# 4.Exploration facs data

Fay

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## Import data

```
MICE <- read.csv("output_data/1.MICE_cleaned_data.csv")
```

## Vectors for selecting cells

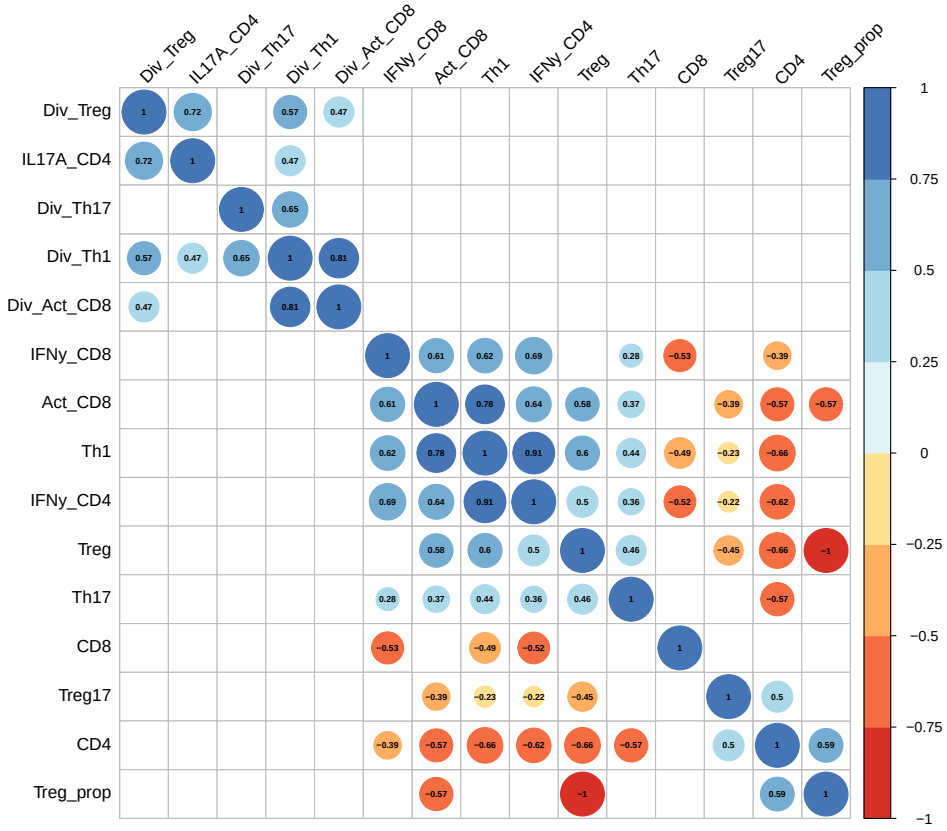
```
Facs_lab <- c("CD4", "Treg", "Div_Treg", "Treg17", "Th1",
                    "Div_Th1", "Th17", "Div_Th17", "CD8", "Act_CD8",
                    "Div_Act_CD8", "IFNy_CD4", "IFNy_CD8","Treg_prop",
                    "IL17A_CD4")

Facs_wild <- c( "Treg", "CD4", "Treg17", "Th1", "Th17", "CD8",
                     "Act_CD8", "IFNy_CD4", "IL17A_CD4", "IFNy_CD8")
```

