



Spatially Visualized Proteomics Solution

Product Introduction

Shenzhen BayOmics Biotechnology Co., Ltd



BACKGROUND INFORMATION

Complete Solution for Spatially Visualized Proteomics

Spatially Visualized Proteomics integrates multiple advanced omics technologies into one complete solution. It is the first time to combine BayOmics' patented, fully-integrated, high-sensitivity proteomic sample preparation technology with multiplex immunohistochemistry and laser microdissection at single-cell resolution. The solution overcomes many of the bottlenecks in conventional technologies, such as artificial cell identification, inaccurate dissection, and low-recovery collection. Moreover, the depth of protein identification in nanogram-scale samples is comparable to that of milligram-scale samples. The solution enables systematic localization, qualitative and quantitative analysis of the tissue microenvironment in multiple dimensions at specific spatial locations in pathological sections. The solution provides an important analytical tool for revealing the highly heterogeneous of the tissue microenvironment, the spatial distribution of different cell types, the relationship of intercellular signal transduction networks, and the mechanisms of major diseases.

Technical Features

Conventional solution

Inaccurate and labor-intensive locating single cells

Excessive width of dissection and burning boundary

Low collection recovery for $\Phi < 100 \mu\text{m}$ sample

Low sample recovery at the ng level

BayOmics Solution

Highly and automatically precisely locate single cells

High-accuracy and high-precision dissection

High recovery for collection and transfer

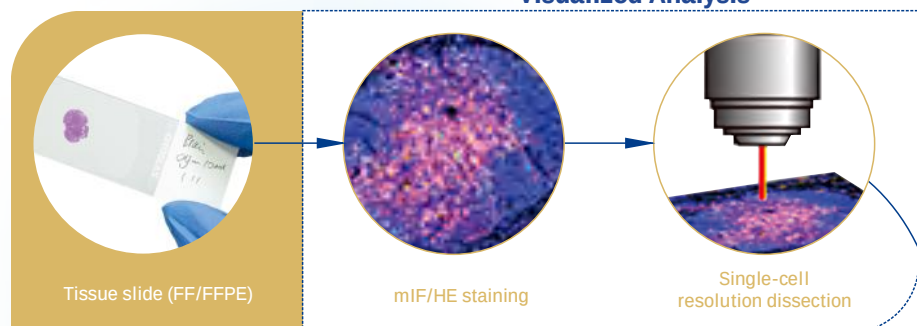
High sensitive preparation for ng-level sample

ANALYTICAL PROCESS

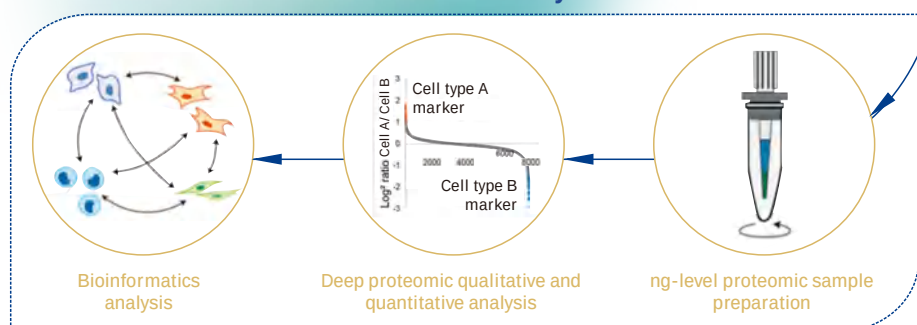
Field of Application



Visualized Analysis

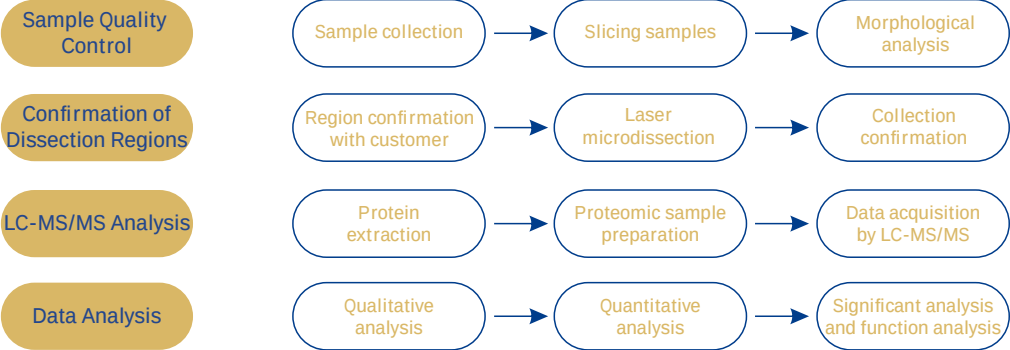


Proteomic Analysis



Develop a complete solution of spatially visualized proteomics by realization of the automatic cell identification, dissection, sample preparation, and data analysis at single-cell resolution.

