

**STOmics**

**STEREO-SEQ ANALYSIS  
WORKFLOW SOFTWARE SUITE  
USER MANUAL**

Software Version: V5.1.3

Manual Version: A3

## Revision History

**Manual Version:** A0  
**Software Version:** V1.0.0  
**Date:** Nov. 2021  
**Description:** Initial release

**Manual Version:** A1  
**Software Version:** V2.1.0  
**Date:** Dec. 2021  
**Description:**

- **New feature:** addition of manual registration function, some fine-tuning will be automatically performed after manually registering;
- **Improvement:** performance improvement for **mapping**; the order of sequencing saturation calculation has switched, in v2.1.0 we only compute the saturation of tissue-covered region;
- **Bug fix:** fixed the bug of indexing at **mapping** step; fix the bug of long waiting time at **register** step.

**Manual Version:** A1.1  
**Software Version:** V2.1.0  
**Date:** Jan. 2022  
**Description:**

- Add error handling;
- Update demo output.

**Manual Version:** A2  
**Software Version:** V4.1.0  
**Date:** Apr. 2022  
**Description:**

- **New feature:** support to process fused micrographs; employ Stereopy in clustering; new gene expression matrix file format; including a file format convertor and a **mapping** memory estimator;
- **Improvement:** performance improvement for **mapping**; update gene annotation approach in count; update image stitching and tissue segmentation model for better performance on image stitching and segmentation for tissue with voids.

**Manual Version:** A3  
**Software Version:** V5.1.3  
**Date:** Aug. 2022  
**Description:**

- **New feature:** addition of cell segmentation on microscopic image in **register** pipeline module and **cellCut** pipeline module to extract cell expression matrix; design IPR file to store image processing record information and TIFF images produced in **register**; output exon expression matrix along with total MID count; addition of cell clustering analysis; addition of cell bin statistic result and image information in HTML report; add pipeline modules to support single-end FASTQ data; addition of option for selecting multi-mapped reads; addition of score system in image processing;
- **Improvement:** addition of poly A filtration in **mapping**; performance improvement for **merge**, **tissueCut** and **saturation**; add data scaling and upgrade clustering analysis pipeline;
- **Bug fix:** fix the bug of plotting scatter plot in **tissueCut**, review and modify the ambiguous metrics names and explanations in HTML report.

**Manual Version:** A3.1  
**Software Version:** V5.1.3  
**Date:** Dec. 2022  
**Description:**

- **Buf fix:** fix the typo in the manual.

**Note: Please download the latest version of the manual and use it with the software specific to this manual.**

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# WORKFLOW

1 G reads

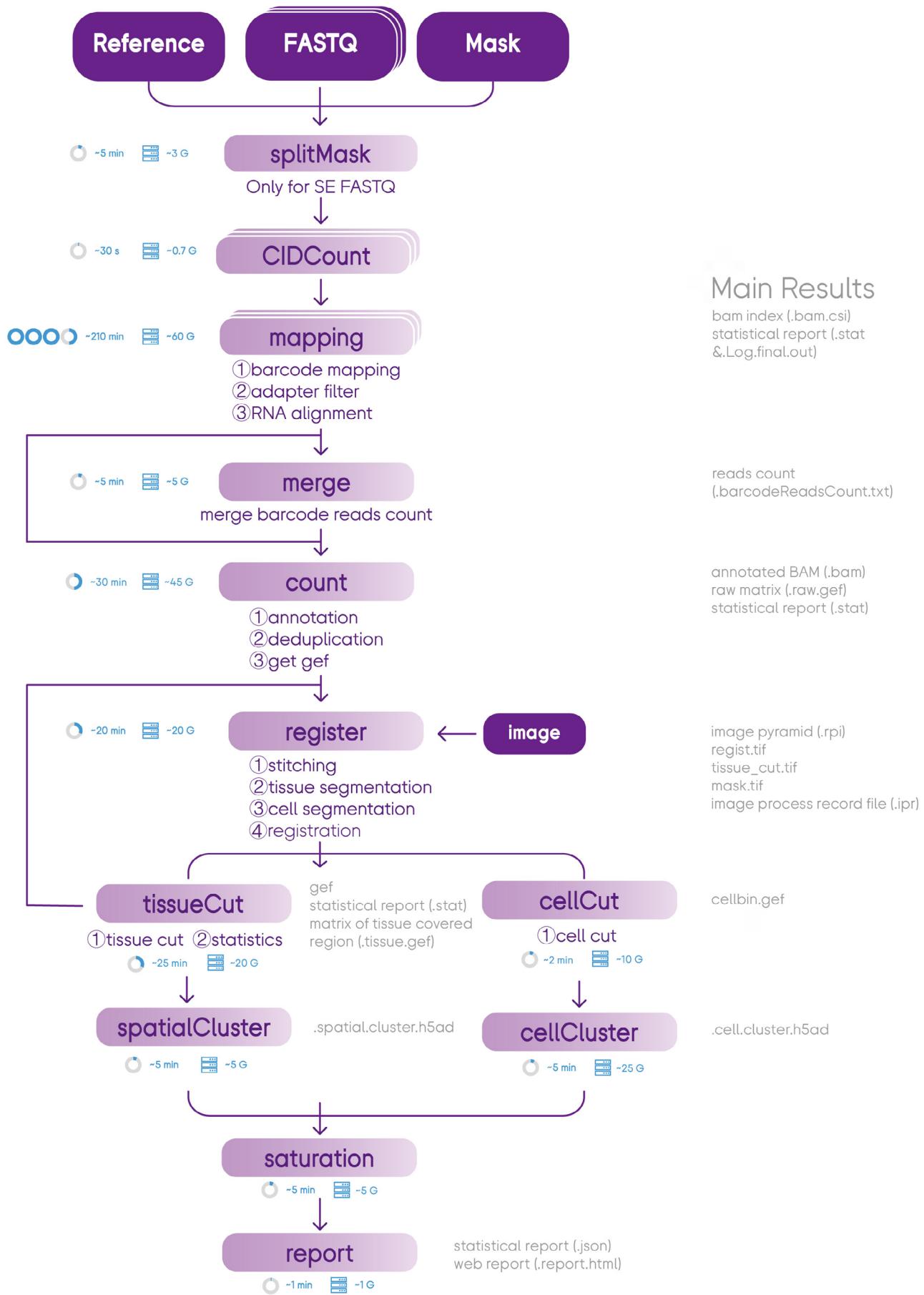
64 bit CentOS/RedHat 7.8  
64 bit Ubuntu 20.04

Minimum requirements:

8 cores 128 G 1 TB

Higher requirements:

12 cores 256 G 1 TB



# TABLE OF CONTENTS

## CHAPTER 1: STEREO-SEQ ANALYSIS WORKFLOW SOFTWARE SUITE

1.1. Software Introduction	1
1.2. System Requirements	2
1.3. Related Software	2
1.4. SAW Docker Image Installation	2
1.5. SAW GitHub	4
1.6. SAW Test Data	4
1.7. SAW Output File Format	4

## CHAPTER 2: SAW PIPELINES & ARGUMENTS

2.1. splitMask	6
2.2. CIDCount	7
2.3. mapping	8
2.4. merge (Optional)	14
2.5. count	15
2.6. register	17
2.7. ipr2img	18
2.8. tissueCut	21
2.9. spatialCluster	23
2.10. cellCut	23
2.11. cellCluster	25
2.12. saturation	25
2.13. report	27
2.14. Other Applications	32

## CHAPTER 3: TEST DATA DEMONSTRATION

3.1. mapping	37
3.2. merge	39
3.3. count	39
3.4. register	41
3.5. tissueCut	42
3.6. cellCut	45
3.7. saturation	46
3.8. report	46

## APPENDICES

Appendix A: Recommend Directory Structure for Raw Data	50
Appendix B: SAW ST Output File List	51
Appendix C: Handling Errors and Exceptions	54
Appendix D: Manual Image Merge Using Image J	55

## REFERENCES

58

## CONTACT US

59



CRITICAL STEPS: Pay extra attention to these instructions/steps to avoid problematic results.



SOLUTION: Provides a solution to handling common errors.

# **CHAPTER 1**

## **STEREO-SEQ ANALYSIS WORKFLOW SOFTWARE SUITE**

## 1.1. Software Introduction

Stereo-seq Analysis Workflow<sup>1</sup> (SAW) software suite is a set of pipelines bundled to position sequenced reads to their spatial location on the tissue section, quantify spatial gene expression and visually present spatial expression distribution. SAW processes the sequencing data of Stereo-seq<sup>2</sup> to generate spatial gene expression matrices, and then users could take these files as the starting point to perform downstream analysis. SAW includes thirteen essential and suggest pipelines and auxiliary tools for supporting other handy functions:

- **splitMask:** Split Stereo-seq Chip T mask file into several pieces according to CID indexing in the SE FASTQ files.
- **CIDCount:** Counting CIDs in the Stereo-seq Chip mask file and roughly estimating memory required to do mapping. (Highly suggested to run this before mapping.)
- **mapping:** Corresponds *in situ* captured sequenced reads recorded in FASTQ<sup>3,4</sup> files by Stereo-seq with their spatial information. It also aligns reads to the reference genome and generates coordination sorted BAM files.
- **merge (optional):** Combines mapping of CID (same as barcodes) listed files with reads count from multiple runs of mapping. Only applicable for an analysis that requires to combine multiple pairs of FASTQ.
- **count:** Reads BAM files generated from mapping to perform gene annotation, de-duplication, and gene expression analysis on the aligned reads.
- **register:** Align microscopic tissue staining image with gene expression matrix file (GEF) generated from count.register is an optional pipeline when image failed QC or input ssDNA image is absent.
- **ipr2img:** Convert TIFF images from IPR, such as template-aligned stitched TIFF image, binarized tissue segmentation and cell segmentation images. Optional module when image failed QC or input ssDNA image is absent.
- **tissueCut:** Identify tissue coverage area on the chip and extract gene expression matrix of the corresponding spatial location by taking inputs from both count and register or count pipeline alone.
- **spatialCluster:** Perform clustering analysis for spots (bin200) according to the gene expression matrix of the tissue covered area generated from tissueCut.
- **cellCut:** Identify cell coverage area on the ssDNA plot and extract gene expression matrix of the corresponding spatial location by taking inputs from both count and register pipeline. Optional module when image failed QC or input ssDNA image is absent.
- **cellCluster:** Perform clustering analysis for cell bins according to the gene expression matrix which generated from cellCut. Optional module when image failed QC or input ssDNA image is absent
- **saturation:** Calculate sequencing saturation of tissue coverage area based on the file that was used for sampling data generated from count.
- **report:** Generate a JSON format statistical summary report that integrate the analysis result from each step, as well as an HTML web analysis report, showing spatial expression distribution of genes, key statistical metrics, sequencing saturation plots, clustering analysis results. Depending on the image input state and register mode, HTML reports may or may not have cell bin statistical data and image processing key results.

Other handy functions:

- **Other applications of cellCut:** Manipulating GEF file.
- **rapidRegister:** Run registration without performing cell segmentation.
- **checkGTF:** Check GTF/GFF file is prepared in the correct format, otherwise, re-format one that meet the compatibility requirements for count.



## 1.2. System Requirements

SAW runs on Linux systems that meet the following minimum requirements:

8-core Intel or AMD processor (>24 cores recommended)
128GB RAM (>256GB recommended)
1TB free disk space
64-bit CentOS/RedHat 7.8 or Ubuntu 20.04

To install and run SAW, please install one kind of the following softwares:

<b>docker</b> <sup>5</sup> : version 20.10.8 or higher
<b>singularity</b> <sup>6</sup> : version 3.8 or higher

## 1.3. Related Software

SAW >= 5.0.0 requires imageQC version >= 1.1.0 that provide IPR file for recording image processing data.

## 1.4. SAW Docker Image Installation

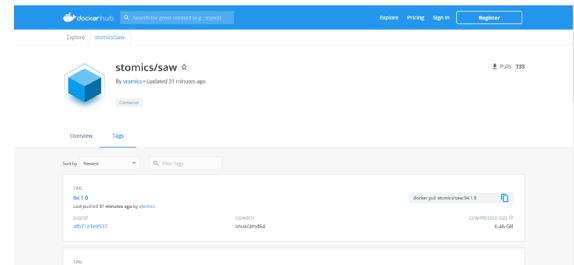
SAW is delivered as a docker image that bundles all of its required software dependencies. You can pull the SAW docker image from Docker Hub to your local system and run analyses offline.

Please download the latest version of the software and use it with the corresponding [Stereo-seq Analysis Workflow Software Suite User Manual](#) version.

Docker Hub link: <https://hub.docker.com/r/stomics/saw/tags>

We support using Singularity and Docker to install and run the SAW.

Here we take SAW version 5.1.3 as an example.



### 1.4.1. SAW Installation via Singularity

⚠️ **CRITICAL STEPS: For yellow highlighted inputs, please replace with your own path or data.**

Step 1: Pull the SAW docker image (2 options):

```
$ singularity build SAW_v5.1.3.sif docker://stomics/saw:05.1.3 ## option 1
$ singularity build --sandbox SAW_v5.1.3/ docker://stomics/saw:05.1.3 ## option 2
```

For non-root users, especially who don't have enough space in the `/home/` directory, please try:

```
$ export SINGULARITY_CACHEDIR=/path/to/build
$ singularity build --sandbox SAW_v5.1.3/ docker://stomics/saw:05.1.3
```

Step 2: Run pipelines (3 options):

ⓘ Note! All the requested paths need to be mounted before input. For example, it is necessary to bind directories that store input files (`/path/to/data`), reference genome (`/path/to/genomeDir`), and outputs (`/path/to/output`).

```
$ export SINGULARITY_BIND="/path/to/data,/path/to/genomeDir,/path/to/output"
```

Option 1: Run pipelines within the container from the host system.

```
$ /path/to/SAW_v5.1.3.sif <application> ## option 1.1
$ singularity exec /path/to/SAW_v5.1.3.sif <application> ## option 1.2
```

Option 2: Shell into the SAW container and interactively run bash commands. Run `exit` to exit the environment.

```
$ /path/to/SAW_v5.1.3.sif /bin/bash ## option 2.1
Singularity>
Singularity> <shell-command>
Singularity> exit
$
$ singularity shell /path/to/SAW_v5.1.3.sif ## option 2.2
Singularity>
Singularity> <shell-command>
Singularity> exit
$
$ singularity shell SAW_v5.1.3 ## option 2.3 for sandbox
Singularity>
Singularity> <shell-command>
Singularity> exit
$
```

Option 3: Use “`-B directory on the host-machine:directory in the container`” to mount a host directory into the container and execute the command in the container.

```
$ singularity shell -B /path/to/directory/on/the/host-machine:/path/to/directory/
mounted/in/the/container /path/to/SAW_v5.1.3.sif
Singularity>
Singularity> <shell-command>
Singularity> exit
$
```

\* Please be noted that these two lines belong to the same line of command.

## 1.4.2. SAW Installation via Docker

Step 1: Pull the SAW docker image

```
$ docker pull stomics/saw:05.1.3
```

Step 2: Run pipelines interactively

```
$ docker run -it stomics/saw:05.1.3
```



## 1.5. SAW Github

SAW GitHub: <https://github.com/BGIResearch/SAW>

Please visit GitHub for instruction regarding the **installation of singularity** and **indexing reference genome**. The page also provides **SAW shell script** examples for users.

 **Note! Please build your reference before running SAW analysis.**

## 1.6. SAW Test Data

SAW test data can be downloaded from SAW GitHub page. Key outputs are shown in [\*\*Chapter 3 Test Data Demonstration\*\*](#). The reference genome version for SAW testing is:

- genome-build: GRCm38.p6
- genome-version: GRCm38
- genome-date: 2012-01
- genome-build-accession: NCBI:GCA\_000001635.8

## 1.7. SAW Output File Format

Please check [\*\*Stereo-seq File Format Manual\*\*](#) to get more information on SAW output files format.



# **CHAPTER 2**

## **SAW PIPELINES & ARGUMENTS**

## 2.1 splitMask

**splitMask** is designed for splitting Stereo-seq Chip T Mask file according to the SE FASTQ CID. The split count is directly related to the number of split FASTQs while writing FASTQ out from sequencer.

Run **splitMask** requires the following files:

- Stereo-seq Chip T Mask file (**.h5 or .bin**)
- ⌚ Expected running time for ~1G reads: ~5 min, Memory: ~3G

### 2.1.1 Arguments and Options

Table 2-1 **splitMask** Arguments and Options

Parameter index	Function
[1]	(Required) Stereo-seq Chip T Mask file path (.h5 or .bin).
[2]	(Required) Output directory stores split mask files.
[3]	(Required) Set the number of threads to be used.
[4]	(Optional) Split count. This count number needs to be set the same as SE FASTQ count. The options are the powers of 4, and the commonly used options are 16 and 64. If a library contains two barcodes sequenced in the same lane and the two barcodes were split when written out FASTQs, then the split count is 16; otherwise, if the barcodes were not split, then 64.
[5]	(Optional) CID position, commonly used option is “2_25”. <b>splitMask</b> uses 24 bases (out of 25, 25 is the read length of CID) to split Stereo-seq Chip T Mask file. This CID position parameter is a string that combines two index numbers with “_”. The two numbers indicate the start and the end base index in the CID, and the bases in this range are used for splitting. For example, “2_25” means start from the 2 <sup>nd</sup> base to the 25 <sup>th</sup> base that are used for splitting mask file.