## Lab data

### Correlations between the cells

### Corrplot of correlations - Laboratory facs data

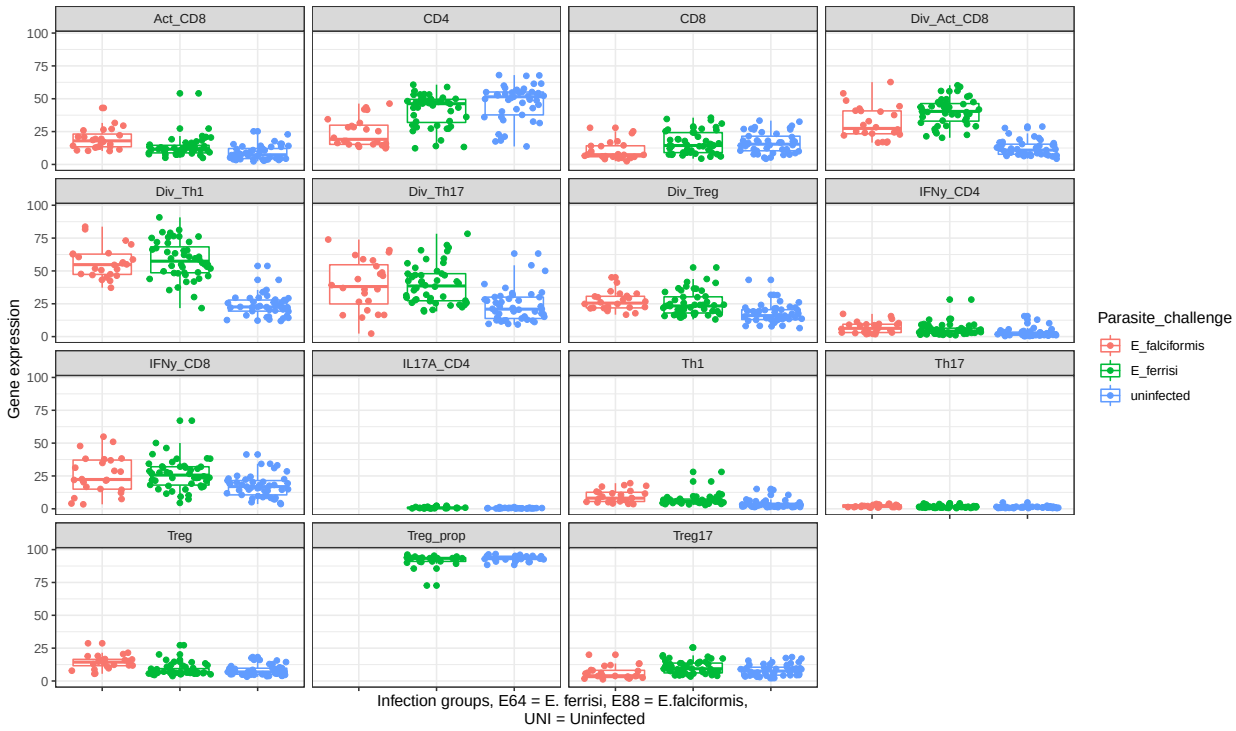
Here is a corrplot of the correlations between the cells




## FACS versus infection intensities - laboratory infections

```
## Warning: Removed 762 rows containing non-finite values (stat_boxplot).
```

