

### 3. Exploration Gene

Fay

2022-10-05

#### Import data

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

#### Vectors for selecting genes

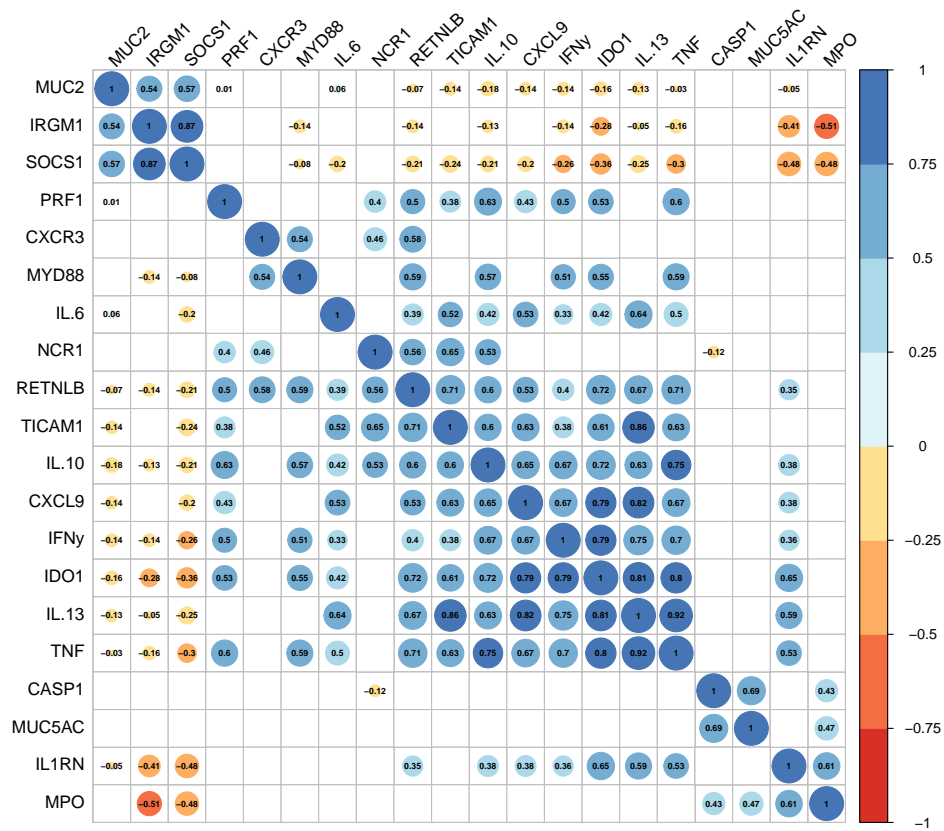
```
Gene_lab <- c("IFNy", "CXCR3", "IL.6", "IL.13", "IL.10",  
             "IL1RN", "CASP1", "CXCL9", "IDO1", "IRGM1", "MPO",  
             "MUC2", "MUC5AC", "MYD88", "NCR1", "PRF1", "RETNLB", "SOCS1",  
             "TICAM1", "TNF") # "IL.12", "IRG6")  
  
Genes_wild <- c("IFNy", "CXCR3", "IL.6", "IL.13", "IL.10",  
              "IL1RN", "CASP1", "CXCL9", "IDO1", "IRGM1", "MPO",  
              "MUC2", "MUC5AC", "MYD88", "NCR1", "PRF1", "RETNLB", "SOCS1",  
              "TICAM1", "TNF") #, "IL.12", "IRG6")
```