### 2.1.2 Usage Example

⌚ Note! Replace **{SN}** with your Stereo-seq Chip T serial number (SN, e.g. SS200000135TL\_D1),

```
...
$ mkdir /path/to/output/00.splitmask
$ singularity exec SAW_v5.1.3.sif splitMask \
    /path/to/data/{SN}.barcodeToPos.h5 \ ## Mask path
    /path/to/output/00.splitmask \ ## output directory
    8 \ ## threads
    16 \ ## split count
    2_25 ## CID position
```

### 2.1.3 Outputs

The output files of **splitMask** are organized as below:

```
...
$ tree /path/to/output/00.splitmask
/path/to/output/00.splitmask
|-- 01.SN.barcodeToPos.bin
|-- 02.SN.barcodeToPos.bin
|-- 03.SN.barcodeToPos.bin
|-- 04.SN.barcodeToPos.bin
|-- 05.SN.barcodeToPos.bin
|-- 06.SN.barcodeToPos.bin
```



```
...
|-- 07.SN.barcodeToPos.bin
|-- 08.SN.barcodeToPos.bin
|-- 09.SN.barcodeToPos.bin
|-- 10.SN.barcodeToPos.bin
|-- 11.SN.barcodeToPos.bin
|-- 12.SN.barcodeToPos.bin
|-- 13.SN.barcodeToPos.bin
|-- 14.SN.barcodeToPos.bin
|-- 15.SN.barcodeToPos.bin
`-- 16.SN.barcodeToPos.bin

0 directories, 16 files
```

## 2.2 CIDCount

**CIDCount** is a small program for computing the number of CIDs in the Stereo-seq Chip T Mask file and roughly estimating how much memory will be needed to do **mapping**.

Run **CIDCount** requires the following files:

- Stereo-Seq Chip T Mask file (**.h5 or .bin**)
- ⌚ Expected running time for ~1G reads: ~30 s, Memory: ~0.7G

### 2.2.1 Arguments and Options

Table 2-2 CIDCount Arguments and Options

Parameter	Function
<b>-i</b>	(Required) Stereo-seq Chip T Mask file path (.h5 or .bin).
<b>-s</b>	(Required) A string of species name.
<b>-g</b>	(Required) Genome file size in GB.

### 2.2.2 Usage Example

For PE FASTQ input cases, run **CIDCount** as below:

```
...
$ singularity exec SAW_v5.1.3.sif CIDCount \
    -i /path/to/data/{SN}.barcodeToPos.h5 \ ## Stereo-seq Chip T Mask file path
    -s {speciesName} \ ## species name
    -g {genomeSize} ## genome file size in GB, can be acquired by "ls -l --block-size=GB ${Genome file of the species after STAR indexing}"
```

For SE FASTQ input cases that require to run **splitMask** first, users may run **CIDCount** only once because the results for each individual small mask are close to each other.

```
...
$ singularity exec SAW_v5.1.3.sif CIDCount \
    -i /path/to/output/00.splitmask/{index}.{SN}.barcodeToPos.bin \ ## Stereo-seq
    Chip T Mask file path
```



```
...  
-s {speciesName} \ ## species name  
-g {genomeSize} ## genome file size in GB, can be acquired by "ls -l --block-size=GB ${Genome file of the species after STAR indexing}"
```

 Note! **{index}** needs to be replaced by the real index number of the split mask file.

## 2.2.3 Outputs

The output of **CIDCount** is shown as below,

```
...  
$ singularity exec SAW_v5.1.3.sif CIDCount -i SN.barcodeToPos.h5 -s mouse -g 3  
645784920 ## CID count  
62 ## estimated memory for mapping
```

If users wish to run **CIDCount**, they may add “**bcNum**” to the required **{lane}.bcPara** file for **mapping**. Please check [2.3.2 Usage Example \(mapping\)](#) for the demo.

## 2.3 mapping

Each Stereo-seq sequenced read contains a CID sequence which is used as a key to spatially map the read back to its original location on the tissue slice. **mapping** pipeline matches CID of the original sequencing reads stored in the FASTQ file with the records of CID-coordinates key-value pairs saved in the Stereo-seq Chip T Mask file. Coordinate information for reads that CID could be paired with will be added based on the records of the Mask file (allow 1 mismatch). Coordinate information for reads that CID could be paired with will be added based on the records of the Mask file. Reads that get the coordinate annotations are Valid CID mRNA Reads (**Valid CID Reads**). After discarding reads with MID quality does not satisfy with further analysis, filtering reads with adapter, and filtering short reads (read length less than 30 after trimming consecutive A bases), the filtered **Valid CID Reads** are the **Clean Reads**. **mapping** pipeline maps **Clean Reads** to the reference genome, and output sorted BAM<sup>7</sup> format alignments and summary report.

Run **mapping** requires the following files:

- Stereo-seq sequenced reads FASTQ files (**.fq.gz**)
- Stereo-seq Chip T Mask file (**.h5 or .bin**)
- Indexed reference genome
- bcPara file (**.bcPara**), please check the content of Table 2-4
-  Expected running time for ~1G reads: ~4 h, Memory: ~67G
-  NOTE! Before proceeding, if users need to estimate the number of CIDs and the memory needed for running **mapping**, please refer to [2.2 CIDcount](#) for more information.

### 2.3.1 Arguments and Options

As **mapping** encapsulate STAR<sup>8</sup> function, it accepts additional options beyond those shown in the table below.

Table 2-3 mapping Arguments and Options

Parameter	Function
<b>--outSAMattributes spatial</b>	Set to turn on spatial BAM file format mode.
<b>--outSAMtype BAM SortedByCoordinate</b>	(STAR option) Set output BAM file sorted by coordinate.
<b>--genomeDir</b>	(STAR option) Path to the directory where the genome indices are stored.
<b>--runThreadN</b>	(STAR option; defaults to 1) Set the number of threads to be used. Usually set to 8 or higher.
<b>--outFileNamePrefix</b>	(STAR option) Custom output file prefix.
<b>--sysShell /bin/bash</b>	(STAR option) Path to the shell binary.
<b>--stParaFile</b>	(Required) Name of a parameters file defines CID mapping options. Options are specified in Table 2-2.
<b>--readNameSeparator \"\\"</b>	(STAR option) Character(s) separating the part of the read names that will be trimmed in output.
<b>--limitBAMsortRAM</b>	(STAR option) Maximum available RAM (bytes) for sorting BAM.
<b>--limitOutSJcollapsed</b>	(STAR option) Max number of collapsed junctions.
<b>--limitIObufferSize</b>	(STAR option) Max available buffers size (bytes) for input/output, per thread.
<b>--outBAMsortingBinsN</b>	(STAR option; defaults to 50) number of genome bins for coordinate-sorting. If the read2 FASTQ file size is greater than 200, it is better to set this value to 100.

Table 2-4 mapping --stParaFile Arguments and Options

Parameter	Function
<b>in</b>	(Required) Path to the Stereo-seq Chip T Mask file (PE) or split mask file (SE).
<b>in1</b>	(Required) Path to the FASTQ file. If PE sequencing, then specify the path to the FASTQ file of read1 here.
<b>in2</b>	(Optional) Path to the FASTQ file of read2. Only valid for PE sequencing.
<b>encodeRule</b>	(Required) Encoding rule for the four bases. ACTG stands for A->0, C->1, T->2, G->3.
<b>out</b>	(Optional) Set output file prefix.
<b>action</b>	(Required; defaults to 1) Action number. Set to 4 in mapping Valid options: 1=CID stat, 2=CID overlap, 3=get CID position map, 4=map CID to slide, or 5=merge CID list.
<b>barcodeReadsCount</b>	(Required) Mapped CID list file with reads counts for each CID. This is an output file in mapping
<b>platform</b>	(Optional) Sequencing platform. Valid options: SEQ500, T1, or T10.
<b>barcodeStart</b>	(Required; defaults to 0) CID start position. Set to 0 for PE, 1 for SE.
<b>barcodeLen</b>	(Required; defaults to 25) CID length. Set to 25 for PE, 24 for SE.
<b>umiStart</b>	(Required; defaults to 25) MID start position.
<b>umiLen</b>	(Required; defaults to 10) MID length.
<b>umiRead</b>	(Required; defaults to 1) Declare the read contains MID.
<b>mismatch</b>	(Required; defaults to 0) Max mismatch tolerant. Usually set to 1 in mapping.
<b>bcNum</b>	(Required) CID count in mask. Please check <a href="#">2.2 CIDCount</a> for more information.
<b>polyAnum=15</b>	(Optional) Number of consecutive A in the read that will be trimmed. Recommend to set this value to 15.
<b>mismatchInPolyA=2</b>	(Optional) Number of mismatch bases in searching poly A. Recommend to set this value to 2



### 2.3.2 Usage Example

Two scenarios for preparing `mapping --stParaFile` input file `{lane}.bcPara` with PE FASTQ input:

- ⌚ Note! Replace `{SN}` with your Stereo-seq Chip T serial number (SN, e.g. SS200000135TL\_D1), and `{lane}` with the FASTQ lane name prefix (e.g. E100026571\_L01)
- ⌚ The same applies to all examples.

PE scenario 1: Prepare `{lane}.bcPara` file for PE one pair FASTQ as `mapping` input:

```
...
$ mkdir /path/to/output/01.mapping
$ vim /path/to/output/01.mapping/{lane}.bcPara
in=/path/to/data/{SN}.barcodeToPos.h5
in1=/path/to/data/{lane}_read_1.fq.gz
in2=/path/to/data/{lane}_read_2.fq.gz
encodeRule=ACTG
out={lane}
barcodeReadsCount=/path/to/ouptut/01.mapping/{lane}.barcodeReadsCount.txt
action=4
platform=T10
barcodeStart=0
barcodeLen=25
umiStart=25
umiLen=10
umiRead=1
mismatch=1
bcNum=645784920 ## Input the first line from output of CIDCount if run ahead mapping
polyAnum=15
mismatchInPolyA=2
```

PE scenario 2: Prepare `{lane}.bcPara` file for PE multiple pair of FASTQ as `mapping` input:

```
...
$ mkdir /path/to/multi_lane_output/01.mapping
$ vim /path/to/multi_lane_output/01.mapping/{lane}.bcPara
in=/path/to/data/{SN}.barcodeToPos.h5
in1=/path/to/data/{lane}_read_1.fq.gz
in2=/path/to/data/{lane}_read_2.fq.gz
encodeRule=ACTG
out={lane}
barcodeReadsCount=/path/to/multi_lane_output/01.mapping/{lane}.barcodeReadsCount.txt
action=4
platform=T10
barcodeStart=0
barcodeLen=25
umiStart=25
umiLen=10
umiRead=1
mismatch=1
bcNum=645784920 ## Input the first line from output of CIDCount if run ahead mapping
polyAnum=15
mismatchInPolyA=2
```

Run **mapping** for PE input:

```
...$ singularity exec SAW_v5.1.3.sif mapping \
    --outSAMattributes spatial \
    --outSAMtype BAM SortedByCoordinate \
    --genomeDir /path/to/genomeDir \
    --runThreadN 8 \
    --outFileNamePrefix /path/to/output/01.mapping/{lane}. \
    --sysShell /bin/bash \
    --stParaFile /path/to/output/01.mapping/{lane}.bcPara \
    --readNameSeparator "\" \" \
    --limitBAMsortRAM 38582880124 \
    --limitOutSJcollapsed 10000000 \
    --limitI0bufferSize=280000000 \
    --outBAMsortingBinsN 50 \
    > /path/to/output/01.mapping/{lane}_barcodeMap.stat
```

Two scenarios for preparing **mapping --stParaFile** input file **{index}.bcPara** with SE FASTQ input:

**SE scenario 1:** Prepare **{index}.bcPara** file for SE FASTQ that contains one barcode in library or did not split barcode when writing FASTQ:

ⓘ Note! **{index}** need to be replaced by the index of the split mask file which is corresponding to the index of the SE FASTQ file.

```
...$ mkdir /path/to/output/01.mapping
$ vim /path/to/output/01.mapping/{index}.bcPara
in=/path/to/output/00.splitmask/{index}.{SN}.barcodeToPos.bin ## split mask file
in1=/path/to/data/{lane}_{index}.fq.gz ## {index}th FASTQ file in {lane}
out={SN}.bc.out${index}
barcodeReadsCount=/path/to/ouptut/01.mapping/{index}.barcodeReadsCount.txt
action=4
platform=T10
barcodeStart=1
barcodeLen=24
umiStart=25
umiLen=10
umiRead=1
mismatch=1
bcNum=38284877 ## Input the first line from output of CIDCount if run ahead mapping
polyAnum=15
mismatchInPolyA=2
```

**SE scenario 2:** Prepare **{idx}.bcPara** file for SE FASTQ that has multiple barcodes in the library and split when writing FASTQ:

ⓘ Note! **{index}** needs to be replaced by the real index number of the split mask file and **{idx}** needs to be replaced by the index number of the input FASTQ file. For example, if a library contains 2 barcodes that sequenced in the same lane, the **{index}** and **{idx}** for the third FASTQ file of barcode 1 are 01 and 03, respectively.

```
...$ mkdir /path/to/output/01.mapping
$ vim /path/to/output/01.mapping/{idx}.bcPara
in=/path/to/output/00.splitmask/{index}.{SN}.barcodeToPos.bin ## split mask file
in1=/path/to/data/{lane}_{index}.fq.gz ## {index}th FASTQ file in {lane}. FASTQ
files for different barcode usually stores in different directory, so /path/to/data/
might change to /path/to/data/{barcode_n}
out={SN}.bc.out${idx}
barcodeReadsCount=/path/to/ouptut/01.mapping/{idx}.barcodeReadsCount.txt
```



```
...
action=4
platform=T10
barcodeStart=1
barcodeLen=24
umiStart=25
umiLen=10
umiRead=1
mismatch=1
bcNum=38284877 ## Input the first line from output of CIDCount if run ahead mapping
polyAnum=15
mismatchInPolyA=2
```

### Run mapping pipeline

```
...
$ singularity exec SAW_v5.1.3.sif mapping \
    --outSAMattributes spatial \
    --outSAMtype BAM SortedByCoordinate \
    --genomeDir /path/to/genomeDir \
    --runThreadN 8 \
    --outFileNamePrefix /path/to/output/01.mapping/{index}. \ ## {index}
or {idx} depending on the scenario
    --sysShell /bin/bash \
    --stParaFile /path/to/output/01.mapping/{index}.bcPara \ ## {index}
or {idx} depending on the scenario
    --readNameSeparator '\" '\" \
    --limitBAMsortRAM 38582880124 \
    --limitOutSJcollapsed 10000000 \
    --limitIObufferSize=280000000 \
    --outBAMsortingBinsN 50 \
    > /path/to/output/01.mapping/{index}_barcodeMap.stat ## {index} or
{idx} depending on the scenario
```

### 2.3.3 Outputs

PE scenario 1 output files are organized as below:

```
...
$ ll -Rth /path/to/output/01.mapping
-rw-rw-r-- 1 ubuntu ubuntu 11M Apr 13 20:57 lane.Aligned.sortedByCoord.out.bam.csi
-rw-rw-r-- 1 ubuntu ubuntu 8.9K Apr 13 20:40 lane.Log.out
-rw-rw-r-- 1 ubuntu ubuntu 2.0K Apr 13 20:40 lane.Log.final.out
-rw-rw-r-- 1 ubuntu ubuntu 17K Apr 13 20:40 lane.Log.progress.out
-rw-rw-r-- 1 ubuntu ubuntu 62G Apr 13 20:40 lane.Aligned.sortedByCoord.out.bam
-rw-rw-r-- 1 ubuntu ubuntu 1.1K Apr 13 20:06 lane_barcodeMap.stat
-rw-rw-r-- 1 ubuntu ubuntu 11M Apr 13 20:06 lane.SJ.out.tab
-rw-rw-r-- 1 ubuntu ubuntu 997M Apr 13 20:06 lane.barcodeReadsCount.txt
-rw-rw-r-- 1 ubuntu ubuntu 528 Apr 13 17:46 lane.bcPara
```

PE scenario 2 output files are organized as below (Here showing example of 2 pairs of FASTQ):

⌚ If one sample has multiple FASTQ files, you need to run `mapping` for each FASTQ pair.

```
...
$ tree /path/to/multi_lane_output/01.mapping
/path/to/multi_lane_output/01.mapping
└── 01.mapping
```



```

└── lane1.Aligned.sortedByCoord.out.bam
└── lane1.Aligned.sortedByCoord.out.bam.csi
└── lane1_barcodeMap.stat
└── lane1_barcodeReadsCount.txt
└── lane1_bcPara
└── lane1_Log.final.out
└── lane1_Log.out
└── lane1_Log.progress.out
└── lane1_SJ.out.tab
└── lane2.Aligned.sortedByCoord.out.bam
└── lane2.Aligned.sortedByCoord.out.bam.csi
└── lane2_barcodeMap.stat
└── lane2_barcodeReadsCount.txt
└── lane2_bcPara
└── lane2_Log.final.out
└── lane2_Log.out
└── lane2_Log.progress.out
└── lane2_SJ.out.tab

```

SE scenario 1 (one barcode in library or did not split barcode when writing FASTQ) output files are organized as below:

```

$ tree /path/to/output/01.mapping
/path/to/output/01.mapping
└── 01.mapping
    ├── 01.Aligned.sortedByCoord.out.bam
    ├── 01.Aligned.sortedByCoord.out.bam.csi
    ├── 01_barcodeMap.stat
    ├── 01_barcodeReadsCount.txt
    ├── 01_bcPara
    ├── 01_Log.final.out
    ├── 01_Log.out
    ├── 01_Log.progress.out
    └── 01_SJ.out.tab
    ...
    ├── 16.Aligned.sortedByCoord.out.bam
    ├── 16.Aligned.sortedByCoord.out.bam.csi
    ├── 16_barcodeMap.stat
    ├── 16_barcodeReadsCount.txt
    ├── 16_bcPara
    ├── 16_Log.final.out
    ├── 16_Log.out
    ├── 16_Log.progress.out
    └── 16_SJ.out.tab

```

SE scenario 2 (multiple barcodes in the library and split when writing FASTQ) output files are organized as below (Here showing example of 2 barcodes):

```

$ tree /path/to/output/01.mapping
/path/to/output/01.mapping
└── 01.mapping
    ├── 01.Aligned.sortedByCoord.out.bam
    ├── 01.Aligned.sortedByCoord.out.bam.csi
    ├── 01_barcodeMap.stat
    ├── 01_barcodeReadsCount.txt

```

```

  └── 01.bcPara
  └── 01.Log.final.out
  └── 01.Log.out
  └── 01.Log.progress.out
  └── 01.SJ.out.tab
...
  └── 128.Aligned.sortedByCoord.out.bam
  └── 128.Aligned.sortedByCoord.out.bam.csv
  └── 128_barcodeMap.stat
  └── 128_barcodeReadsCount.txt
  └── 128.bcPara
  └── 128.Log.final.out
  └── 128.Log.out
  └── 128.Log.progress.out
  └── 128.SJ.out.tab

```

## 2.4 merge (optional)

SAW `merge` pipeline is used to combine the results of `mapping`.

