



German Conference on Bioinformatics

WS8: Spatial domain identification: computational methods for discovering tissue architecture

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Part 0

Background to spatial transcriptomics

Spatial transcriptomics

nature methods

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Review Article | Published: 10 March 2022

Museum of spatial transcriptomics

[Lambda Moses](#) & [Lior Pachter](#) 

[Nature Methods](#) **19**, 534–546 (2022) | [Cite this article](#)

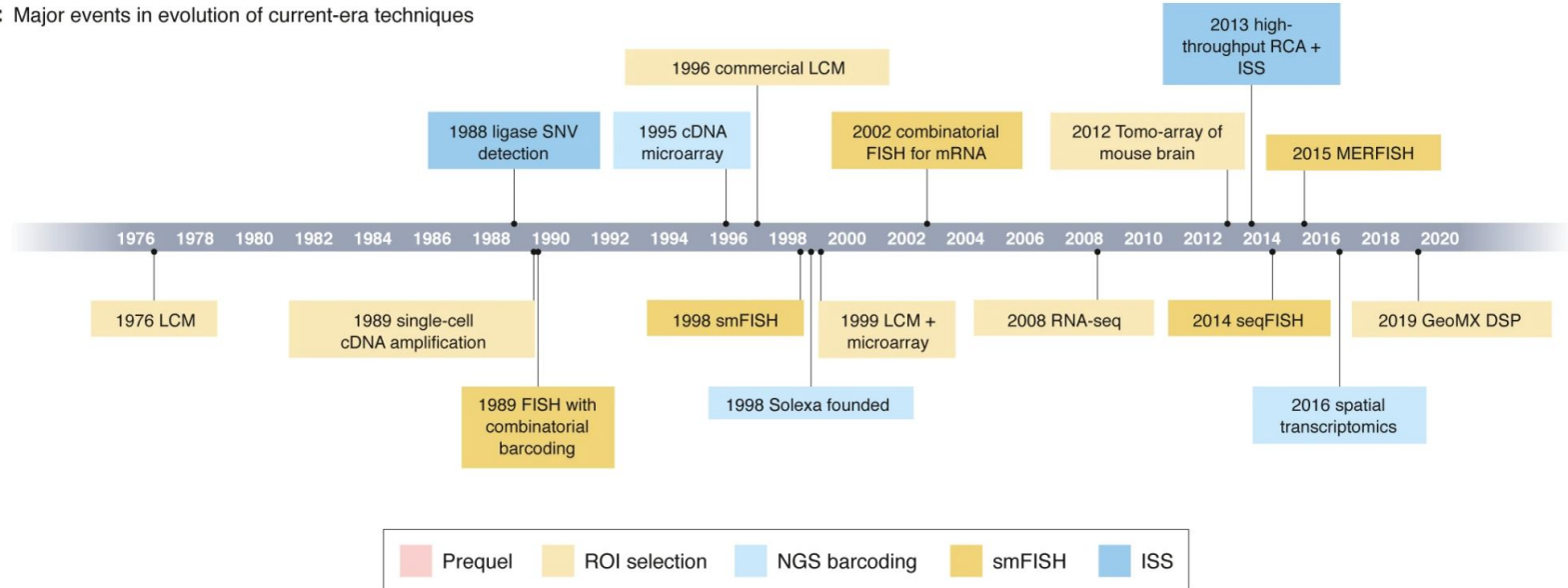
135k Accesses | **895** Citations | **575** Altmetric | [Metrics](#)

