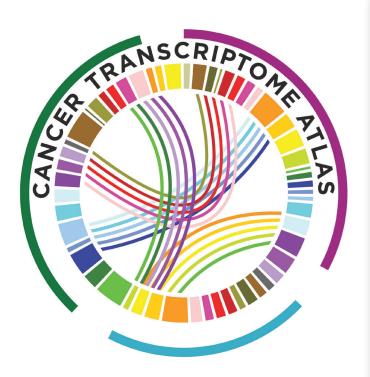
GeoMx® Cancer Transcriptome Atlas

Profile over 1,800 RNA targets simultaneously with spatial resolution in any region of interest from a single tissue section using the GeoMx Digital Spatial Profiler (DSP). The GeoMx Cancer Transcriptome Atlas (CTA) is designed for comprehensive profiling of the tumor, tumor microenvironment, and tumor immune status.



Product Highlights

- Comprehensive RNA content designed for cancer biology research
- Expansive coverage of the immune response, tumor microenvironment, and tumor biology
- Includes clinically relevant gene sets from BC 360 and IO 360 such as the Tumor Inflammation Signature and PAM50
- Over 100 pathways to explore all aspects of cancer
- Compatible with RNAscope™ and antibody morphology markers
- Supplement with up to 60 additional targets of interest
- For use with Illumina next-generation sequencer (NGS) readout
- Utilize the GeoMx Data Center for interactive analysis

GeoMx® Cancer Transcriptome Atlas Design

Designed to profile over 1,800 RNA targets simultaneously with spatial resolution, the Cancer Transcriptome Atlas (CTA) contains targets for broad cell profiling and includes necessary controls for all GeoMx DSP experiments. The CTA covers 112 pathways critical to immune response, tumor biology, and the microenvironment. GeoMx RNA assays contain in situ hybridization (ISH) probes conjugated to unique DNA indexing-oligonucleotides via a UV-photocleavable linker. After selecting regions of interest (ROI) on GeoMx DSP, the DNA oligonucleotides are UV cleaved and then sequenced on an Illumina sequencer. DNA oligonucleotide sequences contain ROI indices mapping them back to their tissue location, an RNA target identification sequence matching them to their ISH probes, and a unique molecular identifier (UMI) to deduplicate reads. Sequenced oligonucleotides are processed, then imported back into the GeoMx Data Center platform for integration with the slide images and ROI selections for spatially-resolved RNA expression.

Curated Content for Cancer Biology

The GeoMx CTA is designed to profile all aspects of tumor and tumor microenvironment biology. Accompanying Morphology Marker Kits are available for tissue visualization and ROI selection.

Adaptive Immunity	#Genes	
T cells B cells	130	
TCR & BCR Signaling	194	
Cancer Antigens	18	
MHC Class I & II Antigen Presentation	86	
T-cell Checkpoints	27	
TH1, TH2, TH9, Th17, and Treg Differentiation	107	

Immune Response	#Genes	
Chemokine Signaling	121	
Cytotoxicity	6	
IL-1, IL-2, IL-6 & IL-17 Signaling	168	
Immune Exhaustion	20	
Interferon Response Genes	25	
Lymphocyte Regulation & Trafficking	202	
NF-kB Signaling	114	
Other Interleukin Signaling	173	
Prostaglandin Inflammation	4	
TNF Signaling	96	
Type I, II, & III Interferon Signaling	103	

Cell Function	#Genes
Apoptosis	121
Autophagy	62
Cell Adhesion & Motility	139
Cell Cycle	167
Cilium Assembly	10
Differentiation	225
DNA Damage Repair	90
EMT	98
Endocytosis	57
Epigenetic Modification	166
Immortality & Stemness	33
Ion Transport	37
Lysosome	14
Oxidative Stress	151
Phagocytosis	105
Proteotoxic Stress	22
RNA Processing	35
Senescence	128

Metabolism	#Genes
Amino Acid Synthesis & Transport	55
Arginine & Glutamine Metabolism	51
Fatty Acid Oxidation & Synthesis	15
Glycolysis & Glucose Transport	29
Glycosylation	12
IDH1/2	10
Lipid Metabolism	78
Mitochondrial Metabolism / TCA	52
Nucleotide Synthesis	10
Pentose Phosphate	7
Tryptophan & Kynurenine Metabolism	4
Vitamin & Cofactor Metabolism	28