Run `merge` requires the following files:

- `mapping` output mapped CID list files (`.txt`)
- ⌚ Expected running time for ~1G reads 2 lanes: ~5 min, Memory: ~5G

### 2.4.1 Arguments and Options

Table 2-5 `merge` Arguments and Options

Parameter	Function
[1]	(Required) Path to the Stereo-seq Chip T Mask file.
[2]	(Required) Mapped CID list files with reads counts for each CID.
[3]	(Required) Mapped CID list file which merges all input files.

### 2.2.2 Usage Example

```

$ mkdir /path/to/multi_lane_output/02.merge
$ singularity exec SAW_v5.1.3.sif merge \
/path/to/data/{SN}.barcodeToPos.h5 \
/path/to/multi_lane_output/01.mapping/{lane1}.barcodeReadsCount.txt,/path/to/multi_*
lanes_output/01.mapping/{lane2}.barcodeReadsCount.txt \ ## change {lane} to {index}
or {idx} for SE and change /path/to/multi_lane_output/ to /path/to/output/ for SE
single lane scenario
/path/to/multi_lane_output/02.merge/{SN}.barcodeReadsCount.txt

```

\* Please be noted that we use the backward slash “\” to indicate the end of a line in a command that spans multiple lines.

### 2.4.3 Outputs

The output file of `merge` has been organized as below:

```

$ ll -Rth /path/to/multi_lane_output/02.merge
-rw-rw-r-- 1 ubuntu ubuntu 997M Apr 13 20:53 SN.barcodeReadsCount.txt

```



## 2.5 count

SAW **count** is an efficient general-purpose read annotation pipeline that label reads with their overlapped genomic features and outputs statistics information for the overall summarization result. Through quantification of annotated reads, **count** generates spatial gene expression data after de-duplicate reads according to CID, gene ID, and MID information. Usually, SAW **count** is run on the **Uniquely Mapped Reads** filtered from **mapping** output based on the reference genome annotation records. Starting from SAW ST v5, **count** added a mode that allows utilizing some **Multi-Mapped Reads** in quantification (**--multi\_map**). The gene expression level in SAW pipeline is the summation of both intron and exon MID count. To support downstream analysis that might be required to differentiate genomic features, **count** also output exon MID count separately.

 Run **count** requires the following files:

- **mapping** output BAM file (**.bam**)
- Reference genome annotation GFF/GTF<sup>9,10</sup> file (**.gtf / .gff**)

Expected running time for ~1G reads: 0.5 h, Memory: ~45 G

### 2.5.1 Arguments and Options

Table 2-6 **count** Arguments and Options

Parameter	Function
<b>-i</b>	(Required) mapping output BAM file. Separate multiple files by comma.
<b>-o</b>	(Required) Set the count output BAM file name.
<b>-a</b>	(Required) Gene annotation GFF/GTF file.
<b>-s</b>	(Required) Set the count output statistical summary report file name.
<b>-e</b>	(Required) Set the count output gene expression file name.
<b>--umi_len</b>	(Required; defaults to 10) MID length.
<b>--sn</b>	(Required) Stereo-seq Chip T serial number (SN).
<b>-c</b>	(Optional; defaults to detected) CPU core number to use.
<b>--save_lq</b>	(Optional; defaults to false) Save low quality reads if set.
<b>--save_dup</b>	(Optional; defaults to false) Save duplicate reads if set.
<b>--umi_on</b>	(Optional; defaults to false) Correct MID if set.
<b>--sat_file</b>	(Optional; defaults to None) Set the saturation sampling file name which is prepared for sequencing saturation (requires <b>--umi_on</b> ).
<b>-m</b>	(Optional; defaults to detected) Set available memory (GB).
<b>--multi_map</b>	(Optional; defaults to disable) Set to enable multi-mapped reads correction. This correction consists of two logics. 1) The first logic is the correction of multi-gene reads which is a read mapped uniquely to a genomic region where multiple genes overlap. In this scenario, the read has to overlap with a genomic locus greater than 50% of its read length. If the genomic feature (exon, intron, or intergenic) of all the mapped genes includes exon and intron, then select the alignment record mapped to exon in preference to intron. If more than one gene locus belongs to the same genomic feature type, then pick the one that has the longest overlap. Otherwise, label the read to “intergenic.” 2) The second logic is to select and correct one of the multi-mapped reads and add the count to gene expression matrix. The first step is to group reads by QNAME. Select reads in the group mapped to exon in preference to those mapped to intron. Then correct the longest overlapped reads (at least overlapped greater than 50% of its read length) in the group to unique read and correct its MAPQ to 255. Set the MAPQ of the remaining reads to 0.



## 2.5.2 Usage Example

```
...
$ mkdir -p /path/to/output/03.count
$ geneExp=/path/to/output/03.count/{SN}.raw.gef
$ saturationSamplingFile=/path/to/output/03.count/{SN}_raw_barcode_gene_exp.txt
$ singularity exec SAW_v5.1.3.sif count \
    -i /path/to/output/01.mapping/{lane}.Aligned.sortedByCoord.out.bam \
    -o /path/to/output/03.count/{SN}.Aligned.sortedByCoord.out.merge.q10.dedup.
[*] target.bam \
    -a /path/to/reference/genes.gtf \
    -s /path/to/output/03.count/{SN}.Aligned.sortedByCoord.out.merge.q10.dedup.
[*] target.bam.summary.stat \
    -e ${geneExp} \
    --umi_len 10 \
    --sat_file ${saturationSamplingFile} \
    --sn {SN} \
    --umi_on \
    --save_lq \
    --save_dup \
    -c 8 \
    -m 128
```

\* Please be noted that we use the backward slash “\” to indicate the end of a line in a command that spans multiple lines.

For more than one pair of FASTQ files (Here showing an example of 2 pairs of FASTQ),

```
...
$ mkdir -p /path/to/multi_lane_output/03.count ## change /path/to/multi_lane_output/ to /path/to/output/ for SE single lane scenario
$ geneExp=/path/to/multi_lane_output/03.count/{SN}.raw.gef
$ saturationSamplingFile=/path/to/multi_lane_output/03.count/{SN}_raw_barcode_gene_exp.txt
$ singularity exec SAW_v5.1.3.sif count \
    -i /path/to/multi_lane_output/01.mapping/{lane1}.Aligned.sortedByCoord.out.bam,/path/to/multi_lane_output/01.mapping/{lane2}.Aligned.sortedByCoord.out.bam \
## change {lane} to {index} or {idx} for SE
    -o /path/to/multi_lane_output/03.count/{SN}.Aligned.sortedByCoord.out.merge.q10.dedup.target.bam \
    -a /path/to/reference/genes.gtf \
    -s /path/to/multi_lane_output/03.count/{SN}.Aligned.sortedByCoord.out.merge.q10.dedup.target.bam.summary.stat \
    -e ${geneExp} \
    --umi_len 10 \
    --sat_file ${saturationSamplingFile} \
    --sn {SN} \
    --umi_on \
    --save_lq \
    --save_dup \
    -c 8 \
    -m 128
```

\* Please be noted that we use the backward slash “\” to indicate the end of a line in a command that spans multiple lines.



For dealing with multi-mapped reads,

```
...$ singularity exec SAW_v5.1.3.sif count \
    -i /path/to/output/01.mapping/{lane}.Aligned.sortedByCoord.out.bam \
    -o /path/to/output/03.count/{SN}.Aligned.sortedByCoord.out.merge.q10.dedup.
target.bam \
    -a /path/to/reference/genes.gtf \
    -s /path/to/output/03.count/{SN}.Aligned.sortedByCoord.out.merge.q10.dedup.
target.
bam.summary.stat \
    -e ${geneExp} \
    --umi_len 10 \
    --sat_file ${saturationSamplingFile} \
    --sn {SN} \
    --umi_on \
    --save_lq \
    --save_dup \
    -c 8 \
    -m 128 \
    --multi_map
```

### 2.5.3 Outputs

The **count** output files are organized as below:

```
...$ ll -Rth /path/to/output/03.count
-rw-rw-r-- 1 ubuntu ubuntu 636M Apr 13 22:11 SN.raw.gef
-rw-rw-r-- 1 ubuntu ubuntu 2.6G Apr 13 22:11 SN_raw_barcode_gene_exp.txt
-rw-rw-r-- 1 ubuntu ubuntu 393 Apr 13 22:11 SN.Aligned.sortedByCoord.out.merge.
q10.dedup.target.bam.summary.stat
-rw-rw-r-- 1 ubuntu ubuntu 46G Apr 13 22:11 SN.Aligned.sortedByCoord.out.merge.
q10.dedup.target.bam
```

## 2.6 register

SAW **register** pipeline aligns the microscopic tissue staining image with the plot of the gene expression matrix generated by **count** based on the track lines on the chip while establishing the mapping relationship between images and spatial gene expression distribution. SAW **register** includes four main modules, stitching, tissue segmentation, cell segmentation, and registration. Stitching combines microscopic images with overlapping sections to create a panoramic image (skip stitching if the input image is already a panoramic image). Tissue and cell segmentation modules detect and mask out tissue and cell coverage region, respectively. Registration module aligns stitched image and expression matrix, and at the same time registered masks from segmentation modules with gene expression matrix using the same parameters.

Run **register** requires the following files:

- **count** output gene expression matrix file (**.raw.gef**)
- ImageQC processed microscopic tissue staining image file (**.tar.gz**)
- ImageQC image process record file (**.ipr**, **require imageQC version >= 1.1.0**)
- ⌚ Expected running time for ~1G reads: ~20 min, Memory: ~20G



## 2.6.1 Arguments and Options

Table 2-7 register Arguments and Options

Parameter	Function
<b>-i</b>	(Required) ImageQC processed staining image TAR.GZ file.
<b>-c</b>	(Required) ImageQC IPR (image process record) file. IPR is designed to efficiently hold images and processing records generated from each image processing step along with metadata in various data types. Please check <a href="#">Stereo-seq File Format Manual</a> to get more information on the IPR file.
<b>-v</b>	(Required) count output gene expression matrix GEF file.
<b>-o</b>	(Required) Path to the directory where to store the register outputs.

## 2.6.2 Usage Example

```
...
$ image=/path/to/data/image
$ image4register=$(find ${image} -maxdepth 1 -name ${SN}*.tar.gz | head -1)
$ imageQC=$(find ${image} -maxdepth 1 -name ${SN}*.ipr | head -1)
$ mkdir -p /path/to/output/04.register
$ singularity exec SAW_v5.1.3.sif register \
    -i ${image4register} \
    -c ${imageQC} \
    -v /path/to/output/03.count/${SN}.raw.gef \
    -o /path/to/output/04.register
```

## 2.6.3 Outputs

register output files are organized as below:

```
...
$ tree /path/to/output/04.register
/path/to/output/04.register
... ## skip setting files, logs and image folder
└── fov_stitched_transformed.tif
└── SN_date_time_version.csv
└── SN_date_time_version.ipr
└── SN_date_time_version.png
```

## 2.7 ipr2img

SAW **ipr2img** pipeline (available sine SAW ST >= v5.0.0) is run to “decode” images from the processed IPR file. SAW **ipr2img** could output TIFF images from IPR such as pre-registered ssDNA stitched image, tissue segmentation and cell segmentation mask TIFFs, as well as registered these three types of images.

Run **ipr2img** requires the following files:

- ImageQC processed microscopic tissue staining image file (**.tar.gz**)
- **register** processed Image process record file (**.ipr**)
- ⌚ Expected running time for ~1G reads: ~5 min, Memory: ~10 G



## 2.7.1 Arguments and Options

Table 2-8 ipr2img Arguments and Options

Parameter	Function
<b>-i</b>	(Required) ImageQC processed staining image TAR.GZ file.
<b>-c</b>	(Required) ImageQC IPR (image process record) file. IPR is designed to efficiently hold image information generated from each processing step and datasets in various compound types along with metadata. Please check <a href="#">Stereo-seq File Format Manual</a> to get more information on IPR file.
<b>-d</b>	(Required) Segmentation module names. Convert segmentation mask TIFF from IPR for the selected modules. Valid options: tissue and cell. Separate modules by space.
<b>-r</b>	(Required; default to True) Whether output registered images or pre-registered images. “Pre-registered” state stands for the images that have been stitched to a single panoramic image and transformed to have the same scale with the gene expression matrix, but still need to be flipped, 90°rotated, or translated. The options are True for output registered images and False for output pre-registered images.
<b>-o</b>	(Required) Path to the directory where to store the ipr2img outputs.

## 2.7.2 Usage Example

```
$ image=/path/to/data/image
$ image4register=$(find ${image} -maxdepth 1 -name {SN}*.tar.gz | head -1)
$ imageIPR=$(find /path/to/output/04.register -maxdepth 1 -name {SN}*.ipr | head -1)
## has to be a processed IPR
$ singularity exec SAW_v5.1.3.sif ipr2img \
    -i ${image4register} \
    -c ${imageIPR} \
    -d tissue cell \ ## output both tissue segmentation mask TIFF
    -r True \
    -o /path/to/output/04.register
```

## 2.7.3 Outputs

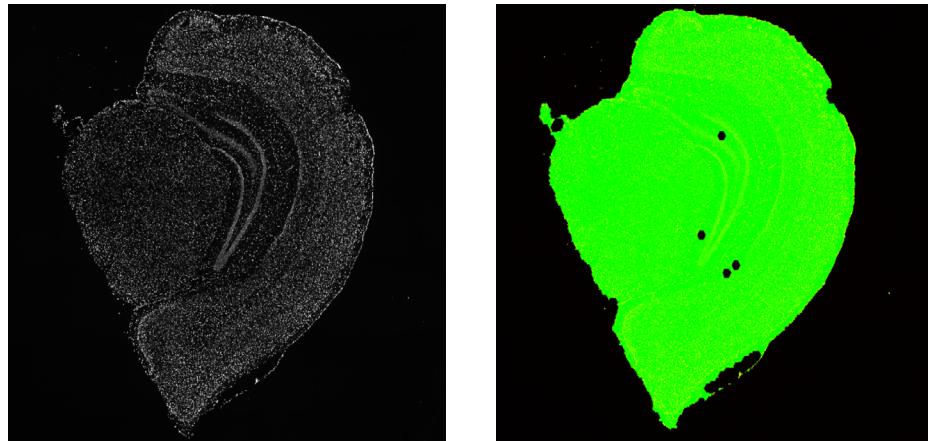
Ipr2img output files are organized as below:

```
$ tree /path/to/output/04.register
/path/to/output/04.register
... ## skip setting files, logs and image folder
├── attrs.json
├── fov_stitched_transformed.tif
├── matrix_template.txt
├── SN_date_time_version.csv
├── SN_date_time_version.ipr
├── SN_date_time_version.png
├── SN_mask.tif
├── SN_regist.tif
├── SN.rpi
├── SN_tissue_bbox.csv
├── SN_tissue_cut.tif
├── transform_template.txt
└── transform_thumb.png
```

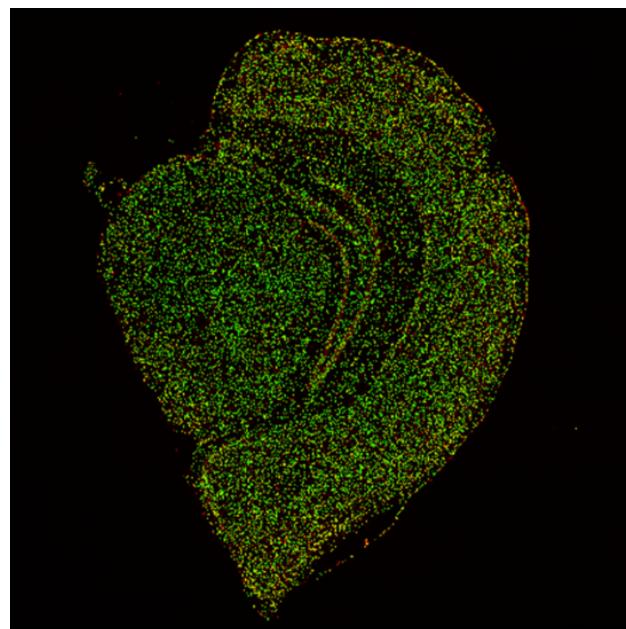


- ⌚ You could pause here and check your tissue segmentation as well as cell segmentation using merged function in ImageJ (images shown below).

