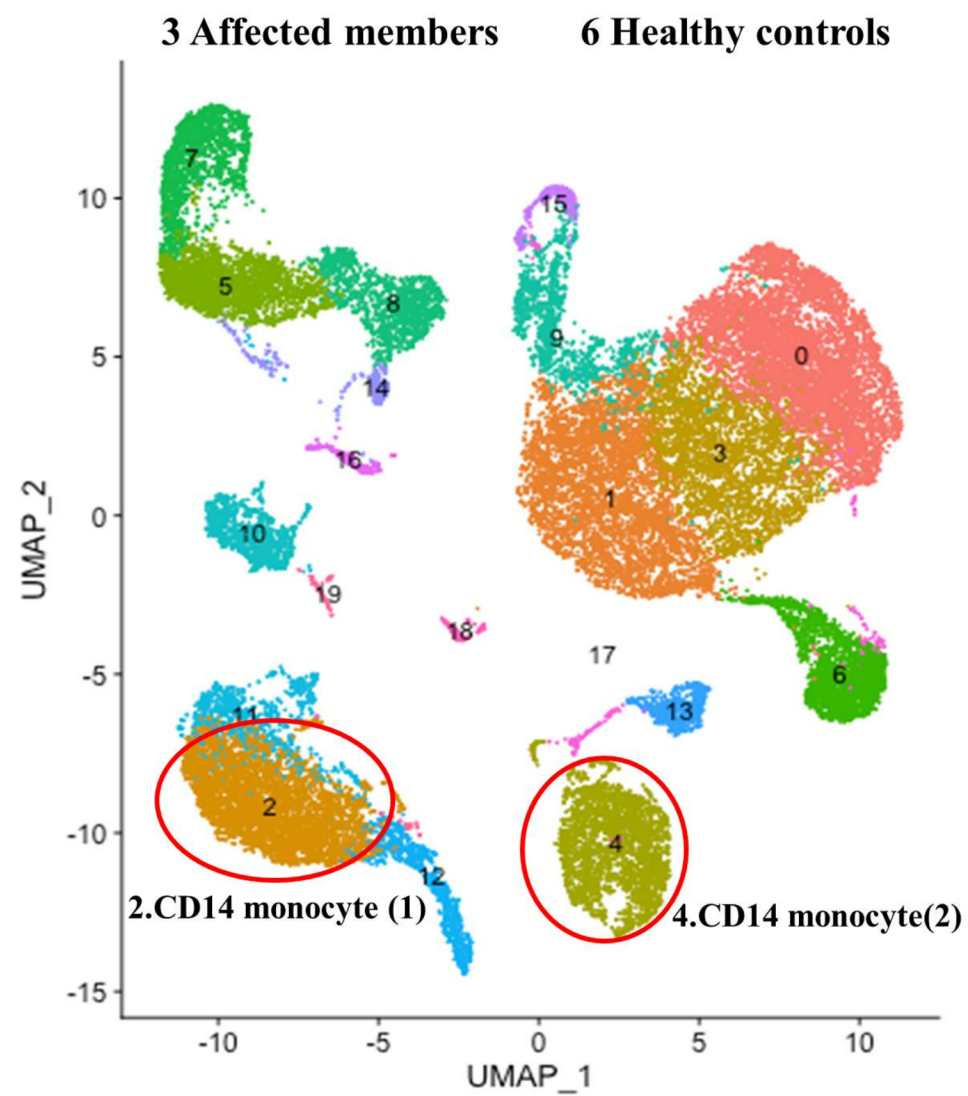




Supplementary Figure S7. UMAP showed the topology of cells of the nine samples (three patients, one Thai healthy control, and five publicly available healthy controls). Visualization of single-cell transcriptome data was done in R (v. 4.2.1; <https://www.R-project.org>) using RStudio (<https://www.rstudio.com>) and R packages tidyverse (v. 1.3.1; <https://doi.org/10.21105/joss.01686>) and ggpubr (v. 0.4.0; <https://CRAN.R-project.org/package=ggpubr>).