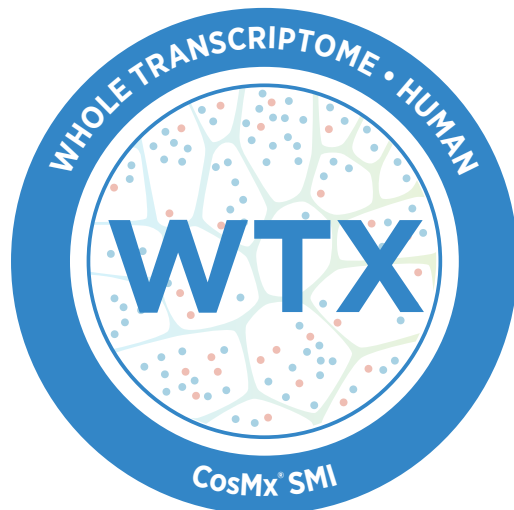




CosMx[®] Human Whole Transcriptome Assay

Reveal complete biology with subcellular whole transcriptome imaging for uncharted discoveries

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. 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.



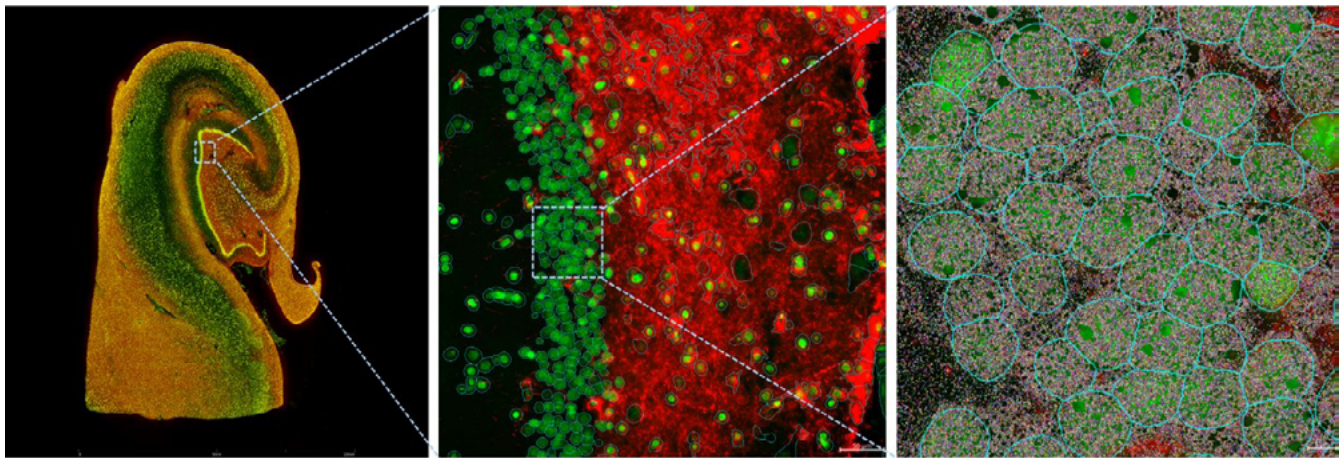
Product Highlights

- Covers ~19,000 RNA targets for full coverage across all protein coding genes
- Best in class, multimodal cell segmentation provides true single-cell resolution
- Compatible with a wide range of tissues including FFPE and Fresh Frozen, to provide full coverage for single-cell spatial biology
- Visualize and analyze data with the interactive, easy to-use AtoMx[™] Spatial Informatics Platform (SIP)

Why use CosMx Human Whole Transcriptome Panel over scRNA-seq?

	scRNA-seq	CosMx SMI
Cells per Sample	10,000	500,000
Data points per sample (Millions)	200	~19,000
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	Maintained

