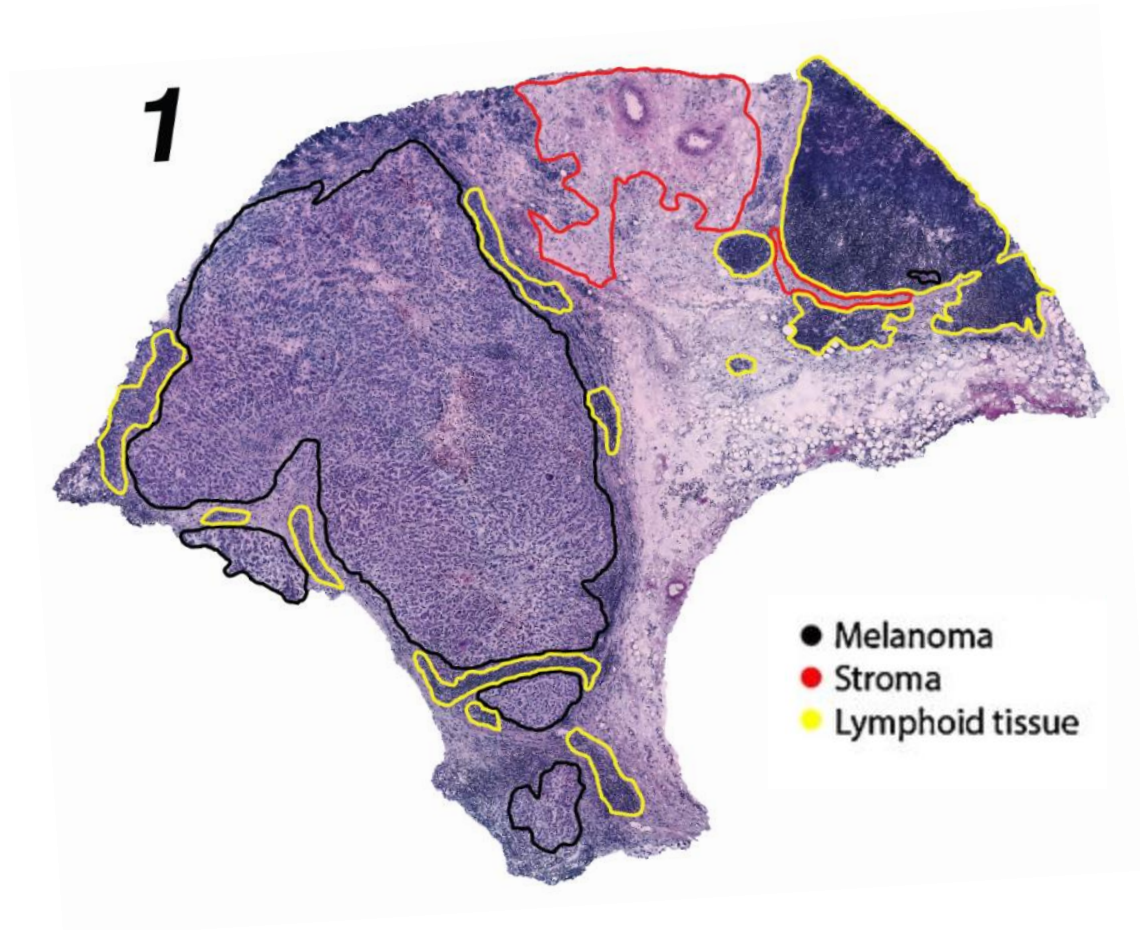
Reuben Moncada<sup>1</sup>, Dalia Barkley<sup>1</sup> , Florian Wagner<sup>1</sup>, Marta Chiodin<sup>1</sup>, Joseph C. Devlin<sup>1</sup>, Maayan Baron<sup>1</sup>, Cristina H. Hajdu<sup>2</sup>, Diane M. Simeone<sup>2,3,4</sup> and Itai Yanai<sup>1,5\*</sup> 

# Sample Melanoma 1

- H&E staining image annotated for histological features (left)
- Each spot (100 $\mu$ m diameter) on spatial transcriptomics (ST) data contains 5-40 cells
  - New VISIUM technology is 55 $\mu$ m diameter
- Hierarchical clustering on top PCs derived from highly variable genes (right)

