

## Vignette Type: Experimental Design (w/Optional Coding)

### Specific Example: Whole Human Brain

User:

Career: Undergraduate Students | Graduate Students | **Post-Docs** | **Senior Scientists/PI** | Teachers

Experience of Cell Types: Novice | Advanced Beginner | **Intermediate** | Expert

Research: Basic | **Translational**

Research Type: **Computational** | **Molecular** | Behavior

Experimental Model: Mouse | Rat | Non-Human Primate | **Human** | Invertebrate | Non-Traditional Vertebrate

A researcher studies the role of astrocytes in the development of multiple sclerosis (M.S.), using postmortem spinal cord samples from humans with and without M.S. They are beginning to design studies for experiments in other commonly affected brain areas, such as the cerebellum. Therefore, they are interested in learning more about astrocyte diversity in other brain areas in the non-M.S. brain.

1. To view the non-neuronal nuclei in the dataset, the researcher clicks on the “Current Views” tab (step 1), clicks on the arrow next to “Dataset” (step 2) and clicks on “Non-Neuronal Cells” (step 3) under “Human brain cellular diversity”. [Link to view in ABC Atlas](#)

The screenshot displays the Brain Knowledge Platform interface. The top navigation bar includes 'ABC Atlas', 'Brain Knowledge Platform', and a 'SIGN IN' button. The main interface is divided into several panels:

- MANAGE LAYOUT:** A sidebar on the left with a 'Current Views' tab (1 out of 4) highlighted by a red box and a red arrow labeled '1'. Below it, a visualization titled 'Non-Neuronal Cells' is shown, with a red arrow labeled '3' pointing to the 'Human brain cell type diversity' entry.
- Edit Panel:** A central panel titled 'Edit' showing a list of datasets. The 'Non-Neuronal Cells' dataset (888k) is selected, with a red arrow labeled '2' pointing to the 'Dataset' dropdown menu. Below the list, there are controls for 'POINT SIZE' (Small, Medium, Large) and 'Low / Fast' vs 'High / Slow'.
- Visualization:** A scatter plot on the right side of the interface showing various cell types represented by colored points.

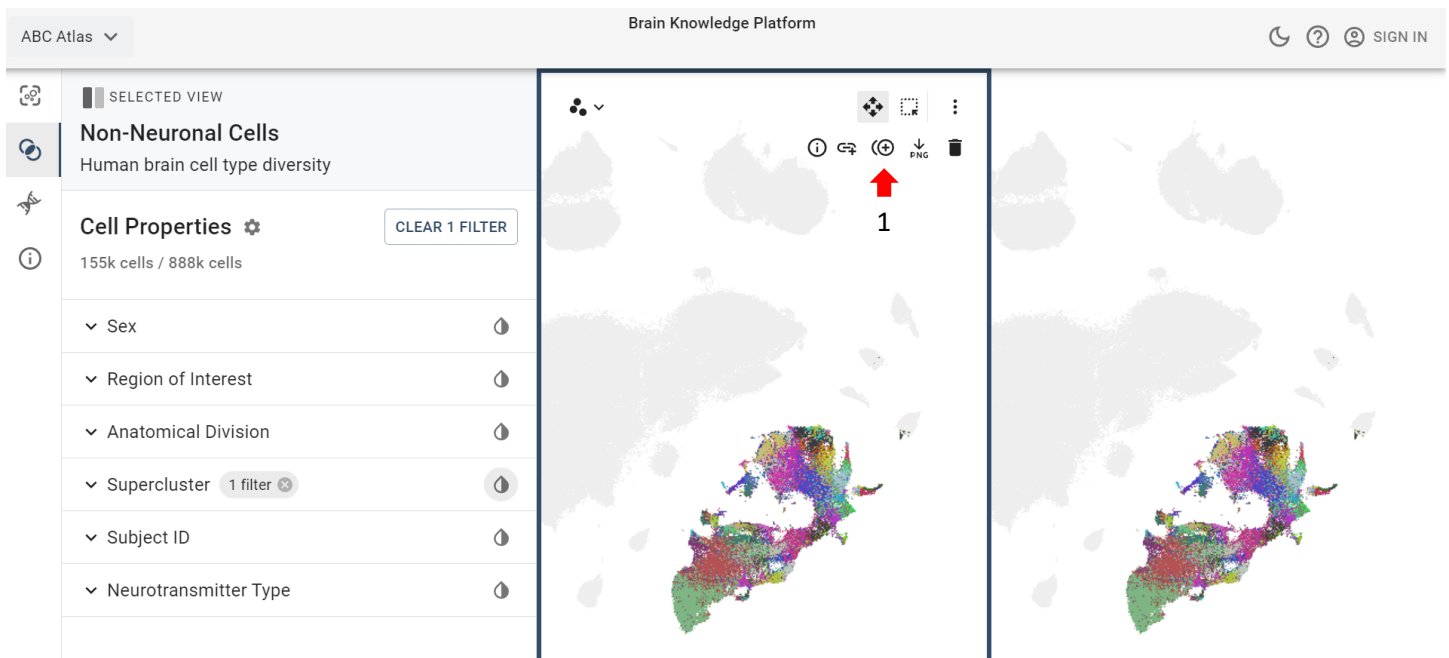
2. To select only astrocytes, the researcher clicks on the “Cell Properties” tab (step 1), then clicks on the arrow next to “Supercluster” and checks the box next to “Astrocyte” (step 2). [Link to view in ABC Atlas](#)

The screenshot shows the ABC Atlas Brain Knowledge Platform interface. The left sidebar is titled "Non-Neuronal Cells" and "Human brain cell type diversity". The "Cell Properties" tab is selected and highlighted with a red box. Below it, the "Supercluster" section is expanded, showing a list of cell types with checkboxes and counts. The "Astrocyte" supercluster is checked and highlighted with a red arrow labeled "2". A red arrow labeled "1" points to the "Cell Properties" tab. The main panel displays a brain map with a purple region highlighted, representing the selected astrocytes.

