Nøvogene

Visium Spatial Transcriptome (FFPE)



Spatial transcriptomics revolutionizes our approach to gene expression analysis by enabling a single cell scale examination across tissue samples. Visium Spatial Gene Expression allows us to unveil the hidden insights within formalin-fixed paraffin-embedded (FFPE) tissue sections. This cutting-edge technology marries the cell morphology with RNA sequencing, offering the comprehensive profiling of RNA expression across entire tissue sections at exceptional resolution. Utilizing Visium Spatial Gene Expression for FFPE, you can uncover spatial gene expression patterns across more than 18,000 genes in both human and mouse FFPE samples, opening new avenues of insight in your research endeavors.

Our Key Features and Advantages

[0]

Diverse Sample Compatibility

• Demostrated data on a wide range of tissue type for human and mouse sepcies.



Multiomics Research

• Uncover novel tissue biomarkers through the simultaneous analysis of histology, protein, and mRNA within the same tissue section.



Professional Service

• Novogene offers a comprehensive technology platform, supported by a skilled service team with extensive project experience.

Project Workflow



Sample Requirements

Sample Type	Sample Amount	Preservation	Sample QC	Shipping
FFPE block*	FFPE block	Store at 4°C after embedding, protected from light	DV200% >30%	4°C or Room Temperature
FFPE slides	5-10 FFPE scrolls in tube for sample QC; 4 FFPE glass slides, tissue section thickness 4~5 μm for library prep	Dry and sealed, storage time at 4°C < 14 days	DV200% >30%	4°C or Room Temperature

* FFPE means formalin fixed & paraffin embedded tissue sample.

Detailed sample requirement of fresh frozen samples, please contact marketing_amea@novogeneait.sg.

Sequencing

Sample Type	Species	Sequencing	Recommended Data	Probe and Cassettes
FFPE block/ slides	Human & Mouse	NovaSeq6000 or NovaSeq X plus PE150	25,000 read pairs/tissue- covered spot	Visium CytAssist Slide and Cassettes, 6.5 mm Visium Human Transcriptome Probe Kit v2 Visium Mouse Transcriptome Probe Kit

Analysis Content

Standard Analysis Pipeline

- 1. Data QC
- 2. Mapping and quantification
- 3. Dimensionality reduction, clustering, and differential analysis: Graphclust clustering K-means clustering
- 4. Seurat analysis:
- PCA analysis

Spatial variable gene expression analysis

Clustering and dimensionality reduction analysis

- 5. Differential expression gene analysis (DEGs):
 - DEGs clustering heatmap

Spatial distribution of DEGs

Violin plot

t-SNE and UMAP dimensional reduction visualization

6. GO, KEGG, Reactome functional enrichment analysis

Demo Analysis Results





T-SNE Projection of Spots Colored by UMI Counts (Space Ranger)



Variable Expressed Genes

Novogene AMEA (Asia Pacific, Middle-East & Africa)

🕼 novogene.com/amea-en 🛛 🐹 marketing_amea@novogeneait.sg

NovogeneAIT

 Image: NovogeneAMEA

© 2024 Novogene Co., Ltd. All Rights Reserved.

Information and specifications are subject to change at any time without notice. Please contact your Novogene representative. AMEA_FFPESpatial_V1_2024