Database - <https://www.nature.com/articles/s41592-022-01409-2#Sec20>

Online supplement: https://pachterlab.github.io/LP_2021/

Spatial transcriptomics

c Major events in evolution of current-era techniques

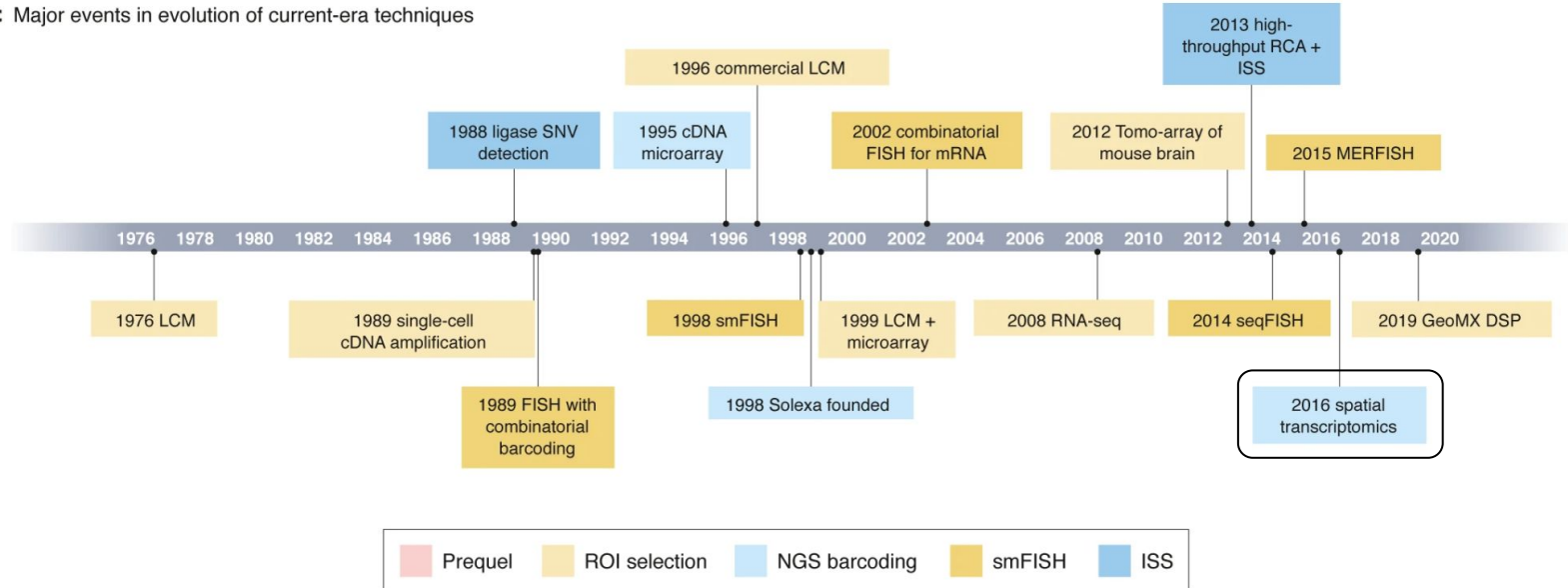


Database - <https://www.nature.com/articles/s41592-022-01409-2#Sec20>

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Spatial transcriptomics

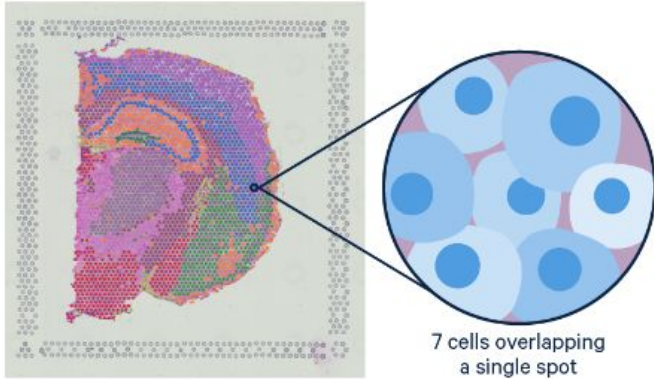
c Major events in evolution of current-era techniques



Database - <https://www.nature.com/articles/s41592-022-01409-2#Sec20>

Online supplement: https://pachterlab.github.io/LP_2021/

Spatial transcriptomics: Visium



Each spot is a mixture of ~1-10 cells, depending on tissue thickness ([source](#))