Merged image of **SN\_regist.tif** and **SN\_tissue\_cut.tif** to check tissue segmentation performance.



Merged image of **SN\_regist.tif** and **SN\_mask.tif** to check cell segmentation performance



Please refer to [\*\*Appendix D: Manual Image Merge Using ImageJ\*\*](#) for further instructions.

## 2.8 tissueCut

SAW **tissueCut** pipeline could delineate and extract the tissue coverage area based on the aligned image generated from **register** and **ipr2img** or from the plot of gene expression matrix (if microscopic tissue staining images are not available). **tissueCut** outputs expression data in GEF format. Users may generate registered image in TIFF or JPG format from image pyramid RPI file using python package Stereopy<sup>11</sup>.

⌚ If the output of **tissueCut** doesn't match the morphology of the tissue, user could use Stereopy to do lasso selection interactively to extract the expression matrix of tissue-covered region. Please check the tutorial, [Stereopy->Examples->Interactive](#).

Run **tissueCut** requires the following files:

- Mapped CID list file (**.txt**)
- count output gene expression matrix file (**.raw.gef**)
- Directory stores aligned microscopic staining image (optional)
- ⌚ Expected running time for ~1G reads: ~25 min, Memory: ~20 G

### 2.8.1 Arguments and Options

Table 2-9 **tissueCut** Arguments and Options

Parameter	Function
<b>--dnbfle</b>	(Required) Mapped CID list file with reads counts for each CID.
<b>-i</b>	(Required) count output gene expression matrix file.
<b>-o</b>	(Required) Path to the directory where to store the <b>tissueCut</b> outputs.
<b>-s</b>	(Optional) Path to the directory where the <b>register</b> outputs are stored. Only valid when <b>register</b> has performed.
<b>-t</b>	(Required) Run for tissue segmentation. Valid options: <b>tissue</b> .
<b>--snId</b>	(Required) Stereo-seq Chip T serial number (SN).
<b>--omics,-o</b>	(Required; default to Transcriptomics) String that specify the omics.
<b>-d</b>	(Required) Set to generate required plots for report.

### 2.8.2 Usage Example

Run **tissueCut** if **register** aligned microscopic staining image is provided:

```
...
$ mkdir -p /path/to/output/05.tissuecut
$ singularity exec SAW_v5.1.3.sif tissueCut \
    --dnbfle /path/to/output/02.merge/{SN}.barcodeReadsCount.txt \
    -i /path/to/output/03.count/{SN}.raw.gef \
    -o /path/to/output/05.tissuecut \
    -s /path/to/output/04.register \
    -t tissue \
    --snId {SN} \
    --omics=Transcriptomics \
    -d
```

Run **tissueCut** if image is not available:

```
...
$ mkdir -p /path/to/output/05.tissuecut
$ singularity exec SAW_v5.1.3.sif tissueCut \
    --dnbfle /path/to/output/02.merge/{SN}.barcodeReadsCount.txt \
    -i /path/to/output/03.count/{SN}.raw.gef \
    -o /path/to/output/05.tissuecut \
    -t tissue \
    --snId {SN} \
    --omics=Transcriptomics \
    -d
```



## 2.8.3 Outputs

**tissueCut** output files:

Image is provided:

```
$ tree /path/to/output/05.tissuecut
/path/to/output/05.tissuecut
└── tissue_fig
    ├── scatter_100x100_MID_gene_counts.png
    ├── scatter_150x150_MID_gene_counts.png
    ├── scatter_200x200_MID_gene_counts.png
    ├── scatter_50x50_MID_gene_counts.png
    ├── SN.ssDNA.rpi
    ├── statistic_100x100_MID_gene_DNB.png
    ├── statistic_150x150_MID_gene_DNB.png
    ├── statistic_200x200_MID_gene_DNB.png
    ├── statistic_50x50_MID_gene_DNB.png
    ├── violin_100x100_MID_gene.png
    ├── violin_150x150_MID_gene.png
    ├── violin_200x200_MID_gene.png
    └── violin_50x50_MID_gene.png
```

Image is not provided:

```
$ tree /path/to/output/05.tissuecut
/path/to/output/05.tissuecut
└── tissue_fig
    ├── scatter_100x100_MID_gene_counts.png
    ├── scatter_150x150_MID_gene_counts.png
    ├── scatter_200x200_MID_gene_counts.png
    ├── scatter_50x50_MID_gene_counts.png
    ├── statistic_100x100_MID_gene_DNB.png
    ├── statistic_150x150_MID_gene_DNB.png
    ├── statistic_200x200_MID_gene_DNB.png
    ├── statistic_50x50_MID_gene_DNB.png
    ├── violin_100x100_MID_gene.png
    ├── violin_150x150_MID_gene.png
    ├── violin_200x200_MID_gene.png
    └── violin_50x50_MID_gene.png
```

## 2.9 spatialCluster

SAW **spatialCluster** pipeline performs clustering analysis for spots using Stereopy. The clustering procedure includes 4 main steps: 1) preprocess gene expression data from the tissue-coverage region (normalize, logarithmize, identify highly-variable genes, and scale each gene), 2) reduce the dimensionality of the data by running PCA on highly variable genes, 3) compute the neighborhood graph and embed neighborhood graph using UMAP, 4) and clustering by Leiden algorithm.

Run **spatialCluster** requires the following files:

- **tissueCut** output GEF file for the tissue-covered region (**.tissue.gef**)

 Expected running time for ~1G reads: ~1 min, Memory: ~5 G

### 2.9.1 Arguments and Options

Table 2-10 **spatialCluster** Arguments and Options

Parameter	Function
<b>-i</b>	(Required) <b>tissueCut</b> output GEF file for the tissue coverage area.
<b>-o</b>	(Required) Output path for the clustering result in H5AD format.
<b>-s</b>	(Required; default to 50) Bin size.

### 2.9.2 Usage Example

```
...
$ mkdir -p /path/to/output/06.spatialcluster
$ singularity exec SAW_v4.1.0.sif spatialCluster \
    -i /path/to/output/05.tissuecut/{SN}.tissue.gef \
    -o /path/to/output/06.spatialcluster/{SN}.spatial.cluster.h5ad \
    -s 200
```

### 2.9.3 Outputs

**spatialCluster** output files are:

```
...
$ tree /path/to/output/06.spatialcluster
/path/to/output/06.spatialcluster
└── SN.spatial.cluster.h5ad
```

## 2.10 cellCut

SAW **cellCut** pipeline runs to extract expression matrix of cells based on the aligned image generated from **register**. **cellCut** outputs expression data in cell bin GEF format.

Run **cellCut** requires the following files:

- **count** output gene expression matrix file (**.raw.gef**)

- **register** output cell segmentation mask TIFF file (**.tif**)

 Expected running time for ~1G reads: ~2 min, Memory: ~10 G

## 2.10.1 Arguments and Options

Table 2-11 `cellCut` Arguments and Options

Commands	Parameters	Function
<code>cgef</code>	<b>-i, --input-file</b>	(Required) Input GEF file.
	<b>-m, --mask-file</b>	(Required) Input cell segmentation mask file.
	<b>-o, --output-file</b>	(Required) Output cell bin GEF file.
	<b>-b, --block</b>	(Optional; default to 256,256) Block size.
	<b>-r, --rand-celltype</b>	(Optional; default to 0) Number of random cell type.
	<b>-t, --threads</b>	(Optional; default to 1) Number of threads.
	<b>-v, --verbose</b>	(Optional) Verbose output.
	<b>-n, --cnum</b>	(Optional; default to 5000) Top level cell number.
	<b>-R, --ratio</b>	(Optional; default to 20) Other level cell number ratio.
	<b>-a, --allocat</b>	(Optional; default to 2) Allocation strategy.
	<b>-g, --raw-gem</b>	(Optional) Raw GEM file.
	<b>-c, --canvas</b>	(Optional; default to 0,0,90000,90000) Set canvas size, minX,minY,maxX maxY.
	<b>-l, --limit</b>	(Optional; default to 16,16) Set block limit.
	<b>-s, --split</b>	(Optional; default to 0) Split cellID to layers and blocks.

ⓘ Please check [2.14.1 Other applications of `cellCut`](#) to learn more about `cellCut`.

## 2.10.2 Usage Example

Run `cellCut` only if `register` aligned microscopic staining image is provided:

```
...
$ mkdir -p /path/to/output/051.cellcut
$ singularity exec SAW_v5.1.3.sif cellCut cgef \
    -i /path/to/output/03.count/{SN}.raw.gef \
    -m /path/to/output/04.register/{SN}_mask.tif \
    -o /path/to/output/051.cellcut/{SN}.cellbin.gef
```

## 2.10.3 Outputs

`cellCut` output files:

```
...
$ tree /path/to/output/051.cellcut
/path/to/output/051.cellcut
└── SN.cellbin.gef
```

## 2.11 cellCluster

SAW **cellCluster** pipeline runs by clustering cells using the Leiden algorithm in the smiliar procedure as **spatialCluster**.

Run **cellCluster** requires the following files.

- **cellCut** output cell bin gene expression matrix file (**.cellbin.gef**)
- ⌚ Expected running time for ~1G reads: ~5 min, Memory: ~25 G

### 2.11.1 Arguments and Options

**Table 2-12 cellCluster Arguments and Options**

Parameter	Function
<b>-i</b>	(Required) <b>cellCut</b> output gene expression matrix file.
<b>-o</b>	(Required) Output path for the clustering result in H5AD format.

### 2.11.2 Usage Example

```
$ mkdir -p /path/to/output/061.cellcluster
$ singularity exec SAW_v5.1.3.sif cellCluster \
    -i /path/to/output/051.cellcut/{SN}.cellbin.gef \
    -o /path/to/output/061.cellcluster/{SN}.cell.cluster.h5ad
```

### 2.11.3 Outputs

**cellCluster** output files:

```
$ tree /path/to/output/061.cellcluster
/path/to/output/061.cellcluster
└── SN.cell.cluster.h5ad
```

## 2.12 Saturation

SAW **saturation** pipeline is performed to compute the sequencing saturation for the tissue coverage area.

- Run **saturation** requires the following files:
- **mapping** output statistical report of CID mapping (**.stat**)
- **count** output saturation sampling file (**.txt**)
- **count** output statistical report of annotation (**.stat**)
- **tissueCut** output GEF file for the tissue coverage area (**.tissue.gef**)
- ⌚ Expected running time for ~1G reads: ~5 min, Memory: ~5 G

## 2.12.1 Arguments and Options

Table 2-13 saturation Arguments and Options

Parameter	Function
<b>-i</b>	(Required) count output saturation sampling file.
<b>--tissue</b>	(Required) tissueCut output GEF file for the tissue coverage area.
<b>-o</b>	(Required) Path to the directory where to store the saturation outputs. Have to be an exist path.
<b>--bcstat</b>	(Required) mapping output statistical report of CID mapping. Separate multiple files by comma.
<b>--summary</b>	(Required) count output statistical report of annotation.

## 2.12.2 Usage Example

```
...
$ mkdir -p /path/to/output/07.saturation
$ singularity exec SAW_v5.1.3.sif saturation \
    -i /path/to/output/03.count/{SN}_raw_barcode_gene_exp.txt \
    --tissue /path/to/output/05.tissuecut/{SN}.tissue.gef \
    -o /path/to/output/07.saturation \
    --bcstat /path/to/output/01.mapping/{lane}_barcodeMap.stat \
    --summary /path/to/output/03.count/{SN}.Aligned.sortedByCoord.out.merge.q10.
[*] dedup.target.bam.summary.stat
```

\* Please be noted that these two lines belong to the same line of command.

For more than one pair of FASTQ files (Here showing an example of 2 pairs of FASTQ),

```
...
$ mkdir -p /path/to/multi_lane_output/07.saturation
$ singularity exec SAW_v5.1.3.sif saturation \
    -i /path/to/multi_lane_output/03.count/{SN}_raw_barcode_gene_exp.txt \
    --tissue /path/to/multi_lane_output/05.tissuecut/{SN}.tissue.gef \
    -o /path/to/multi_lane_output/07.saturation \
    --bcstat /path/to/multi_lane_output/01.mapping/{lane1}_barcodeMap.stat,/path/
[*] to/multi_lane_output/01.mapping/{lane2}_barcodeMap.stat \
    --summary /path/to/multi_lane_output/03.count/{SN}.Aligned.sortedByCoord.out.
[*] merge.q10.dedup.target.bam.summary.stat
```

\* Please be noted that we use the backward slash “\” to indicate the end of a line in a command that spans multiple lines.

## 2.12.3 Outputs

**saturation** output files:

```
...
$ tree /path/to/output/07.saturation
├── plot_1x1_saturation.png
├── plot_200x200_saturation.png
└── sequence_saturation.tsv
```

## 2.13 report

SAW **report** pipeline is performed to integrate analysis report from each step and generate the report in JSON format as well as a web report in HTML format. HTML analytical report integrate genes' spatial expression distribution, key statistical metrics, sequencing saturation plots, clustering analysis result, and image processing information.

Run **report** requires the following files and information:

- **mapping** output statistical reports of CID mapping and **STAR** alignment
  - **count** output statistical report of annotation
  - **register** processed Image process record file (**.ipr**)
  - **tissueCut** and **cellCut** (if available) output GEF file, statistical report of tissue-covered region, plots and image pyramid RPI file (if available)
  - **spatialCluster** and **cellCluster** (if available) output clustering H5AD file
  - **saturation** output bin200 sequence saturation plot
  - species, tissue, and reference information
-  Expected running time for ~1G reads: ~1 min, Memory: 1G

### 2.13.1 Arguments and Options

Table 2-14 **report** Arguments and Options

Parameter	Function
<b>-m</b>	(Required) Statistical report of CID mapping. Separate multiple files by comma.
<b>-a</b>	(Required) Statistical report of STAR alignment. Separate multiple files by comma.
<b>-g</b>	(Required) Statistical report of annotation.
<b>-l</b>	(Required) Statistical report of tissue-covered region.
<b>-n</b>	(Required) GEF file that has wholeExp/bin200.
<b>-b</b>	(Required) tissueCut output bin 200 scatter plot.
<b>-v</b>	(Required) tissueCut output bin 200 violin plot.
<b>-c</b>	(Required) tissueCut output bin 200 statistics plot.
<b>--bin50Saturation</b>	(Required) tissueCut output bin 50 scatter plot.
<b>--bin50violin</b>	(Required) tissueCut output bin 50 violin plot.
<b>--bin50MIDGeneDNB</b>	(Required) tissueCut output bin 50 statistics plot.
<b>--bin100Saturation</b>	(Required) tissueCut output bin 100 scatter plot.
<b>--bin100violin</b>	(Required) tissueCut output bin 100 violin plot.
<b>--bin100MIDGeneDNB</b>	(Required) tissueCut output bin 100 statistics plot.
<b>--bin150Saturation</b>	(Required) tissueCut output bin 150 scatter plot.
<b>--bin150violin</b>	(Required) tissueCut output bin 150 violin plot.
<b>--bin150MIDGeneDNB</b>	(Required) tissueCut output bin 150 statistics plot.
<b>-d</b>	(Required) spatialCluster output H5AD file.
<b>-t</b>	(Required) saturation output bin 200 sequence saturation plot.



Parameter	Function
<b>--bin1Saturation</b>	(Optional) saturation output bin 1 sequence saturation plot.
<b>-r standard_version</b>	(Required) Set to specifying report version.
<b>-s</b>	(Required) The Stereo-seq Chip T serial number.
<b>--pipelineVersion</b>	(Required) Set to specifying analysis pipeline version.
<b>-o</b>	(Required) The directory to store outputs.
<b>-p</b>	(Required) The plotly JS package file path.
<b>--species</b>	(Required) A string of species name.
<b>--tissue</b>	(Required) A string of tissue type.
<b>--logo</b>	(Required) Path of Logo.png.
<b>-reference</b>	(Required) A string of reference used for mapping
<b>--rpi_resolution</b>	(Optional; default to 100) The resolution of RPI. Valid options: <b>2, 10, 50, 100, 150</b> .
<b>-i</b>	(Optional) The image pyramid RPI file.
<b>--iprFile</b>	(Optional) ImageQC IPR (image process record) file.
<b>--cellBinGef</b>	(Optional) The cell bin GEF file.
<b>--cellCluster</b>	(Optional) cellCluster output H5AD file.

