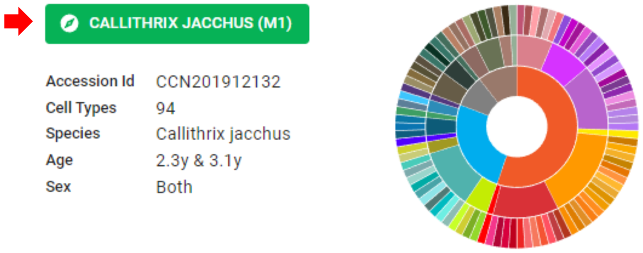
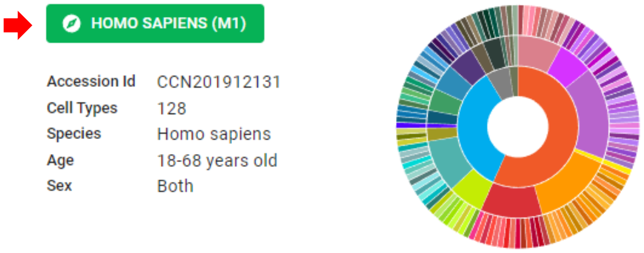
Using the Cell Type Knowledge Explorer

The Cell Type Knowledge Explorer (CTKE) is an interactive tool for exploring data from transcriptomic taxonomies. The CTKE features three transcriptomic taxonomies (from sc-and snRNAseq data): mouse, human, and marmoset primary motor cortex. The CTKE also features an integrated taxonomy of the three species taxonomies, which shows cross-species cell type homologies. Within the mouse taxonomy, there are also patch-seq data to show electrophysiological characteristics and morphological reconstructions at the subclass and cell type levels. In the human L5 ET subclass, there are patch-seq data as well.

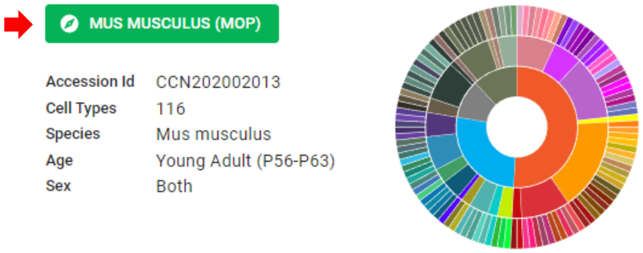
1. Go to brain-map.org https://knowledge.brain-map.org/celltypes to find the Cell Type Knowledge Explorer (CTKE) landing page.
    a. On the landing page, there are three sunburst plots on the right. The three plots represent three transcriptomic taxonomies from the primary motor cortex of marmoset (callithrix jacchus), human (homo sapiens), and mouse (mus musculus). Clicking on the green buttons will take you to the landing page of that species' taxonomy.



Accession Id	CCN201912132
Cell Types	94
Species	Callithrix jacchus
Age	2.3y & 3.1y
Sex	Both

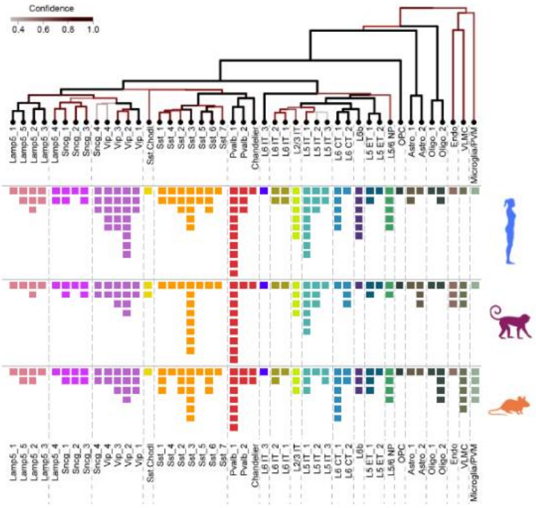


Accession Id	CCN201912131
Cell Types	128
Species	Homo sapiens
Age	18-68 years old
Sex	Both