Spot diameter: 55 μm

Center to center inter-spot distance: 100 μm

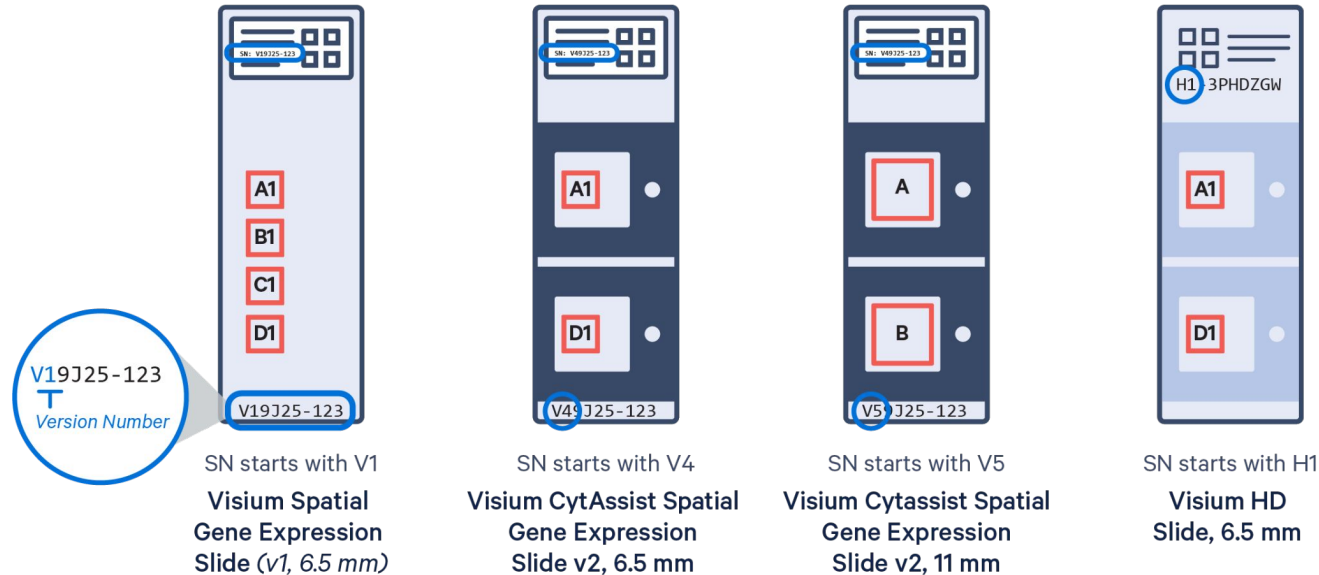
10x Visium

<https://www.10xgenomics.com/platforms/visium>

Spatial transcriptomics: Visium

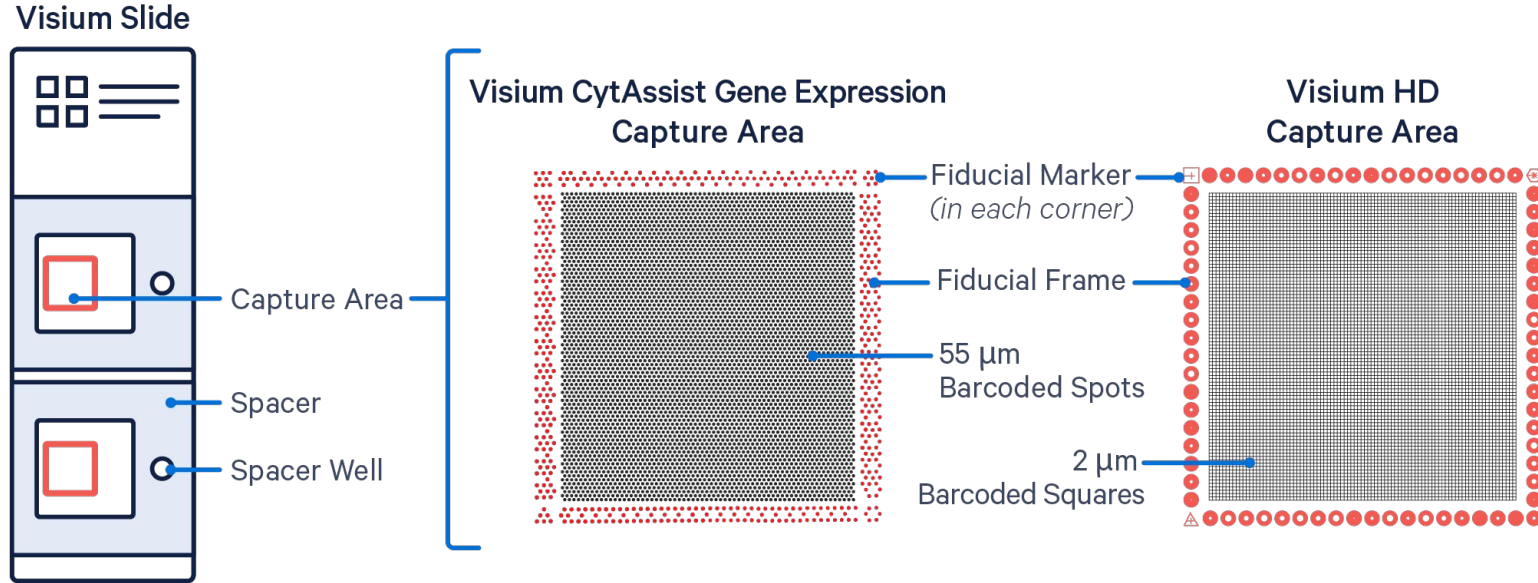
Serial Number locations

Capture Areas



Source: 10x Genomics

Spatial transcriptomics: Visium



Source: 10x Genomics

Spatial transcriptomics: Visium

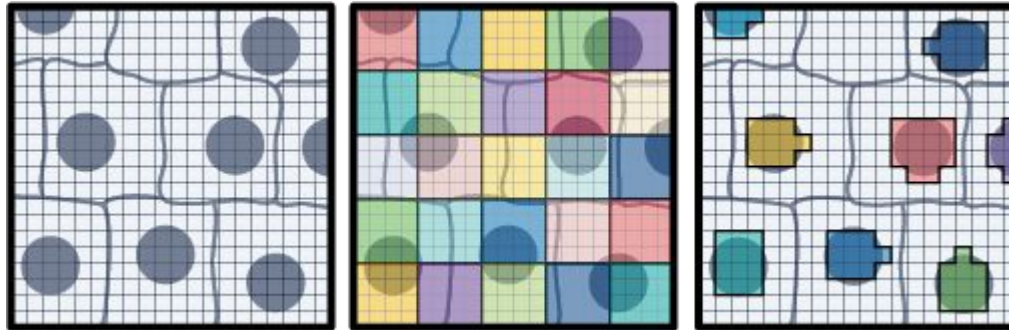


Source: 10x Genomics

Spatial transcriptomics: Visium

Visium v1	Visium v2	Visium HD
<ol style="list-style-type: none">1. 55 μm spots2. 100 μm center-to-center distance3. ~5,000 spots per capture area4. 