

This document was created to introduce users to the Allen Brain Cell (ABC) Atlas and to provide an example use case of the tool and how to accomplish it. Last updated August 2025.

Vignette Type: Experimental Design

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

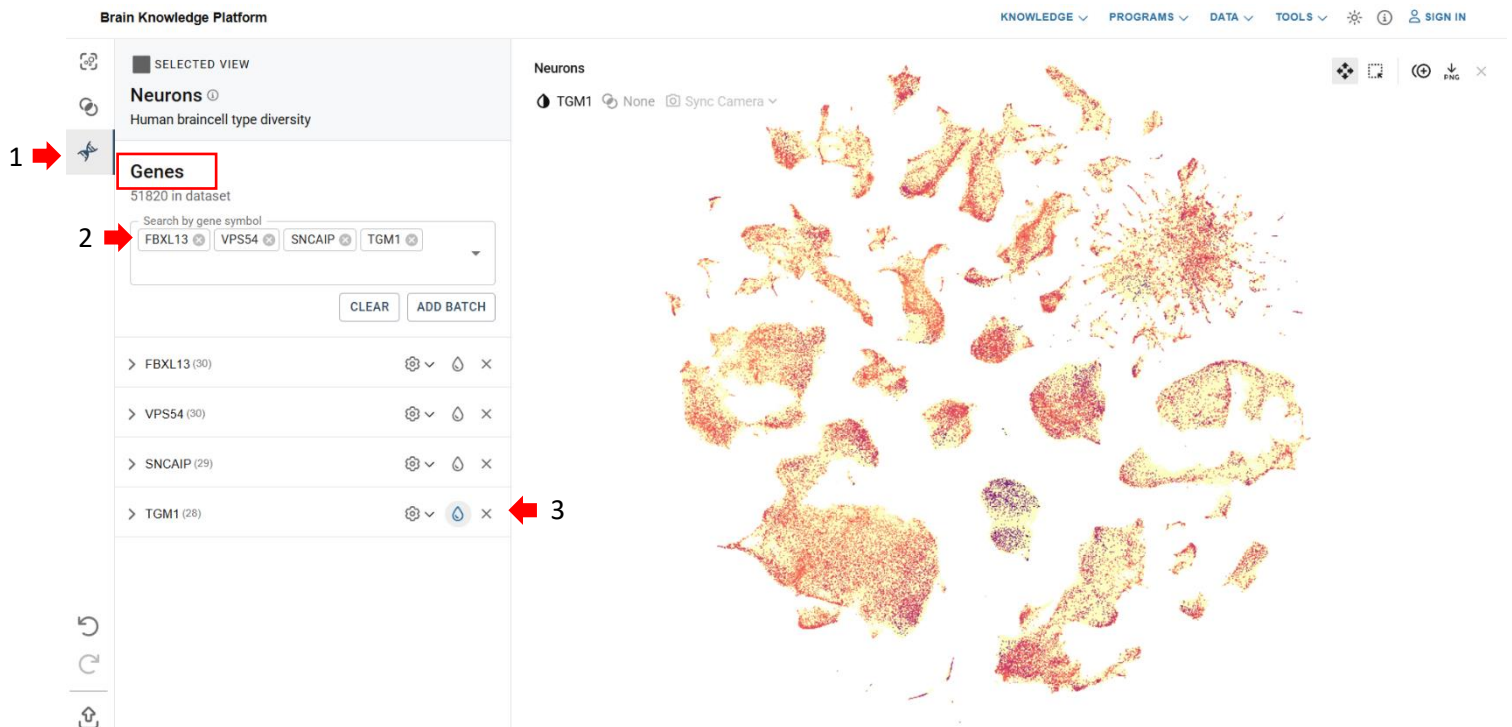
Research: Basic | **Translational**

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