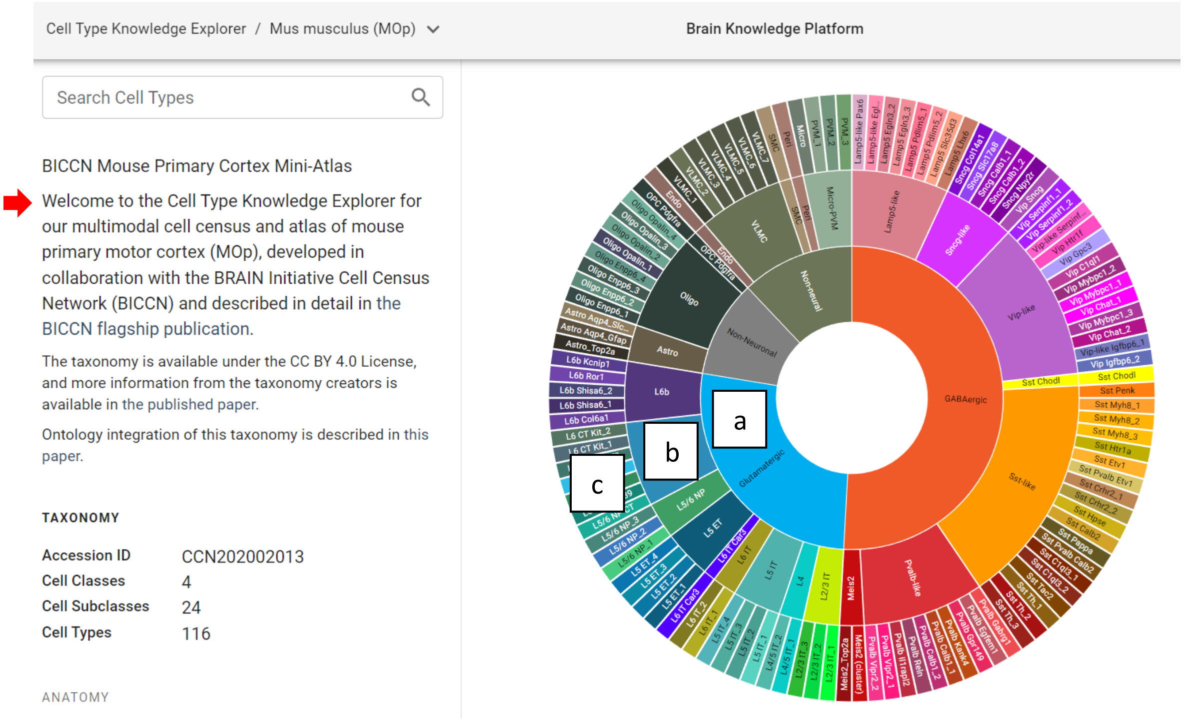


Accession Id	CCN202002013
Cell Types	116
Species	Mus musculus
Age	Young Adult (P56-P63)
Sex	Both

    b. On the left side of the landing page, there is dendrogram that shows an integrated taxonomy, created by combining the three motor cortex taxonomies from the different species.



2. After clicking on one of the green species buttons in step 1a, you will find the species landing page. This page shows an enlarged sunburst plot, representing the primary motor cortex transcriptomic taxonomy of that species. The entire plot is interactive, and any portion can be clicked on to learn more about those specific cell types.
   a. The inner most ring is the broadest level of the taxonomy, showing four classes of cell types. GABAergic cells are red, glutamatergic are blue, non-neuronal cells are grey, and non-neural cells are dark green.
   b. The next layer of the plot shows subclasses of cells that belong to the four classes defined in 2a. Warm colors denote subclasses of cells within the GABAergic class, while cool colors denote subclasses within the glutamatergic class. Brown tones denote subclasses of cells belonging to the non-neuronal or non-neural classes.
   c. The outermost layer of the ring shows individual transcriptomic cell types that belong within the corresponding subclasses and classes.
   d. To learn more about this project, read through the information on the lefthand panel which includes a link to the publications associated with these data.



BICCN Mouse Primary Cortex Mini-Atlas

Welcome to the Cell Type Knowledge Explorer for our multimodal cell census and atlas of mouse primary motor cortex (MOp), developed in collaboration with the BRAIN Initiative Cell Census Network (BICCN) and described in detail in the BICCN flagship publication.

The taxonomy is available under the CC BY 4.0 License, and more information from the taxonomy creators is available in the published paper.

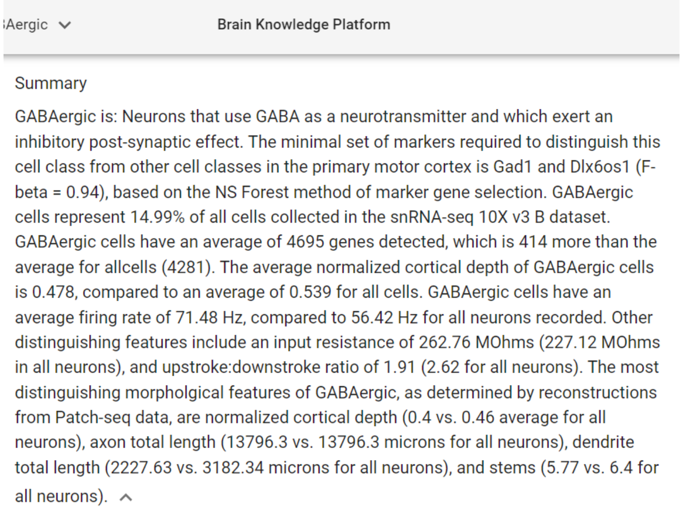
Ontology integration of this taxonomy is described in this paper.

TAXONOMY

Accession ID	CCN202002013
Cell Classes	4
Cell Subclasses	24
Cell Types	116

ANATOMY

3. After clicking on one of the classes (GABAergic, glutamatergic, non-neuronal, or non-neural) in the plot, you will find the page for that cell class. This page includes summary data about that cell class and transcriptomic data.

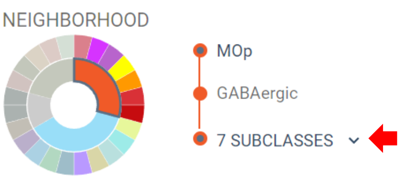


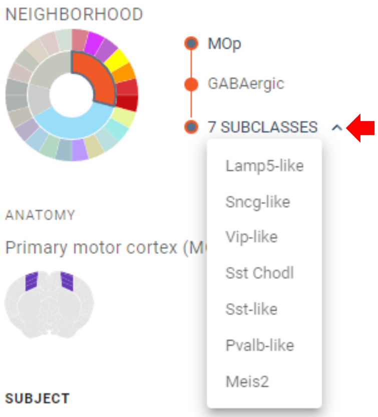
Summary

GABAergic is: Neurons that use GABA as a neurotransmitter and which exert an inhibitory post-synaptic effect. The minimal set of markers required to distinguish this cell class from other cell classes in the primary motor cortex is Gad1 and Dlx6os1 (F-beta = 0.94), based on the NS Forest method of marker gene selection. GABAergic cells represent 14.99% of all cells collected in the snRNA-seq 10X v3 B dataset. GABAergic cells have an average of 4695 genes detected, which is 414 more than the average for allcells (4281). The average normalized cortical depth of GABAergic cells is 0.478, compared to an average of 0.539 for all cells. GABAergic cells have an average firing rate of 71.48 Hz, compared to 56.42 Hz for all neurons recorded. Other distinguishing features include an input resistance of 262.76 MOhms (227.12 MOhms in all neurons), and upstroke:downstroke ratio of 1.91 (2.62 for all neurons). The most distinguishing morpholgical features of GABAergic, as determined by reconstructions from Patch-seq data, are normalized cortical depth (0.4 vs. 0.46 average for all neurons), axon total length (13796.3 vs. 13796.3 microns for all neurons), dendrite total length (2227.63 vs. 3182.34 microns for all neurons), and stems (5.77 vs. 6.4 for all neurons).