6.5 \times 6.5 mm capture area5. Poly(dT)-based (reverse transcription)6. Direct placement of fresh frozen (FF) ~10 μm tissue sections7. Supra-cell resolution8. Easiest to analyze	<ol style="list-style-type: none">1. 55 μm spots2. 100 μm center-to-center distance3. ~5,000 spots per capture area4. 6.5 \times 6.5 mm capture area5. Probe-based with gene-specific probes6. Cytassist placement of FF and FFPE ~10 μm tissue sections7. Supra-cell resolution8. Can be noisy	<ol style="list-style-type: none">1. 2 μm bins2. 2 μm \times 2 μm squares3. ~11 million 2 μm bins4. 6.5 \times 6.5 mm capture area5. Probe-based with gene-specific probes6. Cytassist placement of FF and FFPE ~10 μm tissue sections7. Single-cell resolution8. Lowest depth

Visium HD: cell level analysis



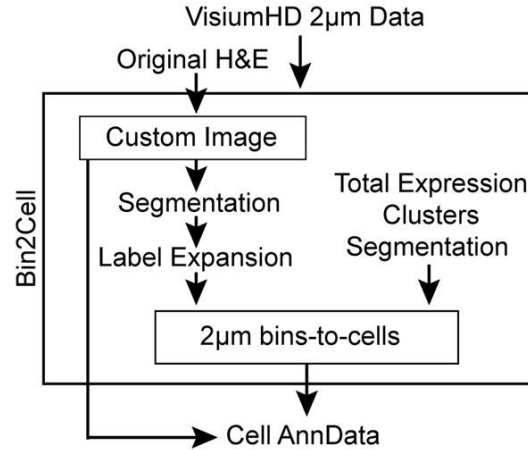
Combined Visium HD + DAPI staining of H&E

