This is a long-format table of single astrocyte & neuron 4-plex data from multiple slides.

It is long-format to show one gene per row but you can cast it back to one astrocyte per row ([cell.id](http://cell.id) column) for single cell comparisons

Each astrocyte slide has Slc1a3/Glast, the astrocyte marker used for cell identification, and 3 astro layer markers.

Each neuron slide has 4 layer markers (an antibody stain was used to identify them)

Some of the columns you would use

“cell.type” – astro or neuron

“normalisedDepth” - cortical depth measurements  of single cells normalised from 0 to 1, upper to deep layers respectively

“spotcounts”  - number of RNA spots for the gene indicated under “genes”

“genes” – neuron or layer astrocyte markers

“[cell.id](http://cell.id)” - unique ID of each cell

“layer” – this is the neuronal layer location of the cell, based on classical markers

This is data from one cortical area (somatosensory barrel cortex). Can provide more areas for validation / comparison