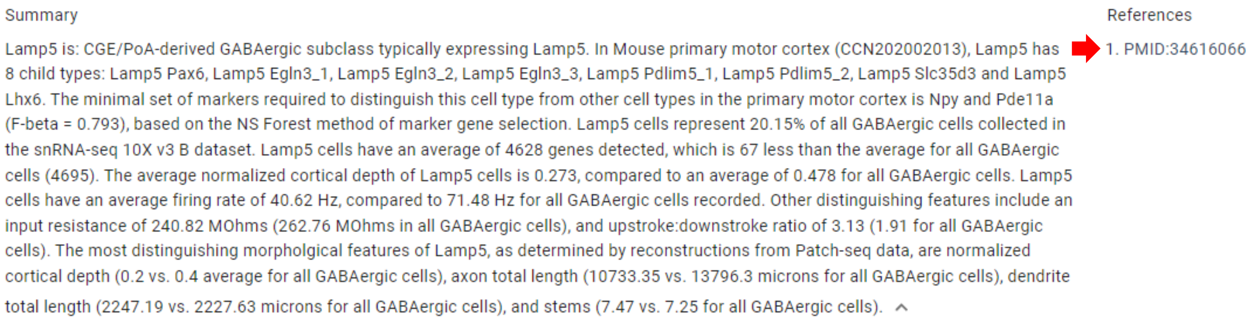
   a. In the gene expression panel, marker genes for the class are colored green. To expand plots, click on the double-edged arrow in the upper righthand corner of the plot. To find out more information about the plot being shown, hover the mouse over the "info" button.

   b. On the lefthand panel, you will find the subclasses within the class listed. To view all of the subclasses, click on the drop-down arrow.





4. After clicking on a subclass in step 3b, you will find the page for that specific subclass. The top of this page features a summary of the subclass, along with a reference in the upper righthand corner.



