

4. Gene_expressions_analysis - Analyzing differences between field and lab gene expression data

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Aims:

- Compare immune gene expression between lab and field data

load libraries

```
library(ggplot2)
library(tidyverse)

## -- Attaching packages ----- tidyverse 1.3.1 --

## v tibble  3.1.8      v dplyr    1.0.9
## v tidyr   1.2.0      v stringr 1.4.0
## v readr   2.1.2      v forcats 0.5.1
## v purrr   0.3.4

## -- Conflicts ----- tidyverse_conflicts() --
## x dplyr::filter() masks stats::filter()
## x dplyr::lag()     masks stats::lag()
```

Import data:

Here, we have the experimental / field data, including imputed data

```
lab <- read.csv("output_data/gene_expression/data_products/lab_imputed_gene_expression.csv")
field <- read.csv("output_data/gene_expression/data_products/field_imputed_gene_expression.csv")
```

Selecting genes

```
# vectors for selecting gene columns
Genes_lab <- c("IFNy", "CXCR3_bio", "IL.6", "IL.10", "IL.13", "IL1RN", "CASP1",
              "CXCL9", "IDO1", "IRGM1", "MPO", "MUC2", "MUC5AC",
              "MYD88", "NCR1", "PRF1", "RETNLB", "SOCS1", "TICAM1", "TNF")

Genes_field <- c("IFNy", "CXCR3", "IL.6", #"GBP2", "IL.12", "IRG6",
                 "IL.10", "IL.13", "IL1RN",
                 "CXCR3", "CASP1", "CXCL9",
                 "IDO1", "IRGM1", "MPO", "MUC2", "MUC5AC", "MYD88",
                 "NCR1", "PRF1", "RETNLB", "SOCS1", "TICAM1", "TNF")
```

Adding a variable that signifies if sample is infected or not

detection threshold: delta ct = -5 (Jarquin Diaz et al)

```
field <- field %>%
  mutate(
    infected_eimeria =
      case_when(
        delta_ct_cewe_MminusE > -5 ~ "infected",
        delta_ct_cewe_MminusE < -5 ~ "uninfected"
      )
  )

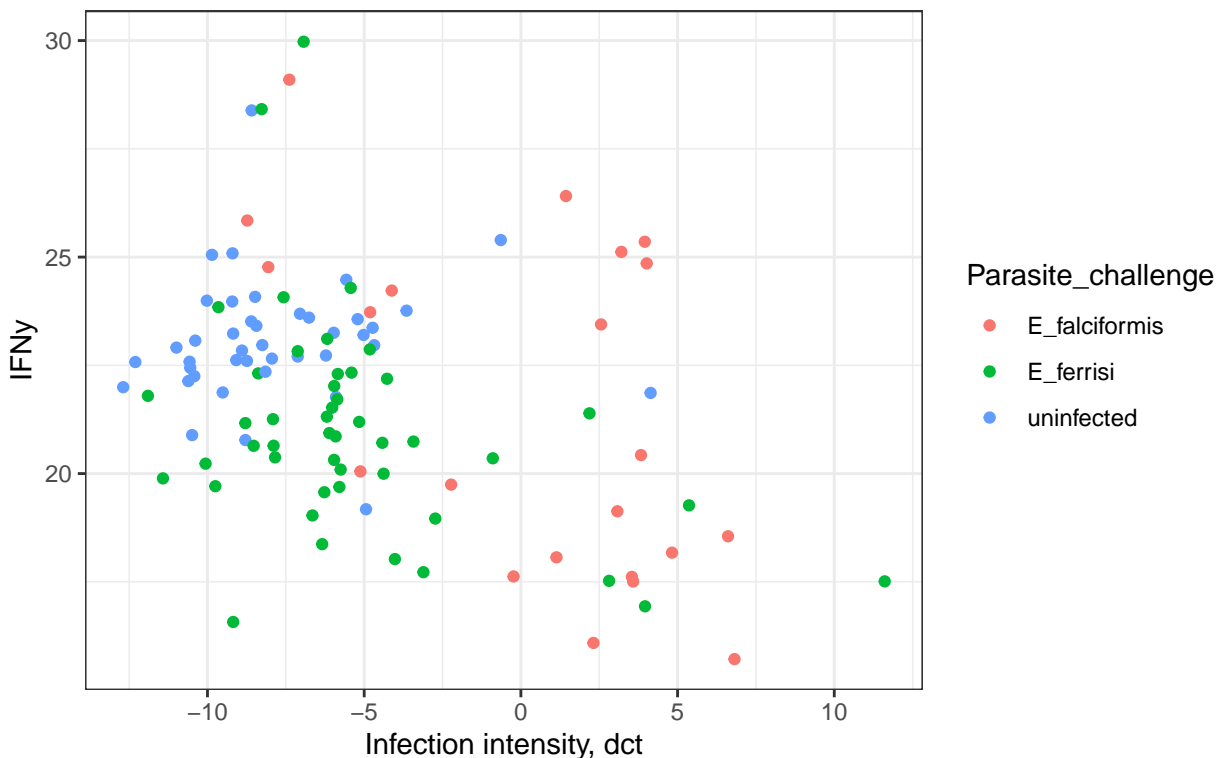
lab <- lab %>%
  mutate(
    infected_eimeria =
      case_when(
        delta > -5 ~ "infected",
        delta < -5 ~ "uninfected"
      )
  )
```

1. IFNy

```
ggplot(lab, aes(x = delta, y = IFNy, color = Parasite_challenge)) +
  geom_jitter() +
  geom_abline() +
  labs(
    x = "Infection intensity, dct",
    title = "Immune gene expression against infection intensity in lab infections"
  ) +
  theme_bw()
```

Warning: Removed 6 rows containing missing values (geom_point).

Immune gene expression against infection intensity in lab infections



```
ggplot(field, aes(x = delta_ct_cewe_MminusE, y = IFNy, color = eimeriaSpecies)) +
  geom_jitter() +
  geom_abline() +
  labs(x = "Infection intensity, dct",
```

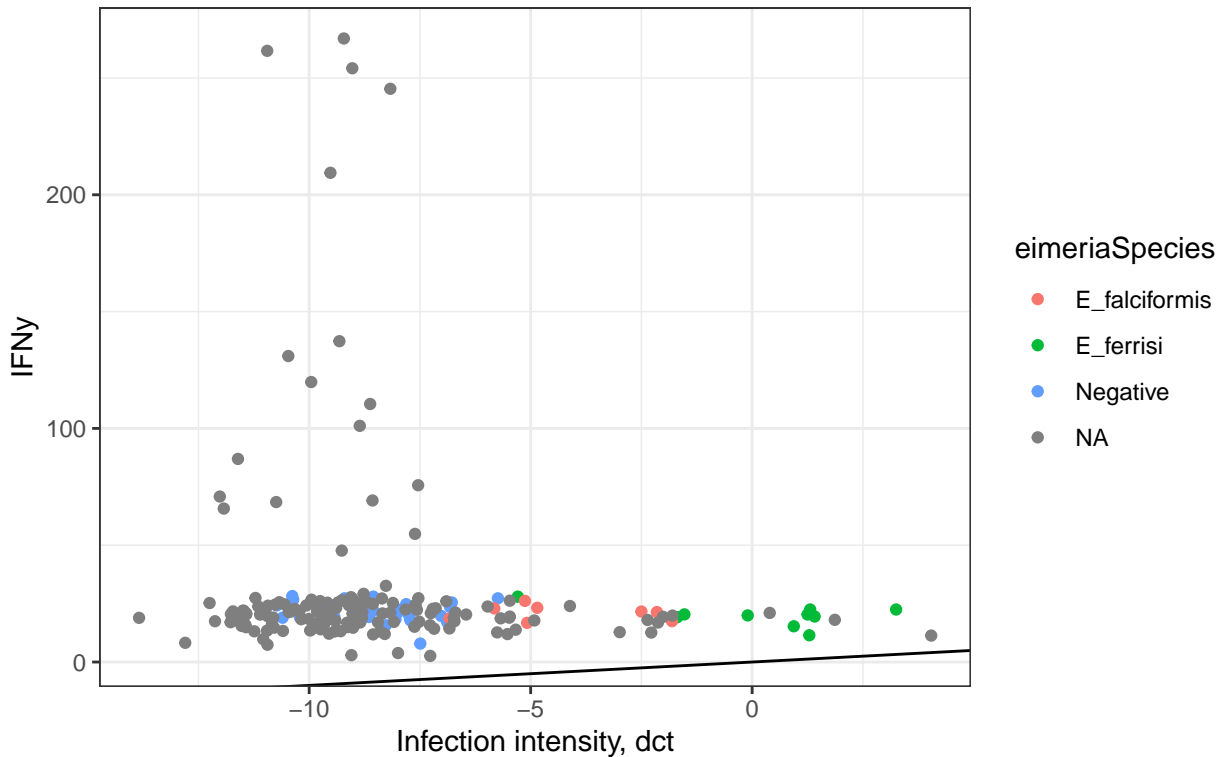
```

    title ="Immune gene expression against infection intensity in field
    samples") +
    theme_bw()

```

Warning: Removed 154 rows containing missing values (geom_point).

Immune gene expression against infection intensity in field samples



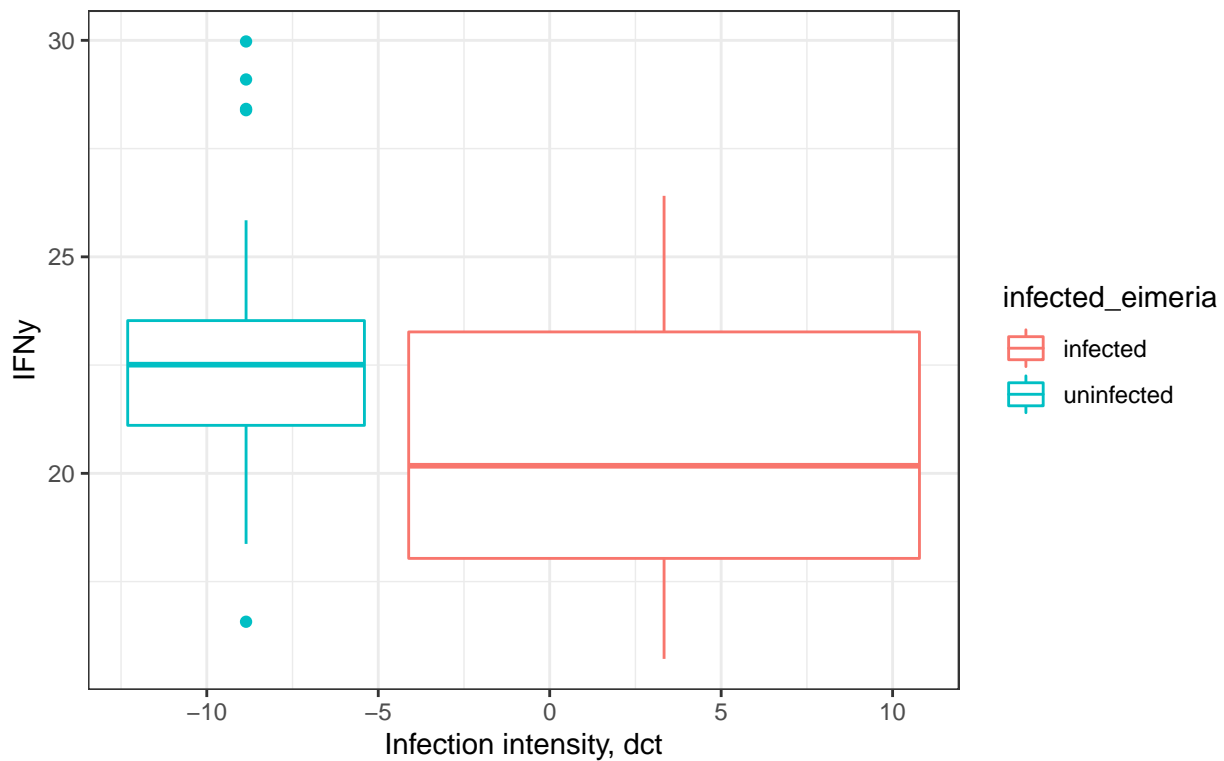
```

ggplot(lab, aes(x = delta, y = IFNγ, color = infected_eimeria)) +
  geom_boxplot() +
  labs(x = "Infection intensity, dct",
       title ="Immune gene expression against infection intensity in lab
       infections") +
  theme_bw()

```

Warning: Removed 6 rows containing missing values (stat_boxplot).

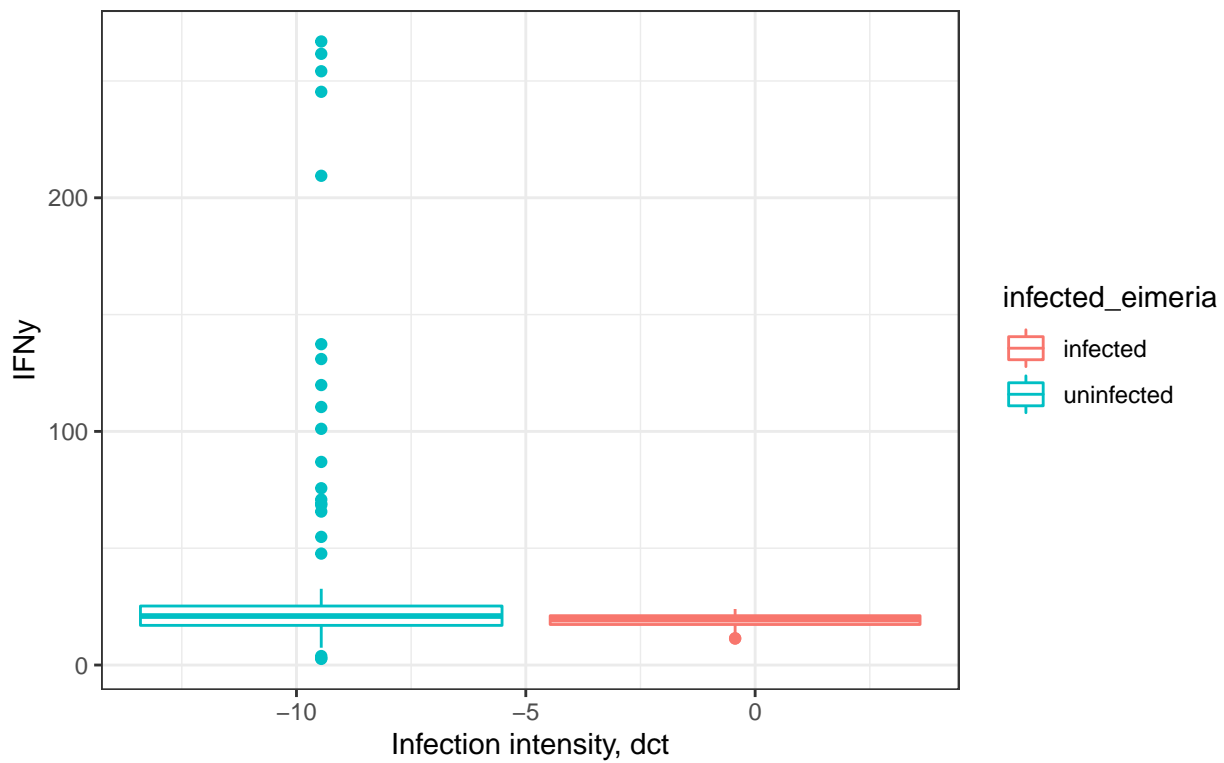
Immune gene expression against infection intensity in lab infections



```
ggplot(field, aes(x = delta_ct_cewe_MminusE, y = IFNγ,  
                  color = infected_eimeria)) +  
  geom_boxplot() +  
  labs(x = "Infection intensity, dct",  
        title = "Immune gene expression against infection intensity in field  
samples") +  
  theme_bw()
```

Warning: Removed 154 rows containing missing values (stat_boxplot).

Immune gene expression against infection intensity in field samples



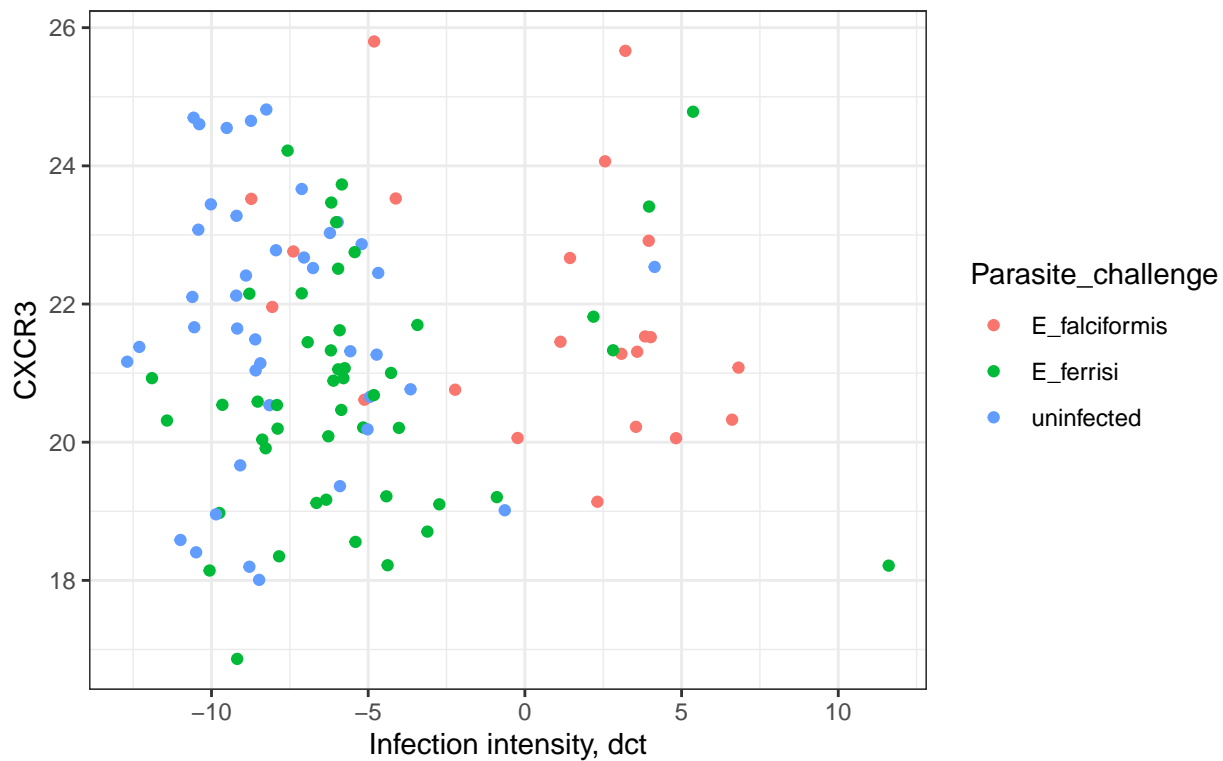
2.

CXCR3

```
ggplot(lab, aes(x = delta, y = CXCR3_bio, color = Parasite_challenge)) +
  geom_jitter() +
  geom_abline() +
  labs(x = "Infection intensity, dct", y = "CXCR3",
       title = "Immune gene expression against infection intensity in lab
infections") +
  theme_bw()
```

Warning: Removed 6 rows containing missing values (geom_point).

