

single_cell

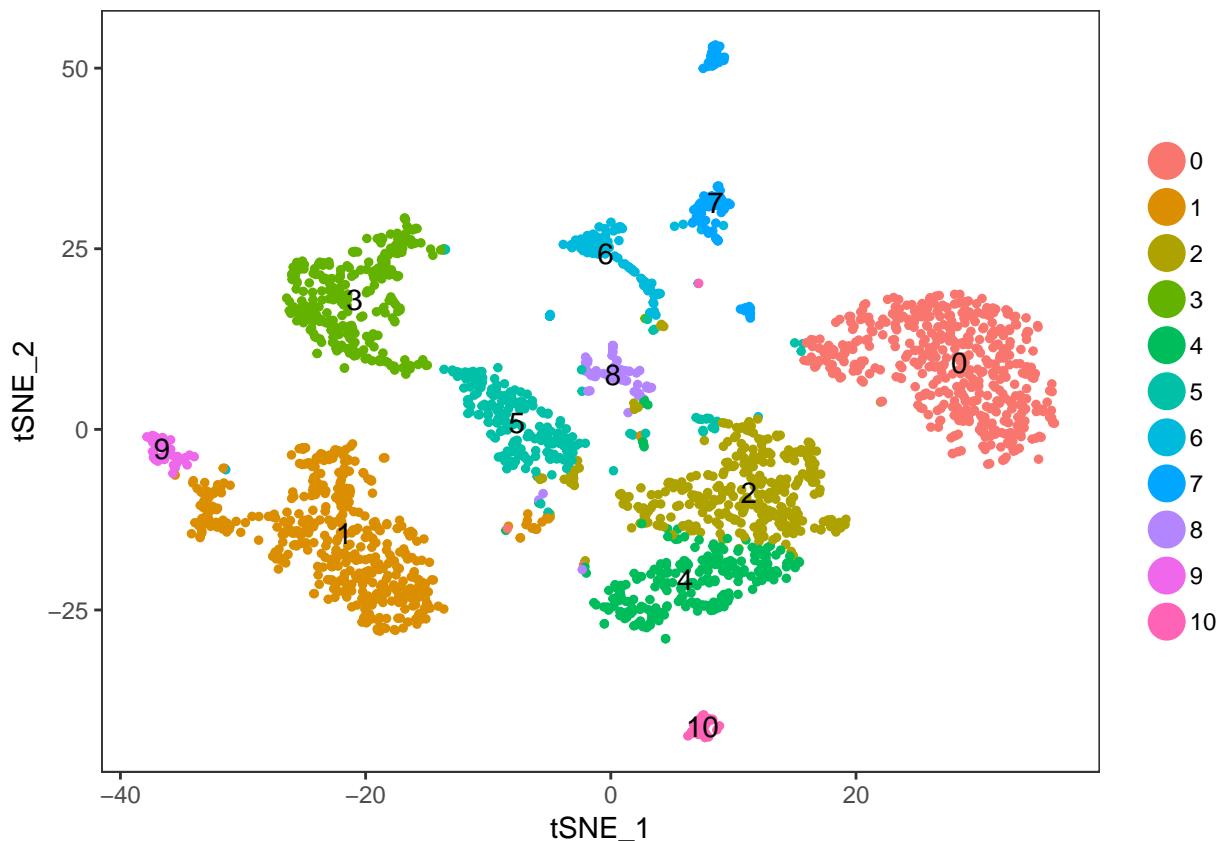
```
library(Seurat)

## Loading required package: ggplot2
## Loading required package: cowplot
##
## Attaching package: 'cowplot'
## The following object is masked from 'package:ggplot2':
##     ggsave
## Loading required package: Matrix
library(dplyr)

##
## Attaching package: 'dplyr'
## The following objects are masked from 'package:stats':
##     filter, lag
## The following objects are masked from 'package:base':
##     intersect, setdiff, setequal, union
library(Matrix)

#KS OBJECT ( 7 DAYS KETOROLAC)
load("KS.Robj", verbose=TRUE)

## Loading objects:
##     KS
#tSNE
KS <- RunTSNE(object = KS, dims.use = 1:13, do.fast = TRUE)
TSNEPlot(object = KS,do.label=TRUE)
```

