

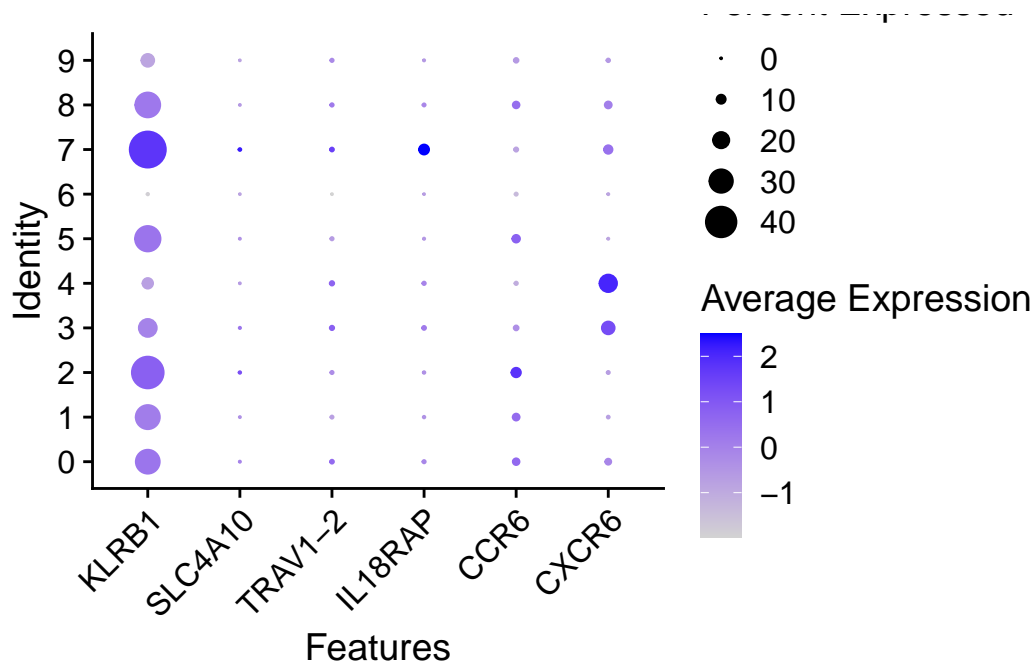
# CSF and Blood MAIT Analysis

```
suppressPackageStartupMessages({  
  library(Seurat)  
  library(ggplot2)  
  library(dplyr)  
})
```

## 1. CSF Analysis

```
csf <- readRDS("../outputs/csf/csf_sct.rds")  
  
# MAIT markers by cluster  
DotPlot(csf, features = c("KLRB1", "SLC4A10", "ZBTB16", "TRAV1-2", "IL18RAP", "CCR6", "CXCR6")) +
```

Warning: The following requested variables were not found: ZBTB16



# I think cluster7 expresses some mait cell marker but not strong, but I still make analysis

# manually map GSM -> diagnosis (from GEO page)

```
lookup <- c(
  GSM3984199_CSF1 = "HC",
  GSM3984200_CSF2 = "AD",
  GSM3984201_CSF3 = "HC",
  GSM3984202_CSF4 = "HC",
  GSM3984203_CSF5 = "MCI",
  GSM3984204_CSF6 = "AD",
  GSM3984205_CSF8 = "HC",
  GSM3984206_CSF9 = "AD",
  GSM3984207_CSF11= "MCI",
  GSM3984208_CSF12= "HC",
  GSM3984209_CSF13= "HC",
  GSM3984210_CSF15= "MCI",
  GSM3984211_CSF16= "HC",
  GSM3984212_CSF17= "MCI",
  GSM3984213_CSF18= "AD",
  GSM3984214_CSF19= "MCI",
  GSM3984215_CSF20= "HC",
  GSM3984216_CSF23= "HC"
)
csf$Diagnosis <- unname(lookup[as.character(csf$sample_id)])
```

```
table(csf$Diagnosis)
```

```
      AD      HC      MCI  
4097 10870  6292
```

```
Idents(csf) <- "seurat_clusters"
```

```
# raw counts  
table(csf$Diagnosis[Idents(csf) == "7"])
```

```
      AD      HC      MCI  
186  474  341
```