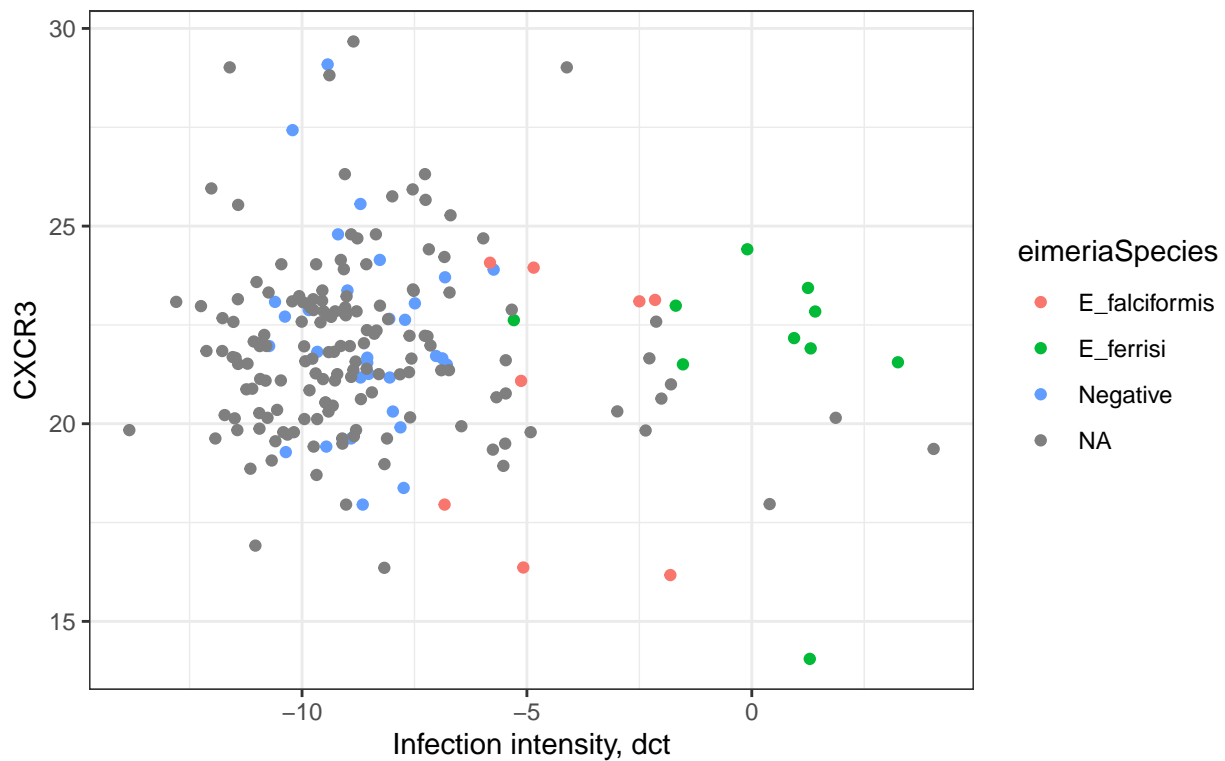
Immune gene expression against infection intensity in lab infections



```
ggplot(field, aes(x = delta_ct_cewe_MminusE, y = CXCR3, color = eimeriaSpecies)) +
  geom_jitter() +
  geom_abline() +
  labs(x = "Infection intensity, dct",
       title = "Immune gene expression against infection intensity in
       field samples") +
  theme_bw()
```

Warning: Removed 154 rows containing missing values (geom_point).

Immune gene expression against infection intensity in field samples

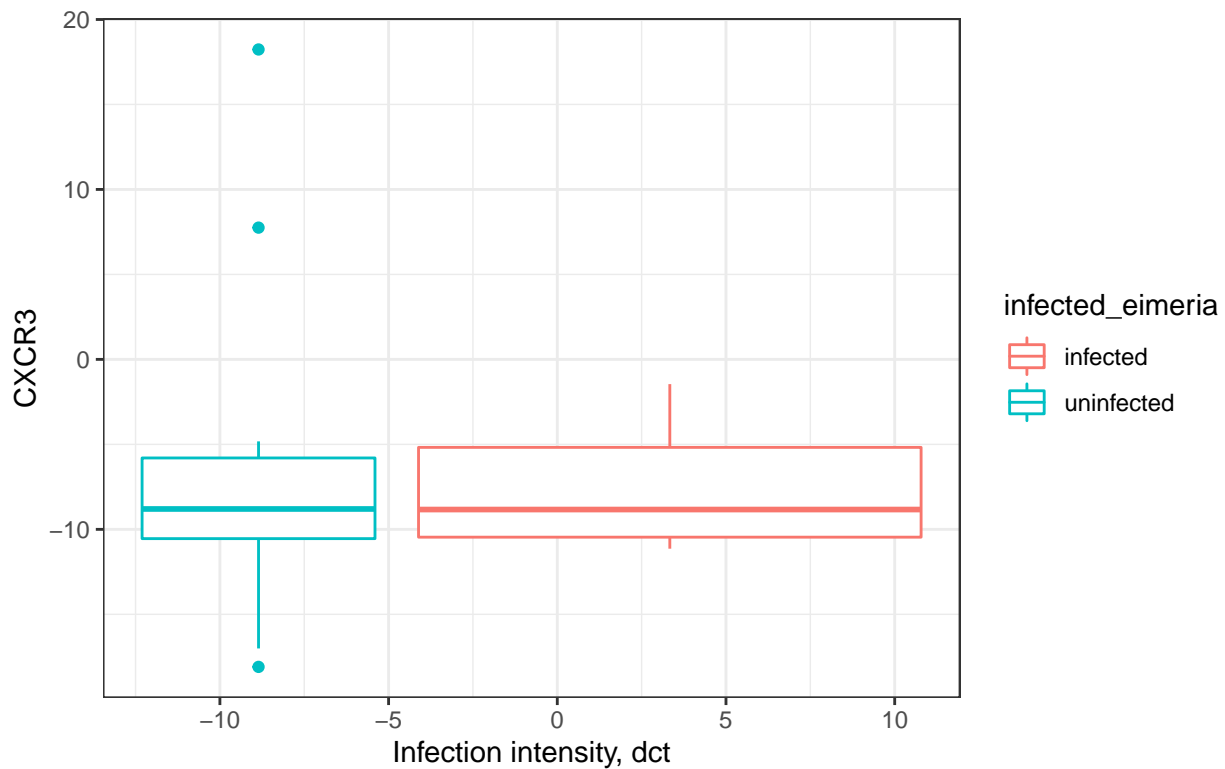


```
ggplot(lab, aes(x = delta, y = CXCR3, color = infected_eimeria)) +
  geom_boxplot() +
  labs(x = "Infection intensity, dct",
       title = "Immune gene expression against infection intensity in lab
infections") +
  theme_bw()
```

Warning: Removed 6 rows containing missing values (stat_boxplot).

Warning: Removed 49 rows containing non-finite values (stat_boxplot).

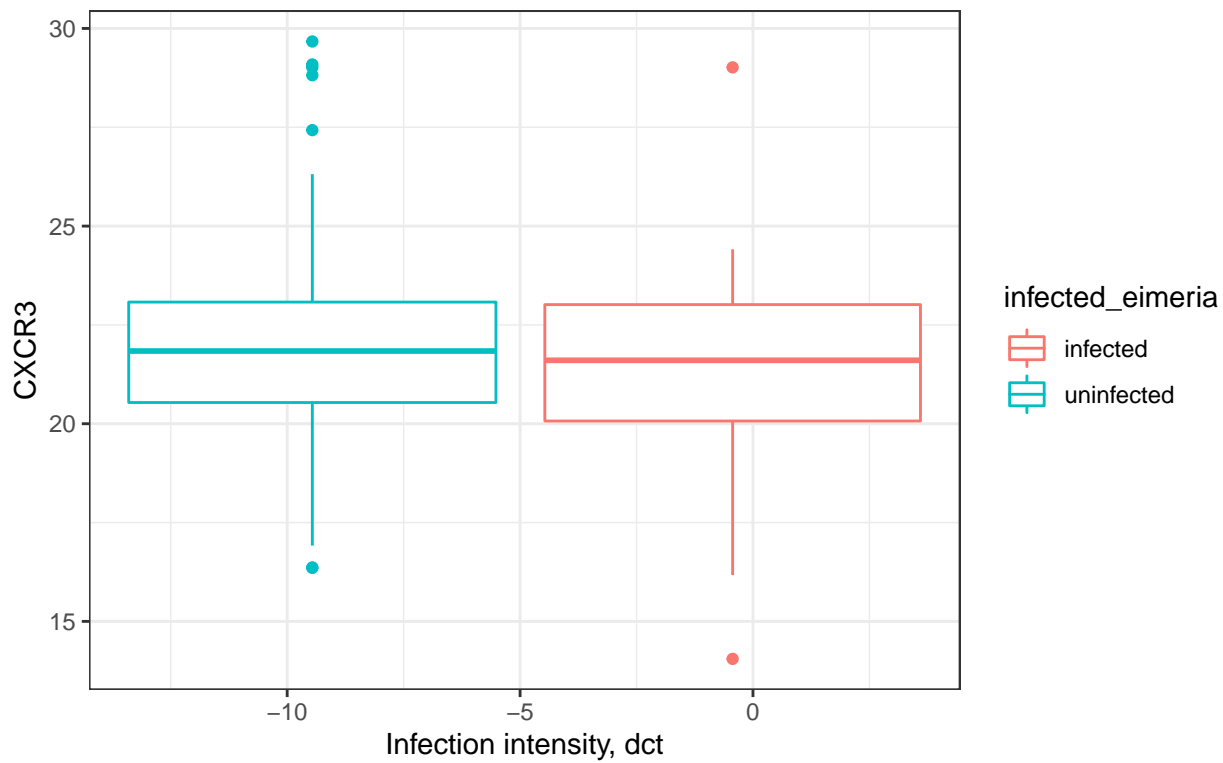
Immune gene expression against infection intensity in lab infections



```
ggplot(field, aes(x = delta_ct_cewe_MminusE, y = CXCR3,
                  color = infected_eimeria)) +
  geom_boxplot() +
  labs(x = "Infection intensity, dct",
       title = "Immune gene expression against infection intensity in field
samples") +
  theme_bw()
```

Warning: Removed 154 rows containing missing values (stat_boxplot).

Immune gene expression against infection intensity in field samples

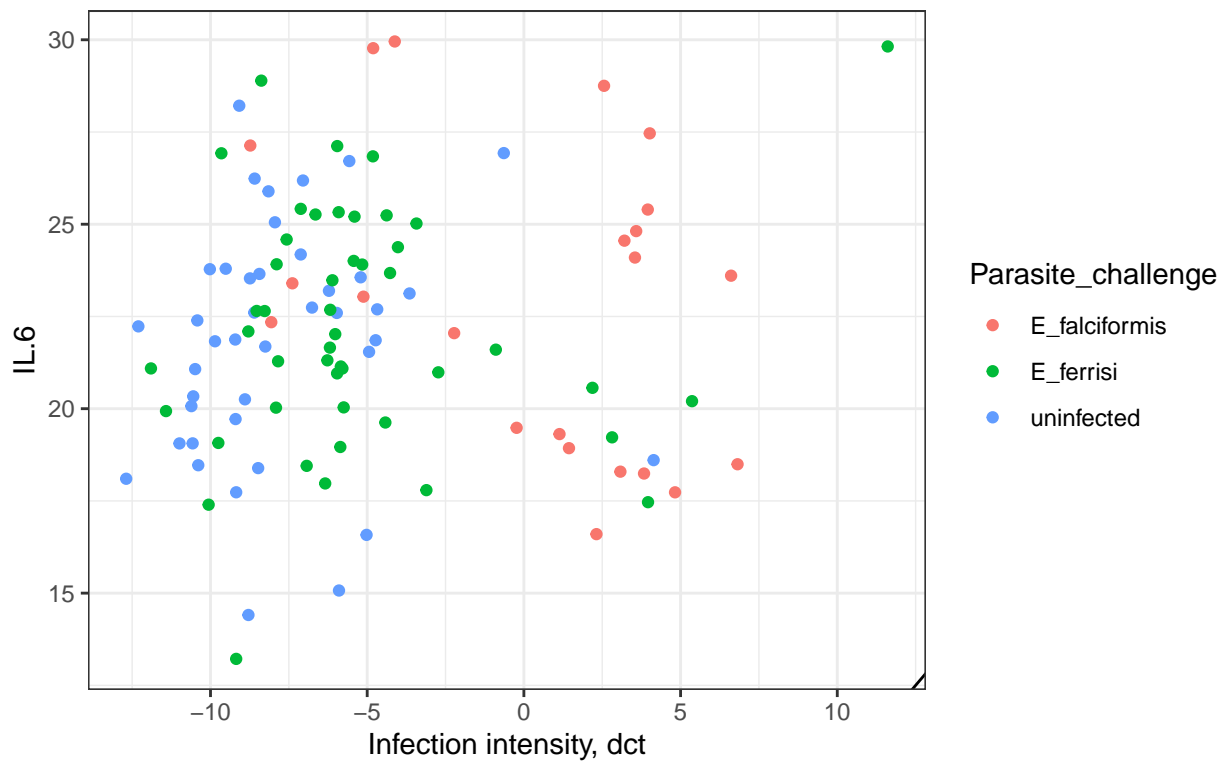


3. IL.6

```
ggplot(lab, aes(x = delta, y = IL.6, color = Parasite_challenge)) +
  geom_jitter() +
  geom_abline() +
  labs(x = "Infection intensity, dct",
       title = "Immune gene expression against infection intensity in lab
infections") +
  theme_bw()
```

Warning: Removed 6 rows containing missing values (geom_point).

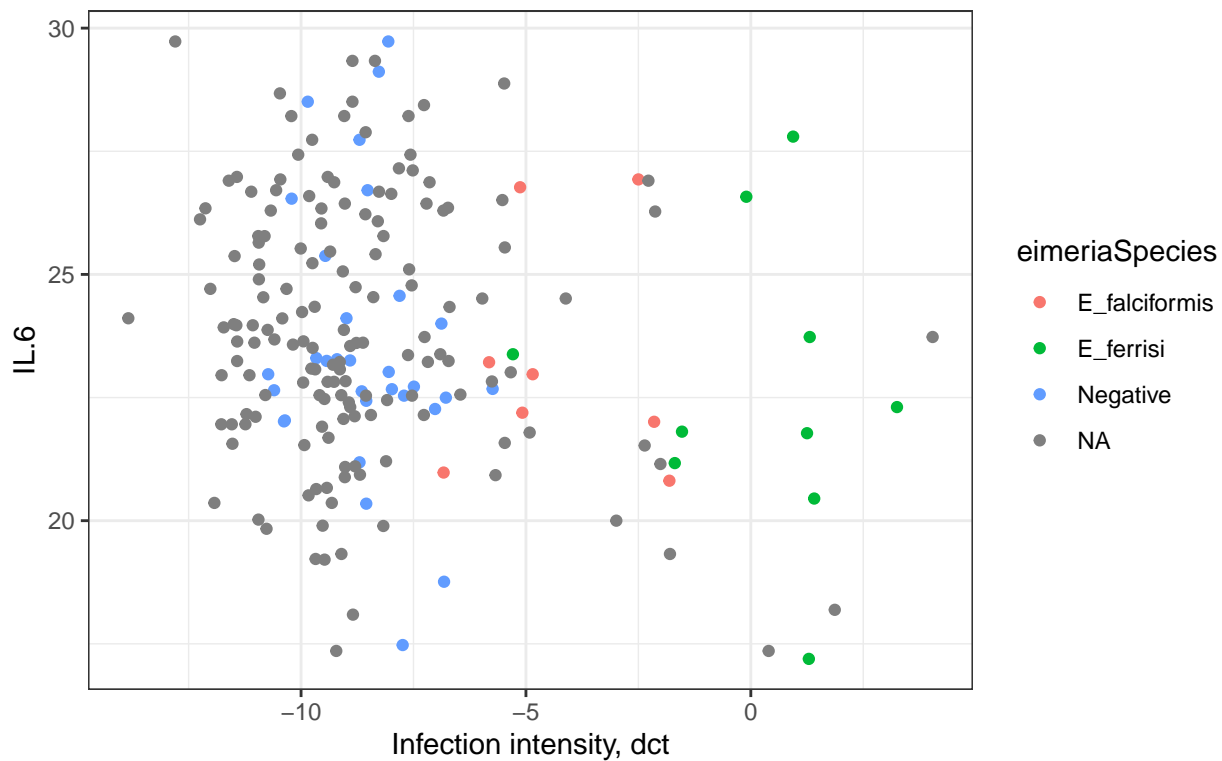
Immune gene expression against infection intensity in lab infections



```
ggplot(field, aes(x = delta_ct_cewe_MminusE, y = IL.6, color = eimeriaSpecies)) +
  geom_jitter() +
  geom_abline() +
  labs(x = "Infection intensity, dct",
       title = "Immune gene expression against infection intensity in field
               samples") +
  theme_bw()
```

Warning: Removed 154 rows containing missing values (geom_point).

Immune gene expression against infection intensity in field samples

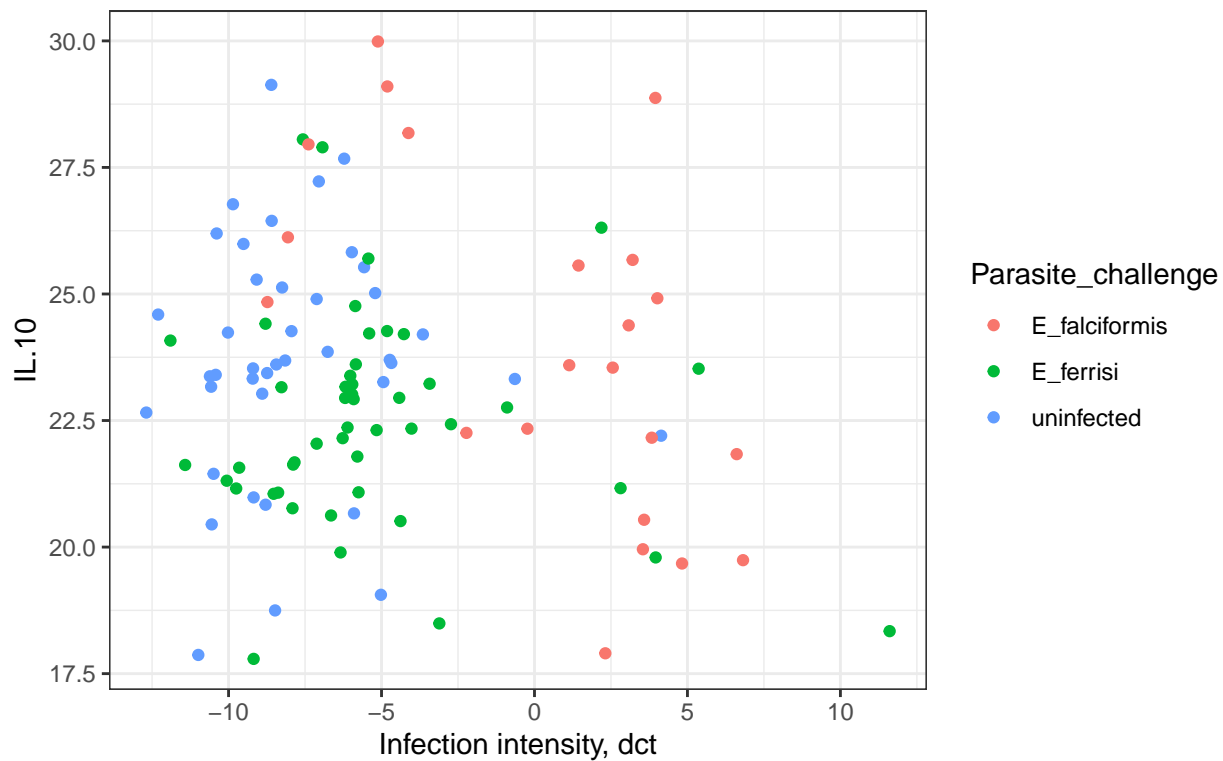


4. IL.10

```
ggplot(lab, aes(x = delta, y = IL.10, color = Parasite_challenge)) +
  geom_jitter() +
  geom_abline() +
  labs(x = "Infection intensity, dct",
       title = "Immune gene expression against infection intensity
in lab infections") +
  theme_bw()
```

Warning: Removed 6 rows containing missing values (geom_point).