## 2.13.2 Usage Example

Run **report** if **register** aligned microscopic staining image is provided and have cell bin output:

ⓘ Note! Replace **{species\_name}**, **{tissue\_type}**, **{reference\_index}** with the real information.

```
...
$ mkdir -p /path/to/output/08.report
$ imageIPR=$(find /path/to/output/04.register -maxdepth 1 -name {SN}*.ipr | head -1)
## has to be a processed IPR
$ singularity exec SAW_v5.1.3.sif report \
    -m /path/to/output/01.mapping/{lane}_barcodeMap.stat \
    -a /path/to/output/01.mapping/{lane}.Log.final.out \
    -g /path/to/output/03.count/{SN}.Aligned.sortedByCoord.out.merge.q10.dedup.
target.bam.summary.stat \
    -l /path/to/output/05.tissuecut/tissuecut.stat \
    -n /path/to/output/05.tissuecut/{SN}.gef \
    -d /path/to/output/06.spatialcluster/{SN}.spatial.cluster.h5ad \
    -t /path/to/output/07.saturation/plot_200x200_saturation.png \
    -b /path/to/output/05.tissuecut/tissue_fig/scatter_200x200_MID_gene_counts.png \
    -v /path/to/output/05.tissuecut/tissue_fig/violin_200x200_MID_gene.png \
    -c /path/to/output/05.tissuecut/tissue_fig/statistic_200x200_MID_gene_DNB.png \
    --bin50Saturation /path/to/output/05.tissuecut/tissue_fig/scatter_50x50_MID_
gene_counts.png \
    --bin50Violin /path/to/output/05.tissuecut/tissue_fig/violin_50x50_MID_gene.
png \
```

\* Please be noted that we use the backward slash “\” to indicate the end of a line in a command that spans multiple lines.



```
...
    --bin50MIDGeneDNB /path/to/output/05.tissuecut/tissue_fig/statistic_50x50_MID_
gene_DNB.png \
    --bin100Saturation /path/to/output/05.tissuecut/tissue_fig/scatter_100x100_MID_
gene_counts.png \
    --bin100violin /path/to/output/05.tissuecut/tissue_fig/violin_100x100_MID_gene
png \
    --bin100MIDGeneDNB /path/to/output/05.tissuecut/tissue_fig/statistic_100x100_
MID_gene_DNB.png \
    --bin150Saturation /path/to/output/05.tissuecut/tissue_fig/scatter_150x150_MID_
gene_counts.png \
    --bin150violin /path/to/output/05.tissuecut/tissue_fig/violin_150x150_MID_gene
png \
    --bin150MIDGeneDNB /path/to/output/05.tissuecut/tissue_fig/statistic_150x150_
MID_gene_DNB.png \
    -r standard_version \
    -i /path/to/output/05.tissuecut/tissue_fig/{SN}.ssDNA.rpi \
    -s {SN} \
    --pipelineVersion SAW_v5.1.3 \
    -p /opt/saw_v5.1.3_software/pipeline/report/plotly_package.txt \
    --iprFile ${imageIPR} \
    --species {species_name} \
    --tissue {tissue_type} \
    --reference {reference_index} \
    --logo /opt/saw_v5.1.3_software/pipeline/report/logo.png \
    -o /path/to/output/08.report
```

\* Please be noted that we use the backward slash “\” to indicate the end of a line in a command that spans multiple lines.

For more than one pair of FASTQ files (Here showing an example of 2 pairs of FASTQ),

```
...
$ mkdir -p /path/to/multi_lane_output/08.report
$ singularity exec SAW_v5.1.3.sif report \
    -m /path/to/multi_lane_output/01.mapping/{lane1}_barcodeMap.stat,/path/to/
multi_lane_output/01.mapping/{lane2}_barcodeMap.stats \
    -a /path/to/multi_lane_output/01.mapping/{lane1}.Log.final.out,/path/to/multi_
lane_output/01.mapping/{lane2}.Log.final.out \
    -g /path/to/multi_lane_output/03.count/{SN}.Aligned.sortedByCoord.out.merge.
q10.dedup.target.bam.summary.stat \
    -l /path/to/multi_lane_output/05.tissuecut/tissuecut.stat \
    -n /path/to/multi_lane_output/05.tissuecut/{SN}.gef \
    -d /path/to/multi_lane_output/06.spatialcluster/{SN}.spatial.cluster.h5ad \
    -t /path/to/multi_lane_output/07.saturation/plot_200x200_saturation.png \
    -b /path/to/multi_lane_output/05.tissuecut/tissue_fig/scatter_200x200_MID_
gene_counts.png \
    -v /path/to/multi_lane_output/05.tissuecut/tissue_fig/violin_200x200_MID_gene.
png \
```



```

    -c /path/to/multi_lane_output/05.tissuecut/tissue_fig/statistic_200x200_MID_
gene_DNB.png \
    --bin50Saturation /path/to/multi_lane_output/05.tissuecut/tissue_fig/scat-
ter_50x50_MID_gene_counts.png \
    --bin50violin /path/to/multi_lane_output/05.tissuecut/tissue_fig/violin_50x50_
MID_gene.png \
    --bin50MIDGeneDNB /path/to/multi_lane_output/05.tissuecut/tissue_fig/statis-
tic_50x50_MID_gene_DNB.png \
    --bin100Saturation /path/to/multi_lane_output/05.tissuecut/tissue_fig/scat-
ter_100x100_MID_gene_counts.png \
    --bin100violin /path/to/multi_lane_output/05.tissuecut/tissue_fig/vio-
lin_100x100_MID_gene.png \
    --bin100MIDGeneDNB /path/to/multi_lane_output/05.tissuecut/tissue_fig/statis-
tic_100x100_MID_gene_DNB.png \
    --bin150Saturation /path/to/multi_lane_output/05.tissuecut/tissue_fig/scat-
ter_150x150_MID_gene_counts.png \
    --bin150violin /path/to/multi_lane_output/05.tissuecut/tissue_fig/vio-
lin_150x150_MID_gene.png \
    --bin150MIDGeneDNB /path/to/multi_lane_output/05.tissuecut/tissue_fig/statis-
tic_150x150_MID_gene_DNB.png \
    -r standard_version \
    -i /path/to/multi_lane_output/05.tissuecut/tissue_fig/{SN}.ssDNA.rpi \
    -s {SN} \
    --pipelineVersion SAW_v5.1.3 \
    -p /opt/saw_v5.1.3_software/pipeline/report/plotly_package.txt \
    --iprFile ${imageIPR} \
    --species {species_name} \
    --tissue {tissue_type} \
    --reference {reference_index} \
    --logo /opt/saw_v5.1.3_software/pipeline/report/logo.png \
    -o /path/to/multi_lane_output/08.report

```

\* Please be noted that we use the backward slash “\” to indicate the end of a line in a command that spans multiple lines.

Run **report** if **register** aligned microscopic staining image is absent (Here showing an example of just one pair of FASTQ, similar to multiple pairs),

```

$ mkdir -p /path/to/output/08.report
$ singularity exec SAW_v5.1.3.sif report \
    -m /path/to/output/01.mapping/{lane}_barcodeMap.stat \
    -a /path/to/output/01.mapping/{lane}.Log.final.out \
    -g /path/to/output/03.count/{SN}.Aligned.sortedByCoord.out.merge.q10.dedup.
target.bam.summary.stat \
    -l /path/to/output/05.tissuecut/tissuecut.stat \
    -n /path/to/output/05.tissuecut/{SN}.gef \
    -d /path/to/output/06.spatialcluster/{SN}.spatial.cluster.h5ad \
    -t /path/to/output/07.saturation/plot_200x200_saturation.png \
    -b /path/to/output/05.tissuecut/tissue_fig/scatter_200x200_MID_gene_counts.png

```



```

    -v /path/to/output/05.tissuecut/tissue_fig/violin_200x200_MID_gene.png \
    -c /path/to/output/05.tissuecut/tissue_fig/statistic_200x200_MID_gene_DNB.png \
    --bin50Saturation /path/to/output/05.tissuecut/tissue_fig/scatter_50x50_MID_
gene_counts.png \
    --bin50violin /path/to/output/05.tissuecut/tissue_fig/violin_50x50_MID_gene.png \
\ \
    --bin50MIDGeneDNB /path/to/output/05.tissuecut/tissue_fig/statistic_50x50_MID_
gene_DNB.png \
    --bin100Saturation /path/to/output/05.tissuecut/tissue_fig/scatter_100x100_MID_
gene_counts.png \
    --bin100violin /path/to/output/05.tissuecut/tissue_fig/violin_100x100_MID_gene.
png \
    --bin100MIDGeneDNB /path/to/output/05.tissuecut/tissue_fig/statistic_100x100_
MID_gene_DNB.png \
    --bin150Saturation /path/to/output/05.tissuecut/tissue_fig/scatter_150x150_MID_
gene_counts.png \
    --bin150violin /path/to/output/05.tissuecut/tissue_fig/violin_150x150_MID_gene.
png \
    --bin150MIDGeneDNB /path/to/output/05.tissuecut/tissue_fig/statistic_150x150_
MID_gene_DNB.png \
    -r standard_version \
    -s {SN} \
    --pipelineVersion SAW_v5.1.3 \
    -p /opt/saw_v5.1.3_software/pipeline/report/plotly_package.txt \
    --species {species_name} \
    --tissue {tissue_type} \
    --reference {reference_index} \
    --logo /opt/saw_v5.1.3_software/pipeline/report/logo.png \
    -o /path/to/output/08.report

```

\* Please be noted that we use the backward slash “\” to indicate the end of a line in a command that spans multiple lines.

### 2.13.3 Outputs

**report** output files that have cell bin data input are organized as below:

```

$ tree /path/to/output/08.report
/path/to/output/08.report
├── scatter_1x1_MID_gene_counts.png
├── SN.report.html
├── SN.statistics.json
└── statistic_1x1_MID_gene_DNB.png
└── violin_1x1_MID_gene.png

```

**report** output files that the cell bin data inputs are absent:

```

$ tree /path/to/output/08.report
/path/to/output/08.report
├── SN.report.html
└── SN.statistics.json

```



## 2.14 Other Applications

### 2.14.1 Other applications of cellCut

SAW **cellCut** is also an application for manipulating GEF file. SAW contains this tool to convert GEF format gene expression matrix to plain table or complete a GEF. Users may also manipulate the GEF files using the separate individual C++ compiled program geftools<sup>12</sup> or its python encapsulated package gefpy<sup>13</sup>.

#### 2.14.1.1 Arguments and Options

Table 2-15 Other applications of **cellCut** Arguments and Options

Commands	Parameters	Function
<b>view</b>	<b>-i, --input-file</b>	(Required) Input bin GEF file or cell bin GEF file.
	<b>-o, --output-file</b>	(Optional; default to stdout) Output GEM file.
	<b>-d, --exp_data</b>	(Optional; default to "") Input bin1 GEF to get cell bin GEM.
	<b>-b, --bin-size</b>	(Optional; default to 1) Set bin size for bin GEF file. Only valid for bin GEF.
	<b>-s, --serial-number</b>	(Required) Stereo-seq Chip T serial number.
<b>bgef</b>	<b>-e, --exon</b>	(Optional; default to 1) Whether or not output exon group.
	<b>-i, --input-file</b>	(Required) Input gene expression matrix file (.gem/.gem.gz) or bin1 GEF file.
	<b>-o, --output-file</b>	(Required) Output bin GEF file.
	<b>-b, --bin-size</b>	(Required; default to 1,10,20,50,100,200,500) Comma-separate bin size list.
	<b>-r, --region</b>	(Optional; default to "") A rectangular region represented by the comma-separated list of vertex coordinates. For example, minX,maxX,minY,maxY.
	<b>-t, --threads</b>	(Optional; default to 8) Number of threads.
	<b>-s, --stat</b>	(Optional; default to true) Whether create stat group. Stat group includes a gene dataset which contains total MIDcount and E10 score for each gene.
	<b>-o, --omics</b>	(Required; default to Transcriptomics) Specify the omics.
	<b>-v, --verbose</b>	(Optional) Verbose output.

#### 2.14.1.2 Usage Examples

Function 1: GEF to plain table GEM format

```
$ singularity exec SAW_v5.1.3.sif cellCut view \ ## convert GEF that only contains
bin1 geneExp
    -s {SN} \
    -i /path/to/output/03.count/{SN}.raw.gef \
    -o {SN}.raw.gem
$ singularity exec SAW_v5.1.3.sif cellCut view \ ## convert a whole GEF
    -s {SN} \
    -i /path/to/output/05.tissuecut/{SN}.gef \
    -o {SN}.gem
$ singularity exec SAW_v5.1.3.sif cellCut view \ ## convert tissue GEF that only
contains bin1 geneExp
```

```
...
-s {SN} \
-i /path/to/output/05.tissuecut/{SN}.tissue.gef \
-o {SN}.tissue.gem
$ singularity exec SAW_v5.1.3.sif cellCut view \ ## convert cellbin GEF to cellbin
GEM
-s {SN} \
-i /path/to/output/051.cellcut/{SN}.cellbin.gef \
-o {SN}.cellbin.gem \
-d /path/to/output/03.count/{SN}.raw.gef
```

## Function 2: completion of a GEF

```
...
$ singularity exec SAW_v5.1.3.sif cellCut bgef \ ## complete GEF that only contains
bin1 geneExp group to a whole GEF, you may specify the bin size you need using “-b”.
Separate multiple bin size with comma
-i /path/to/output/03.count/{SN}.tissue.gef \
-o {SN}.tissue.complete.gef \
-b 1,20,50,100 \
-O Transcriptomics
```

## Function 3: converting GEM to GEF

```
...
$ singularity exec SAW_v5.1.3.sif cellCut bgef \ ## convert GEM to GEF in specific
bin size. Separate multiple bin sizes with comma
-i {SN}.gem \
-o {SN}.gef \
-b 1,20,50 \
-O Transcriptomics
```

Example of GEF to GEM conversion using gefpy, users may specify the bin size.

```
...
$ python
>>> from gefpy.bgef_reader_cy import BgefR
>>> bgef=BgefR(filepath='/path/to/output/05.tissue/{SN}.tissue.gef',bin_size=200,n_
thread=4)
>>> bgef.to_gem('{SN}.tissue.bin200.gem')
```



## 2.14.2 rapidRegister

SAW **rapidRegister** is a lite **register** pipeline that perform all modules in the **register** except cell segmentation.

Run **rapidRegister** requires the following files:

- **count** output gene expression matrix file (**.raw.gef**)
  - ImageQC processed microscopic tissue staining image file (**.tar.gz**)
  - ImageQC Image process record file (**.ipr**, **require imageQC version >= 1.1.0**)
- ⌚ Expected running time for ~1G reads: ~20 min, Memory: ~20 G

### 2.14.2.1 Arguments and Options

Table 2-16 **rapidRegister** Arguments and Options

Parameter	Function
<b>-i</b>	(Required) ImageQC processed staining image TAR.GZ file.
<b>-c</b>	(Required) ImageQC IPR (image process record) file. IPR is designed to efficiently hold images and processing records generated from each image processing step along with metadata in various data types. Please check <a href="#">Stereo-seq File Format Manual</a> to get more information on the IPR file.
<b>-v</b>	(Required) count output gene expression matrix GEF file.
<b>-o</b>	(Required) Path to the directory where to store the rapidRegister outputs.

### 2.14.2.2 Usage Examples

Function 1: GEF to plain table GEM format

```
...
$ image=/path/to/data/image
$ image4register=$(find ${image} -maxdepth 1 -name ${SN}*.tar.gz | head -1)
$ imageQC=$(find ${image} -maxdepth 1 -name ${SN}*.ipr | head -1)
$ mkdir -p /path/to/output/04.register
$ singularity exec SAW_v5.1.3.sif rapidRegister \
    -i ${image4register} \
    -c ${imageQC} \
    -v /path/to/output/03.count/{SN}.raw.gef \
    -o /path/to/output/04.register
```

### 2.14.2.3 Outputs

**rapidRegister** output files are organized as below:

```
...
$ tree /path/to/output/04.register
/path/to/output/04.register
... ## skip setting files, logs and image folder
└── fov_stitched_transformed.tif
└── SN_date_time_version.csv
└── SN_date_time_version.ipr ## rapidRegister output IPR does not have /CellSeg/
CellMask dataset
└── SN_date_time_version.png
```



## 2.14.3 checkGTF

SAW **checkGTF** is an application for checking whether the GTF/GFF file is in the correct format as the input for **count**.

Run**checkGTF** requires the following files:

- Reference genome annotation GFF/GTF<sup>9,10</sup> file (**.gtf / .gff**)

### 2.14.3.1 Arguments and Options

Table 2-17 **checkGTF** Arguments and Options

Parameter	Function
<b>-i</b>	(Required) Gene annotation GFF/GTF file.
<b>-o</b>	(Required) Output a re-format GFF/GTF file.

### 2.14.3.2 Usage Examples

```
$ singularity exec SAW_v5.1.3.sif checkGTF \
    -i /path/to/reference/genes.gtf \
    -o /path/to/reference/genes_new.gtf \
```

# **CHAPTER 3**

## **TEST DATA**

### **DEMONSTRATION**

Users may refer to this section as a format for testing SAW process, of the files show in this chapter as the reference in testing SAW pipelines. This chapter includes the statistics results and examples of critical files for each key step.

SN: SS200000135TL\_D1

ⓘ “...” iin the demo stands for some lines of log information that can be omitted.