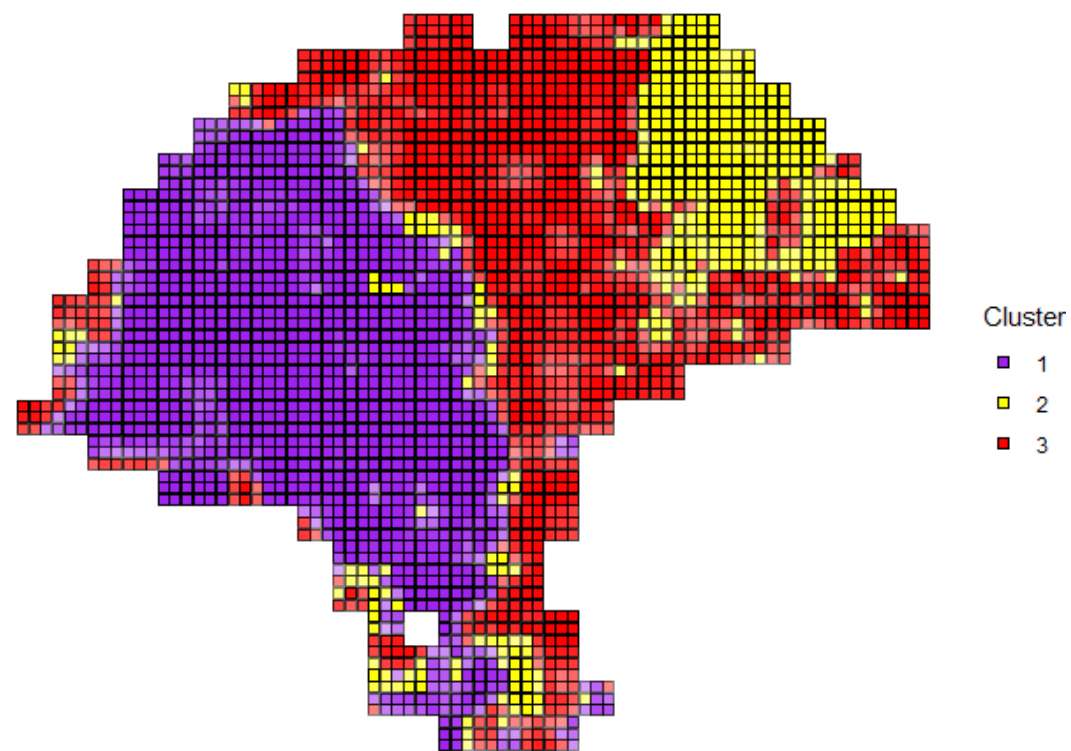
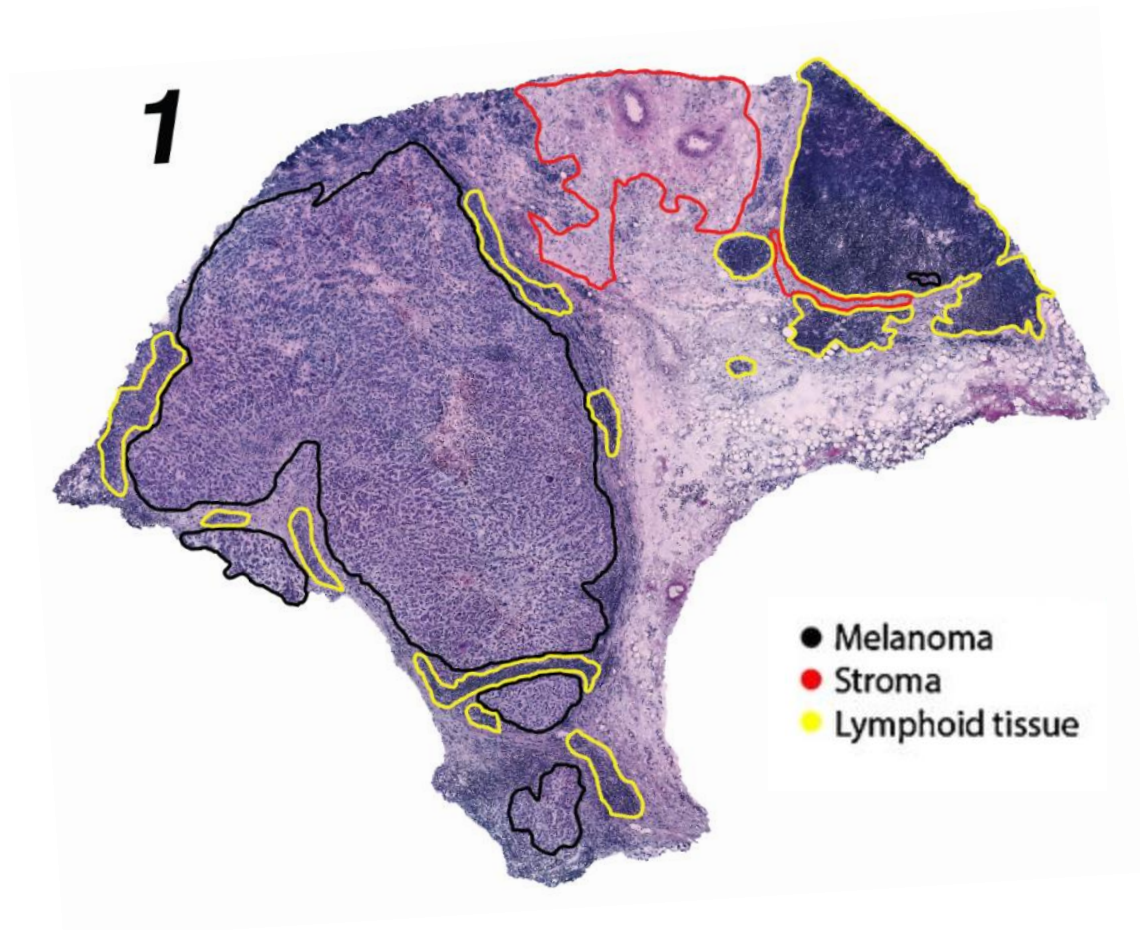


# Spatial clustering



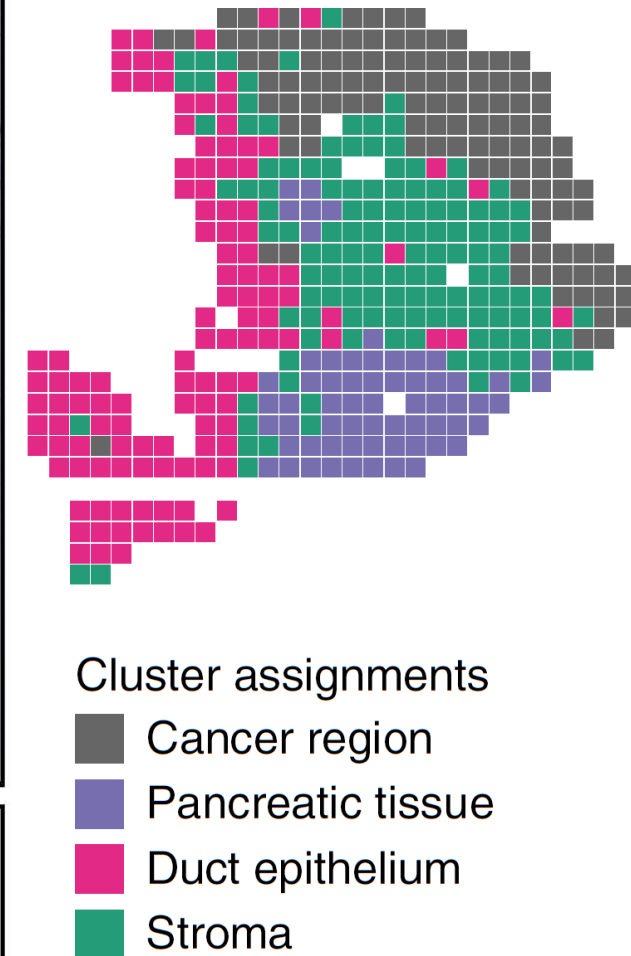
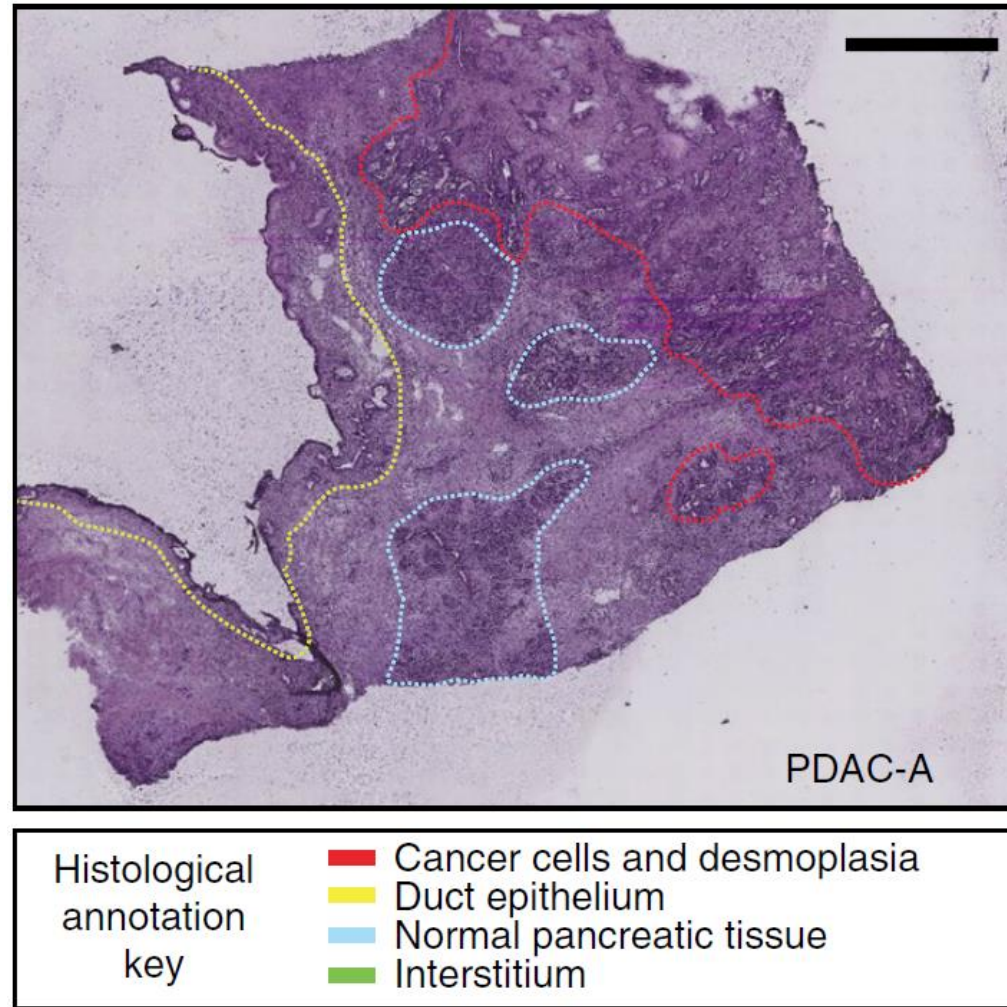


