

ISCVAM - Interactive Single Cell Visual Analytics for Multiomics tutorial

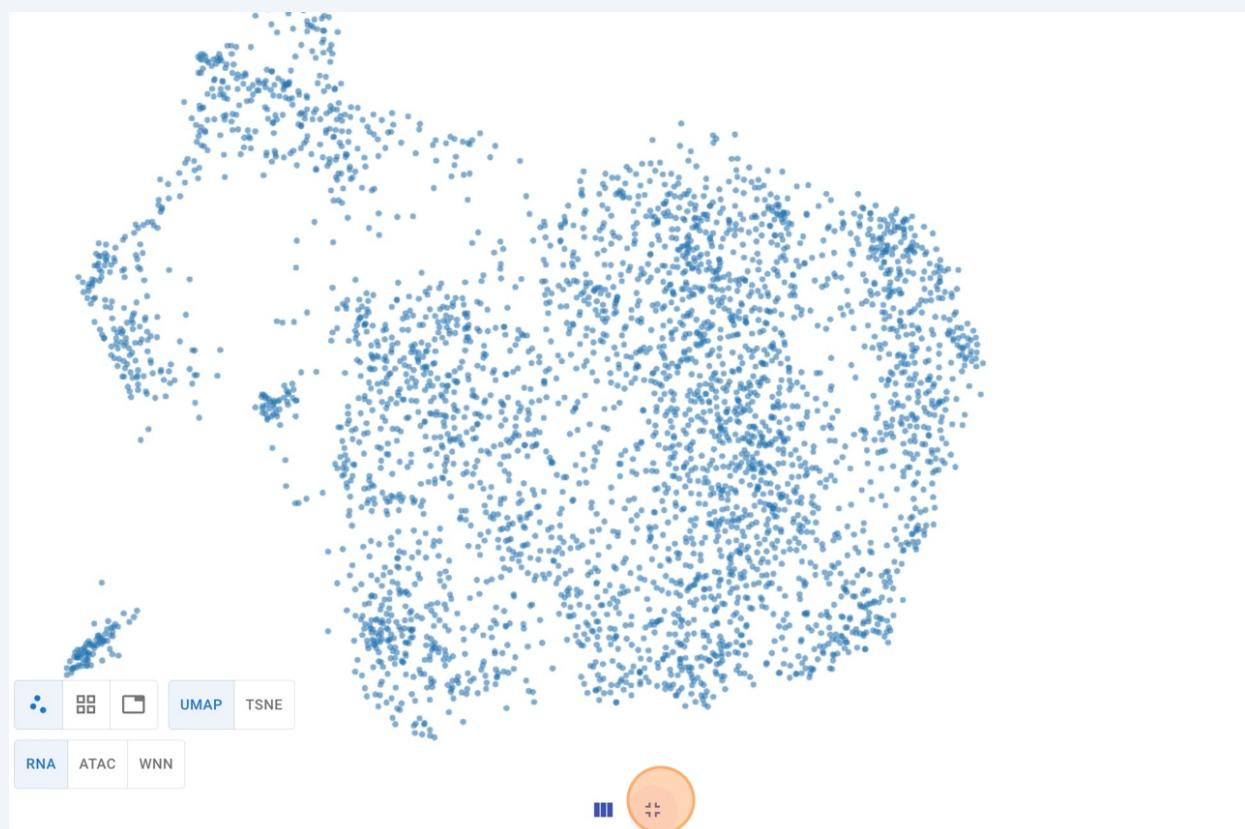
Scribe 

This tutorial is a brief introduction on how to use ISCVAM. Our single-cell multiomics visualization app serves as an investigation tool, which allows users to:

- (1) visualize data under multi-modalities (RNA, ATAC) --> leverage the transcriptomics and epigenetics of the cells
- (2) paint cells with multiple single-cell clustering resolutions --> discover rare cell population
- (3) view 3 datasets simultaneously --> validate findings across datasets

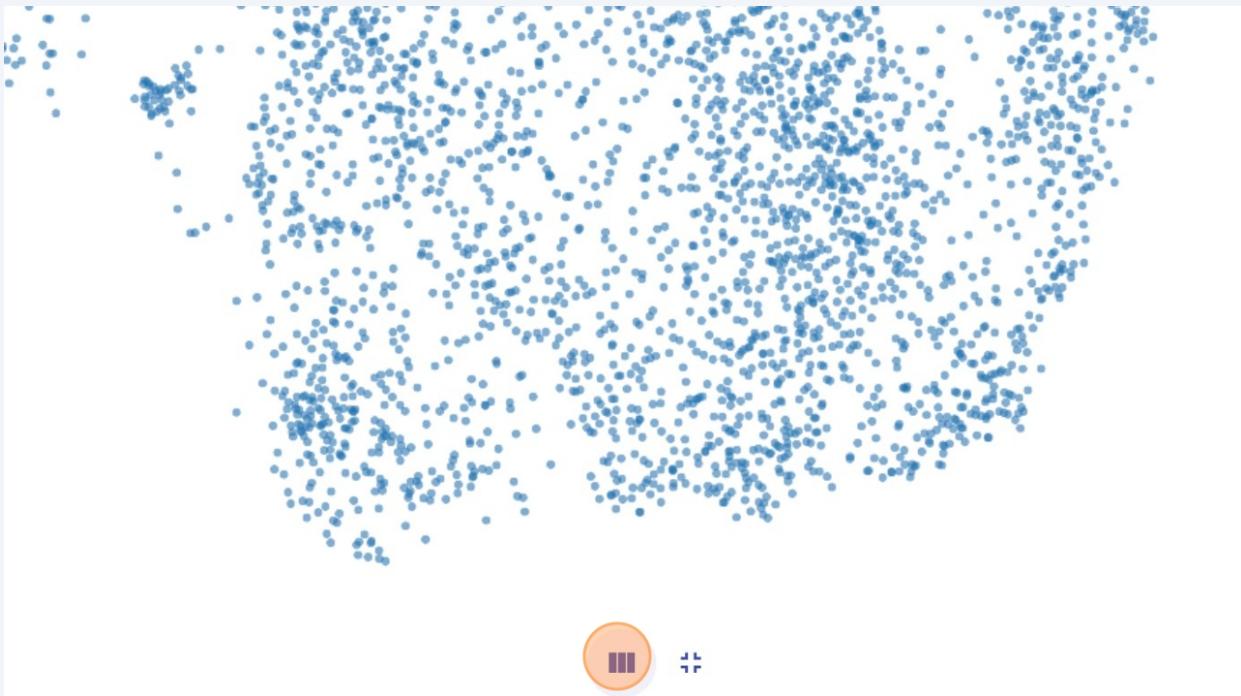
- 1 Navigate to <https://chenlab.utah.edu/iscvam/>

