

3. Exploration Gene

Fay

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Import data

```
MICE <- read.csv("output_data/2.imputed_MICE_data_set.csv")
```

Vectors for selecting genes

```
# Vectors for selecting genes
# Lab genes
# The measurements of IL.12 and IRG6 are done with an other assay and will
# ignore for now
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")

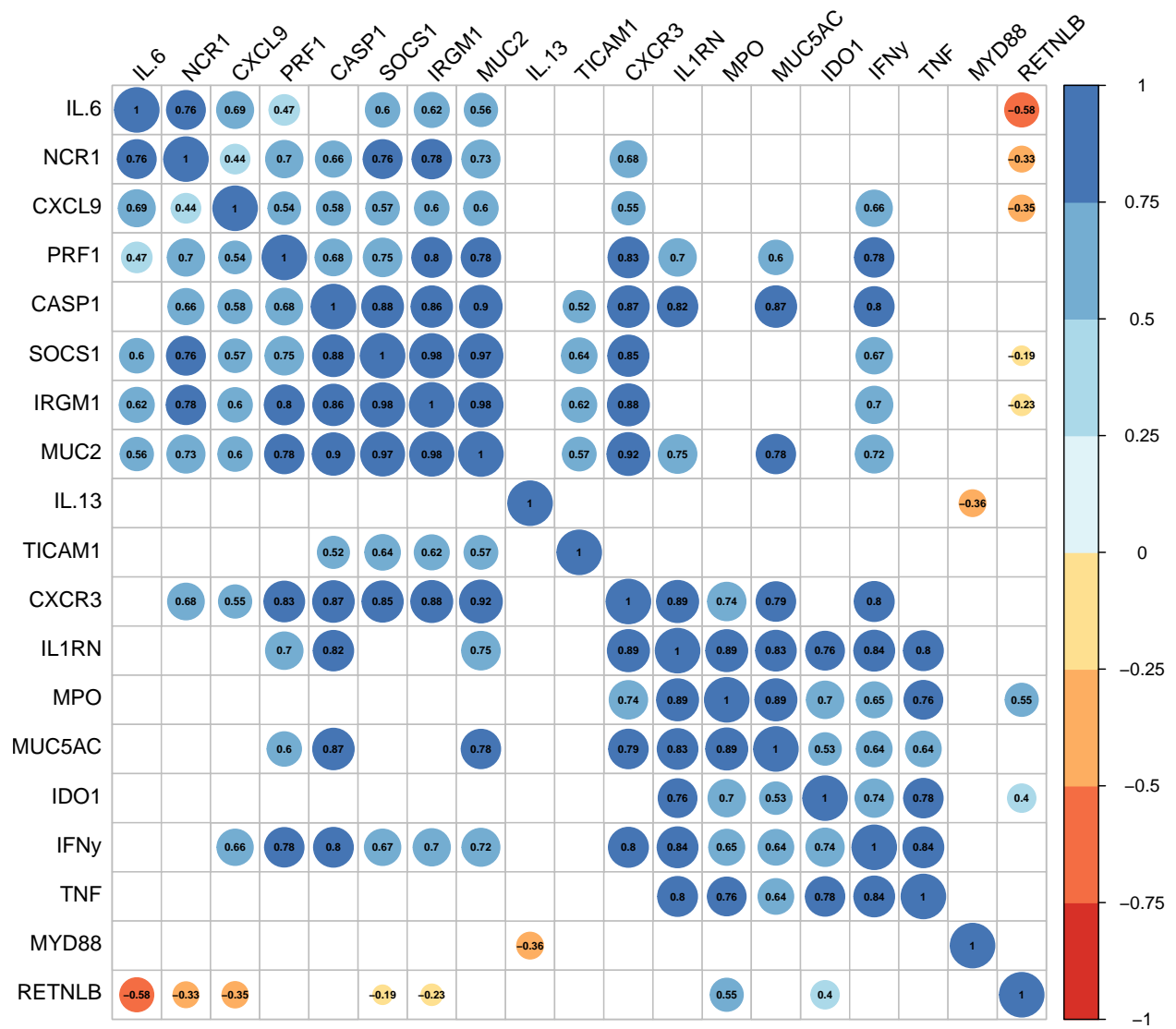