## 3.1 mapping

### 3.1.1 Statistical Report for CID Mapping and Filtering

```
...
$ cat /path/to/output/01.mapping/E100026571_L01_trim_read_barcodeMap.stat
...
getBarcodePositionMap_uniqBarcodeTypes: 645784920
total_reads: 1002214171
reads_with_polyA: 131113905 13.08%
reads_filteredByPolyA: 22008148 2.20%
mapped_reads: 826344259 82.45%
reads_with_adapter: 9007116 0.90%
reads_with_dnb: 42264284 4.22%
barcode_exactlyOverlap_reads: 682746301 68.12%
barcode_misOverlap_reads: 143590127 14.33%
barcode_withN_reads: 7831 0.00%
Q10_bases_in_barcode: 99.54%
Q20_bases_in_barcode: 97.49%
Q30_bases_in_barcode: 91.74%
Q10_bases_in_umi: 99.26%
Q20_bases_in_umi: 96.32%
Q30_bases_in_umi: 89.45%
Q10_bases_in_seq: 99.47%
Q20_bases_in_seq: 97.12%
Q30_bases_in_seq: 91.08%
umi_filter_reads: 8265089 0.82%
umi_with_N_reads: 13025 0.00%
umi_with_polyA_reads: 12365 0.00%
umi_with_low_quality_base_reads: 8239699 0.82%
mapped_dnbs: 75619113
...
```

### 3.1.2 Statistical Report for Reference Genome Alignment

```
$ cat /path/to/output/01.mapping/E100026571_L01_trim_read.Log.final.out
...
Number of input reads | 766807770
Average input read length | 95
UNIQUE READS:
    Uniquely mapped reads number | 643871246
    Uniquely mapped reads % | 83.97%
    Average mapped length | 95.21
    Number of splices: Total | 67595584
    Number of splices: Annotated (sjdb) | 65674308
    Number of splices: GT/AG | 66407685
    Number of splices: GC/AG | 457595
    Number of splices: AT/AC | 41563
    Number of splices: Non-canonical | 688741
    Mismatch rate per base, % | 0.50%
    Deletion rate per base | 0.07%
    Deletion average length | 3.91
    Insertion rate per base | 0.03%
    Insertion average length | 1.25
MULTI-MAPPING READS:
    Number of reads mapped to multiple loci | 87649341
    % of reads mapped to multiple loci | 11.43%
    Number of reads mapped to too many loci | 5301054
    % of reads mapped to too many loci | 0.69%
UNMAPPED READS:
    Number of reads unmapped: too many mismatches | 0
    % of reads unmapped: too many mismatches | 0.00%
    Number of reads unmapped: too short | 28773993
    % of reads unmapped: too short | 3.75%
    Number of reads unmapped: other | 1212136
    % of reads unmapped: other | 0.16%
CHIMERIC READS:
    Number of chimeric reads | 0
    % of chimeric reads | 0.00%
```

### 3.1.3 Example of BAM mapping

```
$ samtools view /path/to/output/01.mapping/E100026571_L01_trim_read.Aligned.sorted-ByCoord.out.bam | head -2
E100026571L1C007R00303973559      256      1      3000644 3      100M      *      0
0      GCCTCATTGTGCCCATATGTTGCCTATGTTGTGGACTTATTTCATTAAACTTAAACATCTTA-
ATTTTTTCTTTATTCATCATTGACCAAGCT      -FCA9D?GFFD<-D<CGFEGD-DG★FGDFBE;E(9BGGE38FFFG-
9GG;0?GGFGB?E@G:GGG3GF79F0GGDG?G<D>F;EG,G?<<CD4>G=>B+C      NH:i:2      HI:i:2      AS:i:94
nM:i:2Cx:i:8839      Cy:i:7539      UR:Z:120CF
E100026571L1C003R03702347721      0      1      3001778 255      100M      *      0
0      GTATGACATCTGTCCAGGATCTTAGCTTCTAGTCTCTGGTGAGAAGTCTGGAGTAATTCTAATAGGCCTG-
CATTATATGTTACTTGACCTTTTC      EEFEDFFEFFFFFEFFFEC@EFFFFDFEEFFFEFFFCEFFAFBFCED??FG-
BEFFDC:FFFDCFAF4FAFFDFFDG?DFBD.F@FECA/FEDEFFAA      NH:i:1      HI:i:1      AS:i:92 nM:i:3Cx-
:i:12136      Cy:i:14034      UR:Z:C0808
```

## 3.2 merge

### 3.2.1 Example of Mapped CID List with Reads Count File

```
$ head /path/to/output/02.merge/SS200000135TL_D1.barcodeReadsCount.txt
0      2960      1
0      2972      1
0      2979      1
0      2989      1
0      3057      1
0      3080      1
0      3695      1
0      3703      1
0      3733      1
0      3734      8
```

### 3.3 count

### 3.3.1 Statistical Report for MID Filtering and Gene Annotation

```
$ cat /path/to/output/03.count/SS200000135TL_D1.Aligned.sortedByCoord.out.merge.q10.dedup.  
target.bam.summary.stat  
## FILTER & DEDUPLICATION METRICS  
TOTAL_READS      PASS_FILTER      ANNOTATED_READS  UNIQUE_READS      FAIL_FILTER_RATE      FAIL_  
ANNOTATE_RATE    DUPLICATION_RATE  
731520587        643871246        532386027        108123310        11.98       17.31       79.69  
## ANNOTATION METRICS  
TOTAL_READS      MAP      EXONIC      INTRONIC      INTERGENIC      TRANSCRIPTOME      ANTISENSE  
643871246        643871246        483163052        49222975        111485219        532386027  
109940618  
100.0  100.0  75.0   7.6   17.3   82.7   17.1
```

### 3.3.2 Example of Annotated BAM

```
$ samtools view /path/to/output/03.count/SS200000135TL_D1.Aligned.sortedByCoord.out.merge.q10.dedup.target.bam | grep GE:Z | head -2
E100026571L1C002R00703943265      1040      1      3082766 255      11M132671N89M      *      0
0      CTGCTGCAGCTTTTTCTTGAGATTTATTTTATGCTATGTATGGTATTTGCCATATATGCTATGCACCAT-
GTGTGTGCAGTGCCTTGAG      FFFFFECGFDCFGDFEE@EEGIBFGCGFFGACGFCGFFDGDFGFFFFFEGCDFCGFFGG@FFF=EFF-
DGGGGGGFDGFFFGGGFGFFGGGGFGGGDFG      NH:i:1  HI:i:1  AS:i:88nM:i:0  Cx:i:7767      Cy:i:18052
UR:Z:7AE49      XF:i:0  GE:Z:Xkr4      GS:Z:-  UB:Z:79E49
E100026571L1C008R03103646063      16      1      3090385 255      16M224429N32M      *      0
0      AATGGATTATGTTGATGGTTGAATATGAAATCCATCAACATAATC      GGGGGGGGGGGGGGGGGGGGGGGGGGG-
FGGGGGGGGGGGGGGGGGGGGGGGGGGG      NH:i:1  HI:i:1  AS:i:36 nM:i:0  Cx:i:9239      Cy:i:8595
UR:Z:E1454      XF:i:1  GE:Z:Xkr4      GS:Z:-
```

### 3.3.3 Example of count Gene Expression Matrix

```
$ h5dump -n /path/to/output/03.count/SS200000135TL_D1.raw.gef
HDF5 “/path/to/output/03.count/SS200000135TL_D1.raw.gef” {
FILE_CONTENTS {
group /
group /geneExp
group /geneExp/bin1
dataset /geneExp/bin1/expression
dataset /geneExp/bin1/gene
}
}
$ h5dump -d /geneExp/bin1/expression /path/to/output/03.count/SS200000135TL_D1.raw.gef | head -15
HDF5 “/path/to/output/03.count/SS200000135TL_D1.raw.gef” {
DATASET “/geneExp/bin1/expression” {
DATATYPE H5T_COMPOUND {
H5T_STD_U32LE “x”;
H5T_STD_U32LE “y”;
H5T_STD_U8LE “count”;
}
DATASPACE SIMPLE { ( 73956787 ) / ( 73956787 ) }
DATA {
(0): {
4888,
10392,
1
},
(1): {
}
$ h5dump -d /geneExp/bin1/gene /path/to/output/03.count/SS200000135TL_D1.raw.gef | head -20
HDF5 “/path/to/output/03.count/SS200000135TL_D1.raw.gef” {
DATASET “/geneExp/bin1/gene” {
DATATYPE H5T_COMPOUND {
H5T_STRING {
STRSIZE 32;
STRPAD H5T_STR_NULLTERM;
CSET H5T_CSET_ASCII;
CTYPE H5T_C_S1;
} “gene”;
H5T_STD_U32LE “offset”;
H5T_STD_U32LE “count”;
}
DATASPACE SIMPLE { ( 24606 ) / ( 24606 ) }
DATA {
(0): {
“Gm1992”,
0,
132
},
(1): {
```

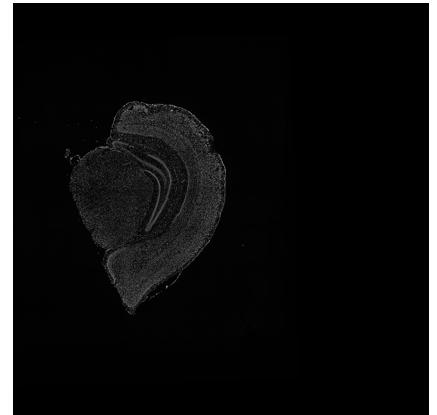
### 3.3.4 Example of count Sampling File

```
$ head -8 /path/to/output/03.count/SS200000135TL_D1_raw_barcode_gene_exp.txt
10392 4888 10551 665954 4
7096 8901 10551 881671 1
7096 8901 10551 357383 20
18783 7397 10551 355789 1
13032 9155 10551 297666 1
13032 9155 10551 298690 1
11778 10617 10551 686313 4
11152 6947 10551 322978 1
```

## 3.4 register

### 3.4.1 Registered image

File /path/to/output/04.register/SS200000135TL\_D1\_register.tif



### 3.4.2 Image Process Record File

```
...
$ h5dump -n /path/to/output/04.register/SS200000135TL_D1_20220527_201353_1.1.0.ipr
HDF5 “/path/to/output/04.register/SS200000135TL_D1_20220527_201353_1.1.0.ipr” {
FILE_CONTENTS {
group      /
group      /CellSeg
dataset    /CellSeg/CellMask
group      /ImageInfo
dataset    /ImageInfo/RGBScale
group      /ManualState
dataset    /Preview
group      /QCInfo
group      /QCInfo/CrossPoints
dataset    /QCInfo/CrossPoints/0_0
...
dataset    /QCInfo/CrossPoints/9_7
dataset    /QCInfo/TrackDistanceTemplate
group      /Register
dataset    /Register/MatrixTemplate
group      /StereoResepSwitch
group      /Stitch
group      /Stitch/BGISTitch
dataset    /Stitch/BGISTitch/StitchedGlobalLoc
group      /Stitch/ScopeStitch
dataset    /Stitch/ScopeStitch/GlobalLoc
group      /Stitch/StitchEval
dataset    /Stitch/StitchEval/StitchEvalH
dataset    /Stitch/StitchEval/StitchEvalV
dataset    /Stitch/TemplatePoint
dataset    /Stitch/TransformTemplate
group      /TissueSeg
dataset    /TissueSeg/TissueMask
}
}
$ h5dump -A /path/to/output/04.register/SS200000135TL_D1_20220527_201353_1.1.0.ipr | head -20
HDF5 “/path/to/output/04.register/SS200000135TL_D1_20220527_201353_1.1.0.ipr” {
GROUP “/” {
    ATTRIBUTE “IPRVersion” {
        DATATYPE H5T_STRING {
            STRSIZE H5T_VARIABLE;
            STRPAD H5T_STR_NULLTERM;
            CSET H5T_CSET_UTF8;
            CTYPE H5T_C_S1;
        }
        DATASPACE SCALAR
        DATA {
            (0): “0.0.1”
        }
    }
}
```

```

}
GROUP "CellSeg" {
    ATTRIBUTE "CellSegShape" {
        DATATYPE H5T_STD_I64LE
        DATASPACE SIMPLE { ( 2 ) / ( 2 ) }
        DATA {
            (0): 21482, 22337

```

## 3.5 tissueCut

### 3.5.1 Statistical Report for Tissue Covered Region

```

$ cat /path/to/output/05.tissuecut/tissuecut.stat
# Tissue Statistic Analysis with Stain Image
Contour_area: 88637560
Number_of_DNB_under_tissue: 36679634
Ratio: 41.38%
Total_gene_type: 24299
MID_counts: 89816137
Fraction_MID_in_spots_under_tissue: 83.07%
Reads_under_tissue: 648371996
Fraction_reads_in_spots_under_tissue: 78.46%

binSize=1
Mean_reads_per_spot: 17.68
Median_reads_per_spot: 11.00
Mean_gene_type_per_spot: 1.71
Median_gene_type_per_spot: 1
Mean_Umi_per_spot: 2.45
Median_Umi_per_spot: 2

binSize=50
Mean_reads_per_spot: 18045.92
Median_reads_per_spot: 16198.00
Mean_gene_type_per_spot: 1151.22
Median_gene_type_per_spot: 1117
Mean_Umi_per_spot: 2499.82
Median_Umi_per_spot: 2309

binSize=100
Mean_reads_per_spot: 71116.81
Median_reads_per_spot: 64454.00
Mean_gene_type_per_spot: 3083.32
Median_gene_type_per_spot: 3081
Mean_Umi_per_spot: 9851.50
Median_Umi_per_spot: 9066

binSize=150
Mean_reads_per_spot: 157601.36
Median_reads_per_spot: 143773.00
Mean_gene_type_per_spot: 4891.22
Median_gene_type_per_spot: 5029
Mean_Umi_per_spot: 21831.83
Median_Umi_per_spot: 20242

binSize=200
Mean_reads_per_spot: 276727.25
Median_reads_per_spot: 254272.00
Mean_gene_type_per_spot: 6403.27
Median_gene_type_per_spot: 6719
Mean_Umi_per_spot: 38333.82
Median_Umi_per_spot: 35679

```



### 3.5.2 Example of Gene Expression Matrix for Tissue Covered Region



### 3.5.3 Example of Gene Expression Matrix for Maximum Area Enclosing Rectangle

```
$ h5dump -n /path/to/output/05.tissuecut/SS200000135TL_D1.gef
HDF5 "/path/to/output/05.tissuecut/SS200000135TL_D1.gef" {
FILE_CONTENTS {
group /
group /geneExp
group /geneExp/bin1
dataset /geneExp/bin1/exon
dataset /geneExp/bin1/expression
dataset /geneExp/bin1/gene
group /geneExp/bin10
dataset /geneExp/bin10/exon
dataset /geneExp/bin10/expression
dataset /geneExp/bin10/gene
group /geneExp/bin100
dataset /geneExp/bin100/exon
dataset /geneExp/bin100/expression
dataset /geneExp/bin100/gene
group /geneExp/bin20
dataset /geneExp/bin20/exon
dataset /geneExp/bin20/expression
dataset /geneExp/bin20/gene
group /geneExp/bin200
dataset /geneExp/bin200/exon
dataset /geneExp/bin200/expression
dataset /geneExp/bin200/gene
group /geneExp/bin50
dataset /geneExp/bin50/exon
dataset /geneExp/bin50/expression
dataset /geneExp/bin50/gene
group /geneExp/bin500
dataset /geneExp/bin500/exon
dataset /geneExp/bin500/expression
dataset /geneExp/bin500/gene
group /stat
dataset /stat/gene
group /wholeExp
dataset /wholeExp/bin1
dataset /wholeExp/bin10
dataset /wholeExp/bin100
dataset /wholeExp/bin20
dataset /wholeExp/bin200
dataset /wholeExp/bin50
dataset /wholeExp/bin500
group /wholeExpExon
dataset /wholeExpExon/bin1
dataset /wholeExpExon/bin10
dataset /wholeExpExon/bin100
dataset /wholeExpExon/bin20
dataset /wholeExpExon/bin200
dataset /wholeExpExon/bin50
dataset /wholeExpExon/bin500
}
}
$ h5dump -d /stat/gene /path/to/output/05.tissuecut/SS200000135TL_D1.gef | head -20
HDF5 "/path/to/output/05.tissuecut/SS200000135TL_D1.gef" {
DATASET "/stat/gene" {
DATATYPE H5T_COMPOUND {
H5T_STRING {
STRSIZE 32;
```



```
STRPAD H5T_STR_NULLTERM;
CSET H5T_CSET_ASCII;
CTYPE H5T_C_S1;
} "gene";
H5T_STD_U32LE "MIDcount";
H5T_IEEE_F32LE "E10";
}
DATASPACE SIMPLE { ( 24661 ) / ( 24661 ) }
DATA {
(0): {
    "Gm42418",
    5861037,
    60.1033
},
(1): {
```

## 3.6 cellCut

### 3.6.1 3.6.1 Example of Gene Expression Matrix for Cell Bins

```
$ h5dump -n /path/to/output/051.cellcut/SS200000135TL_D1.cellbin.gef
HDF5 "/path/to/output/051.cellcut/SS200000135TL_D1.cellbin.gef" {
FILE_CONTENTS {
group      /
group      /cellBin
dataset    /cellBin/blockIndex
dataset    /cellBin/blockSize
dataset    /cellBin/cell
dataset    /cellBin/cellBorder
dataset    /cellBin/cellExon
dataset    /cellBin/cellExp
dataset    /cellBin/cellExpExon
dataset    /cellBin/cellTypeList
dataset    /cellBin/gene
dataset    /cellBin/geneExon
dataset    /cellBin/geneExp
dataset    /cellBin/geneExpExon
}
}
```