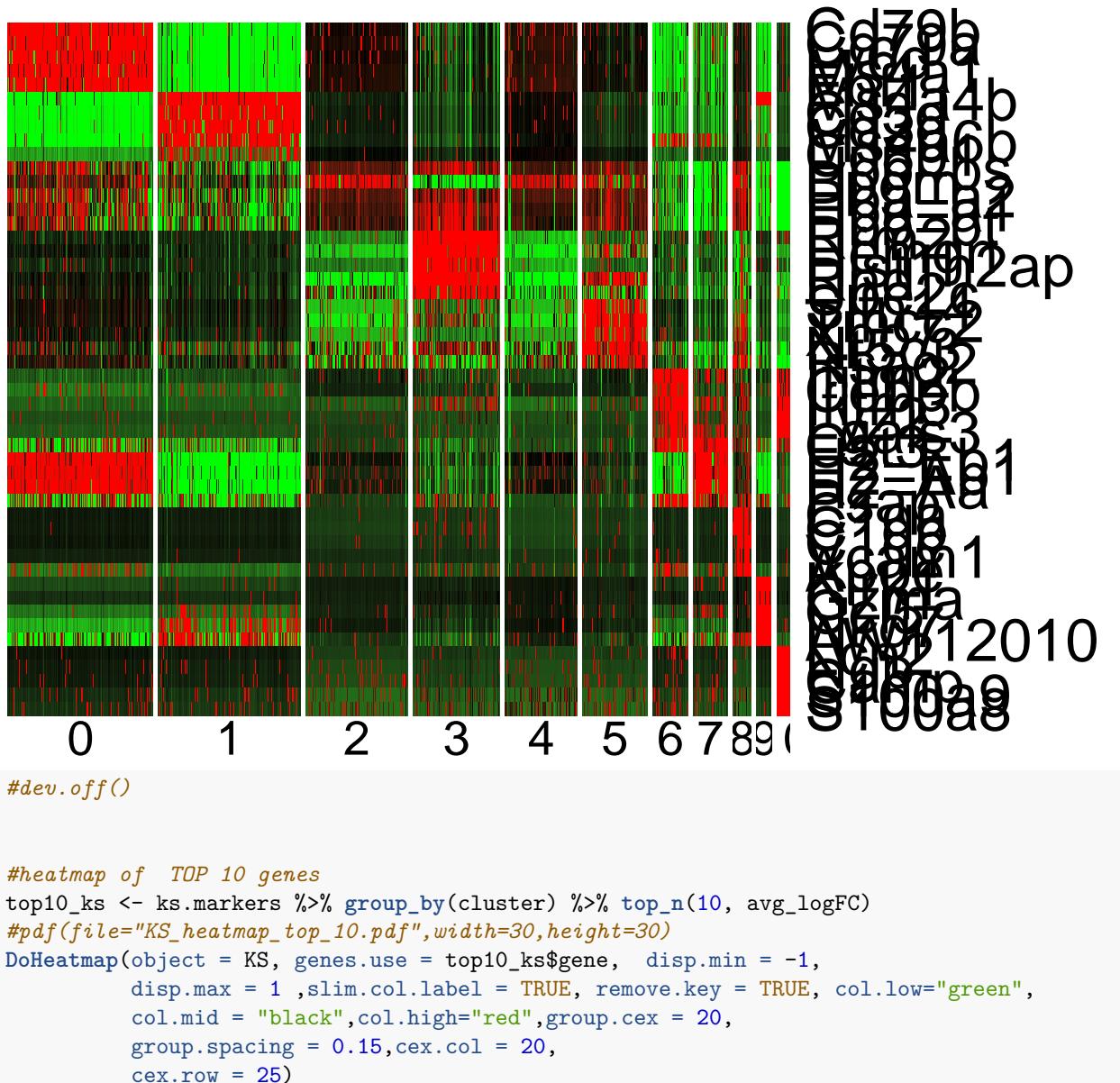


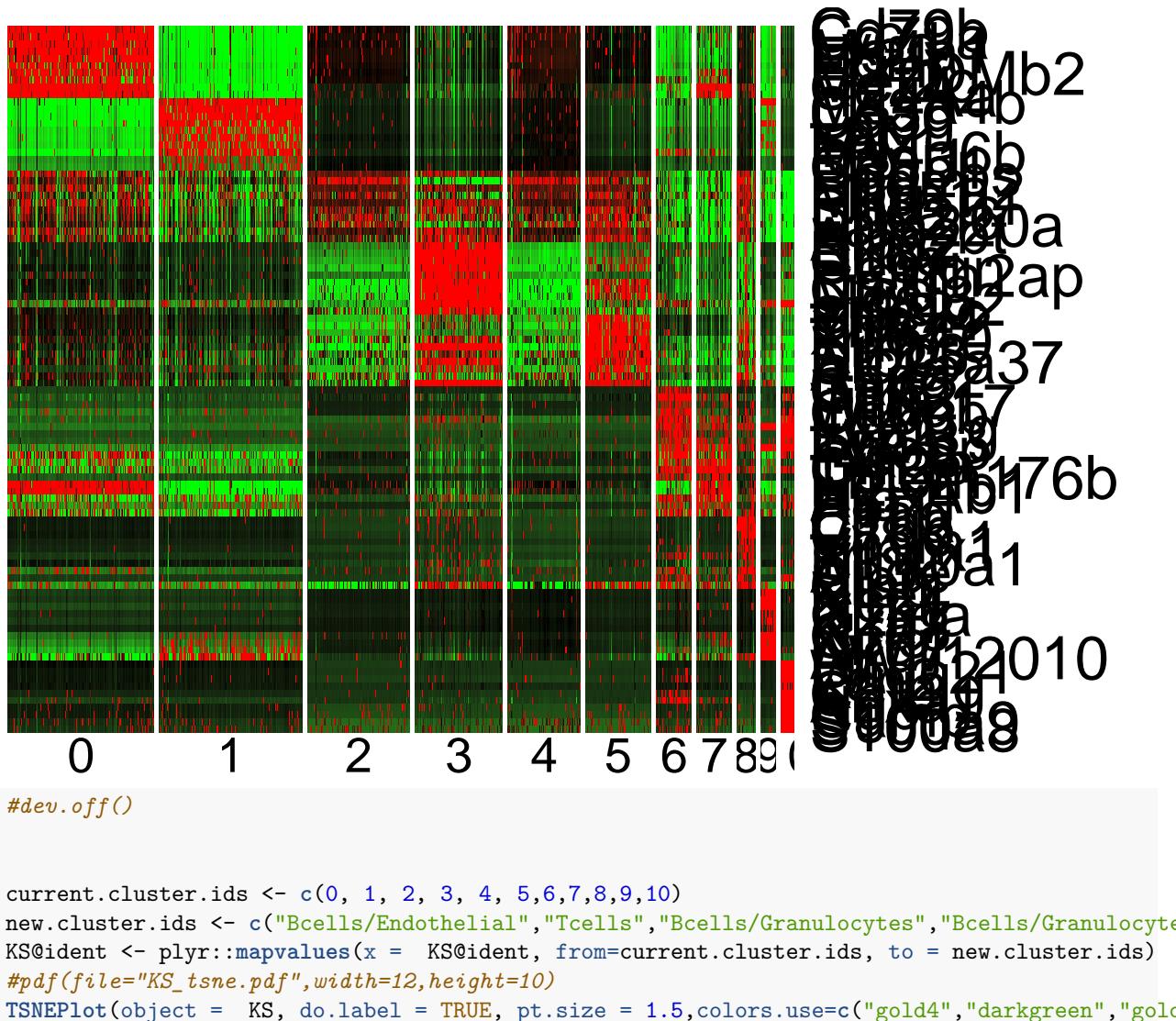
```

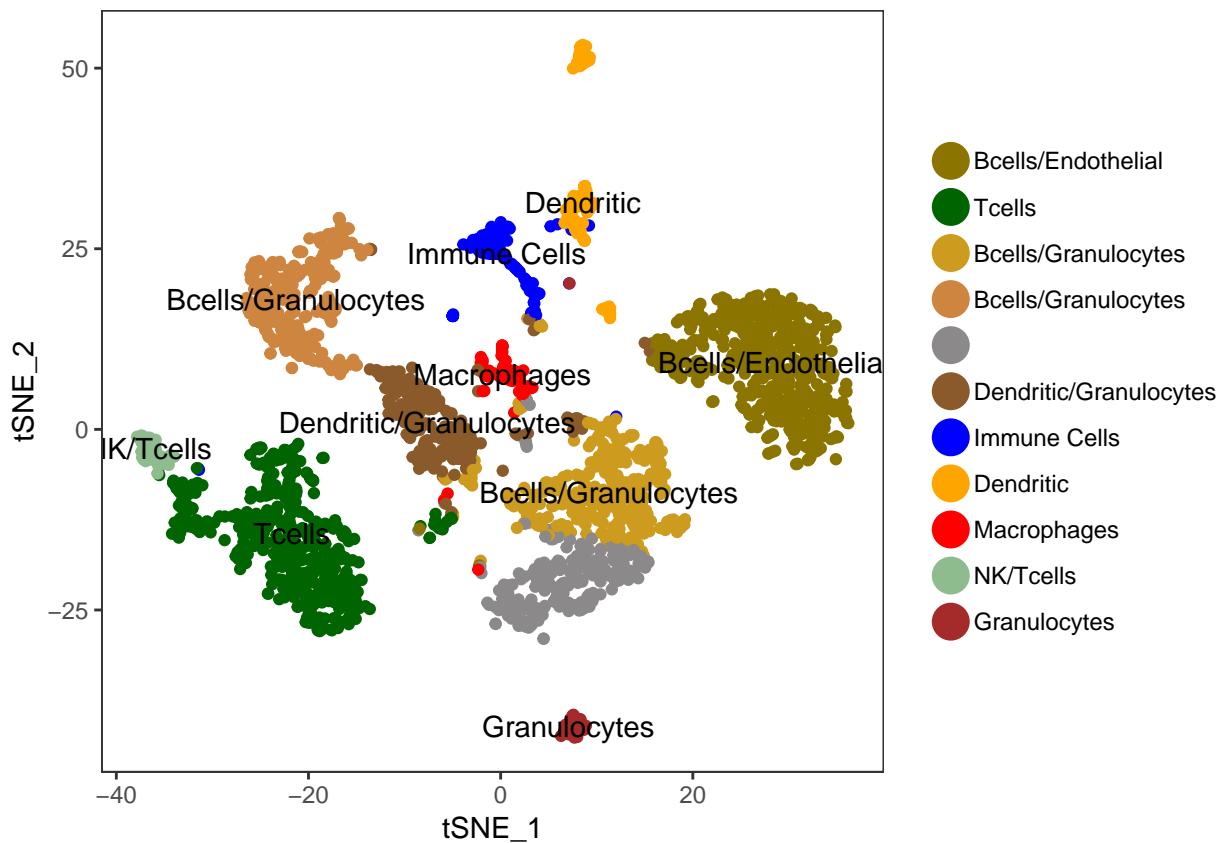
ks.markers <- FindAllMarkers(object = KS , min.pct = 0.25, thresh.use = 0.25)

#heatmap of TOP 5 genes
top5_ks <- ks.markers %>% group_by(cluster) %>% top_n(5, avg_logFC)
#pdf(file="KS_heatmap_top_5.pdf",width=20,height=20)
DoHeatmap(object = KS, genes.use = top5_ks$gene, disp.min = -1,
          disp.max = 1 ,slim.col.label = TRUE, remove.key = TRUE, col.low="green",
          col.mid = "black",col.high="red",group.cex = 20,
          group.spacing = 0.15,cex.col = 20,
          cex.row = 25)

