

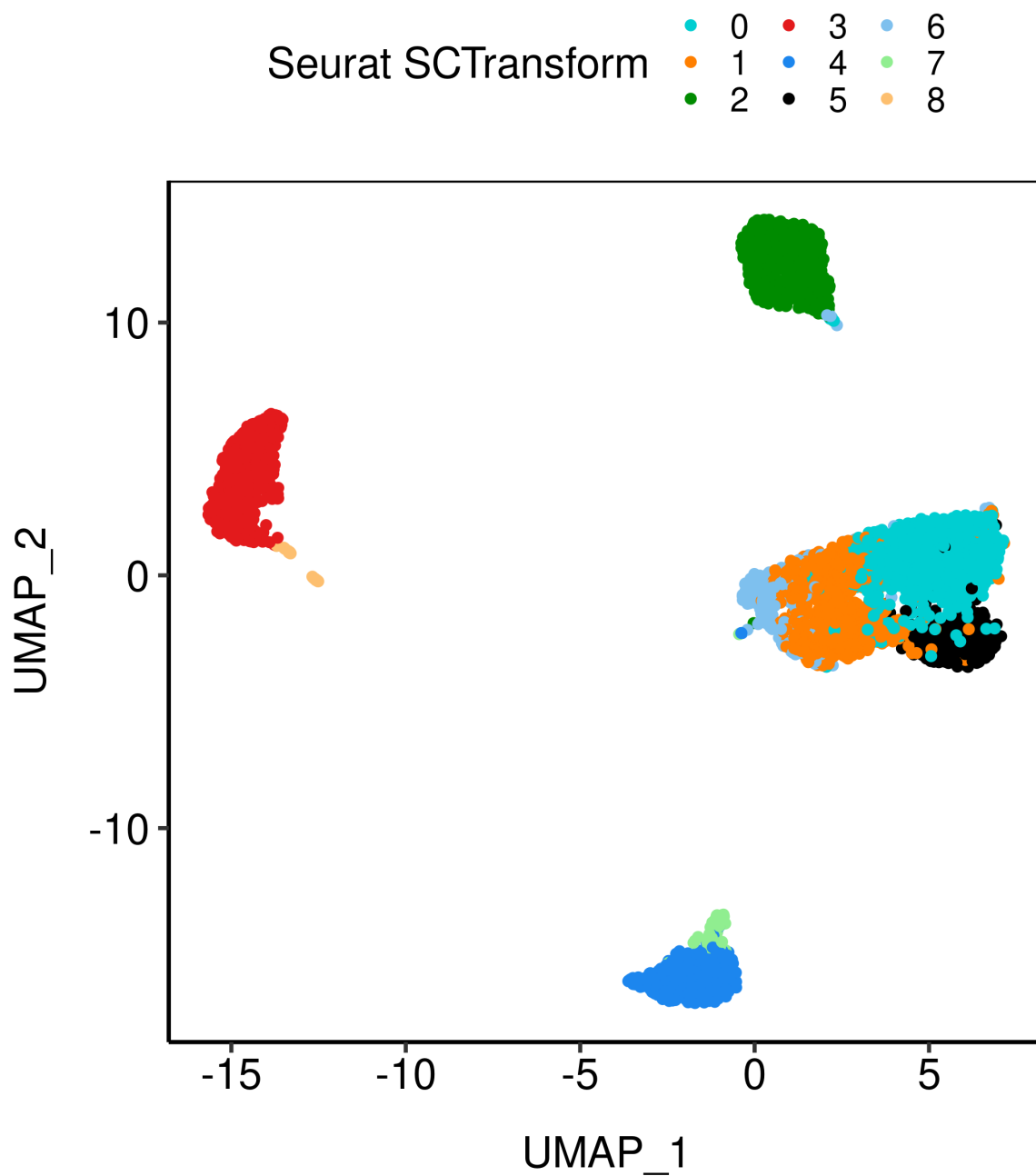


Figure S3: The UMAP plot visualizing the clustering performance in the Zhengmix8eq data set using Seurat SCTransform (15 PCs and resolution parameter 0.8). Each color represents an identified cluster. Similar as the clustering results from Seurat with log-normalized counts, it performs well in identifying the more distinct cell types (NK cells in green, Monocytes in red and B cells in blue), but fails to distinguish T subtypes.