E9.5 scRNA

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Load package

```
library(Seurat)
```

```
## Attaching SeuratObject
```

```
library(FateMapper)
```

```
## Loading required package: ggplot2
```

```
## Warning: package 'ggplot2' was built under R version 4.2.3
```

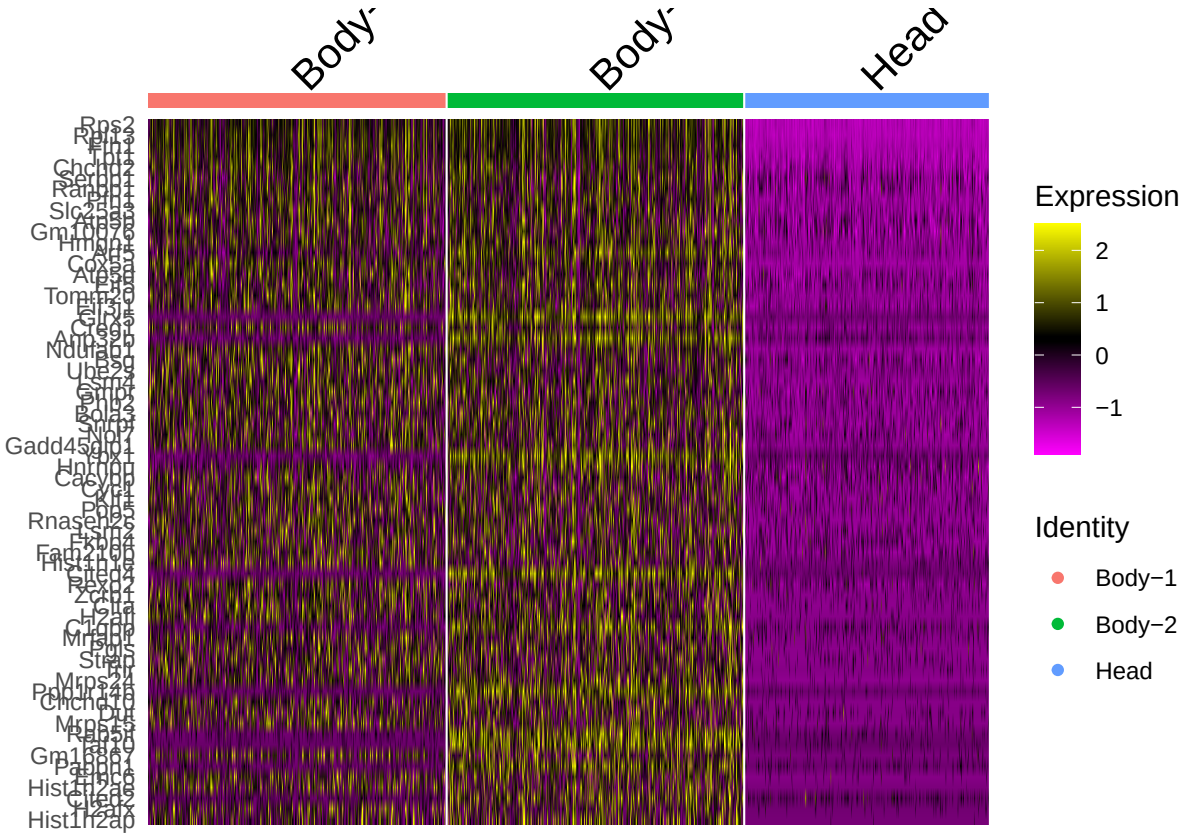
```
rna = readRDS('/data/jiangjunyao/20231205_scRNA/e95_3sample_scanvi_seurat.rds')
