

Stereo-seq Transcriptomics Set User Guidance

01 Introduction

Based on high-resolution, large field-of-view Stereo-seq transcriptomics technology powered by DNBSEQ, this solution enables a seamless “tissue-to-data” workflow through *in situ* capture of whole transcriptome information with nanoscale resolution and a centimeter-sized field of view (FOV). The Stereo-seq Chip T (poly-T-based chip) features spatially encoded capture probes that hybridize with mRNA molecules within tissue sections, followed by cDNA synthesis. With DNBSEQ sequencing and an integrated visualization platform, researchers can obtain ultra-high-resolution spatial transcriptomic data across entire tissue samples.

02 Workflow

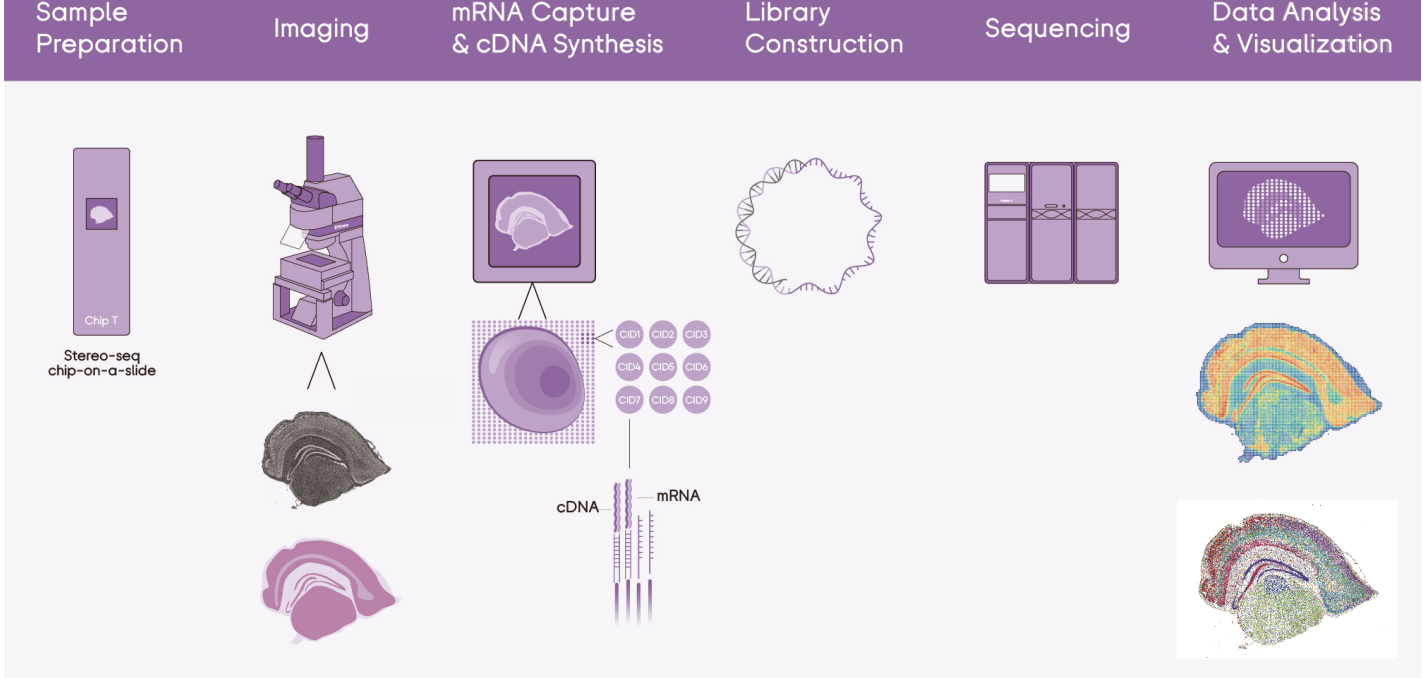


Figure 1 Stereo-seq Transcriptomics Set V1.3 Workflow

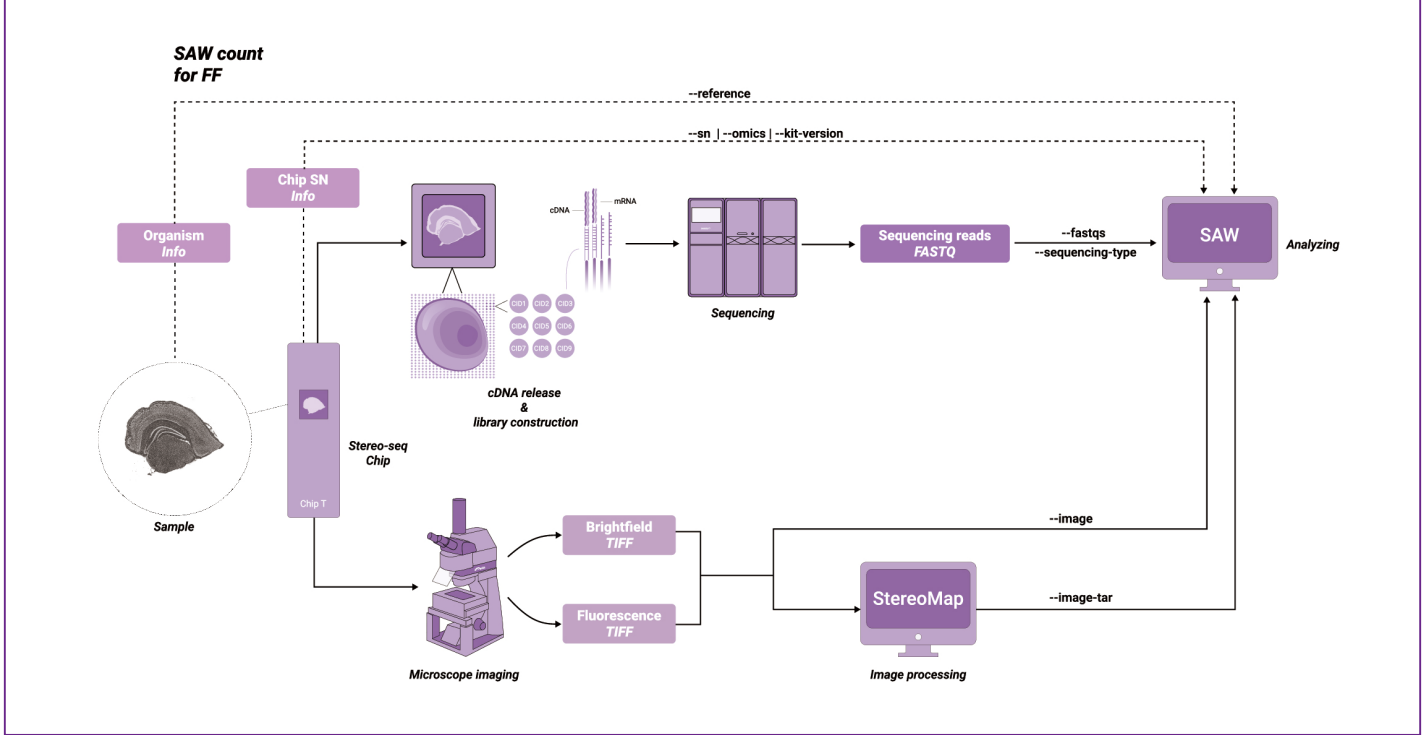


Figure 2 Overview of Stereo-seq Transcriptomics Set V1.3 Data Analysis Workflow

03 Resources Index

Step	Document Title and Description	Link
Experiment Preparation	Stereo-seq Transcriptomics Set User Guidance Document No. : STUM-UG002 This guidance aims to give the user a general view of the Stereo-seq Transcriptomics Set V1.3, with the overview of whole experiment workflow and index of resources to support the users' in-house experiments.	View Document
	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.	View Document
	Stereo-seq Operation Guide For Receiving, Handling And Storing This manual provides receiving, handling and storing guidance of the Stereo-seq Chip Slide.	View Document
