ANOTATION USED:

levels(clusters)[levels(clusters) %in% c("7","14","5","3","11", "24", "32")] <- "Microglia"

levels(clusters)[levels(clusters) %in% c("4","2","29")] <- "Vascular endothelial cells, venous"

levels(clusters)[levels(clusters) %in% c("10","18")] <- "Perivascular macrophages"

levels(clusters)[levels(clusters) %in% c("13")] <- "Oligodendrocytes precursor cells"

levels(clusters)[levels(clusters) %in% c("36","26","23")] <- "Vascular smooth muscle cells, arterial"

levels(clusters)[levels(clusters) %in% c("6","30")] <- "Olfactory ensheathing cells"

levels(clusters)[levels(clusters) %in% c("22")] <- "Vascular leptomeningeal cells"

levels(clusters)[levels(clusters) %in% c("37")] <- "Ependymal cells"

levels(clusters)[levels(clusters) %in% c("25")] <- "Neural stem cells"

levels(clusters)[levels(clusters) %in% c("31")] <- "Astrocytes"

levels(clusters)[levels(clusters) %in% c("27")] <- "Pericytes"

levels(clusters)[levels(clusters) %in% c("19","28")] <- "Oligodendrocytes"

levels(clusters)[levels(clusters) %in% c("34")] <- "Neuroblasts"

levels(clusters)[levels(clusters) %in% c("1")] <- "Vascular endothelial cells, capillary"

levels(clusters)[levels(clusters) %in% c("38")] <- "Enteric glia"

levels(clusters)[levels(clusters) %in% c("16")] <- "Subventricular zone\n radial glia-like cells"

#immuno

levels(clusters)[levels(clusters) %in% c("12","33")] <- "Neutrophils"

levels(clusters)[levels(clusters) %in% c("8","15")] <- "Macrophages/Monocytes"

levels(clusters)[levels(clusters) %in% c("9","21")] <- "DCs"

levels(clusters)[levels(clusters) %in% c("20","16")] <- "Fibroblasts"

levels(clusters)[levels(clusters) %in% c("17")] <- "B cells"

levels(clusters)[levels(clusters) %in% c("35")] <- "NK(T) cells"