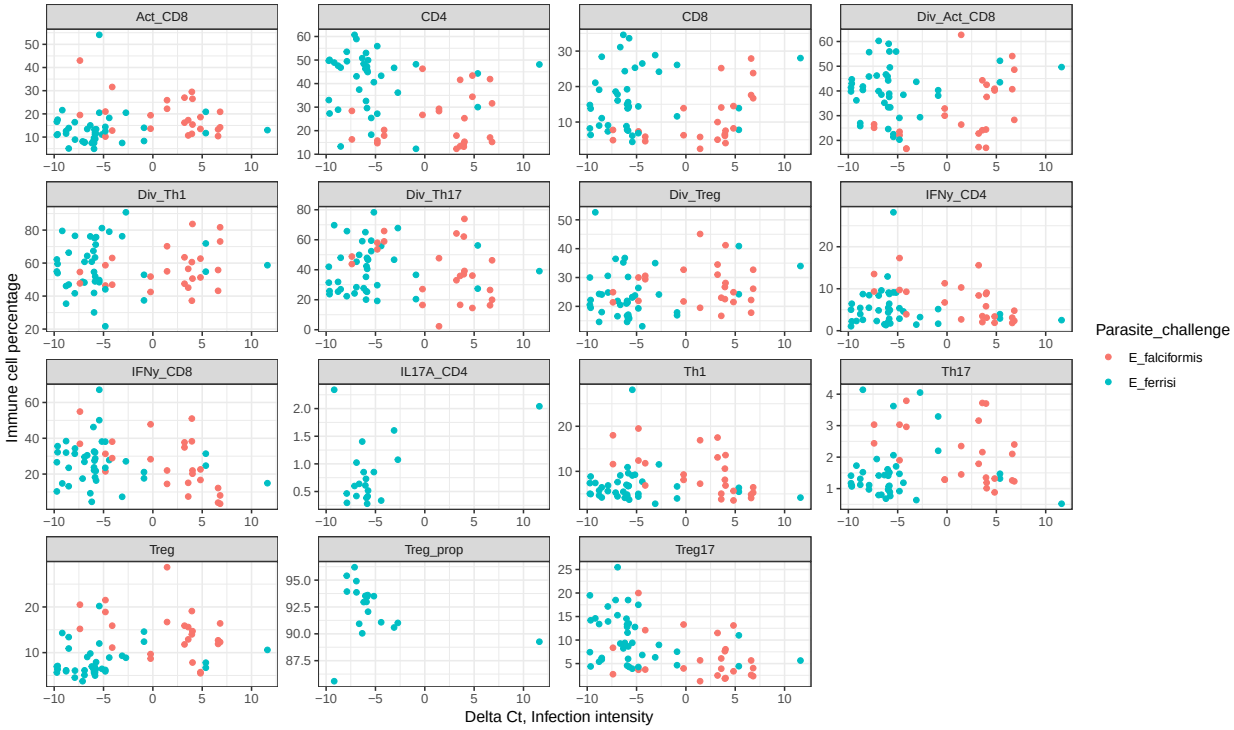
```
## Warning: Removed 762 rows containing missing values (geom_point).
```




```
f %>%
    filter(!Parasite_challenge == "uninfected", MC.Eimeria == "TRUE") %>%
    ggplot(aes(x = delta_ct_cewe_MminusE, y = Percentage,
               color = Parasite_challenge)) +
    geom_jitter() +
    facet_wrap(~ Cells, scales = "free") +
    theme_light() +
    labs(x = "Delta Ct, Infection intensity", y = "Immune cell percentage",
         title = "Immune cells in response to infection intensity -
         laboratory infections") +
    theme_bw() +
  theme(plot.title = element_text(size= 30))
```

