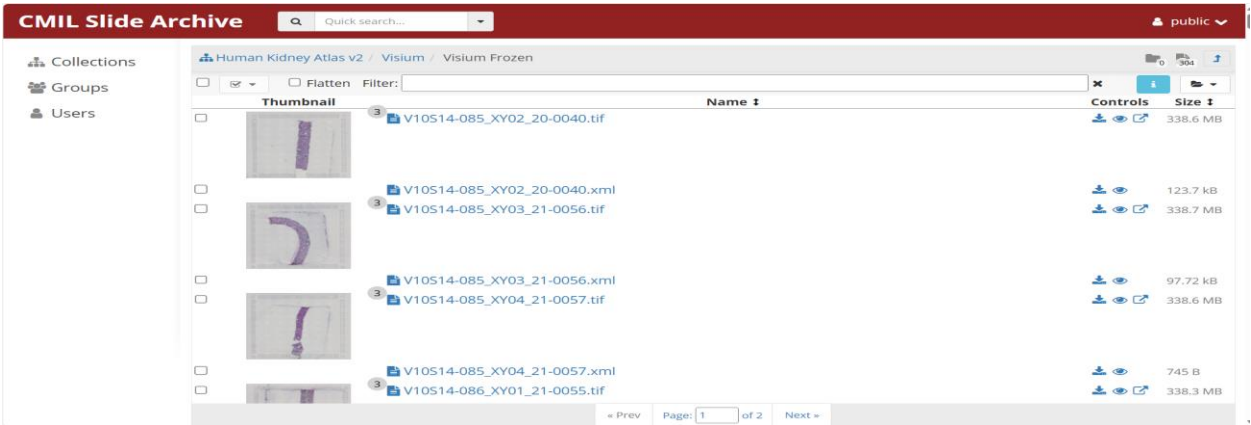
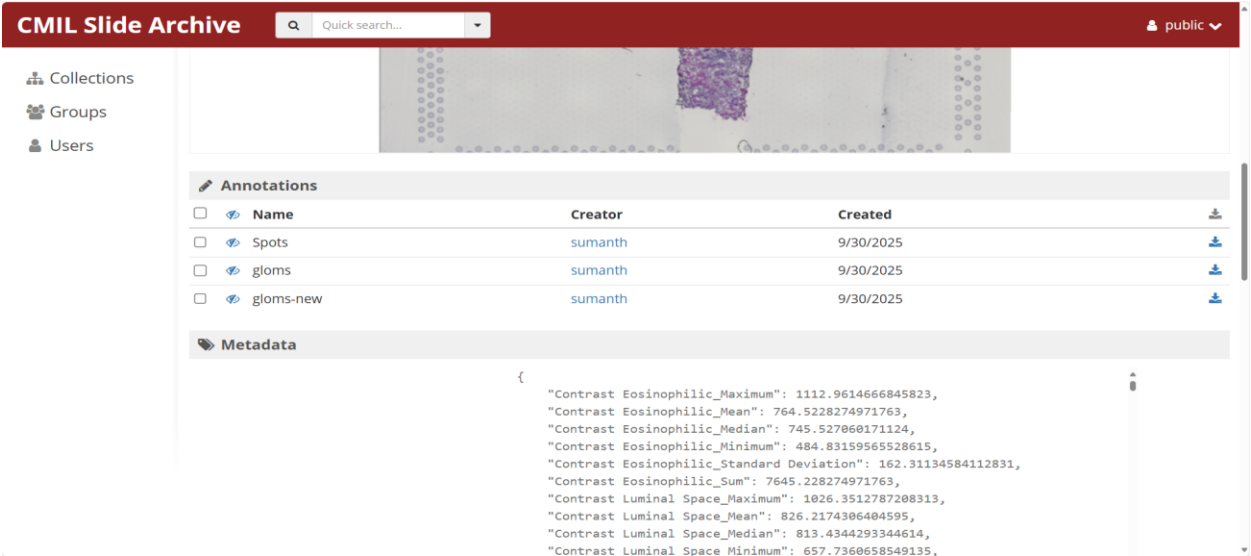