- 2 Click here to view 1 dataset in full-screen mode



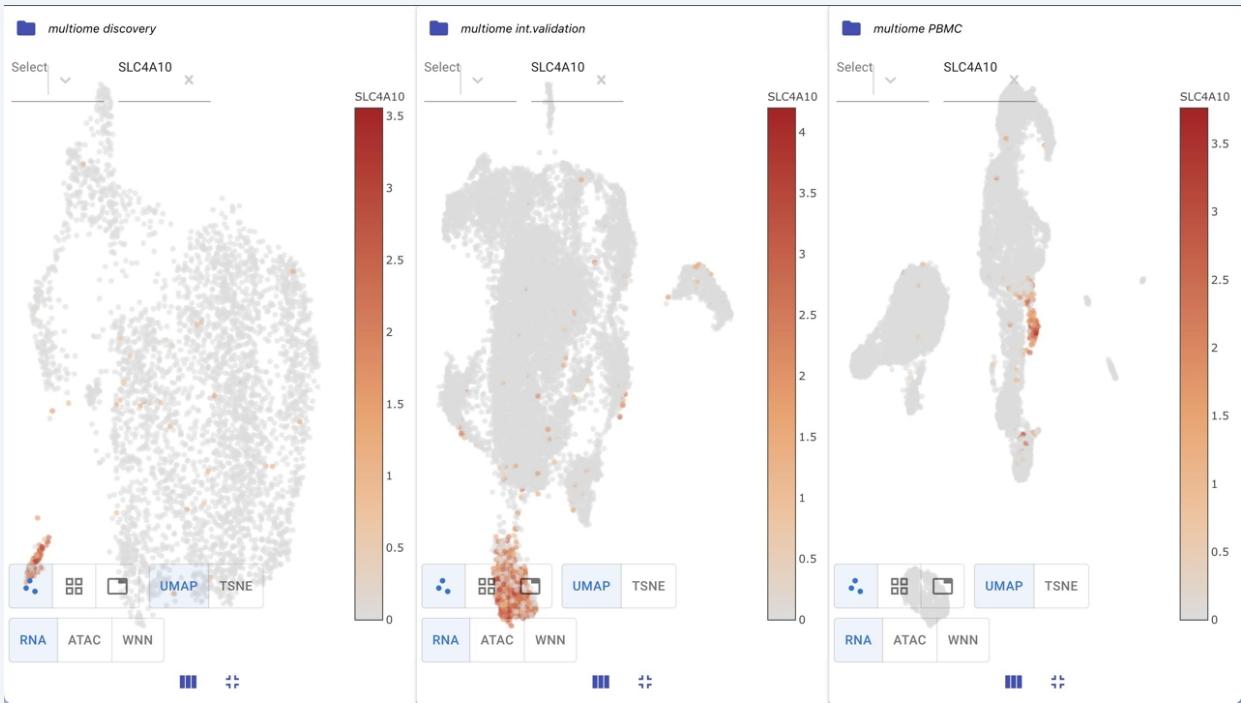
3

Click this icon to view data in 3 panels simultaneously --> for cross-referencing your findings across datasets