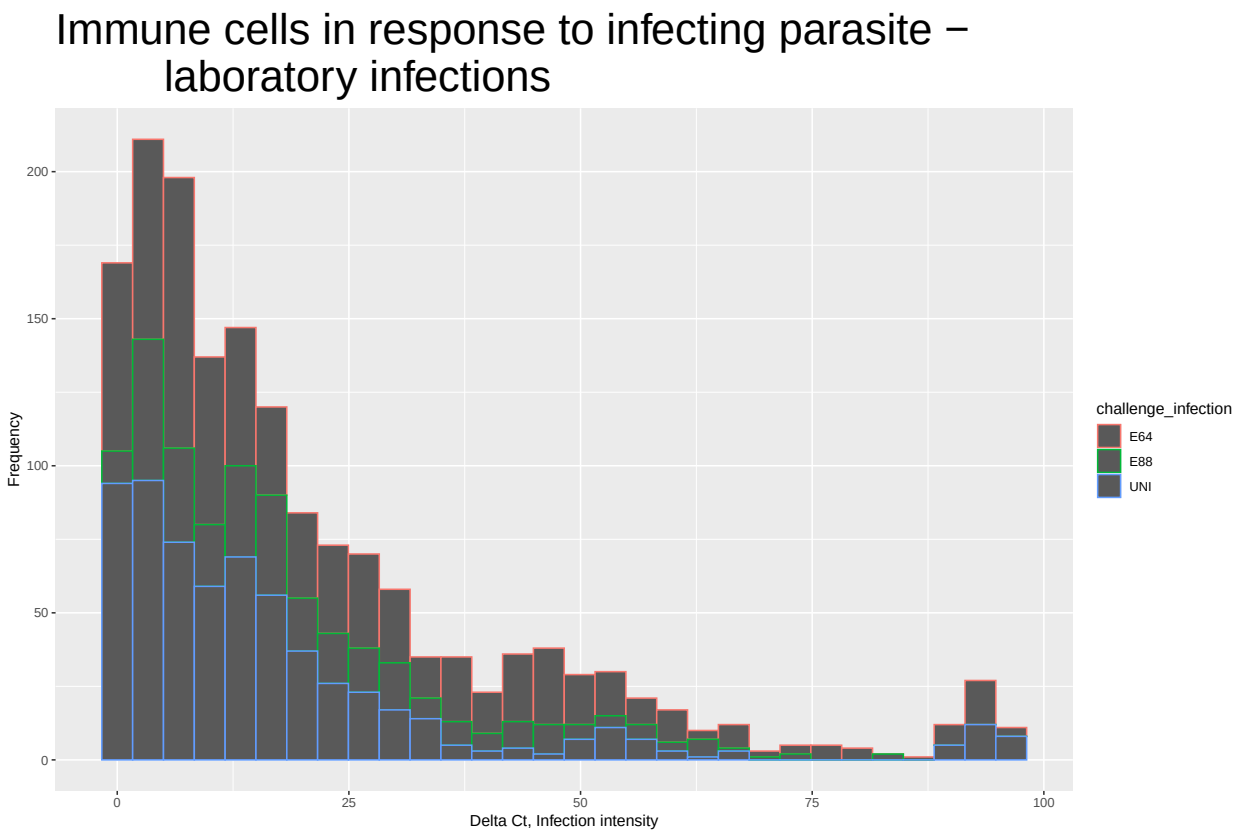
```
## Warning: Removed 463 rows containing missing values (geom_point).
```

# Immune cells in response to infection intensity − laboratory infections




```
## Warning: Ignoring unknown parameters: echo
```

```
## Warning: Removed 762 rows containing non-finite values (stat_bin).
```



