

Breast cancer (BC) is the most common cancer among Polish women. Despite a relatively good prognosis in early stages, the metastatic disease remains hardly manageable and states the main cause of BC mortality. The exact mechanisms involved in the metastatic cascade remain not fully recognised. Thus, there is a strong need for research which can translate to better understanding of BC biology and establishing new molecular targets for adjuvant therapy. Despite advances of molecular biology and detection techniques pathologists struggle to explain mechanisms of the carcinogenesis and lymph node metastases of BC.

The Visium Spatial Gene Expression from 10x Genomics supports and extends contemporary histopathological analysis. It enables comprehensive spatial transcriptomic analysis of genes (not only those whose products can be stained) and types of certain cells. Moreover, it provides a revolutionary data which cannot be ignored.

Originally, Visium Spatial Gene Expression was designed in 2018 and based on usage of fresh-frozen specimen, however, last year the protocol for Formalin-Fixed Paraffin-Embedded (FFPE) was discovered. Based on recent studies the specificity of FFPE is comparable to fresh-frozen samples which enables analysis of thousands of samples, since FFPE or decades was the most popular form of tissue preservation.

The purpose of this project is to provide a proof of concept for the Visium Spatial Gene Expression using Formalin-Fixed Paraffin-Embedded specimen. By analysing the spatial transcriptomic expression of breast tumors and corresponding lymph nodes metastases we would like to provide novel data about its potential mechanisms as well as discover new therapeutic targets for metastatic disease.