```



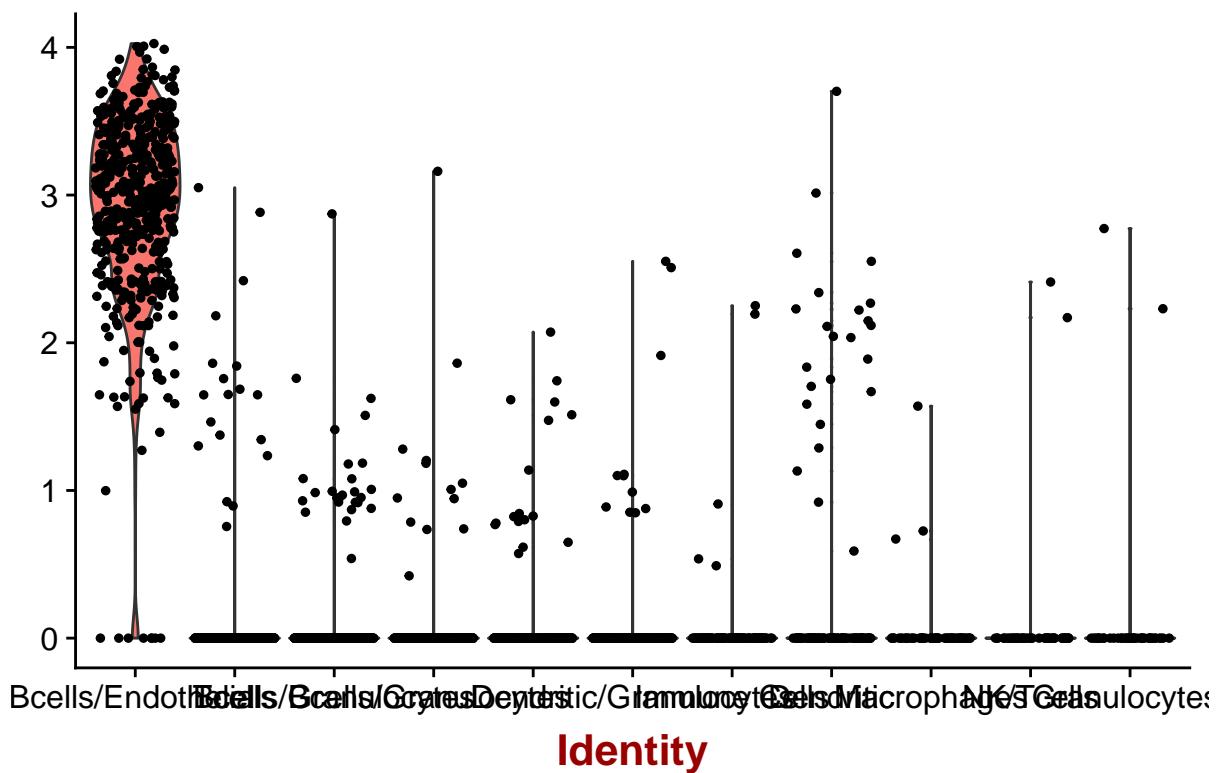




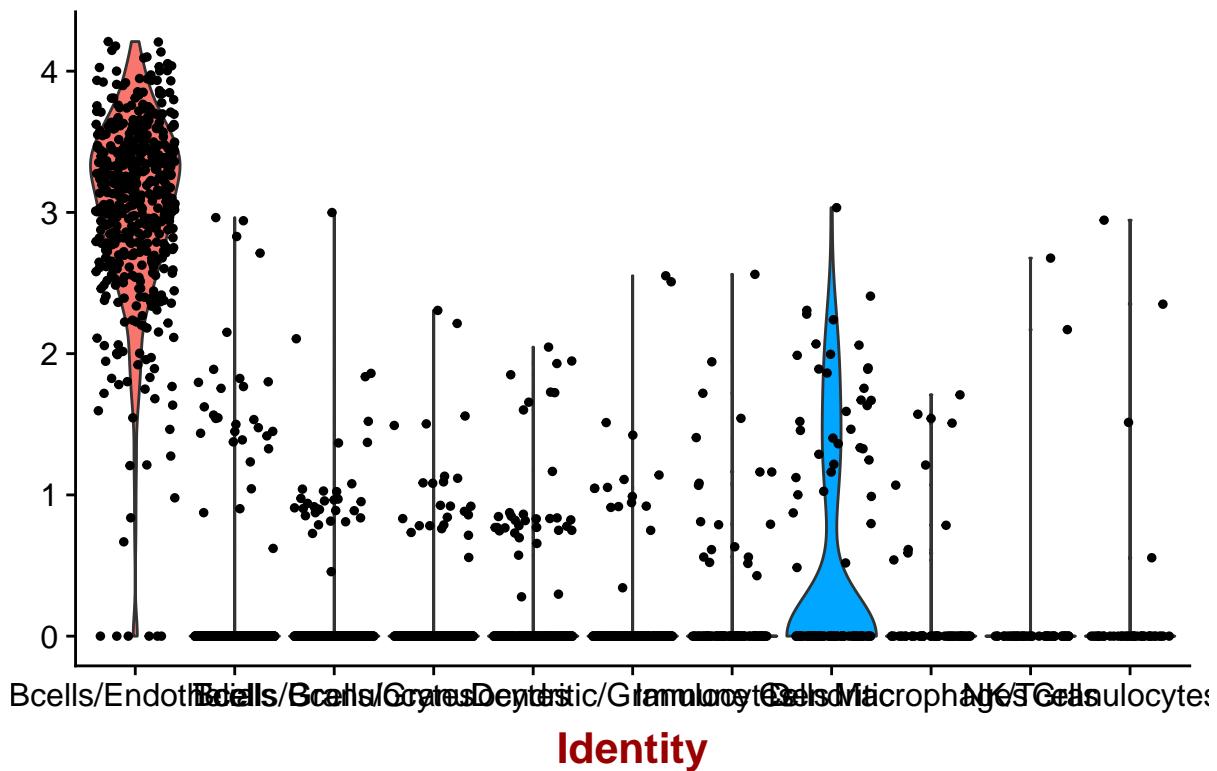
```
#dev.off()

#Violin plots
#B CELLS
#nams <- c("Cd79a", "Cd79b", "Cd19", "Blk")
#pdf(paste(nams, "_Bcells_Markers_KS.pdf"))
VlnPlot(object = KS, features.plot = c("Cd79a"))
```

