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Poster Abstract Form

Single-Section Spatial Transcriptomic and Metabolomic Profiling of the Pancreatic Cancer Microenvironment

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Introduction
Pancreatic ductal adenocarcinoma (PDAC) is one of the most lethal cancers, with a 5-year survival rate of only 13%. Poor prognosis stems from late detection and profound therapeutic resistance, driven in part by the dense desmoplastic stroma and poor vascularity, which limit drug delivery and immune cell infiltration.

Methods
To investigate how the PDAC tumour microenvironment is organised, we performed a spatial multi-omics analysis combining spatial transcriptomics with mass spectrometry imaging (MSI) of lipids and metabolites. By integrating gene expression, histological annotation, and metabolomic data, we developed an approach to spatially map cell-type responses within intact PDAC sections. MSI, using Desorption Electrospray Ionization (DESI) and Matrix-Assisted Laser Desorption Ionization (MALDI), was employed to define the distribution of metabolites, lipids, and pharmaceutical compounds directly on tissue sections.

Results
Preliminary DESI MSI data revealed distinct spatial patterns of drug distribution alongside lipid and metabolite signatures enriched in treated regions. Spatial transcriptomics identified cellular diversity within PDAC tumours, showing that specific transcriptional states and spatial niches are critical determinants of drug response.

Conclusion
We have developed a robust single-section method that enables simultaneous analysis of transcriptomics and metabolites at single-cell resolution. This platform can now be scaled to tissue microarrays, providing unprecedented insight into tumour-stroma interactions and informing the development of novel therapeutic strategies targeting the PDAC microenvironment.