Source: [10x Genomics](https://www.10xgenomics.com)

Workflow:

<https://www.10xgenomics.com/analysis-guides/segmentation-visium-hd>

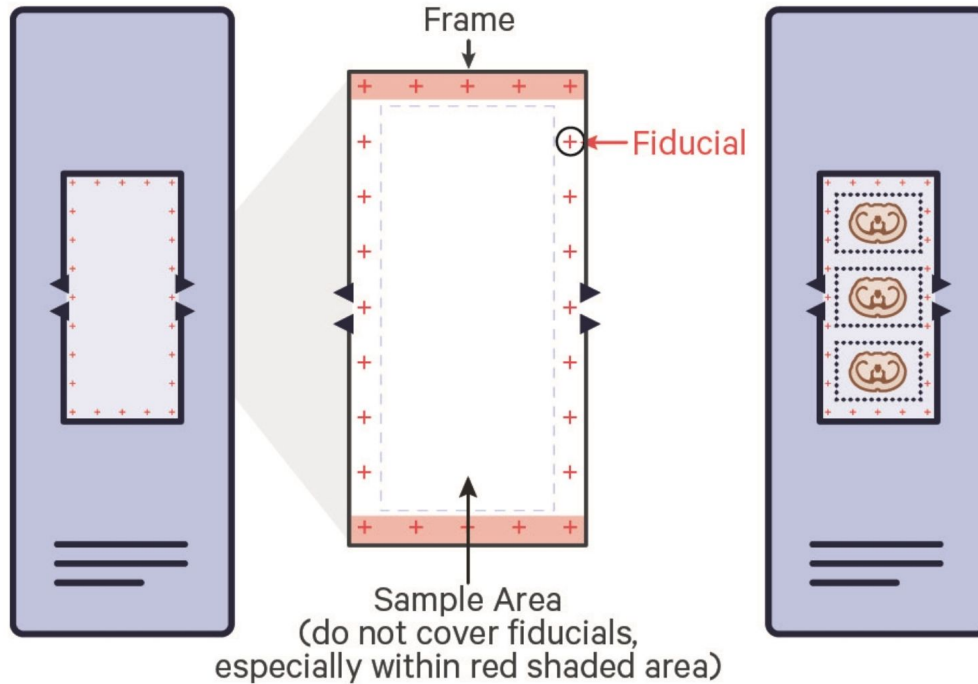
Spatial transcriptomics: Visium



Bin2Cell

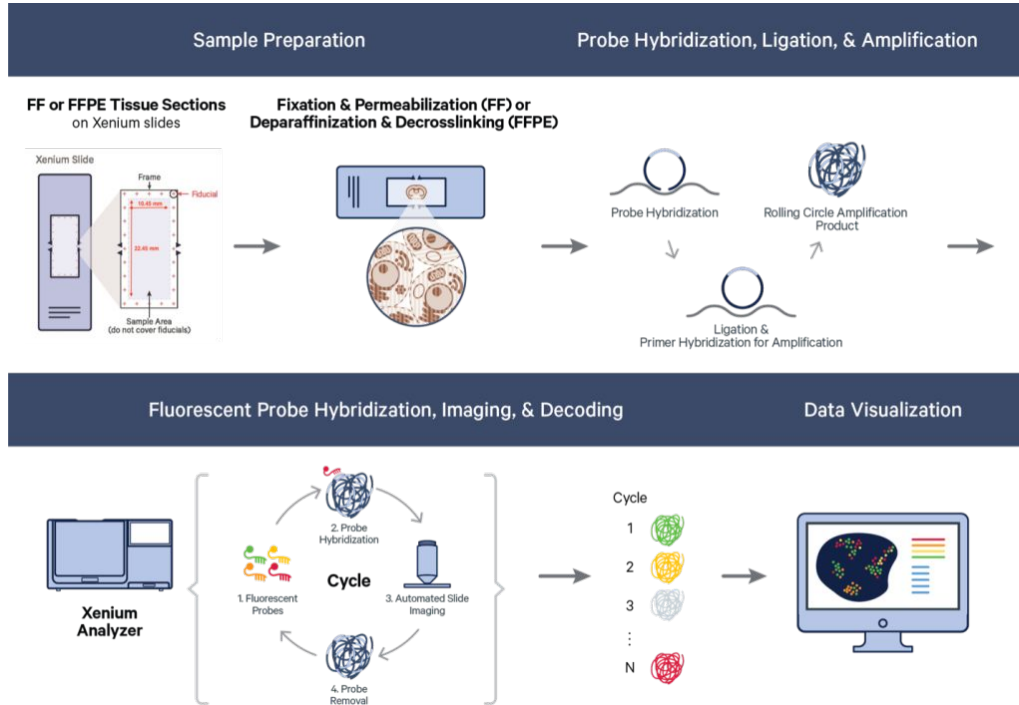
Polański et al., 2024. *Bioinformatics*.