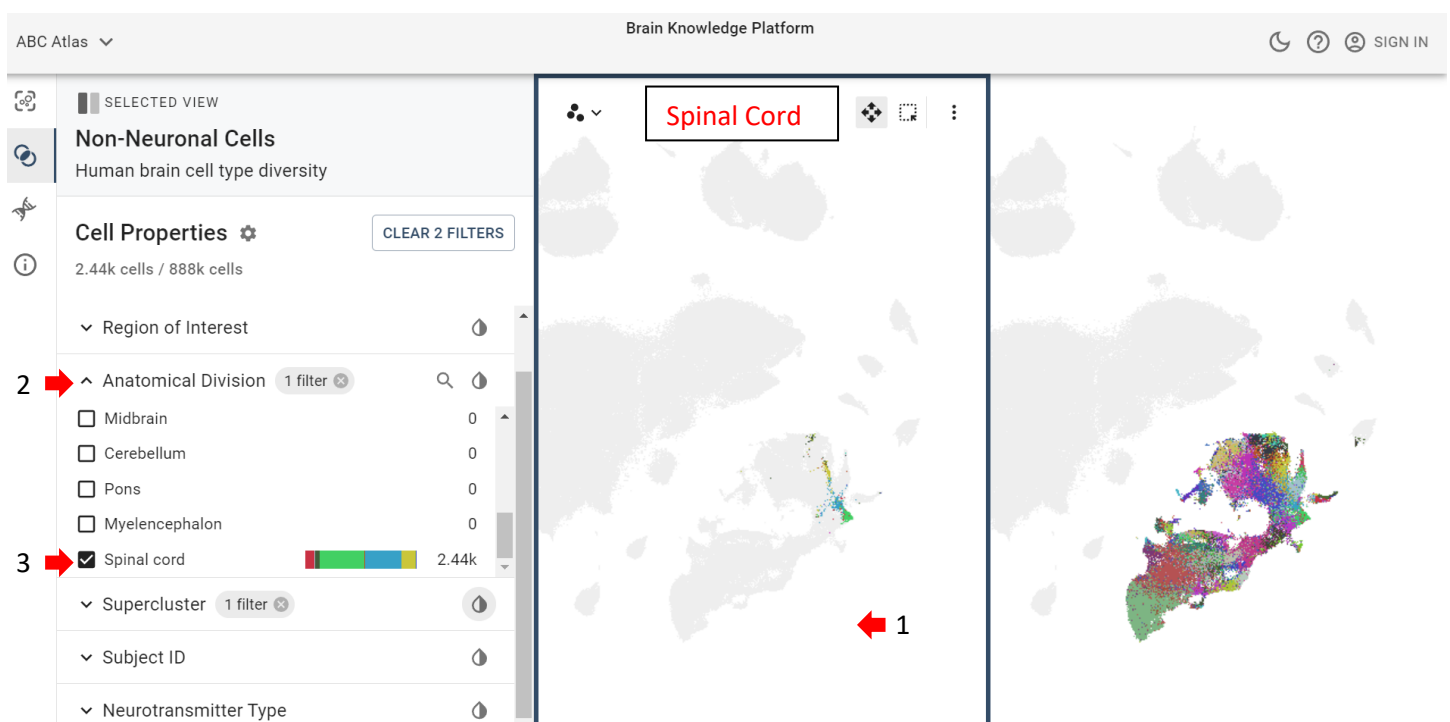
3. To view the subclusters within the Astrocyte supercluster, the researcher clicks on the ink drop symbol (step 1) next to “Supercluster” and clicks on “Subcluster” on the pop-up menu (step 2). [Link to view in ABC Atlas](#)

The screenshot shows the ABC Atlas Brain Knowledge Platform interface. The left sidebar is titled "Non-Neuronal Cells" and "Human brain cell type diversity". The "Cell Properties" tab is selected. The "Supercluster" section is expanded, showing a list of cell types with checkboxes and counts. The "Astrocyte" supercluster is checked and highlighted with a red arrow labeled "2". A red arrow labeled "1" points to the ink drop symbol next to the "Astrocyte" supercluster. A pop-up menu is open, showing options: "Color By", "Supercluster", "Cluster", and "Subcluster". The "Subcluster" option is highlighted with a red arrow labeled "2". The main panel displays a brain map with a multi-colored region highlighted, representing the selected subclusters within the astrocyte supercluster.

