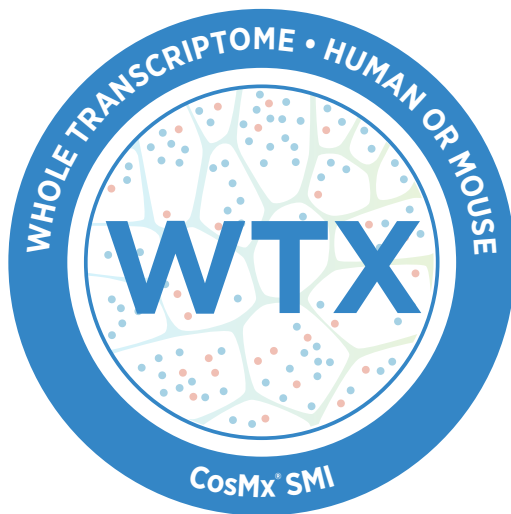




CosMx[®] Whole Transcriptome Assay

Reveal complete biology with whole transcriptome subcellular imaging in human and mouse samples

What if you could uncover the story of every pathway, every cell and every transcript—exactly where they belong? For the first time, image the whole transcriptome of every single cell with spatial context in human and mouse samples. With the CosMx Whole Transcriptome (WTX), project complete pathway biology in space, map every cell-to-cell interaction at the individual transcript level, and discover the unknown and unexpected—all with best-in-class sensitivity and genomic breadth within a single intact FFPE tissue section.



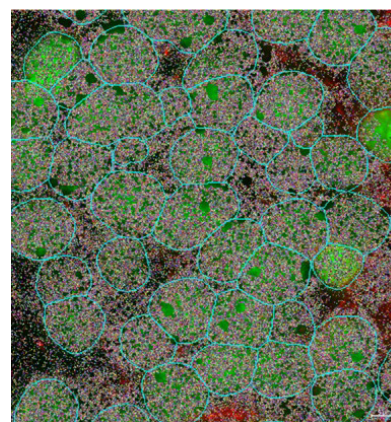
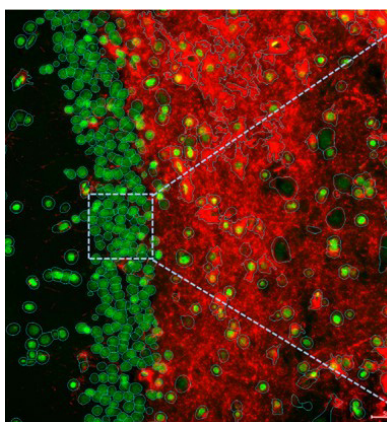
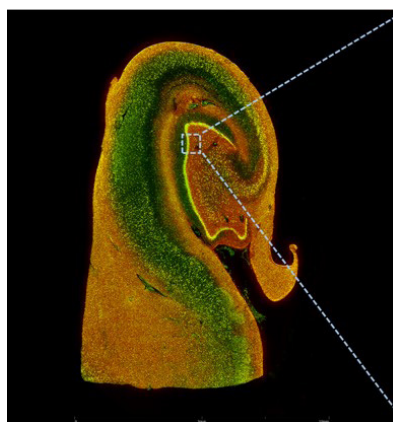
Product Highlights

- Covers >19,000 RNA targets in Human and >21,000 RNA targets in Mouse, providing full coverage across all protein coding genes
- Compatible with a wide range of tissues including FFPE and Fresh Frozen, to provide full coverage for single-cell spatial biology
- Fully customizable for CRISPR screening, TCR profiling and infectious disease applications
- Mouse WTX includes probes for common transgenes (*Cre* and *GFP*); key developmental lncRNAs (*H19*, *Hotair*, *Meg3*, *Neat1*, *Xist*); and isoform-specific probes for *Cdkn2a*; to support advanced applications common in mouse

Why use CosMx Whole Transcriptome Assay over scRNA-seq?

	scRNA-seq	CosMx SMI
Cells per Sample	10,000	500,000
Data points per sample (Millions)	200	>21,000
Cell Sub-sampling	5%	100%
Cell Loss	35%	0%
Cell Coverage	Partial (systematic loss of some cell types)	Full
Cell State	Biased	Full
Spatial Context	Lost	Intact

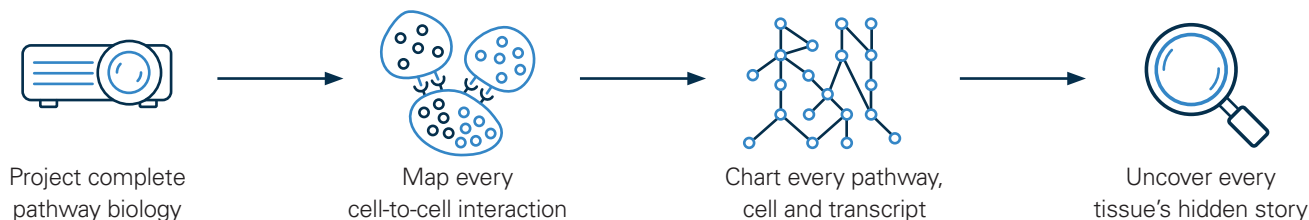
Based on typical values for an FFPE scRNA-seq workflow and CosMx SMI workflow