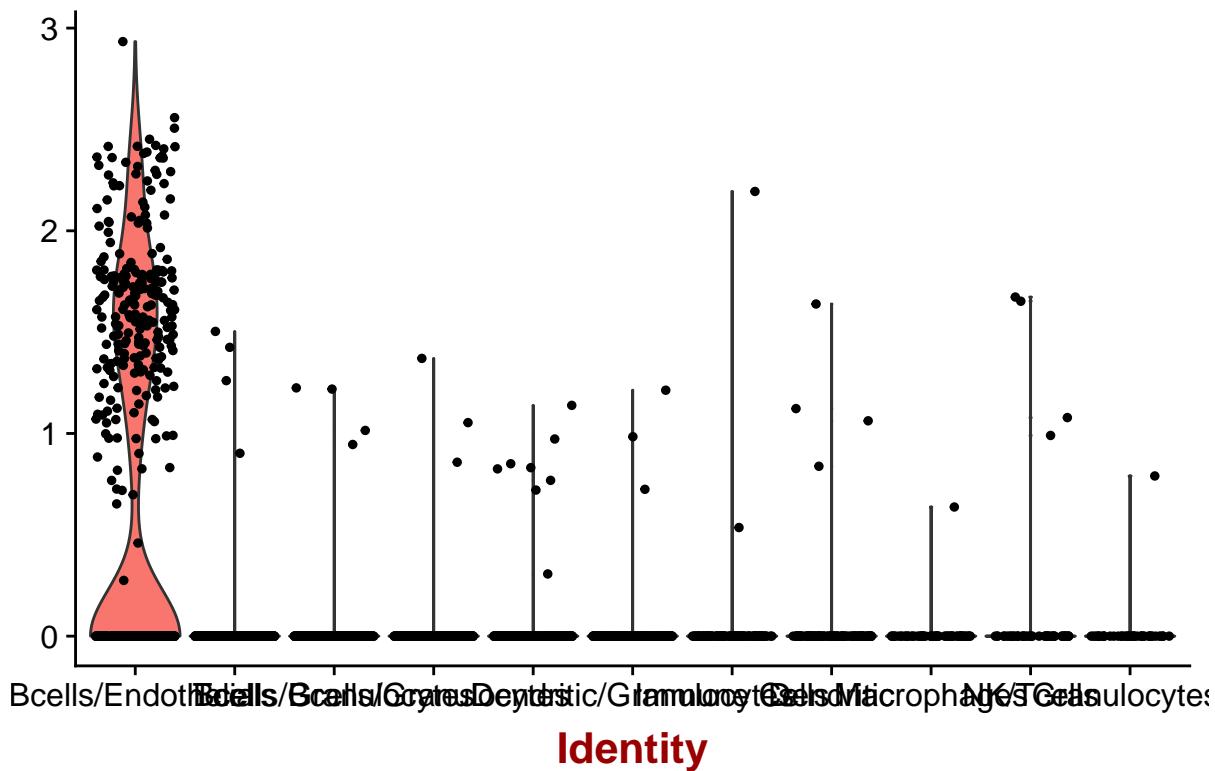
Cd79a



Cd79b

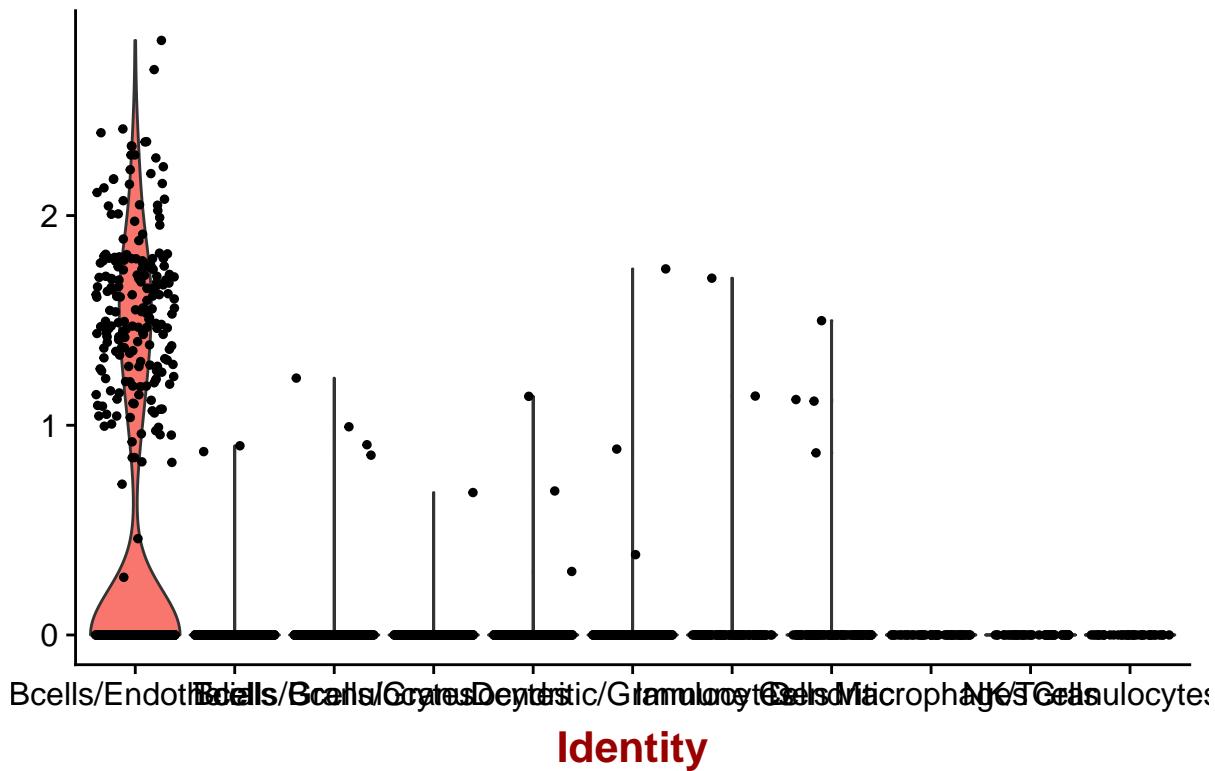


Cd19



Identity

Blk

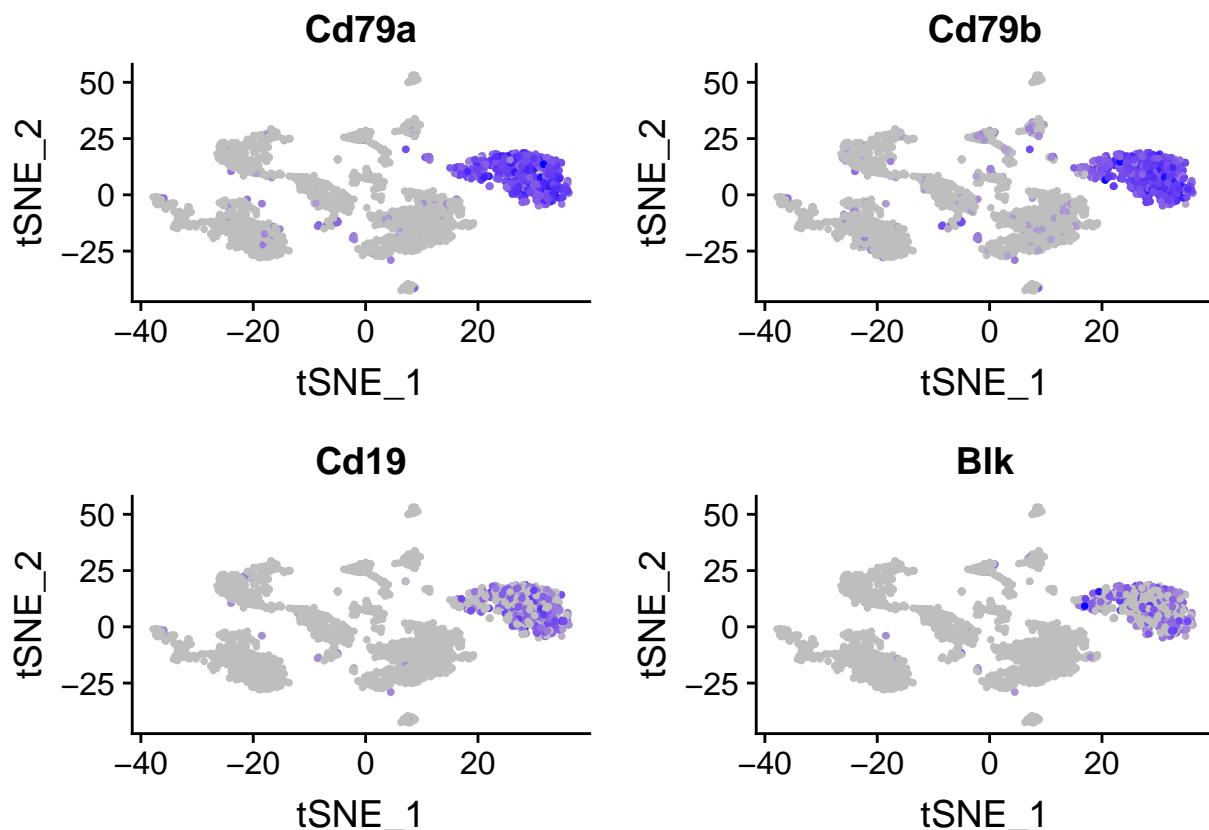


```

#dev.off()

#Featureplot
#B cells
#pdf(file="KS_Bcells.pdf",width=10,height=10)
FeaturePlot(object = KS, features.plot = c("Cd79a","Cd79b","Cd19","Blk"), cols.use = c("grey", "blue"), ...

```



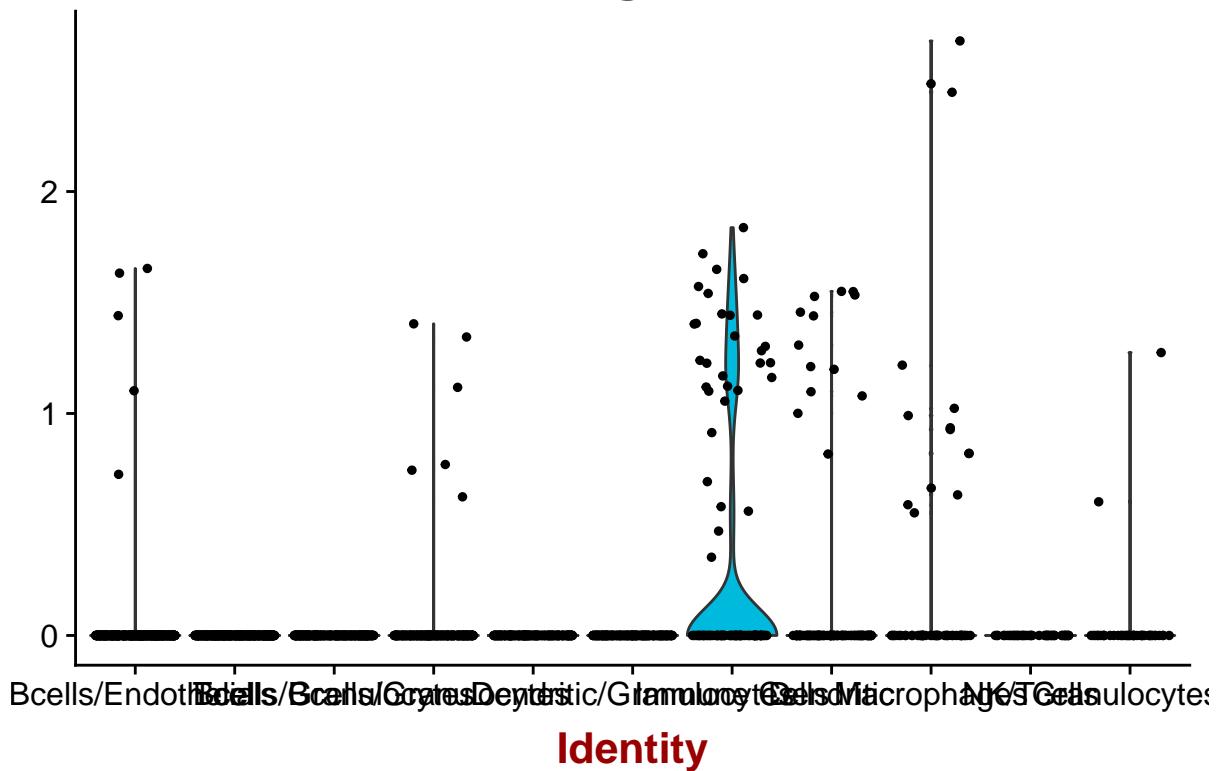
```

#dev.off()

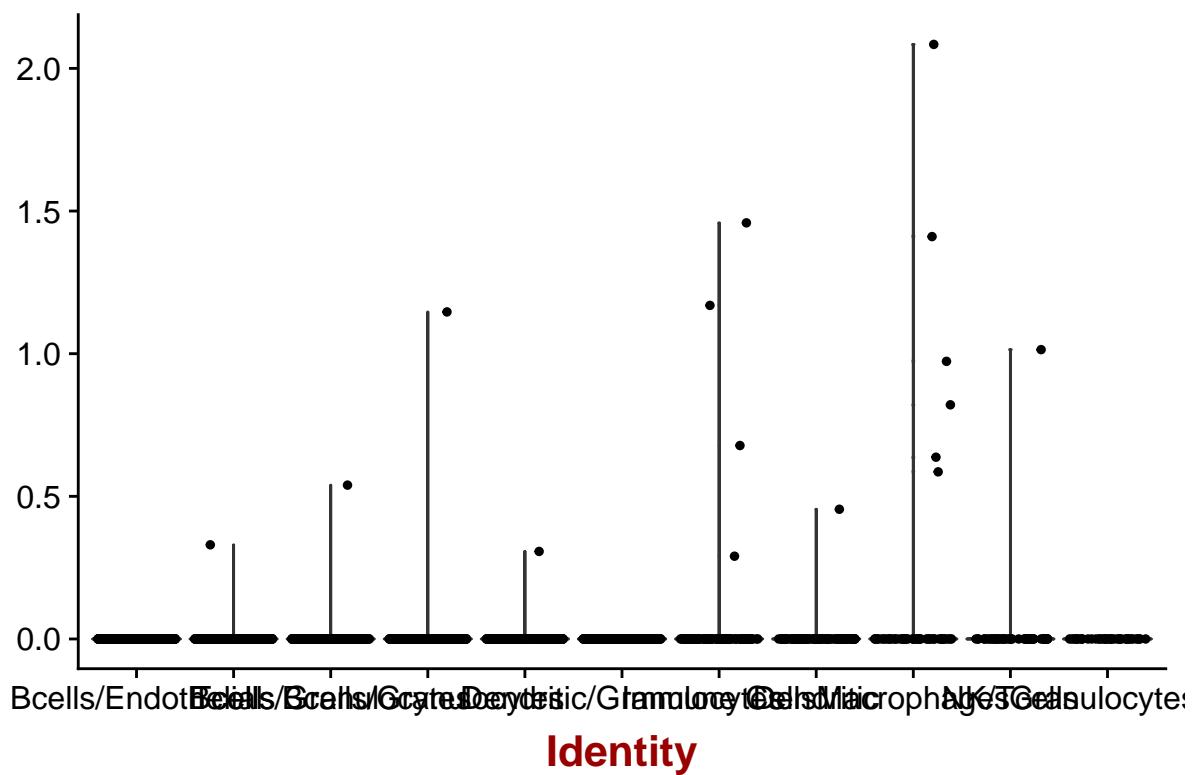
#Macrophages
#nams <- c("Adgre1", "Cd163", "Cd14", "Csf1r", "Ccr2")
#pdf(paste(nams, "_Macrophages_Markers_KS.pdf"))
VlnPlot(object = KS, features.plot = c("Adgre1"))

