

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

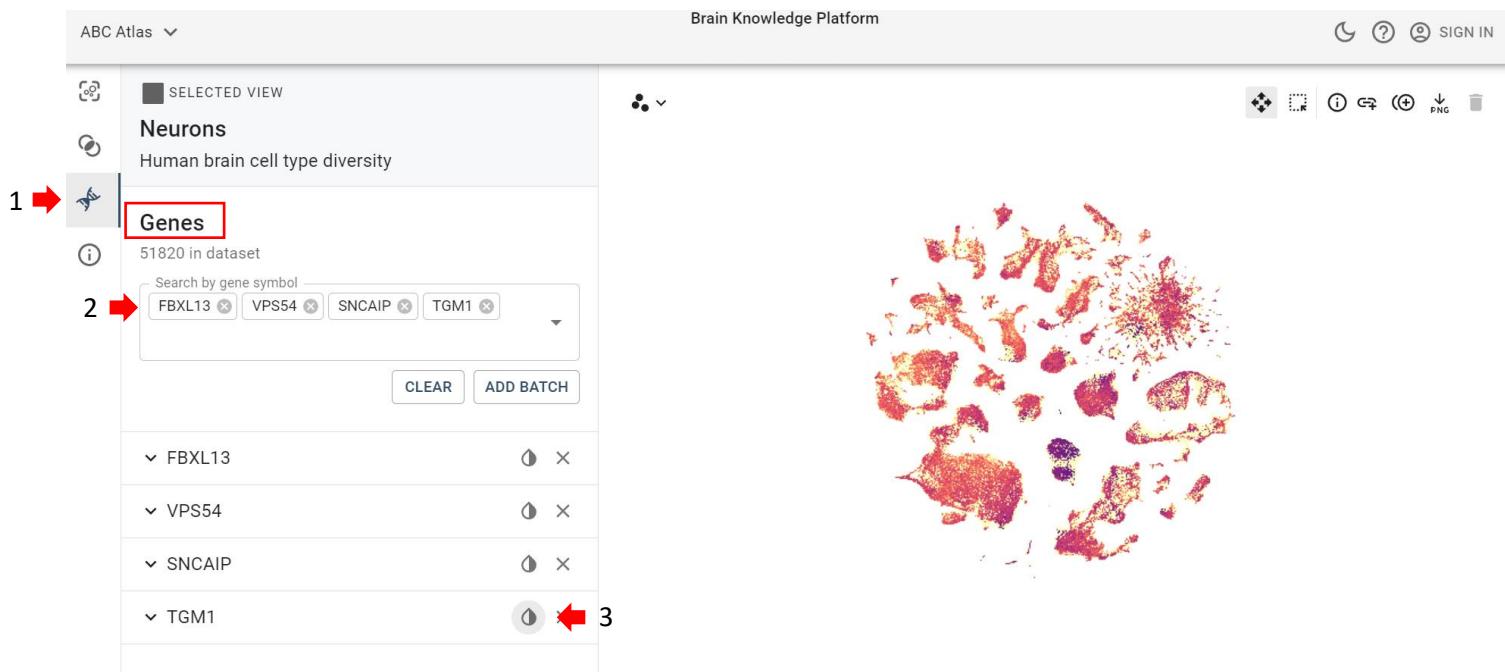
Research: Basic | Translational

Research Type: Computational | Molecular | Behavior

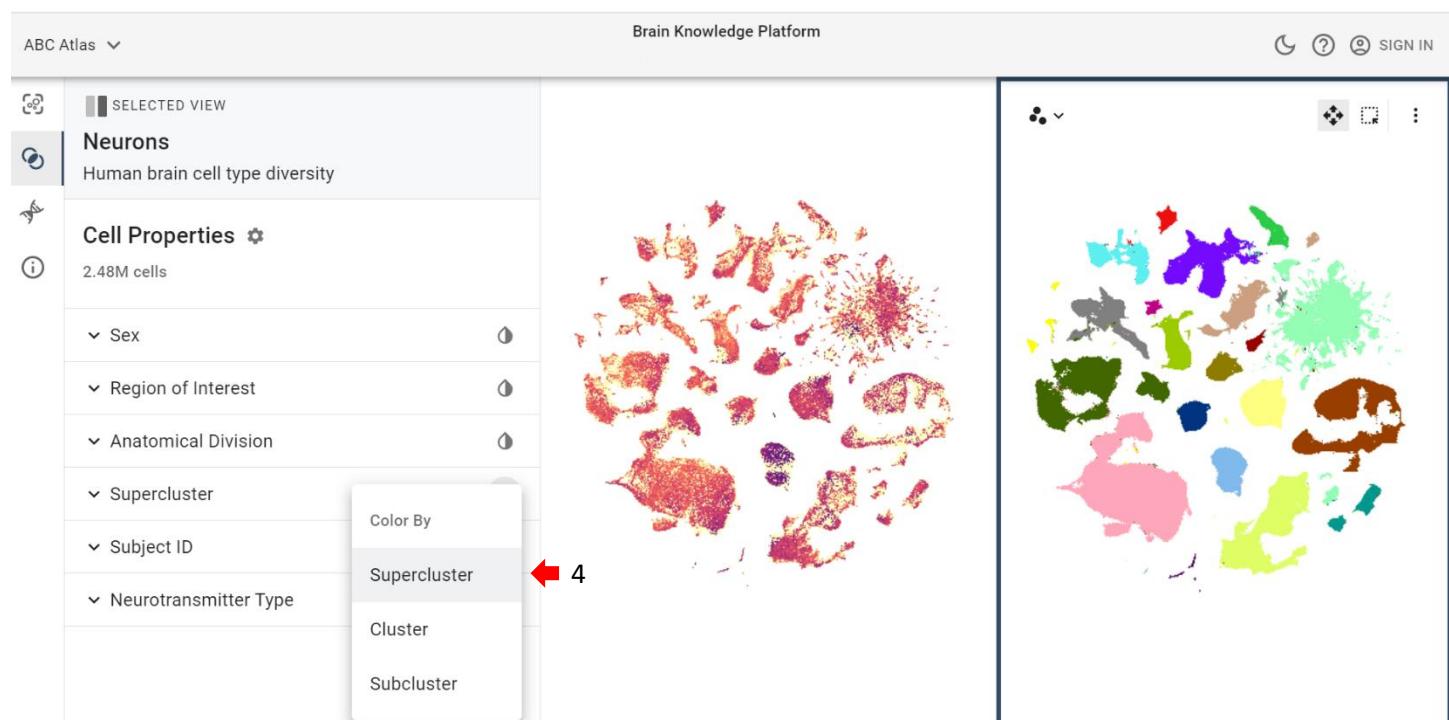