## 3.7 saturation

### 3.7.1 Example of Sequence Saturation File

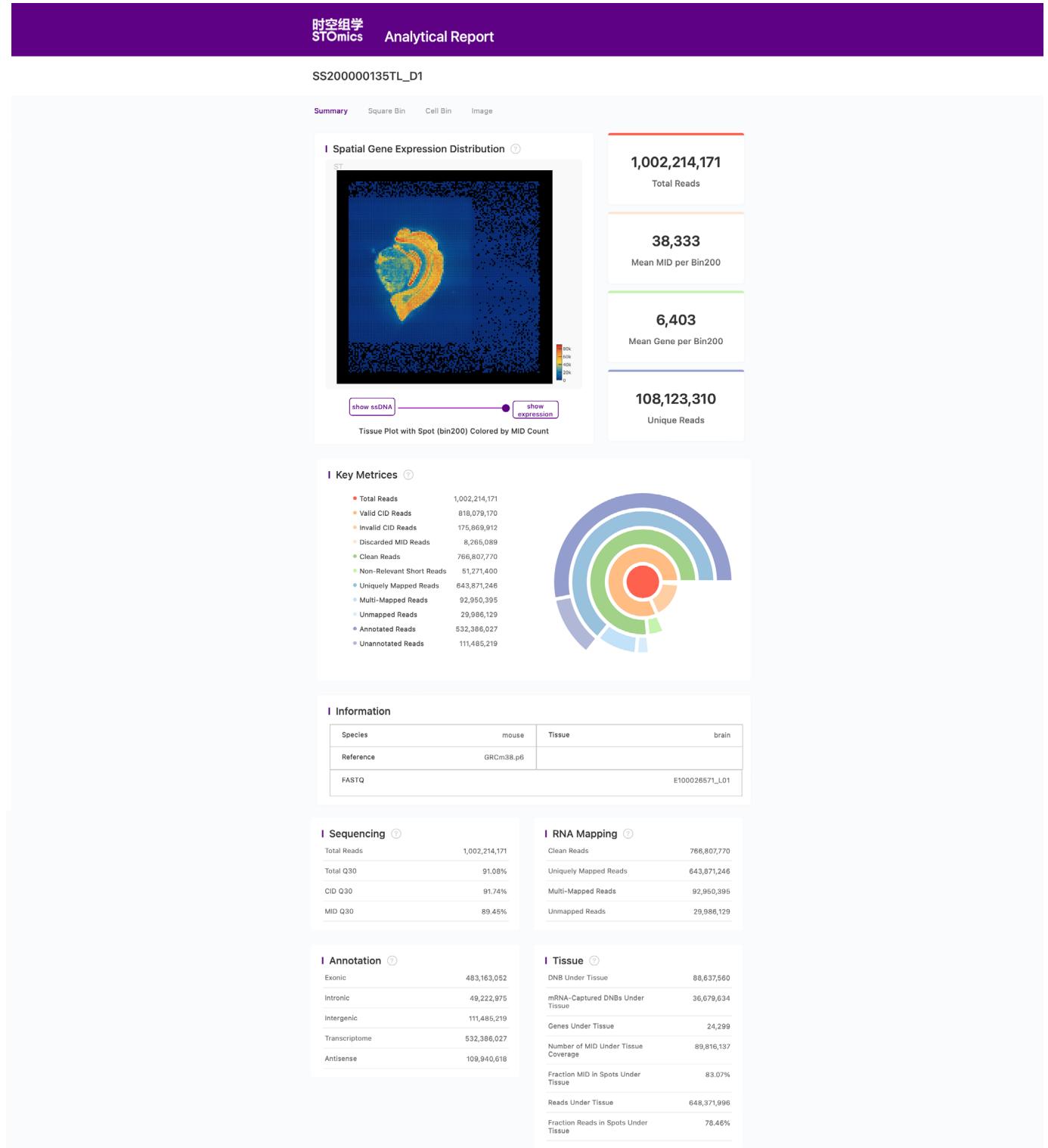
```
...$ cat /path/to/output/07.saturation/sequence_saturation.tsv
sample bar_x bar_y1 bar_y2 bar_umi bin_x bin_y1 bin_y2 bin_umi
0.05 26619302 0.249906 1 19966974 26619302
0.274024 3100 7309
0.1 53238604 0.389633
0.410009 4135 11896
0.2 106477208 0.542708
0.557736 5030 17825
0.3 159715808 0.625397
0.637281 5497 21903
0.4 212954416 0.677911
0.687768 5805 25110
0.5 266193008 0.71435 1 76038055 266193008
0.722835 6032 27836
0.6 319431616 0.741211
0.748708 6213 30262
0.7 372670208 0.762077
0.768813 6337 32459
0.8 425908832 0.77864 1 94279199 425908832
0.784793 6458 34514
0.9 479147392 0.792299
0.797978 6580 36433
1 532386027 0.803707
0.80899 6655 37933
```

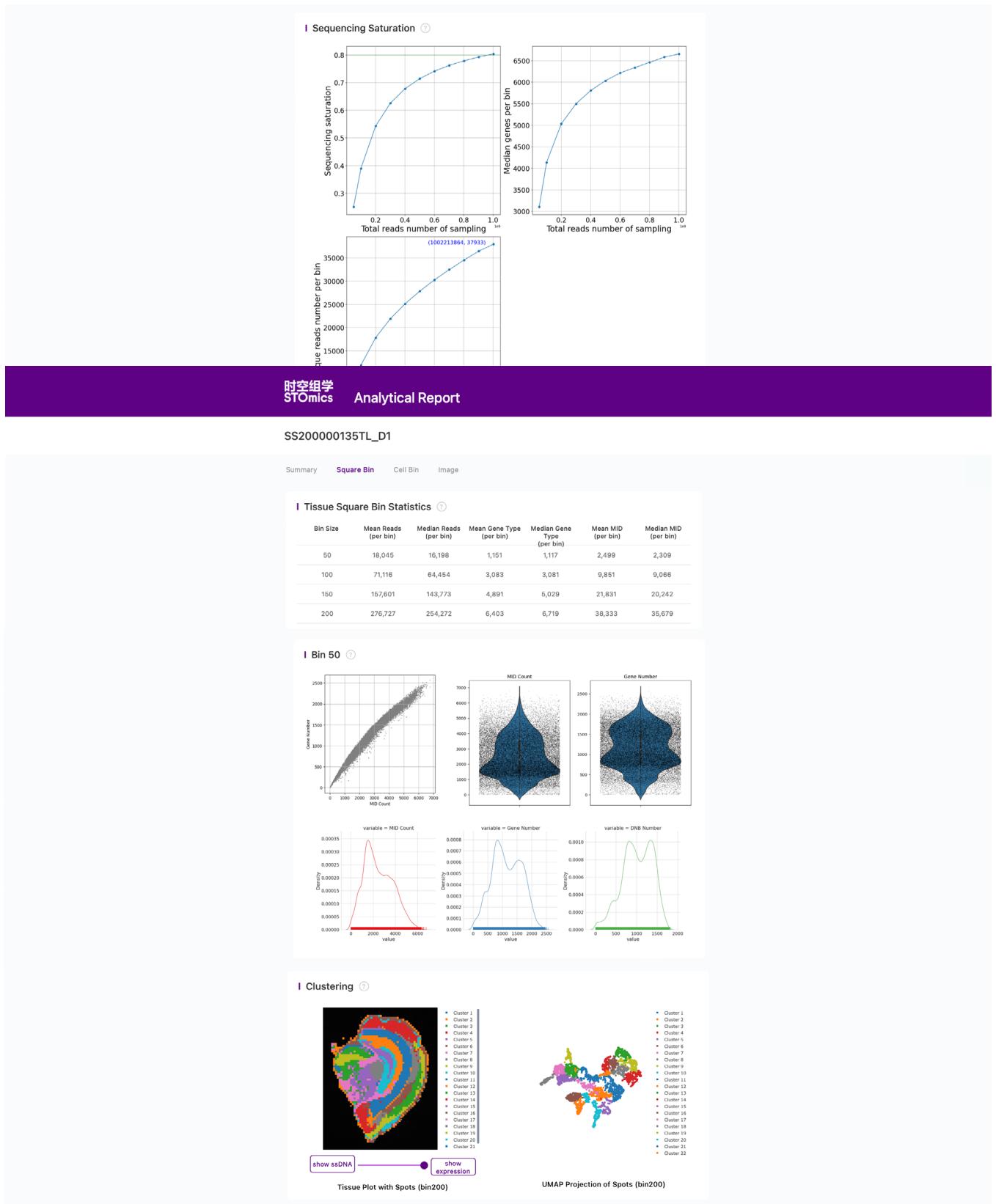
## 3.8 report

### 3.8.1 Example of Statistical Summary Report

```
...$ head /path/to/output/08.report/SS200000135TL_D1.statistics.json
{
    "version": "version_v2",
    "1.Filter_and_Map": {
        "1.1.Adapter_Filter": [
            {
                "Sample_id": "E100026571_L01",
                "getCIDPositionMap_uniqCIDTypes": "645784920",
                "total_reads": "1002214171",
                "mapped_reads": "826344259(82.45%)",
                "CID_misOverlap_reads": "143590127(14.33%)",
                "CID_noOverlap_reads": "143590127(14.33%)"
            }
        ]
    }
}
```

### 3.8.2 HTML Report





**时空组学 STOMics Analytical Report**

**SS200000135TL\_D1**

Summary   Square Bin   **Cell Bin**   Image

### I Cell Bin Statistics

Mean Cell Area	286	Median Cell Area	270
Mean Cell Boundary DNB Count	282	Median Cell Boundary DNB Count	238
Mean Gene Type	229	Median Gene Type	201
Mean MID	411	Median MID	343

### I Cell Bin

### I Clustering

**Tissue Plot with Spots (cell bin)**

**show ssDNA**   **show expression**

**UMAP Projection of Spots (cellbin)**

Cluster 1, Cluster 2, Cluster 3, Cluster 4, Cluster 5, Cluster 6, Cluster 7, Cluster 8, Cluster 9, Cluster 10, Cluster 11, Cluster 12, Cluster 13, Cluster 14, Cluster 15, Cluster 16, Cluster 17, Cluster 18, Cluster 19, Cluster 20, Cluster 21, Cluster 22, Cluster 23, Cluster 24

Summary   Square Bin   Cell Bin   **Image**

### I Image Information

Manufacturer	motic	ImageQC Version	1.1.0
Model	Moticam56 M	QC Pass	Pass
Scan Time	2021-11-26 12:26:19	Track Line Score	70
Overlap	0.1	Clarity Score	94
Exposure Time (ms)	19,009	Good FOV Count	92
Scan Rows	13	Total FOV Count	117
Scan Columns	9	Stitching Score	93
FOV Height	2,039	Tissue Segmentation Score	95
FOV Width	3,064	Registration Score	99
Stain Type	ssDNA		
Stitched Image	No		
Image Name	SS200000135TL_D1_20220527_201353_1.0		

### I QC

ScaleX	0.866
ScaleY	0.866
Rotation	-1.603
Flip	True
Image X Offset	-3,383.29
Image Y Offset	2,065
Counter Clockwise Rotation	90
Matrix X Offset	0.00
Matrix Y Offset	0.00
Matrix Height	26,459
Matrix Width	26,459

### I Registration

### I Stitching

Template Source Row No.	9
Template Source Column No.	6
Global Height	24,071
Global Width	25,128

**Horizontal Image Stitching Deviation Heatmap**

**Vertical Image Stitching Deviation Heatmap**

# Appendices

## Appendix A: Recommend Directory Structure for Raw Data

```
...  
$ tree  
.  
|-- image  
|   |-- SS200000135TL_D1_20220527_201353_1.1.0.ipr  
|   `-- SS200000135TL_D1_20220527_201353_1.1.0.tar.gz  
|-- mask  
|   '-- SS200000135TL_D1.barcodeToPos.h5  
|-- md5  
|-- reads  
|   |-- E100026571_L01_trim_read_1.fq.gz  
|   '-- E100026571_L01_trim_read_2.fq.gz  
`-- reference  
    |-- STAR_SJ100  
    |   |-- Genome  
    |   |-- SA  
    |   |-- SAindex  
    |   |-- chrLength.txt  
    |   |-- chrName.txt  
    |   |-- chrNameLength.txt  
    |   |-- chrStart.txt  
    |   |-- exonGeTrInfo.tab  
    |   |-- exonInfo.tab  
    |   |-- geneInfo.tab  
    |   |-- genomeParameters.txt  
    |   |-- genomeParameters_bkp.txt  
    |   |-- sjdbInfo.txt  
    |   |-- sjdbList.fromGTF.out.tab  
    |   |-- sjdbList.out.tab  
    |   '-- transcriptInfo.tab  
    |-- genes.gtf  
    '-- genome.fa  
  
5 directories, 24 files
```

ⓘ Recommend to organize raw data as above if users prefer to use **SAW shell script** provide on the **SAW GitHub page** (<https://github.com/BGIResearch/SAW>).

## Appendix B: SAW ST Output File List

STEP	OUTPUT	FILE DESCRIPTION
<b>SPLITMASK</b>	<b>*.SN.barcodeToPos.bin</b>	Split Stereo-seq Chip T Mask file according to the CID.
	<b>lane.Aligned.sortedByCoord.out.bam</b>	Binary Alignment/Map file, used for storing the sequence alignment information.
	<b>lane.Aligned.sortedByCoord.out.bam.csi</b>	BAM index file, which is a table of contents for the BAM file that indicating where in the BAM file a specific read or set of reads can be found.
	<b>lane.barcodeReadsCount.txt</b>	Mapped CID list file with reads counts for each CID, the three columns record x, y, and read count.
<b>MAPPING</b>	<b>lane.Log.final.out</b>	Summary mapping statistics after mapping job is complete (STAR output)
	<b>lane.Log.out</b>	Main log file in STAR mapping (STAR output)
	<b>lane.Log.progress.out</b>	Reports job process statistics (STAR output)
	<b>lane.SJ.out.tab</b>	Splice junctions detected in the mapping (STAR output)
	<b>lane.bcPara</b>	A parameters file defines CID mapping options
	<b>lane_barcodeMap.stat</b>	Statistical report of CID mapping, such as CID mapped reads count, reads sequencing quality, mapped DNB count, etc.
<b>MERGE</b>	<b>SN.barcodeReadsCount.txt</b>	Mapped CID list file with reads counts for each CID., the three columns record x, y, and read count.
	<b>SN.Aligned.sortedByCoord.out.merge.q10.dedup.target.bam</b>	Annotated BAM file sorted by coordinate, includes uniquely mapped reads and multi-mapped reads whose Hl:i tag is 1.
<b>COUNT</b>	<b>SN.Aligned.sortedByCoord.out.merge.q10.dedup.target.bam.summary.stat</b>	Statistical summary report file for count. Total reads in filter&deduplication metrics stands for the total alignment record count in bam. Pass filter and total reads in annotation metrics are the same, they represent uniquely mapped reads that will be used for annotation, MID correction and quantification.
	<b>SN.raw.gef</b>	Gene expression file in hdf5 format. This is the first raw matrix that includes the expression information over a complete chip region. It only includes geneExp group for the bin size of 1. The origin of expression matrix has been calibrated to (0,0), and the offset x and y has been record as minX and minY in the attribute of geneExp/expression dataset.
	<b>SN_raw_barcode_gene_exp.txt</b>	A space-separate file records coordinate, gene, MID, and count information. Which is prepared to be a sampling file that performing sequence saturation. The 5 columns are coorY, coorX, geneIndex, MIDIndex, readCount.
	<b>1.ini</b>	Image configuration file.
<b>REGISTER &amp; IPR2IMG</b>	<b>date-hh-mm-ss.log</b>	Log file.
	<b>3.jpg</b>	Microscope stitched image.
	<b>attrs.json</b>	Height and width of gene expression matrix.
	<b>SN or other user specified name for the image folder used when input into imageQC</b>	This subdirectory stores raw small image pieces in TIFF format.
	<b>SN_0000_0000_YYYY-MM-DD_hh-mm-ss-n.tif</b>	Small image pieces in TIFF format.
	<b>fov_stitched_transformed.tif</b>	The stitched panoramic image that has pre-registered with the track line pattern template. So that it will not need to further rotate a non-right angle or scale.