#### Lab data

##### Correlations between the genes

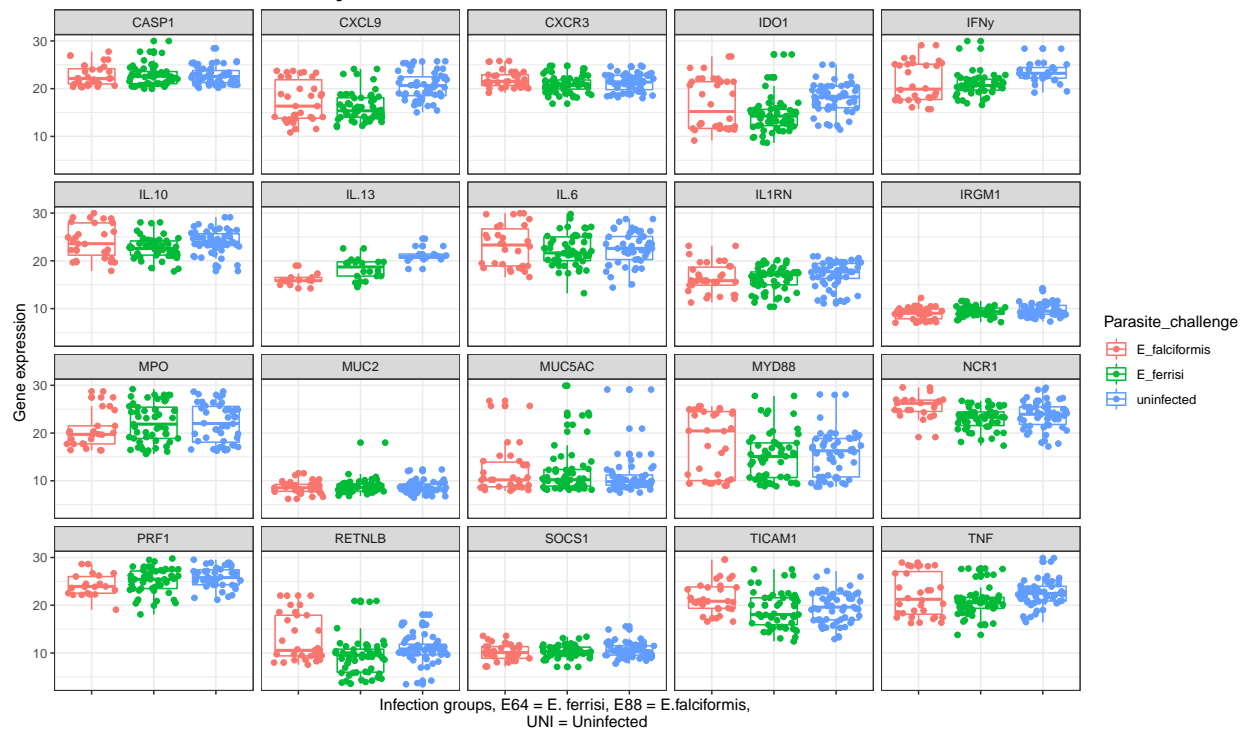
##### Corrplot of correlations - Laboratory gene expression data

Here is a corrplot of the correlations between the genes.



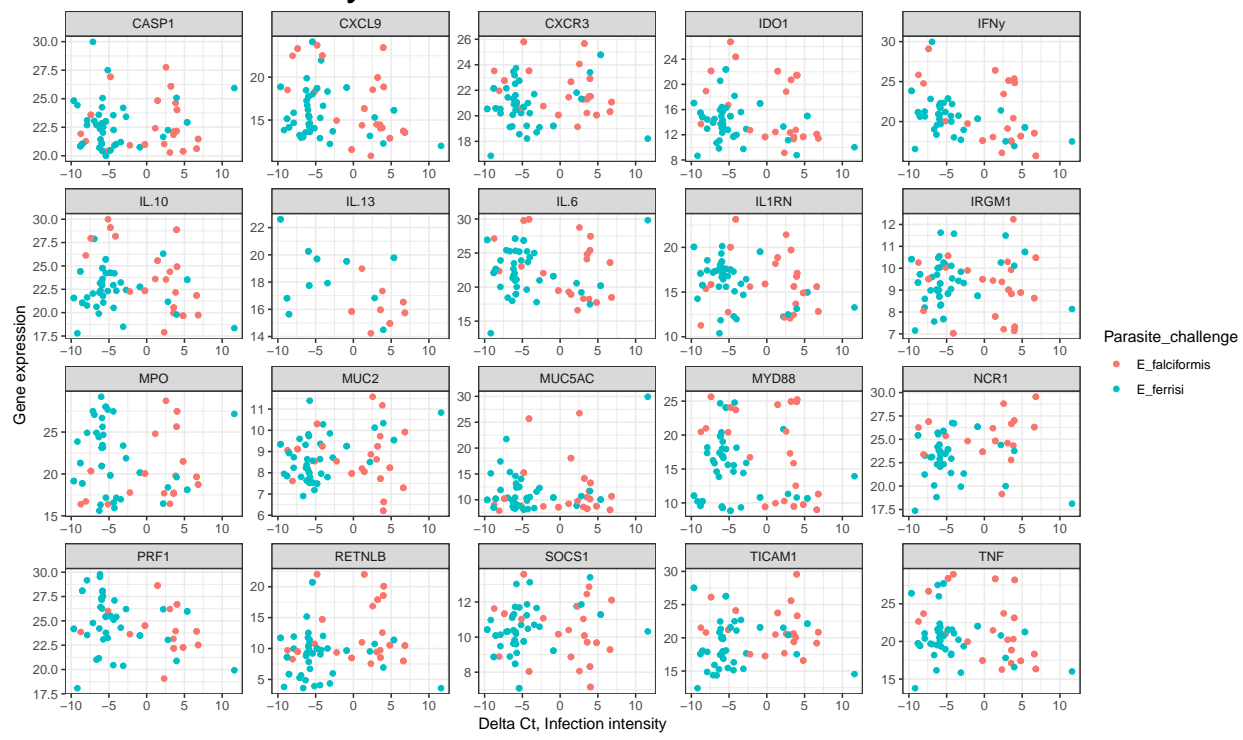
## Gene expression versus infection intensities - laboratory infections