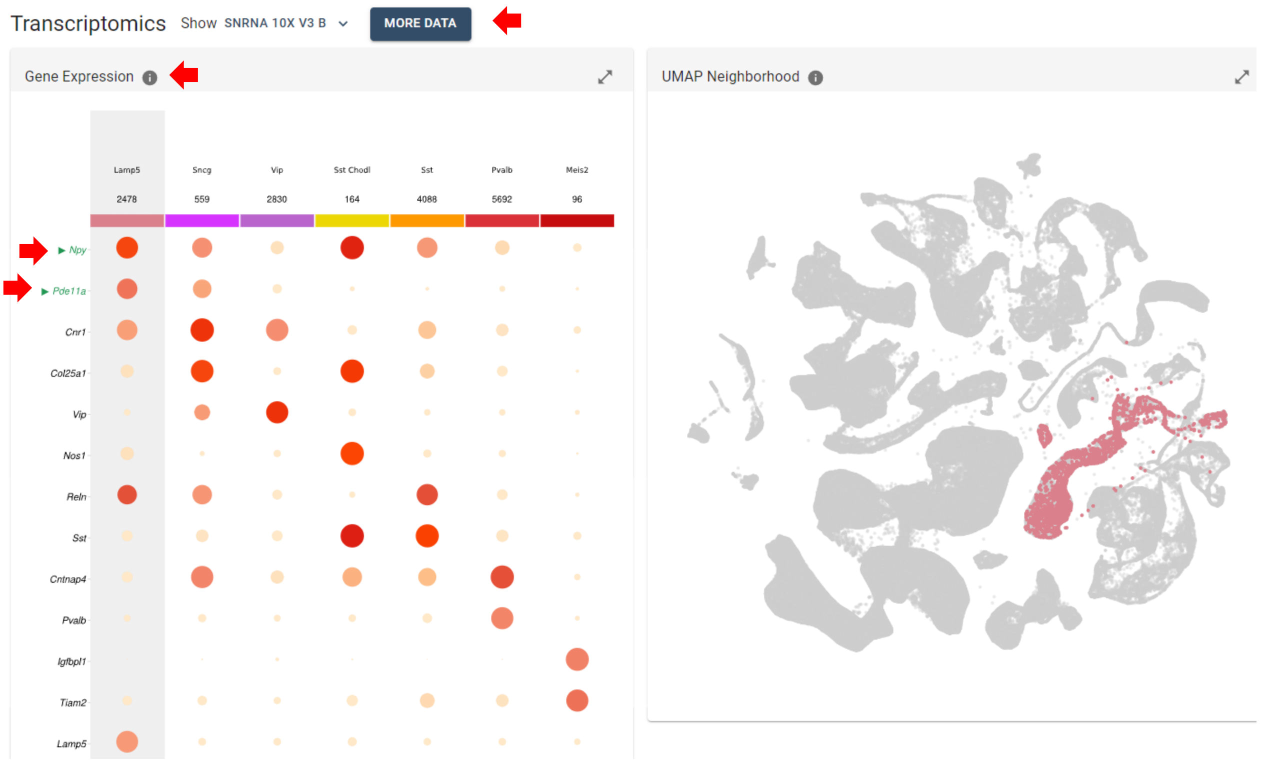
Summary

Lamp5 is: CGE/PoA-derived GABAergic subclass typically expressing Lamp5. In Mouse primary motor cortex (CCN202002013), Lamp5 has 8 child types: Lamp5 Pax6, Lamp5 Egln3_1, Lamp5 Egln3_2, Lamp5 Egln3_3, Lamp5 Pdlim5_1, Lamp5 Pdlim5_2, Lamp5 Slc35d3 and Lamp5 Lhx6. The minimal set of markers required to distinguish this cell type from other cell types in the primary motor cortex is Npy and Pde11a (F-beta = 0.793), based on the NS Forest method of marker gene selection. Lamp5 cells represent 20.15% of all GABAergic cells collected in the snRNA-seq 10X v3 B dataset. Lamp5 cells have an average of 4628 genes detected, which is 67 less than the average for all GABAergic cells (4695). The average normalized cortical depth of Lamp5 cells is 0.273, compared to an average of 0.478 for all GABAergic cells. Lamp5 cells have an average firing rate of 40.62 Hz, compared to 71.48 Hz for all GABAergic cells recorded. Other distinguishing features include an input resistance of 240.82 MOhms (262.76 MOhms in all GABAergic cells), and upstroke:downstroke ratio of 3.13 (1.91 for all GABAergic cells). The most distinguishing morpholgical features of Lamp5, as determined by reconstructions from Patch-seq data, are normalized cortical depth (0.2 vs. 0.4 average for all GABAergic cells), axon total length (10733.35 vs. 13796.3 microns for all GABAergic cells), dendrite total length (2247.19 vs. 2227.63 microns for all GABAergic cells), and stems (7.47 vs. 7.25 for all GABAergic cells).

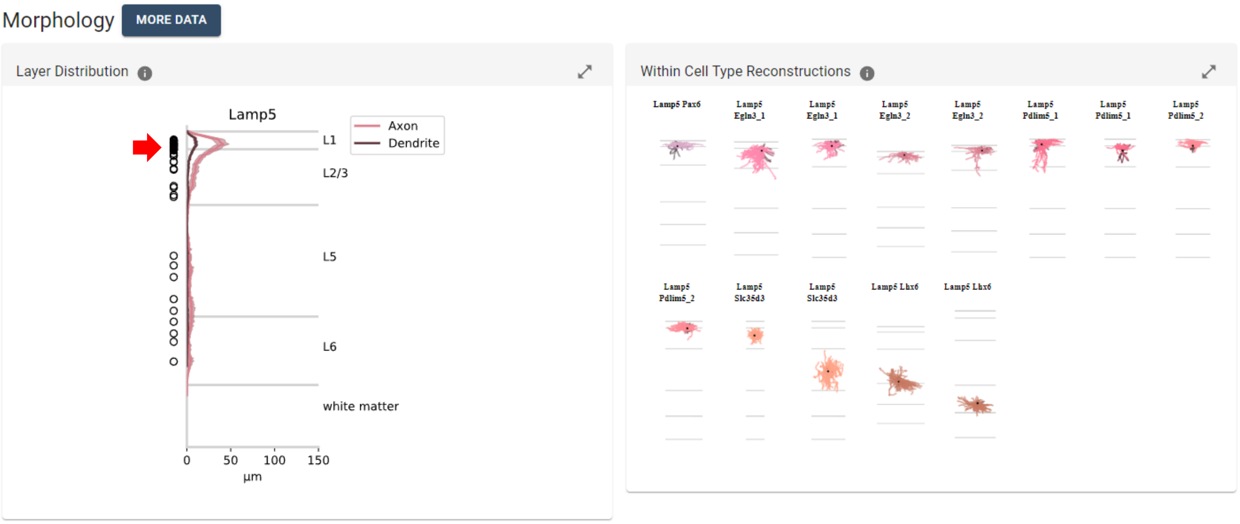
References

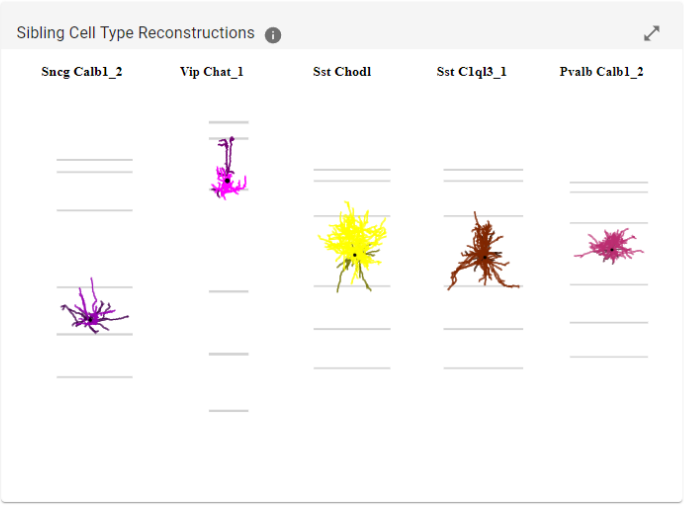
1. PMID:34616066

a. Next, you will find the gene expression data and the marker genes (in green) used to define cells belonging to this subclass. To find out more information about the plot being shown, hover the mouse over the “info” button. To access the raw data, click on the “MORE DATA” button.

