**Available datasets:**

Astrocytes: BAMs and FASTQs (Total size: 95.5 GB)

Microglia: BAMs and FASTQs (Total size: 51 GB)

Neurons: BAMs and FASTQs (Total size: 96 GB)

**Readme for Microglia data set:**

**Description**: RNA sequencing data from laser capture microglia.

**Size**:  26000 MB FASTQs and 25000 MB BAMs = 51000 MB Total

**Platform**: Linux

**Environment**: Centos 6 (or later version)

**Major Component Description**: Raw FASTQs and BAMs generated from alignment (FASTQs aligned to GRCH37 reference using STAR 2.3.1z)

**Detailed Set-up Instructions**: Each BAM/FASTQ is organized as per the brain region they are from. For the BAMs, a BAM index may be required by some tools/programs. It can be generated using Samtools (samtools index). Lastly, keep the index in the same directory with the BAM. No further set up needed

**Detailed Run Instructions**: No special run instructions needed to use this data

**Output Description**: Output from alignment (STAR): BAM files; Output from differential expression analysis (DESeq2): table with list of genes and corresponding p-value, corrected p-value, log2foldchange and baseMean

**Platform used for sequencing**: Illumina HiSeq 2500