	Experiment Checklist for Stereo-seq Transcriptomics Set V1.3 This manual provides a detailed checklist for Stereo-seq Transcriptomics Set V1.3 workflow in terms of different experiment stages.	Download Table
	Sample Preparation Guide for Fresh Frozen Samples on Stereo-seq Chip Slides Document No. : STUM-SP001 This manual aims to guide the users in fresh frozen samples preparing for Stereo-seq Transcriptomics Set V1.3 Workflow.	View Document
Permeabilization Optimization and Transcriptomics Workflow	Stereo-seq Permeabilization Set for Chip-on-a-slide User Manual Document No. : STUM-PR001 This manual aims to guide the users to perform permeabilization optimization on Stereo-seq Chip P Slide for specific fresh frozen samples.	View Document
	Stereo-seq Transcriptomics Set V1.3 for Chip-on-a-slide User Manual Document No. : STUM-TT001 This manual provides a standard operation guidance for Stereo-seq Transcriptomics Set V1.3 for Stereo-seq Chip T Slide (1cm * 1cm).	View Document
	Stereo-seq Transcriptomics Set V1.3 for Chip-on-a-slide (0.5cm * 0.5cm) User Manual Document No. : STUM-TT002 This manual provides a standard operation guidance for Stereo-seq Transcriptomics Set V1.3 for Stereo-seq Chip T Slide (0.5cm * 0.5cm).	View Document
Library Preparation and Sequencing	Stereo-seq Transcriptomics Fresh Frozen 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 Set V1.3 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 hyper-links to all listed manuals to improve accessibility and user experience.

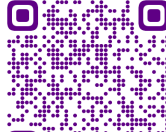
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