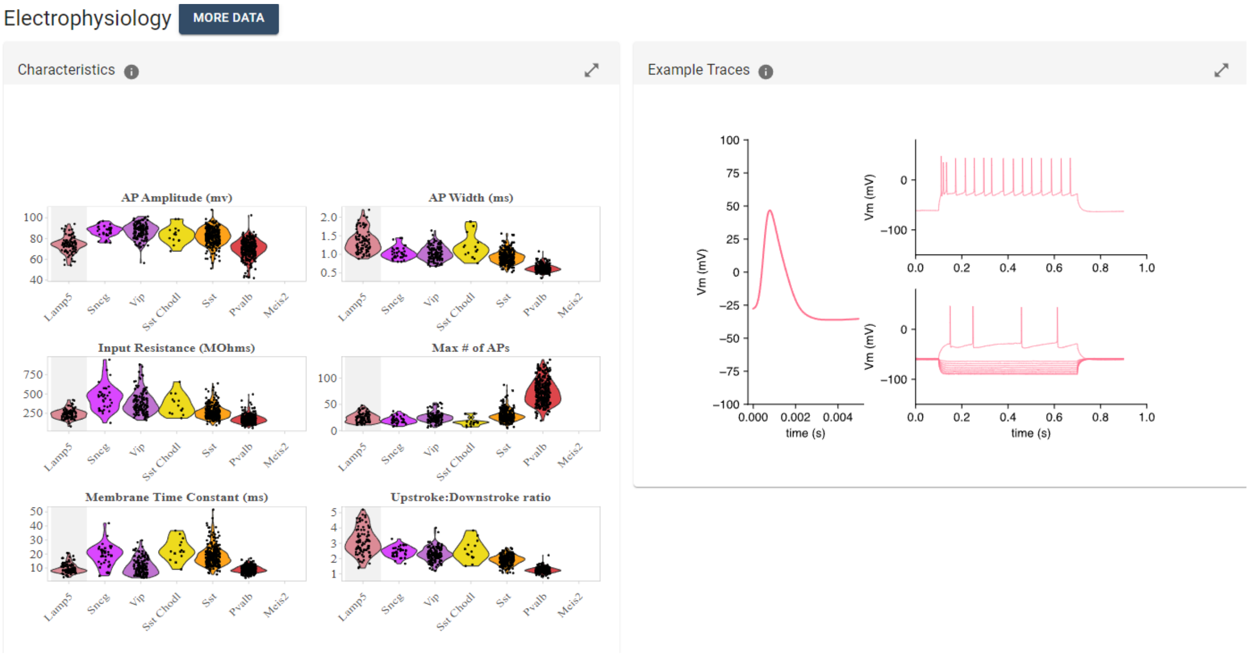


b. Below the transcriptomic data, we have morphological data of cells within this subclass. On the left, we have a histogram which shows the distribution of axonal and dendritic segments throughout the cortical layers, and the distribution of cell bodies (open circles). On the right, we have morphological reconstructions of different cell types within this subclass. Below these panels, we have morphological reconstruction of a cell from this cell subclass compared to other cells from other cell subclasses.

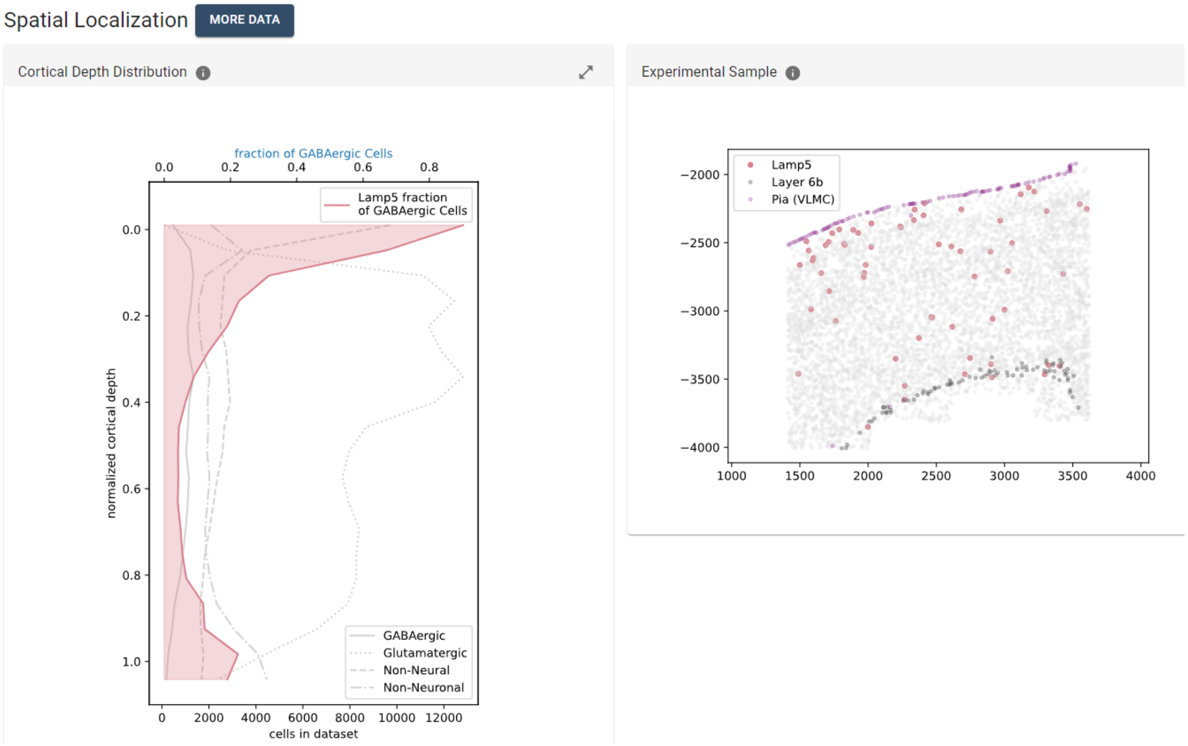




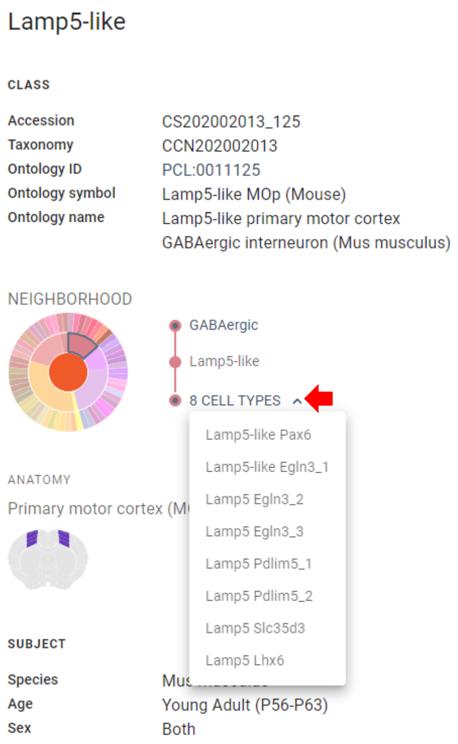
c. Next, we have electrophysiological data. On the left, we have panels comparing electrophysiological characteristics of this cell type compared to other cell types within the same subclass. On the right, we have example traces from a cell within this cell type.



d. Below that we have spatial transcriptomics data. On the lefthand side, the distribution of this subclass as a fraction of its class is shown throughout the cortical layers. On the righthand side, there is an example tissue section and the spatial transcriptomics data, showing the distribuion of cells in this subclass.



e. On the left panel at the top of the page, we have information about our subclass. To view the cell types within the subclass, click on the drop-down arrow.