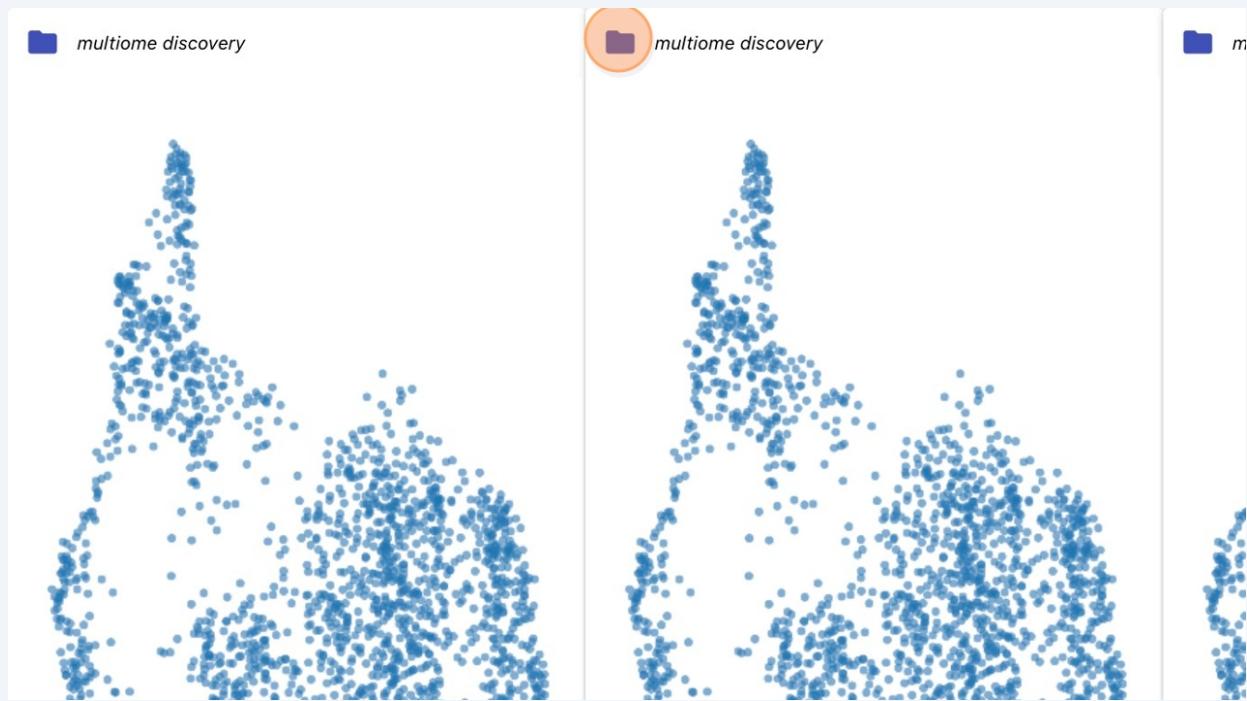


4

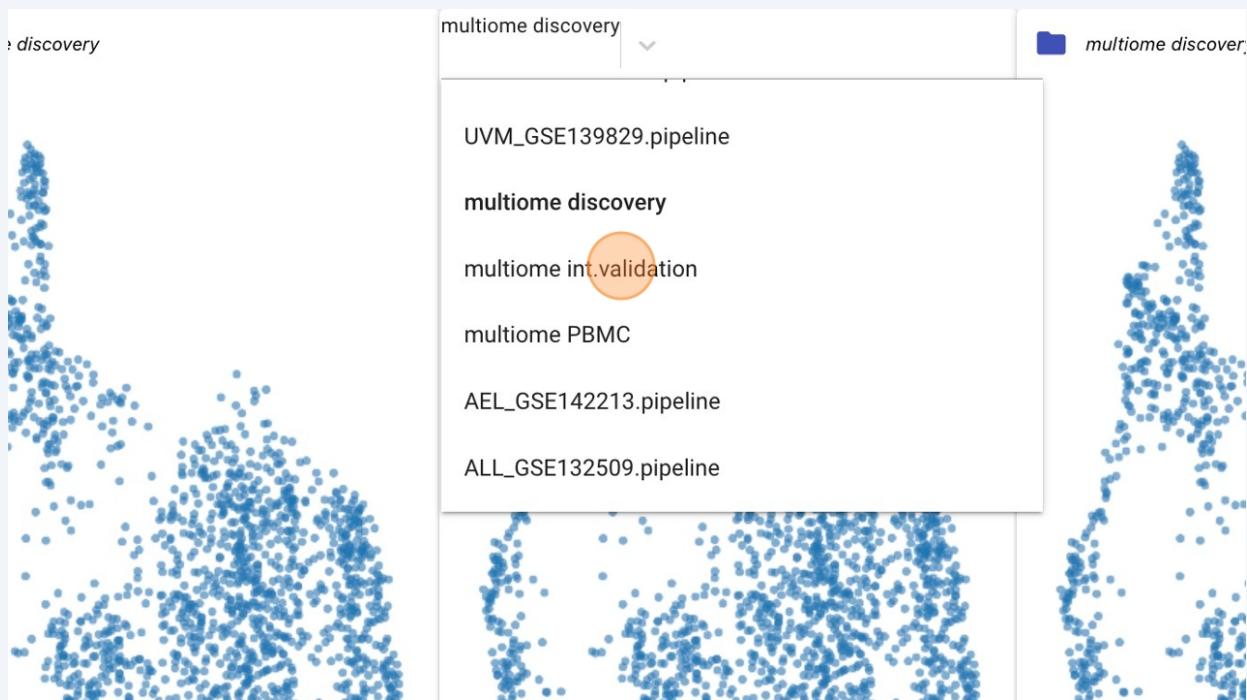
Multi-panels viewing: an example of ISCVAM interface with 3 different datasets painted by the same gene SLC4A10 --> validate findings across datasets



- 5 Click this icon "folder" to load a different dataset

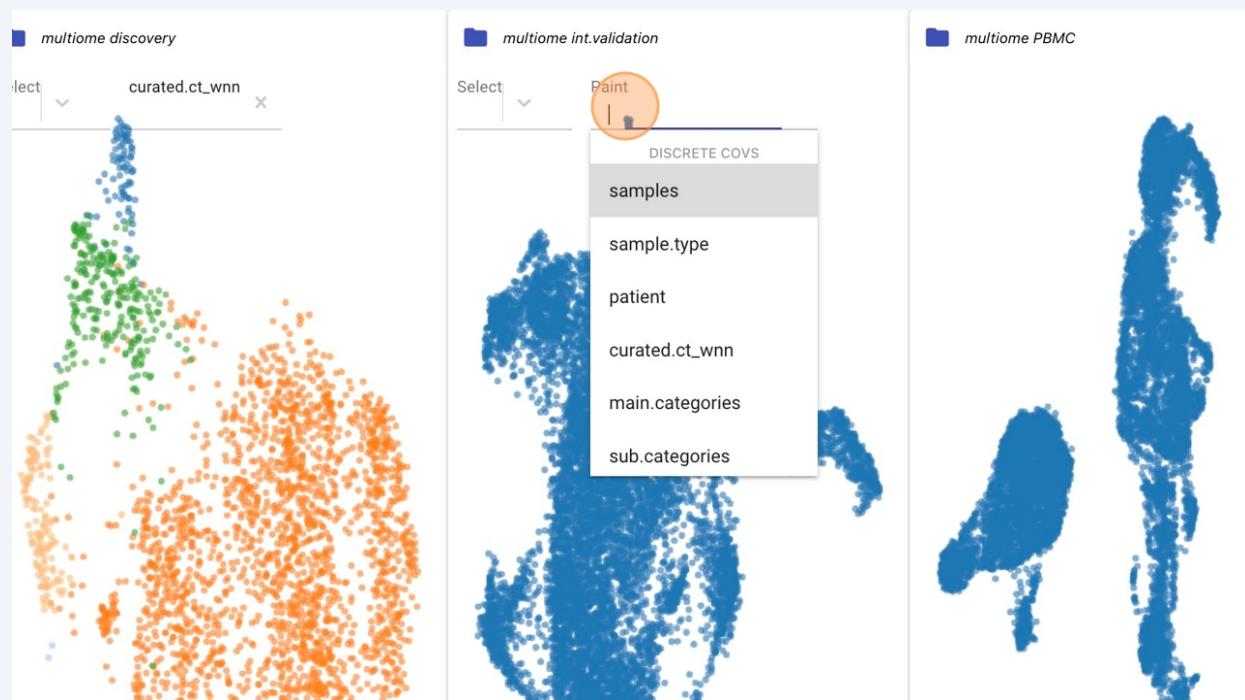


- 6 You can search for a dataset by typing its name here



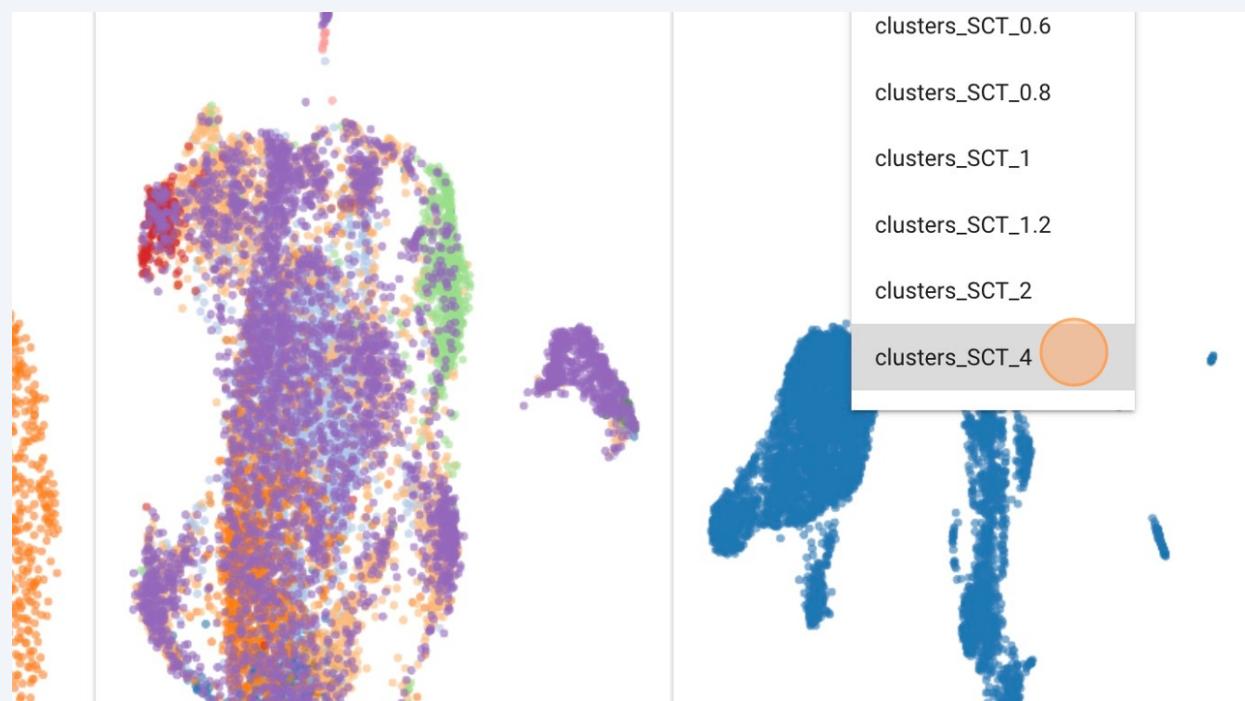
7

Click here to paint cells by different attributes, such as samples, different cell-typing reference panels, QC metrics, etc.