High Fidelity Transcriptomics

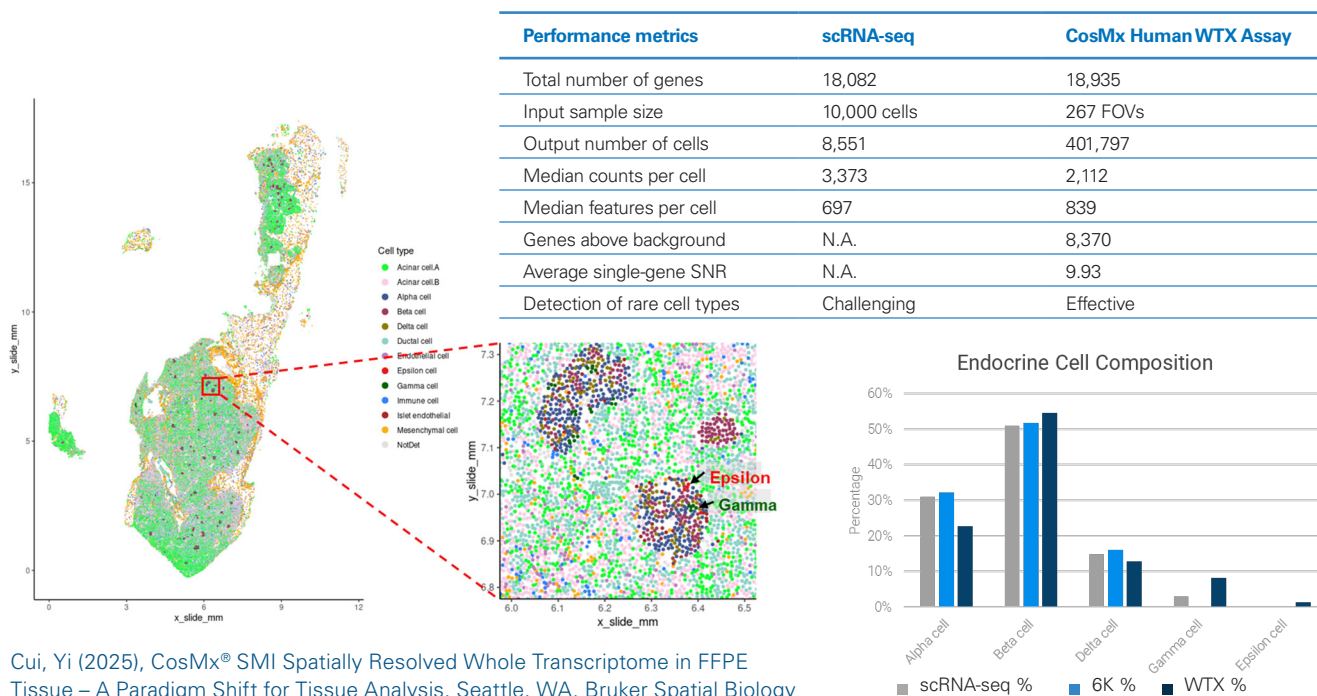
- Designed and validated for FFPE
- >99% protein-coding transcriptome
- Accurate cell segmentation

Key Benefits of Whole Transcriptome Imaging



Explore biology otherwise unmeasured and discoveries otherwise missed

Human Pancreas contains extremely rare Gamma (< 0.5%) and Epsilon (< 0.05%) endocrine cell types. Unbiased whole-transcriptome imaging of human pancreas with CosMx SMI enabled comprehensive detection of cellular diversity, including rare cell populations that are often missed by targeted and single cell approaches.

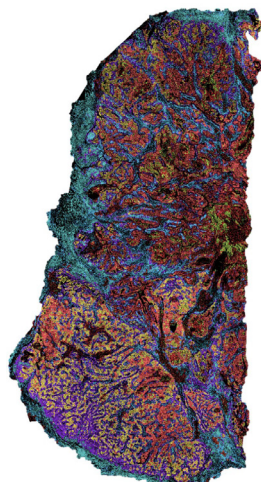


Cui, Yi (2025), CosMx® SMI Spatially Resolved Whole Transcriptome in FFPE Tissue – A Paradigm Shift for Tissue Analysis, Seattle, WA, Bruker Spatial Biology

Paradigm shift from inference to direct measurement

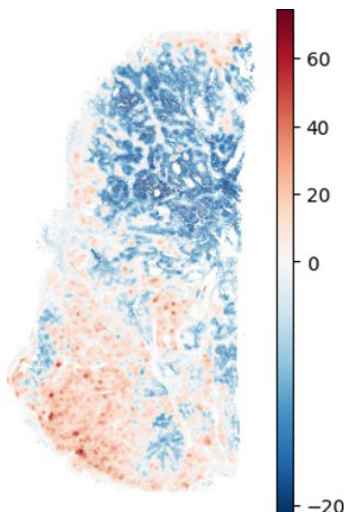
Move beyond inferring biology from cell types to directly measuring functional biological pathways in their spatial context across the tissue.