Lamp5-like

CLASS

Accession	CS202002013_125
Taxonomy	CCN202002013
Ontology ID	PCL:0011125
Ontology symbol	Lamp5-like MOp (Mouse)
Ontology name	Lamp5-like primary motor cortex GABAergic interneuron (Mus musculus)

NEIGHBORHOOD

- Lamp5-like Pax6
- Lamp5-like Egln3_1
- Lamp5 Egln3_2
- Lamp5 Egln3_3
- Lamp5 Pdlim5_1
- Lamp5 Pdlim5_2
- Lamp5 Slc35d3
- Lamp5 Lhx6

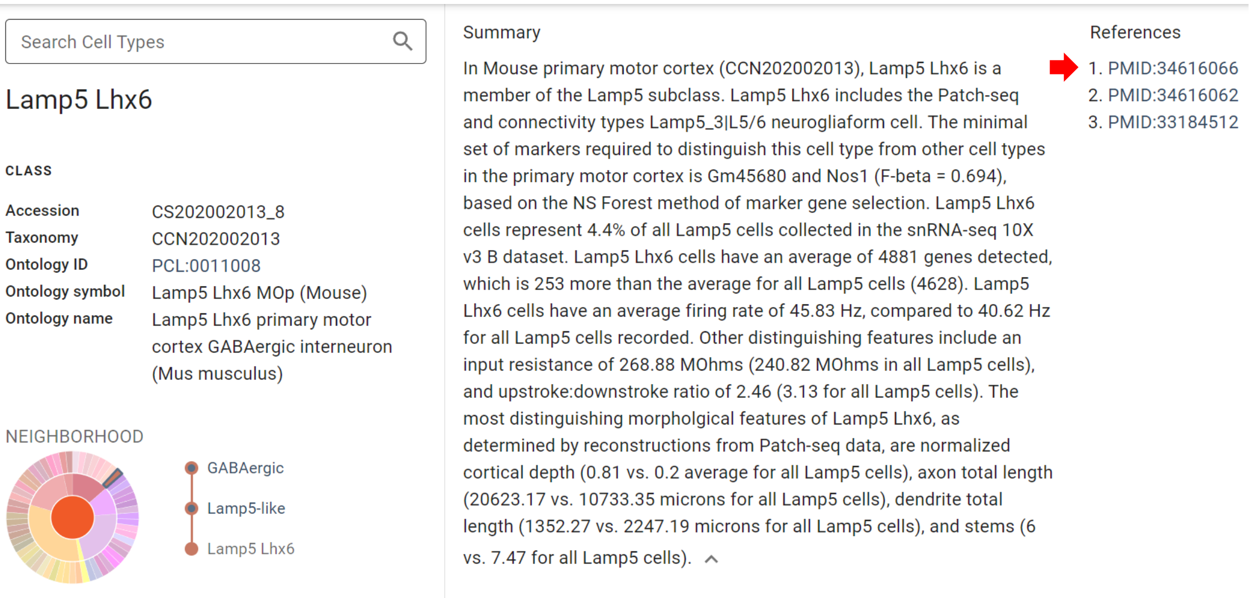
ANATOMY

Primary motor cortex (M

SUBJECT

Species	Mus
Age	Young Adult (P56-P63)
Sex	Both

5. After clicking on a cell type, you will find the main page for that cell type. Here we have a summary of data about the cell type, and references to the data in the upper righthand corner.



Search Cell Types

Lamp5 Lhx6

CLASS

Accession	CS202002013_8
Taxonomy	CCN202002013
Ontology ID	PCL:0011008
Ontology symbol	Lamp5 Lhx6 MOp (Mouse)
Ontology name	Lamp5 Lhx6 primary motor cortex GABAergic interneuron (Mus musculus)