8

You can paint cells at different single-cell resolutions --> discovering smaller cell population

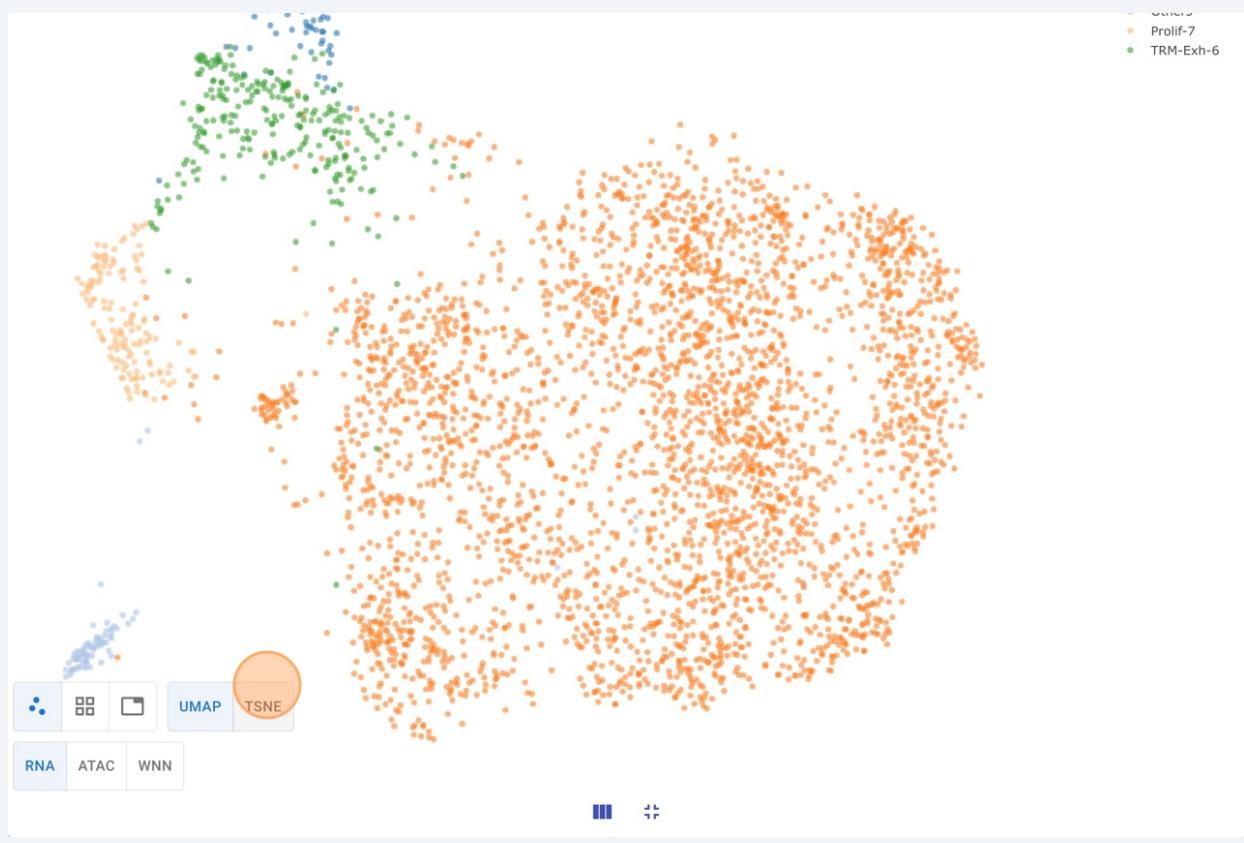


9

Cell annotation with color-coded is on the right side of the screen

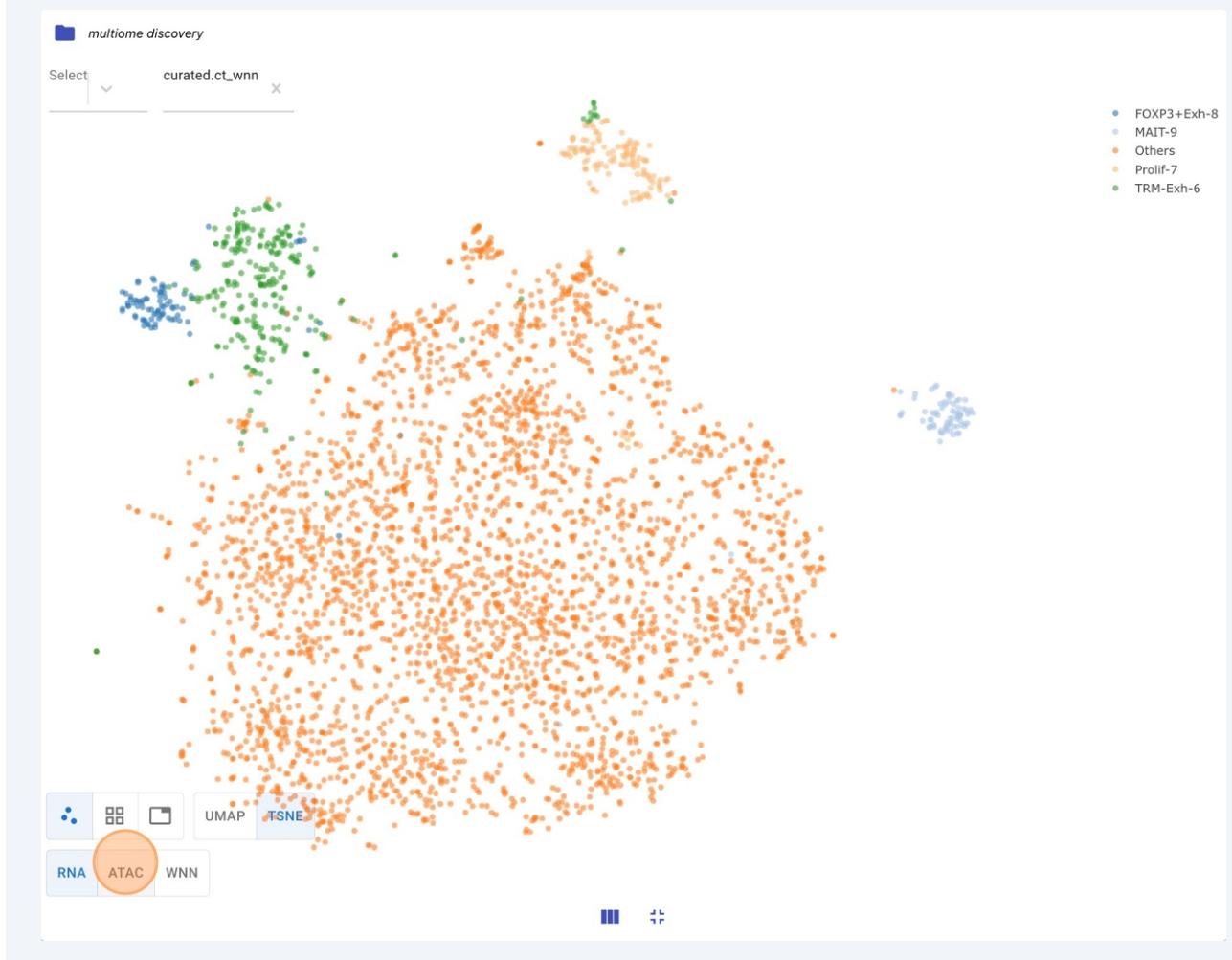