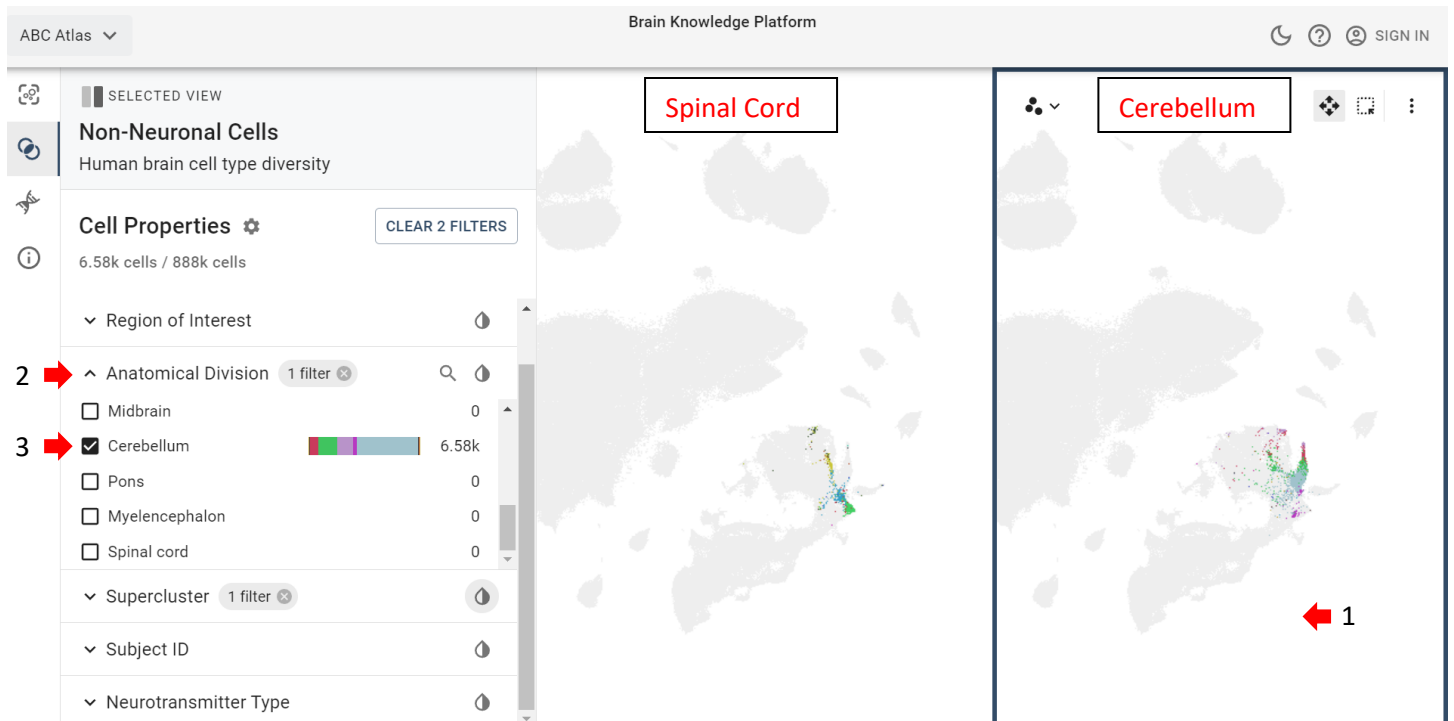
4. To duplicate the view and look at two t-SNE plots at once, the researcher clicks the “Duplicate View” button (step 1). [Link to view in ABC Atlas](#)



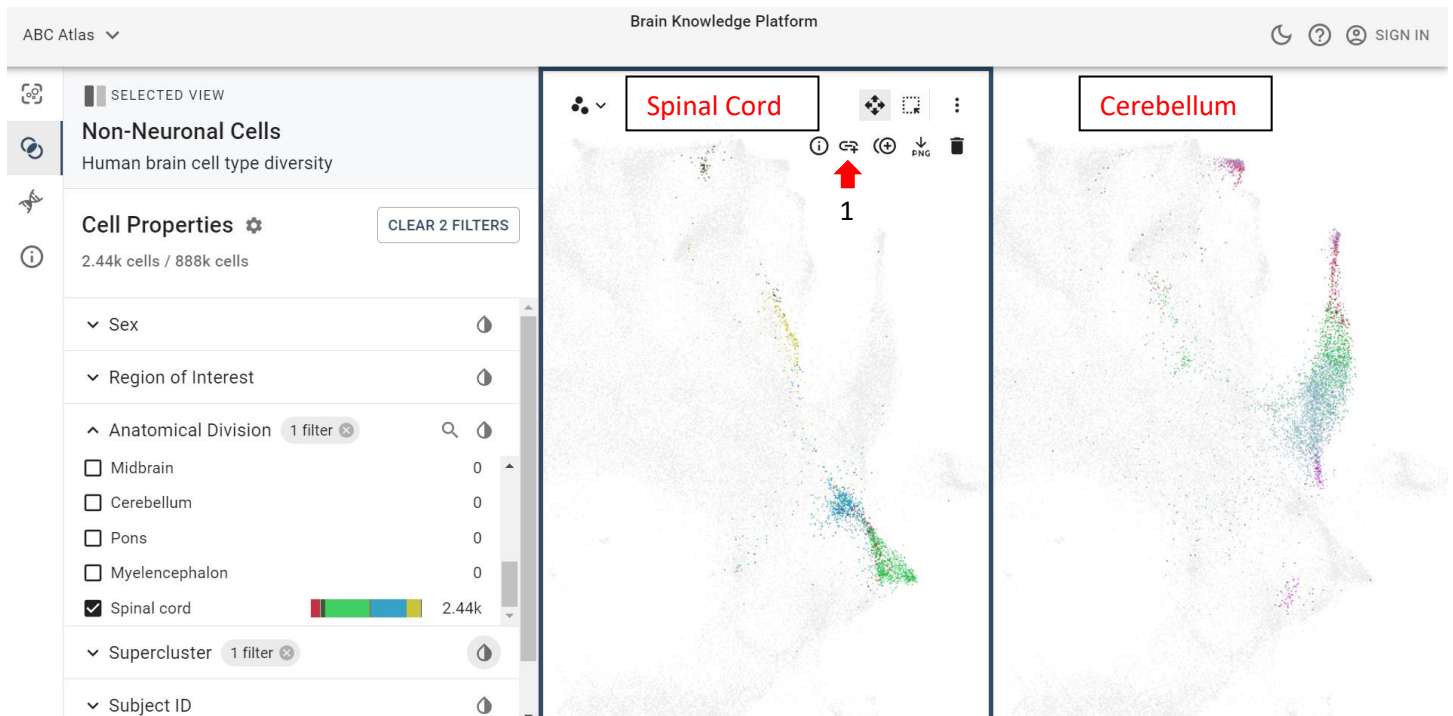
5. To look at just the spinal cord in the lefthand t-SNE, the researcher clicks on the lefthand t-SNE (step 1), clicks on the arrow next to “Anatomical Division” (step 2), and checks the box next to “Spinal cord” (step 3). [Link to view in ABC Atlas](#)



