182 XENIUM IN SITU ANALYSIS AND REPRODUCIBILITY STUDY OF MULTIPLE CARCINOMAS FOR CLINICAL STUDIES

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Background 10x Genomics Xenium assay is the newest in situ spatial transcriptomics platform offering sub-cellular resolution in frozen and FFPE tissue sections for a deeper study of cellular mechanisms and interactions. Mapping RNA targets at high specificity with fully customizable assays and quick workflow, it uses rolling circle amplification and interpretation-ready data is available immediately after the run. At BioChain Institute, Inc. (BioChain), we are conducting validation studies for reproducibility of results with the Xenium platform using BioChain's oncology biospecimen.

Methods FFPE tumor tissues from BioChain's biorepository were screened by our pathologist for tumor content above 30%. Four carcinoma tissues from human breast, colon, lung, and kidney with high DV200 scores were selected. A tissue array was constructed with these tissues to place within the Xenium slide's imageable area. Two serial sections were used in Xenium assay, which were performed according to the 10x Genomics' protocol by different operators independently. The pre-designed Human Multi-Tissue and Cancer Panel was used for targeting 377 genes. The Post-Xenium H&E staining and imaging was performed, and the H&E image was integrated with the DAPI image using Xenium Explorer. Further computational analysis was performed by Aspect Analytics to compare the data between the serial sections.

Results The results were found to be reproducible between two different operators. For example, in the breast section, over 96,000 cells were detected and median transcripts per cell were 70 in both the runs (figure 1). There were 20 clusters representing different cell types/states, 99% transcripts were within cells, and ~85% of the transcripts were found to be high quality. Pearson coefficient between the serial sections data showed positive correlation (figure 2).

Conclusions Xenium platform is a powerful tool for the sub-cellular spatial transcriptomics study of tissues with targeted gene panels.

Consent All samples used in the study were donor consented, de-identified, and IRB approved.

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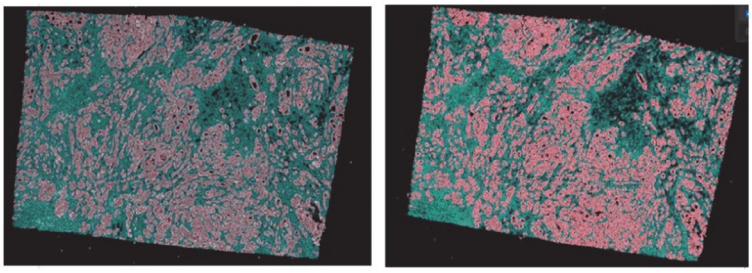
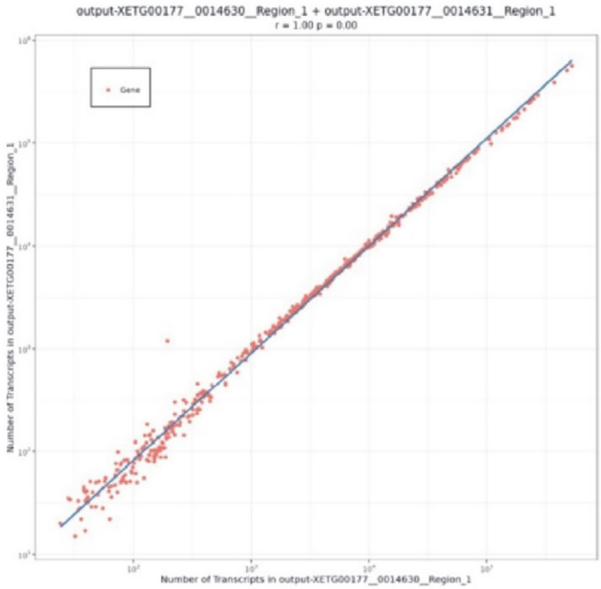


Abstract 182 Figure 1 Xenium Explorer images of the two Breast serial sections at K-2 means clustering showing similar expression distribution across the two sections



Abstract 182 Figure 2 Correlation curve between the Breast carcinoma serial sections' Xenium datasets, showing positive correlation