

Liver

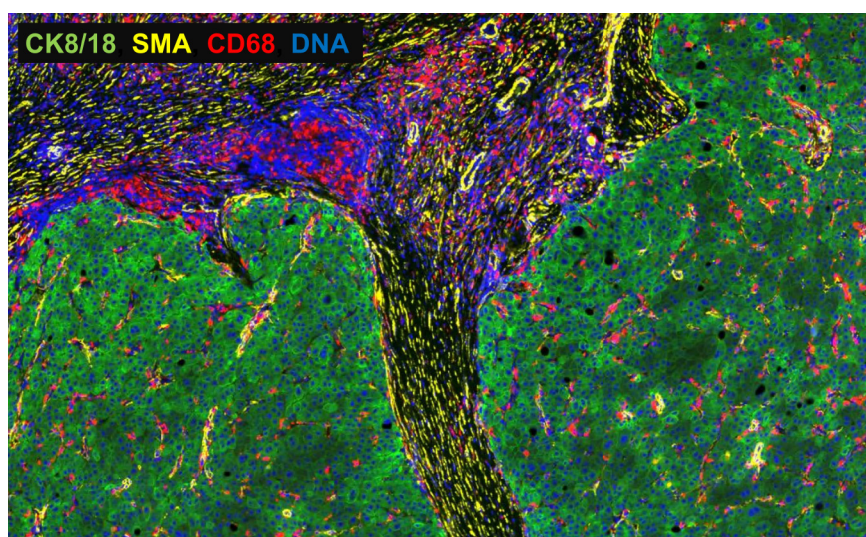
Hepatocellular Carcinoma

Study Purpose

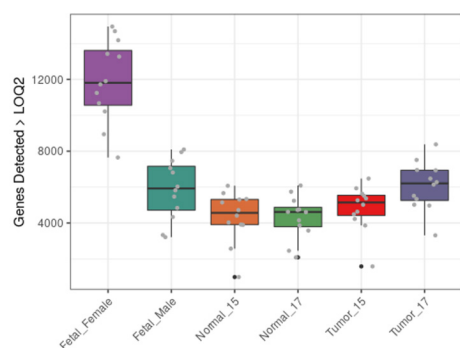
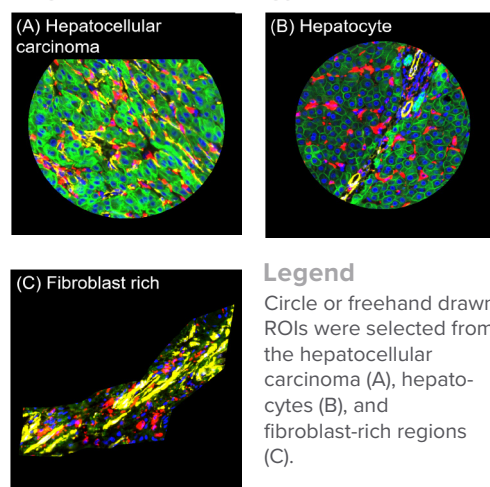
Recent studies have reported that there is a shared immunosuppressive onco-fetal ecosystem between human fetal liver and Hepatocellular Carcinoma (HCC). To further study the interplay of fetal-associated liver cells, fibroblasts and HCC cells, regions of interest (ROIs) were selected on areas of the tissue characterized by HCC, healthy hepatocytes, and fibroblast-rich regions. These regions were profiled using the GeoMx Human Whole Transcriptome Atlas. Differences in the spatial transcriptome of these tissues were explored.

Study Summary

Sample Type	FFPE
Species	Human
AOI* Strategy	Geometric
Assay	Human Whole Transcriptome Atlas
Morphology Markers	CK8/18, CD68, SMA, DNA
Targets Detected	17,834 targets
Application	Biomarker discovery



Segmentation Strategy



Legend

The number of targets detected above the background (LOG2*) by AOI groups.

*AOI = Area of Illumination

Acknowledgement: We sincerely thank Dr. Florent Ginhoux from Singapore Immunology Network (SIgN), A*STAR, for sharing these images.

For more information, please visit

<https://nanosttring.com/geomx-morphology-markers/>

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