NEIGHBORHOOD

- GABAergic
- Lamp5-like
- Lamp5 Lhx6

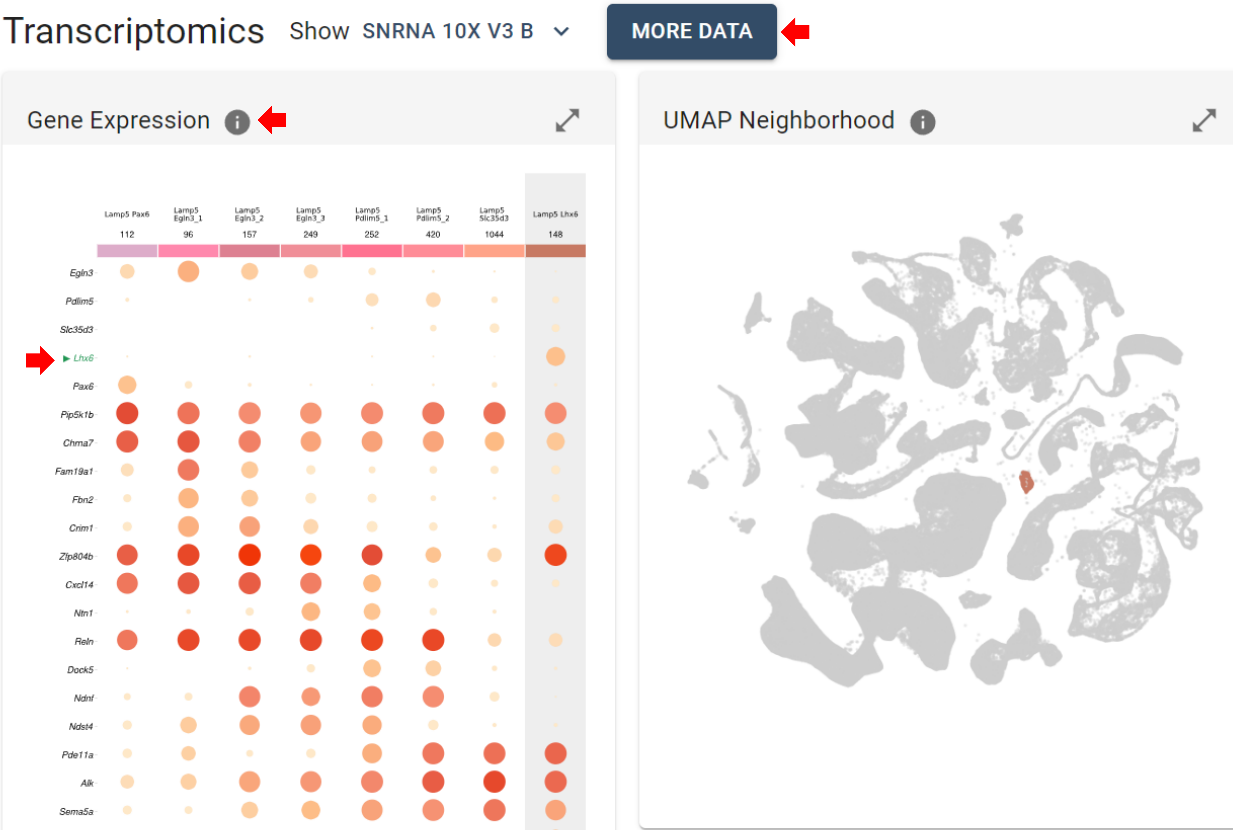
Summary

In Mouse primary motor cortex (CCN202002013), Lamp5 Lhx6 is a member of the Lamp5 subclass. Lamp5 Lhx6 includes the Patch-seq and connectivity types Lamp5_3|L5/6 neurogliaform cell. The minimal set of markers required to distinguish this cell type from other cell types in the primary motor cortex is Gm45680 and Nos1 (F-beta = 0.694), based on the NS Forest method of marker gene selection. Lamp5 Lhx6 cells represent 4.4% of all Lamp5 cells collected in the snRNA-seq 10X v3 B dataset. Lamp5 Lhx6 cells have an average of 4881 genes detected, which is 253 more than the average for all Lamp5 cells (4628). Lamp5 Lhx6 cells have an average firing rate of 45.83 Hz, compared to 40.62 Hz for all Lamp5 cells recorded. Other distinguishing features include an input resistance of 268.88 MOhms (240.82 MOhms in all Lamp5 cells), and upstroke:downstroke ratio of 2.46 (3.13 for all Lamp5 cells). The most distinguishing morpholgical features of Lamp5 Lhx6, as determined by reconstructions from Patch-seq data, are normalized cortical depth (0.81 vs. 0.2 average for all Lamp5 cells), axon total length (20623.17 vs. 10733.35 microns for all Lamp5 cells), dendrite total length (1352.27 vs. 2247.19 microns for all Lamp5 cells), and stems (6 vs. 7.47 for all Lamp5 cells).