### Gene expression in response to infection group, laboratory infections

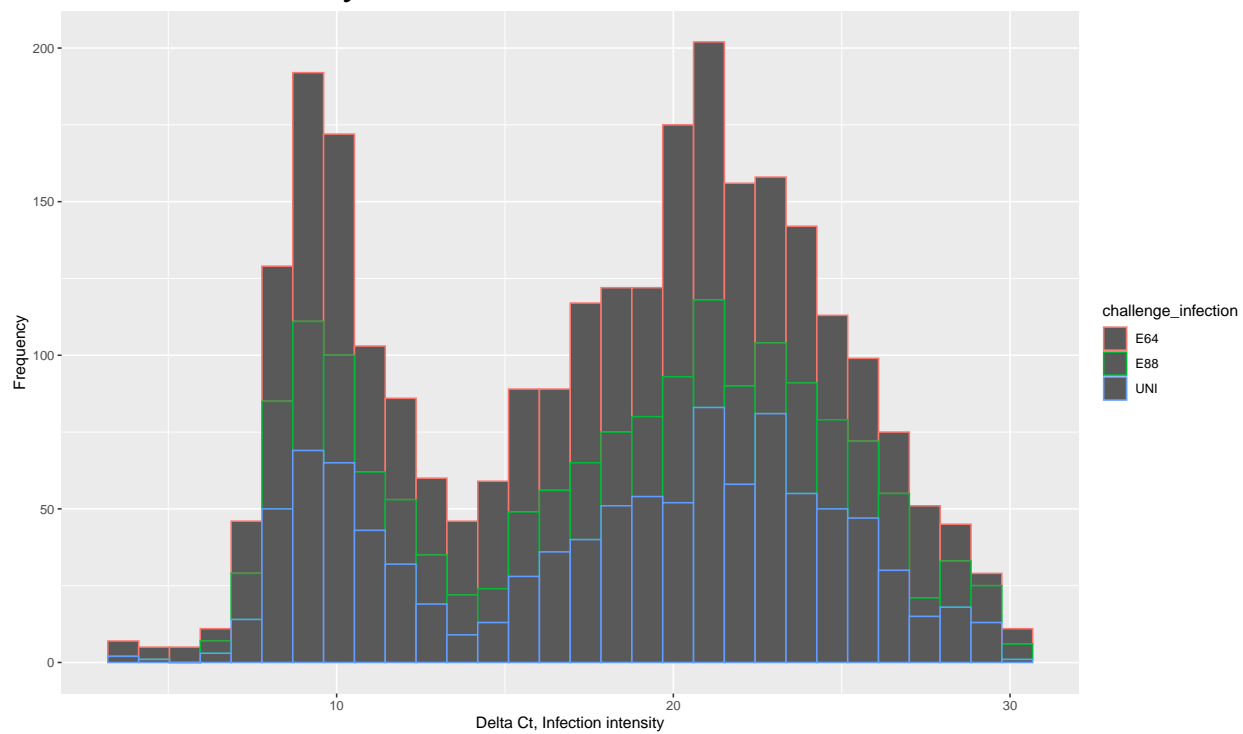


```
g %>%
  filter(!Parasite_challenge == "uninfected", MC.Eimeria == "TRUE") %>%
  ggplot(aes(x = delta_ct_cewe_MminusE, y = gene_expression,
             color = Parasite_challenge)) +
  geom_jitter() +
  facet_wrap(~ Gene, scales = "free") +
  theme_light() +
  labs(x = "Delta Ct, Infection intensity",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