```

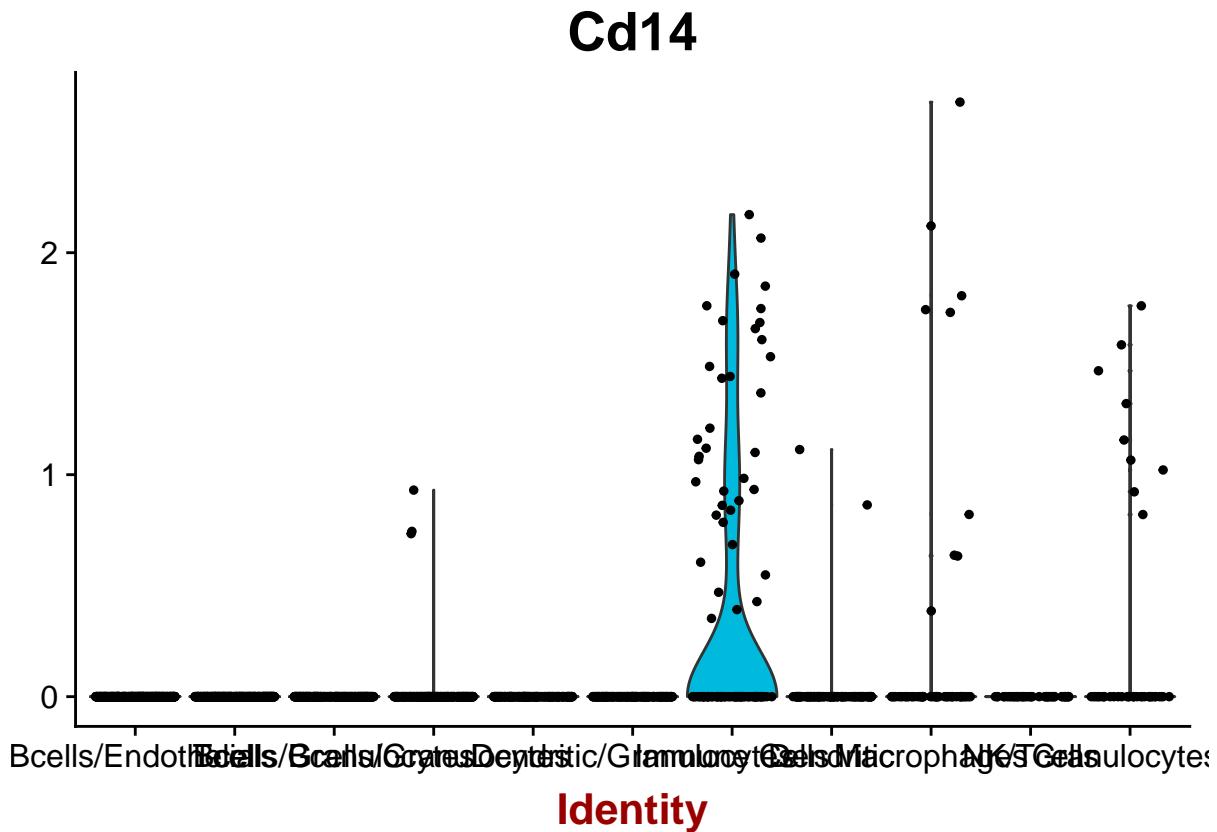
Adgre1



Cd163

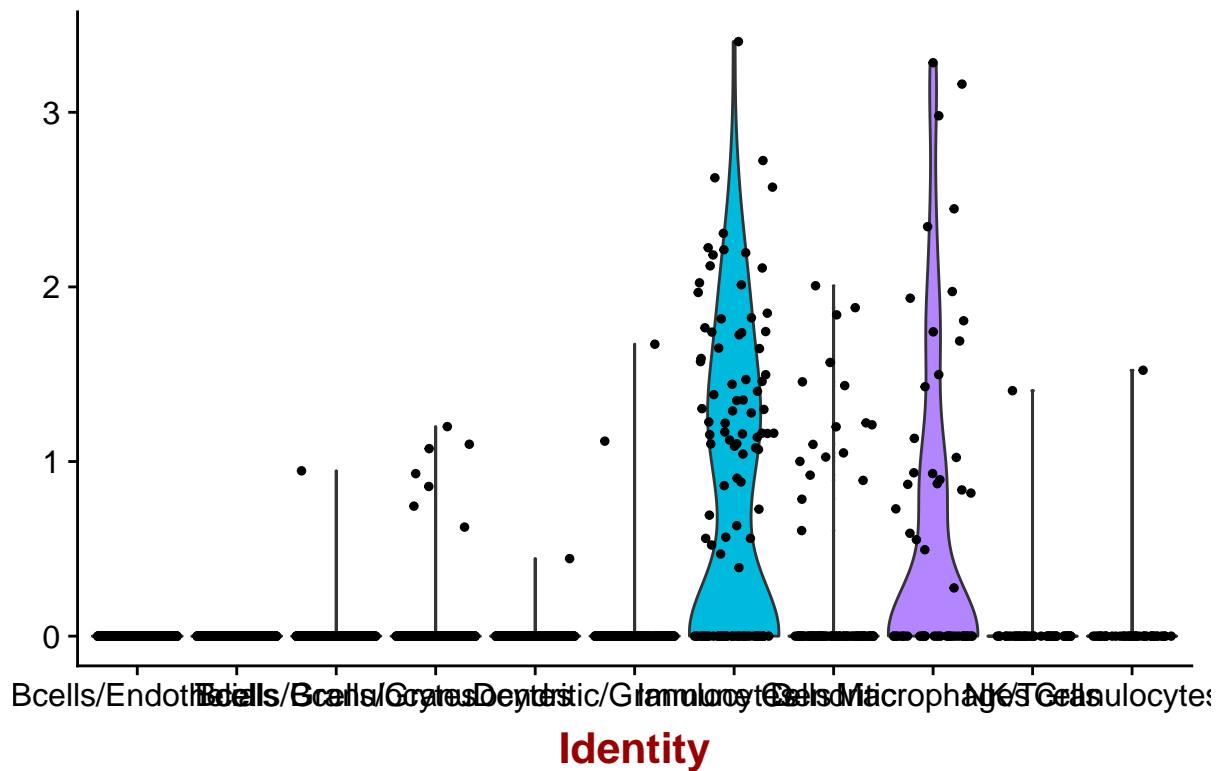


```
VlnPlot(object = KS, features.plot = c("Cd14"))
```

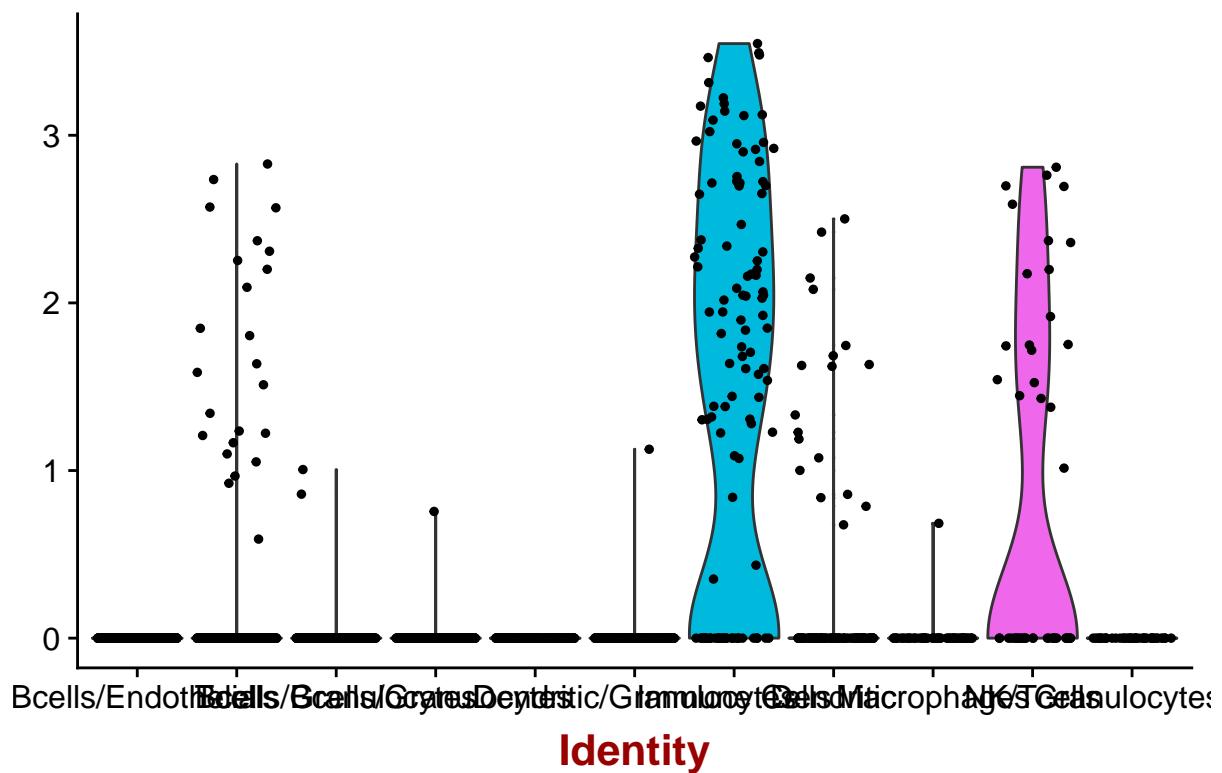


```
VlnPlot(object = KS, features.plot = c("Csf1r"))
```