WORKING PROCESS



DELIVERY REQUESTMENT

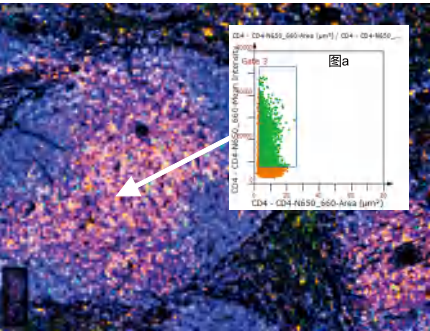
Sample Type	Slicing	Storage and Transportation	Requirement for Sample Amount
FFPE Tissue	By BayOmics	The samples should be stored at 4 °C in sealed bags and transported in ice packs.	1 piece with cut surface ≤ 30 mm x 13 mm
OCT-embedded Tissue	By BayOmics	The samples should be sealed in a freezer at -80 °C and transported on dry ice.	1 piece with cut surface ≤ 30 mm x 13 mm
FFPE Slides	By customer (membrane Slides required)	The slide should be stored, sealed in slide boxes at 4 °C and transported in ice packs.	≥5* continuous slides with a thickness of 4 μm and a cut surface ≤ 30 mm x 13 mm
Fresh Frozen Slides	By customer (membrane Slides required)	The slide should be transported on dry ice.	≥5* continuous slides with a thickness of 10 μm and a cut face ≤ 30 mm x 13 mm

* Note: of 5 slides, 3 are for the pre-staining, 1 for formal experiment and 1 for backup.

RESULT SHOW

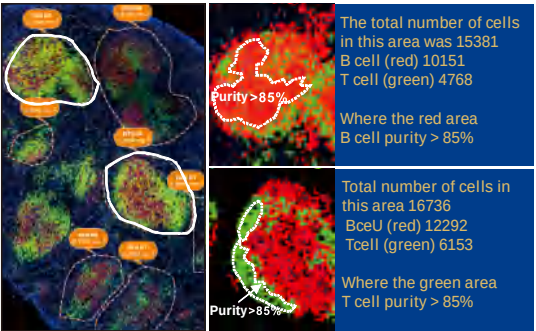
Spatially Visualized Proteomic Analysis of Mouse Spleen FFPE

Visualized Analysis



High-end Contextual Image Analysis with Single Cell Quantification

Cell identification in the tissue was performed by a highly flexible tissue cytometry platform in various configurations. The screening of the CD4 cell in the tissue slide was taken an example as shown in Figure A.

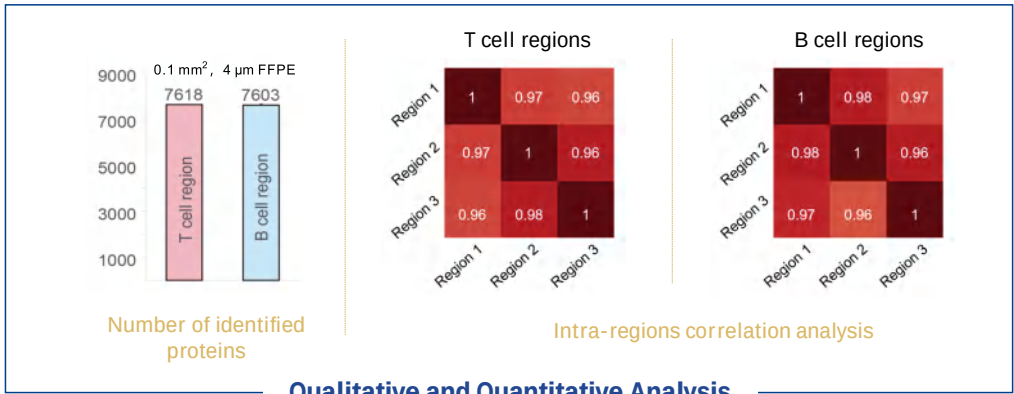


Cell-type Detection Based on Morphologic Characteristics and Evaluation of Cell Purity

