

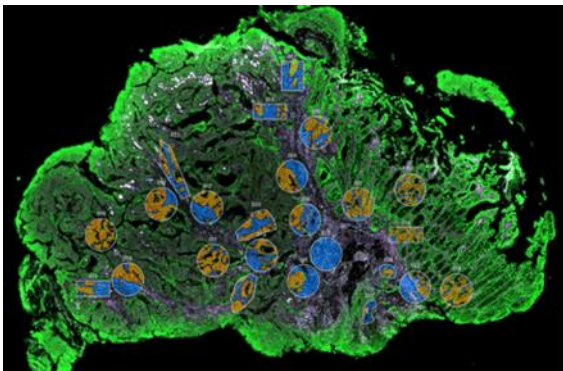
Whole Transcriptome Spatial Analysis

ImaLink Platform, developed by ImaBiotech integrates a unique combination of imaging capabilities. The platform includes the WTA (Whole transcriptome Atlas) GeoMx Nanostring and Illumina NGS instruments, a new technology, designed for comprehensive profiling of the spatial Transcriptome. Dedicated to measure the impact of a drug or a disease to the cell, and with full coverage of protein coding genes, WTA services delivers spatial analysis of any target in any tissue in the biological region that matters most.

ImaBiotech offers a comprehensive service to run the Whole Transcriptome Atlas assay from sample to data in as little as 8 weeks.

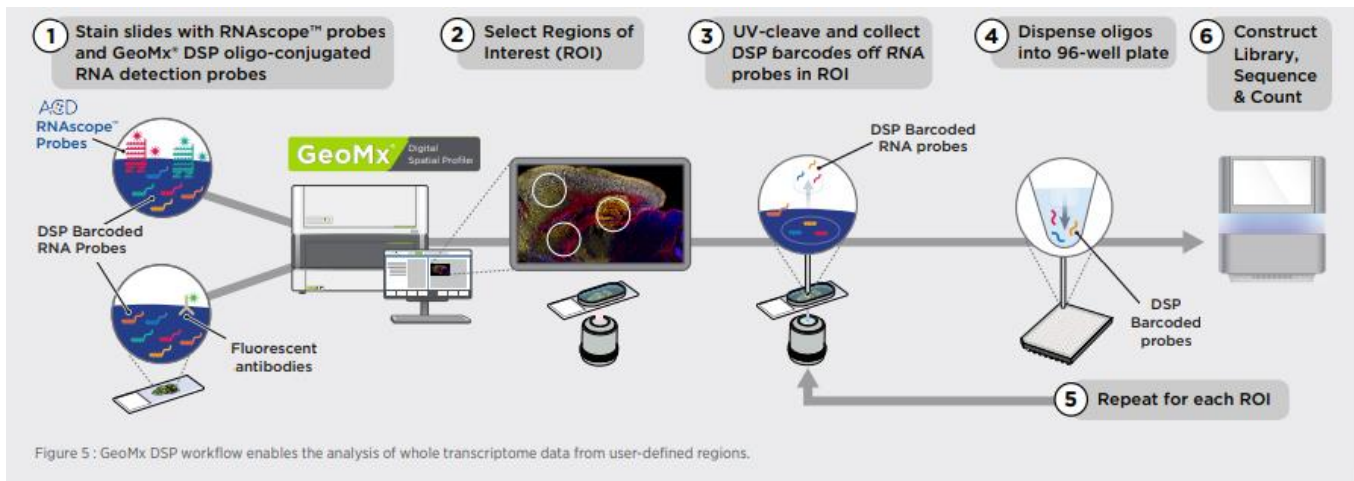
- Whole transcriptome coverage with probes specific to protein coding mRNA sequences
- Superior sensitivity to detect 1000s of unique genes in ≤ 50 mm regions
- Robust performance across sample types including FFPE with high concordance with RNA-seq and RNAscope™
- Map single cell RNA-seq populations to their tissue location
- Integrated Illumina library prep protocols and streamlined NGS analysis pipelines
- Flexibility to customize with up to 60 additional targets, to assay non-coding RNA, synthetic DNA, or exogenous genes

DIGITAL SPATIAL PROFILER



- Spatial Disease Analysis through gene expression of specific cells
- Correlation of Drug exposure to cells and impact to gene expression
- Biomarker discovery/validation in specific cells
- Correlation of gene expression and protein levels in tissues

GEOMX WTA WORKFLOW



HOW IT WORKS

The GeoMx Whole Transcriptome Atlas delivers the maximum amount of sensitivity in each transcript through its unique probe architecture. WTA contains over 18,000 protein coding genes based on the human gene nomenclature committee (HUGO1) database cross-referenced with available mRNA sequences in the National Center for Biotechnology's Information (NCBI) RefSeq database2 (Figure 1). Each probe is assigned a unique DSP barcode for downstream molecular counting on an Illumina sequencer. With GeoMx WTA, researchers can explore pathways across the whole transcriptome in user defined regions of interest.

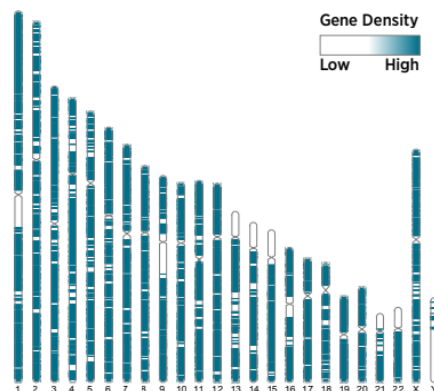


Figure 1: Karyogram illustrating the density of genes in the human genome. The transcripts from these genes make up the human transcriptome and are measured by GeoMx WTA.

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