A User can access the [Digital Slide Archive](https://athena.rc.ufl.edu/) (DSA; <https://athena.rc.ufl.edu/>) by logging in as a public user with the following credentials: **Username:** public; **password:** public. The Whole Slide Images (WSIs) can be found under the path: **Collections → Human Kidney Atlas v2 → Visium → Visium Frozen** (see Supp. Fig. 1). After navigating to the directory, selecting a WSI and clicking on its file name opens a dedicated page where the image is displayed along with its associated computational annotations (in JSON format) and image metadata, available under the Annotations and Metadata sections, respectively (see Supp. Fig. 2). To interactively view the WSI, click the **"Open in HistomicsUI"** button located at the top right of the page (see Supp. Fig. 3). In the HistomicsUI viewer, users can zoom in and out, navigate across the slide, and hover over different regions to examine various structures in fine detail.

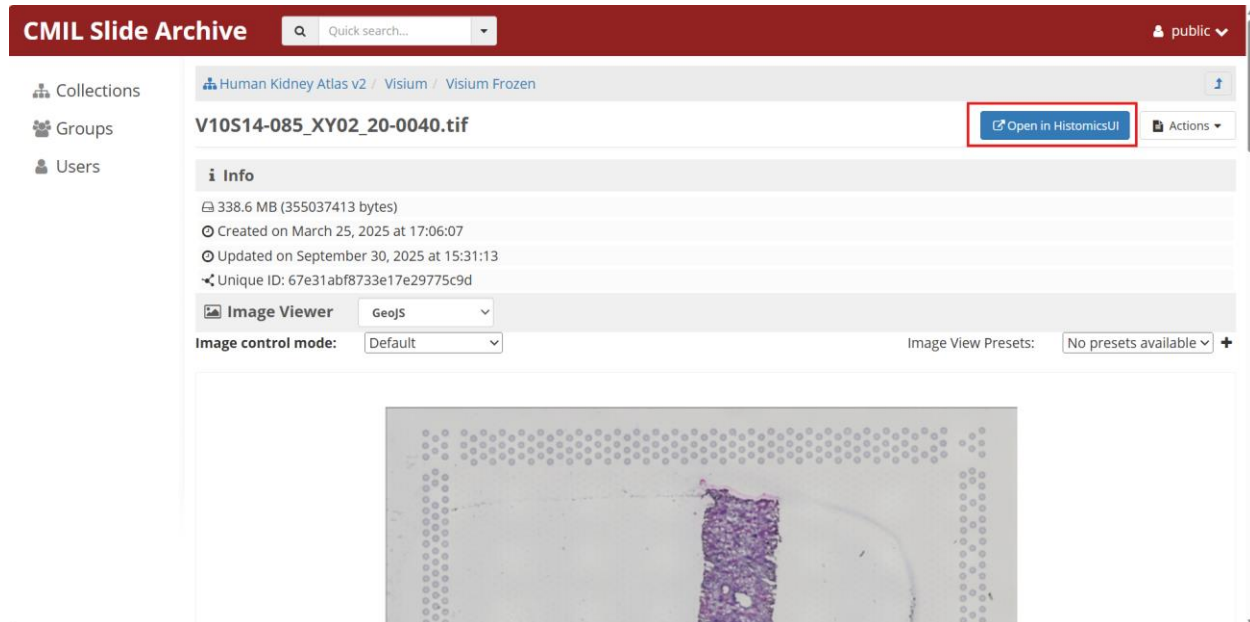


Supp. Fig. 1. DSA interface showing the directory path to WSIs located under Collections → Human Kidney Atlas v2 → Visium → Visium Frozen.



Supp. Fig. 2. Upon opening a WSI in a separate page, the associated computational

segmentation data (downloadable in JSON format) and corresponding non-clinical metadata are accessible from the same interface.



Supp. Fig. 3. The WSI can be viewed in HistomicsUI (a plugin for visualizing large-scale image data in the cloud via DSA) by clicking the “Open in HistomicsUI” button.