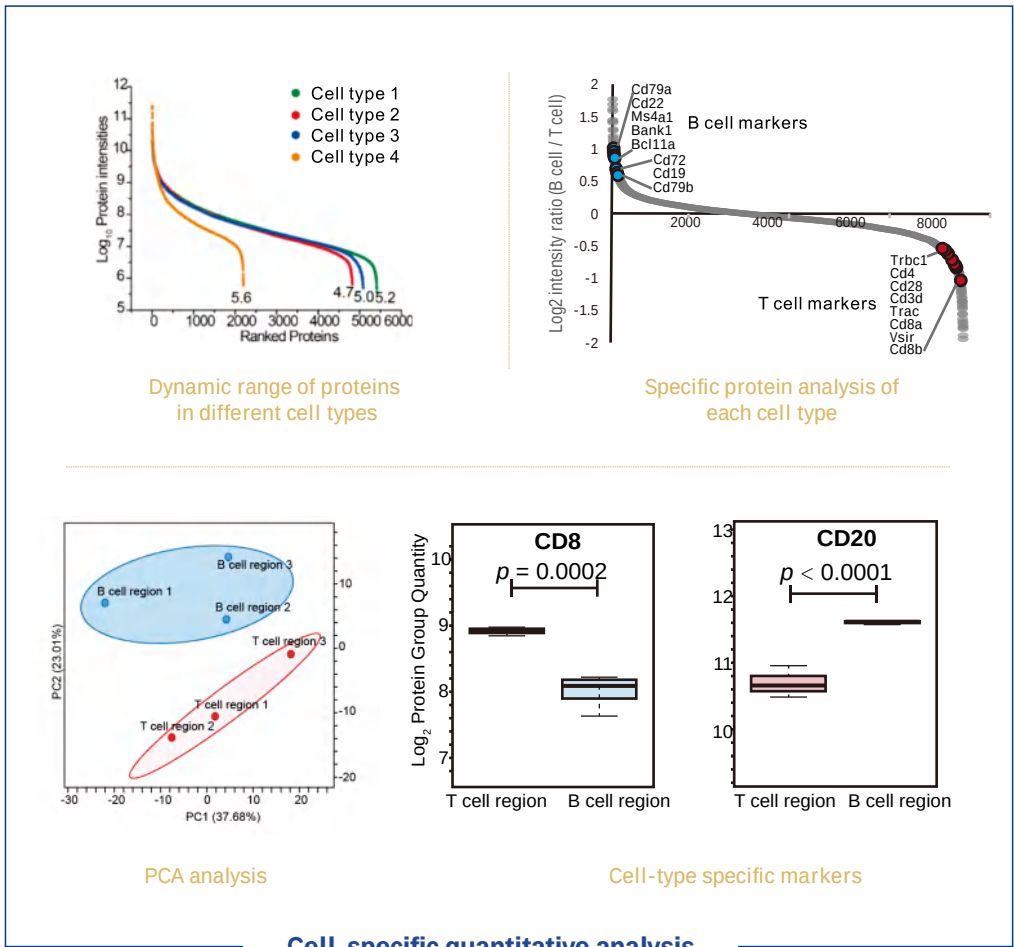
At the single-cell level, the images was analyzed on multi-dimension. The positive cells were selected after the single cells were effective screened from the mouse spleen. Then, the region of each cell type was filled with different color. Each region could be one-to-one corresponded to the flow scatter diagram.