Spatial transcriptomics: Xenium



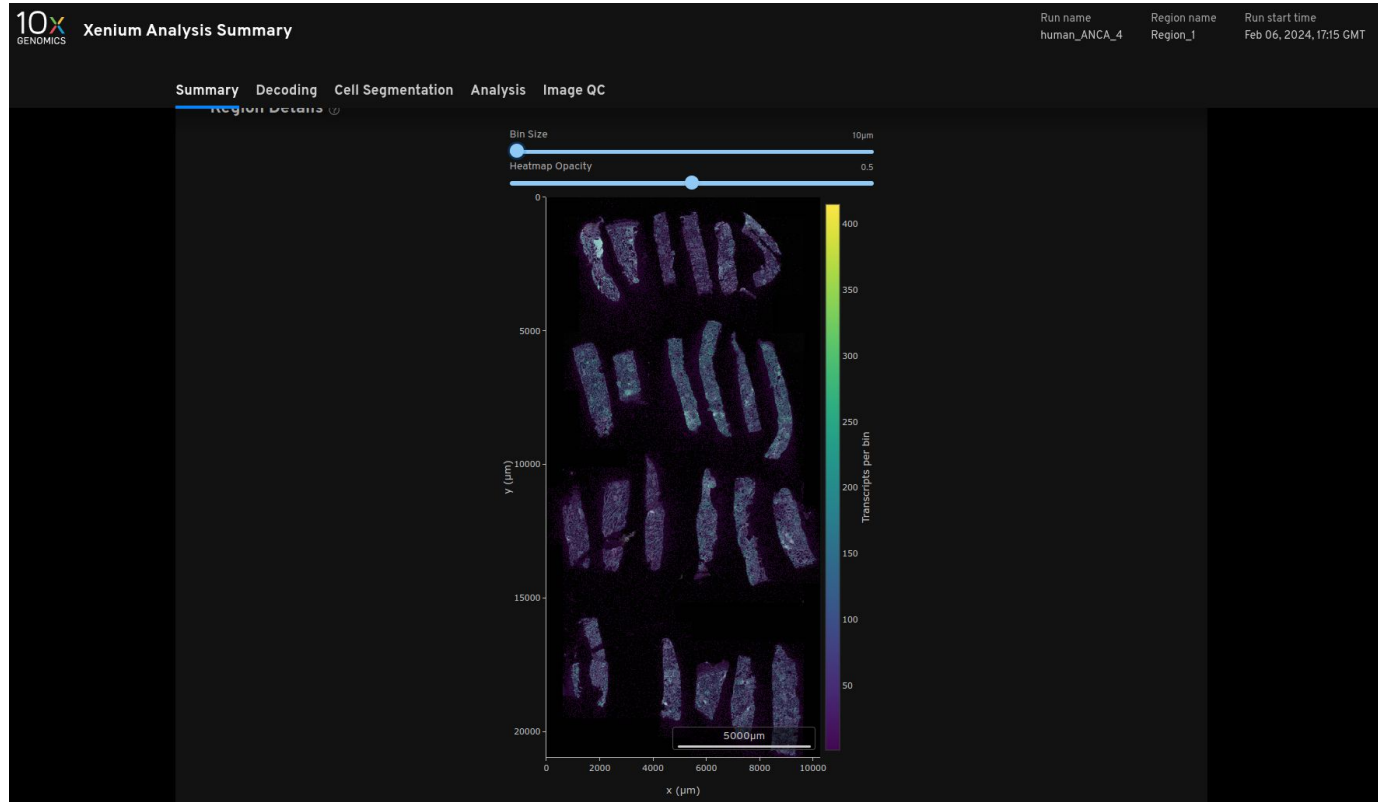
Source: 10x Genomics

Spatial transcriptomics: Xenium



Source: 10x Genomics

Spatial transcriptomics: Xenium

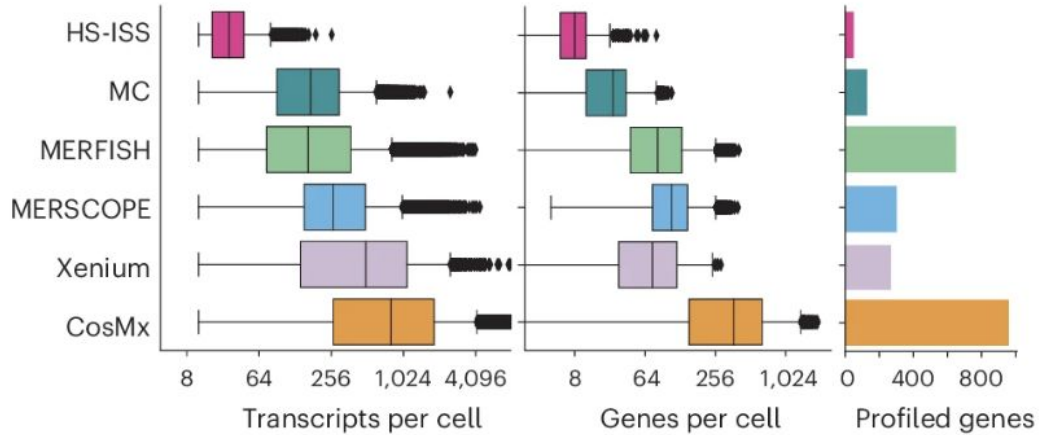


Slide area:
12mm x 24 mm
Capture area:
10.45 x 22.45

Spatial transcriptomics: Xenium

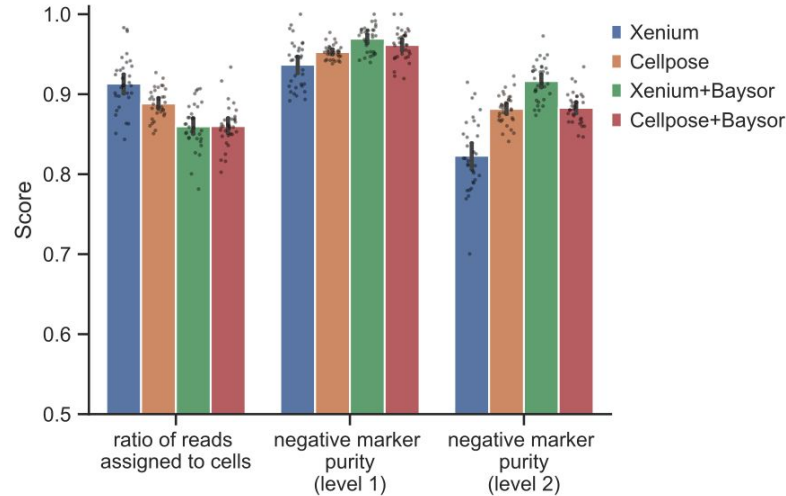
Xenium v1	Xenium prime
<ol style="list-style-type: none">1. Panel size: 480 genes, ~3 probes per gene2. Predesigned panels available: https://www.10xgenomics.com/products/xenium-v1-panel3. Custom panels can be made4. Human, mouse & other species with custom probe design	<ol style="list-style-type: none">1. Panel size: Upto 5,000 genes2. Lower per gene sensitivity3. Predesigned panels available: https://www.10xgenomics.com/products/xenium-5k-panel4. No custom panels - 100 genes can be added to 5000 genes5. Only for humans and mice