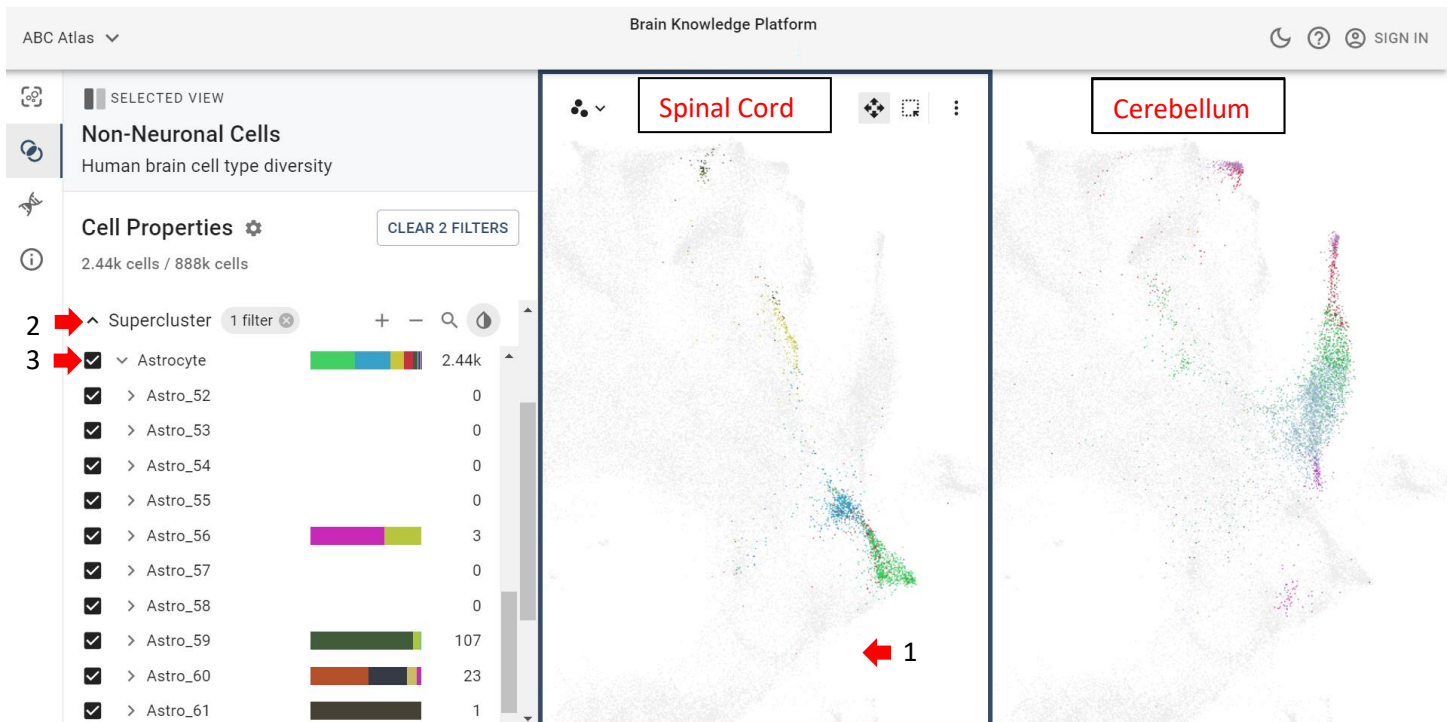
6. To look at just the cerebellum in the righthand t-SNE, the researcher clicks on the righthand t-SNE (step 1), clicks on the arrow next to “Anatomical Division” (step 2), and checks the box next to “Cerebellum” (step 3). [Link to view in ABC Atlas](#)



