

Stereo-seq OMNI Transcriptomics FFPE Set
User Guidance

01 Introduction

Stereo-seq OMNI Transcriptomics Set for FFPE is intended for generating a spatially resolved total 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 using random primers. 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

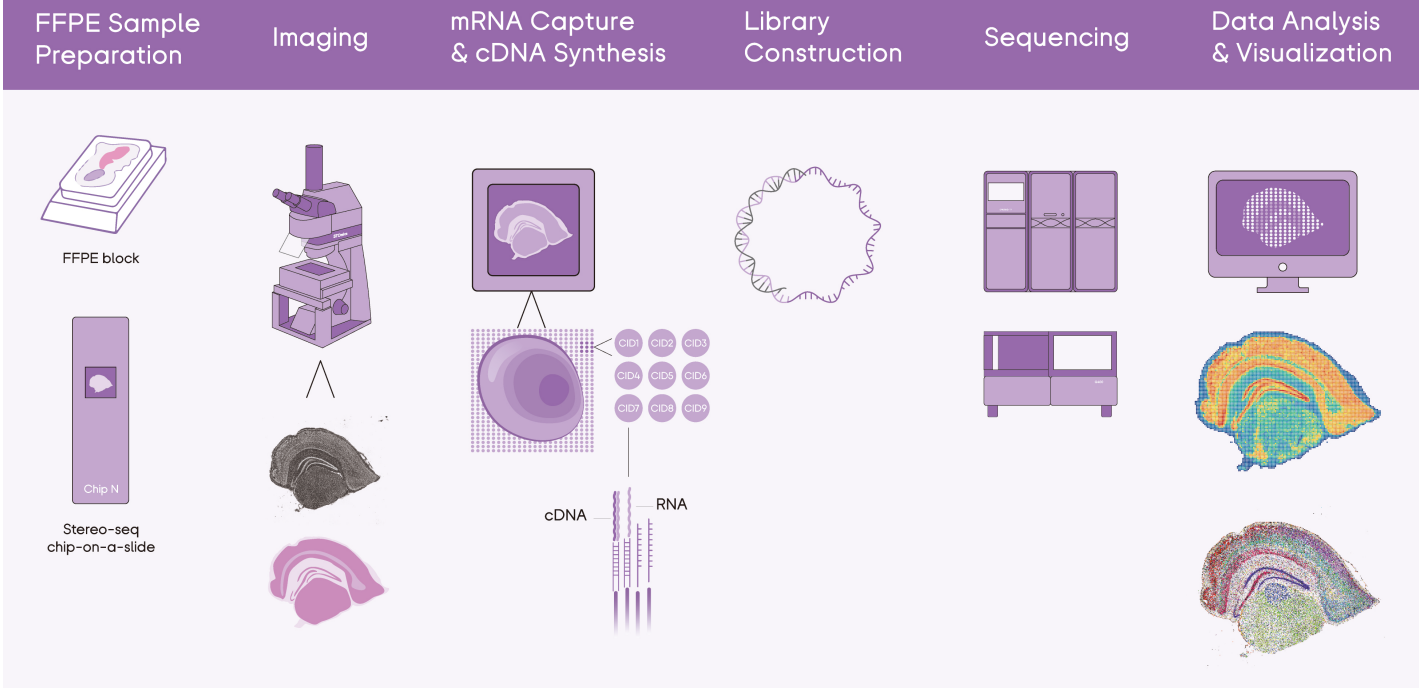


Figure 1 Stereo-seq OMNI Transcriptomics FFPE Set V1.0 Workflow

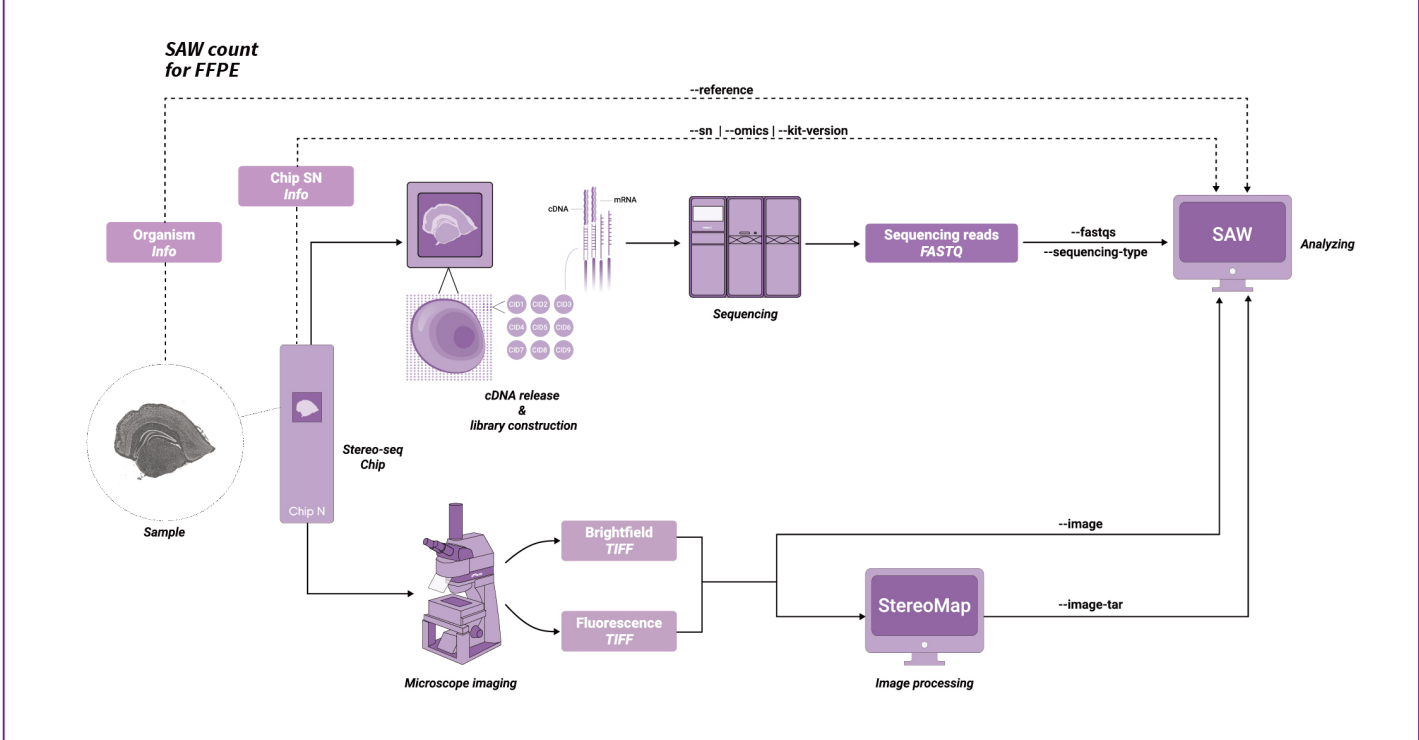



Figure 2 Overview of Stereo-seq OMNI Transcriptomics FFPE Set V1.0 Data Analysis Workflow

03 Resources Index

| Step | Document Title and Description | Link |
|------------------------------------|--|---|
| Experiment Preparation | Stereo-seq OMNI Transcriptomics FFPE Set User Guidance Document No. : STUM-UG004 This guidance aims to give the user a general view of the Stereo-seq Transcriptomics FFPE Set, with the overview of whole experiment workflow and index of resources to support the users' in-house experiments. | https://en.stomics.tech/resources/documents/list.html  |
| | Microscope Assessment Guideline Document No. : STUM-PE001 This manual aims to guide the users to determine a proper microscope for STOmics application, introducing the microscope hardware requirements as well as guidance of imaging acquisition and evaluation. | |
| | Stereo-seq Operation Guide For Receiving, Handling And Storing This manual provides receiving, handling and storing guidance of the Stereo-seq Chip Slide. | |
| | Experiment Checklist For Stereo-seq OMNI FFPE Solutions This checklist enumerates all the necessary equipment and materials required at each individual stage of the Stereo-seq Transcriptomics workflow for FFPE samples. | |
| | 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 Transcriptomics FFPE Set workflow. | |