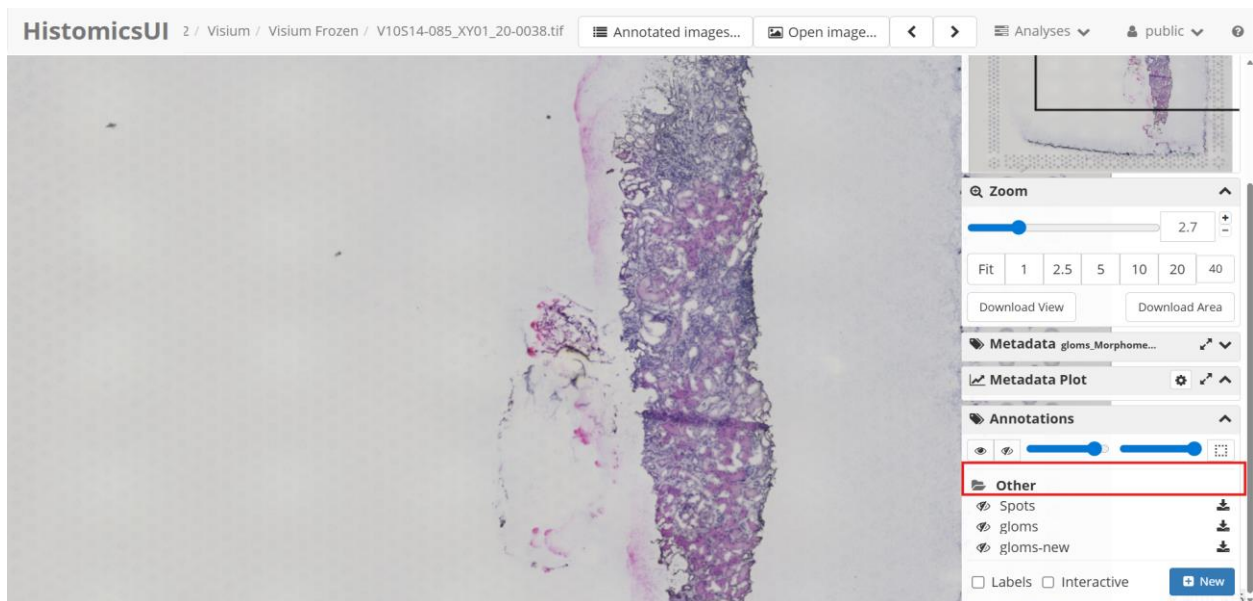
To visualize the computational annotations, the user can click the “**Other**” button under the *Annotations* tab, which expands to display three annotation files in JSON format (see Supp. Fig. 4). Each annotation is listed with an **eye icon** next to its name; clicking this icon overlays the corresponding annotation boundaries on the WSI. For instance, when the *Spots* annotation is activated, the spatial spots become visible on the WSI (see Supp. Fig. 5), and users can zoom in to explore each structure in greater detail. It is important to note that, since these annotations are rendered in the cloud for scalable visualization, loading may take a few seconds depending on the server response time.

There are three available annotations: **Spots**, **Gloms**, and **Gloms-new**.

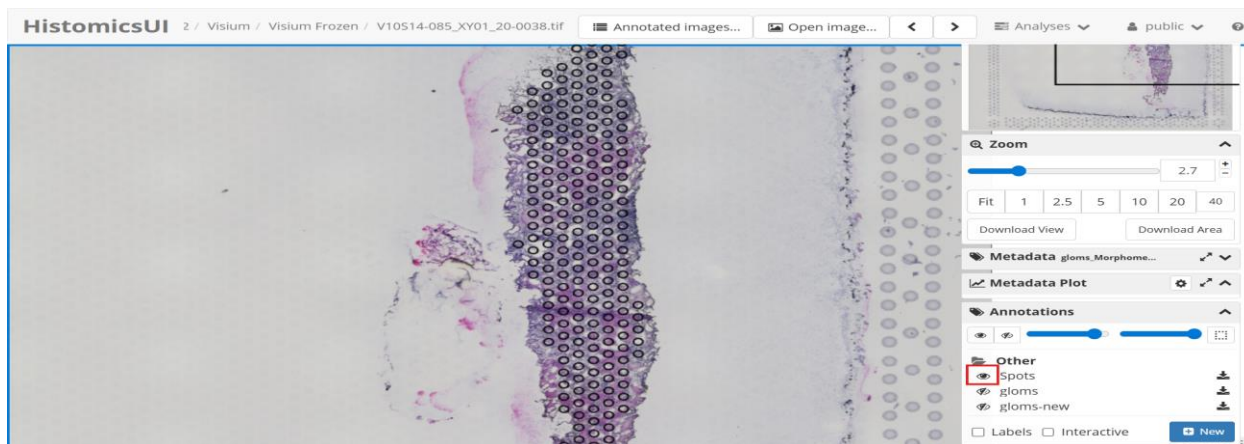
- The **Spots** annotation represents spatial transcriptomics spots, each containing cell-type composition information derived from transcriptomic data.
- The **Gloms** annotation corresponds to the segmented glomerular regions identified directly on the tissue.
- The **Gloms-new** annotation includes the same glomerular boundaries as **Gloms**, but with additional cell-type composition information that has been **spatially aggregated** from the surrounding *Spots* annotations. This integration was