10 Click "TSNE" or "UMAP" to view cells under different dimension reduction

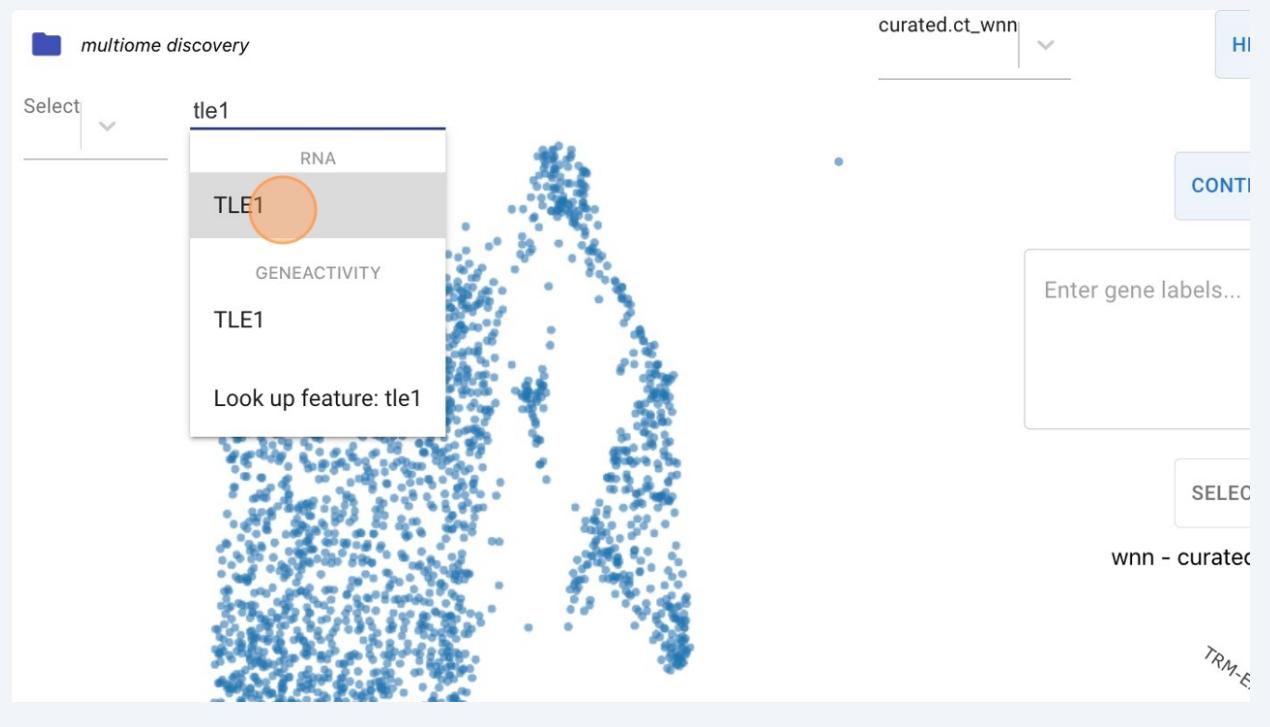


11

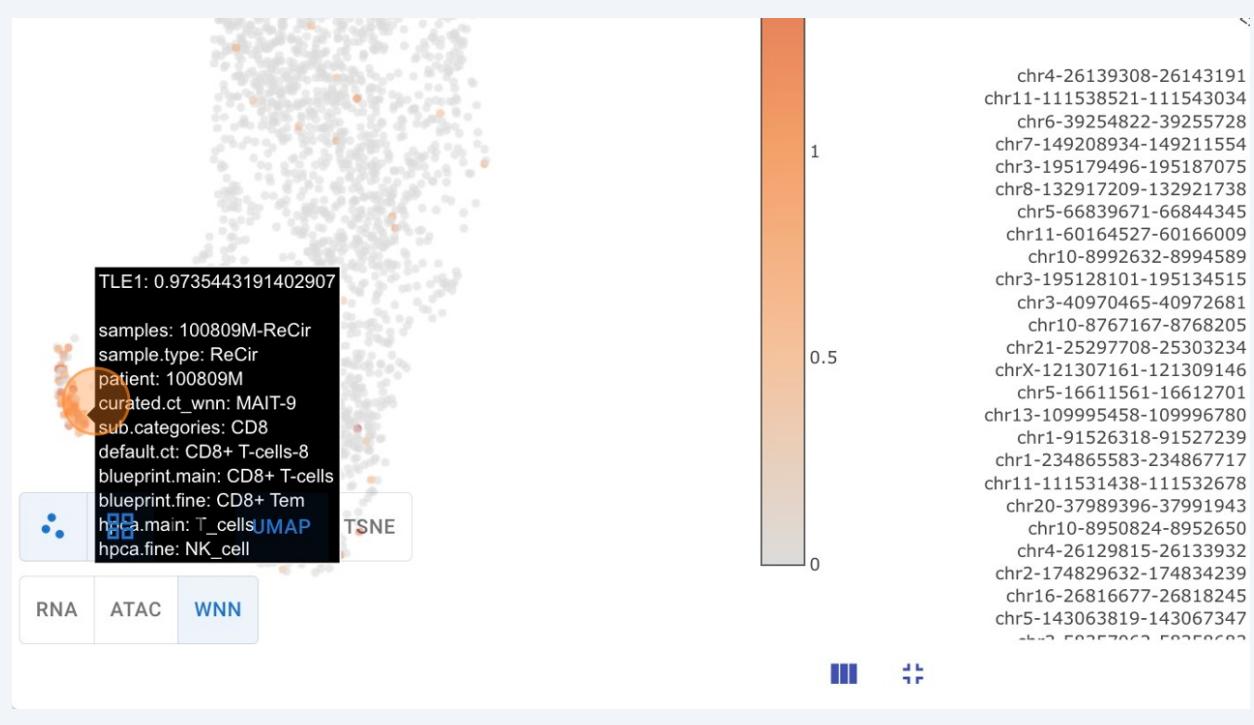
Click here to view cells under different modalities, such as "RNA" or "ATAC" --> leveraging both the transcriptomics and epigenetics of the cells