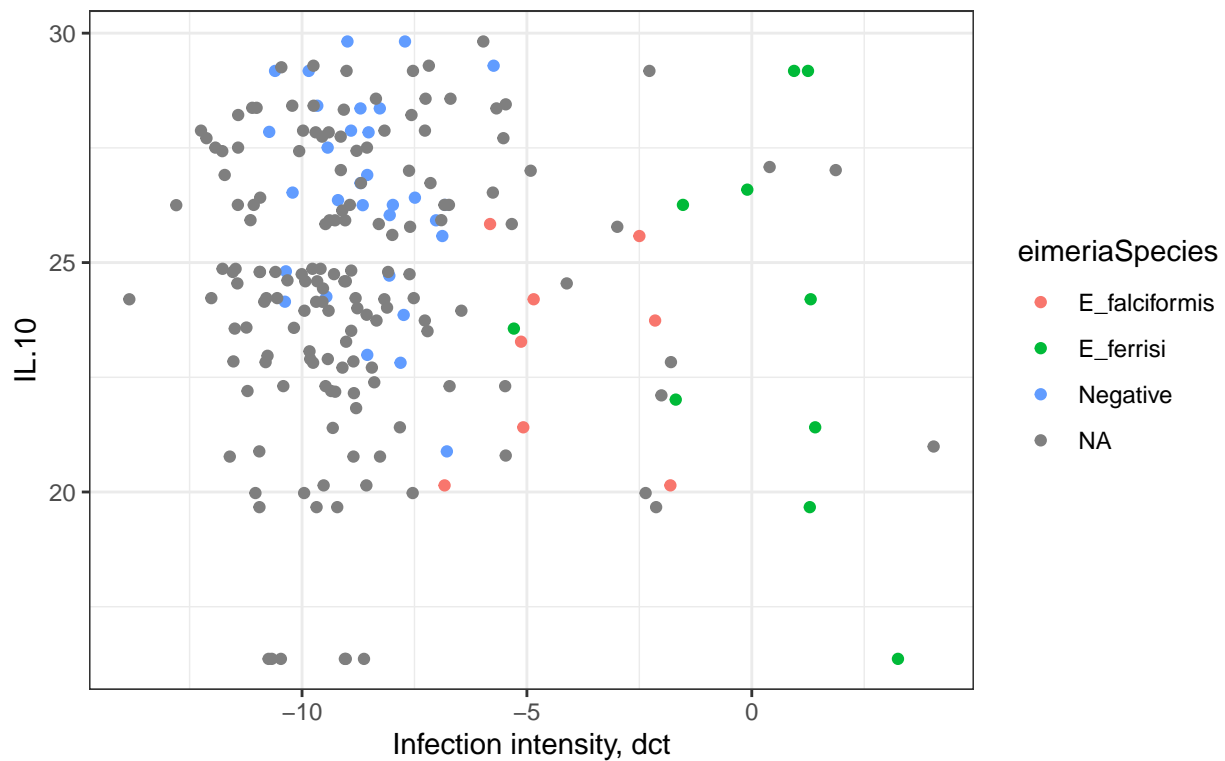
Immune gene expression against infection intensity in lab infections



```
ggplot(field, aes(x = delta_ct_cewe_MminusE, y = IL.10, color = eimeriaSpecies)) +
  geom_jitter() +
  geom_abline() +
  labs(x = "Infection intensity, dct",
       title = "Immune gene expression against infection intensity in field
samples") +
  theme_bw()
```

Warning: Removed 154 rows containing missing values (geom_point).

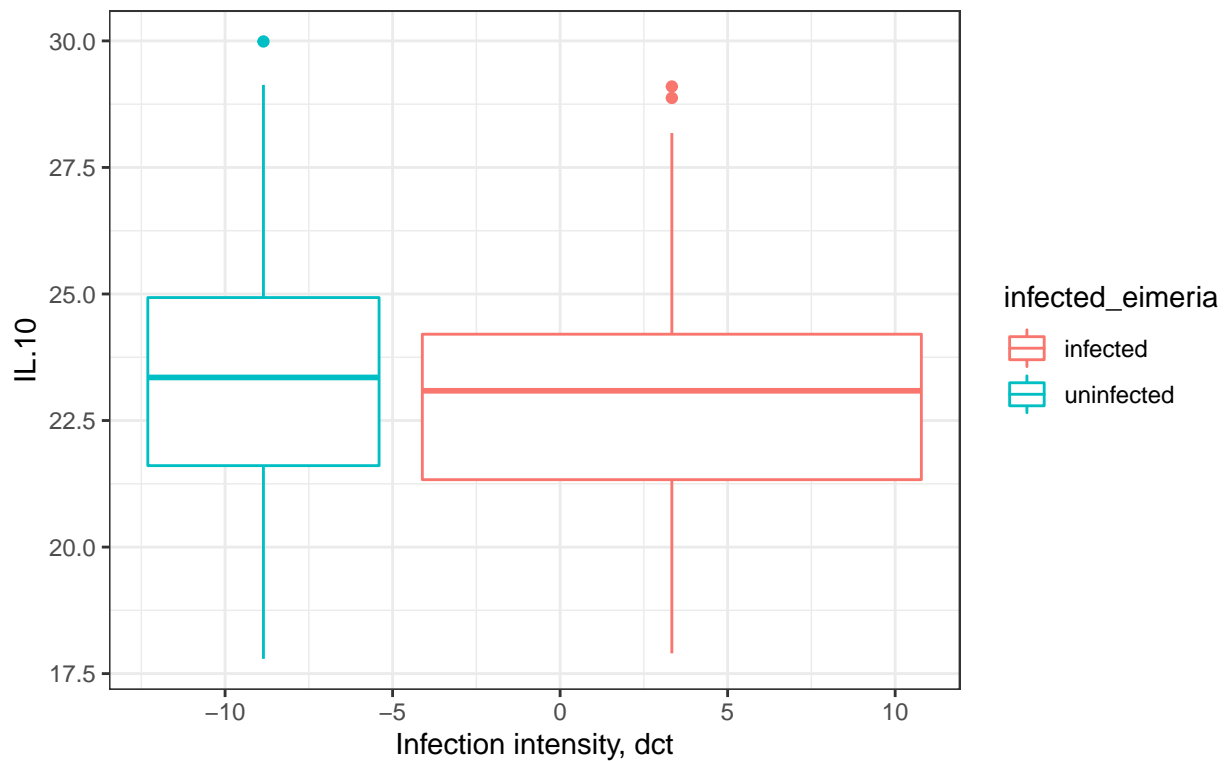
Immune gene expression against infection intensity in field samples



```
ggplot(lab, aes(x = delta, y = IL.10, color = infected_eimeria)) +
  geom_boxplot() +
  labs(x = "Infection intensity, dct",
       title = "Immune gene expression against infection intensity in lab
infections") +
  theme_bw()
```

Warning: Removed 6 rows containing missing values (stat_boxplot).

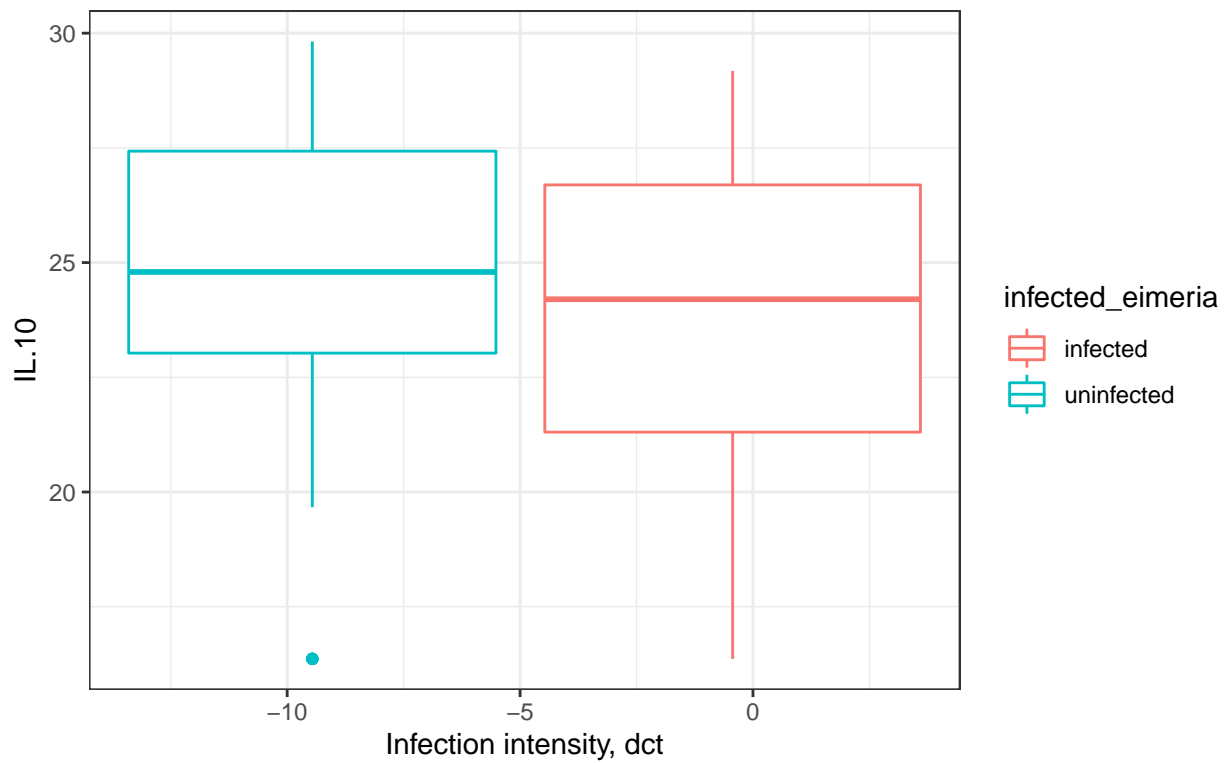
Immune gene expression against infection intensity in lab infections



```
ggplot(field, aes(x = delta_ct_cewe_MminusE, y = IL.10,  
                  color = infected_eimeria)) +  
  geom_boxplot() +  
  labs(x = "Infection intensity, dct",  
       title = "Immune gene expression against infection intensity in field  
samples") +  
  theme_bw()
```

Warning: Removed 154 rows containing missing values (stat_boxplot).

Immune gene expression against infection intensity in field samples

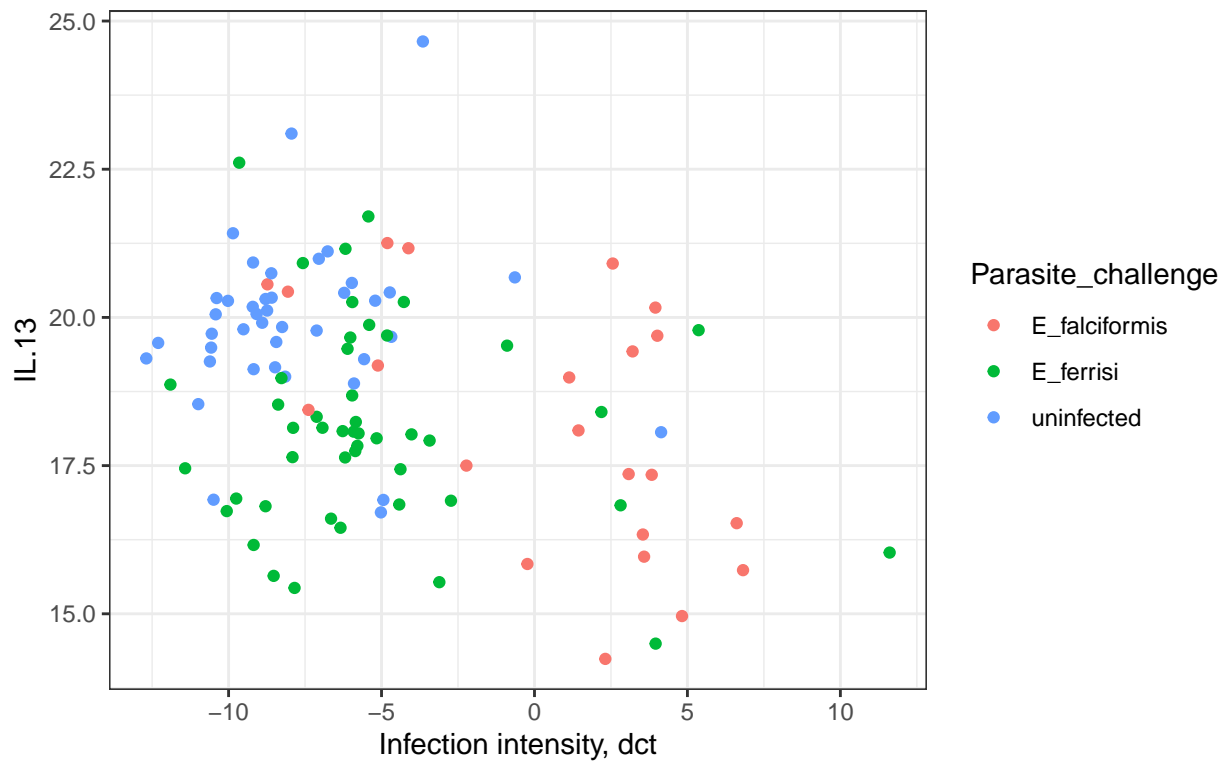


5. IL.13

```
ggplot(lab, aes(x = delta, y = IL.13, color = Parasite_challenge)) +
  geom_jitter() +
  geom_abline() +
  labs(x = "Infection intensity, dct",
       title = "Immune gene expression against infection intensity
in lab infections") +
  theme_bw()
```

Warning: Removed 6 rows containing missing values (geom_point).

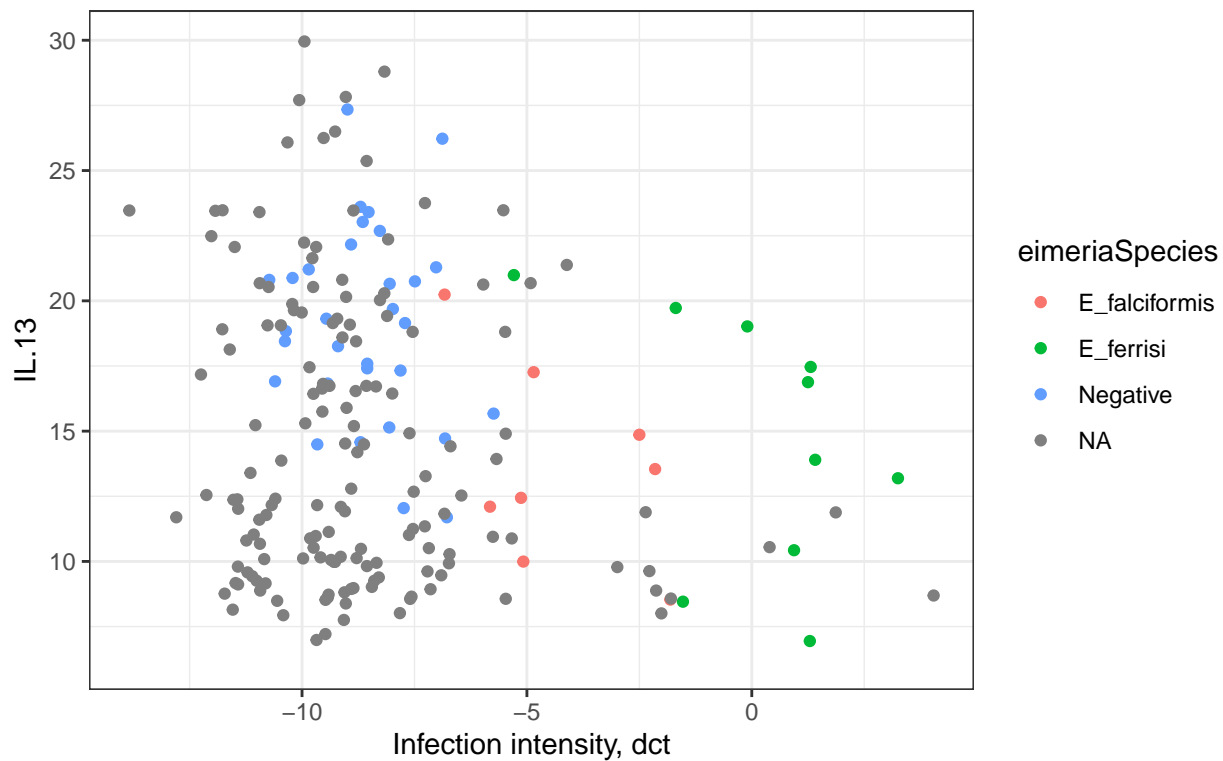
Immune gene expression against infection intensity in lab infections



```
ggplot(field, aes(x = delta_ct_cewe_MminusE, y = IL.13, color = eimeriaSpecies)) +
  geom_jitter() +
  geom_abline() +
  labs(x = "Infection intensity, dct",
       title = "Immune gene expression against infection intensity in field
samples") +
  theme_bw()
```

Warning: Removed 154 rows containing missing values (geom_point).

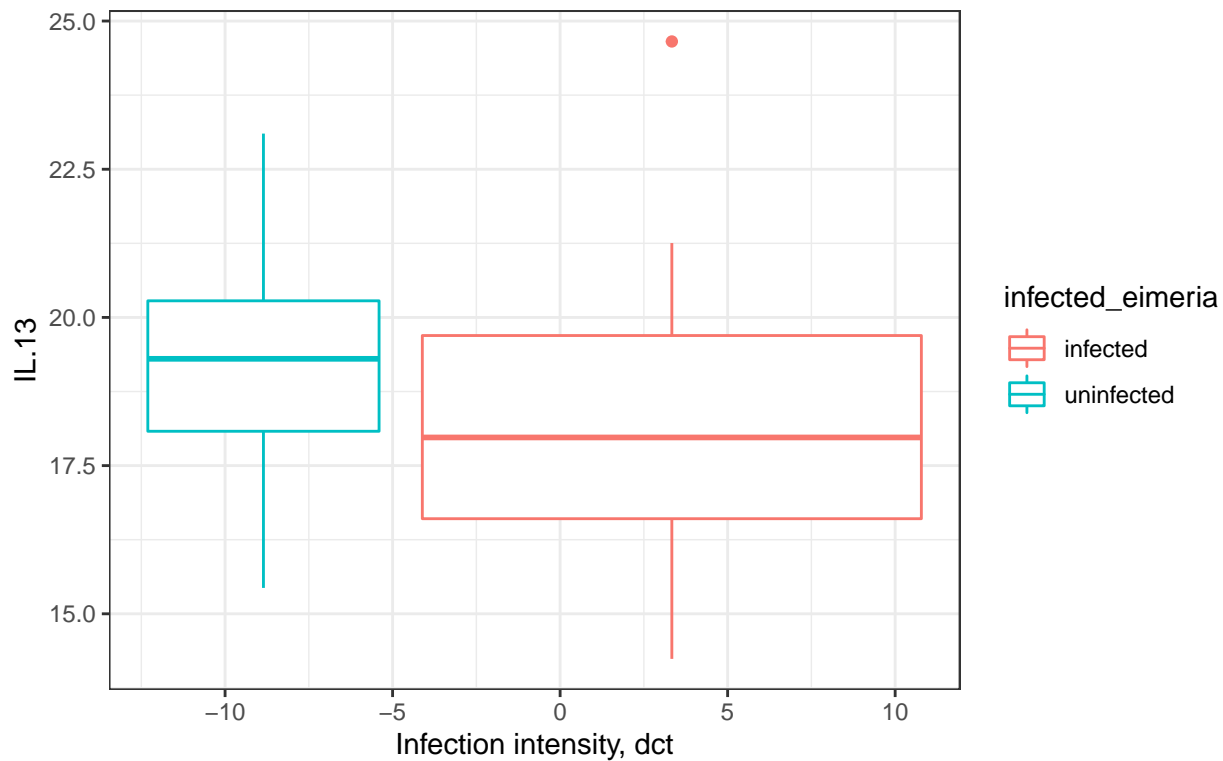
Immune gene expression against infection intensity in field samples



```
ggplot(lab, aes(x = delta, y = IL.13, color = infected_eimeria)) +
  geom_boxplot() +
  labs(x = "Infection intensity, dct",
       title = "Immune gene expression against infection intensity in lab
infections") +
  theme_bw()
```

Warning: Removed 6 rows containing missing values (stat_boxplot).

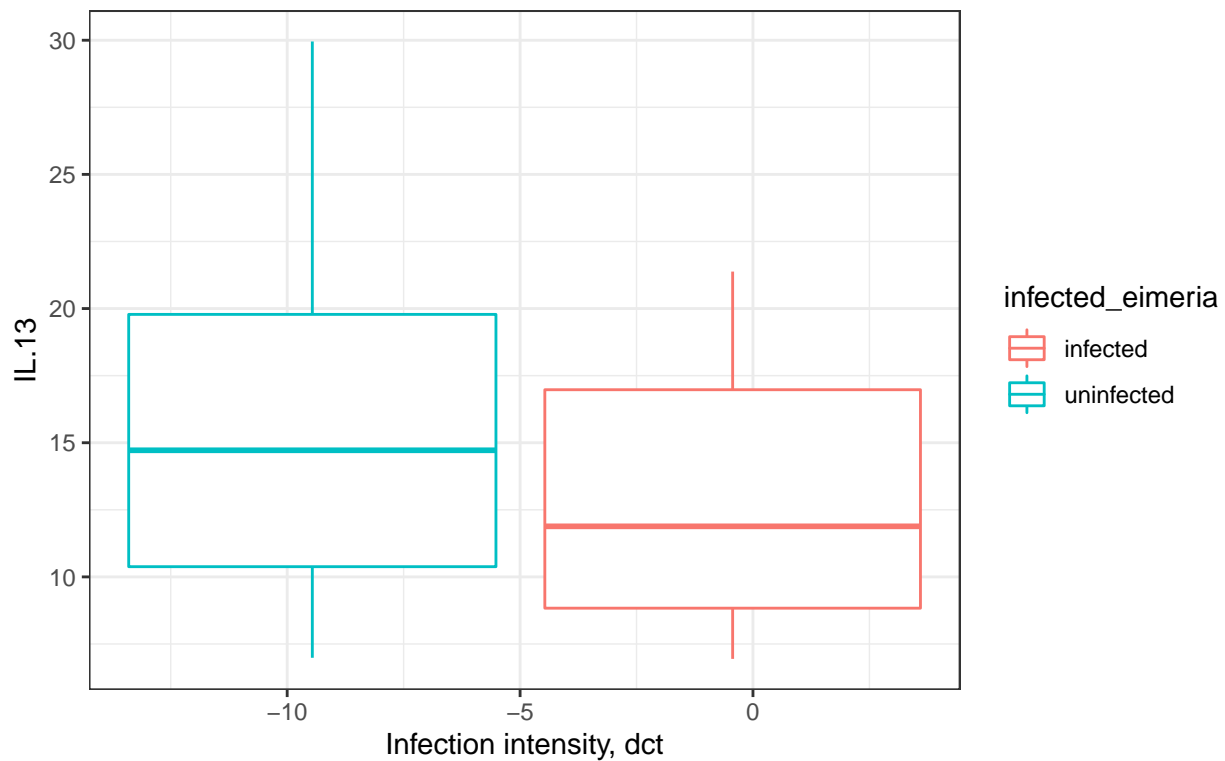
Immune gene expression against infection intensity in lab infections



```
ggplot(field, aes(x = delta_ct_cewe_MminusE, y = IL.13,  
                  color = infected_eimeria)) +  
  geom_boxplot() +  
  labs(x = "Infection intensity, dct",  
        title = "Immune gene expression against infection intensity in field  
        samples") +  
  theme_bw()
```

Warning: Removed 154 rows containing missing values (stat_boxplot).