# Gene expression in response to infection intensity – laboratory infections



# Gene expression in response to infecting parasite – laboratory infections



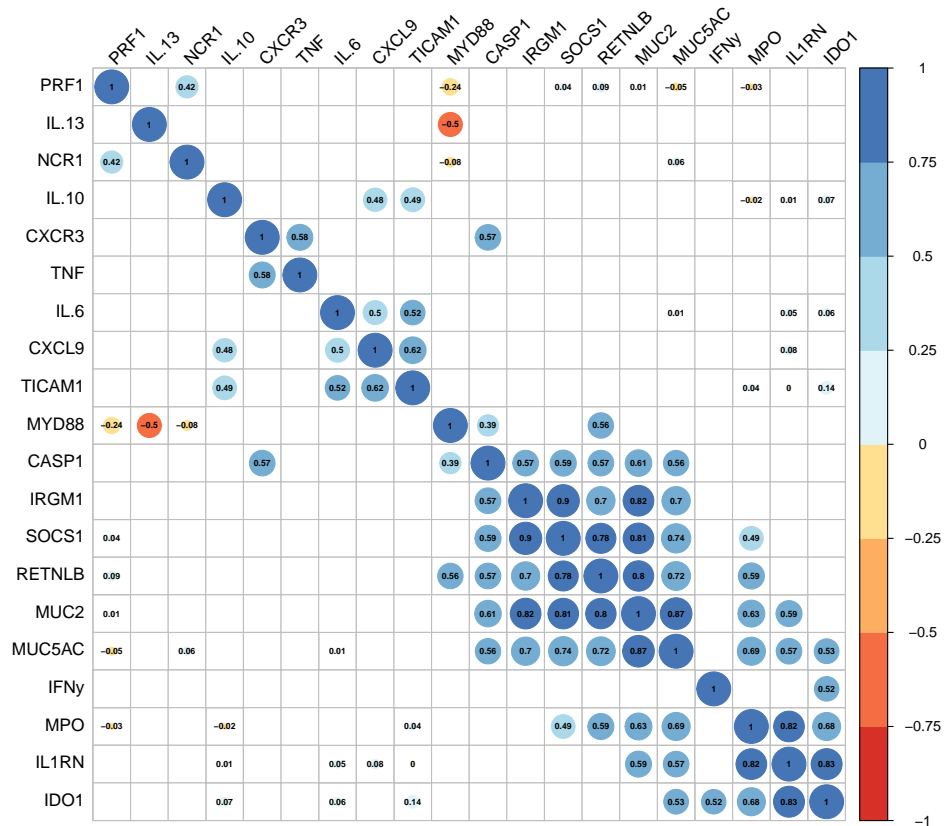
# Repeating for field infections

## Field data

### Correlations between the genes

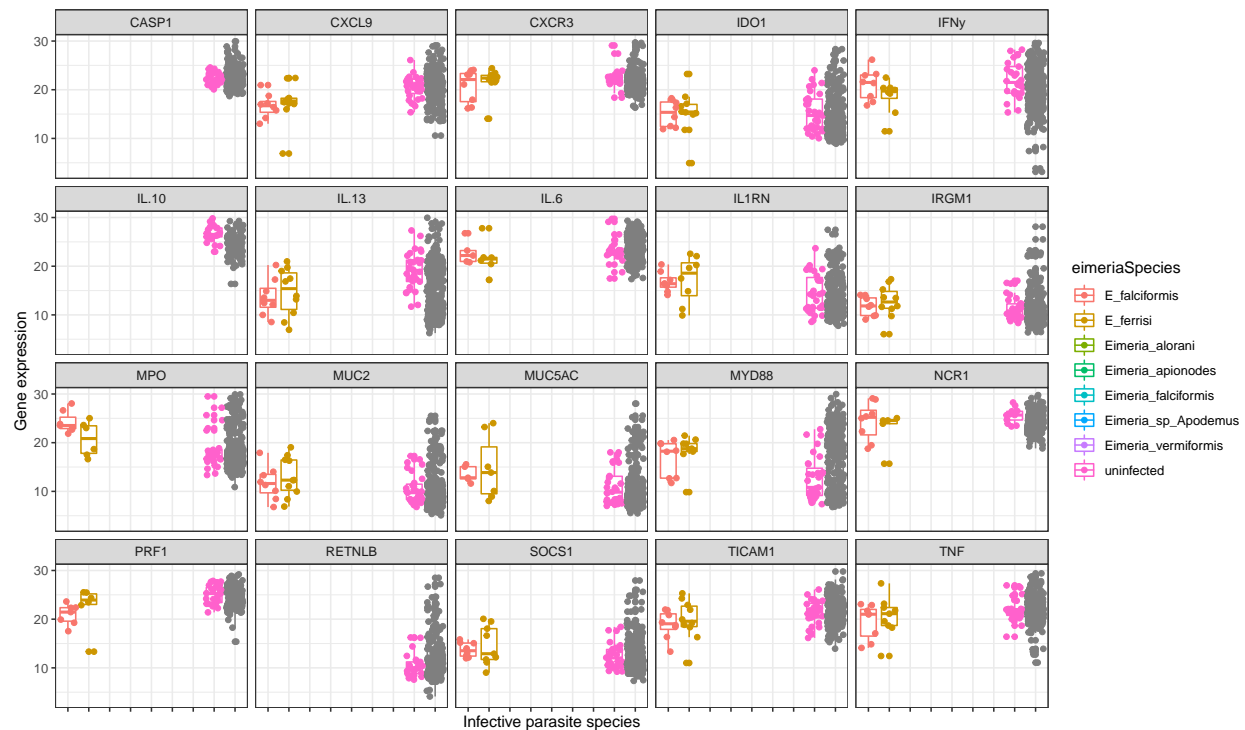
### Corrplot of correlations - Field gene expression data

Here is