12 You can paint gene expression level by typing the gene symbol here

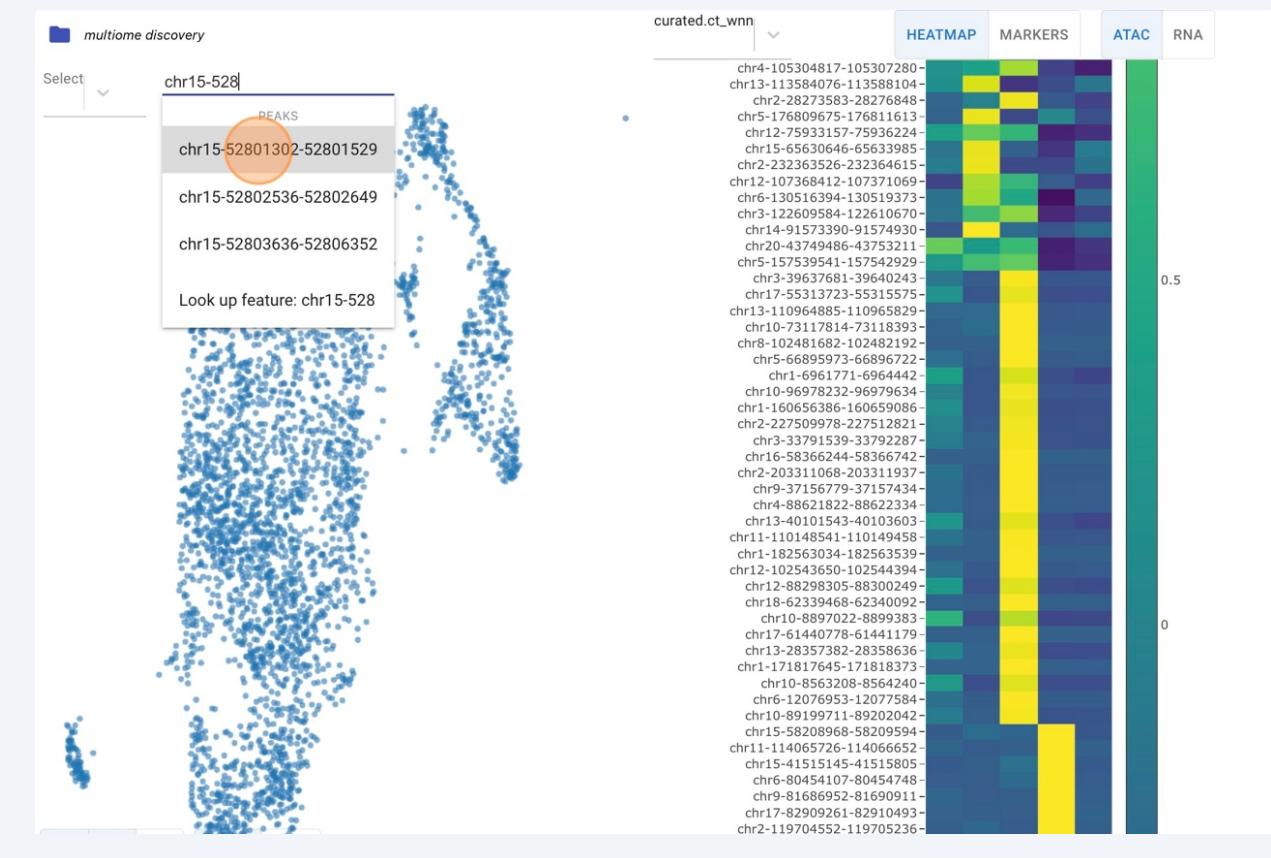


13 Gene expression level of the gene of interested painted



14

Search the peak expression the same way by typing chromosomal location such as "chr15-528" with the help of auto-completion



15

Click here to view heat map at different clustering resolutions --> breaking down clusters of cells at single-cell resolutions



16

Click here to view heatmap markers under different modalities, either RNA or ATAC



17 Click "RNA" to view RNA markers



18 or "ATAC" markers



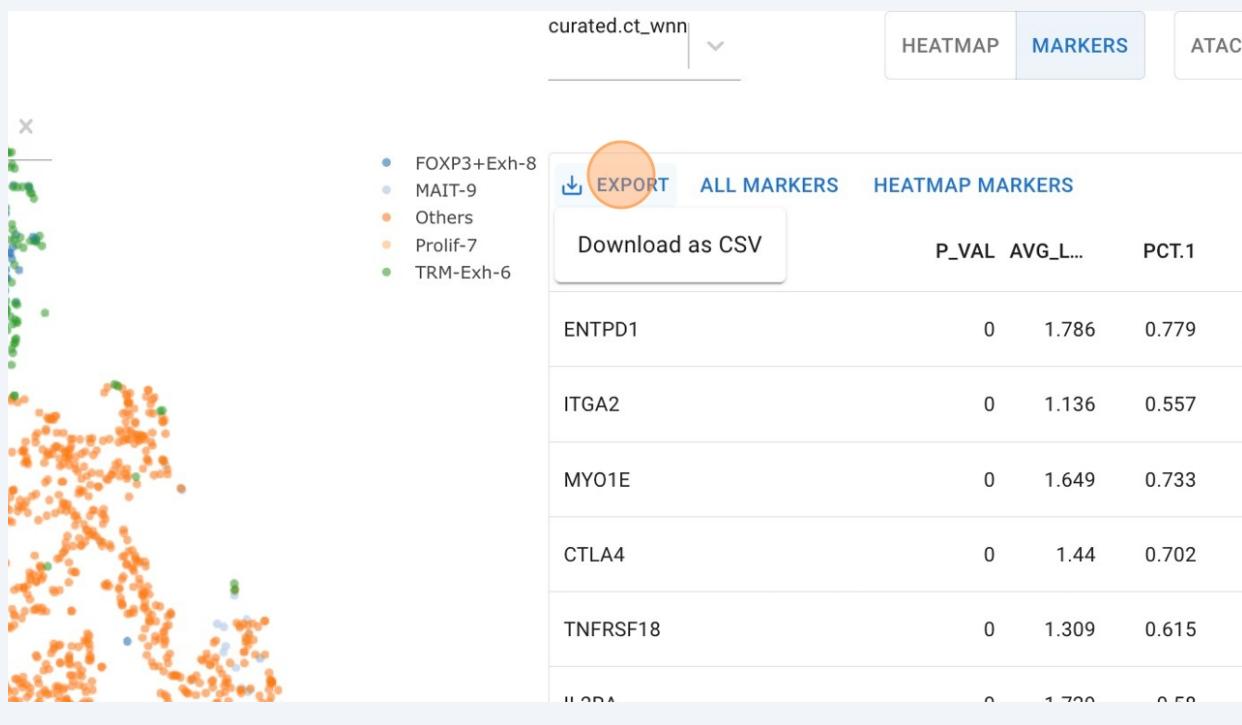
19 View atac markers under log-normalization