Spatial transcriptomics: Xenium



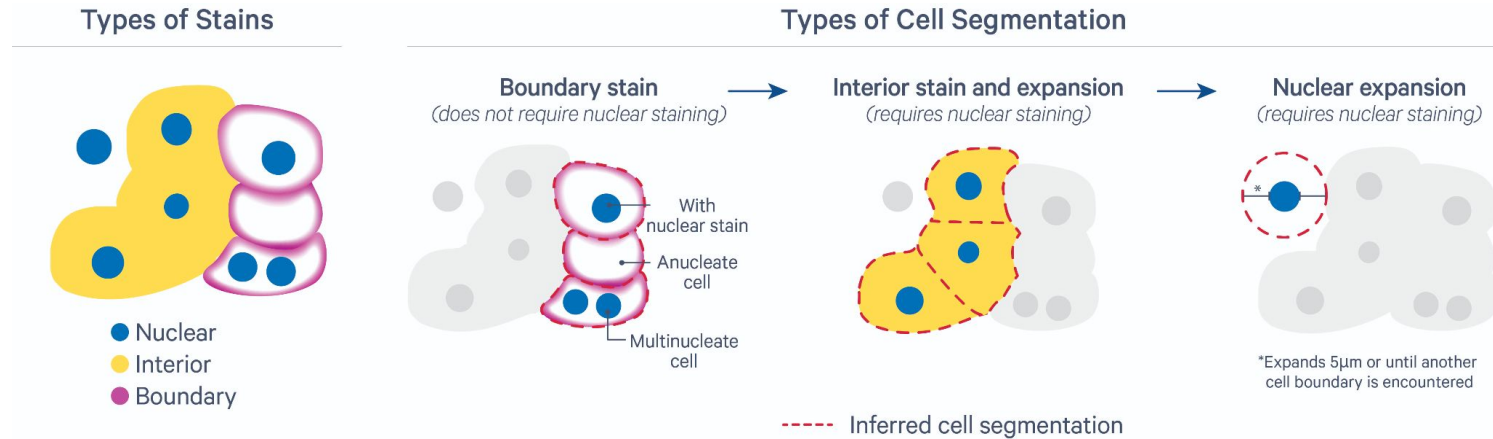
Salas et al., 2025. *Nature Methods*.

Spatial transcriptomics: Xenium



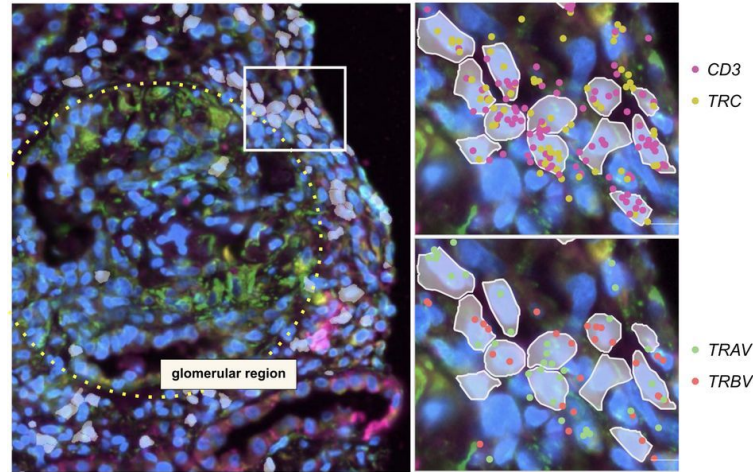
Sultana, Khatri & Yousefi et al., 2025. *Nature Immunology*. In press.
Baysor: Petukhov et al., 2021. *Nature Biotechnology*.
Cellpose: Stringer et al., 2020. *Nature Methods*.

Spatial transcriptomics: Xenium



Source: 10x Genomics

Spatial transcriptomics: Xenium



Ly & Schaub et al., 2025. *bioRxiv*.

Questions?