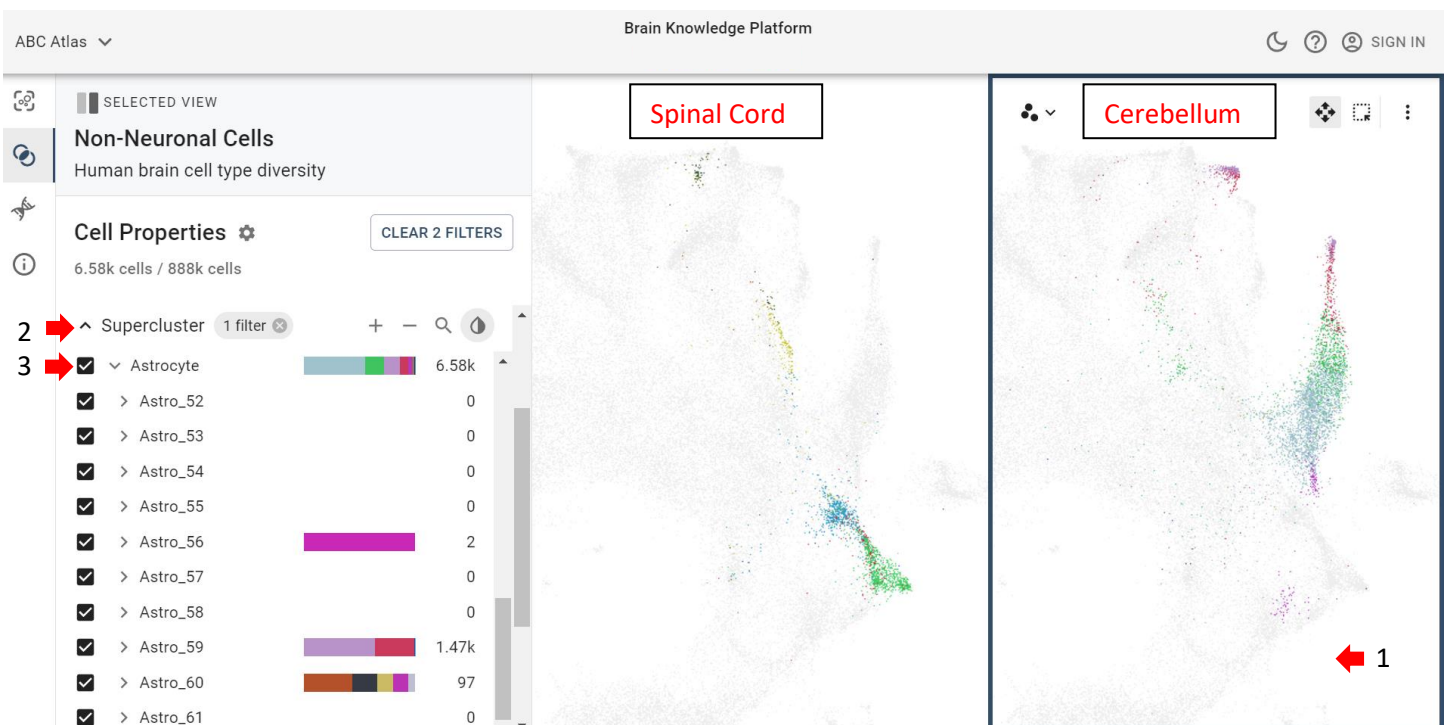
7. To zoom in on both t-SNE plots at the same time, the researcher clicks the “Enable Zoom & Pan Sync” button (accessible by clicking on the three dots) on both t-SNE plots to link them together (step 1) and then zooms in by scrolling their mouse. [Link to view in ABC Atlas](#)



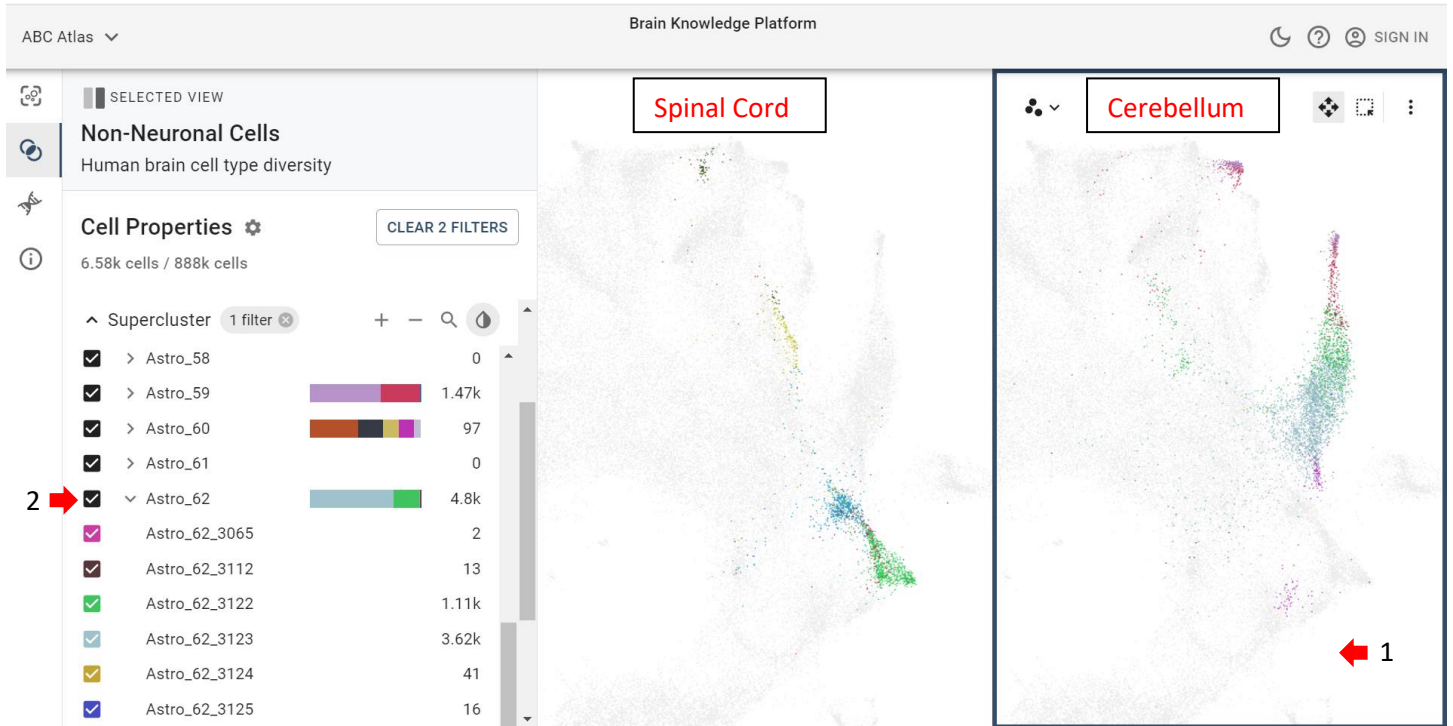
- To view the clusters within the “Astrocyte” supercluster in the spinal cord, the researcher clicks on the lefthand t-SNE (step 1), clicks on the arrow next to Supercluster (step 2), then clicks on the arrow next to “Astrocyte” (step 3) to reveal the clusters. [Link to view in ABC Atlas](#)