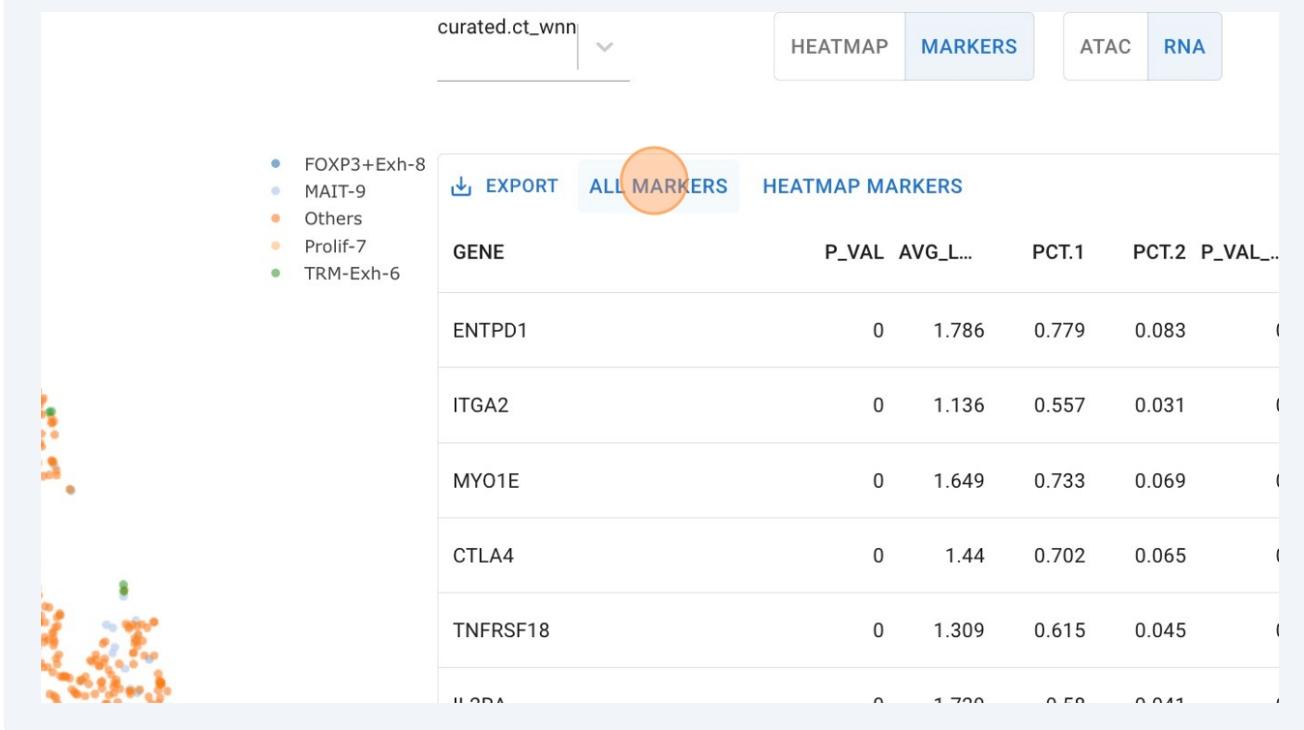
20 Click "MARKERS" to view marker in spreadsheet format



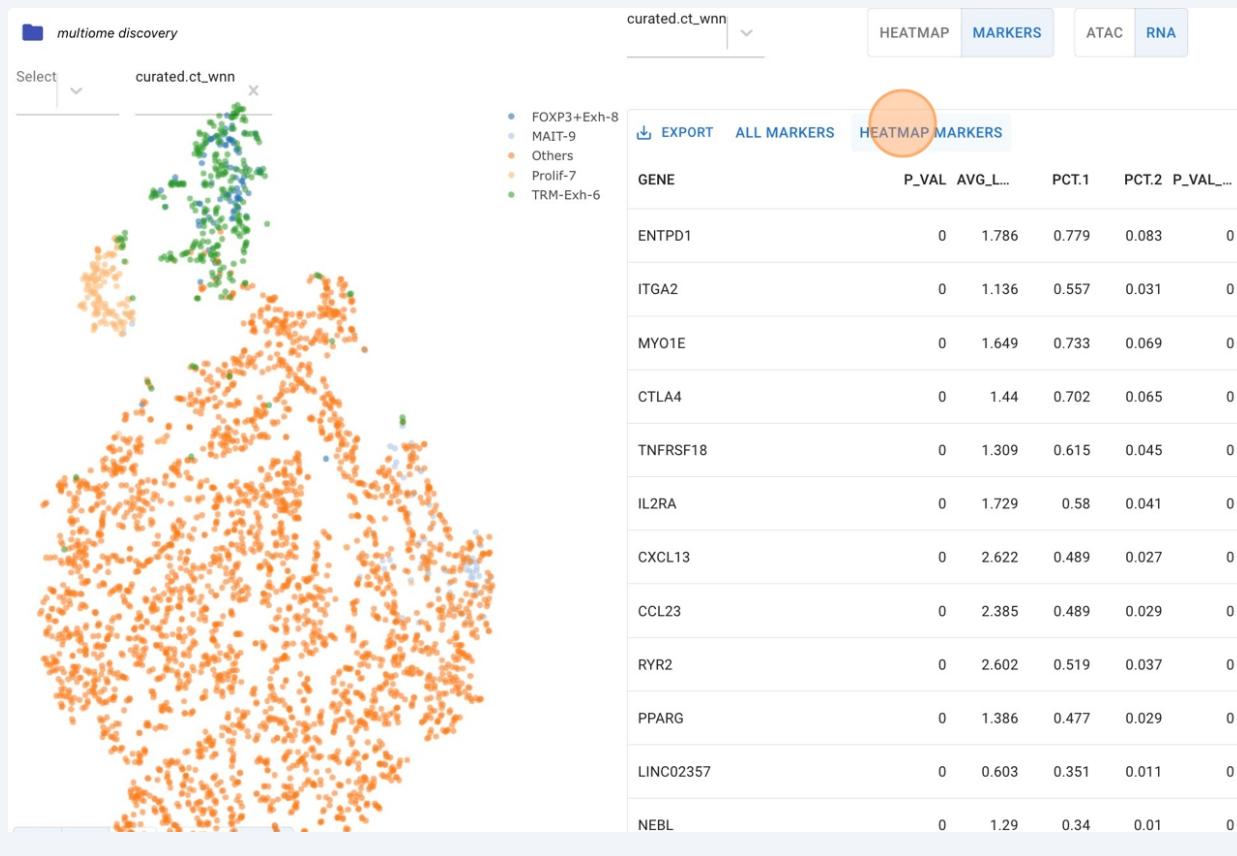
21 Click "EXPORT" to download these marker spreadsheets



