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 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. 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 Transcriptomics Set V1.3 This manual provides a detailed checklist for Stereo-seq Transcriptomics Set V1.3 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 Set V1.3 Workflow.	https://en.stomics. tech/resources/ documents/ list.html ••••••••••••••••••••••••••••••••••••
Permeabilization Optimization and Transcriptomics Workflow	Stereo-seq Permeabilization Set for Chip-on-a-slide User ManualDocument No. : STUM-PR001This manual aims to guide the users to perform permeabilzia- tion optimization on Stereo-P Chip Slide for specific fresh frozen samples.Stereo-seq Transcriptomics Set V1.3 for Chip-on-a-slide User ManualDocument No. : STUM-TT001This manual provides a standard operation guidance for Stereo-seq Transcriptomics Set V1.3 for Stereo-seq Chip T Slide (1 cm * 1 cm).Stereo-seq Transcriptomics Set V1.3 for Chip-on-a-slide (0.5cm * 0.5cm) User ManualDocument No. : STUM-TT002This manual provides a standard operation guidance for Stereo-seq Transcriptomics Set V1.3 for Stereo-seq Chip T Slide (0.5cm * 0.5cm).	
Library Preparation and Sequencing	Stereo-seq Transcriptomics Fresh Frozen Library Preparation User ManualDocument No. : STUM-LP002This manual aims to provide guidance for the whole-transcriptome library construction from cDNA products obtained via Stereo-seq Transcriptomics Set V1.3 workflow.Related Sequencing ManualsCG DNBSEQ-T7RS Stereo-seq Visualization Reagent Set Instructions for UseCG DNBSEQ-G400RS Stereo-seq Visualization Reagent Set Instructions for UseMGI DNBSEQ-T7RS Stereo-seq Visualization Reagent Set 	https://www. completegenomics. com/documentation/ 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. 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/ stereoMap-operation -manual.html https://en.stomics. tech/service/new- saw-operation- manual.html

04 Revision History

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