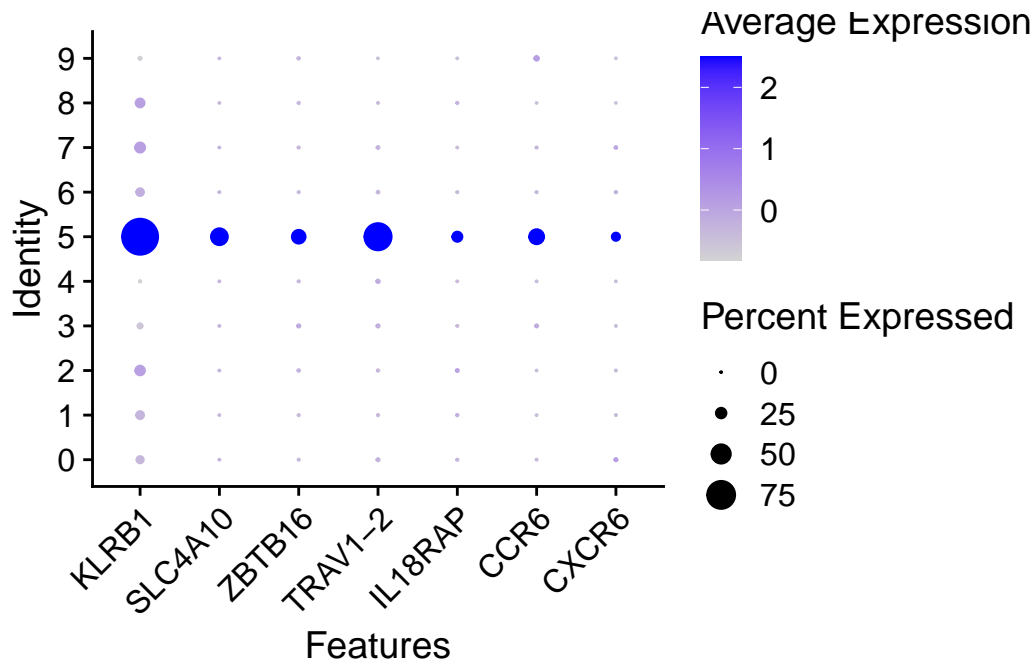
```
# proportions per diagnosis group  
prop.table(table(csf$Diagnosis, Idents(csf)), margin = 1)[,"7"]
```

```
      AD      HC      MCI  
0.04539907 0.04360626 0.05419580
```

## 2. Blood Analysis

```
blood <- readRDS("../outputs/blood/blood_sct.rds")
```

```
DotPlot(blood, features = c("KLRB1", "SLC4A10", "ZBTB16", "TRAV1-2", "IL18RAP", "CCR6", "CXCR6"))
```



```
# I think cluster5 is mait cells
#Make a lookup table inside R
lookup_blood <- c(
  GSM3956366_T1 = "AD",
  GSM3956367_T2 = "MCI",
  GSM3956368_T3 = "HC",
  GSM3956369_T4 = "HC",
  GSM3956370_T5 = "AD",
  GSM3956371_T6 = "AD",
  GSM3956372_T7 = "HC",
  GSM3956373_T8 = "HC",
  GSM3956374_T9 = "AD",
  GSM3956375_T10 = "HC",
  GSM3956376_T11 = "HC",
  GSM3956377_T12 = "HC",
  GSM3956378_T14 = "MCI"
)
#Add diagnosis to Seurat metadata
blood$Diagnosis <- unname(lookup_blood[as.character(blood$sample_id)])
table(blood$Diagnosis) # sanity check
```

AD      HC      MCI

```
4672 11084 2451
```

```
#count cluster5 by diganosis
Idents(blood) <- "seurat_clusters"

# Raw counts of cluster 5 cells by diagnosis
table(blood$Diagnosis[Idents(blood) == "5"])
```

```
AD  HC MCI
550 831 206
```

```
# Or proportion of each diagnosis group in cluster 5
prop.table(table(blood$Diagnosis, Idents(blood)), margin = 1)[, "5"]
```

```
      AD      HC      MCI
0.11772260 0.07497293 0.08404733
```