# Spatial deconvolution

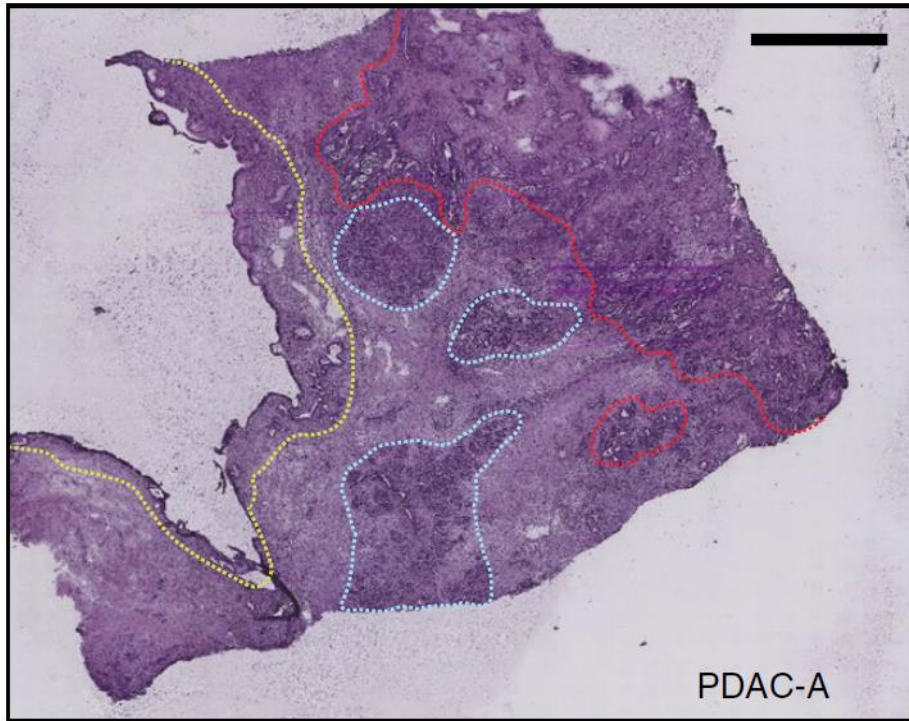


## Sample PDAC-A

- H&E staining image annotated for histological features (left)
- Each spot (100 $\mu$ m diameter) on spatial transcriptomics (ST) data contains 20-70 cells
  - New VISIUM technology is 55 $\mu$ m diameter
- Hierarchical clustering on top PCs derived from highly variable genes (right)