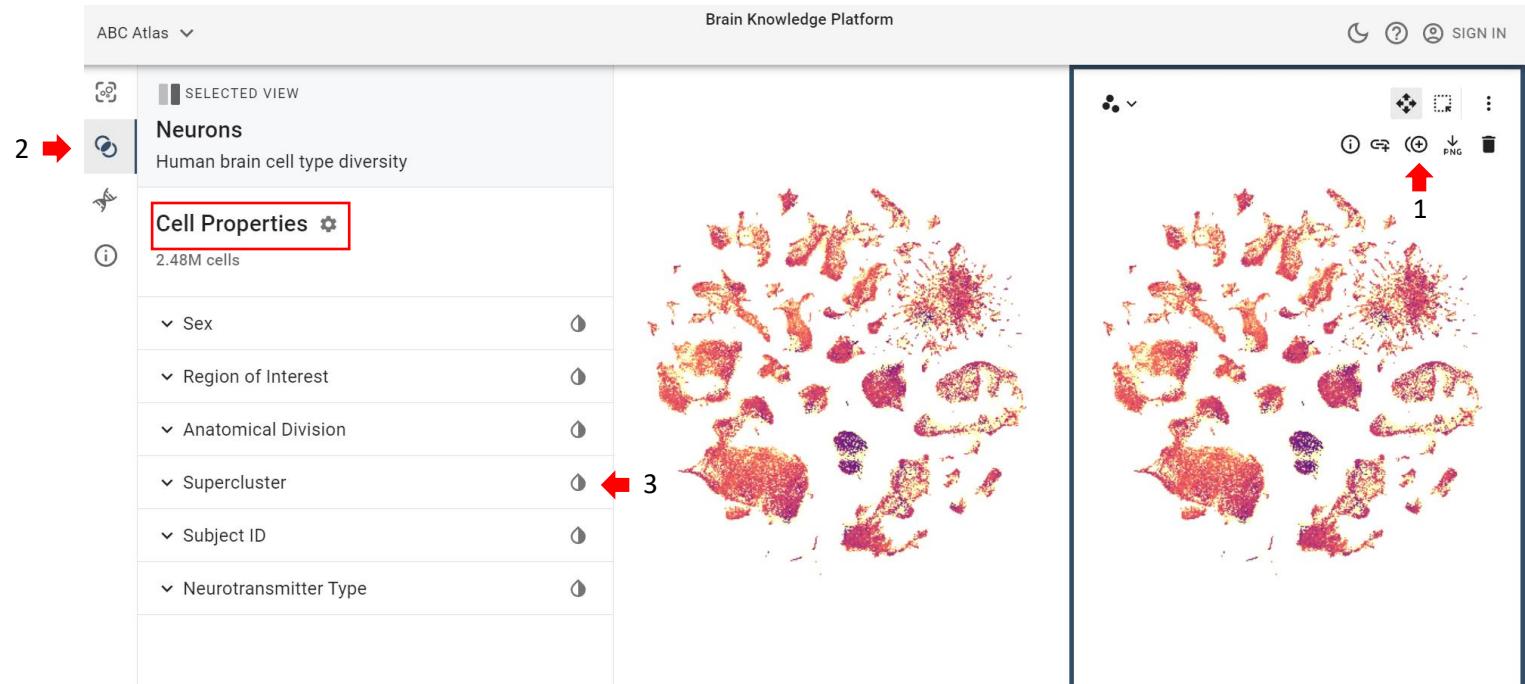
Experimental Model: Mouse | Rat | Non-Human Primate | Human | Invertebrate | Non-Traditional Vertebrate

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.