Genes_wild <- c("IFNy", "CXCR3", "IL.6", "IL.13", # "IL.10",
                "IL1RN", "CASP1", "CXCL9", "IDO1", "IRGM1", "MPO",
                "MUC2", "MUC5AC", "MYD88", "NCR1", "PRF1", "RETNLB", "SOCS1",
                "TICAM1", "TNF") #, "IL.12", "IRG6")
```

Lab data

Correlations between the genes

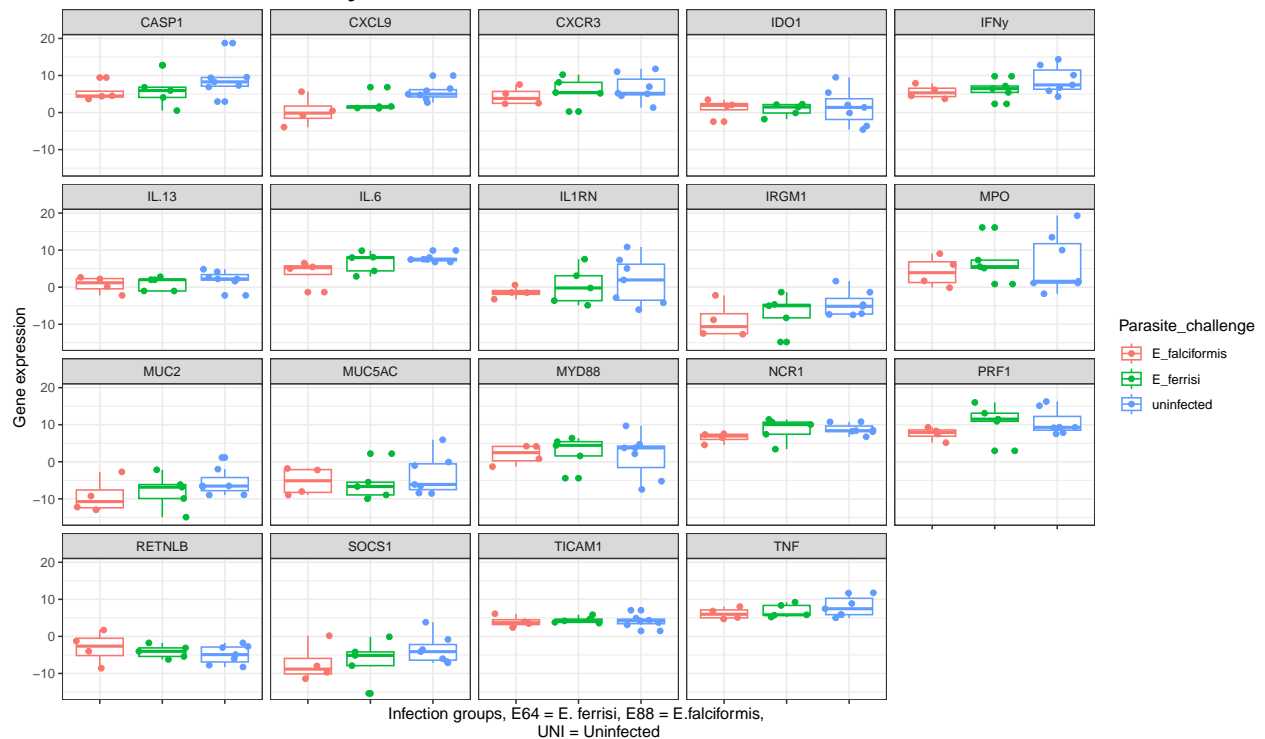
Corrplot of correlations - Laboratory gene expression data

Here is a corrplot of the correlations between the genes.



