**Head and Neck sc-RNA-seq .gz file generation:**

We downloaded sequencing file from the public database and reformatted it with a script, ***createInputFile***. After this, the gene names are in single quotes, which we removed in the cell using sed.  Run script by following command line input in terminal window using Unix:

**$ perl createInputFileML GSE103322\_HNSCC\_all\_data.txt.gz | gzip > HNSCC\_all\_data\_all\_cell\_types.gz**

HNSCC\_all\_data\_all\_cell\_types.gz is the file used in the scRNAseqDataAnalysis.R file for head and neck analysis.

**Ovarian sc-RNA-seq .gz file generation:**

We downloaded all the csv files from the public database and combined and reformatted these files using ovarianCancerCombineDataFiles.R script. This script creates and saves the following gz file that is then used in the scRNAseqDataAnalysis.R script for ovarian data analysis: ovarian\_all\_data\_all\_cell\_types\_with\_headers.gz