```

head & body ery deg

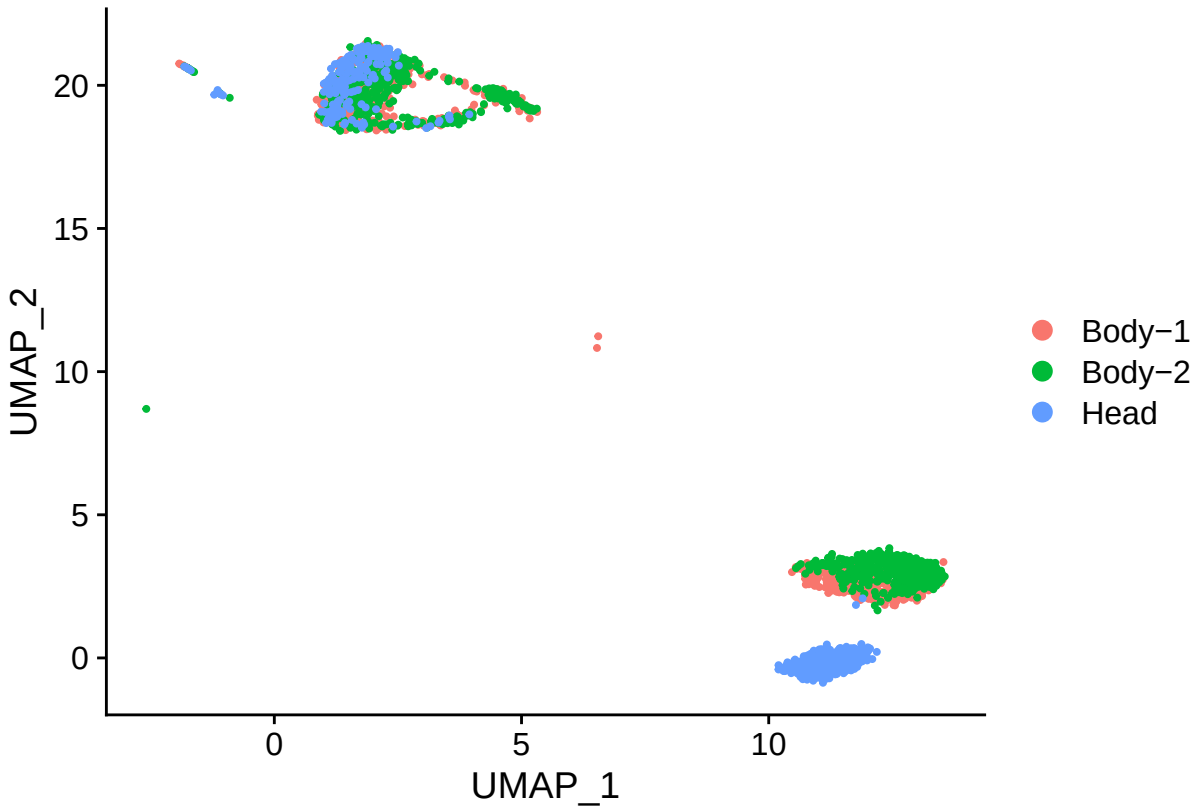
```
deg_use = deg[deg$avg_log2FC>1,]
DefaultAssay(ery) = 'RNA'
ery = ScaleData(ery)
```

```
## Centering and scaling data matrix
```

```
DoHeatmap(ery,deg_use$gene,group.by = 'orig.ident')
```

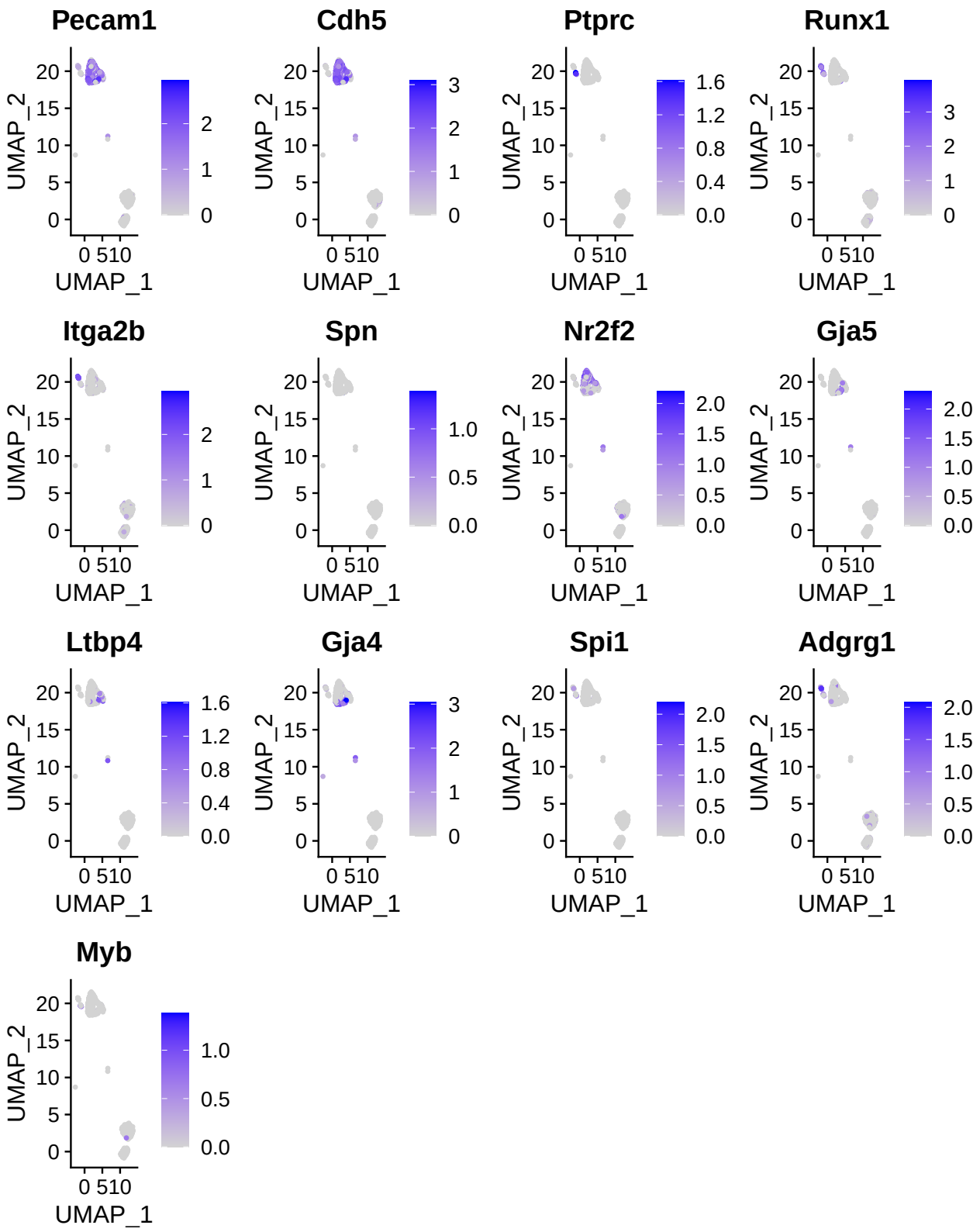



```
blood = subset(rna,celltype %in% c('Primitive erythroid cells','Blood progenitors','Endothelium'))