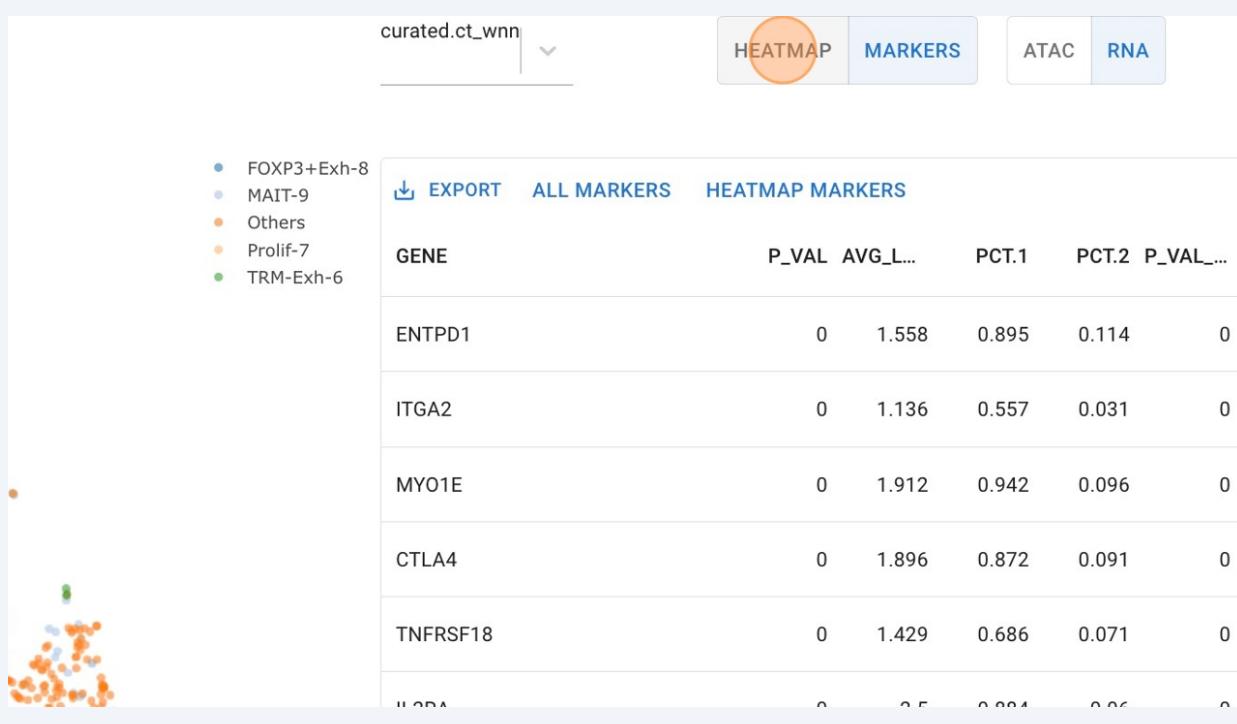
22 Can view markers under "ALL MARKERS"



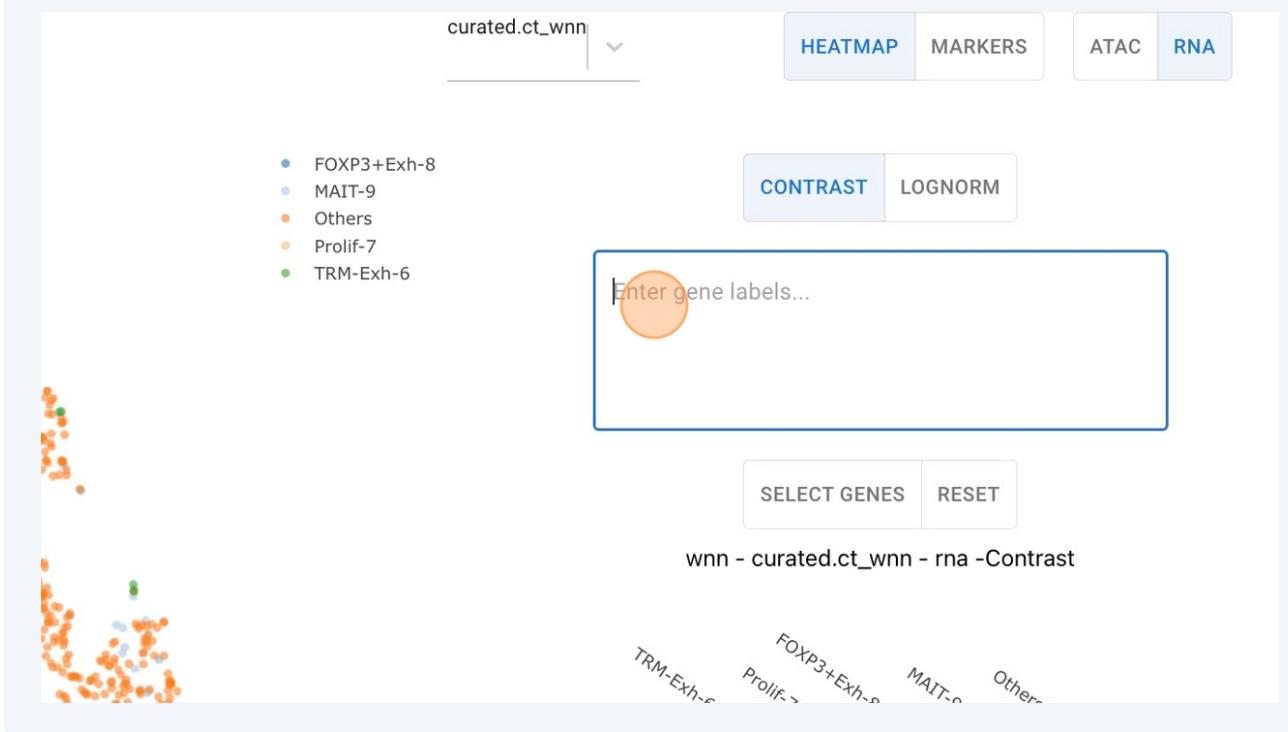
23 or only "HEATMAP MARKERS"



24 Click "HEATMAP" to go back to heatmap



25 Click the "Enter gene labels..." field.



26 Type "itga2 enter top2a enter tle1 enter slc4a10"

27

Click "SELECT GENES" to plot your interested gene expression



28 Click "RESET" to come back to precomputed heatmap