| Transcriptomics Workflow | Stereo-seq Transcriptomics Set for FFPE User Manual Document No. : STUM-TT004 This manual provides a standard operation guidance for Stereo-seq Transcriptomics FFPE Set workflow. | |
| Library Preparation and Sequencing | Stereo-seq OMNI 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 Transcriptomics FFPE Set workflow. | |
| | 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

©2025 STOmics Tech Co., Ltd. All rights reserved.

1. The products shall be for research use only, not for use in diagnostic procedures.
2. The contents of this manual may be protected in whole or in part by applicable intellectual property laws. STOmics Tech Co., Ltd. and/or corresponding right subjects own their intellectual property rights according to law, including but not limited to trademark rights, copyrights, etc.
3. STOmics Tech Co., Ltd. does not grant or imply the right or license to use any copyrighted content or trademark (registered or unregistered) of ours or any third party's. Without our written consent, no one shall use, modify, copy, publicly disseminate, change, distribute, or publish the program or contents of this manual without authorization, and shall not use the design or the design skills to use or take possession of the trademarks, the logo, or other proprietary information (including images, text, web design or form) of ours or those of our affiliates.
4. Nothing contained herein is intended to or shall be construed as any warranty, expression or implication of the performance of any products listed or described herein. Any and all warranties applicable to any products listed herein are set forth in the applicable terms and conditions of sale accompanying the purchase of such product. STOmics Tech Co., Ltd. makes no warranty and hereby disclaims any and all warranties as to the use of any third-party products or protocols described herein.

05 Contact Us



STOmics Website: <https://en.stomics.tech>