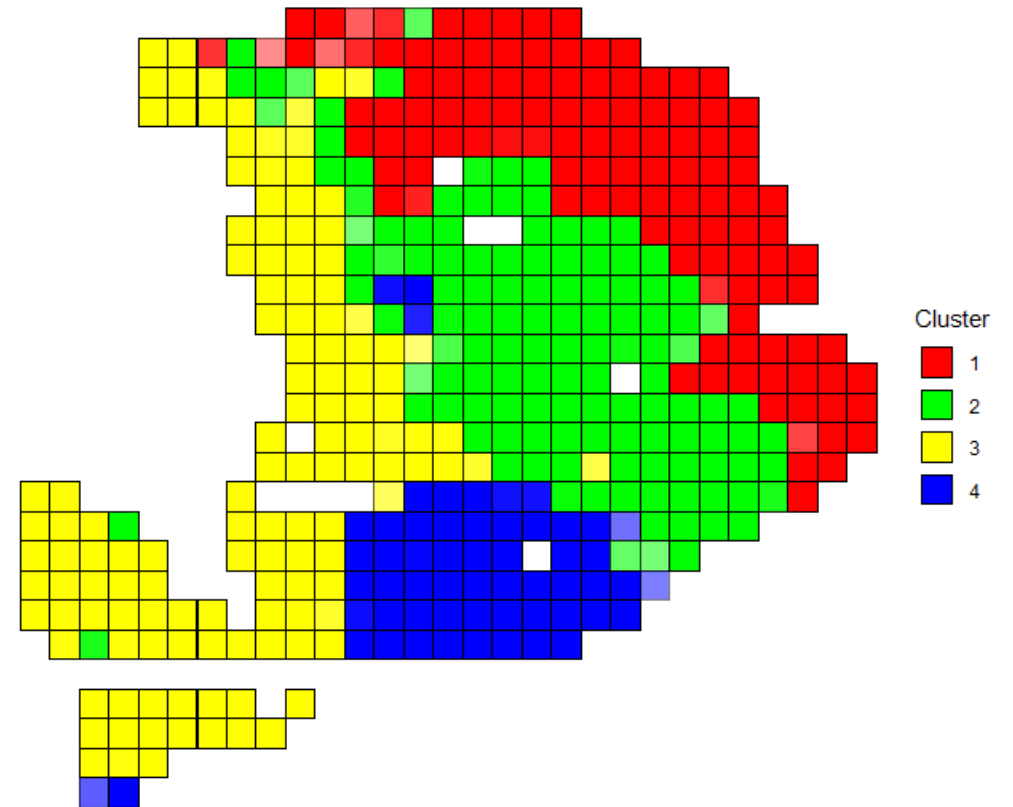


# Spatial Clustering



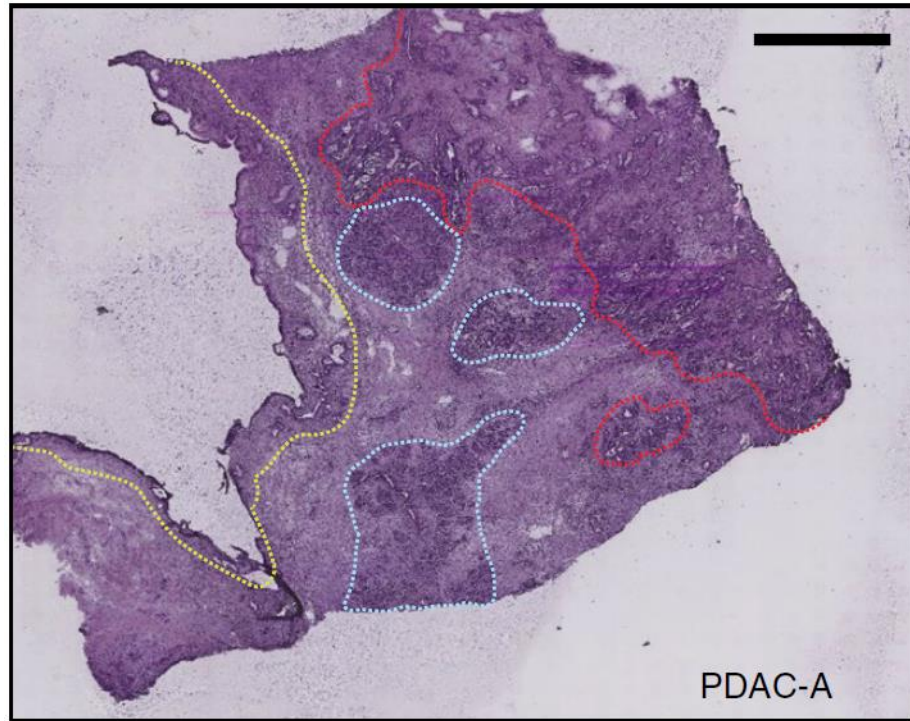
Histological  
annotation  
key

<span style="color: red;">■</span>	Cancer cells and desmoplasia
<span style="color: yellow;">■</span>	Duct epithelium
<span style="color: lightblue;">■</span>	Normal pancreatic tissue
<span style="color: green;">■</span>	Interstitium



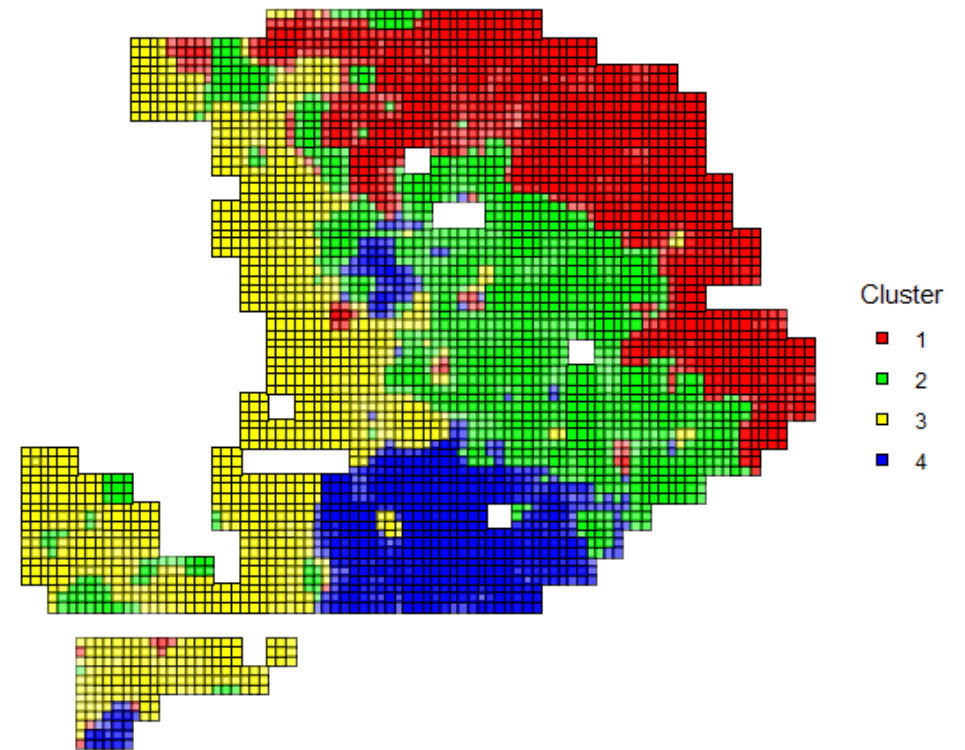


# Spatial Deconvolution



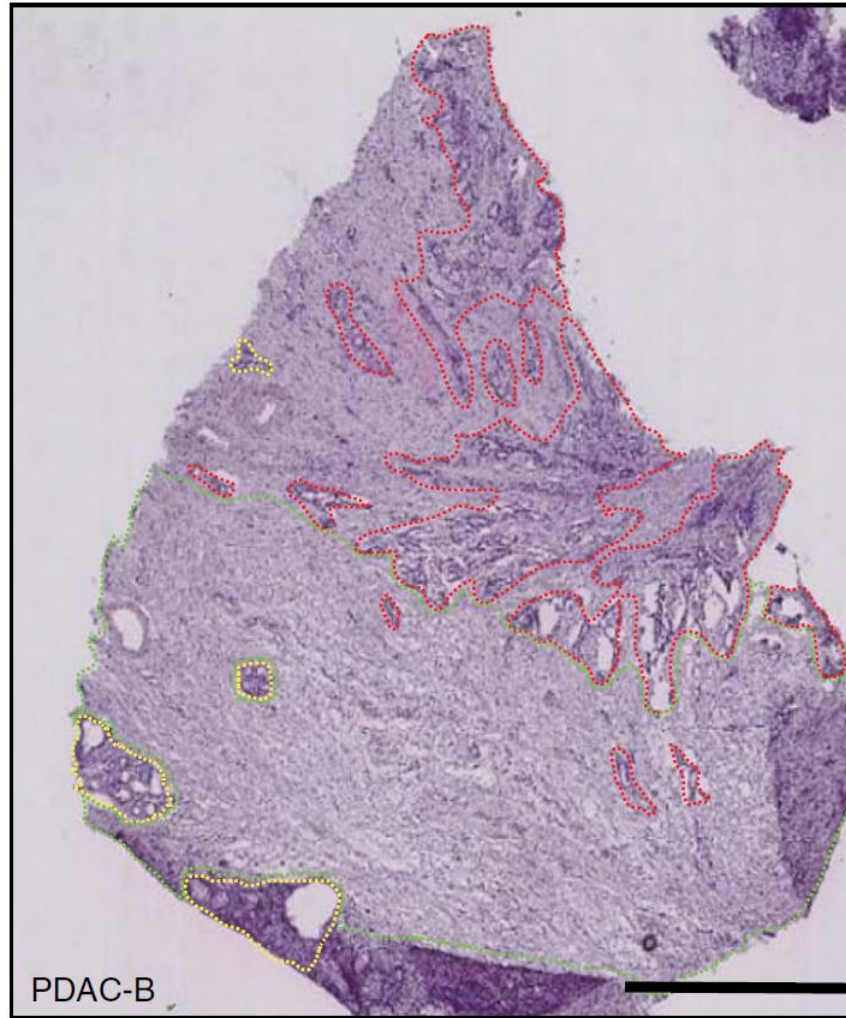
Histological  
annotation  
key

■	Cancer cells and desmoplasia
■	Duct epithelium
■	Normal pancreatic tissue
■	Interstitium