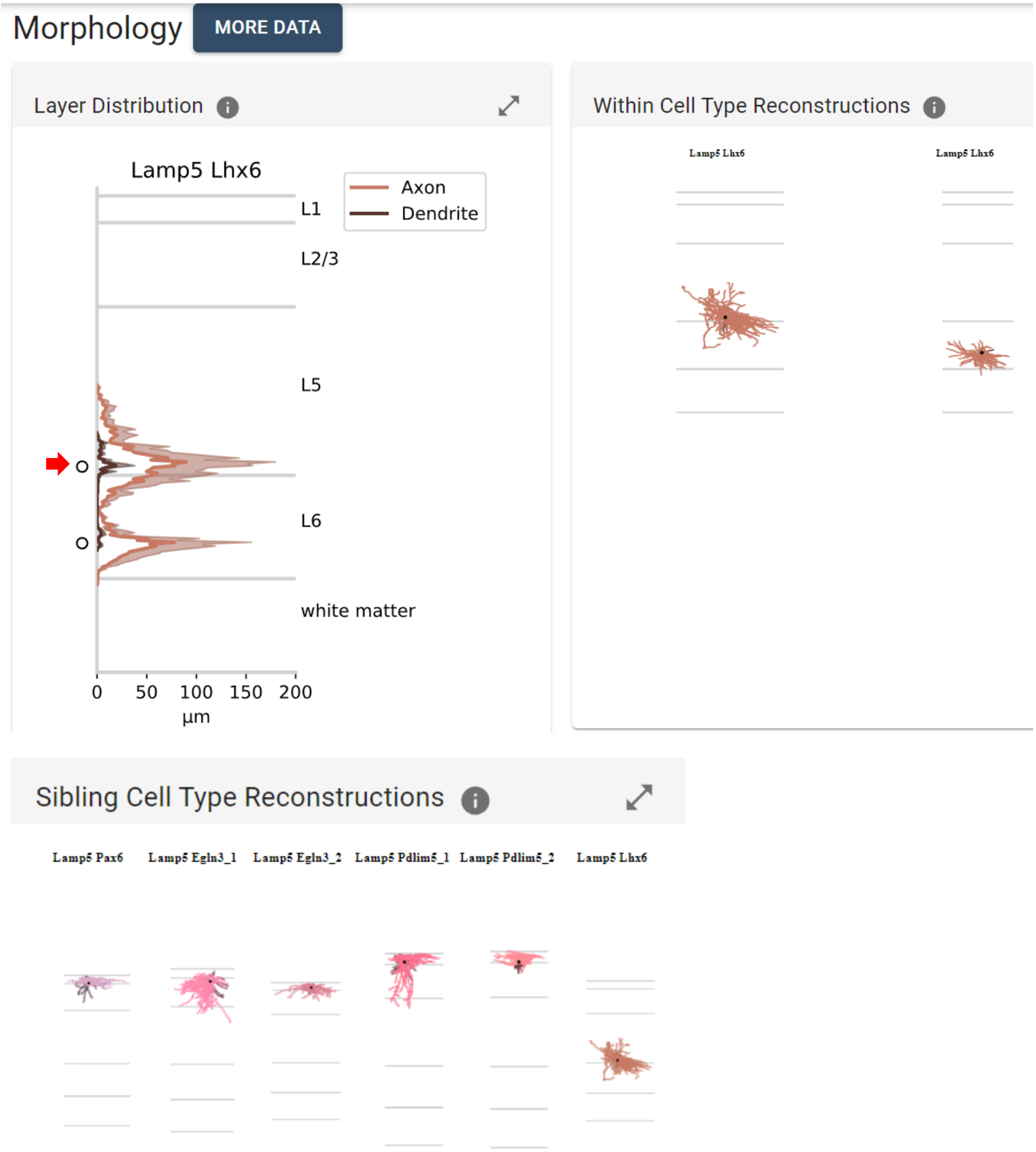
References

1. PMID:34616066
2. PMID:34616062
3. PMID:33184512

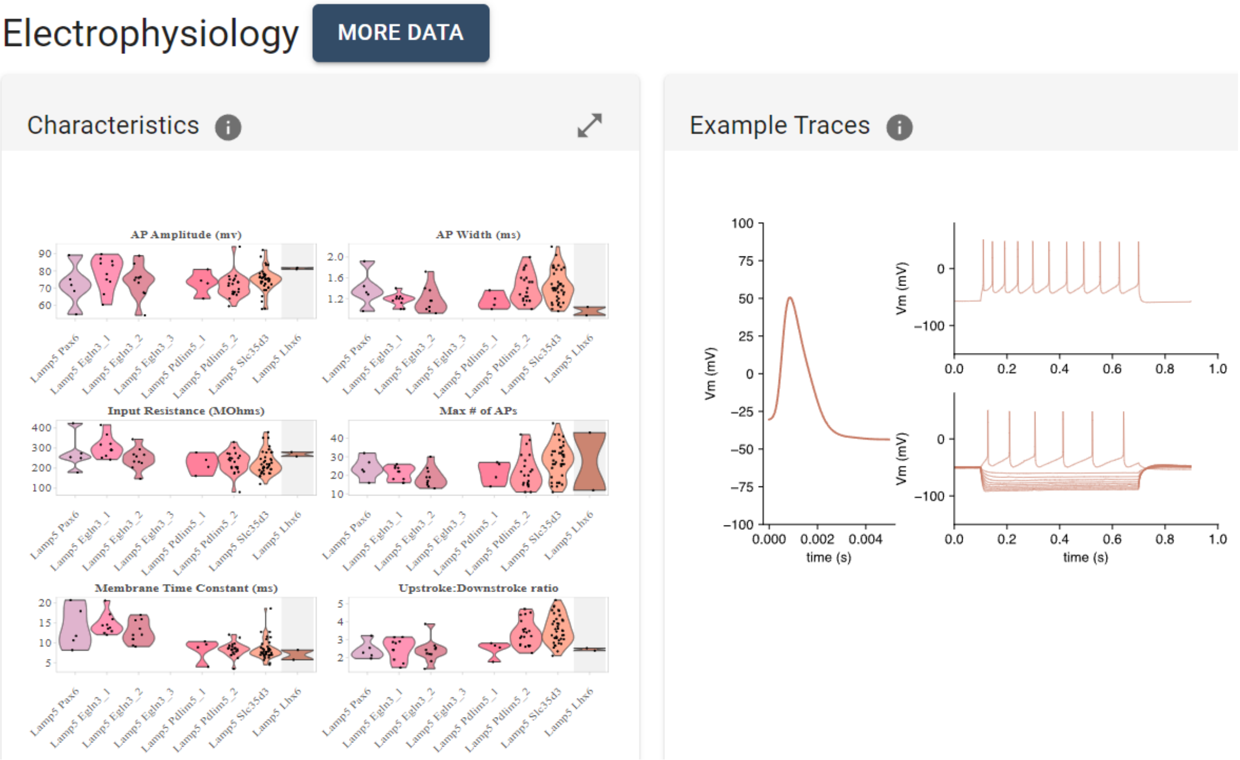
   a. Below the summary, you will find transcriptomic data for this cell type, with marker genes listed in green. To find out more information about the plot being shown, hover the mouse over the "info" button. To access the raw data, click on the "MORE DATA" button.



b. Below the transcriptomic data, we have morphological data of cells within this cell type. On the left, we have a histogram which shows the distribution of axonal and dendritic segments throughout the cortical layers, and the distribution of cell bodies (open circles). On the left, we have morphological reconstructions of different cells within this cell type. Below these panels, we have morphological reconstruction of a cell from this cell type, compared to other cell types within the same subclass.



c. Below the morphological data, we have the electrophysiological data. On the left, we have panels comparing electrophysiological characteristics of this cell type compared to other cell types within the same subclass. On the right, we have example traces from a cell within this cell type.



d. After the electrophysiological data, we have heatmaps; these heatmaps show homologous cell types between the three species (mouse, marmoset, and human) based on the integrated taxonomy featured on the CTKE landing page in step 1. Darker color on the heatmap indicates higher similarity and homologous cell types are outlined in black squares. To view homologous cell types in other species, click directly on the portion of the heat map corresponding to a homologous cell type, which will lead you to the page for that species cell type.