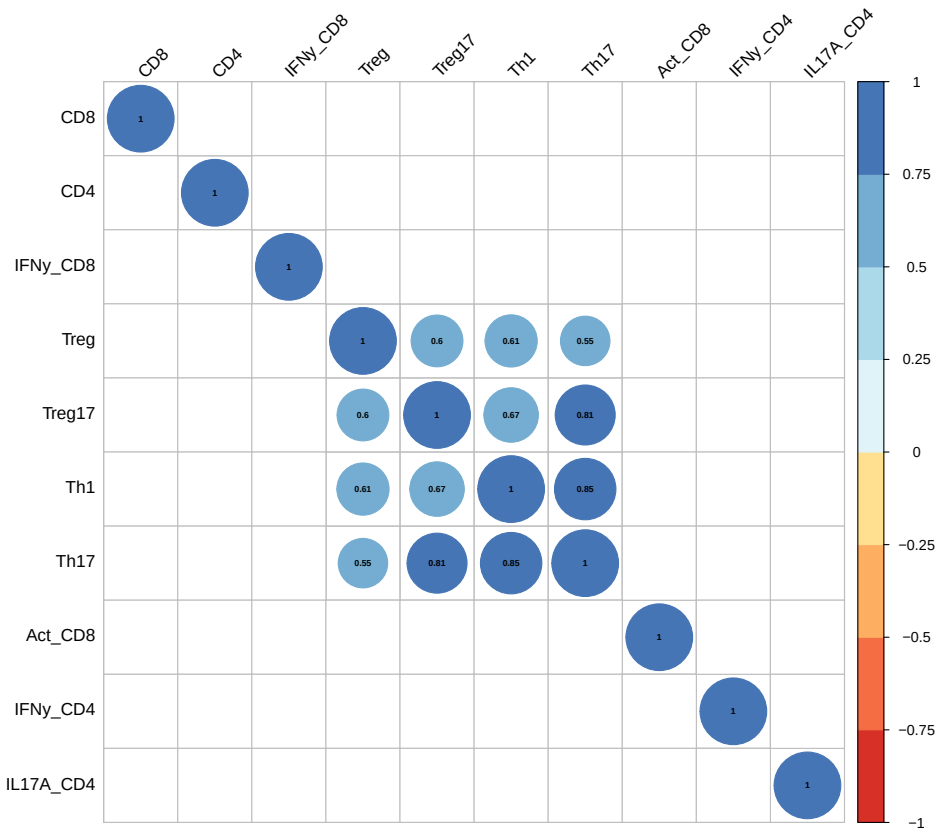

# Repeating for field infections

# Field data

## Correlations between the cells

## Corrplot of correlations - Field facs data

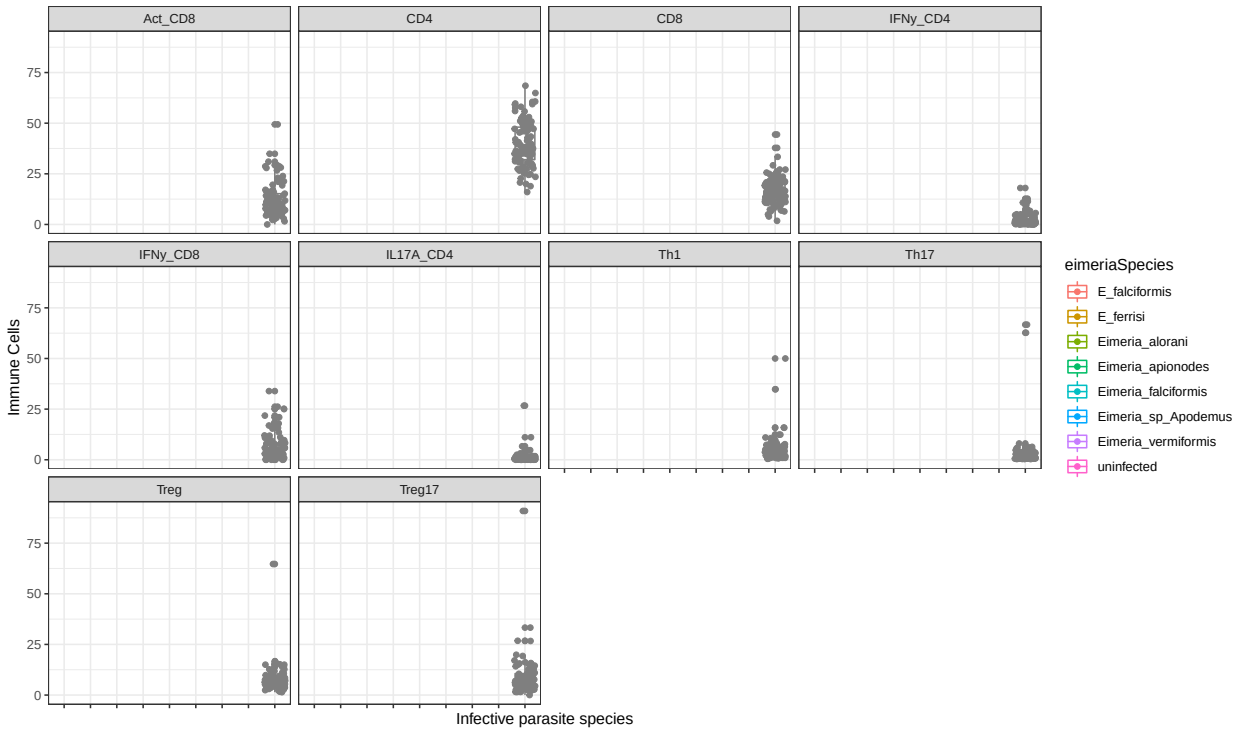
Here is a corrplot of the correlations between the cells