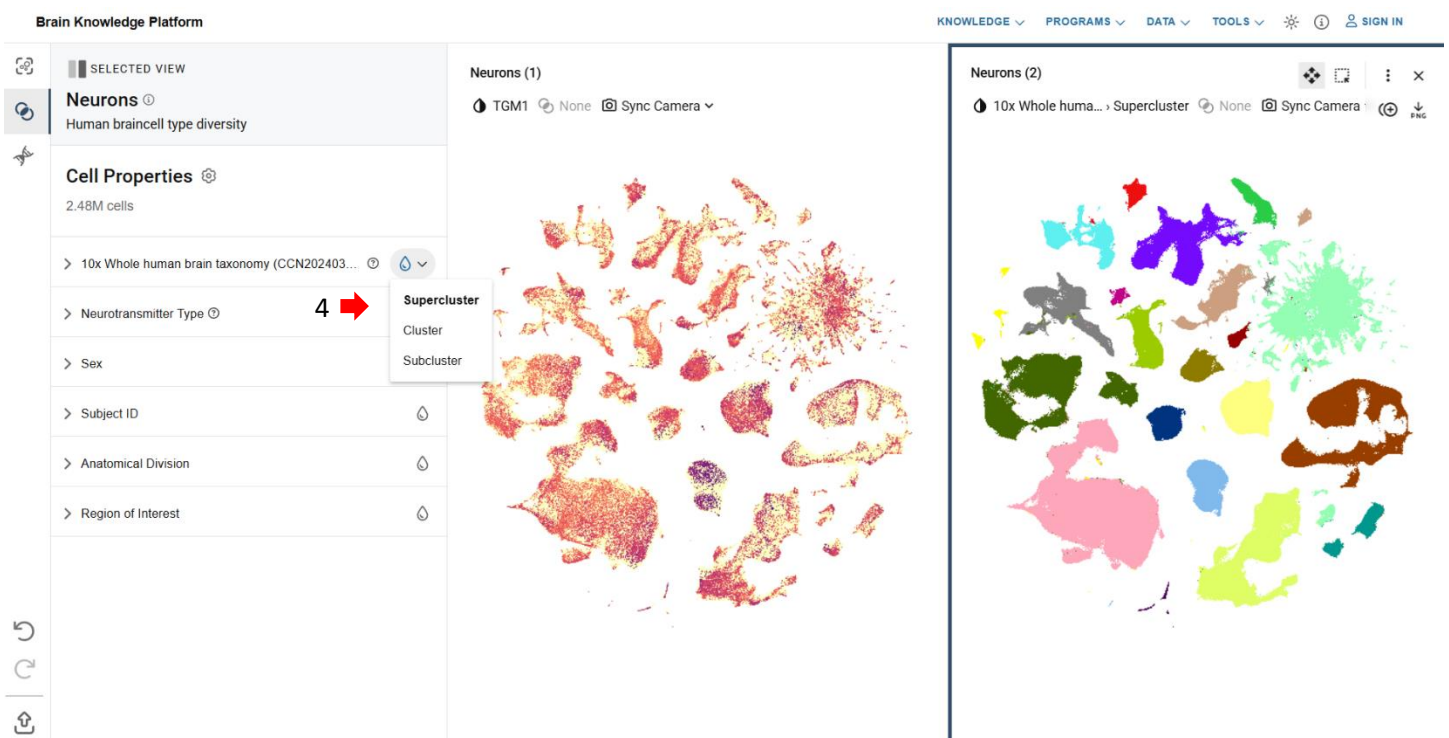
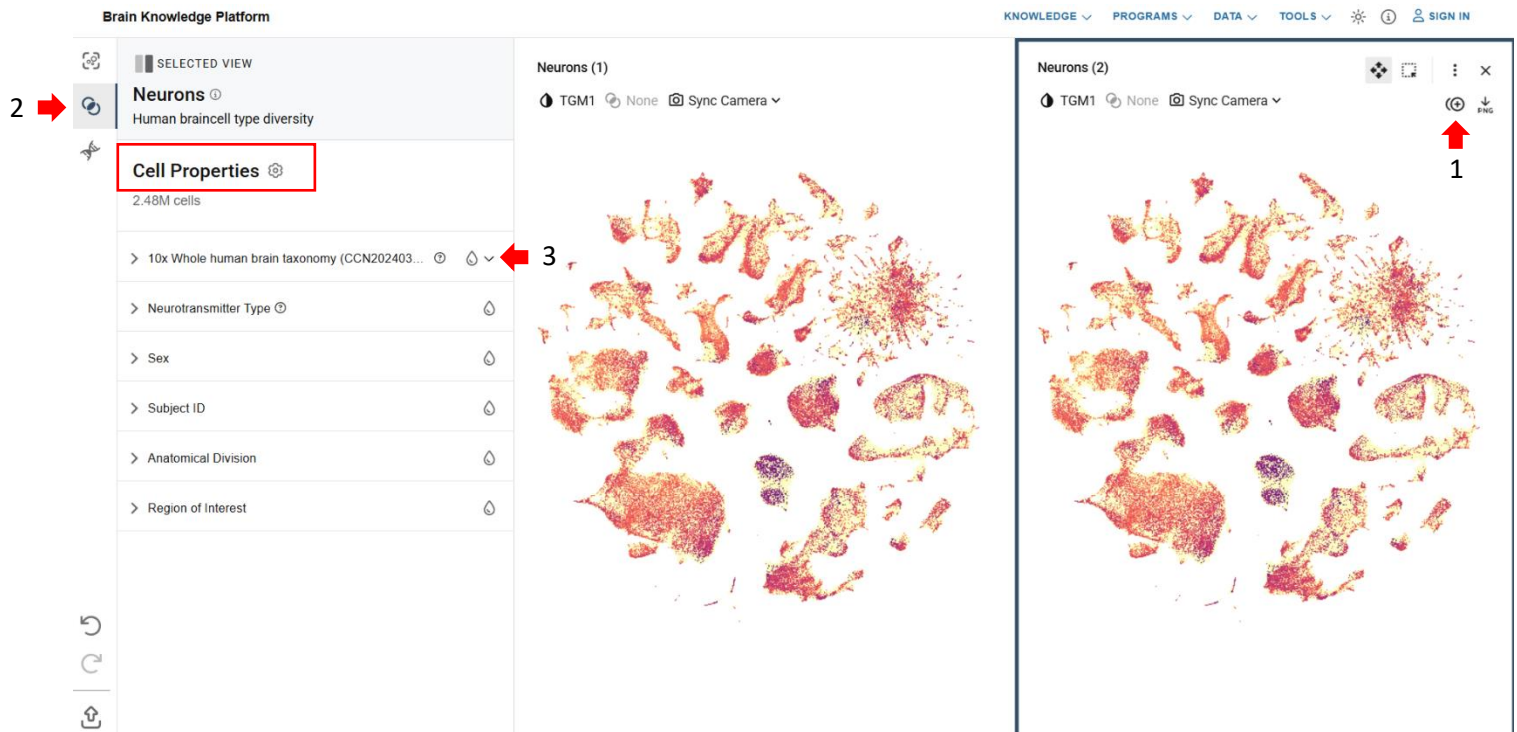
Experimental Model: Mouse | Rat | Non-Human Primate | **Human** | Invertebrate | Non-Traditional Vertebrate

