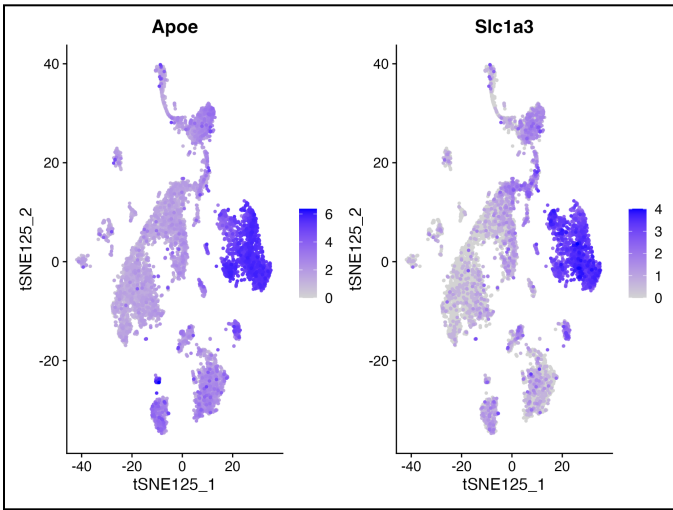
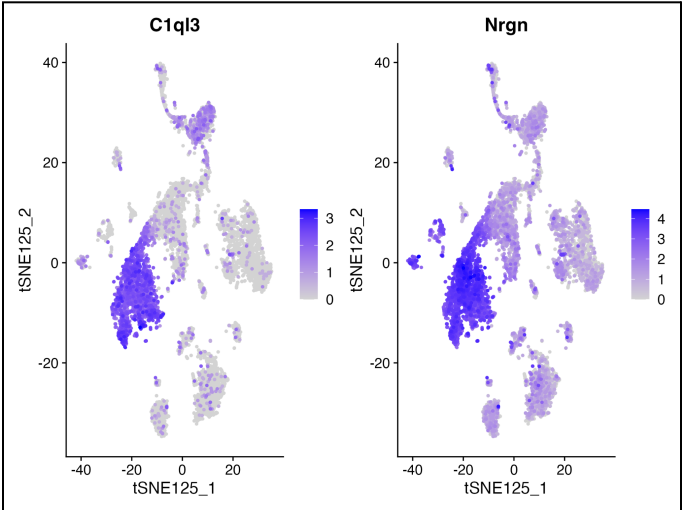


t-SNE Plot of Clusters

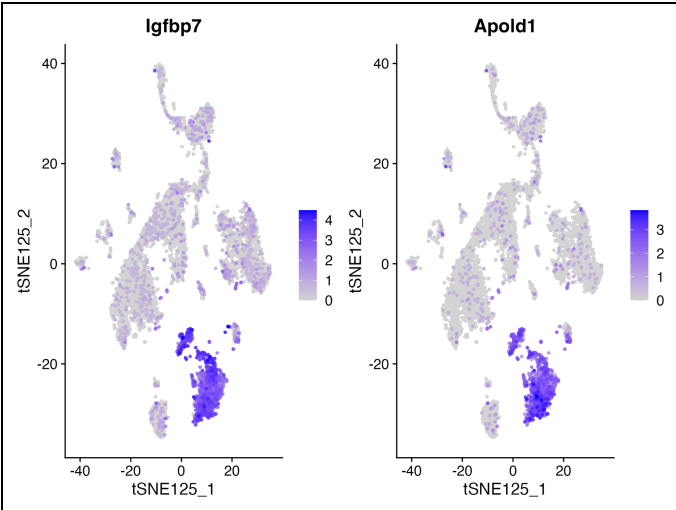
I chose the k value of 30 instead of the default value of 20 because this value produced more clusters with splits rather than having a good amount of clusters with splits with any change in resolution. I tested out various resolution values and saw that lower ones worked best in terms of necessary cluster separations; I initially thought 0.05 had too few clusters in obviously distinct areas and 0.06 had too many clusters in obviously singular-grouped areas so in-between worked the best for necessary separations. From the cowplot, I determined that a 125 perplexity worked the best in forming distinct clusters that were separate from each other. While some clusters included sub-clusters (like cluster 3 and 6), testing out any adjustments from these parameters caused overclustering in other areas that did not deem necessary to be clustered and less efficient/useful groupings. However, this may be improved by merging clusters.



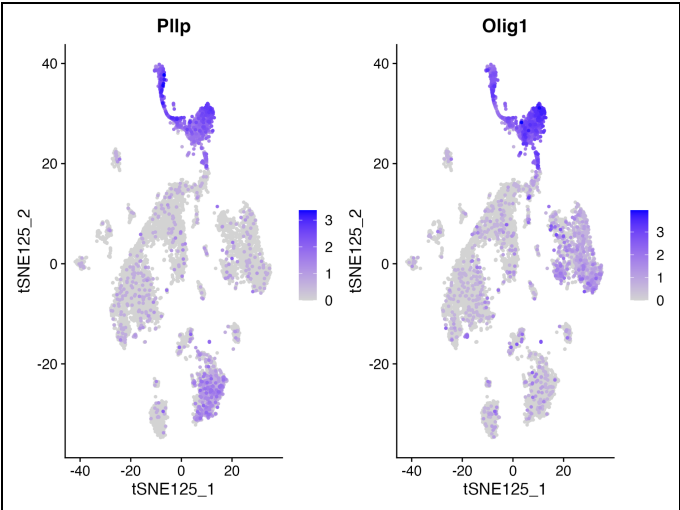
Feature Plot of Apoe and Slc1a3 Genes in Cluster One



Feature Plot of C1ql3 and Nrgn Genes in Cluster Two



Feature Plot of Igfbp7 and Apold1 Genes in Cluster Three



Feature Plot of Plip and Olig1 Genes in Cluster Four