## Immune cells versus infection intensities - Field infections

```
## Warning: Removed 18260 rows containing non-finite values (stat_boxplot).
```

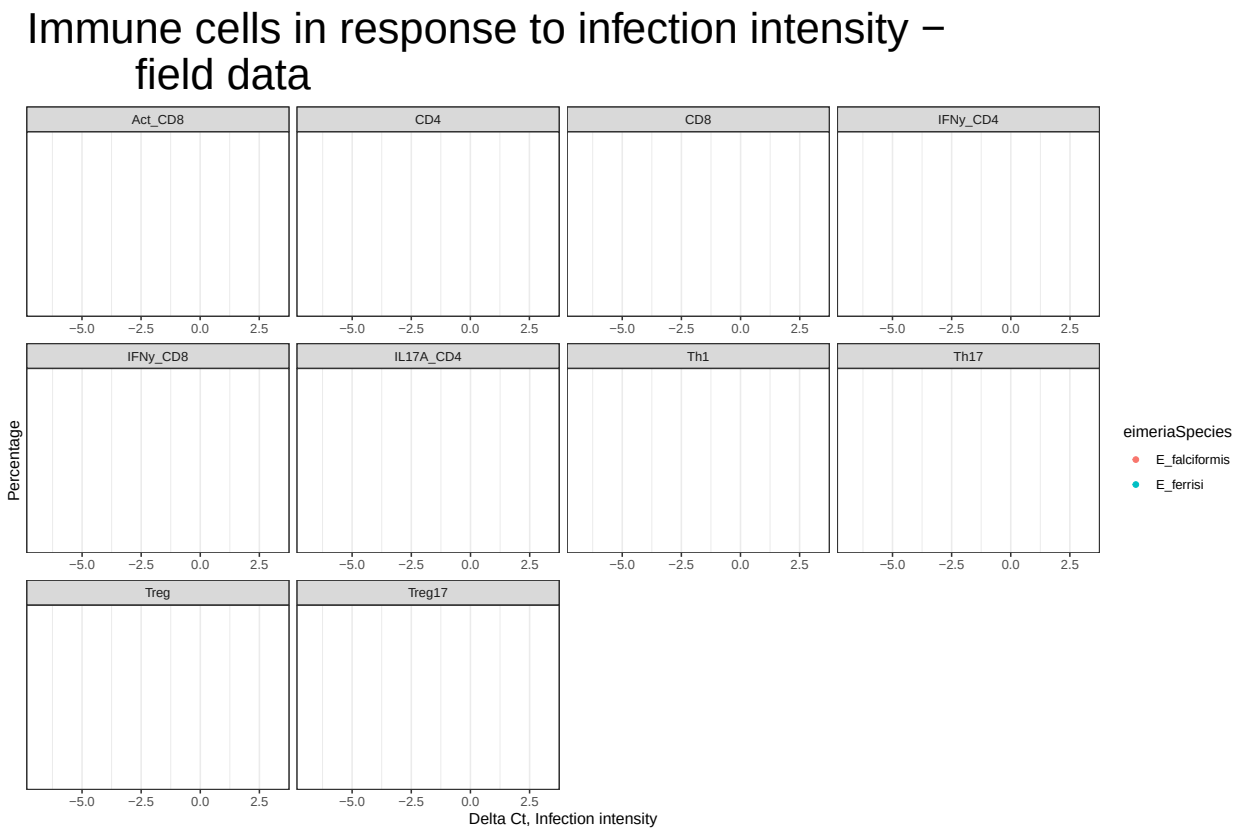
```
## Warning: Removed 18260 rows containing missing values (geom_point).
```




```
f %>%
    filter(!eimeriaSpecies == "uninfected", MC.Eimeria == "TRUE") %>%
    ggplot(aes(x = delta_ct_cewe_MminusE, y = Percentage,
               color = eimeriaSpecies)) +
    geom_jitter() +
    facet_wrap(~ Cells, scales = "free") +
    theme_light() +
    labs(x = "Delta Ct, Infection intensity", y = "Percentage",
         title = "Immune cells in response to infection intensity -
         field data") +
    theme_bw() +
  theme(plot.title = element_text(size= 30))
```

```
## Warning in min(x): no non-missing arguments to min; returning Inf

## Warning in max(x): no non-missing arguments to max; returning -Inf

## Warning in min(diff(sort(x))): no non-missing arguments to min; returning Inf

## Warning in min(x): no non-missing arguments to min; returning Inf

## Warning in max(x): no non-missing arguments to max; returning -Inf

## Warning in stats::runif(length(x), -amount, amount): NAs produced
```