UMAPPlot(blood)
```

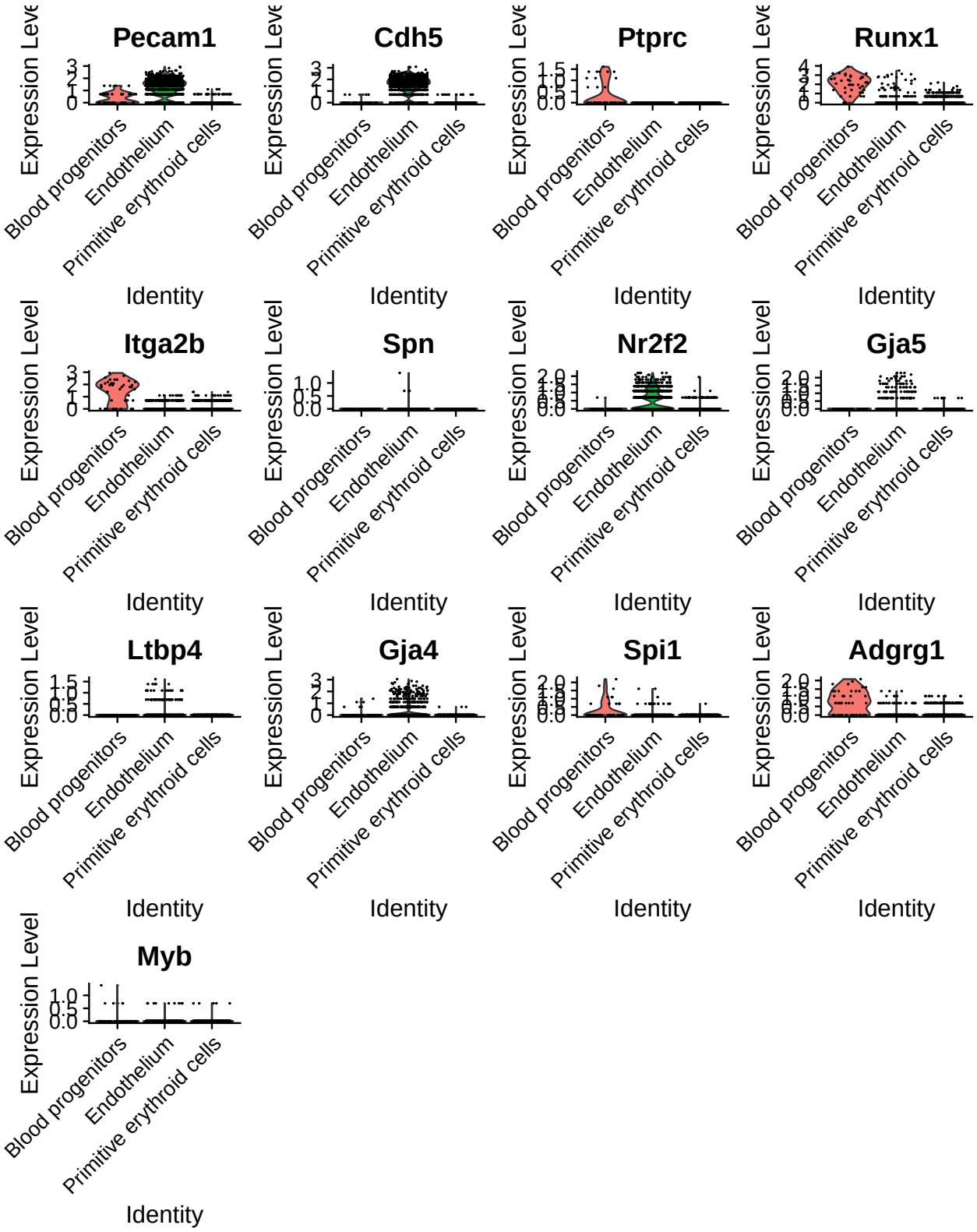


some markers

```
blood_marker = c('Pecam1', 'Cdh5', 'Ptprc', 'Runx1', 'Itga2b', 'Spn', 'Nr2f2',
                 'Gja5','Ltbp4','Gja4', 'Spi1','Adgrg1', 'Myb')
FeaturePlot(blood,blood_marker)
```



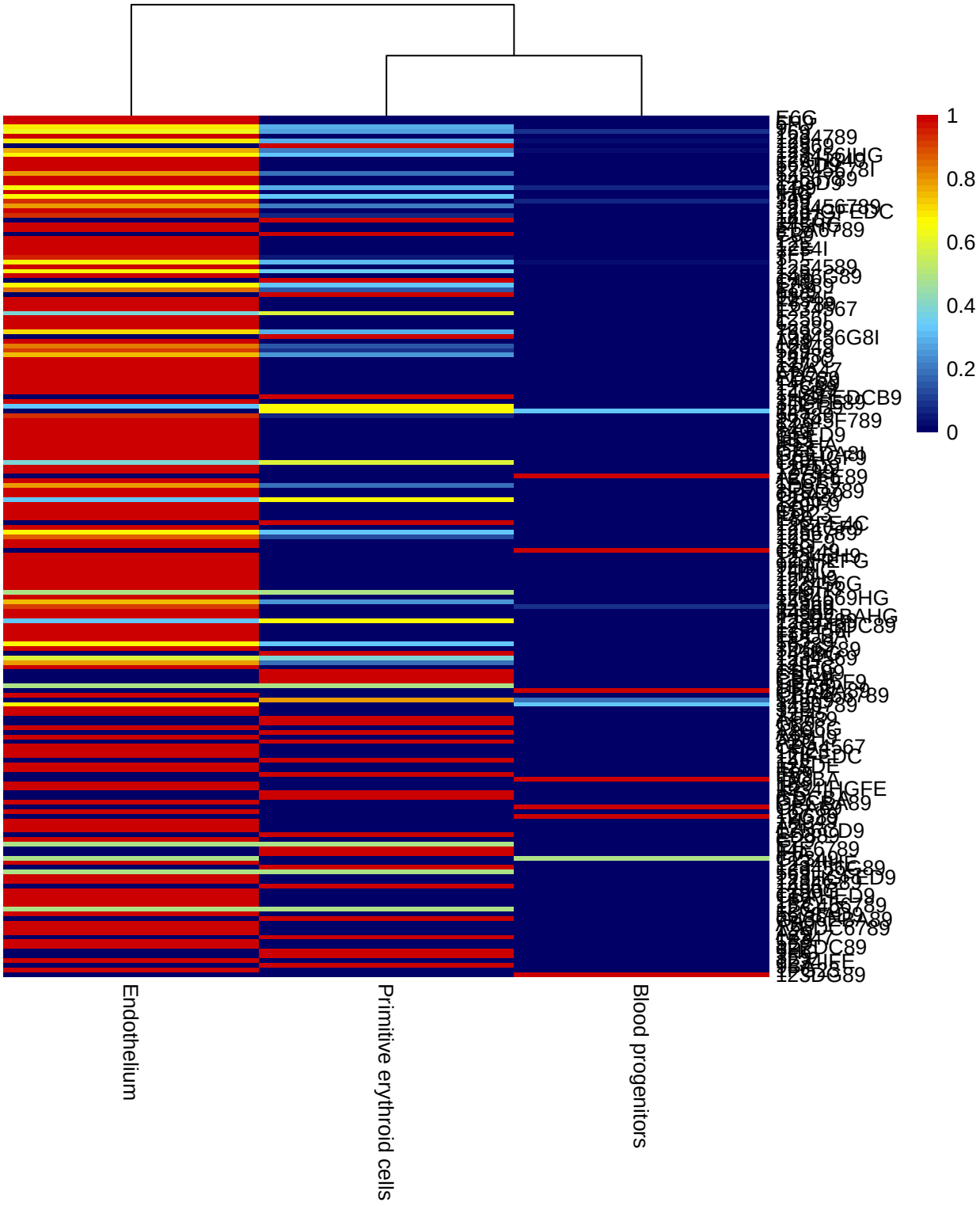

```
VlnPlot(blood,blood_marker,group.by = 'celltype')
```



endo deg

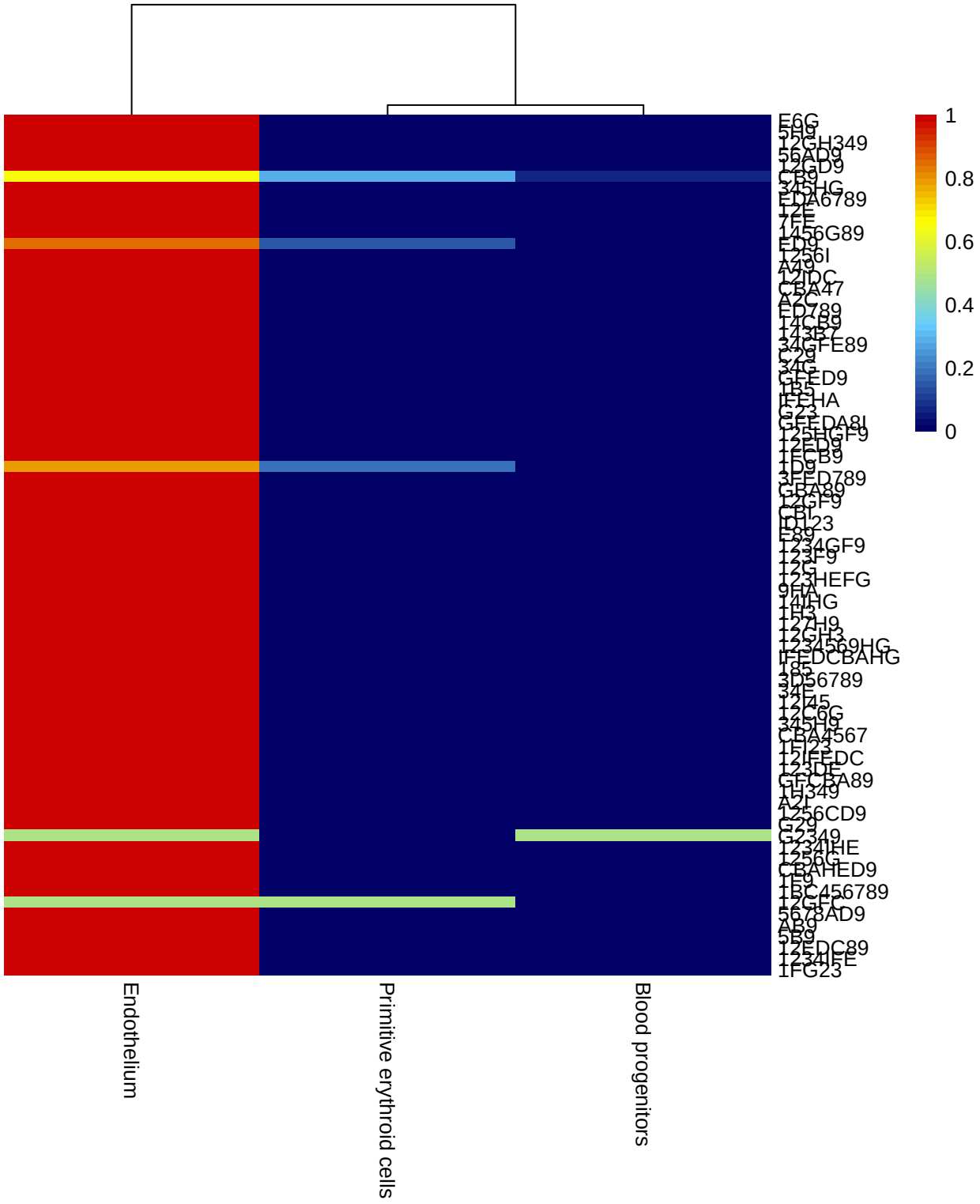