A researcher specializes in studying genes associated with autism spectrum disorder (ASD). While designing experiments for their next grant, they read a paper identifying novel ASD risk genes from a human GWAS study; they are now interested in seeing if these genes are co-expressed in specific human neuron populations and/or brain regions.

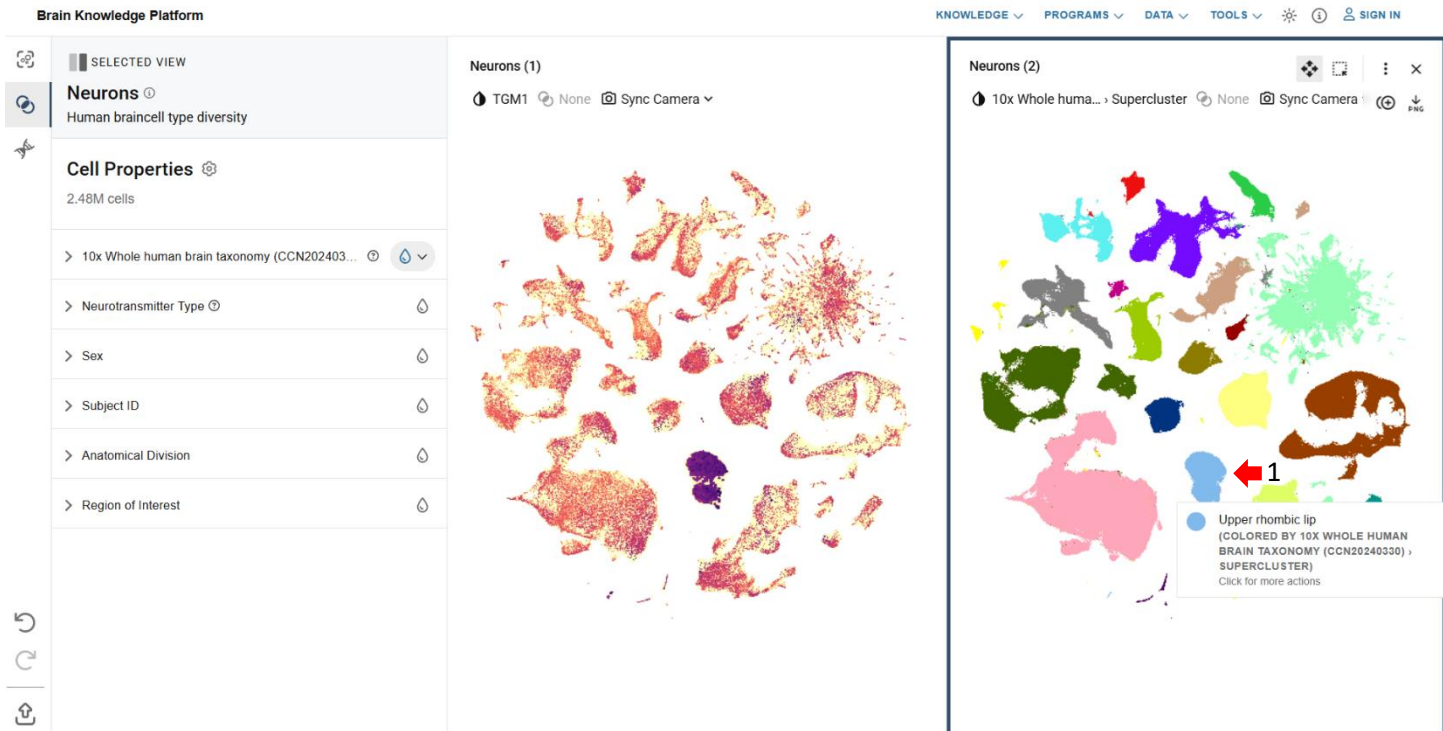
1. To find genes of interest, the researcher clicks on the gene tab (step 1), searches for different genes (step 2), and colors the t-SNE plot for each gene by clicking on the ink drop symbol (step 3). The current plot is colored for *TGM1*. [Link to view in ABC Atlas](#)



- To see which superclusters highly express the gene of interest (*TGM1*), the researcher first duplicates the t-SNE plot by clicking on the “Duplicate View” symbol (step 1). Next, the researcher clicks on the “Cell Properties” tab (step 2). They then color the duplicated plot by superclusters by clicking on the ink drop symbol next to “10x Whole human brain taxonomy” (step 3) and clicking on “Supercluster” in the pop-up menu (step 4). [Link to view in ABC Atlas](#)



- The researcher notices that the highest gene expression (darkest color) is restricted to a specific t-SNE island. To determine which supercluster that is, the researcher hovers their mouse over the plot (step 1) and learns that these cells belong to the “Upper rhombic lip” supercluster. [Link to view in ABC Atlas](#)



4. To isolate nuclei from the upper rhombic lip supercluster, the researcher clicks on the arrow next to “10x Whole human brain taxonomy” (step 1) and checks the “Upper rhombic lip” box (step 2). [Link to view in ABC Atlas](#)

