Stereo-seq Transcriptomics Solution V1.3 for mIF User Guidance

01 Introduction

Stereo-seq Transcriptomics Solution V1.3 for mIF is an extended application of Stereo-seq Transcriptomics Solution V1.3. By integrating multiplex immunofluorescence (mIF) staining method into the process of Stereo-seq Transcriptomics standard workflow, Stereo-seq transcriptome and mIF co-detection technology enables spatial visualization of multiple proteins on top of the unbiased whole transcriptome information on the same tissue slice. Without affecting mRNA capturing, the additional detected protein information can be integrated with gene expression data to evaluate valuable samples in depth, and to parse complex pathological and physiological processes.

02 Workflow

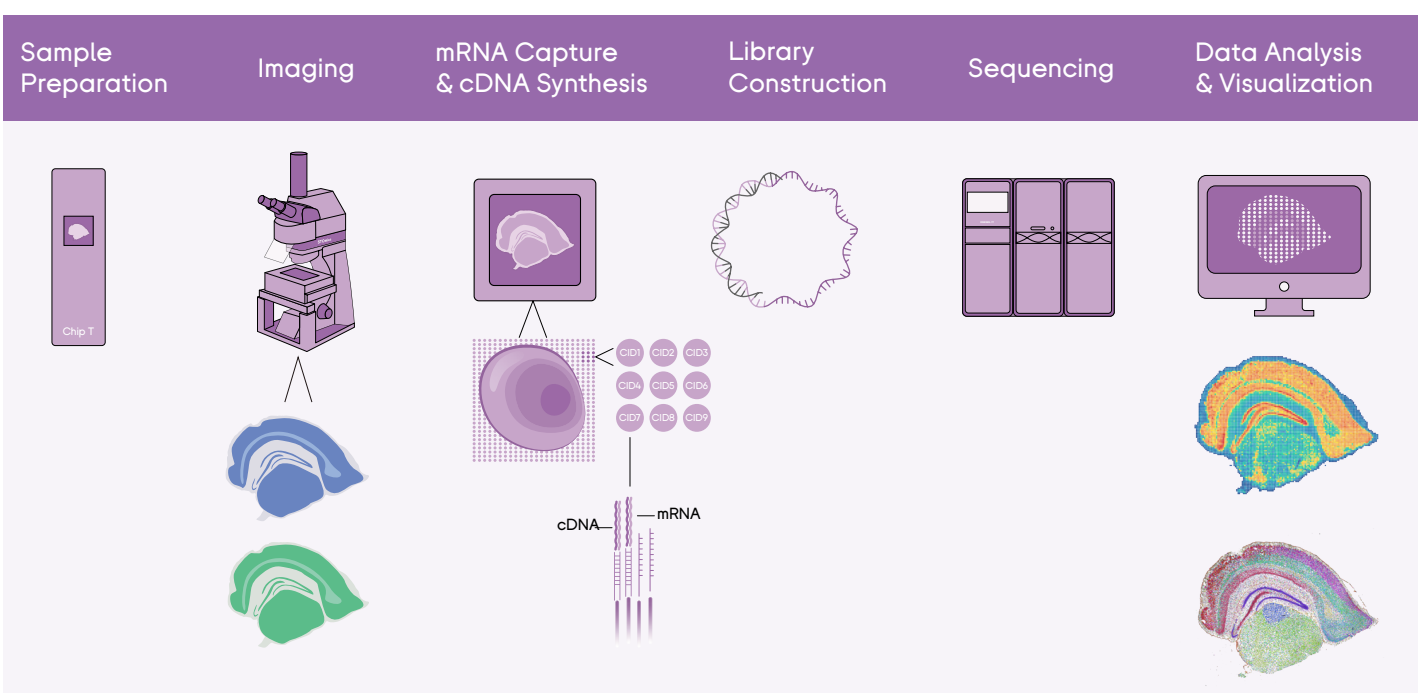

Figure 1 Stereo-seq Transcriptomics Solution V1.3 for mIF Workflow

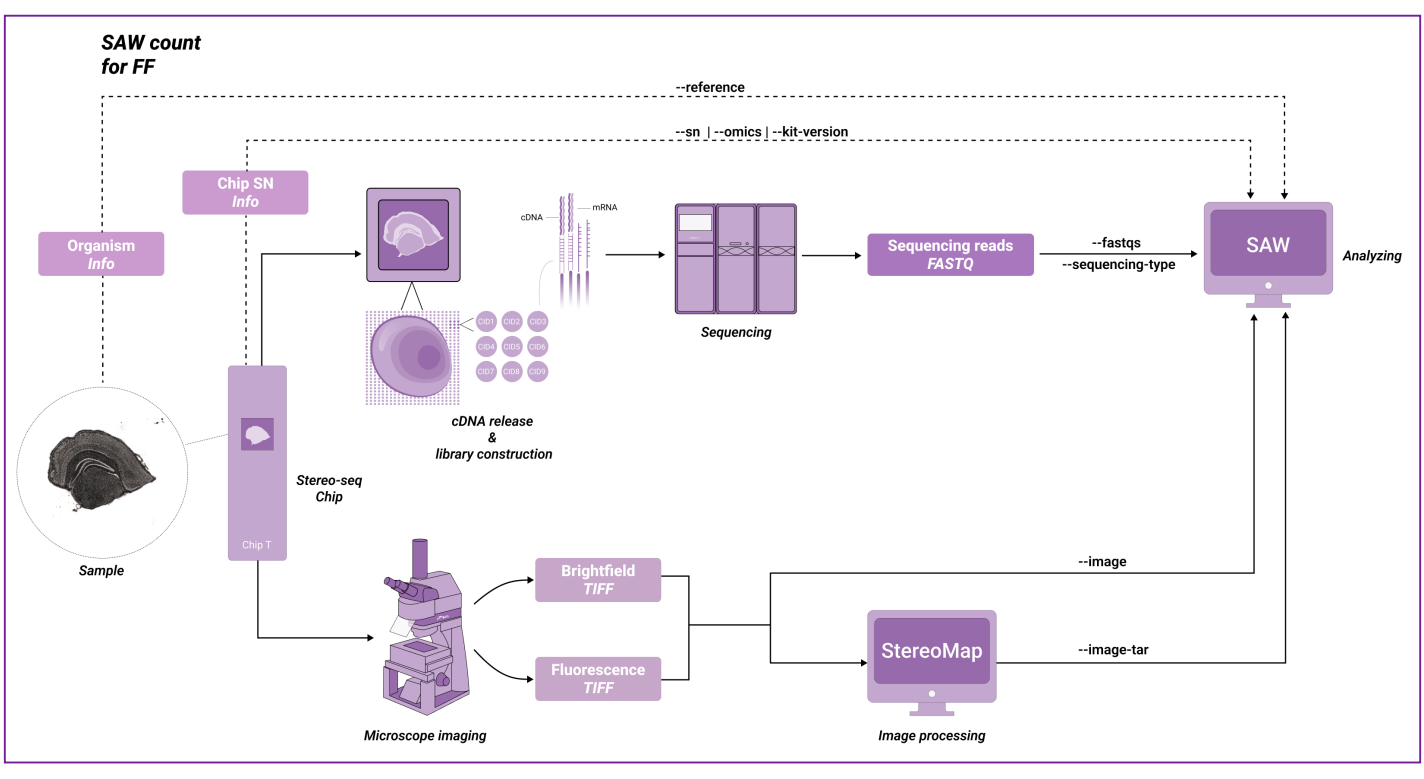

Figure 2 Overview of Stereo-seq Transcriptomics Solution V1.3 for mIF Data Analysis Workflow

03 Resources Index

Step	Document Title and Description	Link
Experiment Preparation	**Stereo-seq Transcriptomics Solution V1.3 for mIF User Guidance** Document No. : STUM-UG003 This guidance aims to give the user a general view of the Stereo-seq Transcriptomics Solution V1.3 for mIF, 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 Chip Slide 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 Transcriptomics Solution V1.3 for mIF This manual provides a detailed checklist for Stereo-seq Transcriptomics Solution V1.3 for mIF workflow in terms of different experiment stages.	
	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 Solution V1.3 for mIF applications.	
Permeabilization Optimization and Transcriptomics Workflow	**Stereo-seq Permeabilization Set for mIF User Manual** Document No. : STUM-PR003 This manual aims to guide the users in permeabilziation optimization for specific samples that are used for Stereo-seq Transcriptomics Solution V1.3 for mIF applications.	
	Stereo-seq Transcriptomics Set for Chip-on-a-slide mIF User Manual Document No. : STUM-TT003 This manual provides a standard operation guidance for Stereo-seq Transcriptomics Solution V1.3 mIF applications, in terms of antibody titration, mIF pilot experiment and transcritomics standard procedure. This manual is suitable for Stereo-seq Chip Slide(1cm * 1cm).	
Library Preparation and Sequencing	**Stereo-seq Transcriptome FF 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 Solution V1.3 for mIF 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: Jan. 2025
Description: Initial release

05 Contact Us

STOmics Website: https://en.stomics.tech
STOmics Email Address: info_global@stomics.tech