Csf1r

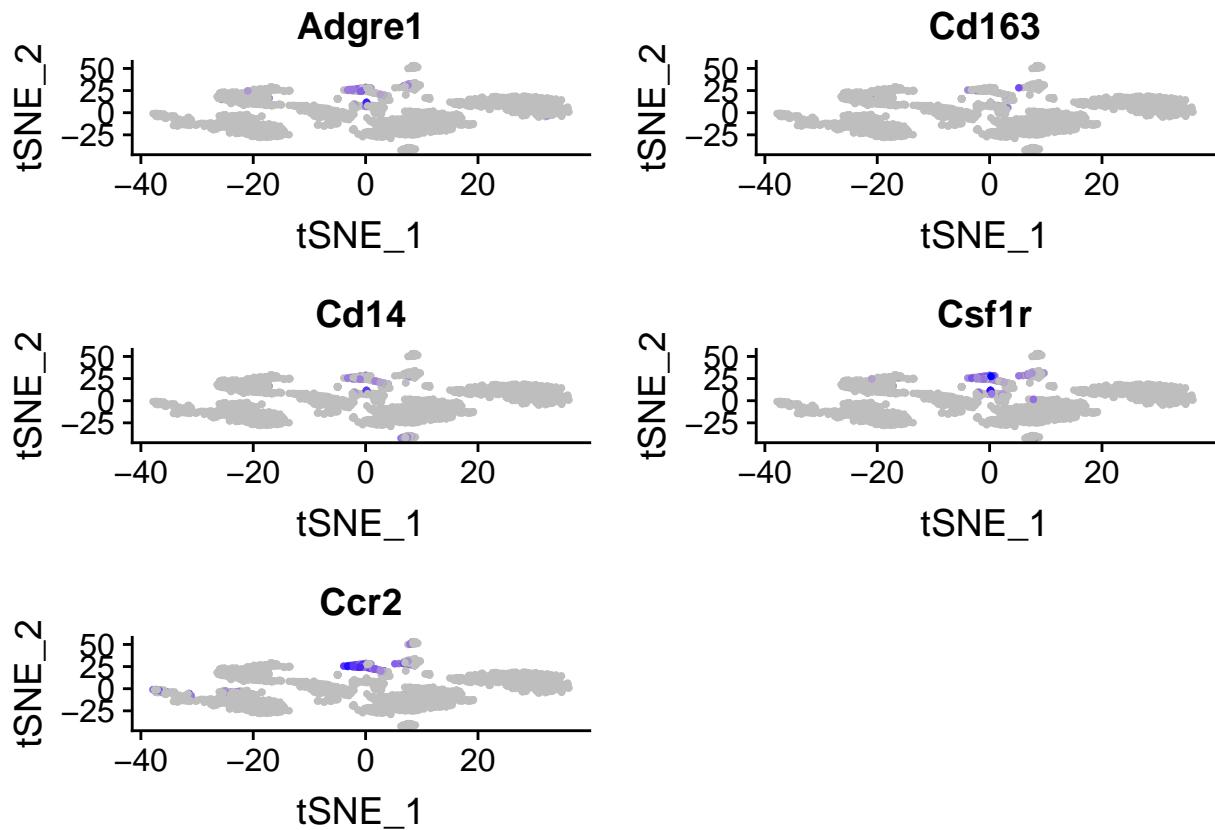


Ccr2



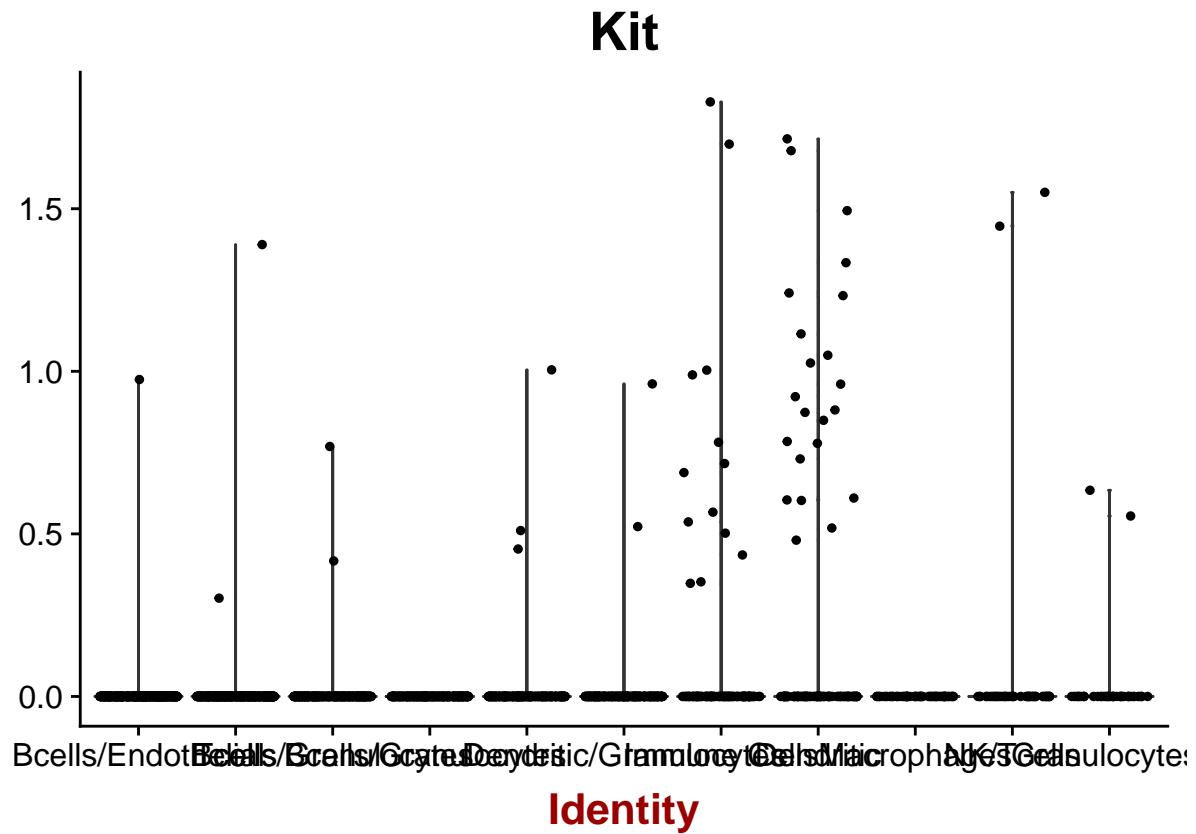
Identity

```
#dev.off()  
  
#pdf(file="KS_Macrophages.pdf",width=10,height=10)  
FeaturePlot(object =KS, features.plot = c("Adgre1","Cd163","Cd14","Csf1r","Ccr2"), cols.use = c("grey",
```



```
#dev.off()

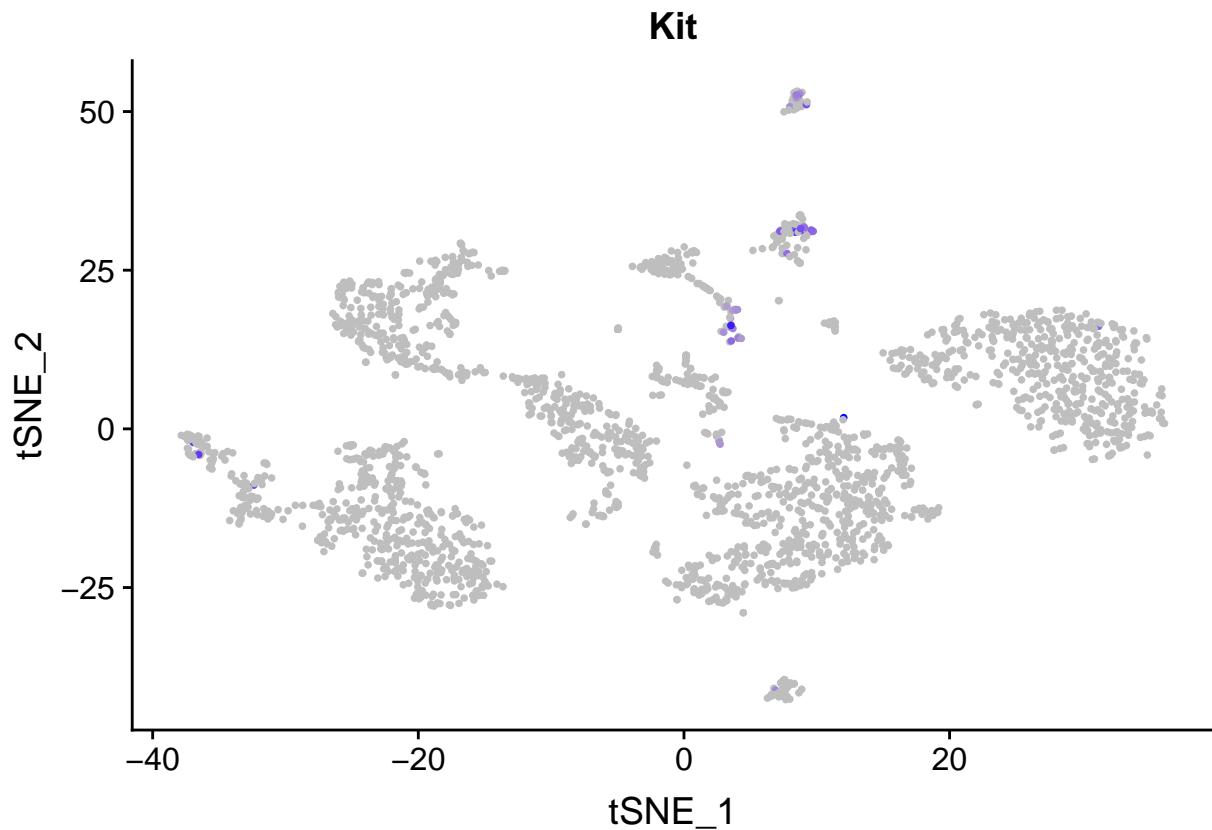
#Mast cells
#nams <- c("Kit")
#pdf(paste(nams, "_Mast_Markers_KS.pdf"))
#VlnPlot(object = KS, features.plot = c("Fcera1a"))
VlnPlot(object = KS, features.plot = c("Kit"))
```



```
#VlnPlot(object =KS, features.plot = c("Tpsab1"))
#dev.off()
```