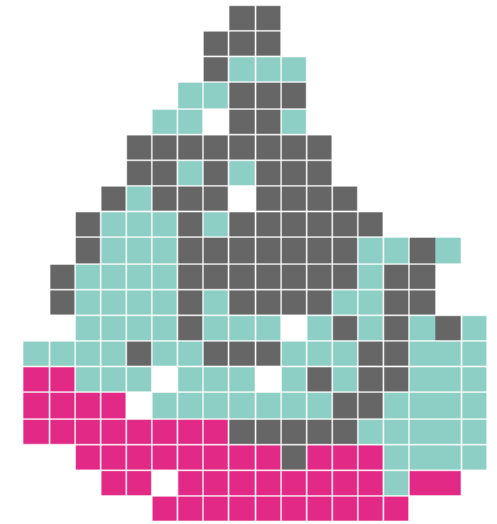


# Sample PDAC-B

- H&E staining image annotated for histological features (left)
- Each spot (100μm diameter) on spatial transcriptomics (ST) data contains 20-70 cells
  - New VISIUM technology is 55μm diameter
- Hierarchical clustering on top PCs derived from highly variable genes (right)



Histological annotation key	<span style="color: red;">—</span>	Cancer cells and desmoplasia
	<span style="color: yellow;">—</span>	Duct epithelium
	<span style="color: lightblue;">—</span>	Normal pancreatic tissue
	<span style="color: green;">—</span>	Interstitium

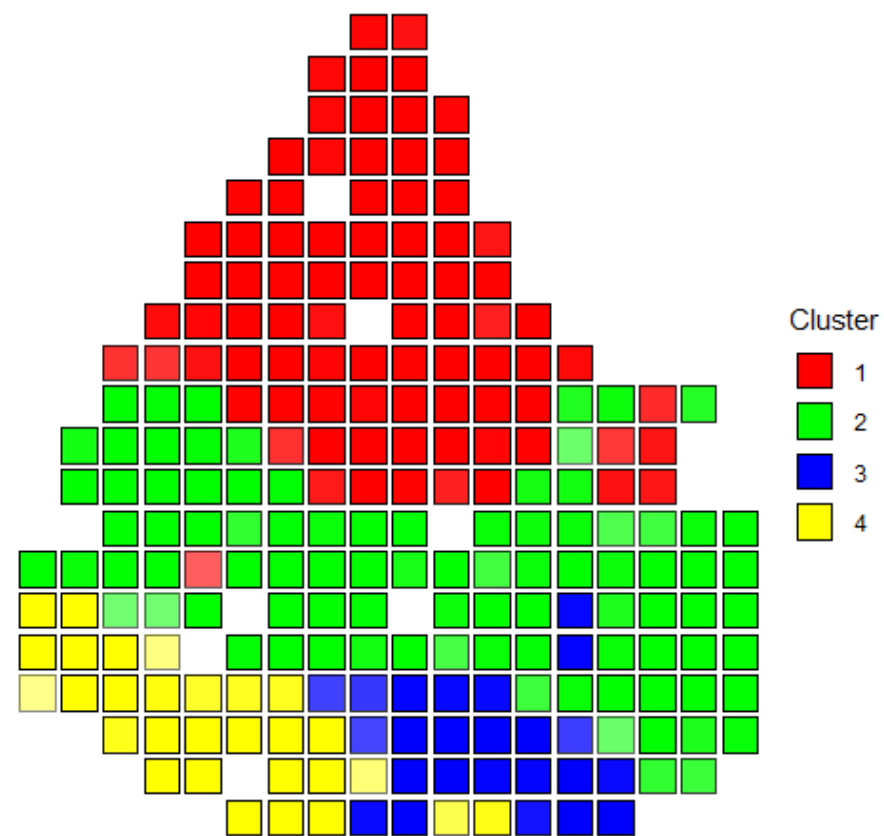
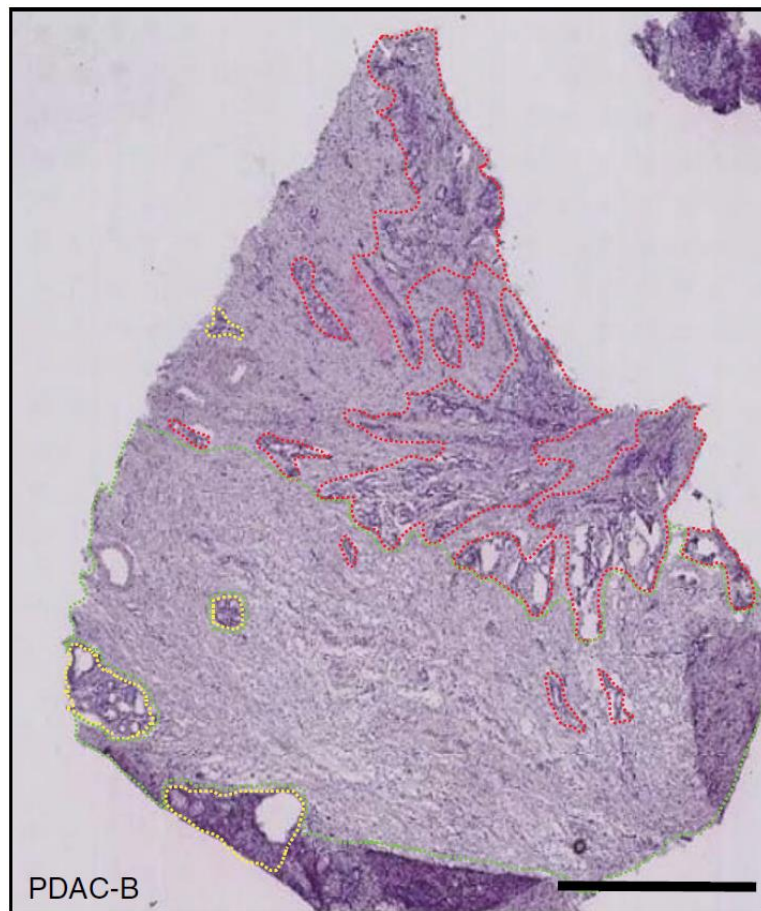