```
pgen <- read.delim("~/20231205_scRNA/pgen")
rare_barcode = pgen[pgen$pgen< 0.001,1]
blood_fate = blood@meta.data[,c('barcodes','celltype')]
```

```
blood_fate = blood_fate[!is.na(blood_fate[,1]),]
fate_count = fate_mapping(blood_fate)
```



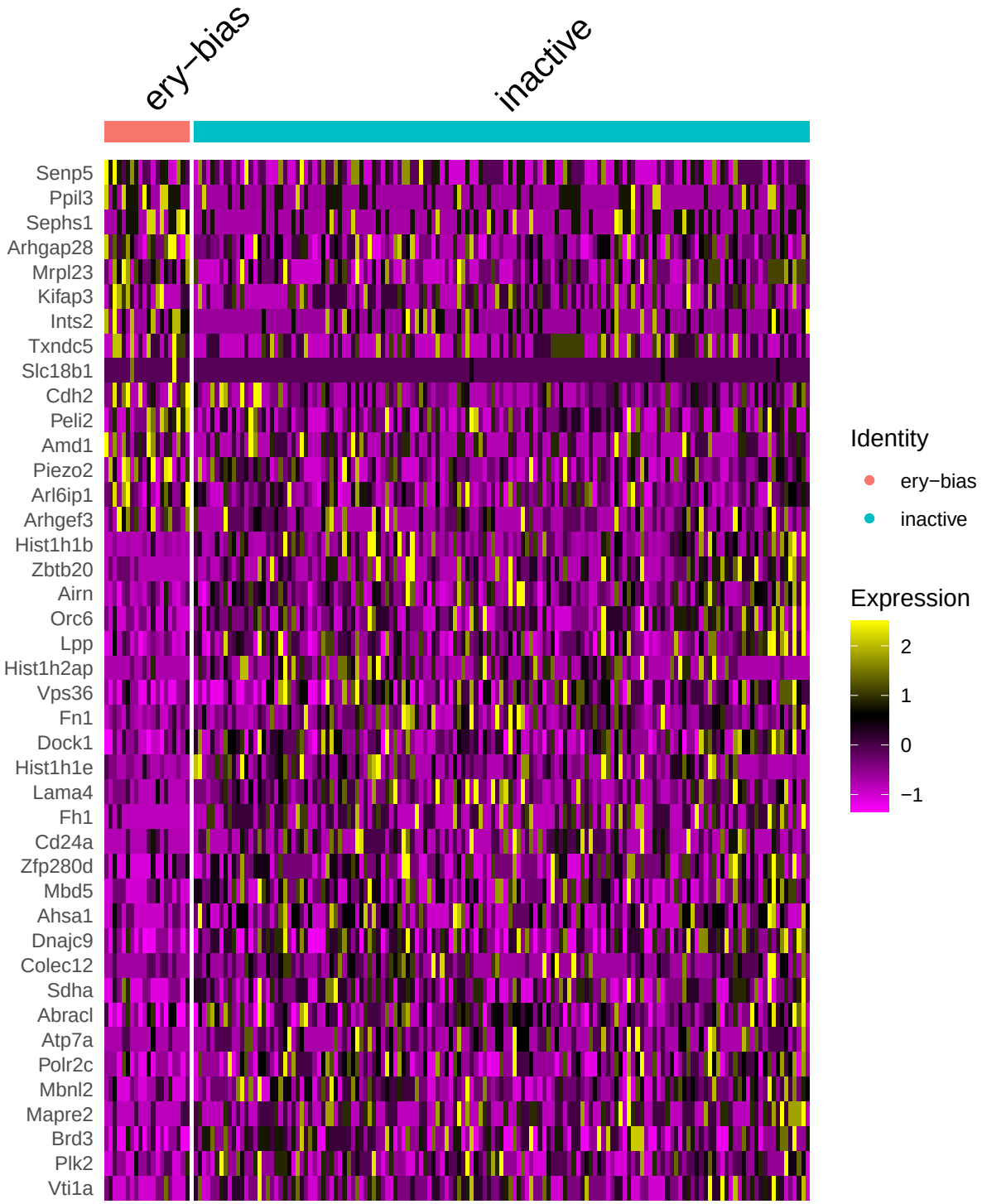

```
fate_count = fate_count[fate_count$Endothelium!=0,]
fate_count = fate_count[rownames(fate_count)%in%rare_barcode,]