Immune gene expression against infection intensity in field samples

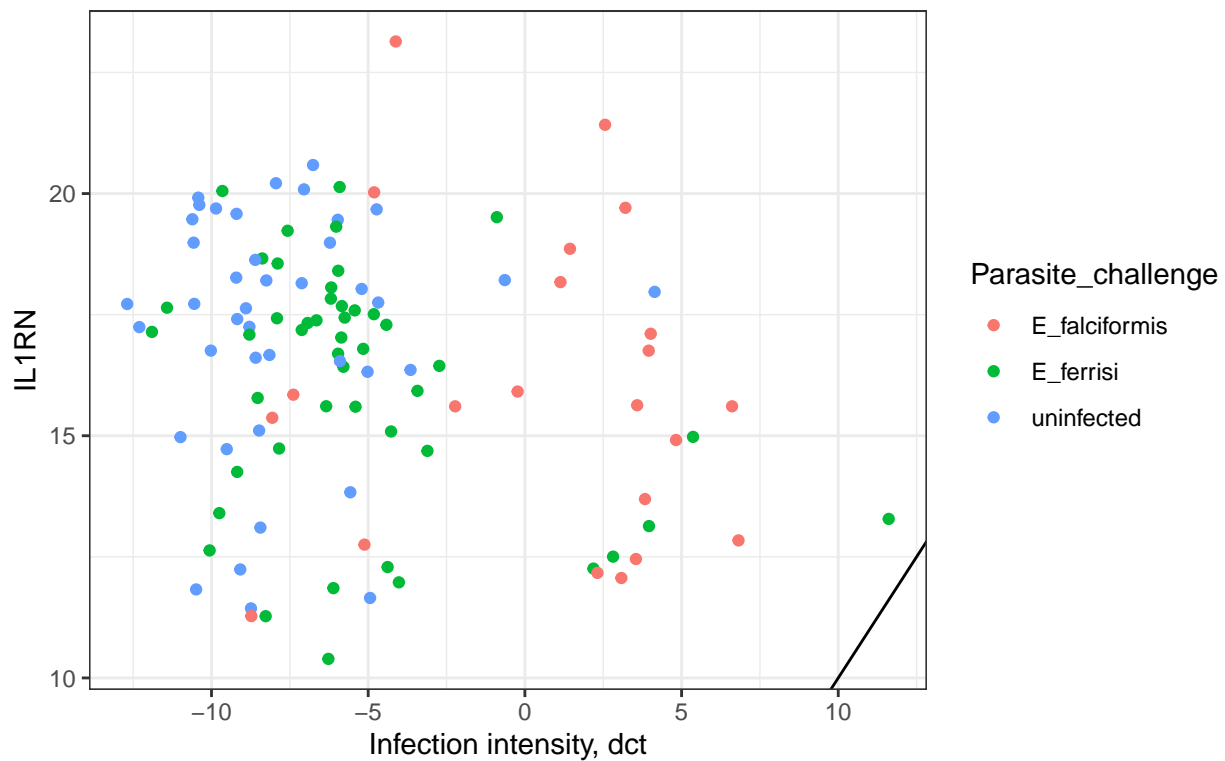


6. IL1RN

```
ggplot(lab, aes(x = delta, y = IL1RN, color = Parasite_challenge)) +  
  geom_jitter() +  
  geom_abline() +  
  labs(x = "Infection intensity, dct",  
        title = "Immune gene expression against infection intensity  
in lab infections") +  
  theme_bw()
```

Warning: Removed 6 rows containing missing values (geom_point).

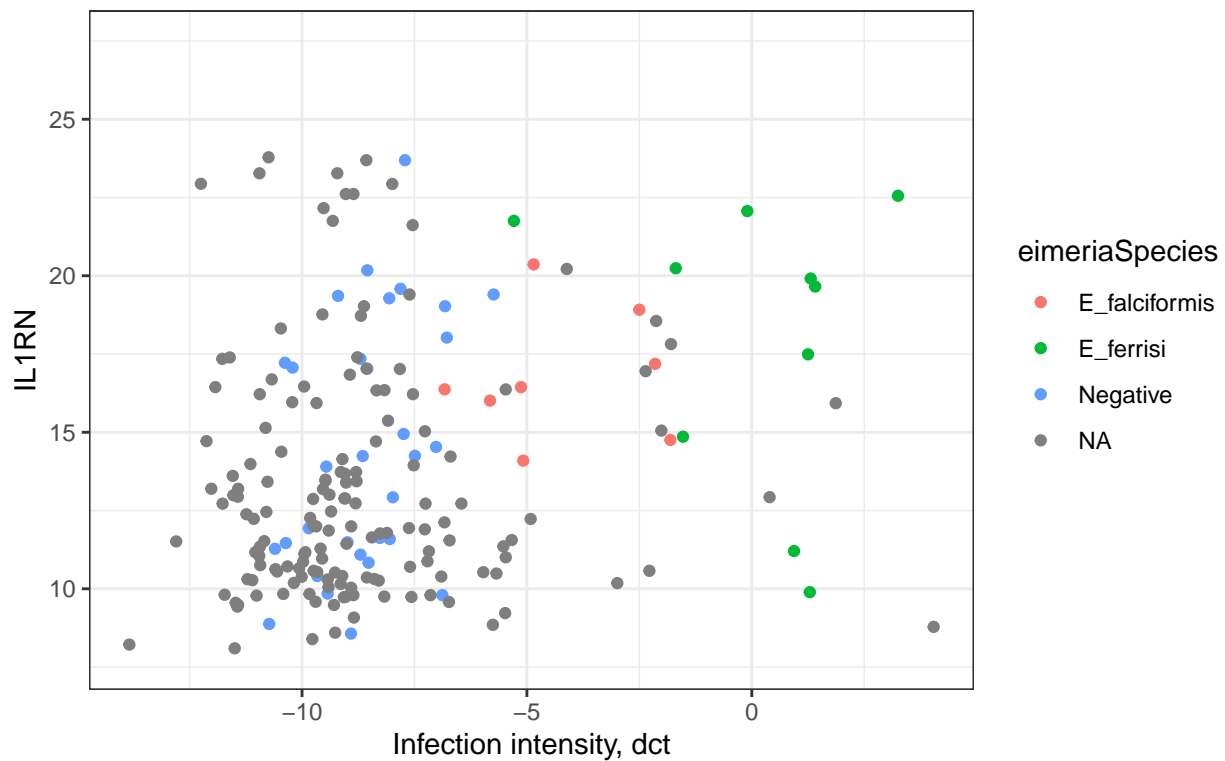
Immune gene expression against infection intensity in lab infections



```
ggplot(field, aes(x = delta_ct_cewe_MminusE, y = IL1RN, color = eimeriaSpecies)) +
  geom_jitter() +
  geom_abline() +
  labs(x = "Infection intensity, dct",
       title = "Immune gene expression against infection intensity in field
samples") +
  theme_bw()
```

Warning: Removed 154 rows containing missing values (geom_point).

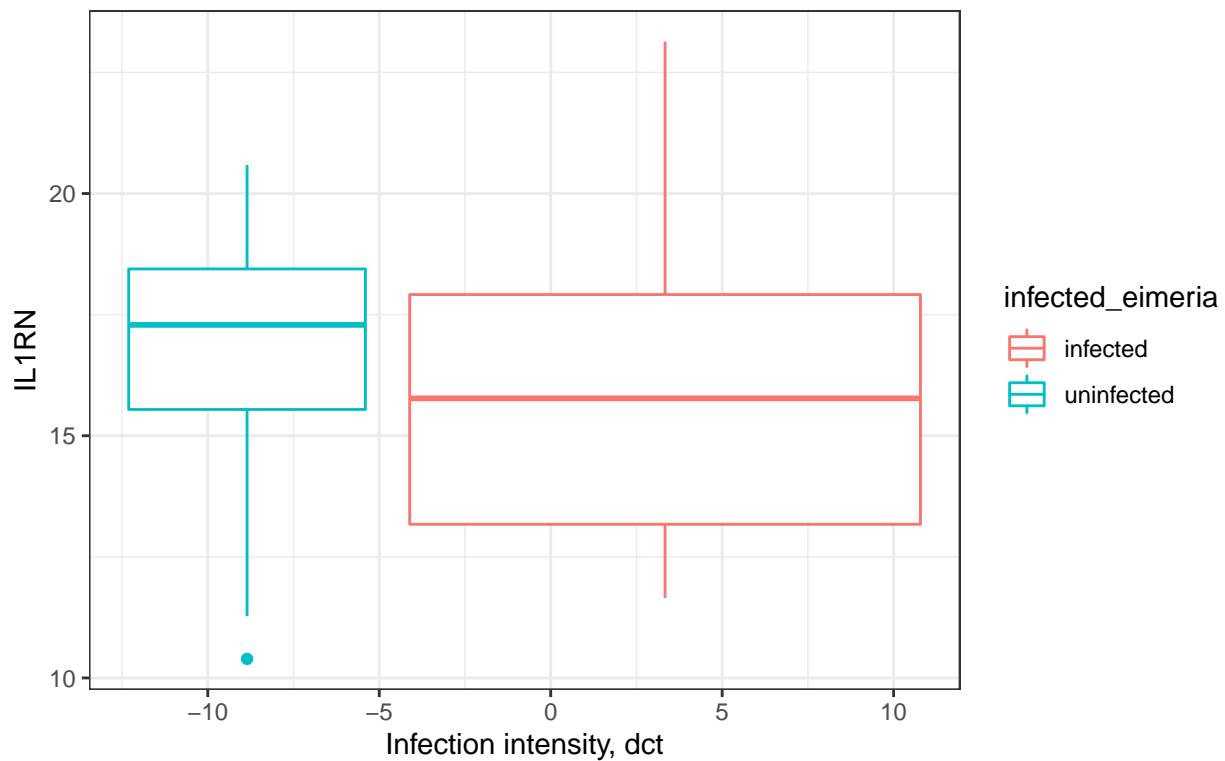
Immune gene expression against infection intensity in field samples



```
ggplot(lab, aes(x = delta, y = IL1RN, color = infected_eimeria)) +
  geom_boxplot() +
  labs(x = "Infection intensity, dct",
       title = "Immune gene expression against infection intensity in lab
infections") +
  theme_bw()
```

```
## Warning: Removed 6 rows containing missing values (stat_boxplot).
```

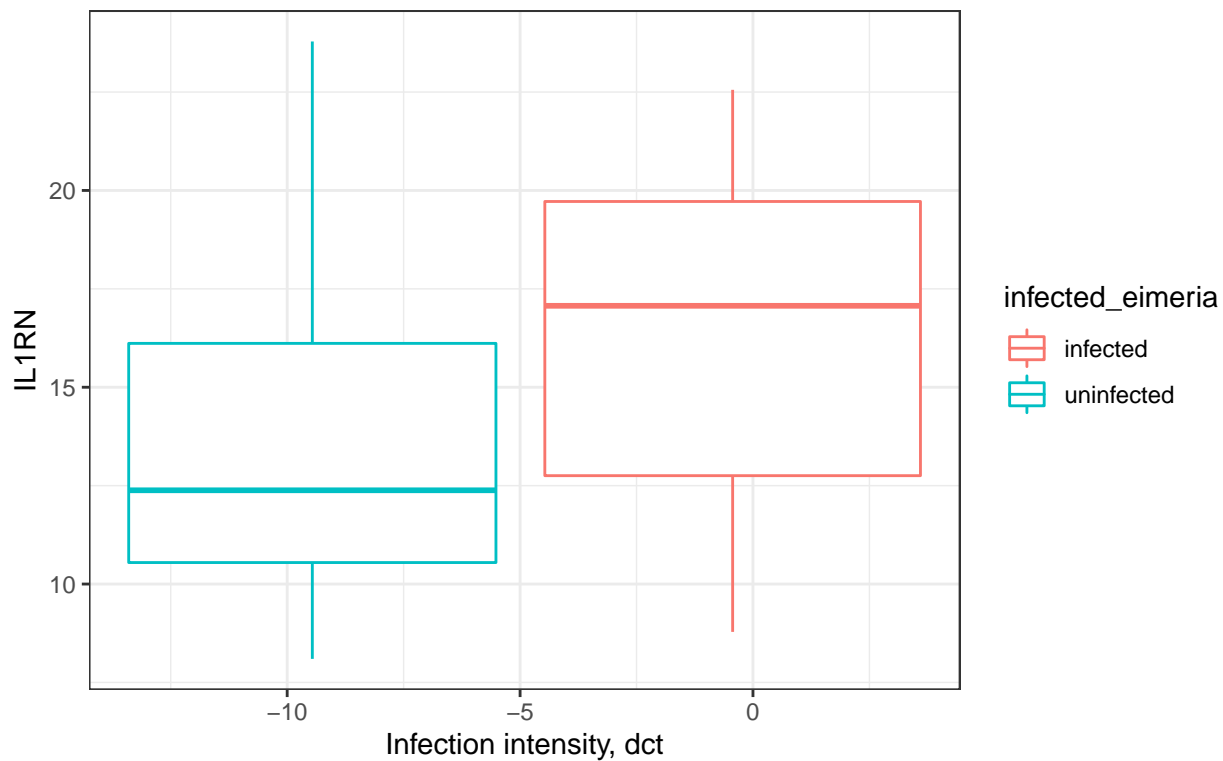
Immune gene expression against infection intensity in lab infections



```
ggplot(field, aes(x = delta_ct_cewe_MminusE, y = IL1RN,
                  color = infected_eimeria)) +
  geom_boxplot() +
  labs(x = "Infection intensity, dct",
       title = "Immune gene expression against infection intensity in field
samples") +
  theme_bw()
```

Warning: Removed 154 rows containing missing values (stat_boxplot).

Immune gene expression against infection intensity in field samples

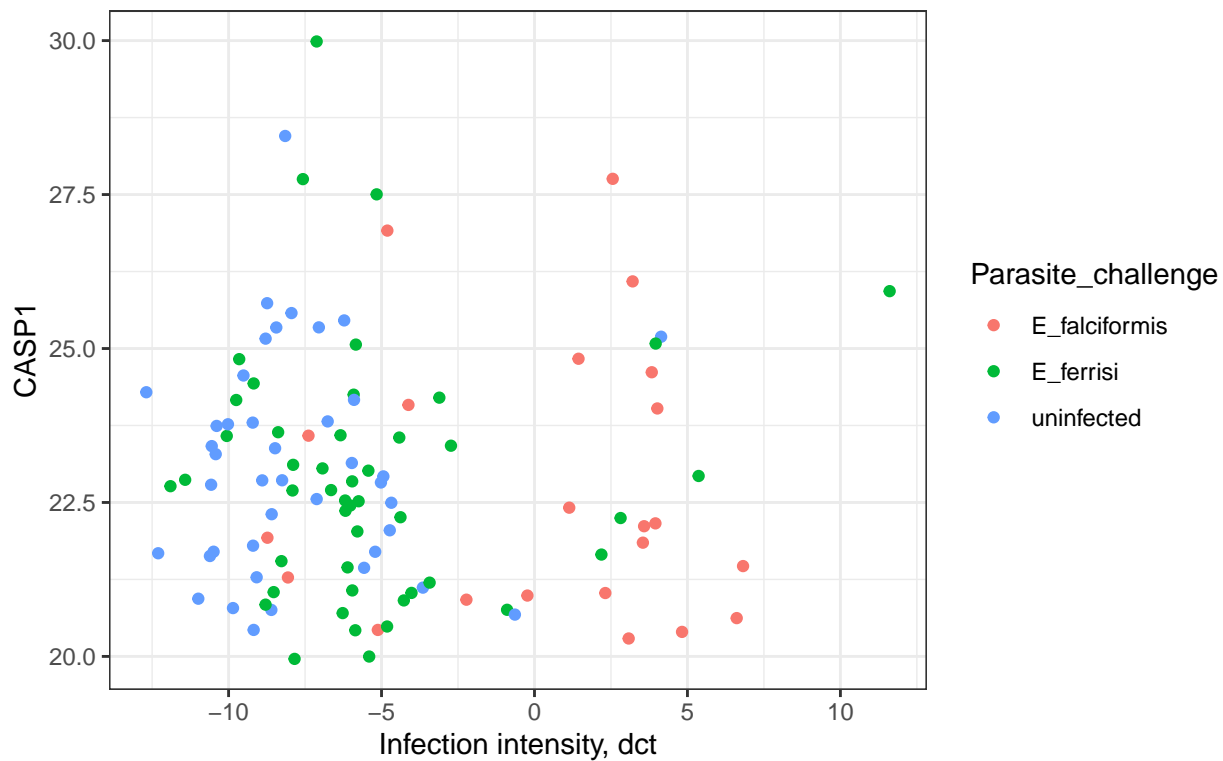


7. CASP1

```
ggplot(lab, aes(x = delta, y = CASP1, color = Parasite_challenge)) +  
  geom_jitter() +  
  geom_abline() +  
  labs(x = "Infection intensity, dct",  
        title = "Immune gene expression against infection intensity  
in lab infections") +  
  theme_bw()
```

Warning: Removed 6 rows containing missing values (geom_point).

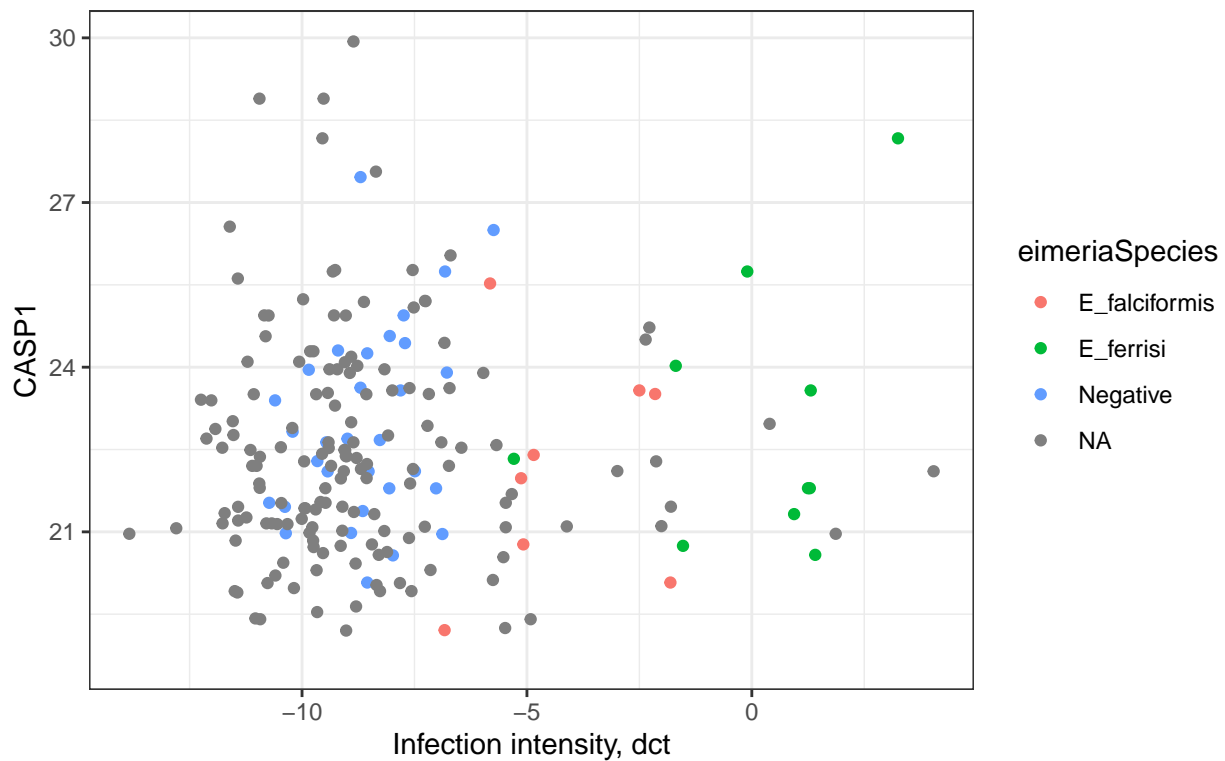
Immune gene expression against infection intensity in lab infections



```
ggplot(field, aes(x = delta_ct_cewe_MminusE, y = CASP1, color = eimeriaSpecies)) +
  geom_jitter() +
  geom_abline() +
  labs(x = "Infection intensity, dct",
       title = "Immune gene expression against infection intensity in field
samples") +
  theme_bw()
```

Warning: Removed 154 rows containing missing values (geom_point).