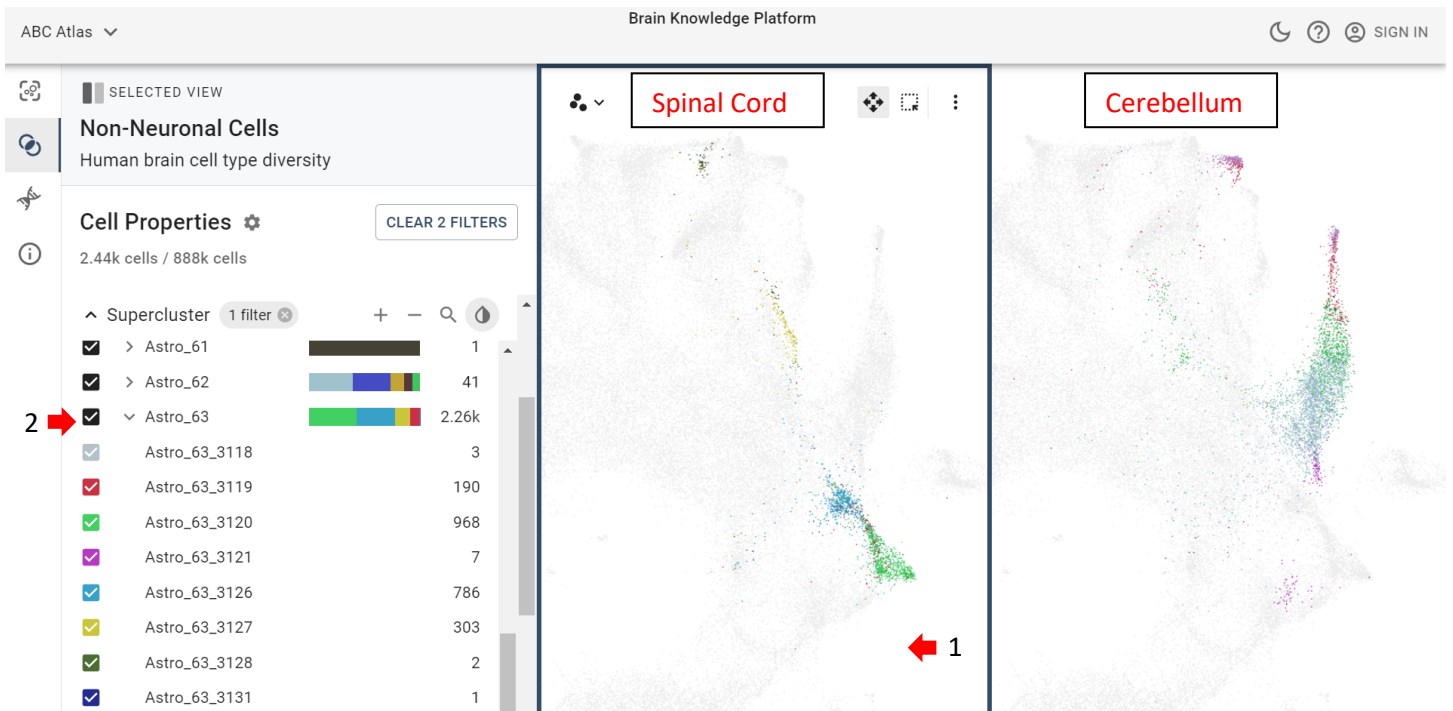
- To view the clusters within the “Astrocyte” supercluster in the cerebellum, the researcher clicks on the righthand t-SNE (step 1), then click on the arrow next to Supercluster (step 2), then clicks on the arrow next to “Astrocyte” (step 3) to reveal the clusters. [Link to view in ABC Atlas](#)



10. When looking at the cerebellum astrocyte clusters in step 9, the researcher notices that the majority of nuclei (4.8k) belong to the Astro\_62 cluster. To learn more about the Astro\_62 cluster, the researcher clicks on the righthand t-SNE (step 1), then clicks on the arrow next to Astro\_62 (step 2) to reveal the subclusters within the Astro\_62 cluster. Here the researcher sees that the majority of the nuclei (3.62k) belong to the Astro\_62\_3123 subcluster. [Link to view in ABC Atlas](#)



11. When looking at the spinal cord astrocyte clusters in step 8, the researcher notices that the majority of nuclei (2.26k) belong to the Astro\_63 cluster. To learn more about the Astro\_63 cluster, the researcher first clicks on the lefthand t-SNE (step 1), then clicks the arrow next to Astro\_63 (step 2) to reveal the subclusters within the Astro\_63 cluster. Here the researcher sees that the majority of the nuclei (968) belong to the Astro\_63\_3120 subcluster. [Link to view in ABC Atlas](#)