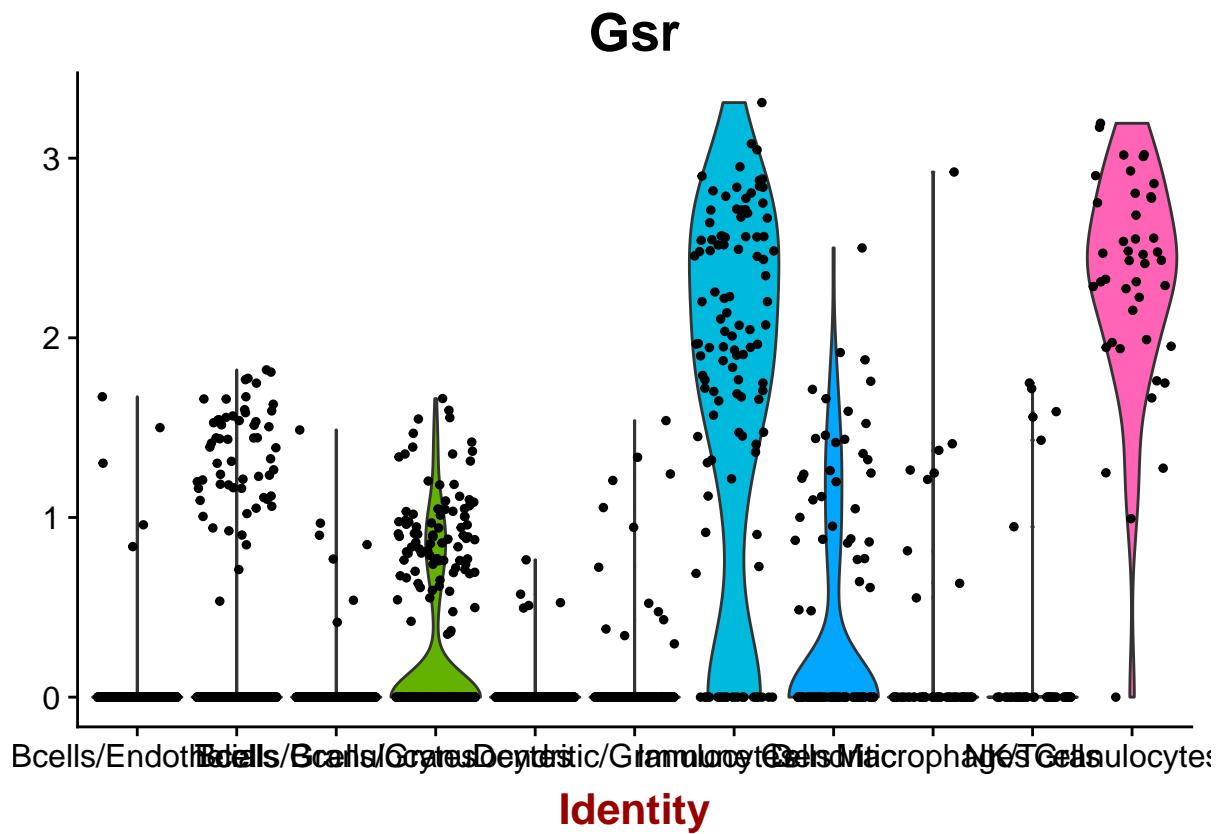
```
#pdf(file="KS_Mast.pdf",width=10,height=10)
```

```
FeaturePlot(object =KS, features.plot = c("Kit"), cols.use = c("grey", "blue"), reduction.use = "tsne")
```



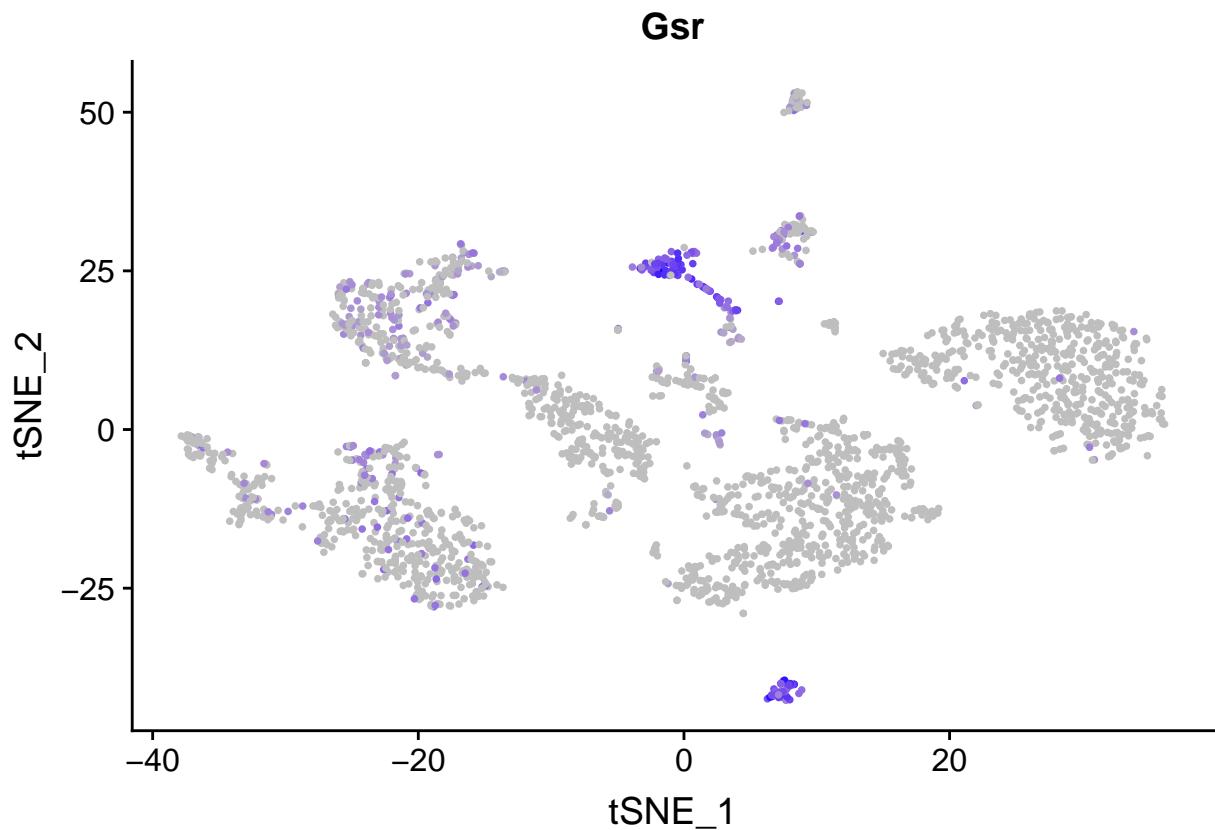
```
#dev.off()

#Neutrophil
#nams <- c("Gsr")
#pdf(paste(nams, "_Neutrophils_Markers_KS.pdf"))
VlnPlot(object = KS, features.plot = c("Gsr"))
```



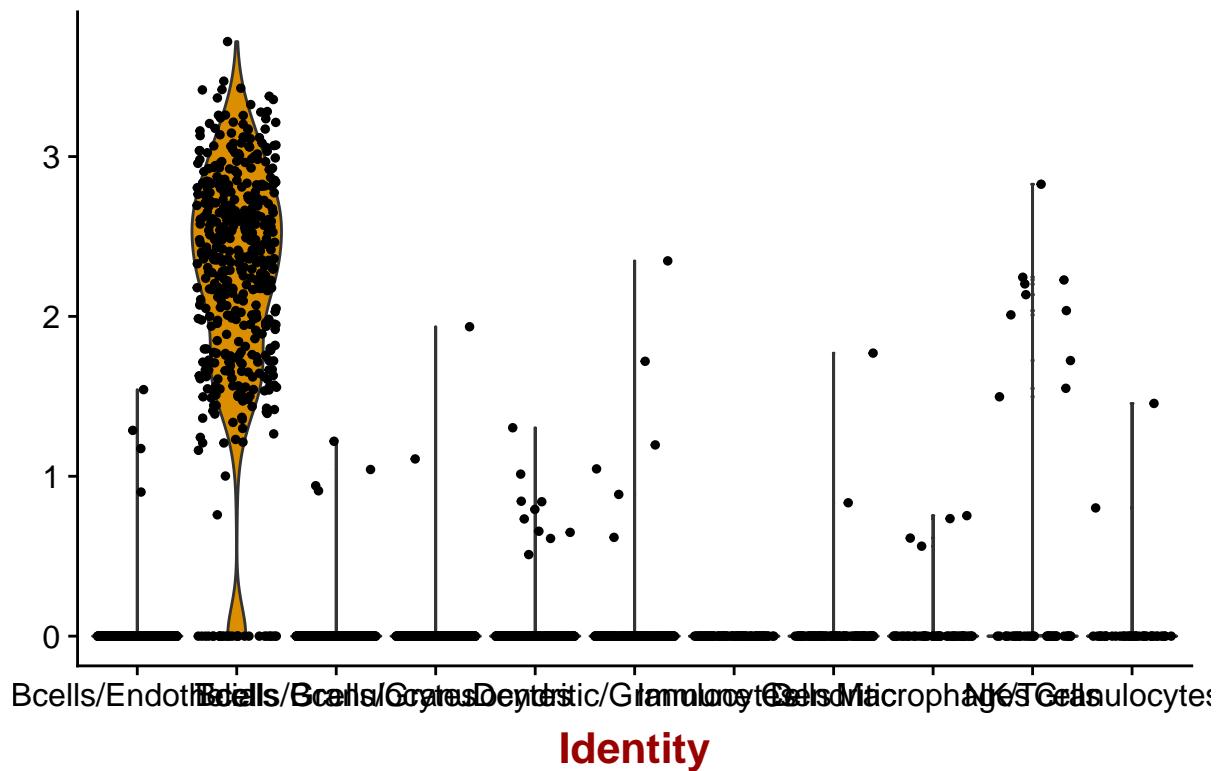
```
#dev.off()

#pdf(file="KS_Neutrophil.pdf",width=10,height=10)
FeaturePlot(object =KS, features.plot = c("Gsr"), cols.use = c("grey", "blue"), reduction.use = "tsne")
```