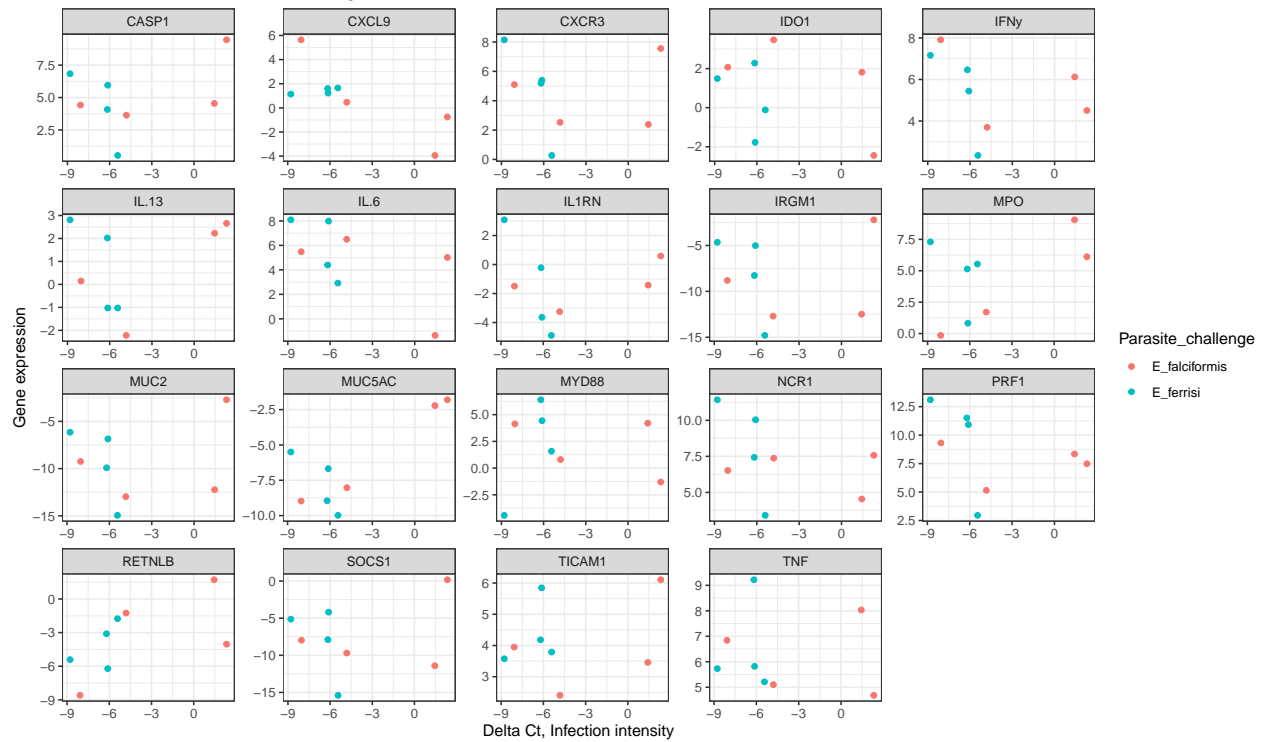
Gene expression versus infection intensities - laboratory infections

Gene expression in response to infection group, laboratory infections

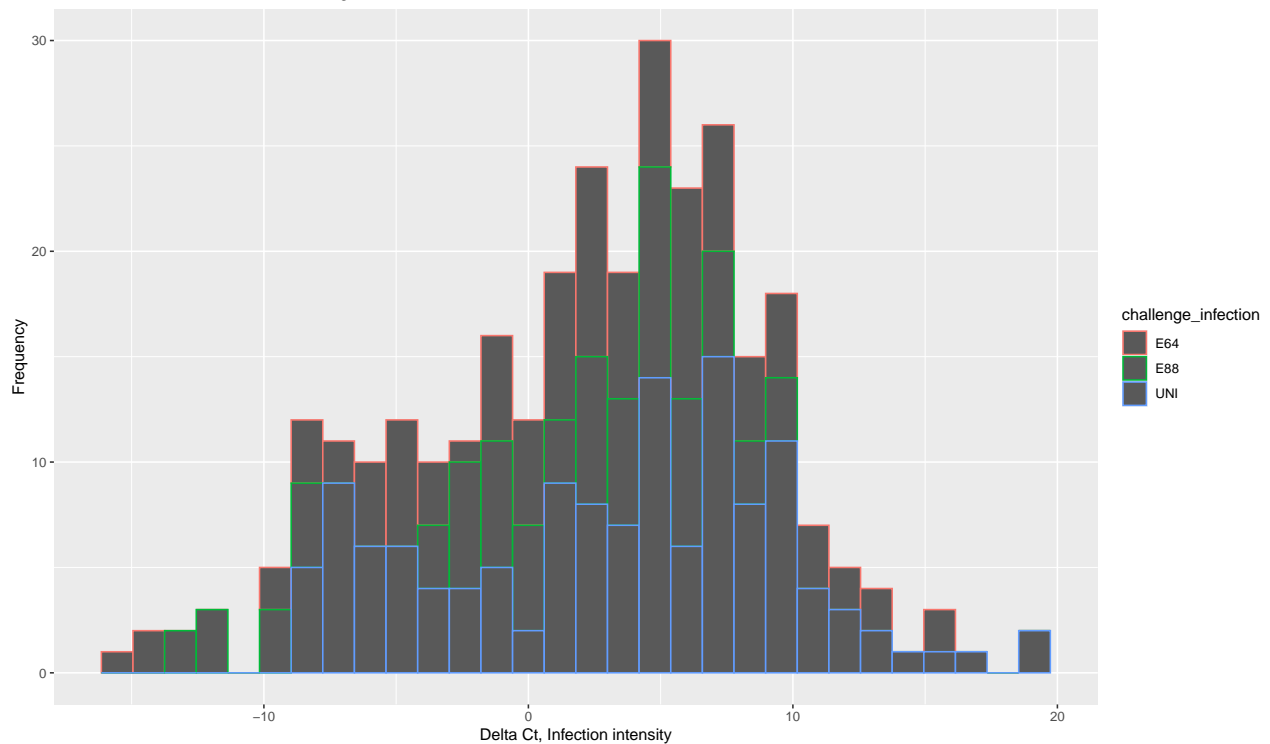


```
g %>%
  filter(!Parasite_challenge == "uninfected", MC.Eimeria == "TRUE") %>%
