

Stereo-seq OMNI Transcriptomics FFPE Set V1.1

User Guidance

01 Introduction

Stereo-seq OMNI Transcriptomics FFPE Set V1.1 is intended for generating a spatially resolved coding and non-coding RNA library from formalin-fixed and paraffin-embedded (FFPE) tissue sections. Built upon DNA Nanoball (DNB) technology, STOmics Stereo-seq OMNI Transcriptomics Set for FFPE enables a "tissue-to-data" solution through in situ capture of the whole transcriptome at nanoscale resolution and large field-of-view. Each cDNA synthesized from RNA captured on a particular spot is linked to its spatially-barcoded probe, allowing subsequent gene expression mapping of a tissue section following sequencing based on DNBSEQ platform, and achieve data analysis and visualization using the STOmics developed software.

02 Workflow

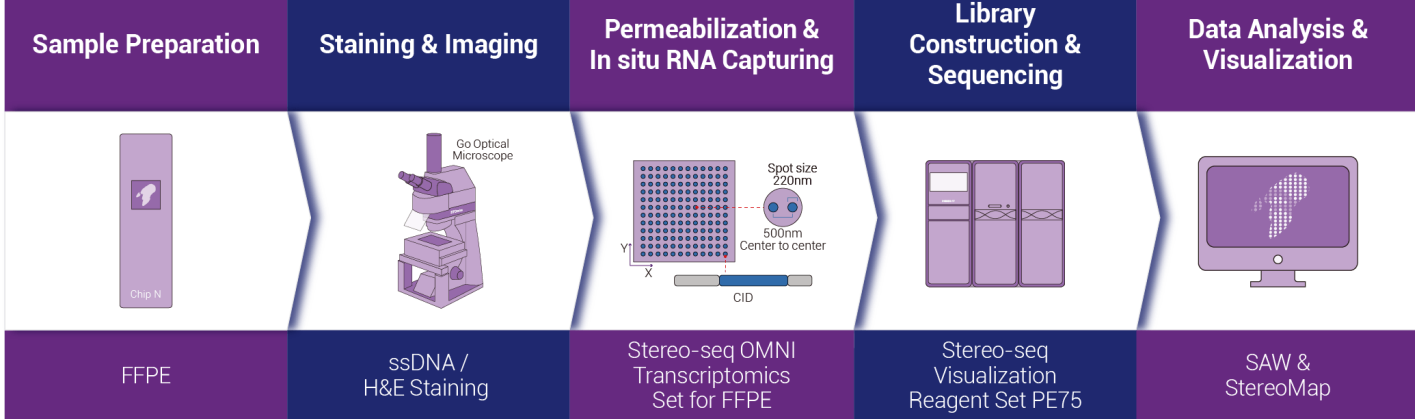


Figure 1 Stereo-seq OMNI Transcriptomics FFPE Set V1.1 Workflow

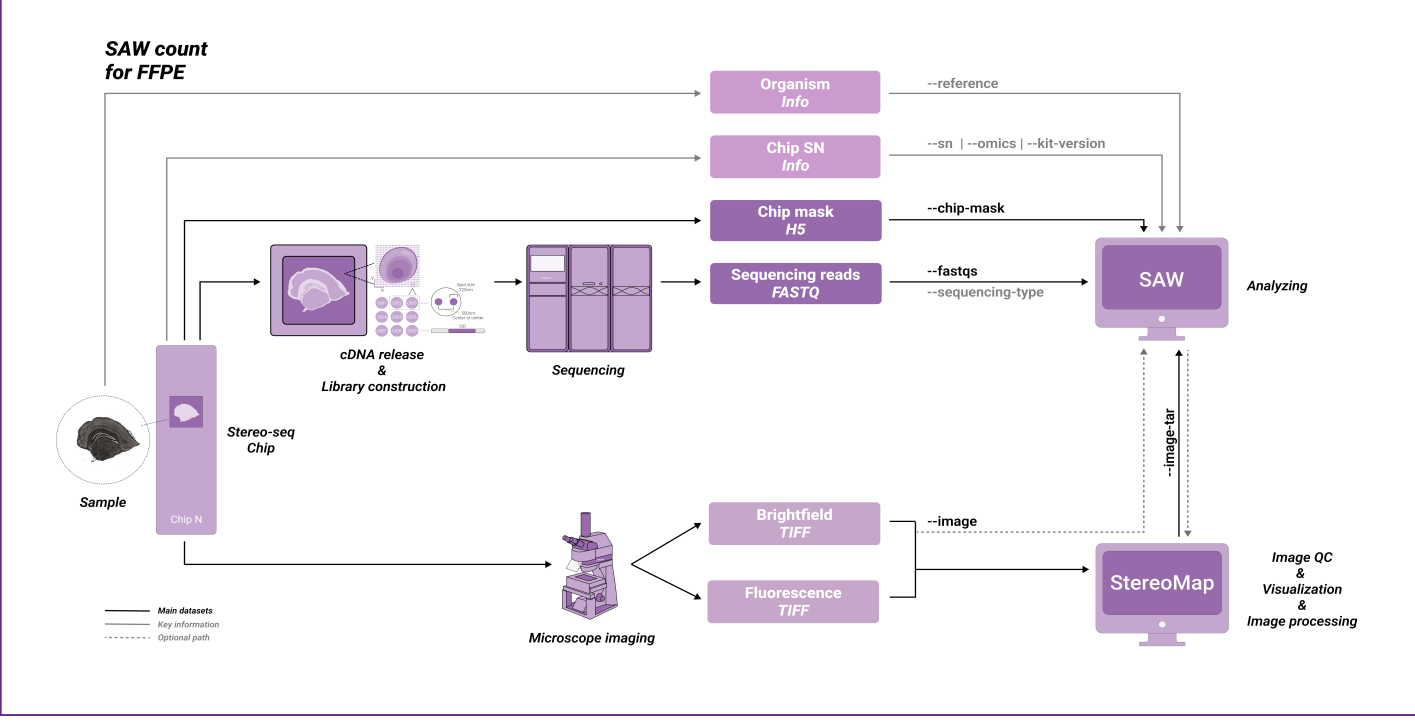


Figure 2 Overview of Stereo-seq OMNI Transcriptomics FFPE Set V1.1 Data Analysis Workflow

03 Resources Index

Step	Document Title and Description	Link
Experiment Preparation	UG004 Stereo-seq OMNI Transcriptomics FFPE Set V1.1 User Guidance Document No. : STUM-UG004 This guidance aims to give the user a general view of the Stereo-seq OMNI Transcriptomics FFPE Set V1.1, with the overview of whole experiment workflow and index of resources to support the users' in-house experiments.	View Document
	Stereo-seq Imaging Requirements and Guidelines Document No. : STUM-PE002 This manual aims to provide users guidance for assessing their imaging system including the hardware parameters and imaging quality for STOmics application, introducing the imaging system requirements, microscope assessment guidelines as well as preliminary image assessment and analysis.	View Document
	Stereo-seq Operation Guide For Receiving, Handling And Storing Document No. : STUM-PE005 This manual provides receiving, handling and storing guidance of the Stereo-seq Chip Slide.	View Document
	Experiment Preparation Checklist for Stereo-seq OMNI FFPE Transcriptomics Set V1.1 Document No. : STUM-PE007 This checklist enumerates all the necessary equipment and materials required at each individual stage of the Stereo-seq OMNI Transcriptomics V1.1 workflow for FFPE samples.	View Document
	Stereo-seq Sample Preparation, Sectioning and Mounting Guide for FFPE Samples on Stereo-seq Chip Slides Document No. : STUM-SP003 This manual aims to guide the users in FFPE tissue samples preparation, sectioning and mounting for Stereo-seq OMNI Transcriptomics FFPE Set V1.1 workflow.	View Document