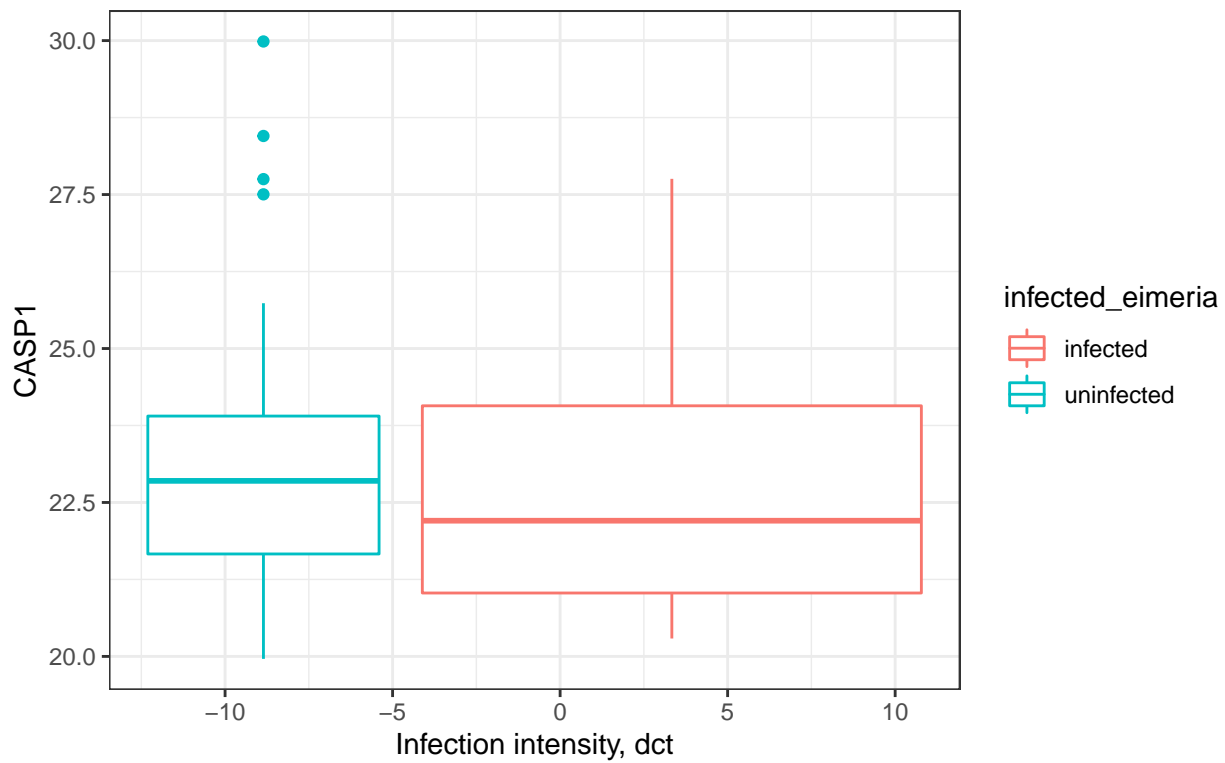
Immune gene expression against infection intensity in field samples



```
ggplot(lab, aes(x = delta, y = CASP1, color = infected_eimeria)) +
  geom_boxplot() +
  labs(x = "Infection intensity, dct",
       title = "Immune gene expression against infection intensity in lab
infections") +
  theme_bw()
```

```
## Warning: Removed 6 rows containing missing values (stat_boxplot).
```

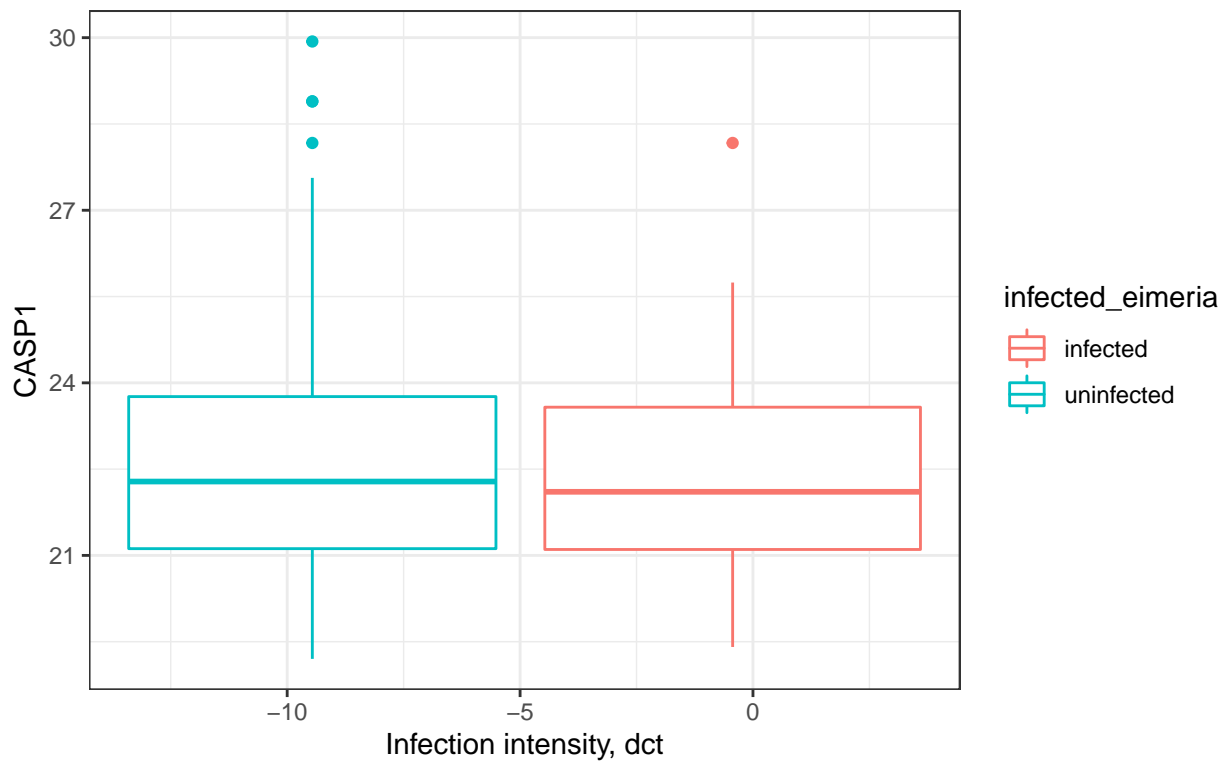
Immune gene expression against infection intensity in lab infections



```
ggplot(field, aes(x = delta_ct_cewe_MminusE, y = CASP1,
                  color = infected_eimeria)) +
  geom_boxplot() +
  labs(x = "Infection intensity, dct",
       title = "Immune gene expression against infection intensity in field
samples") +
  theme_bw()
```

Warning: Removed 154 rows containing missing values (stat_boxplot).

Immune gene expression against infection intensity in field samples

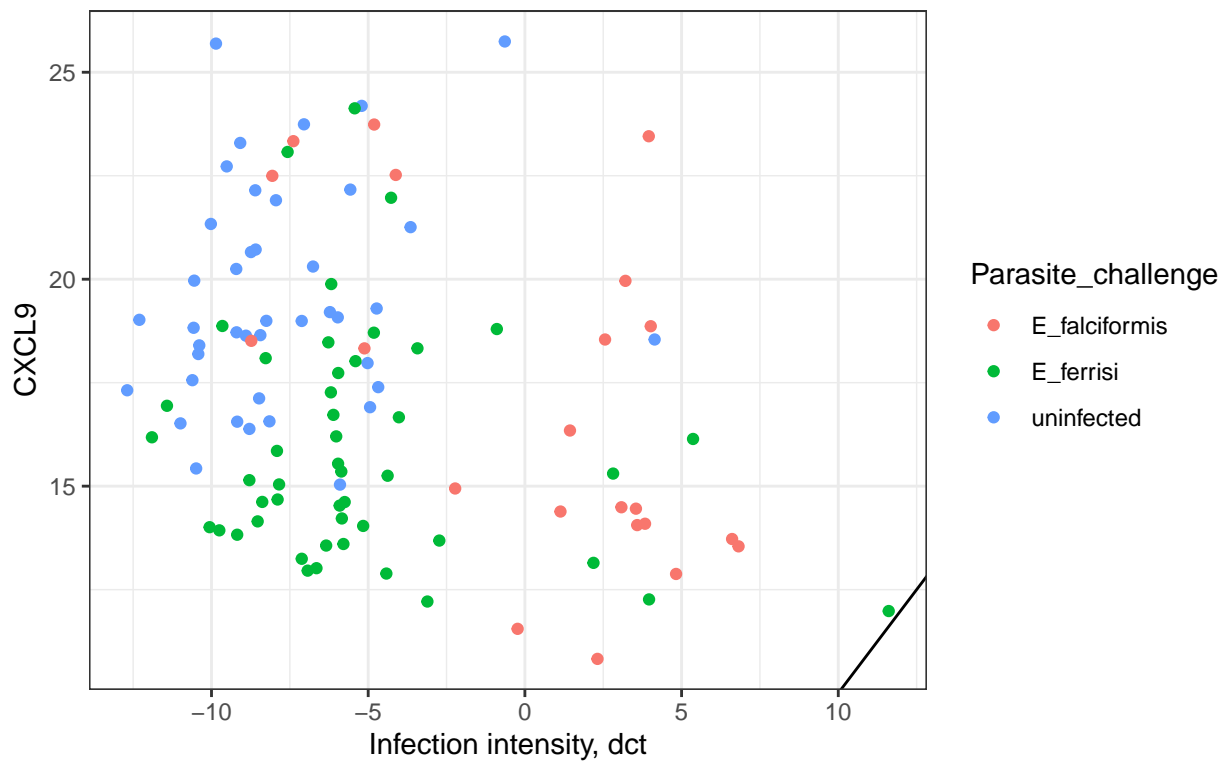


8. CXCL9

```
ggplot(lab, aes(x = delta, y = CXCL9, color = Parasite_challenge)) +
  geom_jitter() +
  geom_abline() +
  labs(x = "Infection intensity, dct",
       title = "Immune gene expression against infection intensity
in lab infections") +
  theme_bw()
```

Warning: Removed 6 rows containing missing values (geom_point).

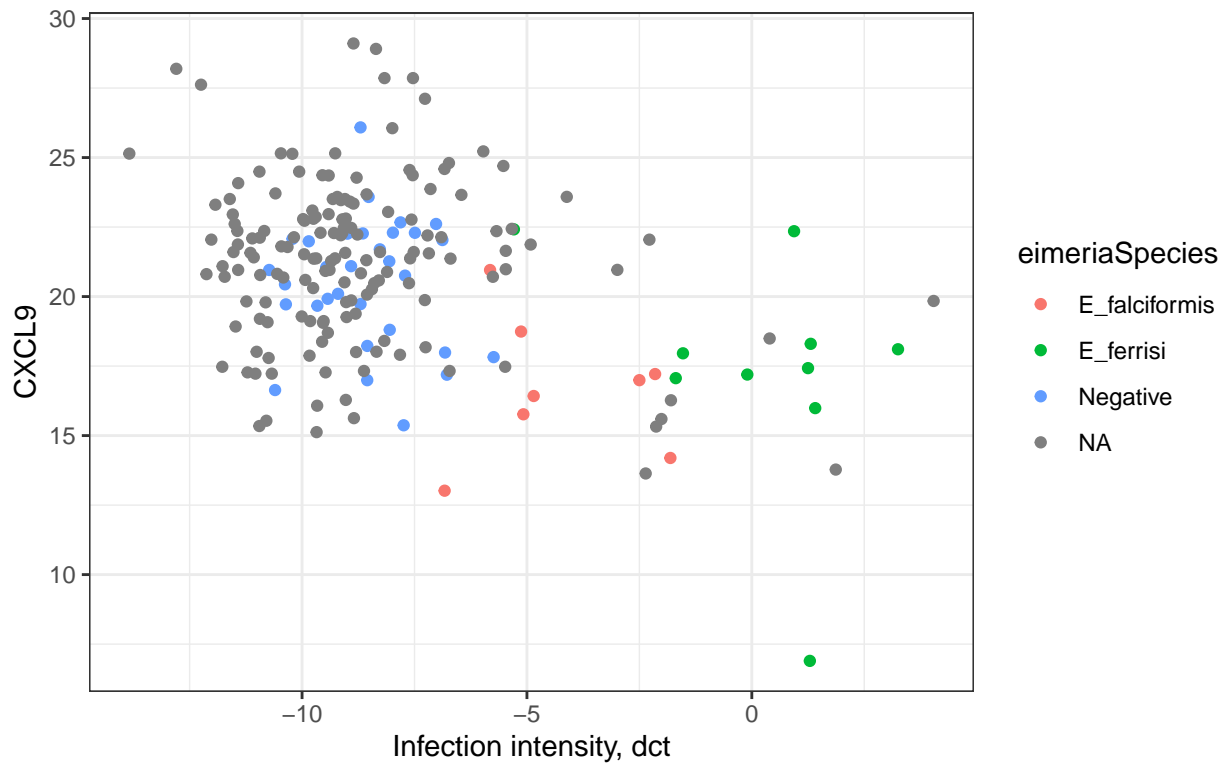
Immune gene expression against infection intensity in lab infections



```
ggplot(field, aes(x = delta_ct_cewe_MminusE, y = CXCL9, color = eimeriaSpecies)) +
  geom_jitter() +
  geom_abline() +
  labs(x = "Infection intensity, dct",
       title = "Immune gene expression against infection intensity in field
       samples") +
  theme_bw()
```

Warning: Removed 154 rows containing missing values (geom_point).

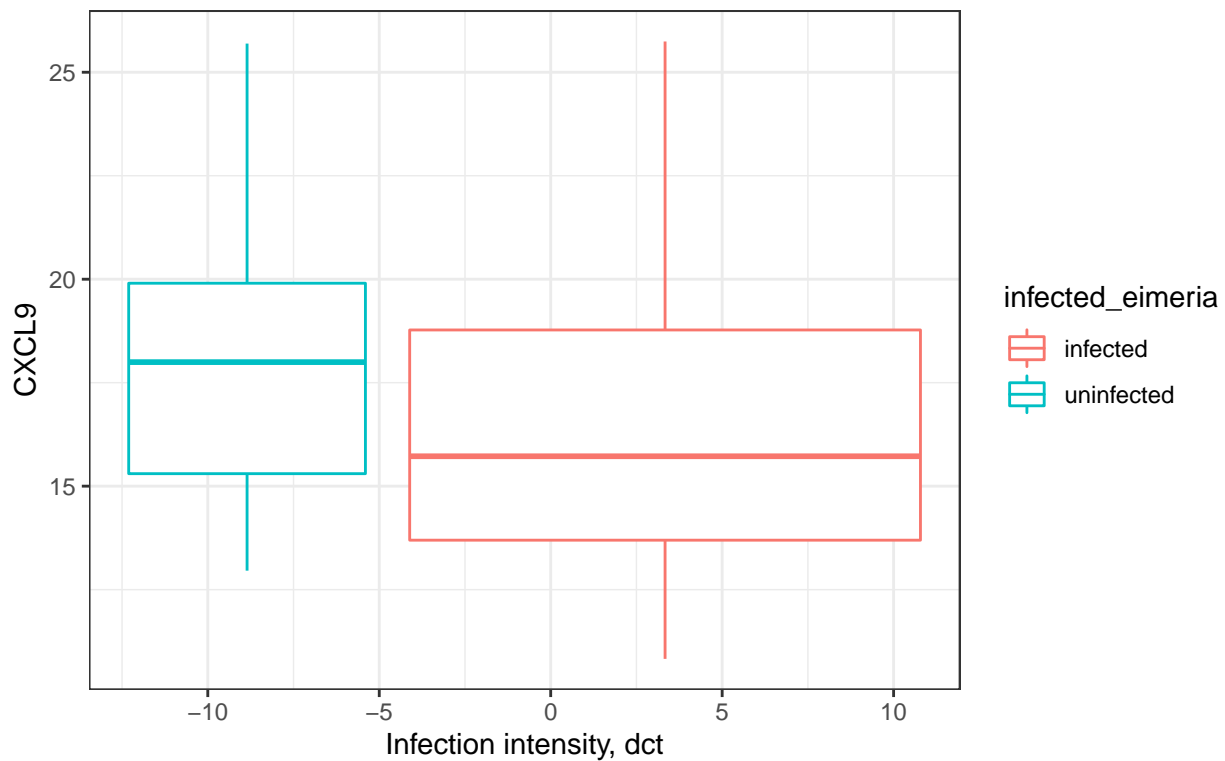
Immune gene expression against infection intensity in field samples



```
ggplot(lab, aes(x = delta, y = CXCL9, color = infected_eimeria)) +
  geom_boxplot() +
  labs(x = "Infection intensity, dct",
       title = "Immune gene expression against infection intensity in lab
infections") +
  theme_bw()
```

Warning: Removed 6 rows containing missing values (stat_boxplot).

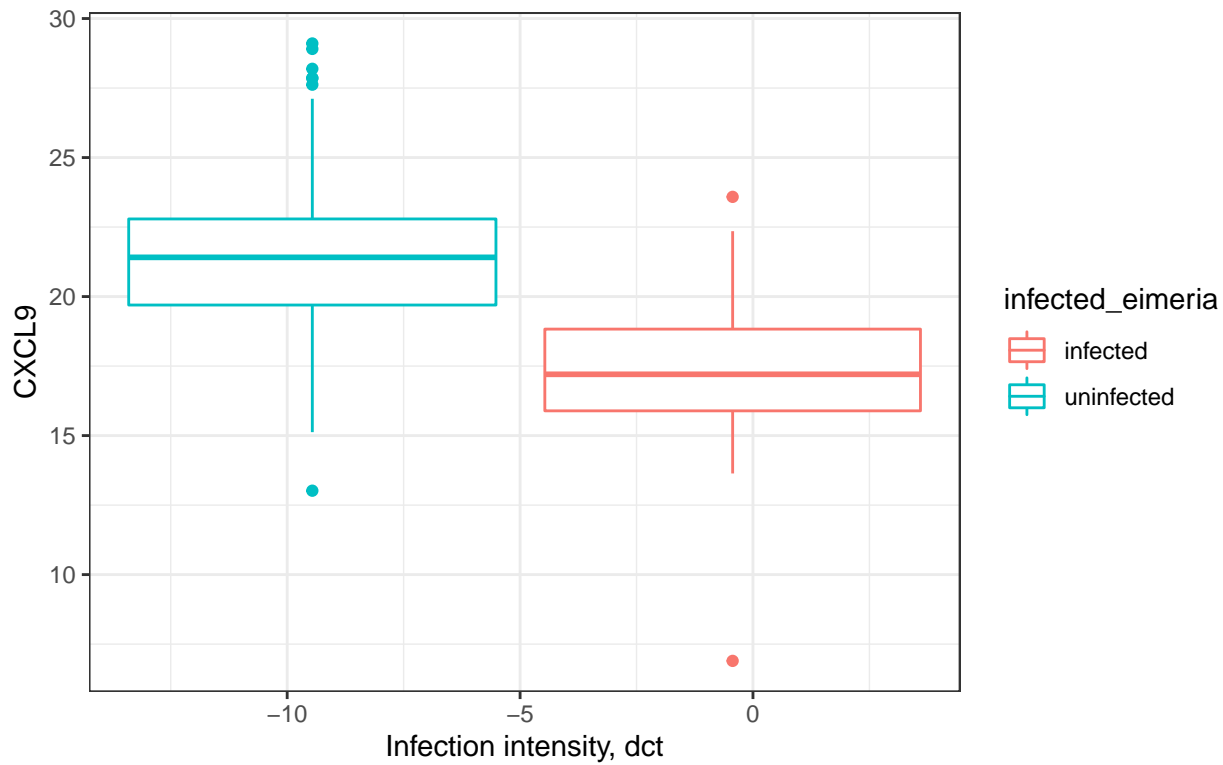
Immune gene expression against infection intensity in lab infections



```
ggplot(field, aes(x = delta_ct_cewe_MminusE, y = CXCL9,  
                  color = infected_eimeria)) +  
  geom_boxplot() +  
  labs(x = "Infection intensity, dct",  
       title = "Immune gene expression against infection intensity in field  
samples") +  
  theme_bw()
```

Warning: Removed 154 rows containing missing values (stat_boxplot).