Breast Cancer



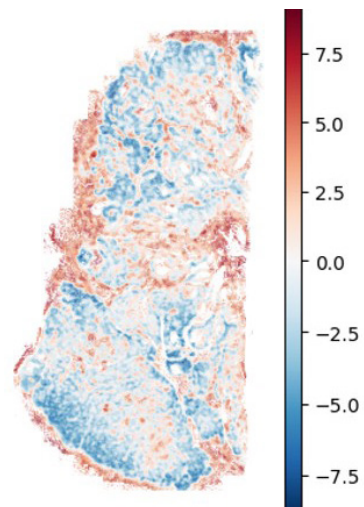
Novae spatial domains (K = 15)

Trail



Evading apoptosis

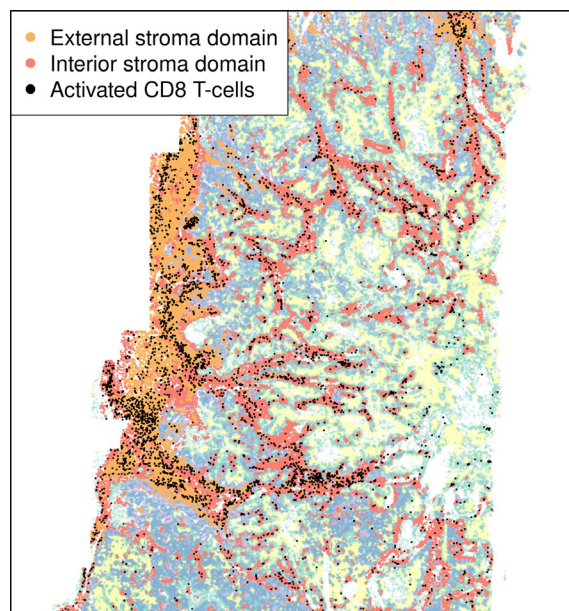
Jak-Stat



Dichotomy in immune response

From high-level pathways to unexpected biological discoveries in space

Develop a new understanding of genes in pathways otherwise missed without WTX



51 high-confidence T cell genes
enriched in tumor interior:

ADRA2B, ARMC2, B3GNT4, CDIP1, CEMP1, CNNM2, CRISP2, CTF1, CUBN, DDX28, ERMN, FAM98C, FBXO24, FEV, FOXD1, FOXH1, GAGE12H, GCGR, GLTPD2, GPR152, HACD4, HBM, JSRP1, KCNA3, KISS1R, KRT85, LHB, MBOAT4, MED140S, MPI, NEIL3, NRN1L, OR8U1, PGLYRP2, PRR33, PSD, RASGEF1A, RTL6, RTN4R, SAMD10, SMIM45, SPACA5B, SYNGR3, TBX10, TESC, TMEM145, **TNFRSF18**, TSPOAP1, UPK2, XCR1, ZNF80

Enriched for REACTOME
metabolism pathways

T-cell activation and survival

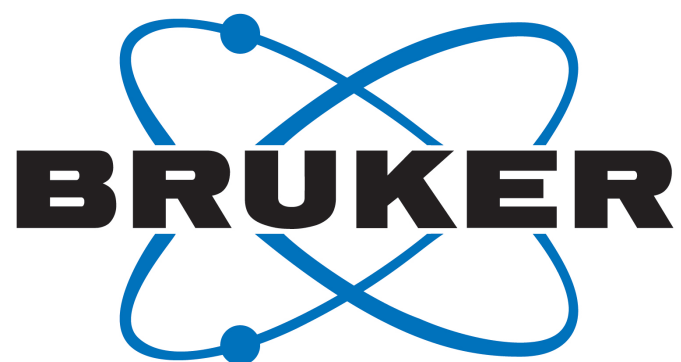
31 genes **depleted** in tumor
interior:

ARL4C, C11orf21, CCND3, CD52, CD69, CDAN1, CTRL, EPHA1, FCMR, **GIMAP2**, **GNG2**, GPRIN3, **GZMK**, **HLA-E**, IKZF3, IL2RG, IL32, IL7R, LCP1, MSL2, MYCBP2, POLG2, PRKACB, RGS1, RPS29, RUNX3, THEMIS, TRAF1, TRDC, TTC13, USP7

Enriched for REACTOME
cell cycle and adaptive
immune pathways

T-cell survival (not in any
other high-plex spatial panel)

Cytotoxic killing



For more information, please visit brukerspatialbiology.com/CosMxWTX

Bruker Spatial Biology

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