```

```
blood_fate = blood_fate[blood_fate$barcodes %in% rownames(fate_count),]
fate_count = fate_mapping(blood_fate)
```




```
barcode_ery = rownames(fate_count[fate_count$`Primitive erythroid cells`!=0,])
barcode_no = rownames(fate_count[fate_count$`Primitive erythroid cells`==0,])
```

```
rna_blood_ery = subset(blood,barcodes %in% c(barcode_ery,barcode_no))
rna_blood_ery$fate = ifelse(rna_blood_ery$barcodes %in% barcode_ery,
                            'ery-bias','inactive')
rna_blood_ery = subset(rna_blood_ery,celltype=='Endothelium')
rna_blood_ery@active.ident =as.factor(rna_blood_ery$fate)
fate_deg = FindAllMarkers(rna_blood_ery,test.use = 'negbinom')
fate_deg = fate_deg[fate_deg$avg_log2FC>0.5,]
DefaultAssay(rna_blood_ery) = 'RNA'
rna_blood_ery = ScaleData(rna_blood_ery)
DoHeatmap(rna_blood_ery,fate_deg$gene)
```



endo deg body

```
rna_blood_ery_head = subset(rna_blood_ery,orig.ident %in% c('Body-1','Body-2'))
fate_deg = FindAllMarkers(rna_blood_ery_head,test.use = 'negbinom')
fate_deg = fate_deg[fate_deg$avg_log2FC>0.5,]
DefaultAssay(rna_blood_ery_head) = 'RNA'
rna_blood_ery_head = ScaleData(rna_blood_ery_head)
```

```
DoHeatmap(rna_blood_ery_head,fate_deg$gene)
```