Spatial Transcriptomics
Digital Pathology to Investigate Intratumor Heterogeneity in Breast Cancer

Fredrik Salmén1, Sanja Vickovic1, Anders Jemt1, Joseph Bergenstahle1, Jose Fernandez2, Annelie Mollibrink3, Johan Vallon-Christersson1, Johan Staat1, Jan Hakkinen4, Anna Ehinger5, Fredrik Pontén5, Bill Day6, Samina Jafri7, Jonas Frisén7, Åke Borg7, Joakim Lundeberg8 and Patrik Ståhl1,2

An Overview of the Spatial Transcriptomics Method

1. Sectioning and Imaging on Spatially Barcoded Array
2. Permeabilization and cDNA Synthesis
3. Sequencing, Analysis and Visualization

Fluorescently Labeled cDNA Proves Localized RNA Capture

Detection of Tissue Specific Genes in FFPE Xenograft Samples

Compared to Regular RNA-seq

Analysis of Clinical Breast Cancer Sampes

Selecting Spots in Areas of Interest
Dimensionality Reduction and Hierarchical Clustering
Visualize the Location of Clusters and Find Marker Genes
Combine Several Sections and Visualize Spatial Expression Patterns in 3D