performed using the *Spatial Aggregation* plugin, enabling visualization of cell-type distributions within individual glomeruli.

In addition to cell-type composition information, a set of **72 quantitative morphometric and intensity-based features** is extracted for each annotated structure using the *Expanded Granular Feature Extraction* plugin. These features capture detailed histomorphometric properties such as **object size, shape, color intensity, texture, and spatial organization** of tissue components including nuclei, eosinophilic regions, and luminal spaces. Together, these measurements provide a comprehensive representation of both **molecular and morphological characteristics** of each glomerulus or spot, facilitating downstream analyses and visualization.



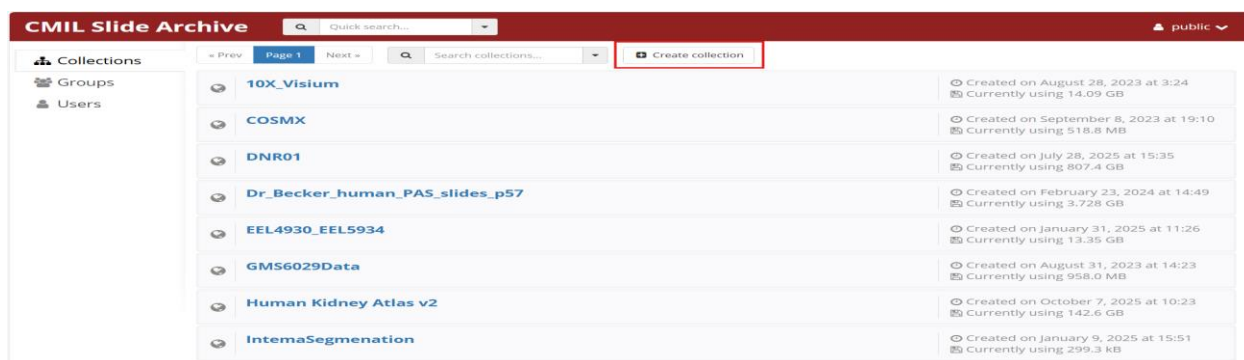
Supp. Fig. 4. Annotations tab in the DSA interface showing the “Other” button expanded to reveal three available annotation files in JSON format.



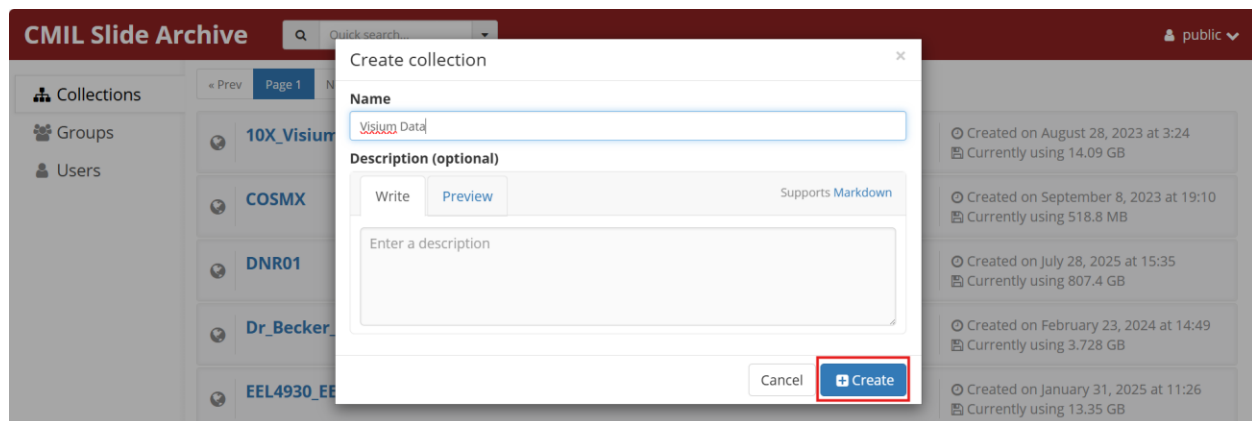
Supp. Fig. 5. Visualization of spatial spot annotations overlaid on the WSI after activating the **Spots** layer; users can zoom in to examine individual structures in detail.

