Background Colorectal cancer (CRC) is a leading cause of cancer-related deaths, often attributed to genetic and epigenetic modification. The investigation of tumor microenvironment (TME) profiling through an in-depth analysis of tissue samples reveals the spatial gene expression patterns of known CRC markers and visualizes cell composition and localization. The aim of this study is to uncover potential therapeutic targets by delving into the mechanisms of tumor formation.

Methods The formalin-fixed paraffin-embedded (FFPE) tissue samples from three primary colon adenocarcinoma tissues (PT) and their matched adjacent normal tissues (PN) were selected from BioChain’s biorepository. The tissue sections were stained with Hematoxylin and Eosin (H&E), and the stained images were annotated by pathologists. The 10x Genomics Visium Spatial Gene Expression for FFPE assay was performed with more than 18,000 gene probe pairs in human spatial profile, followed by whole transcriptome analysis. This technique used mRNA-binding oligonucleotides to capture gene expression within 4,992 spatially barcoded spots. Integrating imaging and sequencing data enabled the acquisition of a spatially resolved transcriptome of CRC heterogeneity.

Results The results showed a strong correlation between the annotations of both PT and PN tissue samples and the spatial gene expression clustering. By overlaying the total gene counts on the H&E-stained tissue image, approximately 16,000–17,000 genes were detected in each sample. The PT samples expressed a median of around 5,500 genes per spot, while the PN samples expressed a median of around 1,600 genes per spot. Notably, the study of gene expression in PT samples showed overexpression of well-known CRC markers (APOE, SCD, IGFBP3, TIMP1, SPARC), while several markers (DES, CA1, KLF4) were down-regulated.

Conclusions These findings provide valuable insights into tumor heterogeneity, spatial organization of cells within the TME, and the identification of biomarkers. BioChain Institute, Inc. is uniquely positioned to assist researchers in studying various oncologic and diseased tissue types by offering comprehensive spatial whole transcriptome analysis. This assay enhances understanding of the TME, aids in discovering diagnostic and prognostic targets, and assists in development of personalized therapies for individual patients.

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