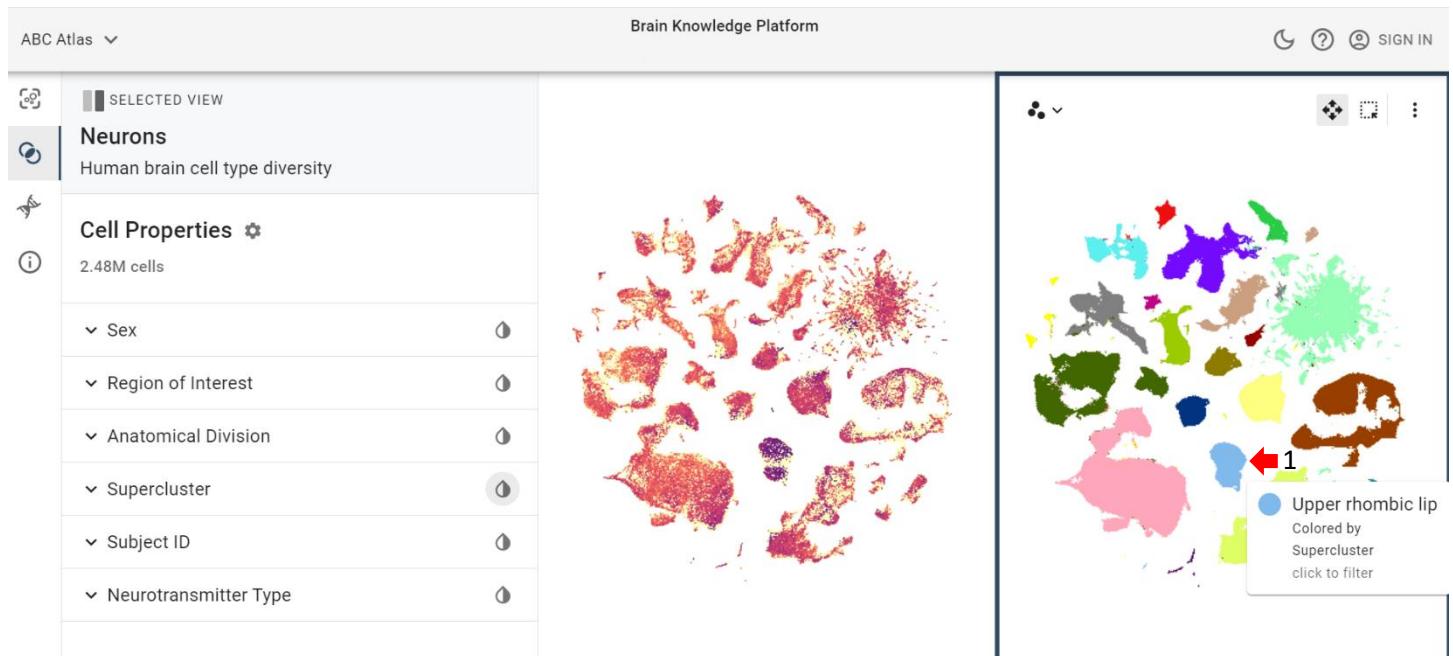
1. To find genes of interest, the researcher clicks on the gene tab (step 1), searches for different genes (step 2), and colors the t-SNE plot for each gene by clicking on the ink drop symbol (step 3). The current plot is colored for *TGM1*. [Link to view in ABC Atlas](#)