a corrplot of the correlations between the genes. I am using the non-normalized genes



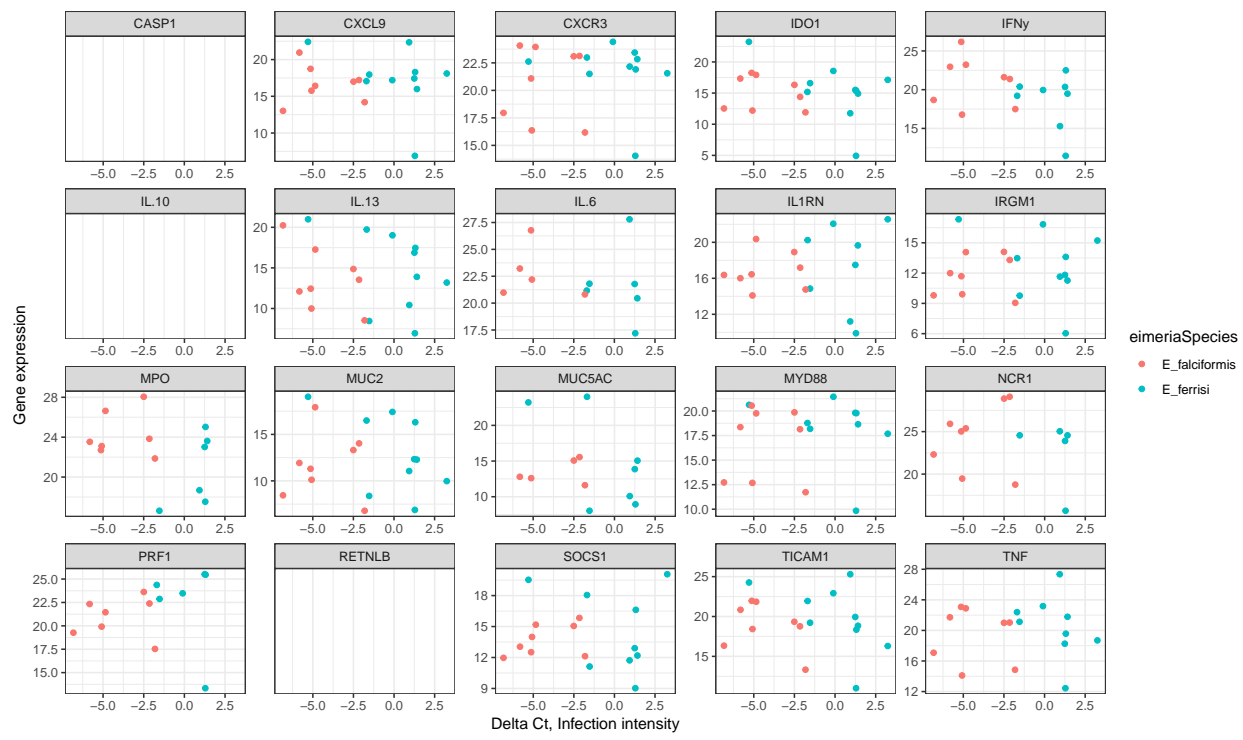
## Gene expression versus infection intensities - Field infections

### Gene expression in response to parasite species – field data

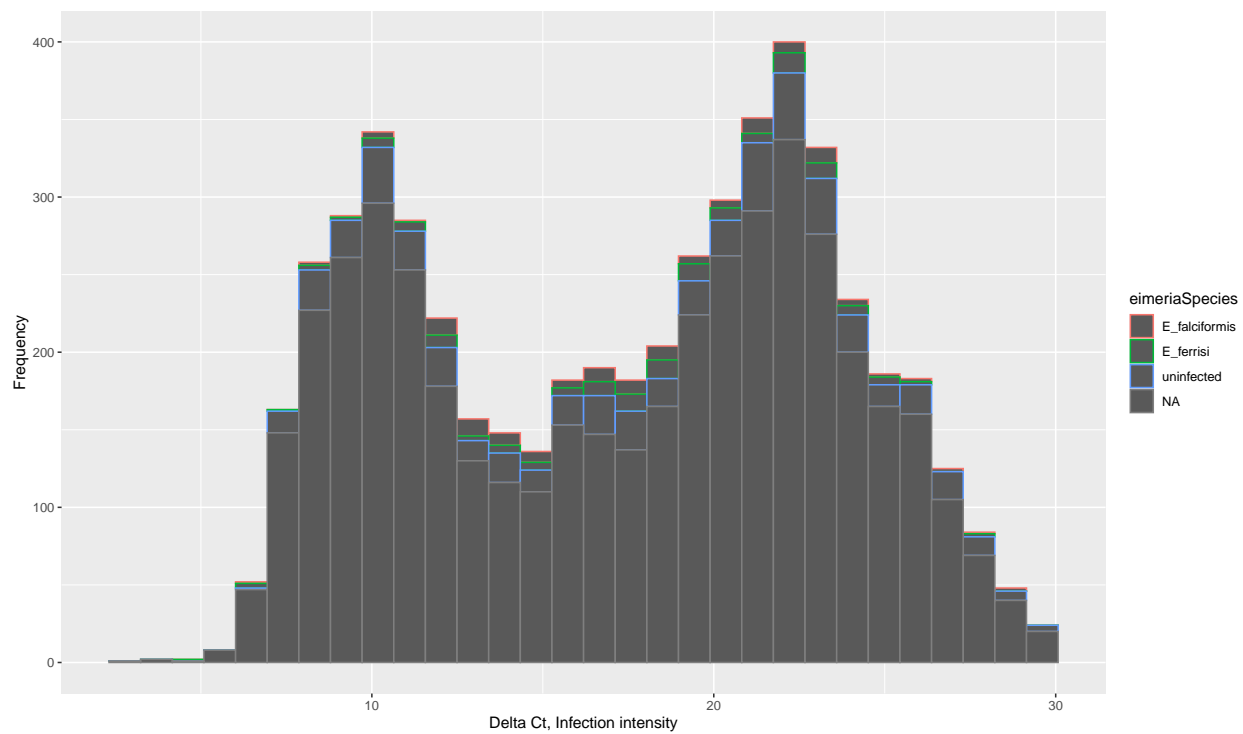


```
g %>%
  filter(!eimeriaSpecies == "uninfected", MC.Eimeria == "TRUE") %>%
  ggplot(aes(x = delta_ct_cewe_MminusE, y = gene_expression,
             color = eimeriaSpecies)) +
  geom_jitter() +
  facet_wrap(~ Gene, scales = "free") +
  theme_light() +
  labs(x = "Delta Ct, Infection intensity", y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

# Gene expression in response to infection intensity – field data



# Gene expression in response to infecting parasite – field data



# Gene expression 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.