Immune gene expression against infection intensity in field samples

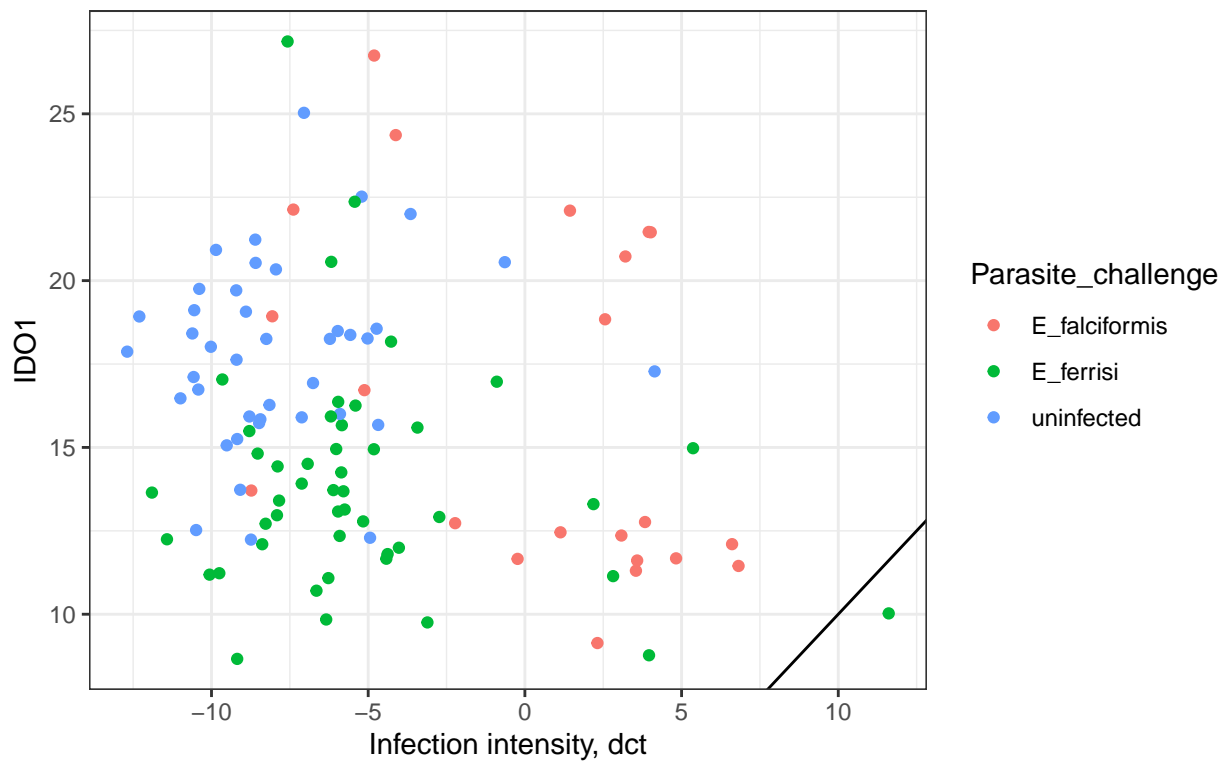


9. IDO1

```
ggplot(lab, aes(x = delta, y = IDO1, color = Parasite_challenge)) +
  geom_jitter() +
  geom_abline() +
  labs(x = "Infection intensity, dct",
       title = "Immune gene expression against infection intensity
in lab infections") +
  theme_bw()
```

Warning: Removed 6 rows containing missing values (geom_point).

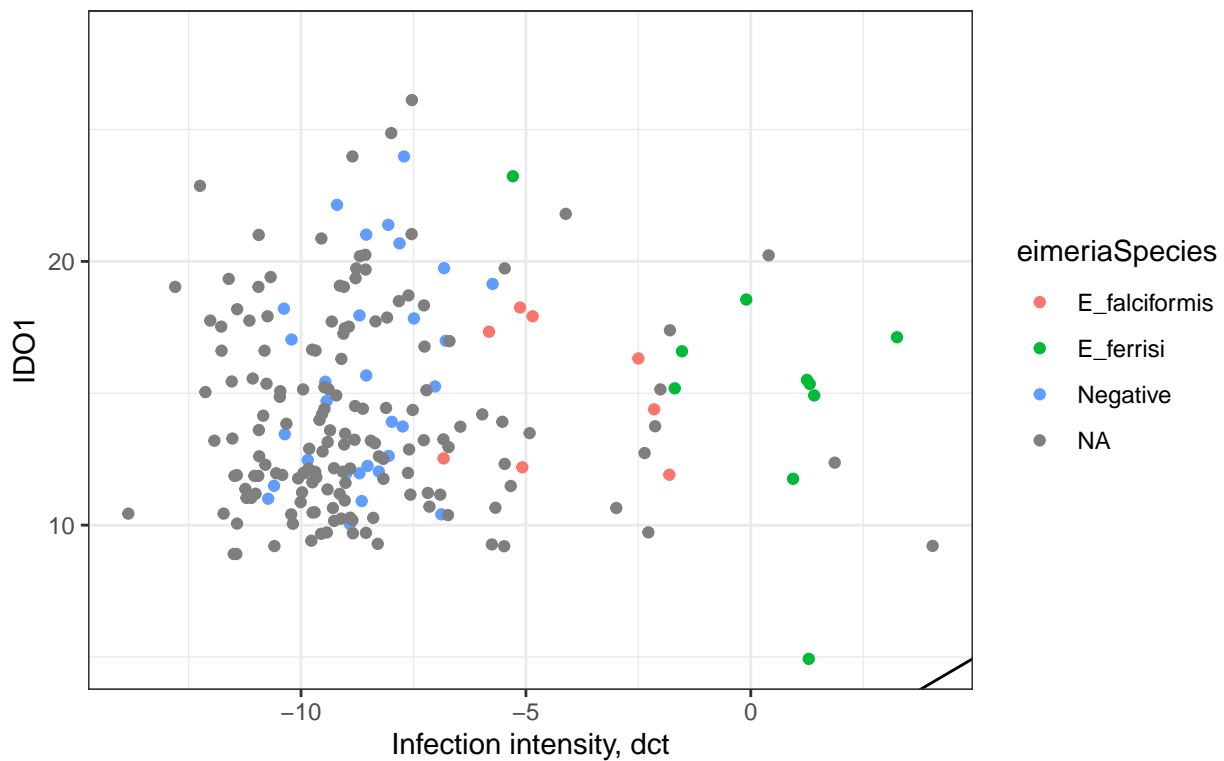
Immune gene expression against infection intensity in lab infections



```
ggplot(field, aes(x = delta_ct_cewe_MminusE, y = IDO1, color = eimeriaSpecies)) +
  geom_jitter() +
  geom_abline() +
  labs(x = "Infection intensity, dct",
       title = "Immune gene expression against infection intensity in field
       samples") +
  theme_bw()
```

Warning: Removed 154 rows containing missing values (geom_point).

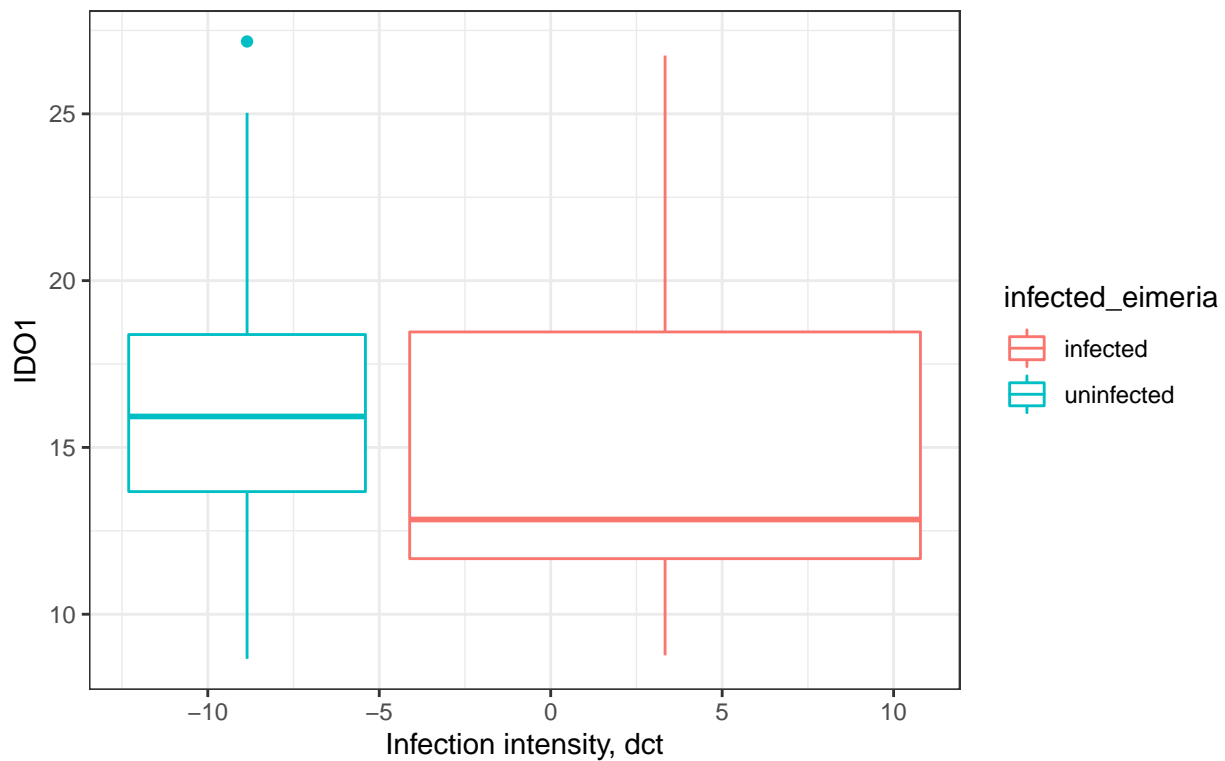
Immune gene expression against infection intensity in field samples



```
ggplot(lab, aes(x = delta, y = IDO1, color = infected_eimeria)) +
  geom_boxplot() +
  labs(x = "Infection intensity, dct",
       title = "Immune gene expression against infection intensity in lab
infections") +
  theme_bw()
```

Warning: Removed 6 rows containing missing values (stat_boxplot).

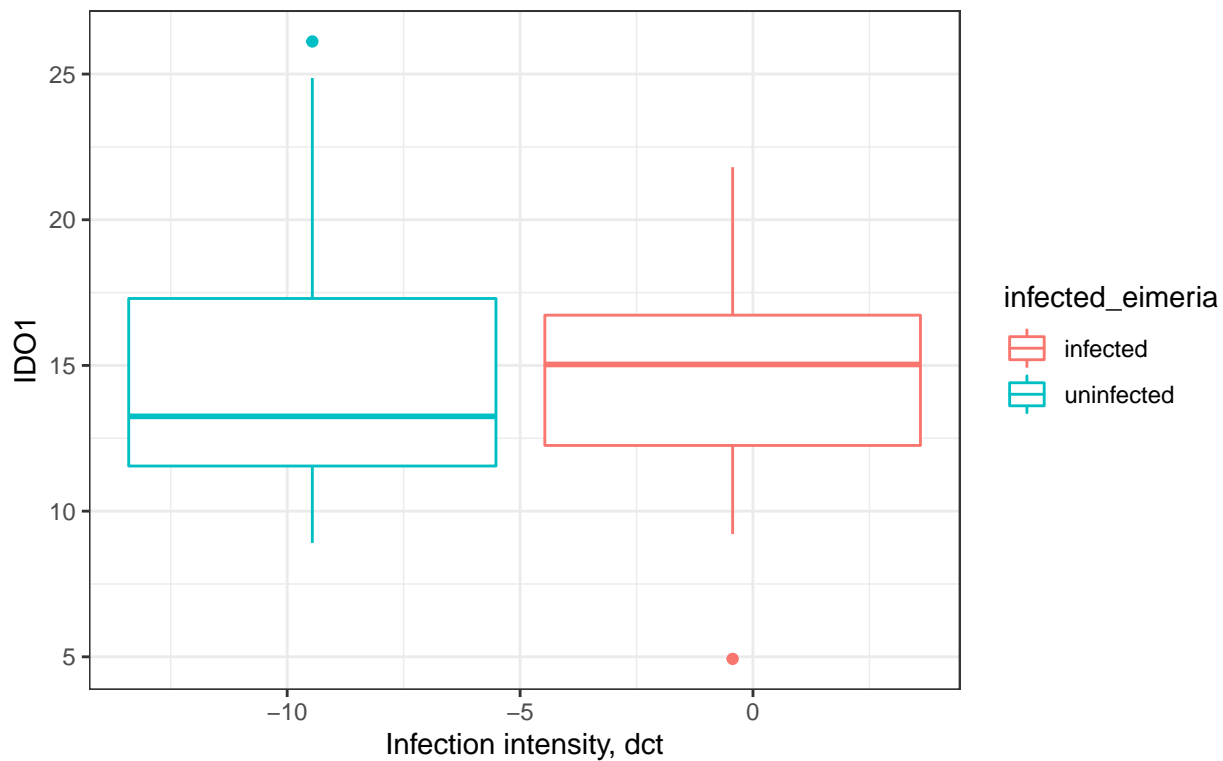
Immune gene expression against infection intensity in lab infections



```
ggplot(field, aes(x = delta_ct_cewe_MminusE, y = IDO1,
                  color = infected_eimeria)) +
  geom_boxplot() +
  labs(x = "Infection intensity, dct",
       title = "Immune gene expression against infection intensity in field
samples") +
  theme_bw()
```

Warning: Removed 154 rows containing missing values (stat_boxplot).

Immune gene expression against infection intensity in field samples

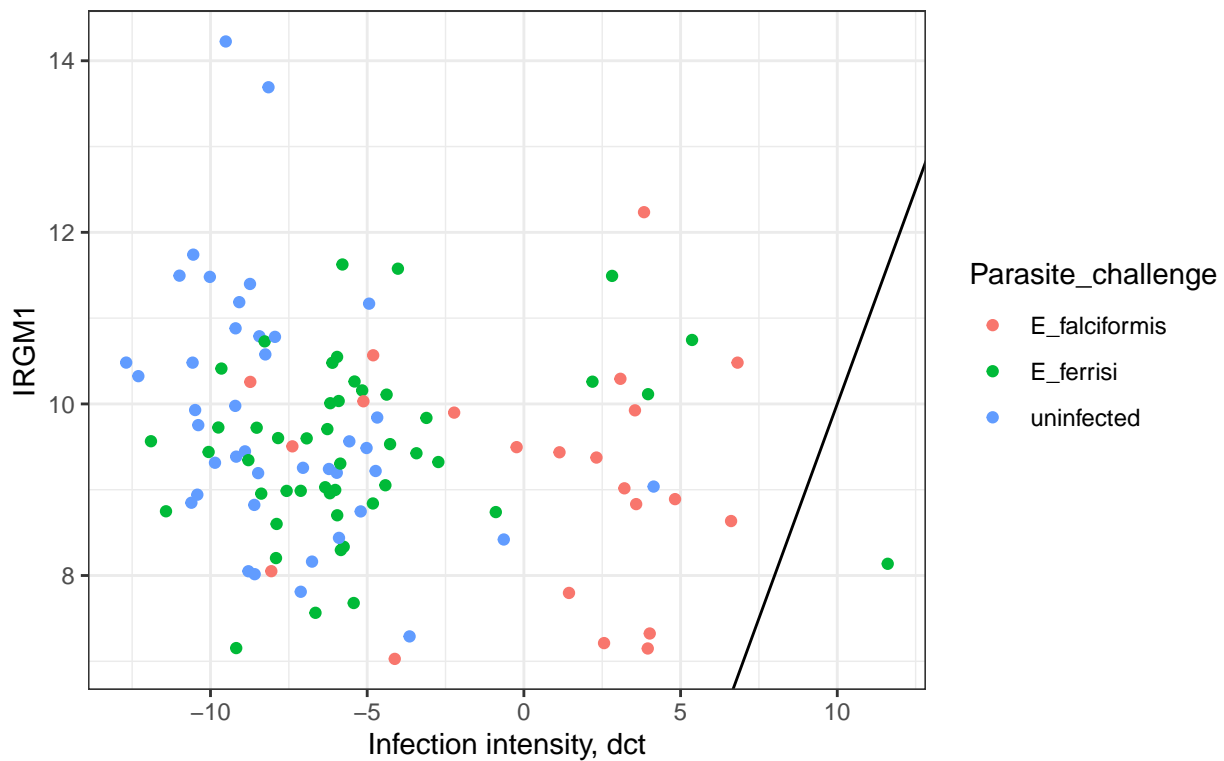


10. IRGM1

```
ggplot(lab, aes(x = delta, y = IRGM1, color = Parasite_challenge)) +
  geom_jitter() +
  geom_abline() +
  labs(x = "Infection intensity, dct",
       title = "Immune gene expression against infection intensity
in lab infections") +
  theme_bw()
```

Warning: Removed 6 rows containing missing values (geom_point).

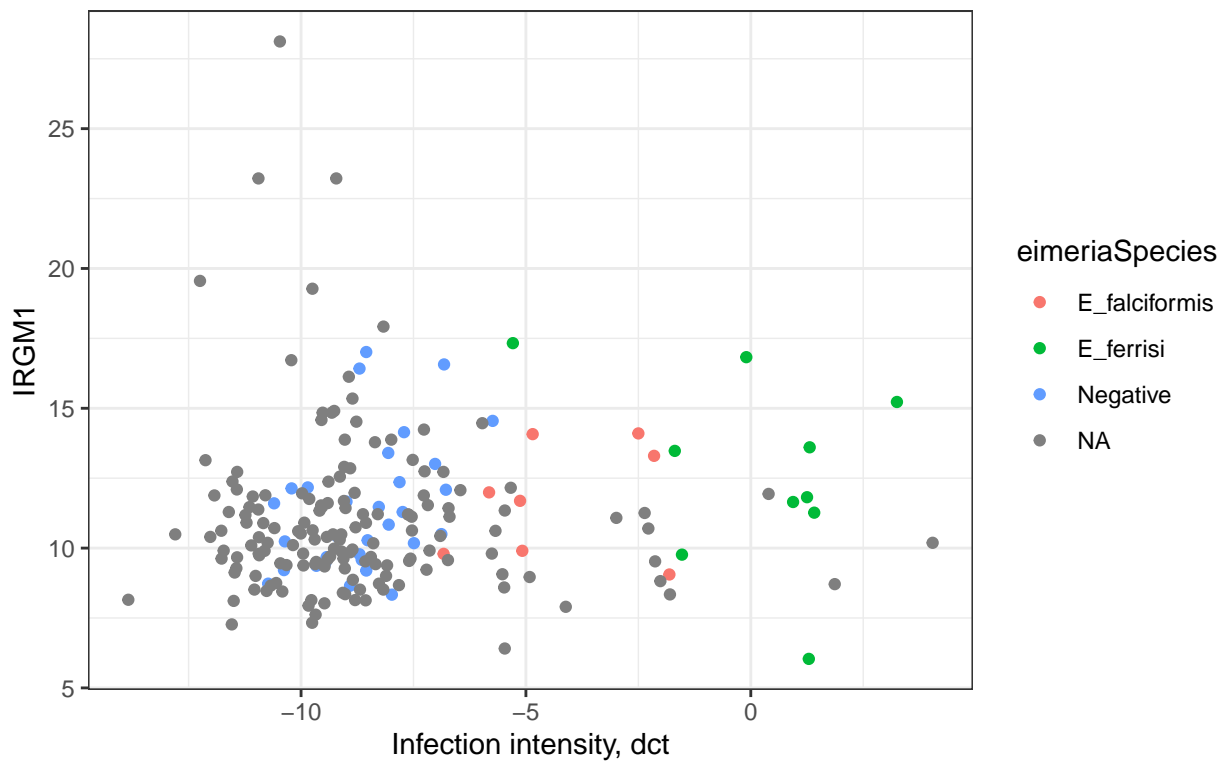
Immune gene expression against infection intensity in lab infections



```
ggplot(field, aes(x = delta_ct_cewe_MminusE, y = IRGM1, color = eimeriaSpecies)) +
  geom_jitter() +
  geom_abline() +
  labs(x = "Infection intensity, dct",
       title = "Immune gene expression against infection intensity in field
       samples") +
  theme_bw()
```

Warning: Removed 154 rows containing missing values (geom_point).