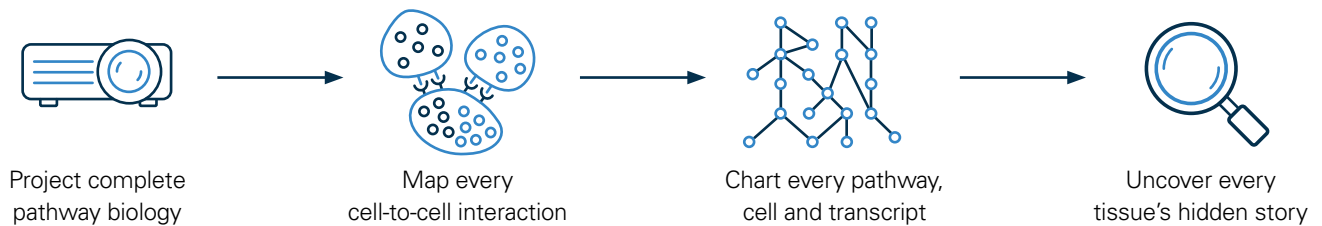
Based on typical values for an FFPE scRNA-seq workflow and CosMx SMI workflow



High Fidelity Transcriptomics

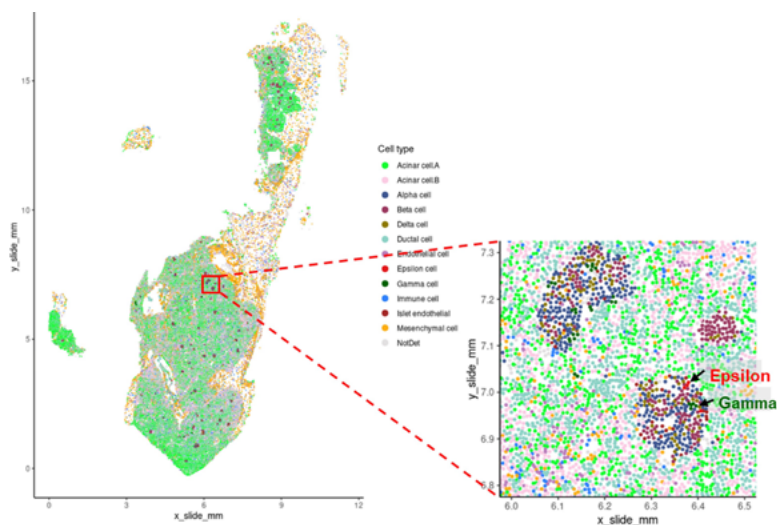
- Designed and validated for FFPE
- >99% protein-coding transcriptome
- Accurate cell segmentation

Key Benefits of Whole Transcriptome Imaging



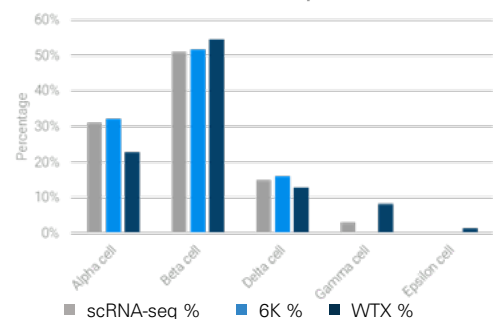
Detect rare cell types missed by lower plex panels and lower throughput platforms

Pancreas contains extremely rare Gamma (< 0.5%) and Epsilon (< 0.05%) endocrine cell types



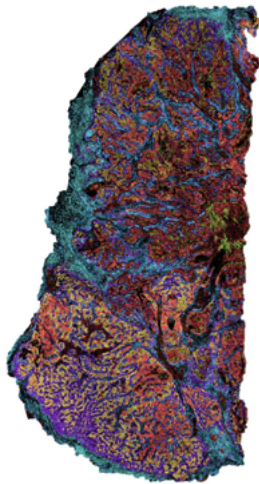
Performance metrics	scRNA-seq	CosMx
Total number of genes	18,082	18,935
Input sample size	10,000 cells	267 FOVs
Output number of cells	8,551	401,797
Median counts per cell	3,373	2,112
Median features per cell	697	839
Genes above background	N.A.	8,370
Average single-gene SNR	N.A.	9.93
Detection of rare cell types	Challenging	Effective

