

The impact of aSTI on the foreskin: spatial transcriptome and ex vivo HIV-1 infection - Support #152

Understanding the Slide seq data and analysis pipelines

05/11/2023 12:34 PM - Ephie Geza

Status:	New	Start date:	04/04/2023
Priority:	High	Due date:	04/12/2023
Assignee:		% Done:	100%
Category:		Estimated time:	10.00 hours
Target version:		Spent time:	14.00 hours
Description			
This is to clarify whether single-cell RNA for the skin should be done or we use it as reference for slide seq analysis.			

History

#1 - 05/11/2023 02:50 PM - Ephie Geza

- Subject changed from Meeting to discuss the reference single-cell of skin and spatial data to Understanding the Slide seq data and analysis pipelines
- Due date changed from 03/17/2023 to 04/12/2023
- Start date changed from 03/17/2023 to 04/04/2023
- Estimated time changed from 1.00 h to 10.00 h

1. Started by investigating the ssHippo data from the SeuratData package in R
  - the data
  - the code upto the creation of the Seurat object.
2. Manipulate the slide seq input data to a format similar to ssHippo