RESULT SHOW

Spatial Proteomic Analysis

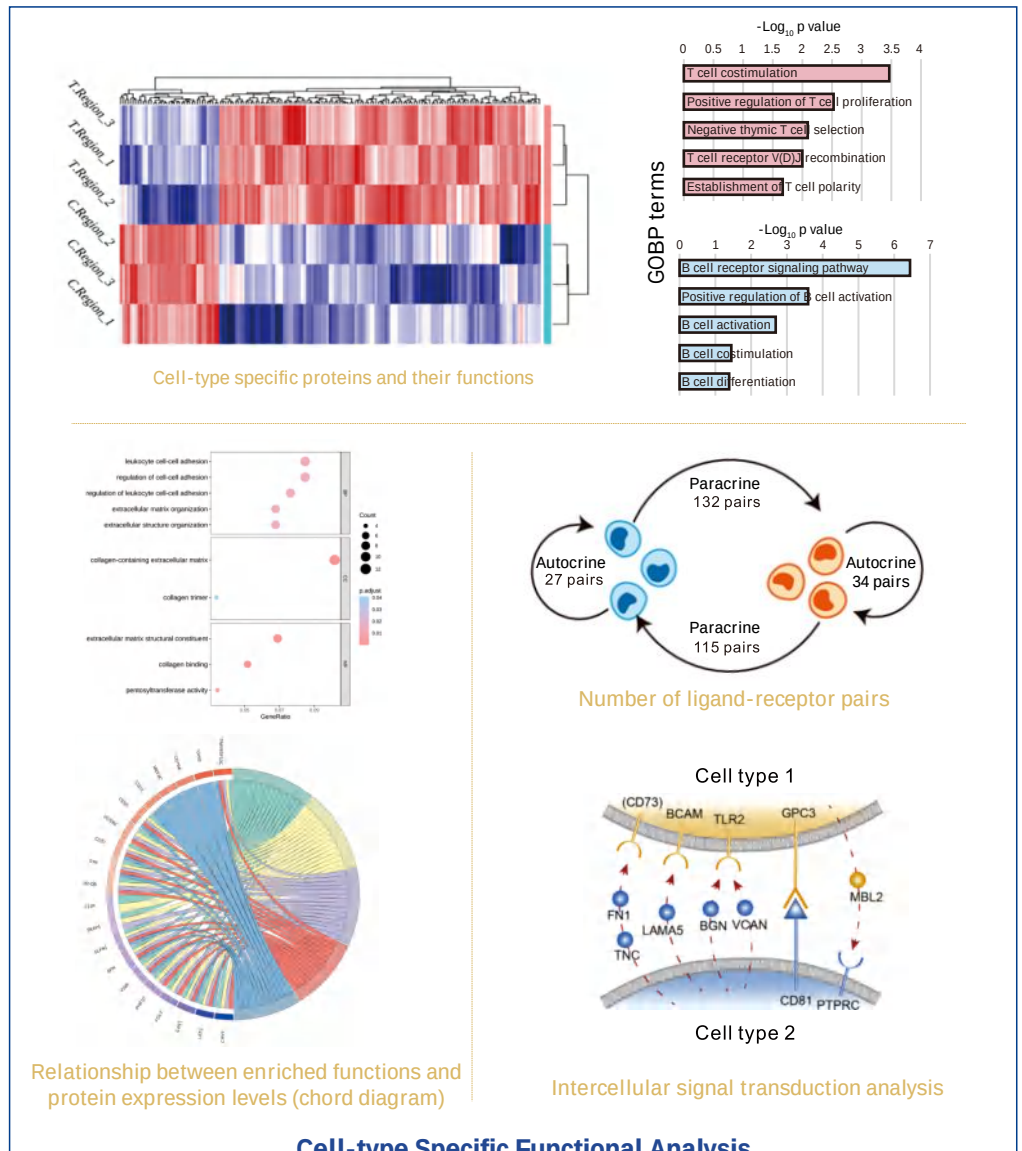


SISPROT-based high-sensitivity proteomic sample preparation ensures in-depth qualitative analysis and accurate quantification of the nanogram-level amount of samples.



RESULT SHOW

Spatial Proteomic Analysis



Relevant Literature

- Spatial-resolution cell type proteome profiling of cancer tissue by fully integrated proteomics technology, Anal. Chem., 2018, 90(9): 5879-5886.
- A fully integrated spintip-based approach for sensitive and quantitative profiling of region-resolved in vivo brain glycoproteome, Anal. Chem., 2019, 91(14): 9181-9189.
- Spatial proteome profiling by immunohistochemistry-based laser capture microdissection and data-independent acquisition proteomics, Anal. Chim. Acta., 2020, 1127: 140-148.
- Spatial proteomics for understanding the tissue microenvironment, Analyst, 2021, 146(12):3777-3798.
- Deep Visual Proteomics defines single-cell identity and heterogeneity, Nat. Biotechnol., 2022, 40(8): 1231-1240.
- Unbiased spatial proteomics with single-cell resolution in tissues, Mol. Cell., 2022, 82(12):2335-2349.



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Global Service Hotline

Innovative Proteomics Technology Decoding the Micro World of Life



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