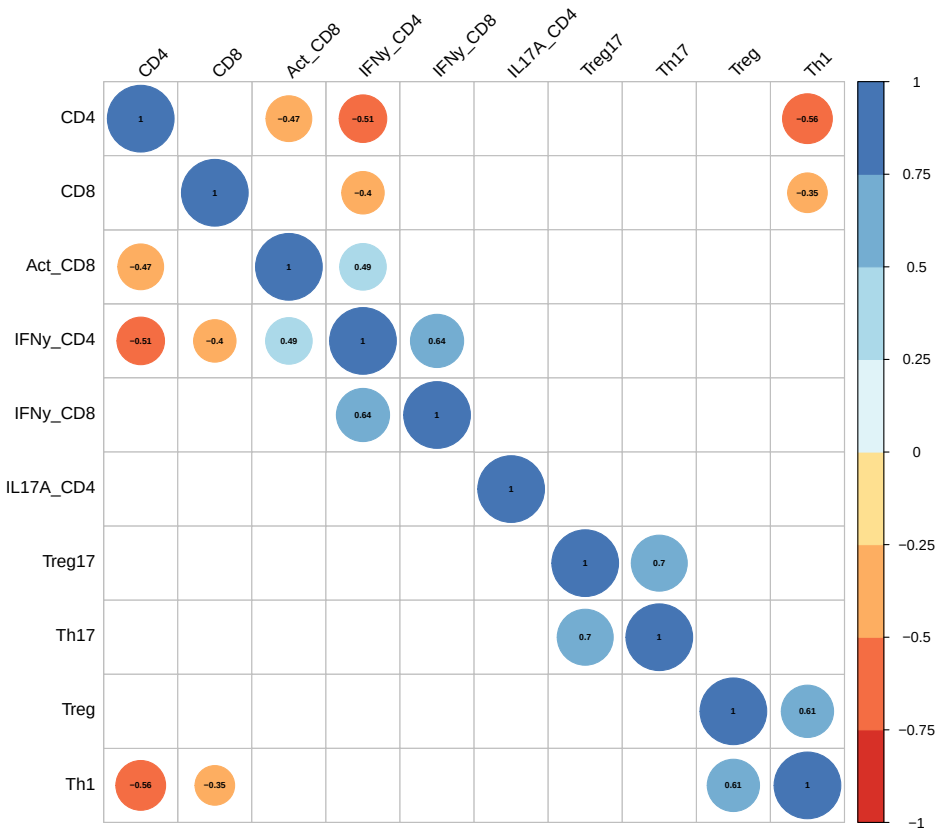
```
## Warning: Removed 180 rows containing missing values (geom_point).
```




# FACS correlations in lab and field data

## Corrplot of correlations - *Laboratory and field* gene expression data

Here is a corrplot of the correlations between the genes.


CD4
CD8
Act_CD8
IFNy_CD4
IFNy_CD8
IL17A_CD4
Treg17
Th17
Treg
Th1
1
0.75
0.5
0.25
0
−0.25
−0.5
−0.75
−1