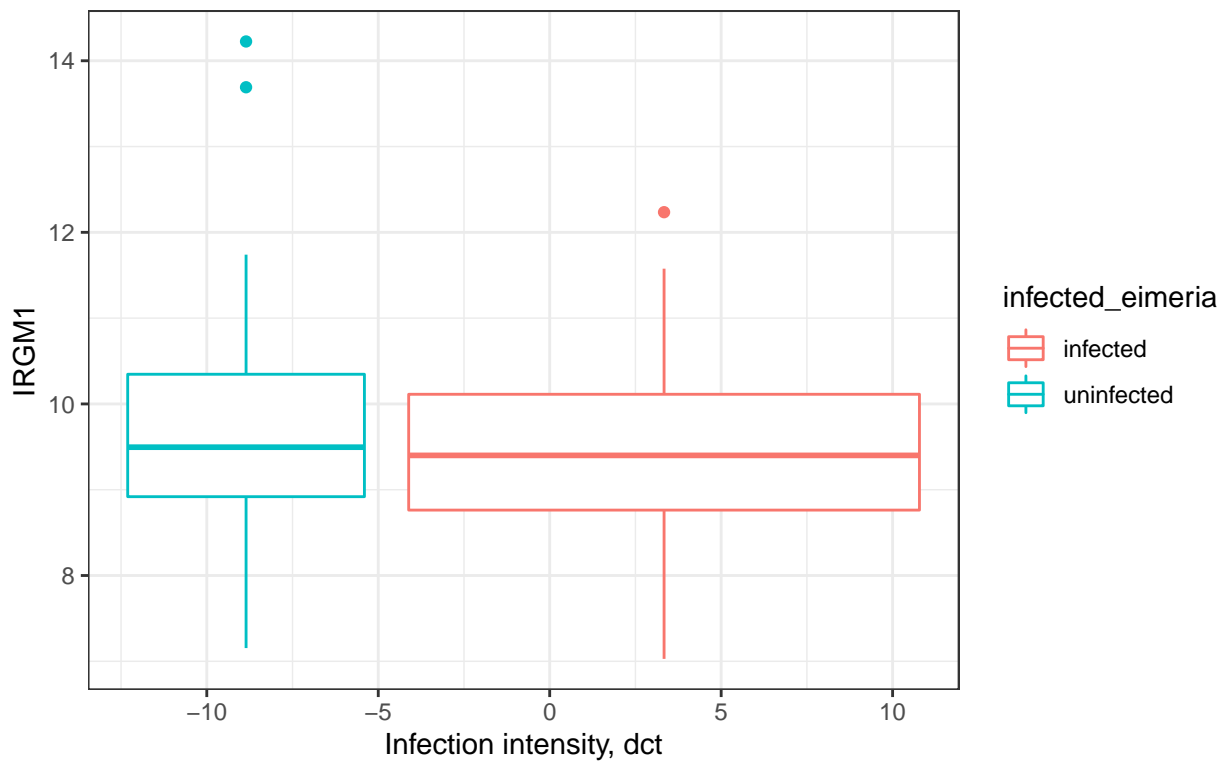
Immune gene expression against infection intensity in field samples



```
ggplot(lab, aes(x = delta, y = IRGM1, color = infected_eimeria)) +
  geom_boxplot() +
  labs(x = "Infection intensity, dct",
       title = "Immune gene expression against infection intensity in lab
infections") +
  theme_bw()
```

Warning: Removed 6 rows containing missing values (stat_boxplot).

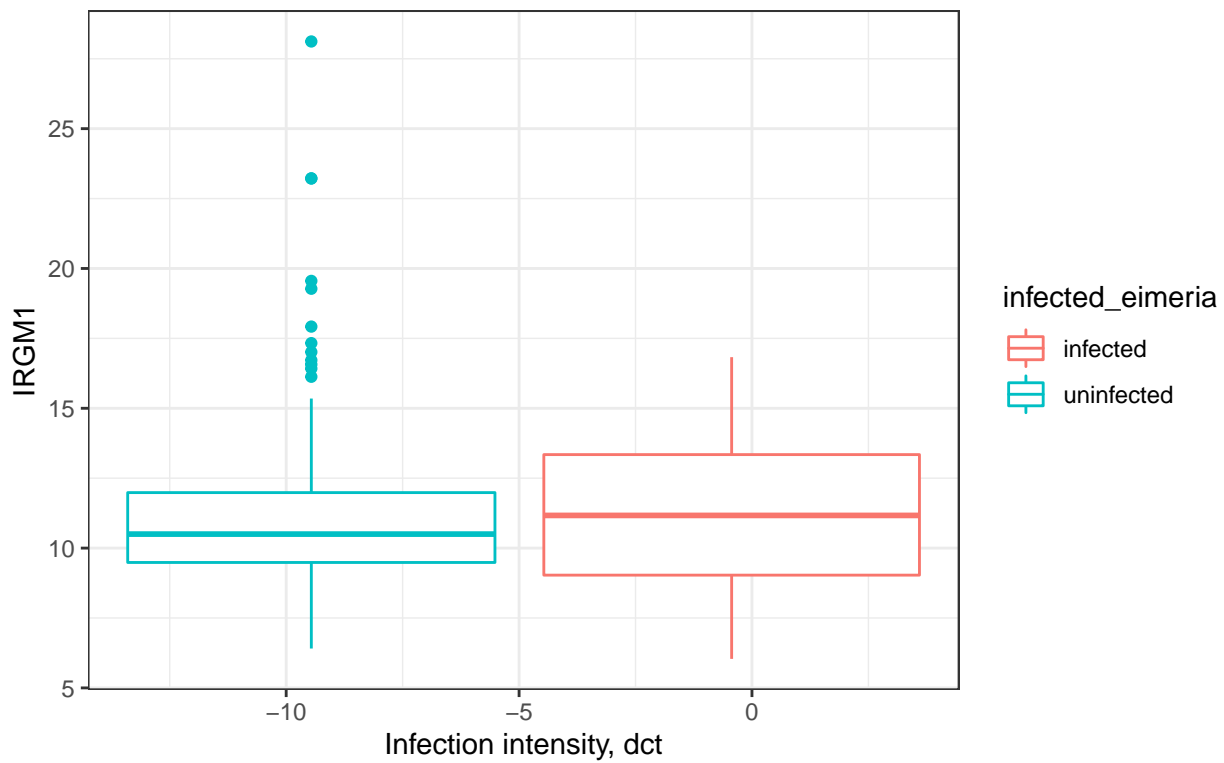
Immune gene expression against infection intensity in lab infections



```
ggplot(field, aes(x = delta_ct_cewe_MminusE, y = IRGM1,
                  color = infected_eimeria)) +
  geom_boxplot() +
  labs(x = "Infection intensity, dct",
       title = "Immune gene expression against infection intensity in field
samples") +
  theme_bw()
```

Warning: Removed 154 rows containing missing values (stat_boxplot).

Immune gene expression against infection intensity in field samples

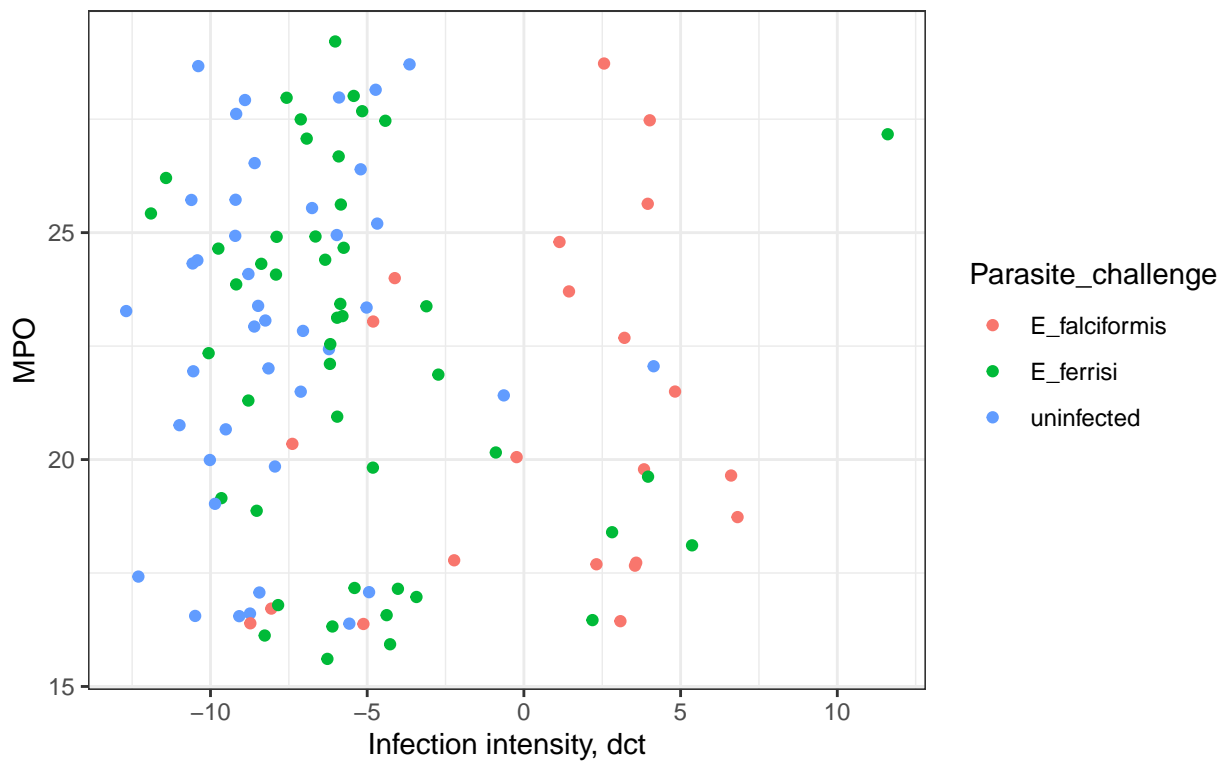


11. MPO

```
ggplot(lab, aes(x = delta, y = MPO, color = Parasite_challenge)) +
  geom_jitter() +
  geom_abline() +
  labs(x = "Infection intensity, dct",
       title = "Immune gene expression against infection intensity
               in lab infections") +
  theme_bw()
```

Warning: Removed 6 rows containing missing values (geom_point).

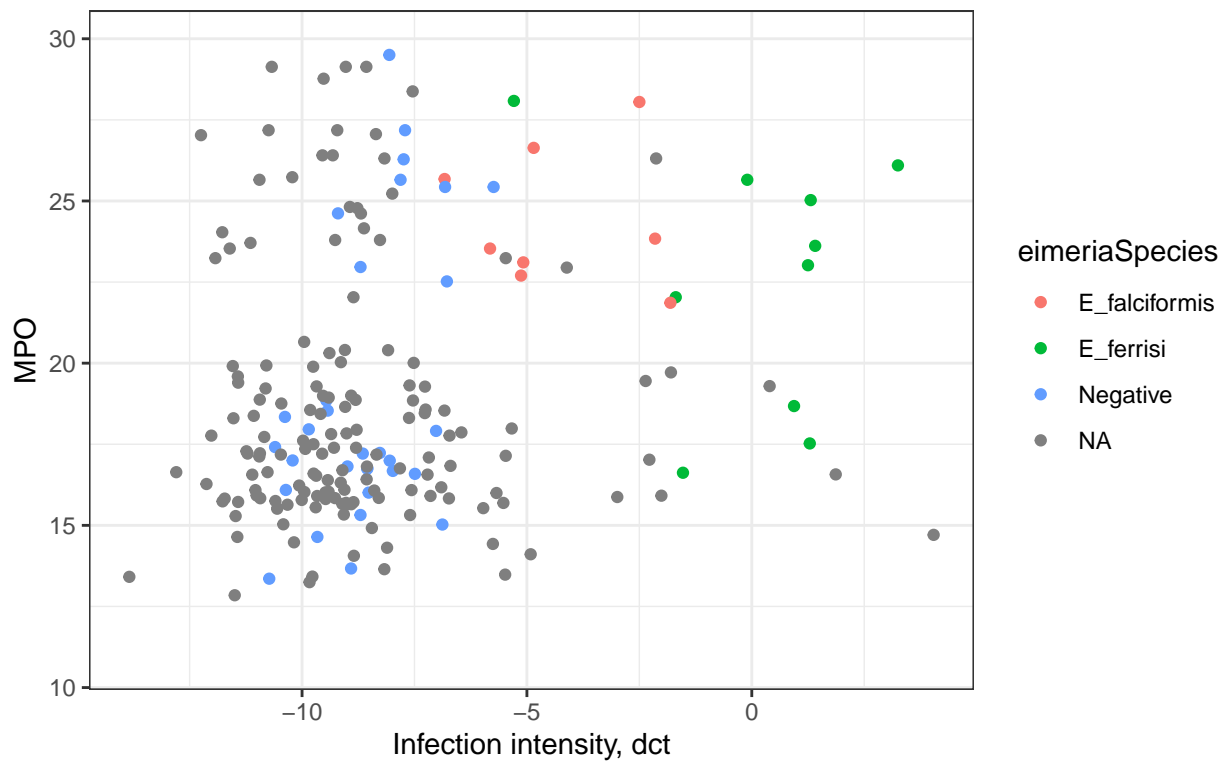
Immune gene expression against infection intensity in lab infections



```
ggplot(field, aes(x = delta_ct_cewe_MminusE, y = MPO, color = eimeriaSpecies)) +
  geom_jitter() +
  geom_abline() +
  labs(x = "Infection intensity, dct",
       title = "Immune gene expression against infection intensity in field
       samples") +
  theme_bw()
```

Warning: Removed 154 rows containing missing values (geom_point).

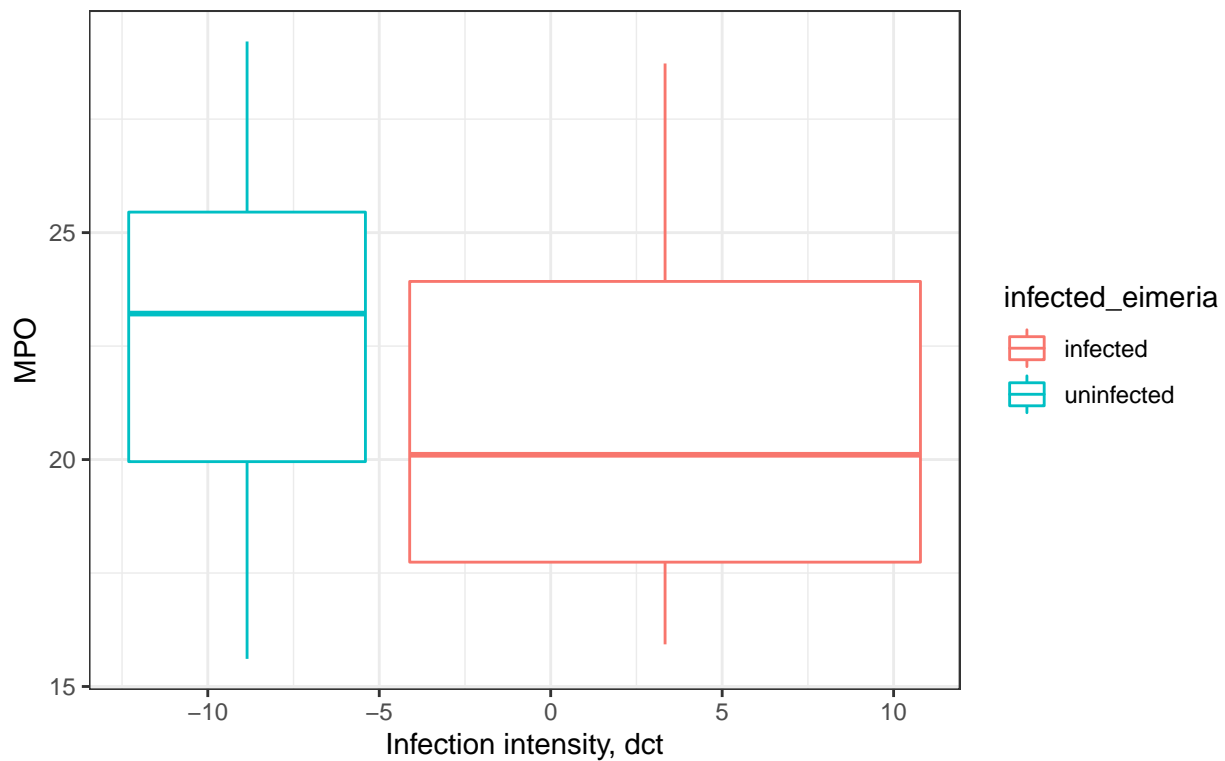
Immune gene expression against infection intensity in field samples



```
ggplot(lab, aes(x = delta, y = MPO, color = infected_eimeria)) +
  geom_boxplot() +
  labs(x = "Infection intensity, dct",
       title = "Immune gene expression against infection intensity in lab
infections") +
  theme_bw()
```

Warning: Removed 6 rows containing missing values (stat_boxplot).

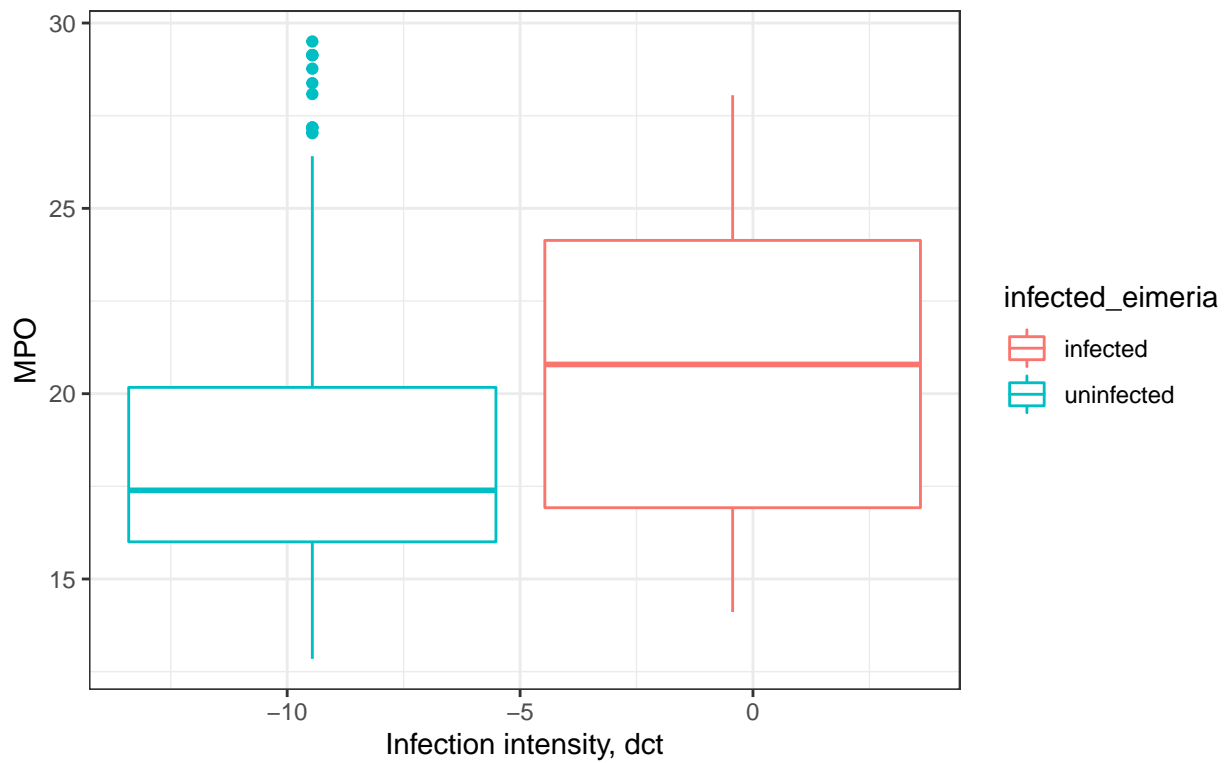
Immune gene expression against infection intensity in lab infections



```
ggplot(field, aes(x = delta_ct_cewe_MminusE, y = MPO,  
                  color = infected_eimeria)) +  
  geom_boxplot() +  
  labs(x = "Infection intensity, dct",  
       title = "Immune gene expression against infection intensity in field  
samples") +  
  theme_bw()
```

Warning: Removed 154 rows containing missing values (stat_boxplot).