12. To learn more about the subcluster Astro\_63\_3120 (found in the spinal cord) and subcluster Astro\_62\_3123 (found in the cerebellum), the researcher goes to the [subcluster annotation table](#) to find the marker genes for these subclusters. In the table, the researcher finds the marker genes 'LINC01094' 'CD44' 'GFAP' 'ID3' 'APLNR' 'AL096709.1' 'AL627316.1' 'HSPB8' 'AC012405.1' 'FOS' for Astro\_63\_3120 and marker genes 'CPAMD8' 'GFAP' 'AC012405.1' 'AL627316.1' 'AC073941.1' 'CD44' 'AC097450.1' 'SLC14A1' 'PAX3' 'TNC' for Astro\_62\_3123.
13. After finding marker genes from the subcluster annotation table, the researcher decides to compare the expression of these genes across the two subcluster populations. The researcher does this by accessing the [WHB Jupyter Notebooks](#), and running the “Getting started” notebook. Afterwards, they click on “Accessing 10x RNA-seq gene expression data” notebook (step 1), scroll to “loading specific genes from the data,” and replace the example gene names listed with the subcluster marker genes (step 2.) Then they combine with the “getting started” notebook and run the cells. Since the researcher is looking at non-neuronal data, they only need to download the non-neuron dataset.

The screenshot shows the Allen Institute Jupyter Notebook interface. On the left, the navigation pane highlights the notebook "Accessing 10x RNA-seq gene expression data" with a red arrow and the number "1". The main content area shows the notebook's text and code cells.

At the top, there is a table of gene annotations:

ENSG00000288643	AC114982.3	protein_coding	novel transcript
ENSG00000288645	AC084756.2	protein_coding	novel protein

Below the table, it says "59357 rows x 3 columns".

The notebook content includes a section titled "Loading specific genes from the data". The text explains that the Whole Human Brain dataset consists of Neuron cells and Non-neuron cells, and that the data is loaded in chunks to avoid memory issues. It then specifies a set of genes to load:

```
gene_names = ['SLC17A6', 'SLC17A7', 'SLC32A1', 'PTPRC', 'PLP1', 'AQP4', 'TTR']
```

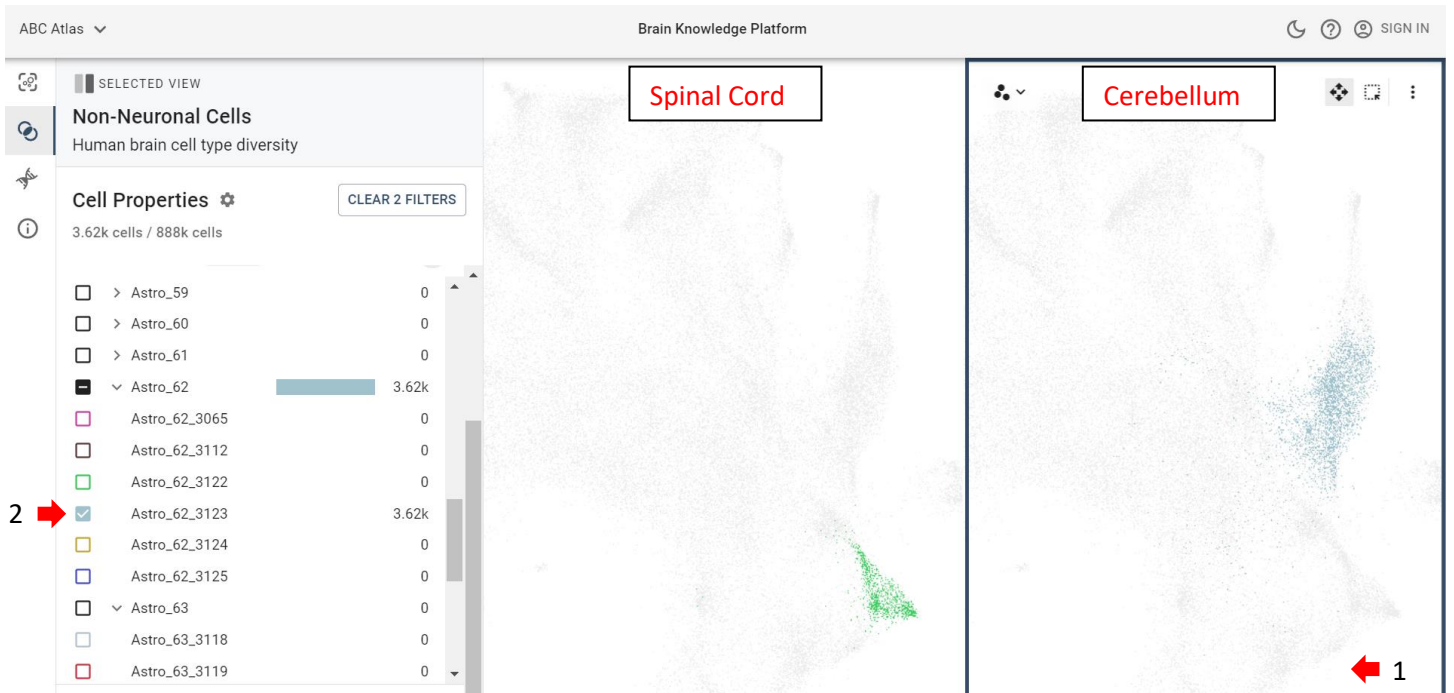
A red arrow and the number "2" point to this code cell, indicating the step where the example gene names are replaced with the subcluster marker genes.