Brain Knowledge Platform

KNOWLEDGE ▾ PROGRAMS ▾ DATA ▾ TOOLS ▾ SIGN IN

SELECTED VIEW

Neurons ⓘ
Human braincell type diversity

Cell Properties ⓘ CLEAR 1 FILTER
137k cells / 2.48M cells

1 → 10x Whole human brain taxon... ⓘ + - 🔍

2 → ☒ > Upper rhombic lip Learn more 137k

☐ > Cerebellar inhibitory 0

☐ > Lower rhombic lip 0

☐ > Oligodendrocyte 0

☐ > Committed oligodendrocyt... 0

☐ > Oligodendrocyte precursor 0

☐ > Astrocyte 0

☐ > Ependymal 0

☐ > Microglia 0

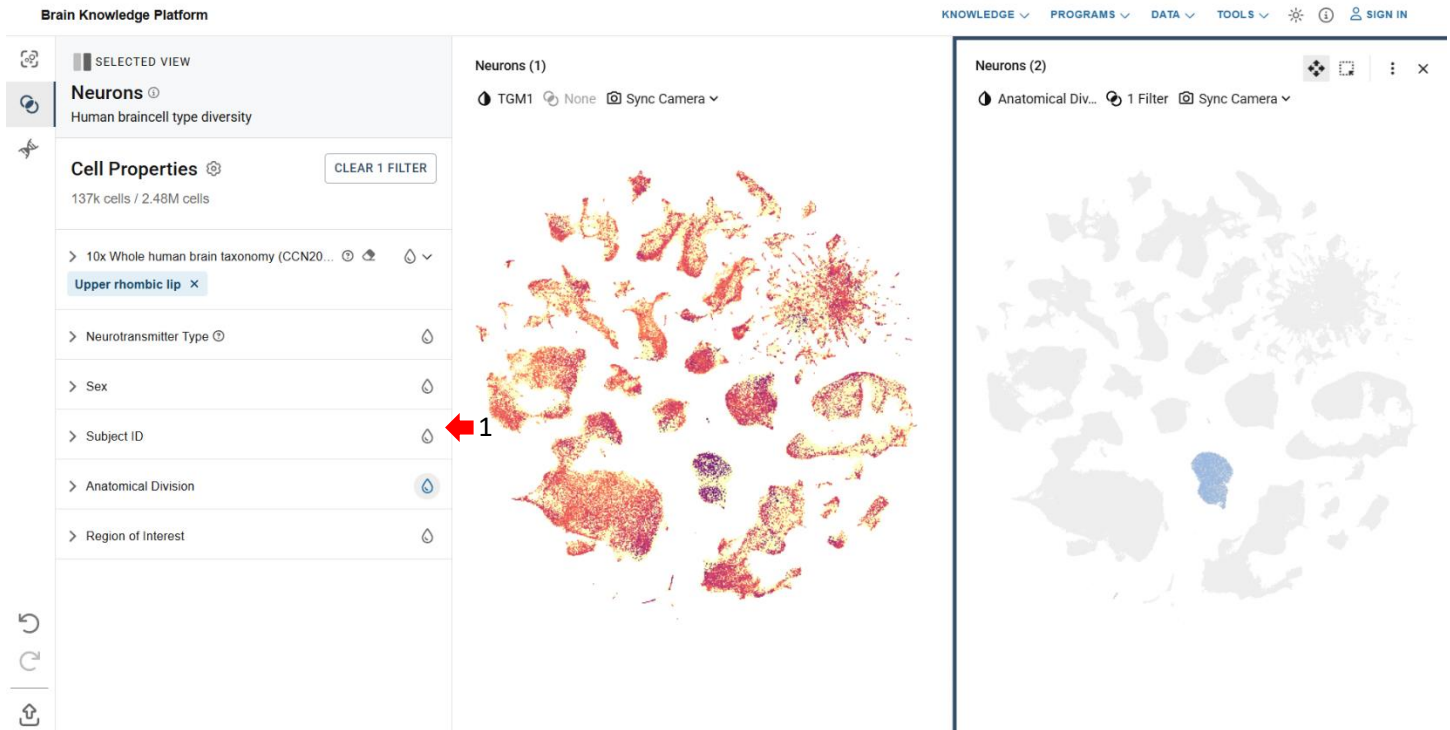
☐ > Vascular 0

> Neurotransmitter Type ⓘ

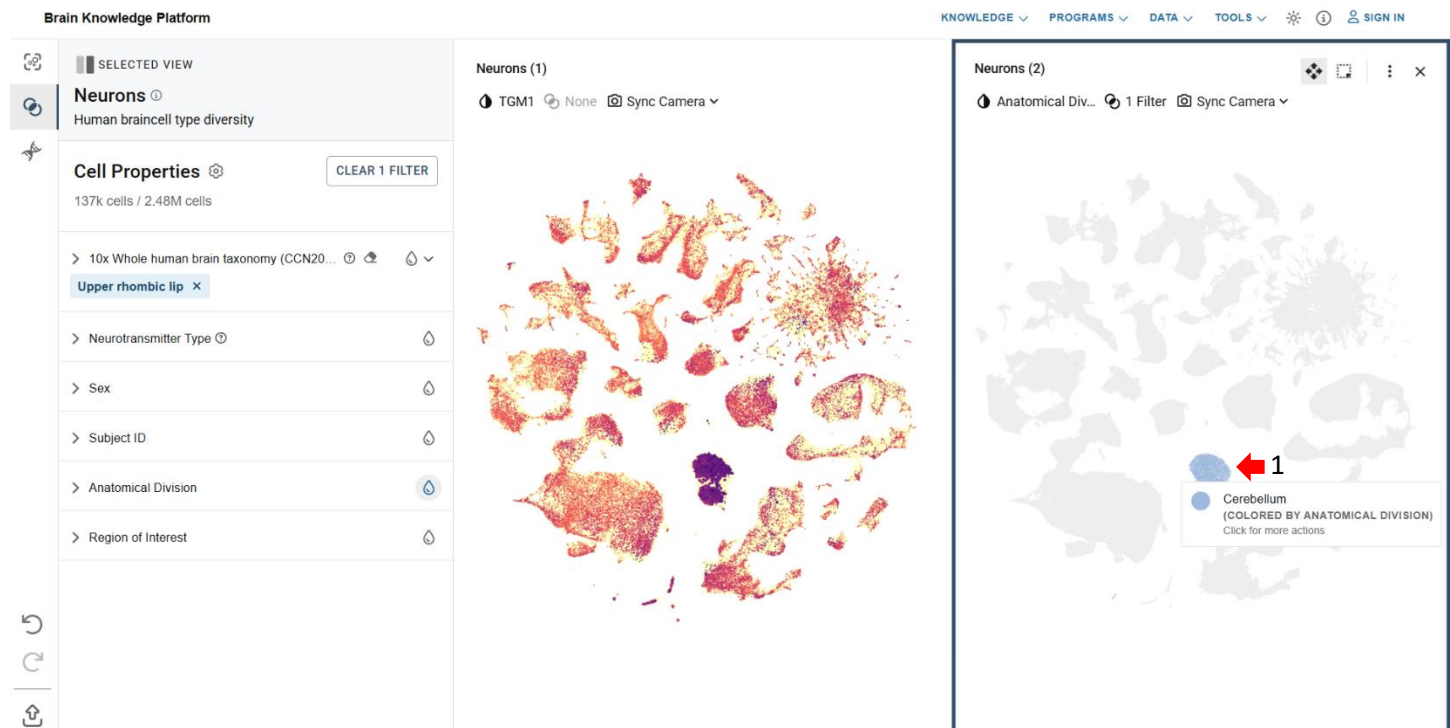
Neurons (1)
TGM1 Sync Camera ▾

Neurons (2)
10x Whole huma... > Supercluster 1 Filter Sync Camera ▾

- To determine which anatomical region the “Upper rhombic lip” supercluster is in, the researcher colors the t-SNE by anatomical division by clicking on the ink drop symbol next to “Anatomical Division” (step 1). [Link to view in ABC Atlas](#)