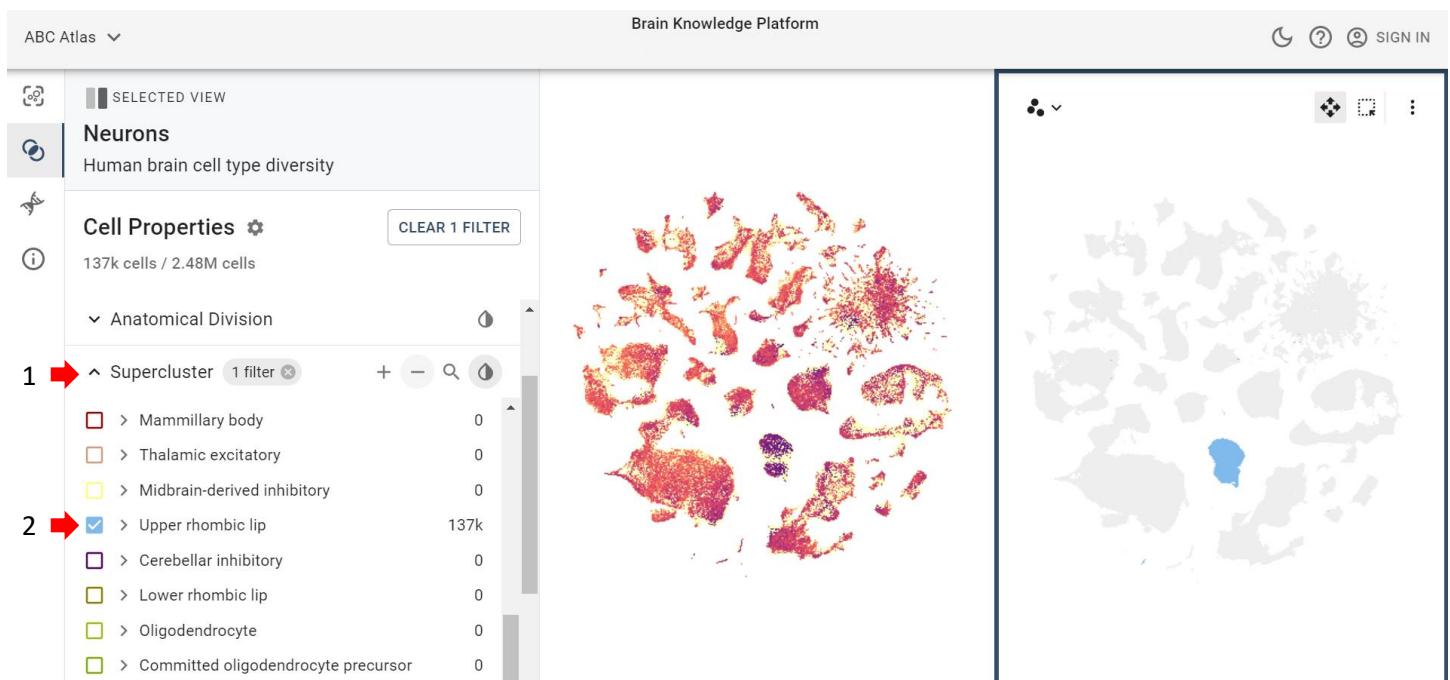
2. To see which superclusters highly express the gene of interest (*TGM1*), the researcher first duplicates the t-SNE plot by clicking on the “Duplicate View” symbol (step 1). Next, the researcher clicks on the “Cell Properties” tab (step 2). They then color the duplicated plot by superclusters by clicking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



3. 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 “Supercluster” (step 1) and checks the “Upper rhombic lip” box (step 2). [Link to view in ABC Atlas](#)



5. 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](#)



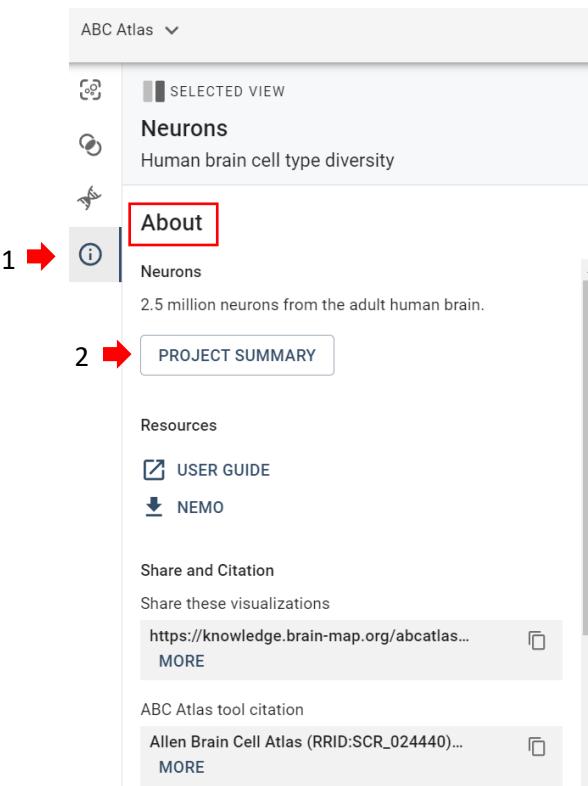
6. Next, the researcher sees that the majority of the “Upper rhombic lip” nuclei are one color (light blue); they hover their mouse over the plot (step 1) and learn that light blue nuclei belong to the cerebellum. [Link to view in ABC Atlas](#)



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 “About” tab (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.



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