  ggplot(aes(x = delta_ct_cewe_MminusE, y = gene_expression,
             color = Parasite_challenge)) +
  geom_jitter() +
  facet_wrap(~ Gene, scales = "free") +
  theme_light() +
  labs(x = "Delta Ct, Infection intensity", 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



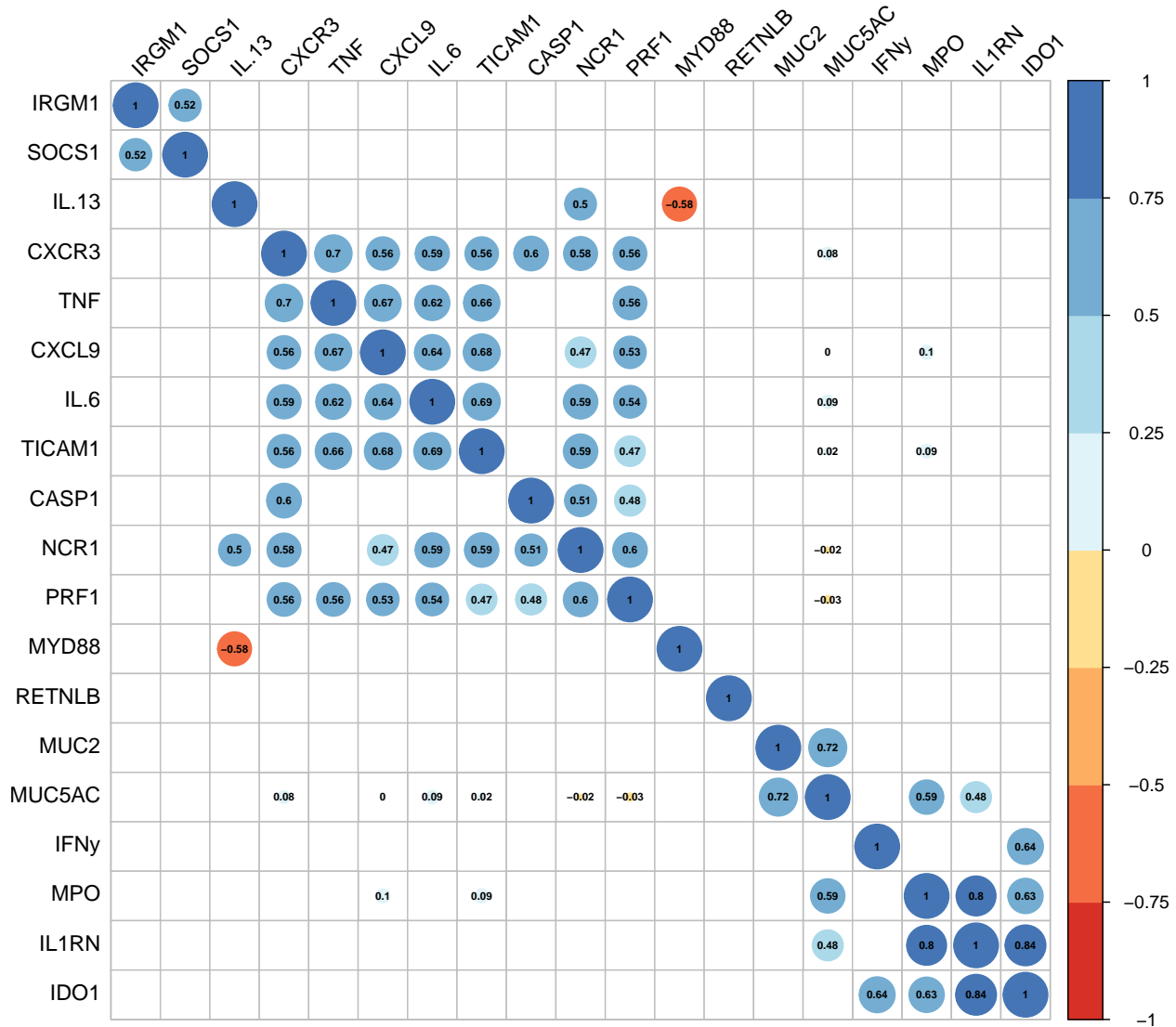
Repeating for field infections

Field data

Correlations between the genes

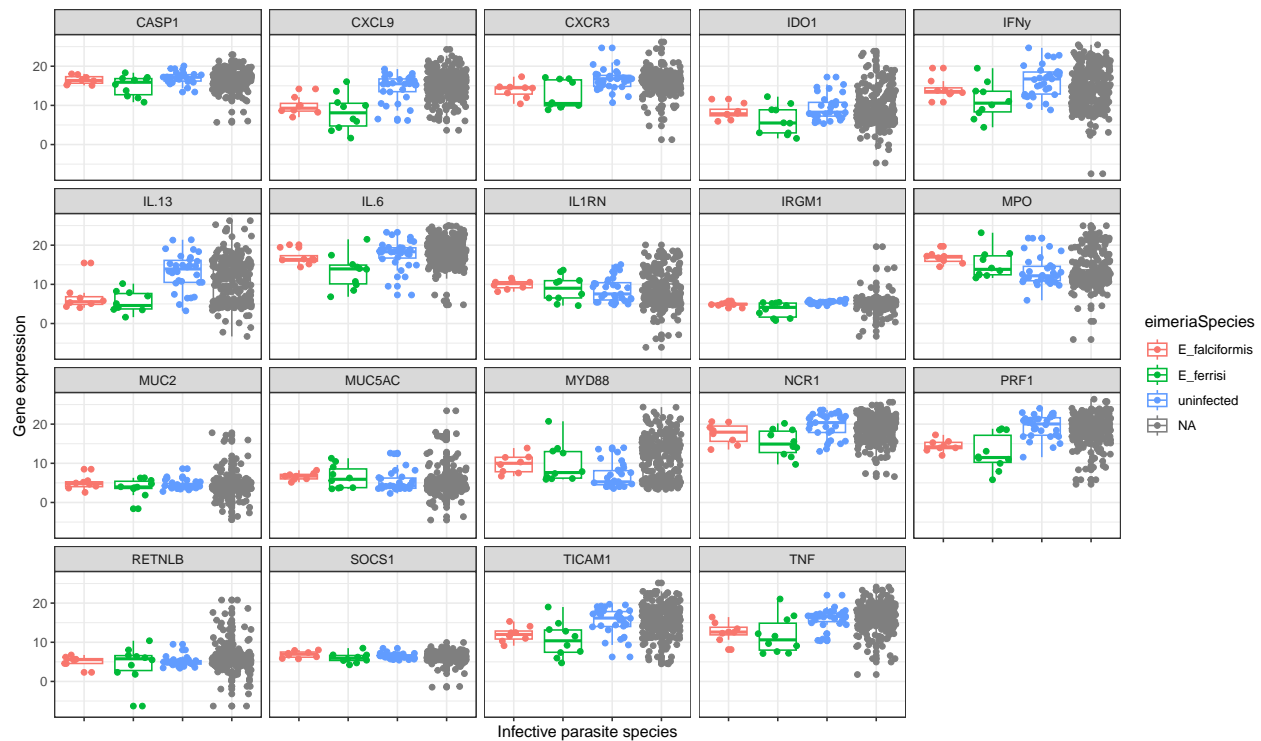
Corrplot of correlations - Field gene expression data

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