If the user wishes to upload their own data, they can create a new collection by selecting **“Collections”** from the menu on the left in DSA interface, clicking the **“Create Collection”** button (see Supp. Fig. 6), and entering the desired name for the collection (see Supp. Fig. 7). Once created, Whole Slide Images (WSIs) can be uploaded to the collection in either **.svs** or **.tiff** format.

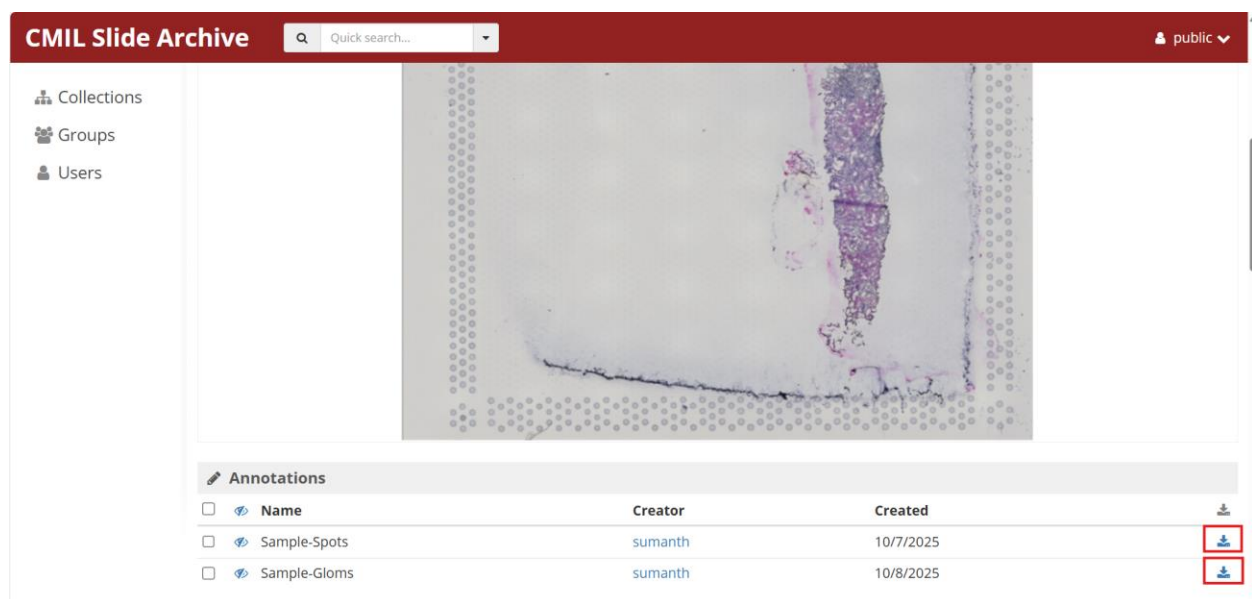
Each uploaded WSI should be associated with **spot and glom annotations**, which should follow a specific JSON structure to ensure compatibility with the visualization tools. To review the required format, users can visit this [image](#) and download the sample annotations by clicking on the download icon under the Annotations section (see Supp. Fig. 8). Each spot in the annotation should include cell-type information and related metadata consistent with the structure illustrated in the sample annotation.



Supp. Fig. 6. Creating a new collection in the Digital Slide Archive (DSA) by selecting **“Collections”** from the left menu and clicking the **“Create Collection”** button.



Supp. Fig. 7. Interface for specifying the name and details of the newly created collection in the DSA before uploading Whole Slide Images (WSIs).



Supp. Fig. 8. Example WSI in the DSA interface showing downloadable sample annotation files under the *Annotations* section, which illustrate the required JSON structure for spot and glom annotations.