

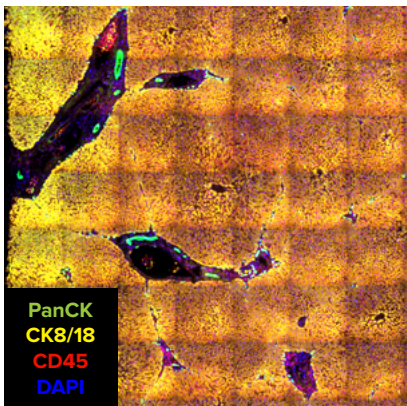
Human Healthy Liver

Study Purpose

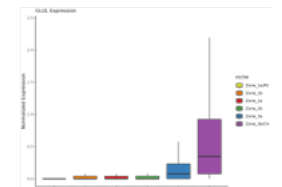
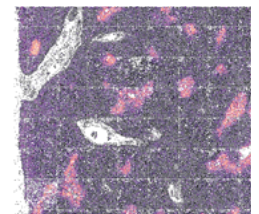
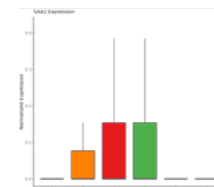
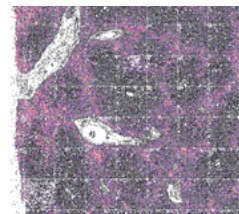
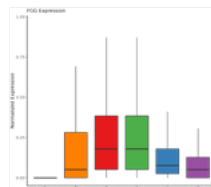
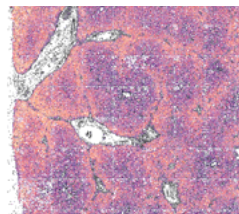
A whole 5 µm slide of FFPE human normal liver from a 35-year-old male was profiled with CosMx Human Universal Cell Characterization RNA panel. In addition to the segmentation markers CD298 and B2M, the same tissue section was also co-stained with a la carte marker CK8/18 to improve cell segmentation quality on normal liver tissue. Like many archived FFPE tissue blocks, this sample has medium-quality RNA with a DV200 of 58.59%. Differential expression of genes (e.g., FGG, SAA1 and GLUL) was observed in 3 hepatocytes zones (Zone1, Zone2 and Zone3). Liver lobular structure is apparent and agrees well with the histologist's annotation. SMI RNA profile was compared against GTEx bulk RNAseq datasets of normal liver profiles and showed high correlation, indicating high specificity of SMI RNA profiling on liver tissue.

Study Summary

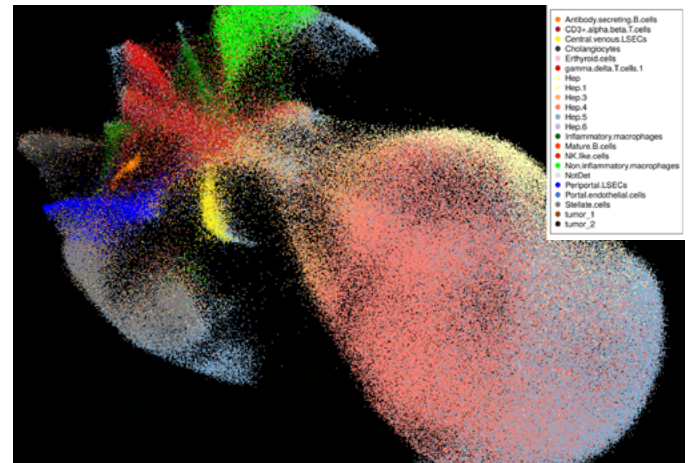
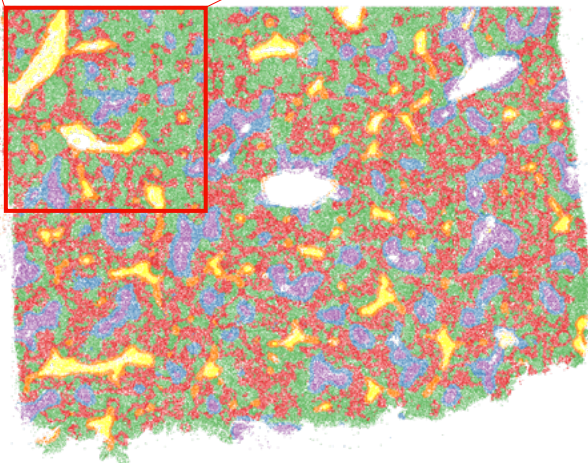
Tissue Type	FFPE Liver
Panel	1000-plex Human RNA Universal Cell Characterization
Segmentation Markers	PanCK, CK8/18, CD45, DAPI
Total tissue area analyzed	76 mm ²
Cells analyzed	340,517
% Cells passed QC	98 %
Number of Genes detected above background	589
% of transcripts assigned a cell	93 %
Mean total transcripts/cell	583
Maximum transcripts/ cell	5,916



Upfront segmentation marker staining



Liver lobule structure apparent from Hepatic zone gene expression



Tissue Neighborhoods

UMAP

For more information, please visit nanosttring.com/CosMx

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