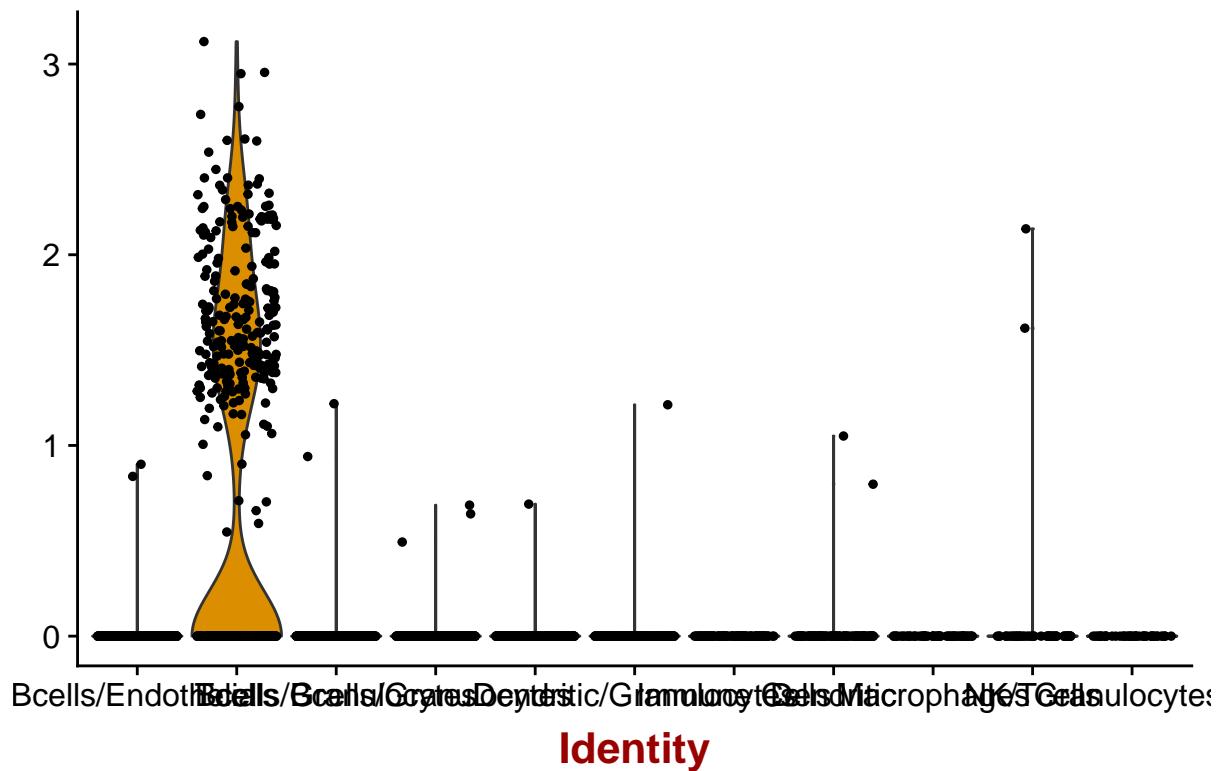


```
#dev.off()  
  
#T cells  
#nams <- c("Cd3d", "Cd3e", "Cd3g", "Cd247")  
#pdf(paste(nams, "_Tcells_other_Markers_KS.pdf"))  
VlnPlot(object = KS, features.plot = c("Cd3d"))
```

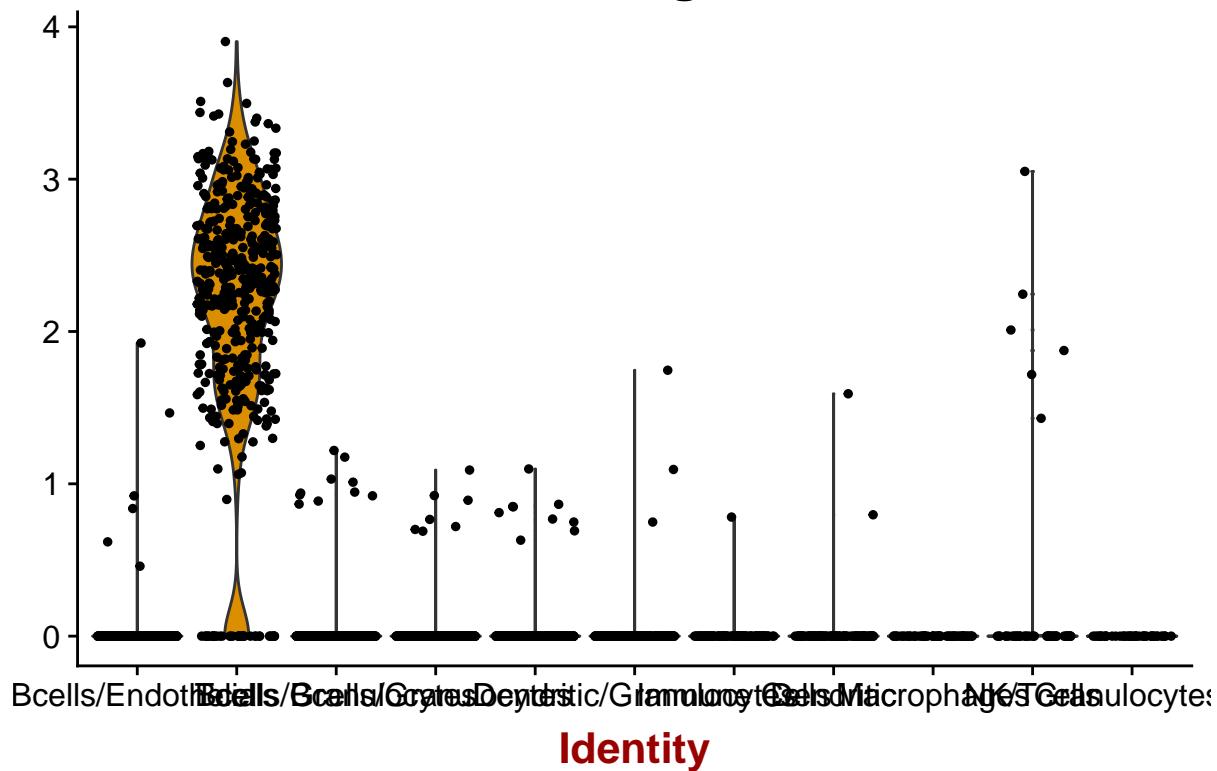
Cd3d



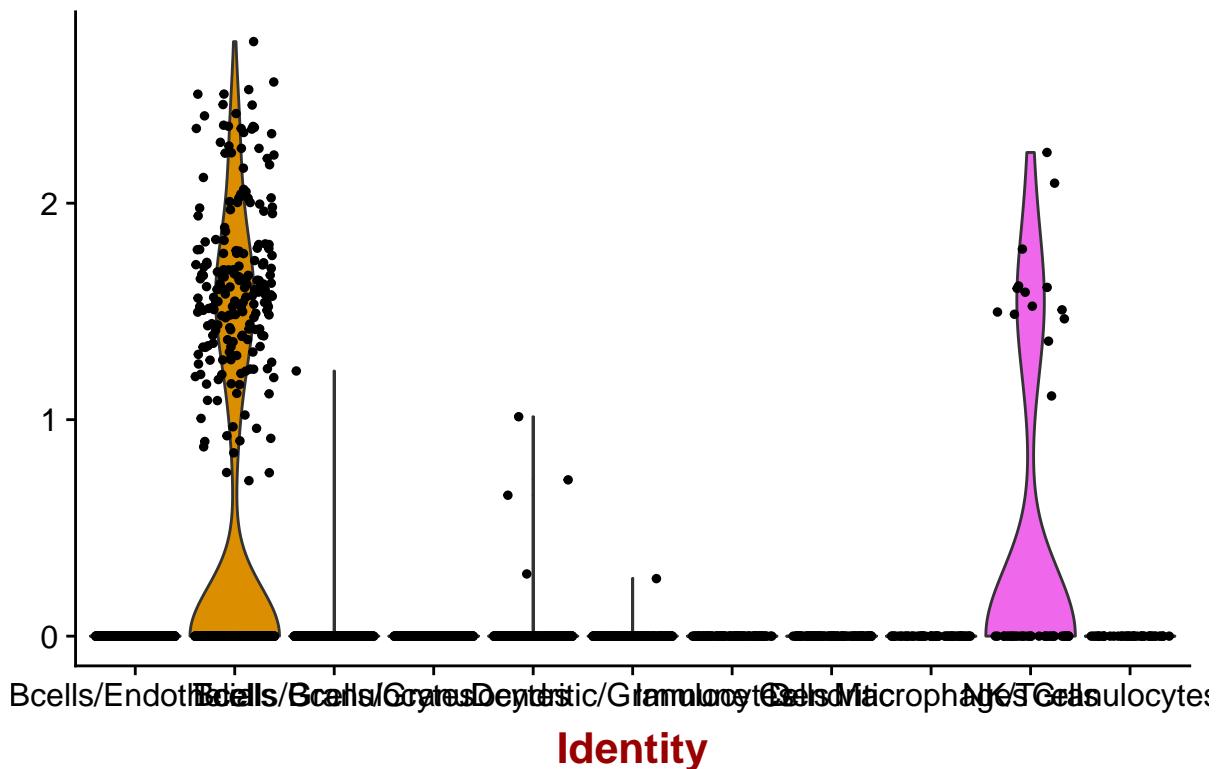
Cd3e



Cd3g



Cd247



Identity

```
#dev.off()  
  
#pdf(file="KS_Tcell_other_markers.pdf",width=10,height=10)  
FeaturePlot(object =KS, features.plot = c("Cd3d","Cd3e","Cd3g","Cd247"), cols.use = c("grey", "blue"),
```

