

## Cluster 7: Immune-Cancer doublets

```
library(Seurat)
library(ggplot2)
```

```
subdataset <- readRDS('../tmp/crc_smc.malignantcells.Rds')
head(subdataset@meta.data, n=3); nrow(subdataset@meta.data)
```

```
##
## AAACCTGCATACGCCG-1-PM-PS-0001-T-A1      35998      4823 PM-PS-0001-T-A1
## AAACCTGGTCGCATAT-1-PM-PS-0001-T-A1      31383      5252 PM-PS-0001-T-A1
## AAACCTGTCCTTGCA-1-PM-PS-0001-T-A1       7302      1713 PM-PS-0001-T-A1
##
## Patient Sample Cell_subtype RNA_snn_res.0.3
## AAACCTGCATACGCCG-1-PM-PS-0001-T-A1 SMC01 SMC01-T CMS2 2
## AAACCTGGTCGCATAT-1-PM-PS-0001-T-A1 SMC01 SMC01-T CMS2 0
## AAACCTGTCCTTGCA-1-PM-PS-0001-T-A1 SMC01 SMC01-T CMS2 2
```

```
## [1] 17334
```

```
epcam <- grep(rownames(subdataset), value = T, pattern = "^EPCAM-ENSG")[1]
krt19 <- grep(rownames(subdataset), value = T, pattern = "^KRT19-ENSG")[1]
krt8 <- grep(rownames(subdataset), value = T, pattern = "^KRT8-ENSG")[1]
```

```
cd45 <- grep(rownames(subdataset), value = T, pattern = "^PTPRC-ENSG")[1]
```

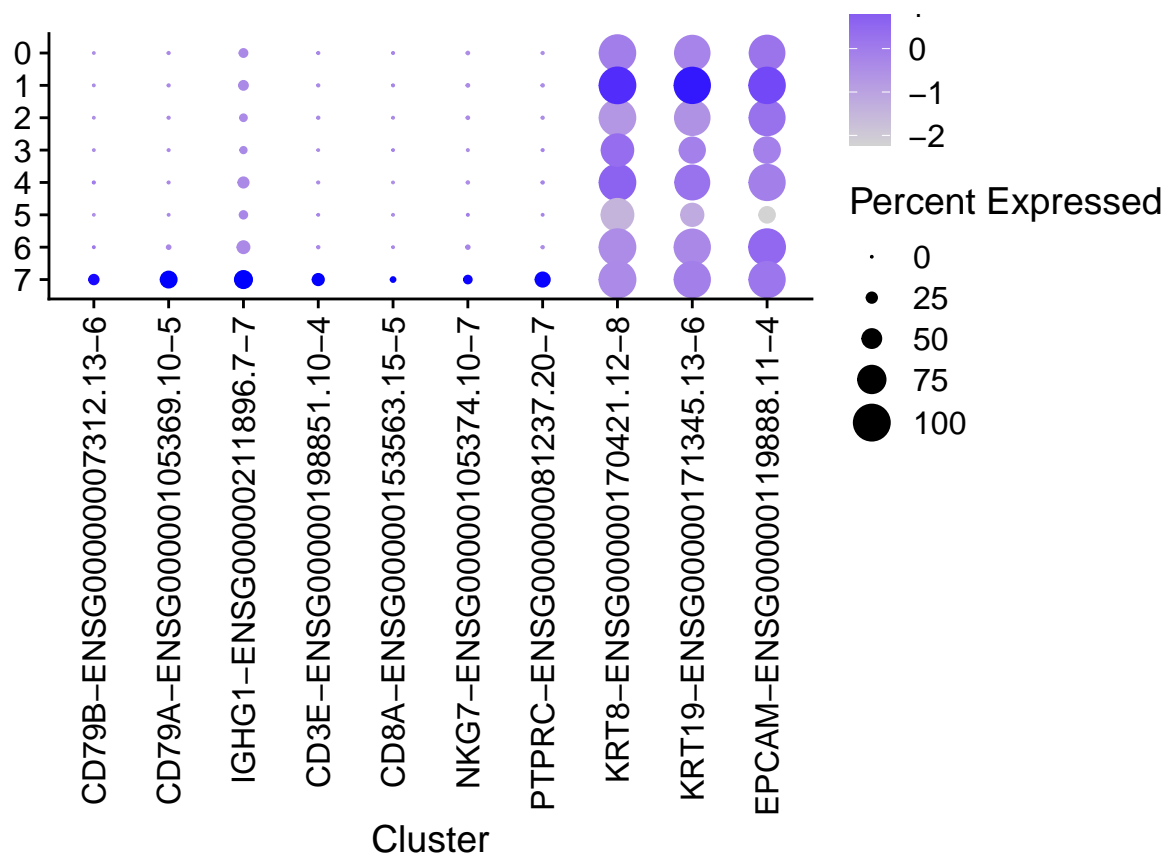
```
nkg7 <- grep(rownames(subdataset), value = T, pattern = "^NKG7-ENSG")[1]
cd8a <- grep(rownames(subdataset), value = T, pattern = "^CD8A-ENSG")[1]
cd3e <- grep(rownames(subdataset), value = T, pattern = "^CD3E-ENSG")[1]
```

```
ighg1 <- grep(rownames(subdataset), value = T, pattern = "^IGHG1-ENSG")[1]
cd79b <- grep(rownames(subdataset), value = T, pattern = "^CD79B-ENSG")[1]
cd79a <- grep(rownames(subdataset), value = T, pattern = "^CD79A-ENSG")[1]
```

```
#dir.create('../res_various/res_0.3/cluster7')
```

```
Idents(subdataset) <- factor(Idents(subdataset), levels = rev(levels(Idents(subdataset))))
```

```
DotPlot(subdataset, features = c(epcam, krt19, krt8, cd45, nkg7, cd8a, cd3e, ighg1, cd79a, cd79b)) +
  labs(x = 'Cluster', y = '') +
  theme(axis.text.x = element_text(angle = 90, hjust = 1, vjust = .5))
```



```
#ggsave('../res_various/res_0.3/cluster7/cluster7.pdf', units = 'cm', width = 8, height = 10)
```