Endocrine Cell Composition



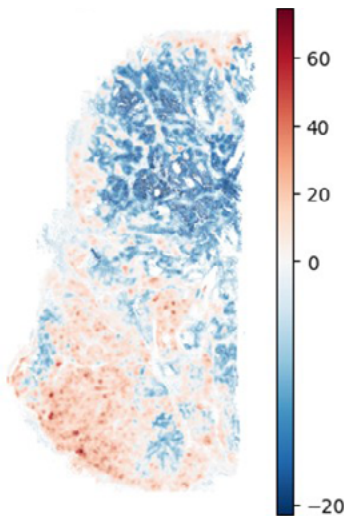
Paradigm shift from cell types to inference biology to direct measurements of functional biological pathways

Breast Cancer



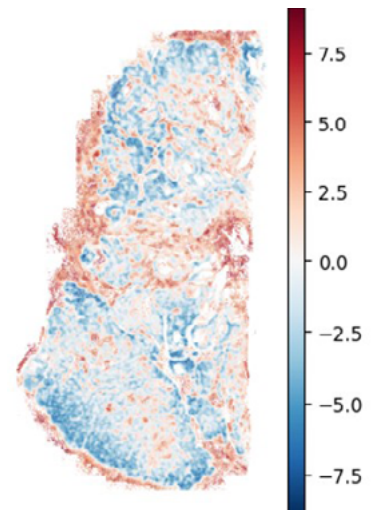
Novae spatial domains (K = 15)

Trail



Evading apoptosis

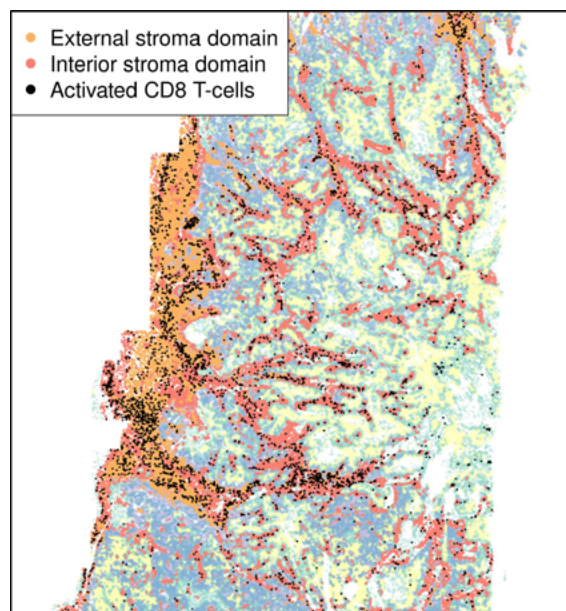
Jak-Stat



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, ORBU1, PGLYRP2, PRR33, PSD, RASGEF1A, RTL6, RTN4R, SAMD10, SMIM45, SPACASB, SYNGR3, TBX10, TESC, TMEM145, **TNFRSF18**, TSPOAP1, UPK2, XCR1, ZNF80

Enriched for REACTOME metabolism pathways

T-cell activation and survival

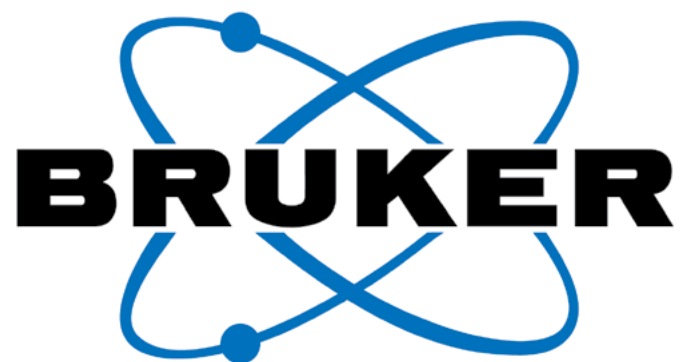
31 genes depleted in tumor interior:

ARL4C, C11orf21, CCND3, CD52, CD69, CDAN1, CTRL, EPHA1, FCMR, **GIMAP2**, **GNG2**, GPRIN3, **GZMK**, **HLA-E**, IKZF3, IL2RG, IL32, IL7R, LCP1, MSL2, MYCOP2, 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 nanosttring.com/CosMxWTX

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