Tissue Compartment	#Genes
Tumor Biology	1454
Immune Response	1481
Microenvironment	978

Innate Immunity	#Genes
Complement System	49
Dendritic Cells	19
DNA & RNA Sensing	107
Glycan Sensing	63
Host Defense Peptides	22
Inflammasomes	11
Myeloid Inflammation	96
Neutrophil Degranulation	124
NK Activity	94
NLR Signaling	88
RAGE Signaling	8
TLR Signaling	135

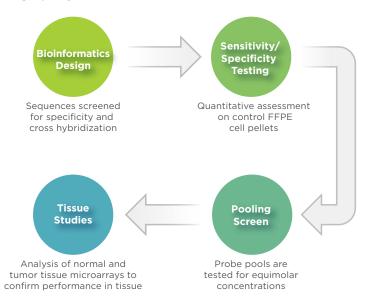
Signaling Pathways	#Genes
AMPK Signaling	44
Androgen Signaling	32
EGFR Signaling	17
ERBB2 Signaling	21
Estrogen Signaling	84
FGFR Signaling	40
FoxO Signaling	79
GPCR Signaling	177
Hedgehog Signaling	45
HIF1 Signaling	68
Insulin Signaling	81
JAK-STAT Signaling	118
MAPK Signaling	261
MET Signaling	34
mTOR Signaling	76
Мус	26
NO Signaling	10
Notch Signaling	74
p53 Signaling	76
PDGF Signaling	30
PI3K-Akt Signaling	242
PPAR Signaling	15
Purinergic Signaling	3
Retinoic Acid Signaling	5
TGF-beta Signaling	69
VEGF Signaling	69
Wnt Signaling	124

Physiology & Disease	#Genes
Angiotensin System	5
Circadian Clock	22
Drug Resistance	3
Glioma	60
Leukemia	93
Matrix Remodeling and Metastasis	52
Melanoma	70
Neuroendocrine Function	8
Prostate Cancer	92

Tissue Compartment	#Genes
Tumor	1622
Immune	1396
Stroma	1024

Validated Assays Ready for Use

All GeoMx RNA assays undergo extensive validation to ensure high quality GeoMx DSP data.



Spatial RNA Profiling with High Reproducibility

RNA detection shows high reproducibility between regions of interest selected from 6 cell lines within a cell pellet array (FIGURE 1).

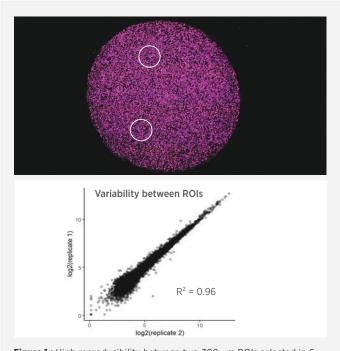


Figure 1: High reproducibility between two 300 μm ROIs selected in 6 different cell lines. An example cell pellet is pictured above with ROIs selected.

High Sensitivity Across All Targets

The GeoMx CTA detects high, medium, and low expressing genes with broad coverage of the genes in The Cancer Genome Atlas (TCGA)².

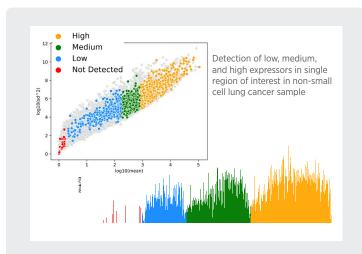


Figure 2: Coverage of the CTA compared to the TCGA with equally-sized bins of low, medium, and high expressors based on TCGA expression level data (left). Average TCGA expression levels below 1 FPKM are categorized as not detected.

Reveal Tissue Heterogeneity

Segmentation analysis of a region of interest (ROI) from a non-small cell lung cancer (NSCLC) sample demonstrates distinct RNA expression profiles in the tumor and tumor microenvironment segments, which would be lost if profiling the ROI as a whole (**FIGURE 3**).

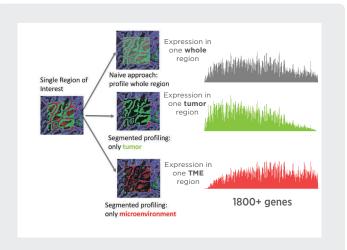


Figure 3: ROIs were selected with mixed tumor and tumor microenvironment (immune) segments in NSCLC tissue. ROIs were segmented based on PanCK and SYTO 13 (nuclear) morphology stain. RNA expression demonstrates distinct profiles in the tumor as compared to the microenvironment segments.