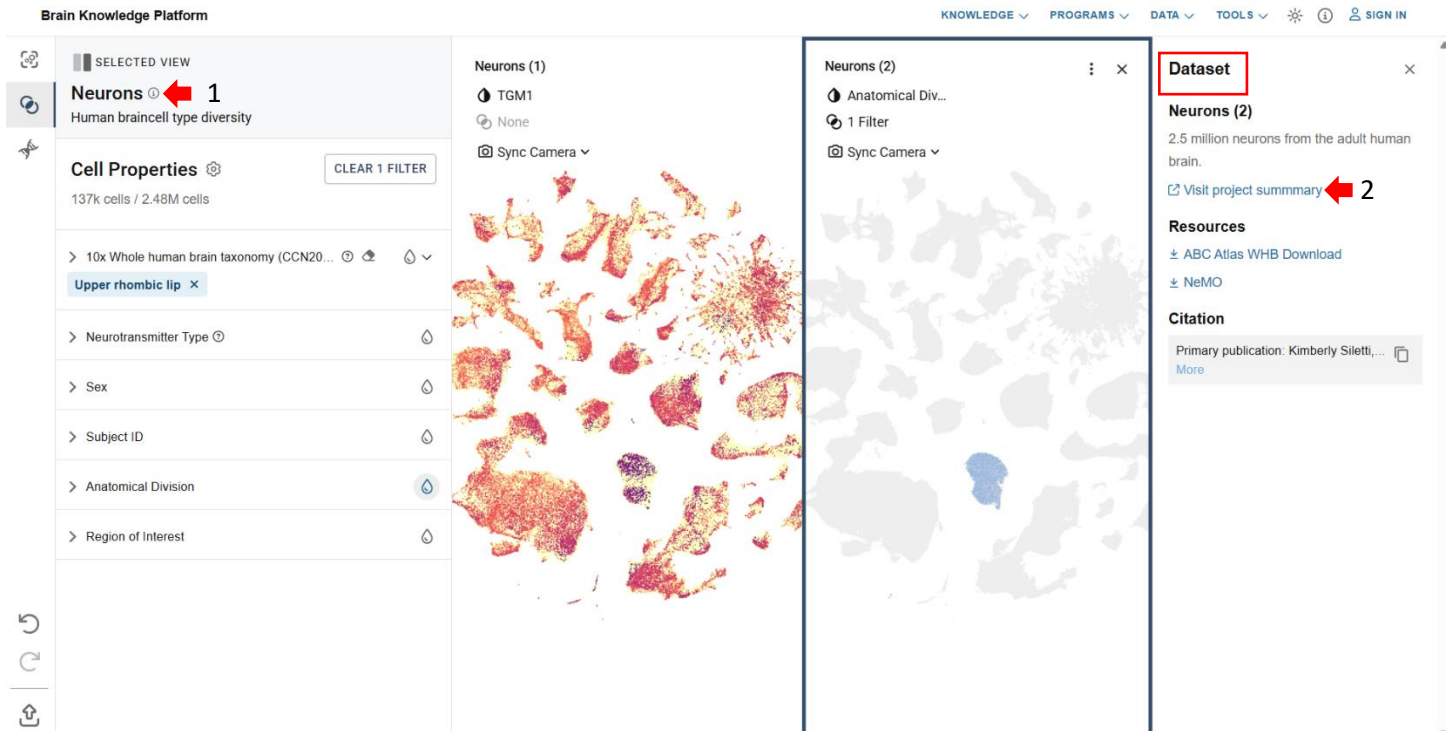
6. Next, the researcher sees that the majority of the “Upper rhombic lip” nuclei are one color (light blue); they hover their mouse over the plot (step 1) and learn that light blue nuclei belong to the cerebellum. [Link to view in ABC Atlas](#)



7. To see if the gene *TGM1* is co-expressed with the other novel ASD markers, the researcher repeats steps 1-7 by coloring the other genes instead.*

*This step can also be done in a Jupyter notebook (see WHB Vignette #3, step 13).

8. After searching through the different genes, the researcher decides to learn more about the “Upper rhombic lip” supercluster. They click on the “Info” symbol (step 1), which leads to the “Project Summary” link (step 2). On the project summary page, they find information (Siletti et al., 2023 DOI) to help them learn about the dataset.



The screenshot displays the Brain Knowledge Platform interface. On the left, the 'SELECTED VIEW' panel shows 'Neurons' with a red arrow pointing to the 'Info' icon (1). Below this, the 'Cell Properties' panel lists various filters, with 'Upper rhombic lip' selected. The main central area shows two brain maps: 'Neurons (1)' with 'TGM1' expression and 'Neurons (2)' with 'Anatomical Div...' expression. On the right, the 'Dataset' panel is highlighted with a red box. It contains the following information:

- Neurons (2)**: 2.5 million neurons from the adult human brain.
- Visit project summary**: A link with a red arrow pointing to it (2).
- Resources**:
 - ABC Atlas WHB Download
 - NeMO
- Citation**:
 - Primary publication: Kimberly Siletti, ...
 - More

9. Now that the researcher has more information on these novel ASD risk genes, they start designing their next experiments with this new knowledge.