## Cluster assignments

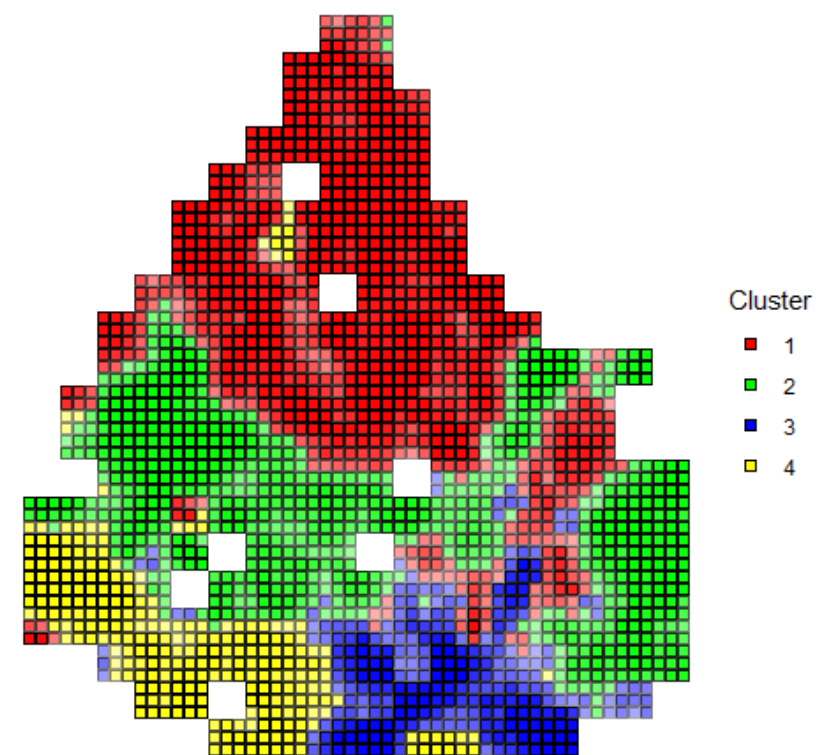
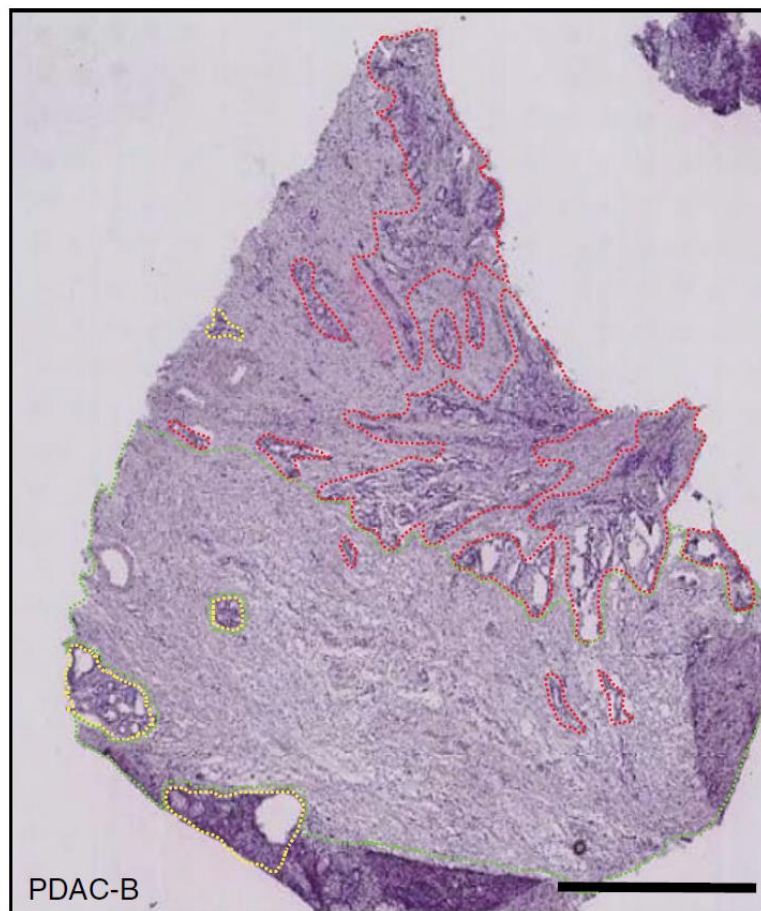
- Cancer region
- Interstitium
- Duct epithelium



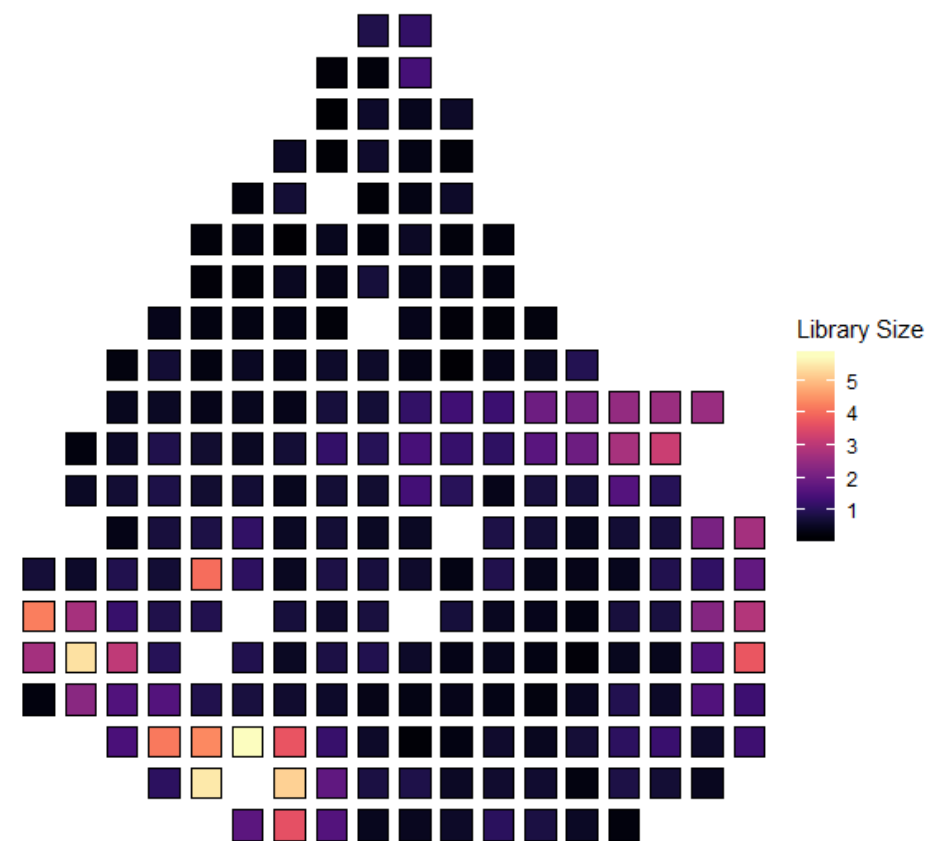
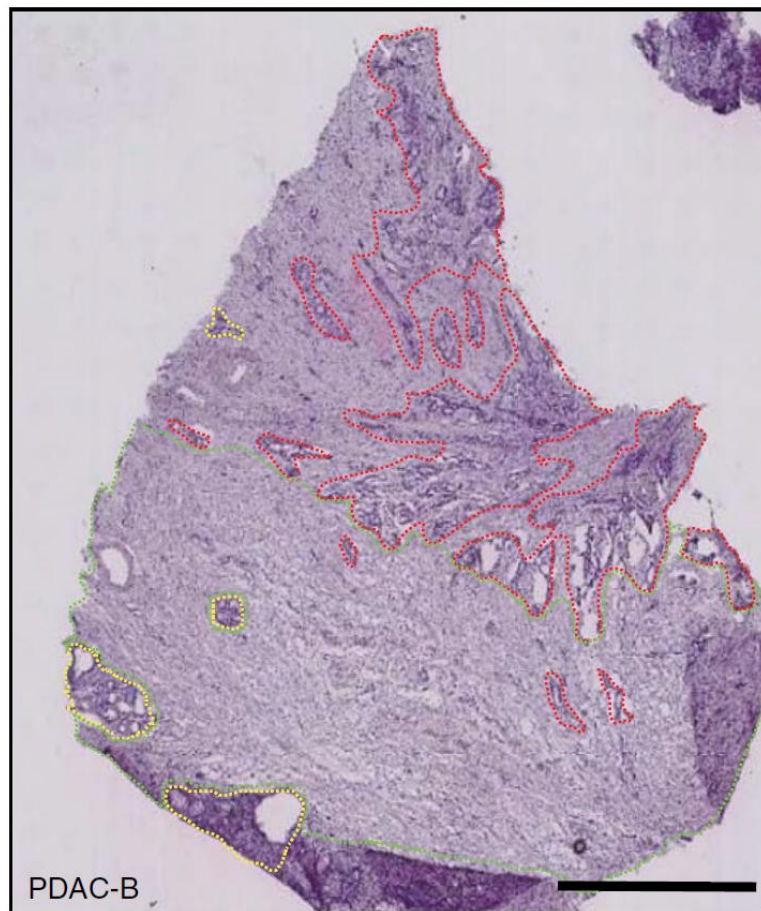
# Spatial clustering



