

**Title:** Decoding Prostate Tumor Immune Dynamics Through Spatial transcriptome Profiling**Authors:**

*Karishma Sajnani, Eirik Høye, Sini Eerola, Antti Kiviaho, Heini Kallio, Teuvo Tammela, Teemu Murtola, Tapio Visakorpi, Matti Nykter, Anthony Mathellier and Alfonso Urbanucci*

**Keywords:**

Molecular biology, cancer, immune cell spatial architecture

**Abstract**

Prostate cancer (PC) progression and relapse are strongly influenced by the tumor immune microenvironment. However, conventional molecular profiling lacks spatial context, limiting insights into how immune dynamics shape patient outcomes. This project aims to integrate spatial transcriptomics (ST) with spatially resolved T- and B-cell receptor (TCR/BCR) repertoires to stratify PC patients for risk and therapeutic response.

We will apply a modified 10x Genomics Visium protocol that enables both gene expression (GEX) and enrichment of TCR/BCR repertoires, profiled by a combination of both short-read and long-read sequencing to spatially barcoded cDNA, enabling full-length mRNA isoforms resolution and quantification of alternative transcript usage in different areas of the tumor and in the tumor microenvironment. This combined strategy provides a unique opportunity to decode both clonal immune dynamics and complex splicing patterns in the preserved tissue architecture.

For our study we will use specimens from a cohort of 48 prostate tumors already profiled with traditional ST using 10x Genomics Visium protocol.

Expected outcomes include the discovery of immune signatures and alternative associated with specific interplaying tumor compartments (stroma and immune) and predictive of metastatic potential and treatment response. This work will contribute to employ stratification methods in precision cancer medicine through the use of companion biomarkers to select candidate patients for potentially benefiting from immunotherapy.