Transcriptomics Workflow	Stereo-seq OMNI Transcriptomics FFPE Set V1.1 for Chip-on-a-slide User Manual Document No. : STUM-TT004 This manual provides a standard operation guidance for Stereo-seq OMNI Transcriptomics FFPE Set V1.1 workflow on Stereo-seq Chip N Slide (1cm * 1cm).	View Document
	Stereo-seq OMNI Transcriptomics FFPE Set V1.1 for Chip-on-a-slide (0.5cm * 0.5cm) User Manual Document No. : STUM-TT007 This manual provides a standard operation guidance for Stereo-seq OMNI Transcriptomics FFPE Set workflow on Stereo-seq Chip N Slide (0.5cm * 0.5cm).	View Document
Library Preparation and Sequencing	Stereo-seq OMNI V1.1 FFPE Library Preparation User Manual Document No. : STUM-LP002 This manual aims to provide guidance for the whole-transcriptome library construction from cDNA products obtained via Stereo-seq OMNI Transcriptomics FFPE Set V1.1 workflow.	View Document
	Related sequencing manuals: CG DNBSEQ-T7RS Stereo-seq Visualization Reagent Set Instructions for Use CG DNBSEQ-G400RS Stereo-seq Visualization Reagent Set Instructions for Use	https://www.completegenomics.com/documentation/
	MGI DNBSEQ-T7RS Stereo-seq Visualization Reagent Set Instructions for Use MGI DNBSEQ-G400RS Stereo-seq Visualization Reagent Set Instructions for Use	https://en.mgi-tech.com/download/files/
Data Analysis	StereoMap User Manual StereoMap is a desktop application designed to provide the essential analysis functionality you need to explore your Stereo-seq data interactively. This manual provides guidance in using StereoMap.	https://en.stomics.tech/service/stereoMap-operation-manual.html
	SAW User Manual Stereo-seq Analysis Workflow (SAW) software suite is a set of pipelines bundled to map sequenced reads to their spatial location on the tissue section, quantify spatial feature expression, and visually present spatial expression distribution. SAW processes the data from the Stereo-seq sequencing platform, combined with microscope images, to generate spatial feature expression matrices. Analysts can use the output files as a starting point to perform downstream analysis. This manual provides guidance in using SAW.	https://en.stomics.tech/service/new-saw-operation-manual.html

04 Revision History

Version: A
Date: Apr. 2025
Description: Initial release

Version: A_1
Date: Jun. 2025
Description: Added hyperlinks to all listed manuals to improve accessibility and user experience.

Version: B
Date: Aug. 2025
Description: Updated the diagrams of the solution and data analysis workflows.

Version: C
Date: Nov. 2025
Description: Compatible for Stereo-seq OMNI Transcriptomics Set V1.1.

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