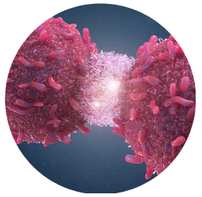


## The Power of Multiomics

Multiomics and spatial multiomics analyses have become critical methods in studying tumor samples. Considering the spatial proximity of cells within a tissue sample alongside differential expression analysis offers a more comprehensive picture of disease development, key driver mutations, and possible therapeutic targets.

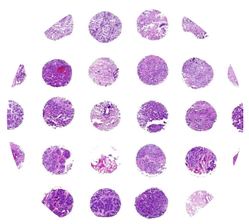
## A 2021 publication by Rico et al.

FFPE tissues (both tumor and normal) were analyzed by:

- RNA sequencing for differential gene expression
- whole exome sequencing for SNPs and indels
- immunohistochemistry (IHC) for expression and cellular localization of proteins of interest
- Digital Spatial Profiling (DSP) (NanoString) to view expression patterns in spatial context, i.e. tumor cells and cells proximal that may provide clues to tumorigenesis
- qPCR for confirmation of differential gene expression

## Hypothesis

This spatial multiomics study led to a hypothesis for the mechanism driving the development of DGASTs from normal tissue, as well as a potential therapeutic not previously considered for this disease subtype



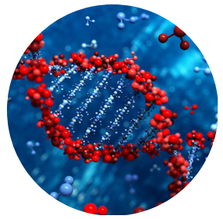
## The Importance of Tissue Controls

- As with any comparative study, utilizing proper control groups is critical
- Since DGASTs are rare tumors, samples in this study were limited, and adjacent normal tissue was not available
- To resolve this issue, normal tissue was obtained from various sources, including normal pancreas and duodenum from BioChain (Newark, California)

# Multiomics Analysis

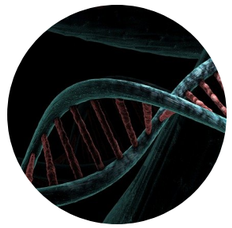
*Multiomics Analysis Leads to Tumorigenesis Hypothesis and Identification of Possible Therapeutic in Rare GI Tumor Subtype*

**www.biochain.com**



## Multiomics Profiling

- RNA sequencing followed by differential expression analysis was used to identify genes with high expression in DGASTs vs. other GI tumors
- Once target genes were identified, IHC, qPCR and DSP were performed to explore differential expression in BG vs. DGAST tumors



- One particular gene of interest (NKX6.3) was found by IHC and qPCR to be expressed in DGAST cells but not in normal tissue – suggesting it plays a role in tumorigenesis or precursor events in the tissue prior to tumor formation
- FFPE samples were analyzed with DSP to quantify a 40 target panel of neural-related antibodies and tumor morphology

- DSP enables “visualization” of spatial context in samples that is otherwise missed by bulk RNA sequencing
- In this study, DSP helped to identify pathways likely involved in the reprogramming of normal BG cells into DGAST tumors
- This was possible by comparing expression patterns in stromal cells surrounding the tumors with cells of similar tissues to identify unique patterns.

BioChain Institute Inc.