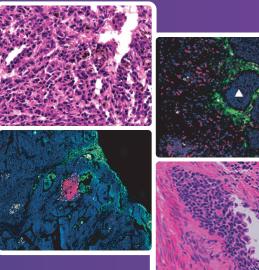
Cancer Research

STOmics | MG

Tumor cell heterogeneity and microenvironment are key to research on tumor mechanism, prevention, and treatment. Spatial transcriptome technology -- Stereo-seq, can map tumor cell heterogeneity and microenvironment structure at subcellular resolution, bringing significant breakthroughs in tumor research. Similarly, spatial multi-omics technology can also be applied to other diseases that are tied to spatial structures, providing a powerful tool for further exploration.



Technology highlights

• Subcellular resolution allowing visualization on cellular heterogeneities and efficient cell type annotations

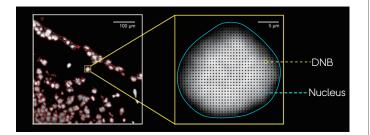
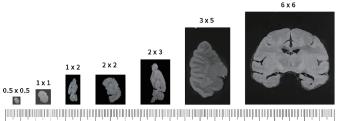


Figure 1. Stereo-seq capturing spots (DNBs) arranged down to single cell resolution, allowing mRNA within one cell to be captured with hundreds of coordinate ID containing DNBs

• Multiple chip sizes allowing various tissue types and scalable capture areas



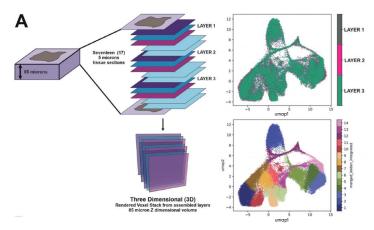
10 11 12 13 14 15 16 17 18 19 20 21 22

Figure 2. Demonstration of Stereo-seq chip at different sizes

Featured publication

Molecular, Metabolic, and Subcellular Mapping of the Tumor Immune Microenvironment via 3D Targeted and Non-Targeted Multiplex **Multi-Omics Analyses**

Ferri-Borgogno & Burks et al., Cancers , 2024



Highlights

- This approach aims to unveil intricate signaling networks between different cell types and the extracellular matrix (ECM) in the 3D tumor microenvironment (TIME) using two FFPE gynecologic tumor samples (HGSOC & AEH)
- Stereo-seq for FFPE enabled the capture of not only human coding and non-coding RNA but also microbiome RNAs with subcellular resolution

STOmics product: Stereo-seq Transcriptomics Solution

Featured publication

An invasive zone in human liver cancer identified by Stereo-seq promotes hepatocyte-tumor cell crosstalk, local immunosuppression and tumor progression.

Wu et al., Cell Research , 2023

Highlights

- Spatial transcriptomics reveals the heterogeneity in tumor margin area
- Characterization of distinctive immune cells, the suppressive immune microenvironment, and metabolic reprogramming of tumor cells in invasive zone
- Tissue resection Single-cell RNA-seq & Slareo-seq Cell type projection Tumor margin identification Margin area (n=8) Union tissue (n=7) Tumor tissue (n=6) Spatial transcriptome Spatial transcriptome Solution Spatial cell profile Spatial cell profile Solution Tumor Margin area (n=8) Tumor tissue (n=6) Solution Spatial transcriptome Solution Solution
- In the invasive zone, hepatocyte injury upregulates SAAs, further recruiting and polarizing macrophages to assist tumor progression

STOmics product: Stereo-seq Transcriptomics Solution

Additional publications

Publication		Experiment snapshot	Link
Molecular, Metabolic, and Subcelle the Tumor Immune Microenvironmer and Non-Targeted Multiplex Multi- <i>Cancers</i> 2024, 16(5), 846	nt via 3D Targeted	STOmics product : Early Access Stereo-seq Transcriptomics Solution for FFPE Sample type : Human, FFPE	
A cellular hierarchy in melanoma un and metastasis. <i>Nature</i> 610: 190–198 (2022)	ncouples growth	STOmics product : Stereo-seq Transcriptomics Solution Sample type : Mouse, Fresh frozen	
Presence of onco-fetal neighborho hepatocellular carcinoma is associ and response to immunotherapy <i>Nature Cancer</i> 5:167–186 (2024)		STOmics product : Stereo-seq Transcriptomics Solution Sample type : Human, Fresh frozen	
Single-cell landscape of idiopathic Castleman Disease in identical twin <i>Blood</i> 2023021992.		STOmics product : Stereo-seq Transcriptomics Solution Sample type : Human, Fresh frozen	



Contact us

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