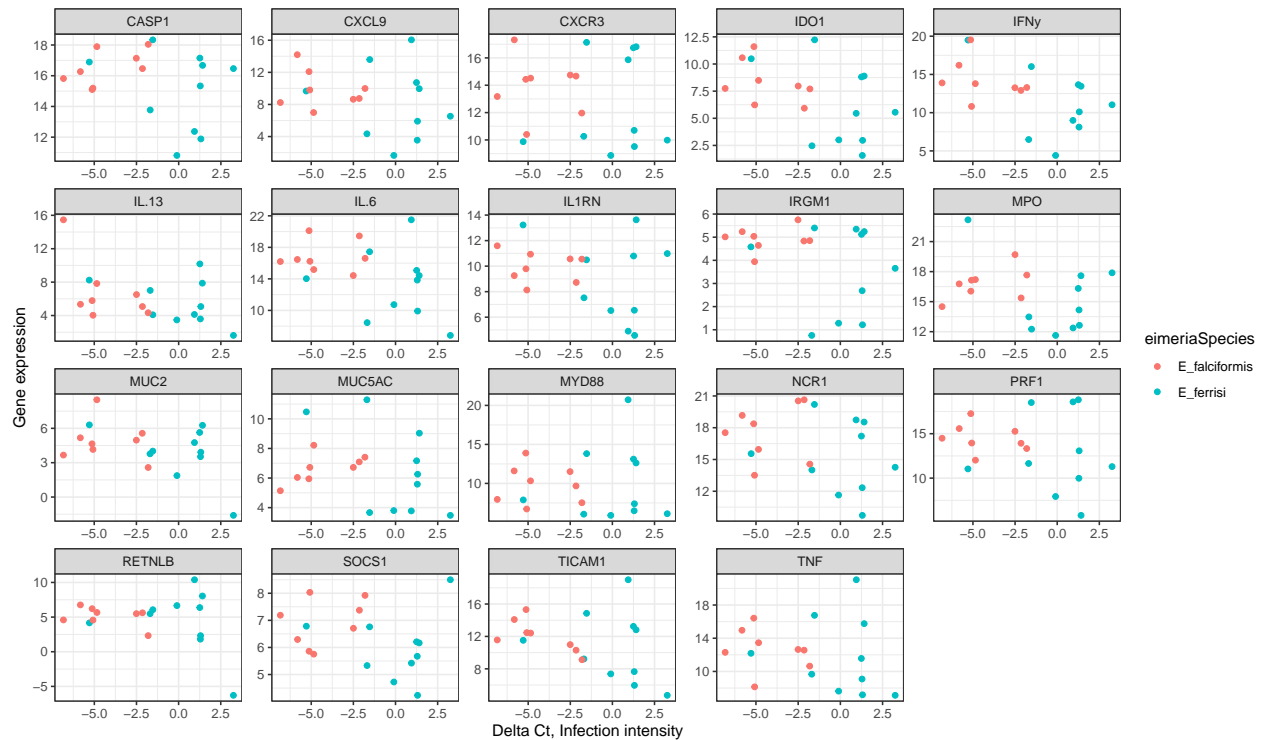
Gene expression versus infection intensities - Field infections

Gene expression in response to parasite species – field data

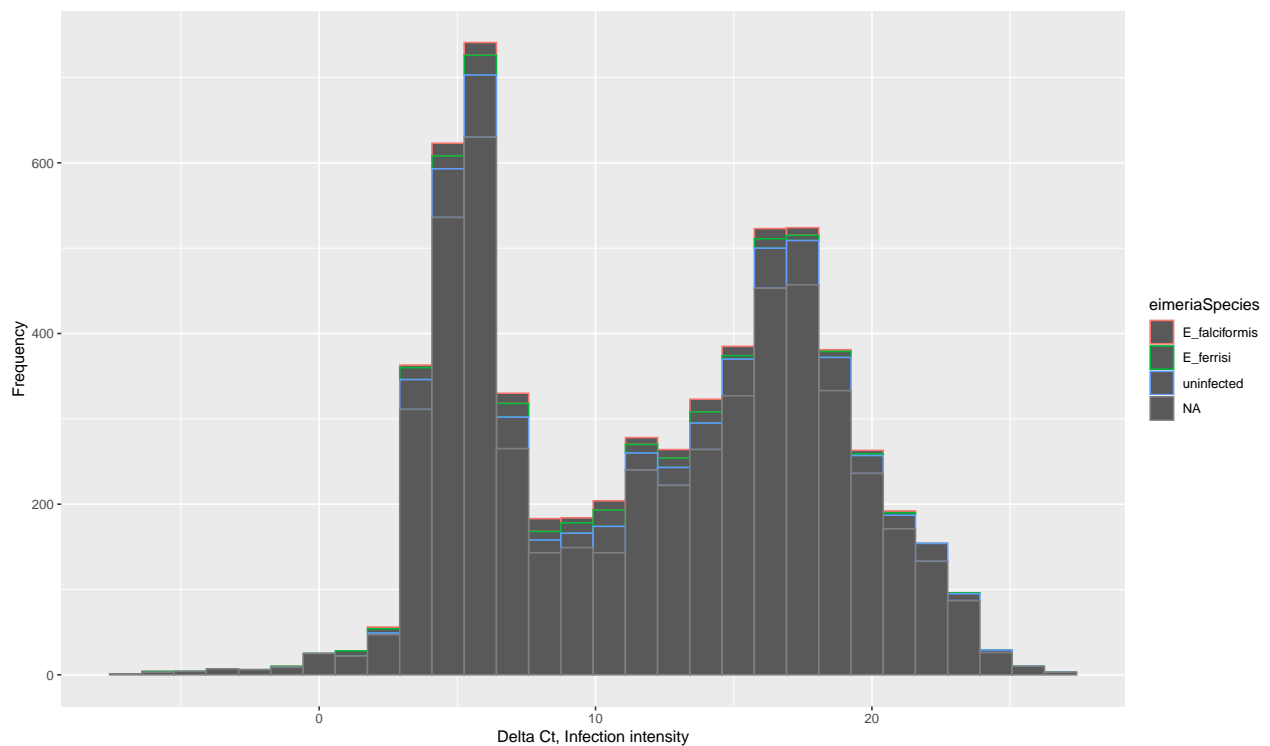


```
g %>%
  filter(!eimeriaSpecies == "uninfected", MC.Eimeria == "TRUE") %>%
  ggplot(aes(x = delta_ct_cewe_MminusE, y = gene_expression,
             color = eimeriaSpecies)) +
  geom_jitter() +
  facet_wrap(~ Gene, scales = "free") +
  theme_light() +
  labs(x = "Delta Ct, Infection intensity", y = "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.