# Spatial Deconvolution

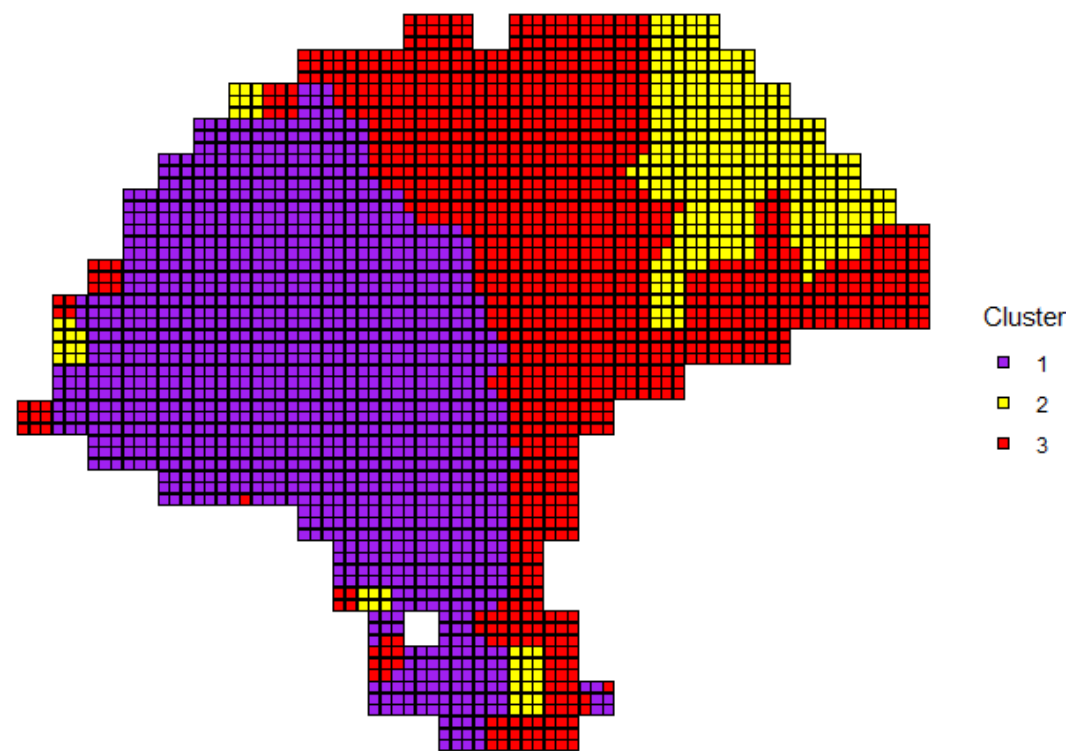
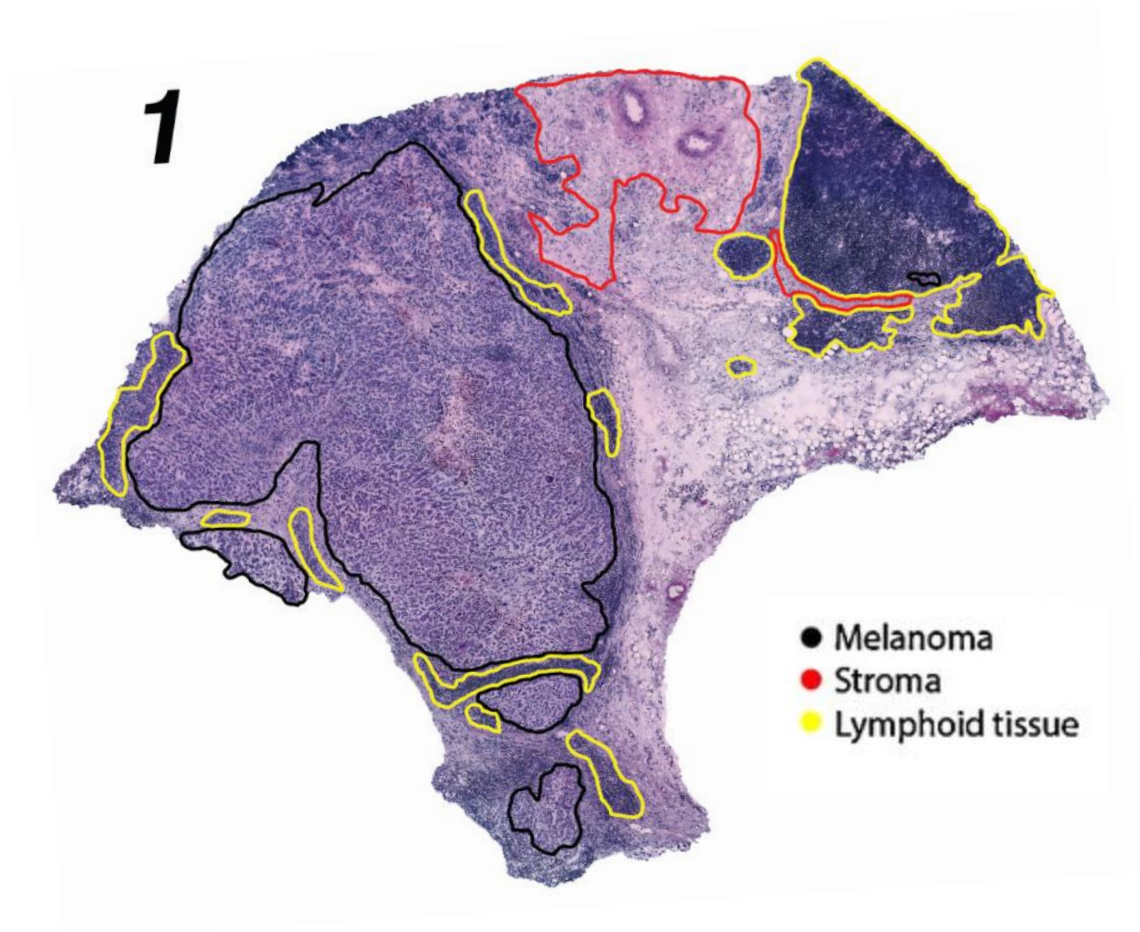