14. To compare gene expression across subclusters, the researcher clicks on the “Whole Human Brain 10x RNA-seq gene expression” tab under notebooks and clicks on “part 2.” Next, they change “example\_cells\_with\_genes” to “gene\_data” to use the genes they typed in for step 13, then combine with the notebook in the previous step and run the cells.

15. After looking at the heatmaps of 'LINC01094' 'CD44' 'GFAP' 'ID3' 'APLNR' 'AL096709.1' 'AL627316.1' 'HSPB8' 'AC012405.1' 'FOS' and 'CPAMD8' 'GFAP' 'AC012405.1' 'AL627316.1' 'AC073941.1' 'CD44' 'AC097450.1' 'SLC14A1' 'PAX3' 'TNC', the researcher sees that *PAX3* has higher expression in Astro\_62\_3123 than Astro\_63\_3120.


16. To isolate individual subclusters in the t-SNEs, the researcher then filters the lefthand spinal cord t-SNE by the Astro\_63\_3120 subcluster and the righthand cerebellum t-SNE by the Astro\_62\_3123 subcluster by clicking on the respective t-SNE plots (step 1) and then checking only those boxes under the “Supercluster” tab (step 2).

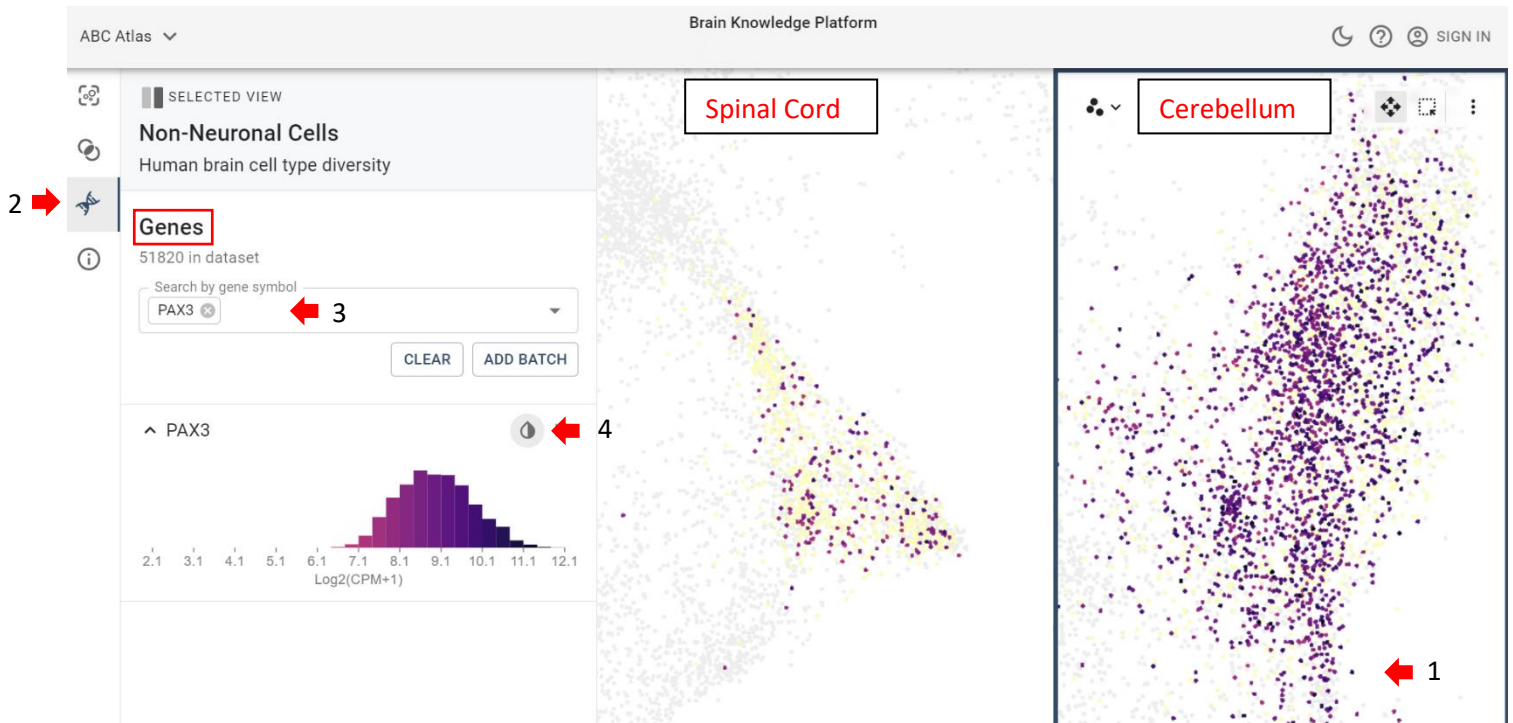
[Link to view in ABC Atlas](#)





17. To color the Astro\_63\_3120 (spinal cord t-SNE) and Astro\_62\_3123 (cerebellum t-SNE) subclusters by the *PAX3* gene, the researcher clicks on a t-SNE plot (step 1), clicks on the “Genes” tab (step 2), types in “PAX3” (step 3), and clicks on the ink drop symbol (step 4), and then repeats these steps with the second t-SNE plot.

The researcher then zooms in on the two t-SNE plots individually by undoing the pan and zoom feature by clicking on the “Enable Zoom & Pan Sync”  symbol (accessible by clicking the three dots in the upper right corner) on both of the t-SNE plots, and scrolls on each plot with their mouse to zoom. [Link to view in ABC Atlas](#)



18. Now the researcher begins to design experiments based on their new knowledge of astrocyte diversity in the spinal cord vs. cerebellum.