STEP	OUTPUT	FILE DESCRIPTION
REGISTER & IPR2IMG	<b>matrix_template.txt</b>	Track line cross point template for the registered ssDNA image. Used for assessing registration result.
	<b>SN_date_time_version.csv</b>	Clarity score for each small image.
	<b>SN_date_time_version.ipr</b>	IPR format image process record file which records basic image information gathered from imageQC.
	<b>SN_date_time_version.png</b>	Clarity score heatmap for each small image.
	<b>SN_mask.tif</b>	Registered cell segmentation binary image file in TIFF format.
	<b>SN_regist.tif</b>	Registered panoramic image file in TIFF format.
	<b>SN.rpi</b>	Registered panoramic image file, tissue area boundary, and cell boundaries (downsampled) that stores as an image pyramid.
	<b>SN_tissue_bbox.csv</b>	Registered panoramic image size.
	<b>SN_tissue_cut.tif</b>	The tissue segmentation result of registered panoramic image file in TIFF format.
	<b>transform_template.txt</b>	Track line cross point template for the fov_stitched_transformed.tif. Used for assessing stitching result.
TISSUECUT	<b>transform_thumb.png</b>	A downsampled pre-registered panoramic image.
	<b>SN_date_time_version.txt</b>	Txt file records track line cross point coordinates.
	<b>SN.gef</b>	A gene expression file in hdf5 format. This file is a complete GEF format which includes geneExp group and wholeExp group in bin1, 10, 20, 50, 100, 200, and 500. It also includes a stat group. The origin of expression matrix has been calibrated to (0,0), and the offset x and y has been recorded as minX and minY in the attribute of geneExp/expression dataset.
	<b>SN.tissue.gef</b>	A gene expression file in hdf5 format. Tissue GEF includes the expression information of the tissue coverage region. It only includes geneExp group for the bin size of 1. The origin of expression matrix has been calibrated to (0,0), and the offset x and y has been record as minX and minY in the attribute of geneExp/expression dataset same to raw GEF.
	<b>dnb_merge/bin200.png</b>	A thumbnail image converts from gene expression matrix in bin200.
	<b>tissue_fig</b>	This directory stores the statistical plots for the tissue coverage region
	<b>SN.ssDNA.rpi</b>	Registered panoramic image file (downsampled) that stores as an image pyramid. Same to the register output 7_result/SN.rpi
	<b>scatter_100x100_MID_gene_counts.png</b>	Scatter plot of MID count and gene number in each bin (bin100)
	<b>scatter_150x150_MID_gene_counts.png</b>	Scatter plot of MID count and gene number in each bin (bin150)
	<b>scatter_200x200_MID_gene_counts.png</b>	Scatter plot of MID count and gene number in each bin (bin200)
	<b>scatter_50x50_MID_gene_counts.png</b>	Scatter plot of MID count and gene number in each bin (bin50)
	<b>statistic_100x100_MID_gene_DNB.png</b>	Univariate distribution of MID count, gene numbers, and DNB numbers with rug along the x axis (bin100)
	<b>statistic_150x150_MID_gene_DNB.png</b>	Univariate distribution of MID count, gene numbers, and DNB numbers with rug along the x axis (bin150)
	<b>statistic_200x200_MID_gene_DNB.png</b>	Univariate distribution of MID count, gene numbers, and DNB numbers with rug along the x axis (bin200)
	<b>statistic_50x50_MID_gene_DNB.png</b>	Univariate distribution of MID count, gene numbers, and DNB numbers with rug along the x axis (bin50)
	<b>violin_100x100_MID_gene.png</b>	Violin plots show the distribution of deduplicated MID count and gene number in each bin (bin100)



STEP	OUTPUT	FILE DESCRIPTION
TISSUECUT	<b>violin_150x150_MID_gene.png</b>	Violin plots show the distribution of deduplicated MID count and gene number in each bin (bin150)
	<b>violin_200x200_MID_gene.png</b>	Violin plots show the distribution of deduplicated MID count and gene number in each bin (bin200)
	<b>violin_50x50_MID_gene.png</b>	Violin plots show the distribution of deduplicated MID count and gene number in each bin (bin50)
	<b>tissuecut.stat</b>	Statistical report for tissue coverage region.
CELLCUT	<b>SN.cellbin.gef</b>	A gene expression file for cells in hdf5 format. Cellbin GEF includes the expression information of the cells, such as the coordinate of the centroid, boundary coordinates, expression of genes, and cell area. The cell is record by its boundary. The origin of expression matrix has been calibrated to (0,0), and the coordinate offset x and y has been recorded as offsetX and offsetY in the attribute of the GEF file same to minX and minY in the raw GEF file.
SPATIAL-CLUSTER	<b>SN.spatial.cluster.h5ad</b>	H5AD file for spatial clustering analysis result.
CELLCLUSTER	<b>SN.cell.cluster.h5ad</b>	H5AD file for cell clustering analysis result.
SATURATION	<b>plot_1x1_saturation.png</b>	Sequencing saturation analysis plots for bin1. Calculated by 1- (unique reads/total reads) for each bin (bin1).
	<b>plot_200x200_saturation.png</b>	Sequencing saturation analysis plots for bin200. Calculated by 1- (unique reads/total reads) for each bin (bin1).
	<b>sequence_saturation.txt</b>	Sequence saturation file. The nine columns are sampling component (#sample), bin1 total reads (bar_x), sequence saturation value at bin1 (bar_y1), median gene count at bin1 (bar_y2), unique reads at bin1 (bar_umi), bin200 total reads (bin_x), sequence saturation value at bin200 (bin_y1), median gene count at bin200 (bin_y2), and unique reads at bin200 (bin_umi), respectively.
	<b>SN.report.html</b>	HTML analytical report.
REPORT	<b>SN.statistics.json</b>	Statistical summary report in JSON format. It gathers all important statistical metrics from the statistical report in each step.
	<b>scatter_1x1_MID_gene_counts.png</b>	Scatter plot of MID count and gene number in each cell
	<b>statistic_1x1_MID_gene_DNB.png</b>	Univariate distribution of MID count, gene numbers, and DNB numbers with rug along the x axis of each cell
	<b>violin_1x1_MID_gene.png</b>	Violin plots show the distribution of deduplicated MID count and gene number in each cell

## Appendix C: Handling Errors and Exceptions

### Common Errors

- **File access error:**

Some examples of file access error:

```
...
terminate called after throwing an instance of 'std::invalid_argument'
what(): Could not open the file: xxxxxxx
...
```

Or

```
...
#006: H5FDsec2.c line 352 in H5FD__sec2_open(): unable to open file: name = '/path/
to/hdf5/file', errno = 2, error message = 'No such file or directory', flags = 0, o_
flags = 0
    major: File accessibility
    minor: Unable to open file
...
```

 bind file path before execute command.

```
...
$ export SINGULARITY_BIND="/path/to/file/directory"
```

### mapping

- **readNameSeparator error:**

```
...
EXITING: FATAL INPUT ERROR: empty value for parameter "readNameSeparator" in input
"Command-Line"
SOLUTION: use non-empty value for this parameter
```

 try to delete --readNameSeparator \\" \" from the command.

- **limitBAMsortRAM error:**

```
...
Error code: SAW-A10183

EXITING because of fatal ERROR: not enough memory for BAM sorting:
SOLUTION: re-run STAR with at least -limitBAMsortRAM xxxxxxxxxxx
```

 Modify the value specified by the --limitBAMsortRAM refer to the SOLUTION in the stderr.

## Appendix D: Manual Image Merge Using ImageJ

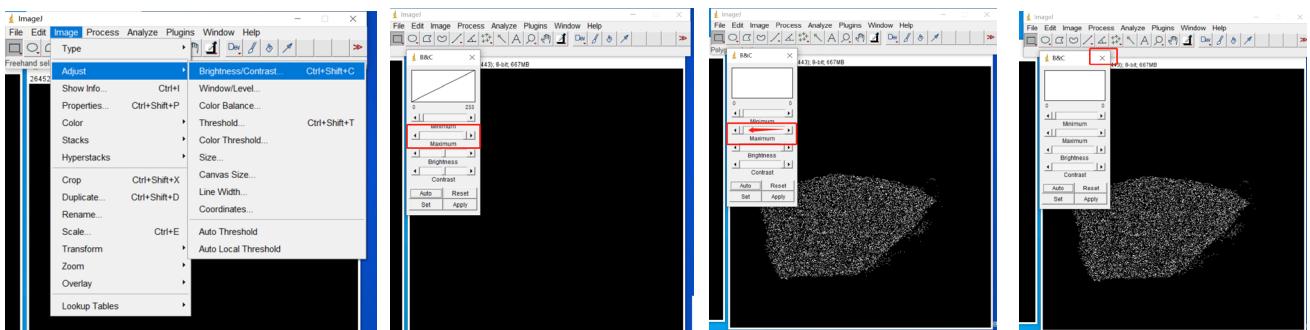
We provide step-by-step procedures demonstrating how to merge your SN\_regist.tif image with your SN\_tissue\_cut.tif image or SN\_mask.tif image to check for tissue segmentation and cell segmentation performance, respectively. Please make sure you have ImageJ installed on your computer.

- Obtain your SN\_regist.tif image and SN\_mask.tif (SN\_tissue\_cut.tif) image from your output files generated after running **ipr2img**.

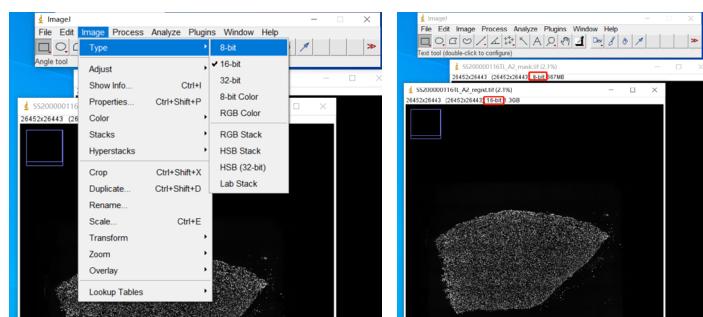
### Here showing an example using

- **SS200000116TL\_A2\_regist.tif** (post-registered ssDNA image, image bit depth of 16 bit)
- and **SS200000116TL\_A2\_mask.tif** (post-registered cellcut image mask, image bit depth of 8 bit).

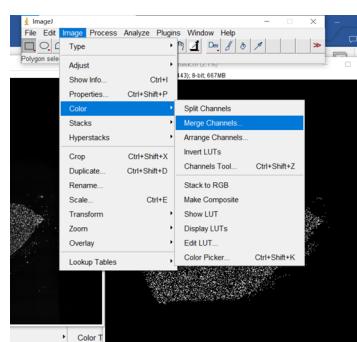
- 1) First, open both SN\_regist.tif image and SN\_mask.tif image using ImageJ.
- 2) Once opened both files, if SN\_mask.tif image is not showing, click **Image > Adjust > Brightness/Contrast**, and pull the maximum bar to the left. The image should appear. Do not click apply, just simply close the B&C interface.



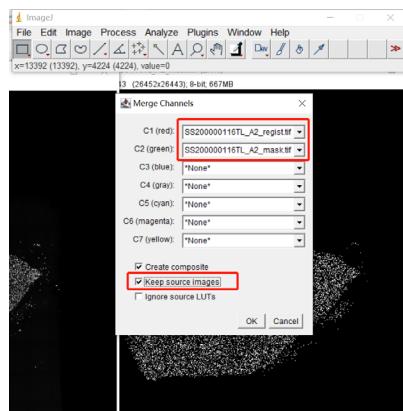
- 3) Now, if your SN\_regist.tif and SN\_mask.tif were set to different sizes, make sure to adjust the image that was in 16 bit to 8 bit. Click **Image > Type > 8 bit**.



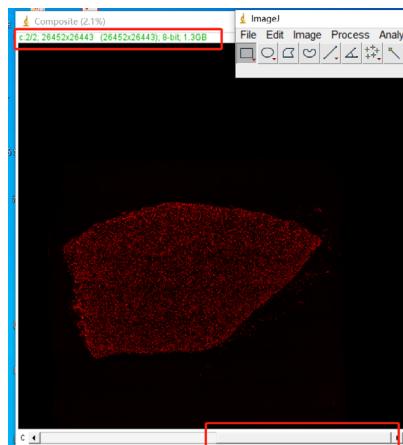
- 4) Merge your SN\_regist.tif and SN\_mask.tif images by selecting **Image > Color > Merge Channels**



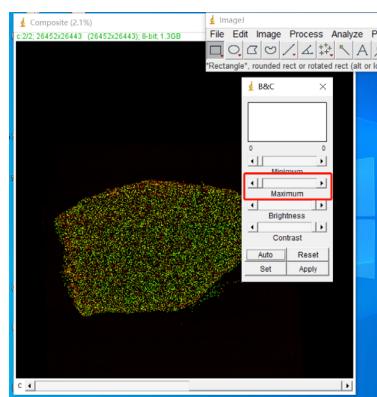
- 5) Assign your SN\_regist.tif to the red channel, and your SN\_mask.tif (or SN\_tissue\_cut.tif) to the green channel. Click the “Keep source images” box so your original images won’t be closed after the merged image is generated.



- 6) If green channel did not show on your merged image, set the bottom bar to the green channel (image info shown in green once switched to green channel).



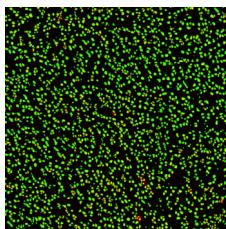
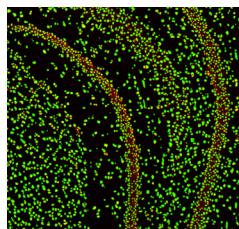
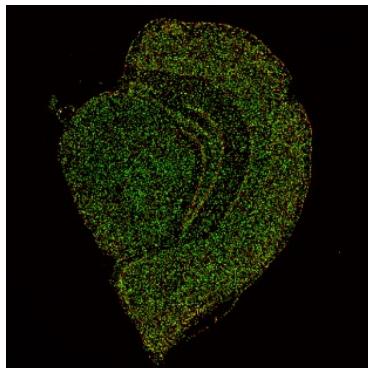
- 7) Go to **Image > Adjust > Brightness/Contrast**, pull the maximum bar to the left. Mask image of cell segmentation should appear in green.



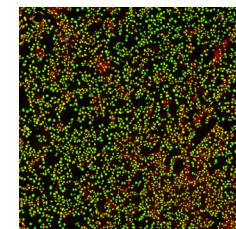
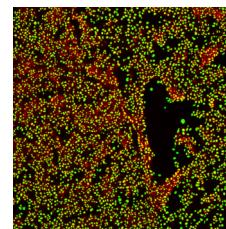
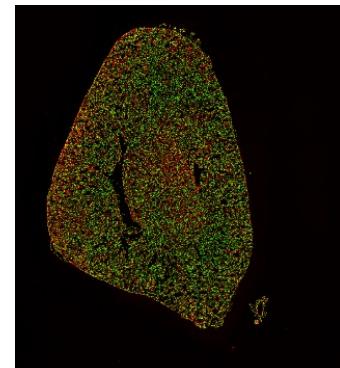
- 8) Zoom in on your merged image and check if green area has more coverage than the red.

Examples of good cell segmentation vs bad cell segmentation:

Good



Bad



Overall segmentation of this sample is good as there is no large area coverage of red in the image. Besides the denser area within the tissue or tissue edge with strong exposure showing incomplete segmentation, the remaining area have clear boundaries of segmented cells, which could be determined as having good cell segmentation.

This is a kidney sample which exhibit very dense tissue morphology, resulting in poor overall segmentation performance and was determined as not suitable for further cell binning analysis

## References

1. BGIResearch/SAW. Accessed October 13, 2021. <https://github.com/BGIResearch/SAW>
2. Chen A, Liao S, Cheng M, et al. Large field of view-spatially resolved transcriptomics at nanoscale resolution Short title: DNA nanoball stereo-sequencing. *bioRxiv*. Published online January 24, 2021:2021.01.17.427004. doi:10.1101/2021.01.17.427004
3. Cock PJA, Fields CJ, Goto N, Heuer ML, Rice PM. The Sanger FASTQ file format for sequences with quality scores, and the Solexa/Illumina FASTQ variants. *Nucleic Acids Res.* 2009;38(6):1767-1771. doi:10.1093/nar/gkp1137
4. Archives SR, Sra T, Nucleotide I, et al. File Format Guide 1. Published online 2009:1-11. Accessed May 21, 2021. <https://www.ncbi.nlm.nih.gov/sra/docs/submitformats/>
5. Merkel D. Docker: lightweight Linux containers for consistent development and deployment. *Linux J.* 2014;2014(239):2. Accessed October 15, 2021. <https://www.linuxjournal.com/content/docker-lightweight-linux-containers-consistent-development-and-deployment>
6. Kurtzer GM, Sochat V, Bauer MW. Singularity: Scientific containers for mobility of compute. *PLoS One*. 2017;12(5):e0177459. doi:10.1371/journal.pone.0177459
7. Sequence Alignment/Map Format Specification.; 2021. Accessed May 21, 2021. <https://github.com/samtools/hts-specs>.
8. Dobin A, Davis CA, Schlesinger F, et al. STAR: Ultrafast universal RNA-seq aligner. *Bioinformatics*. 2013;29(1):15-21. doi:10.1093/bioinformatics/bts635
9. Ensembl. GFF/GTF File Format. Published 2020. Accessed May 27, 2021. <http://www.ensembl.org/info/website/upload/gff.html?redirect=no>
10. GFF2 - GMOD. Accessed May 27, 2021. <http://gmod.org/wiki/GFF2>
11. GitHub - BGIResearch/stereopy: A toolkit of spatial transcriptomic analysis. Accessed July 4, 2021. <https://github.com/BGIResearch/stereopy>
12. BGIResearch/geftools: Tools for manipulating GEFs. Accessed April 7, 2022. <https://github.com/BGIResearch/geftools>
13. BGIResearch/gefpy: gef io, draw out from stereopy. Accessed April 7, 2022. <https://github.com/BGIResearch/gefpy>

## Contact Us

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Please raise GitHub issues for reporting bugs and requesting features:

SAW GitHub Issue Page: <https://github.com/BGIResearch/SAW/issues>