# Library size

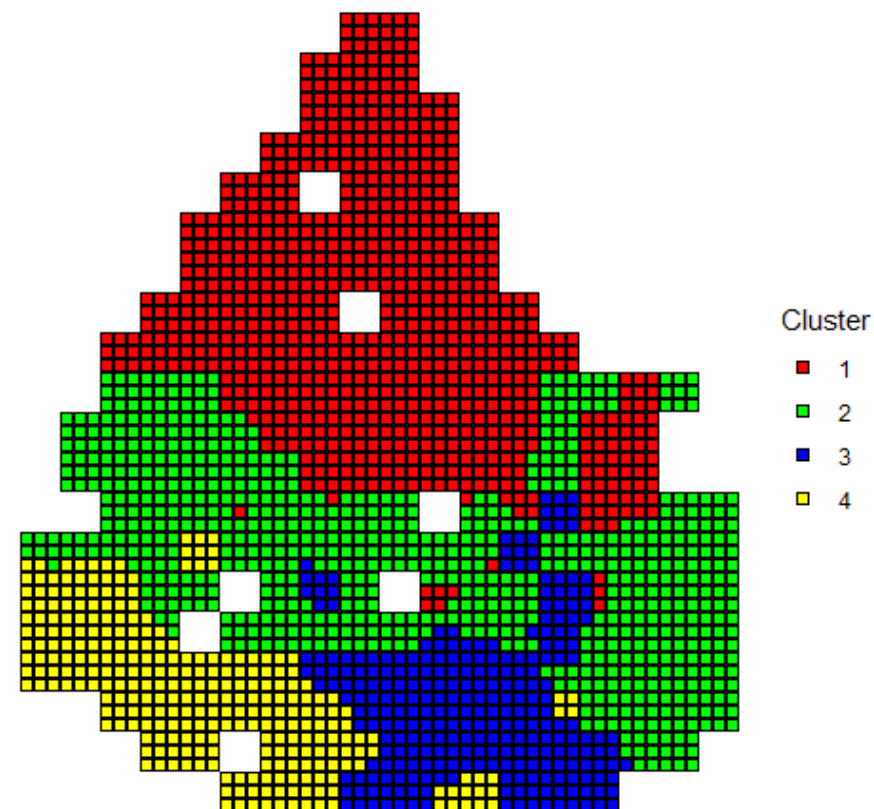
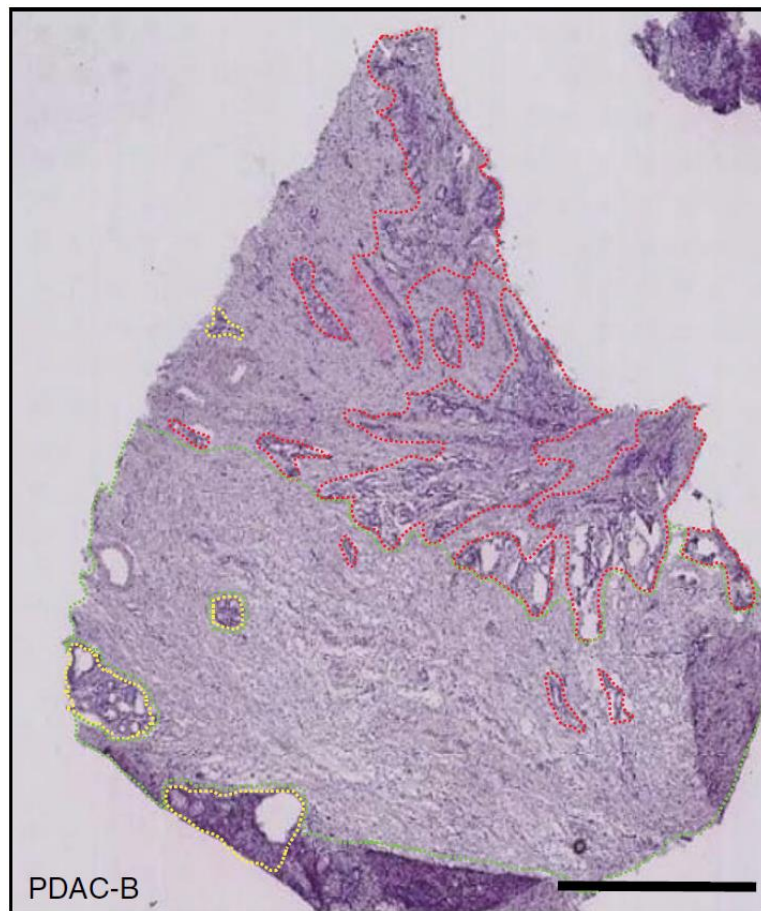




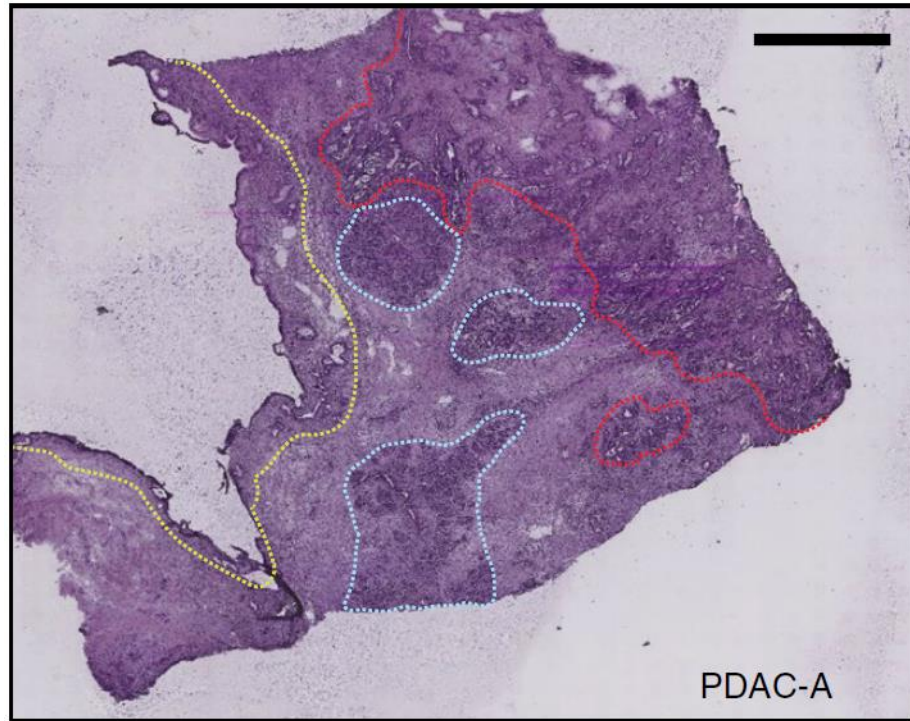
# Spatial edge refinement



# Spatial Deconvolution



# Spatial Deconvolution



Histological  
annotation  
key

<span style="color: red;">■</span>	Cancer cells and desmoplasia
<span style="color: yellow;">■</span>	Duct epithelium
<span style="color: lightblue;">■</span>	Normal pancreatic tissue
<span style="color: green;">■</span>	Interstitium