Comprehensive Coverage for Cancer Biology

Designed for cancer biology research, the Cancer Transcriptome Atlas provides complete coverage of tumor biology, the microenvironment, and the immune response, without sequencing unnecessary targets.





Figure 4: Cancer Transcriptome Atlas Pathways Analysis (left) compared to the Whole Transcriptome Pathways Analysis (right) illustrates the comprehensive coverage of the Cancer Transcriptome Atlas, which encompasses all areas of biology including signal transduction, metabolism, and the immune system³. Increasing the number of RNA targets from the 1,800+ CTA targets to the whole transcriptome yields only a minimal increase in coverage of cancer biology.

GeoMx® Data Center

Unique GeoMx Data Center software uniquely combines whole tissue visualization at single cell resolution with advanced ROI selection to enable comprehensive spatial profiling of tissue sections. The fully integrated workflow tracks image data to corresponding profiling data, allowing users to easily go from data collection to data analysis and to interact with either dataset in real time. The data analysis module assesses the quality of the raw data and provides a number of options to normalize data sets. Moreover, a variety of data visualization formats are enabled to export publication-quality figures. Visualization plots include: heatmap, cluster, bar graph, box plot, scatter plot, line/trend plot, strip plot, volcano plot, and PCA.

To view the RNA probe list visit: nanostring.com/geomxassays

Ordering Information

GeoMx Cancer Transcriptome Atlas			
Product	Product Description	Quantity	Catalog Number
GeoMx Cancer Transcriptome Atlas Human RNA for Illumina Systems	RNA panel including over 1,800 targets plus controls for human immune response, tumor biology, and microenvironment. Includes RNA probes for Illumina NGS readout.	4 slides	GMX-RNA-NGS-CTA-4
	GeoMx Morphology Kits		
Product	Product Description	Quantity	Catalog Number
GeoMx Solid Tumor TME Morphology Kit Human RNA Compatible	Morphology kit for visualization of human solid tumors and the tumor microenvironment. For use with RNA assays. Includes fluorescent antibodies against PanCK, CD45, and a nuclear stain.	12 slides	GMX-RNA-MORPH-HST-12
GeoMx Melanoma TME Morphology Kit Human RNA Compatible	Morphology kit for visualization of human melanoma and the tumor microenvironment. For use with RNA assays. Includes fluorescent antibodies against \$100B/Pmel17, CD45, and a nuclear stain.	12 slides	GMX-RNA-MORPH-HMEL-12
Additional Assay Reagents			
Product	Product Description	Quantity	Catalog Number
GeoMx Seq Code Pack Compatible with Illumina Systems	NGS readout reagents for GeoMx DSP RNA and protein analysis. Includes two Seq Code primer plates (choice of A&B, C&D, E&F, or G&H) and two universal enzyme master mixes.	192 AOI	GMX-NGS-SEQ-[XX]
GeoMx RNA Slide Prep Kit for FFPE	Sample prep reagents for GeoMx DSP RNA analysis. Includes Buffer W, Buffer S, and Buffer R.	12 slides	GMX-PREP-RNA-FFPE-12
GeoMx DSP Collection Plate	Barcoded collection plates for use on the GeoMx DSP. Required for AOI tracking. Kit includes 12 plates covering 1,152 AOI.	1 Pack	GMX-DSP-COLL-PLT-4
GeoMx DSP Instrument Buffer Kit	Buffer kit for the GeoMx DSP. Includes Buffer S and Buffer H. Sufficient for ~48 samples with ~18 AOI each. Volume requirements may vary based on experimental design.	1 Kit	GMX-DSP-BUFF-KIT

References

- 1. Ayers, Mark, et al. IFN-γ-related mRNA profile predicts clinical response to PD-1 blockade. Journal of Clinical Investigation. 127.8 (2017).
- 2. National Cancer Institute: The Cancer Genome Atlas Program. cancer.gov/tcga
- 3. Pathway Analysis figures from Reactome, Copyright 2020 Reactome, License CC BY 4.0. Image cropped from original.

For more information, please visit nanostring.com/GeoMxDSP

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