Immune gene expression against infection intensity in field samples

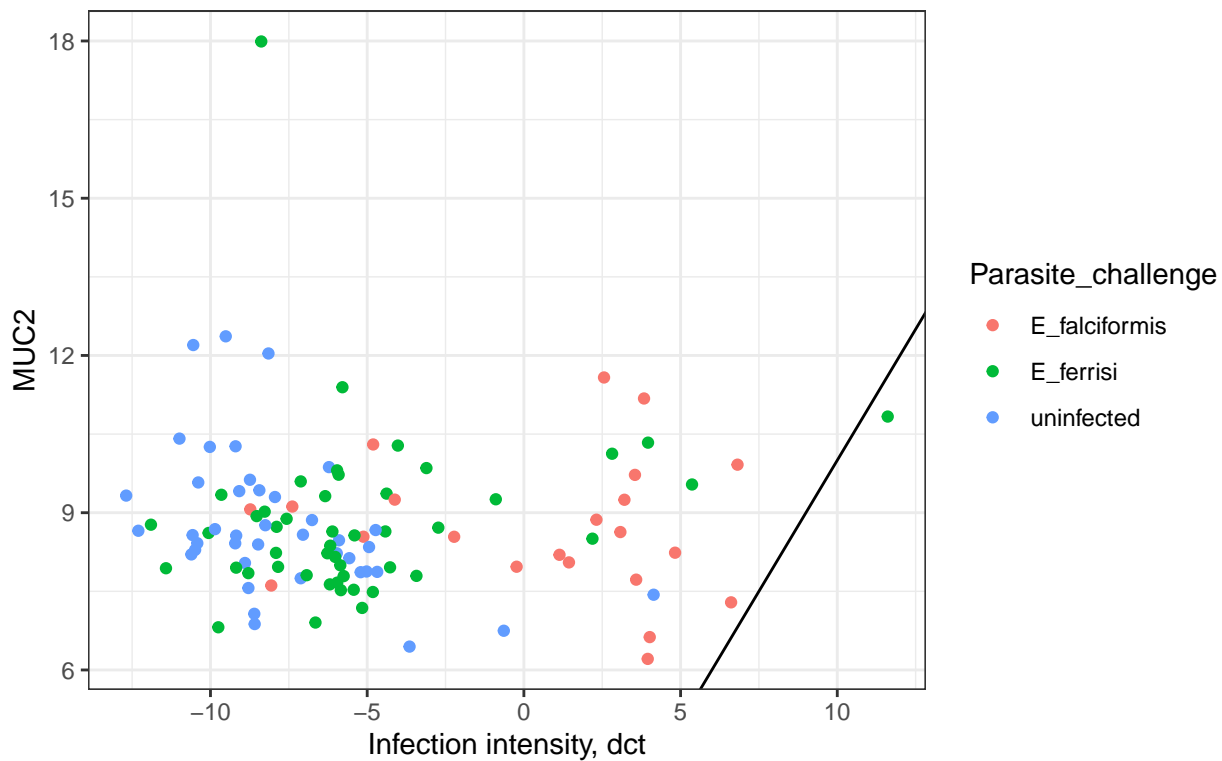


12. MUC2

```
ggplot(lab, aes(x = delta, y = MUC2, color = Parasite_challenge)) +  
  geom_jitter() +  
  geom_abline() +  
  labs(x = "Infection intensity, dct",  
        title = "Immune gene expression against infection intensity  
in lab infections") +  
  theme_bw()
```

Warning: Removed 6 rows containing missing values (geom_point).

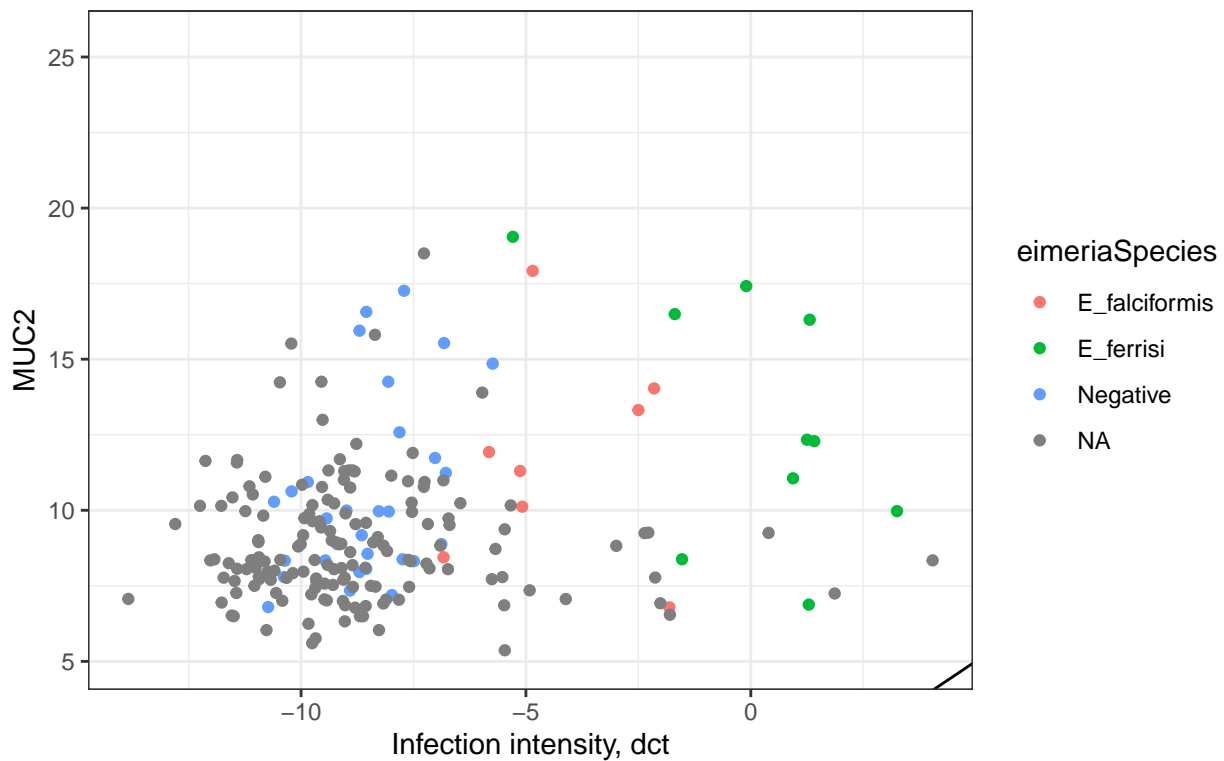
Immune gene expression against infection intensity in lab infections



```
ggplot(field, aes(x = delta_ct_cewe_MminusE, y = MUC2, color = eimeriaSpecies)) +
  geom_jitter() +
  geom_abline() +
  labs(x = "Infection intensity, dct",
       title = "Immune gene expression against infection intensity in field
               samples") +
  theme_bw()
```

Warning: Removed 154 rows containing missing values (geom_point).

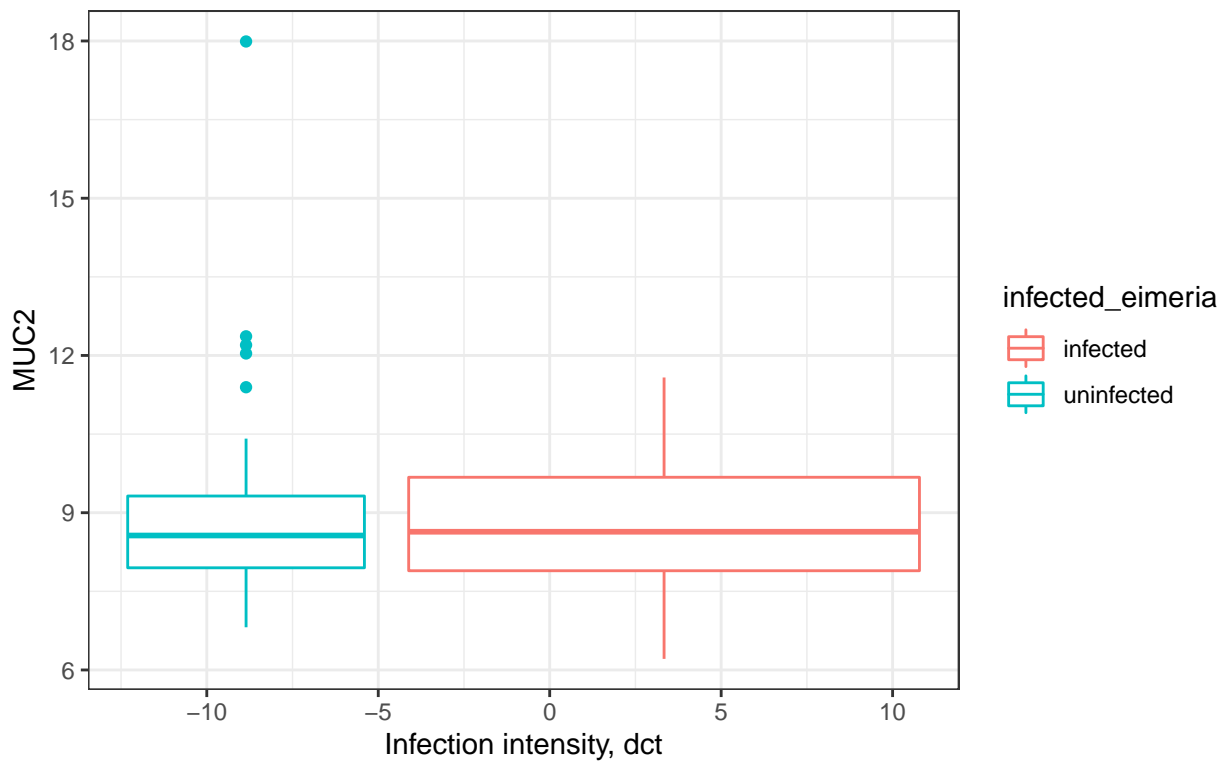
Immune gene expression against infection intensity in field samples



```
ggplot(lab, aes(x = delta, y = MUC2, color = infected_eimeria)) +  
  geom_boxplot() +  
  labs(x = "Infection intensity, dct",  
       title = "Immune gene expression against infection intensity in lab  
infections") +  
  theme_bw()
```

```
## Warning: Removed 6 rows containing missing values (stat_boxplot).
```

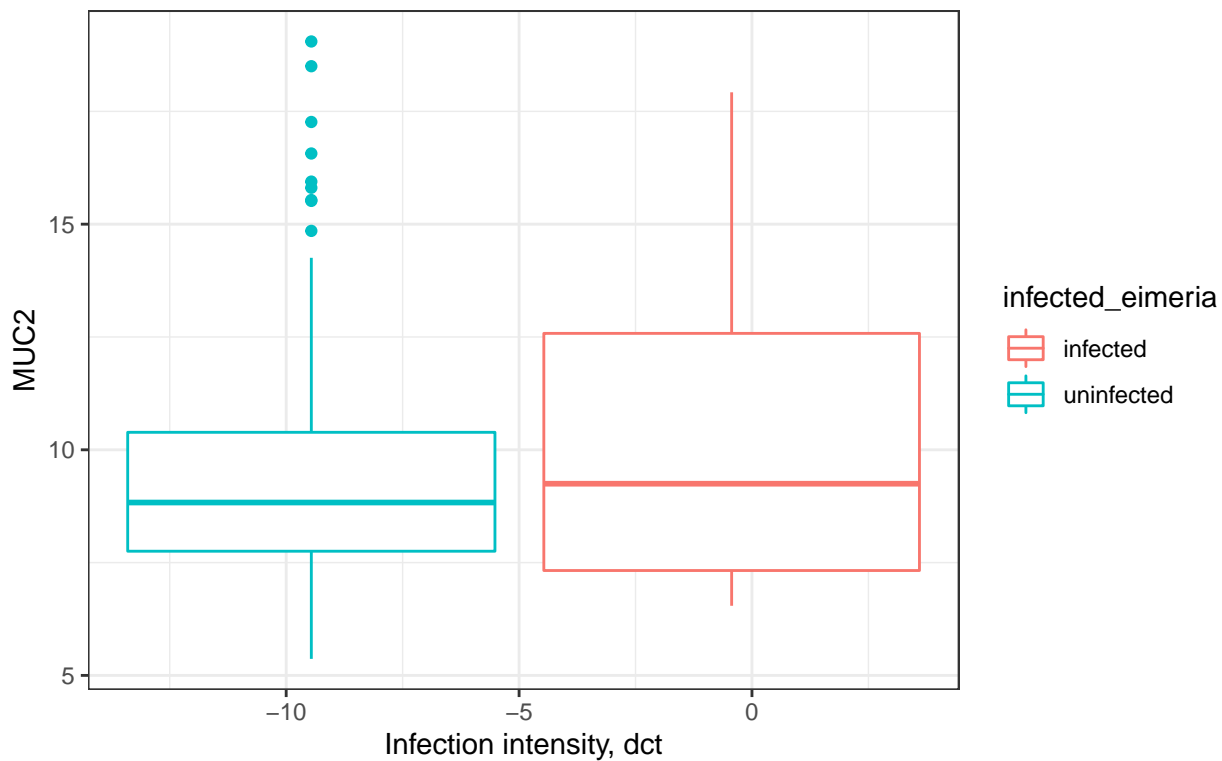
Immune gene expression against infection intensity in lab infections



```
ggplot(field, aes(x = delta_ct_cewe_MminusE, y = MUC2,
                  color = infected_eimeria)) +
  geom_boxplot() +
  labs(x = "Infection intensity, dct",
       title = "Immune gene expression against infection intensity in field
samples") +
  theme_bw()
```

Warning: Removed 154 rows containing missing values (stat_boxplot).

Immune gene expression against infection intensity in field samples

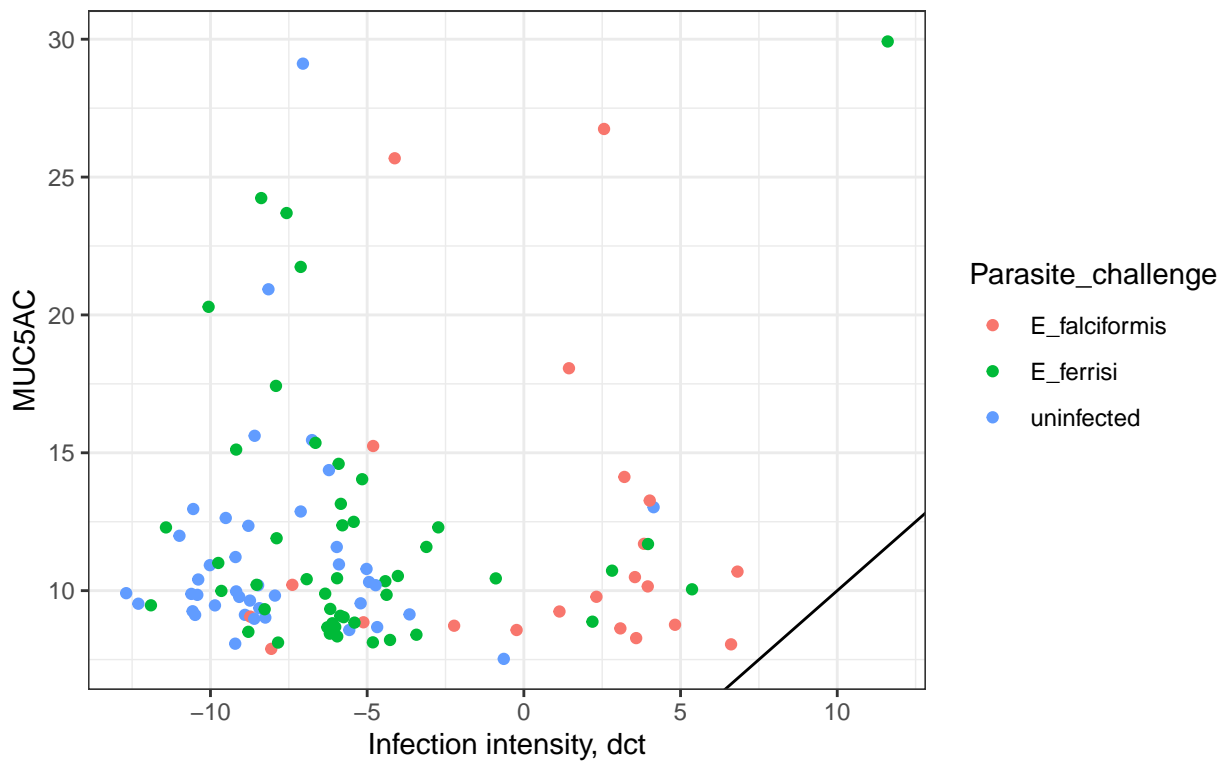


13. MUC5AC

```
ggplot(lab, aes(x = delta, y = MUC5AC, color = Parasite_challenge)) +  
  geom_jitter() +  
  geom_abline() +  
  labs(x = "Infection intensity, dct",  
       title = "Immune gene expression against infection intensity  
in lab infections") +  
  theme_bw()
```

Warning: Removed 6 rows containing missing values (geom_point).

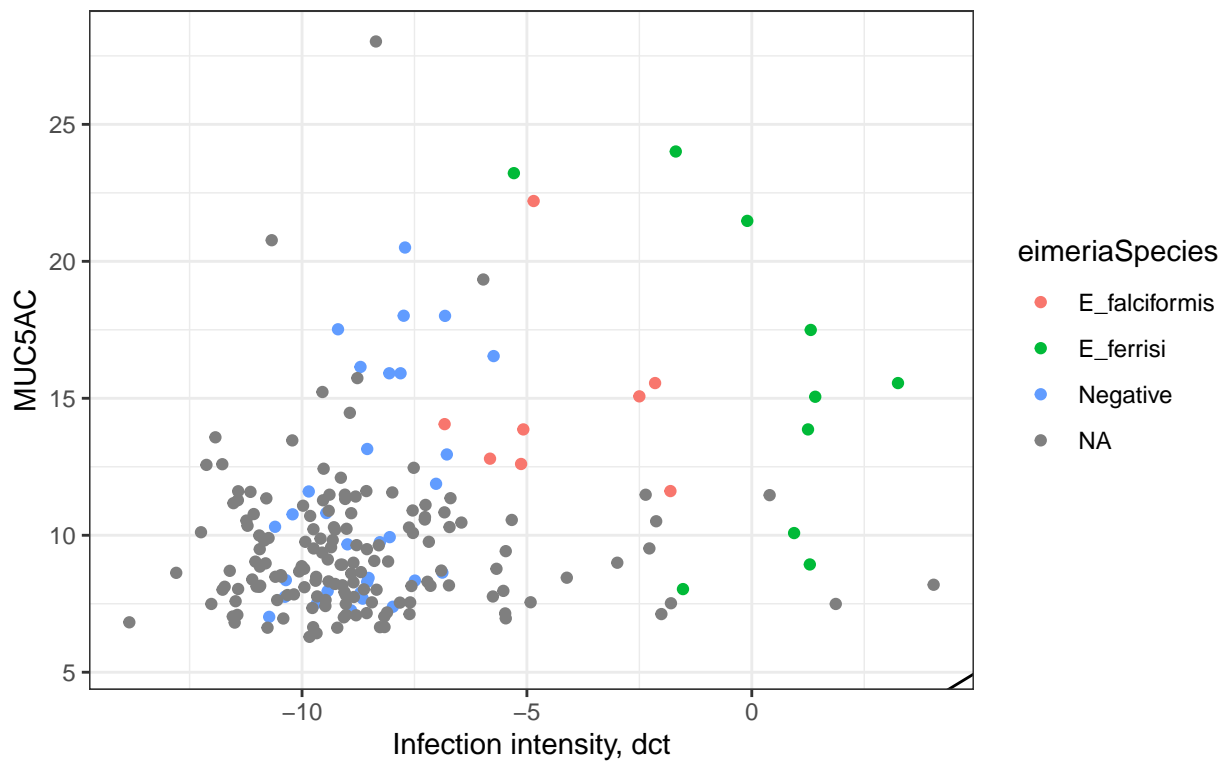
Immune gene expression against infection intensity in lab infections



```
ggplot(field, aes(x = delta_ct_cewe_MminusE, y = MUC5AC, color = eimeriaSpecies)) +
  geom_jitter() +
  geom_abline() +
  labs(x = "Infection intensity, dct",
       title = "Immune gene expression against infection intensity in field
       samples") +
  theme_bw()
```

Warning: Removed 154 rows containing missing values (geom_point).

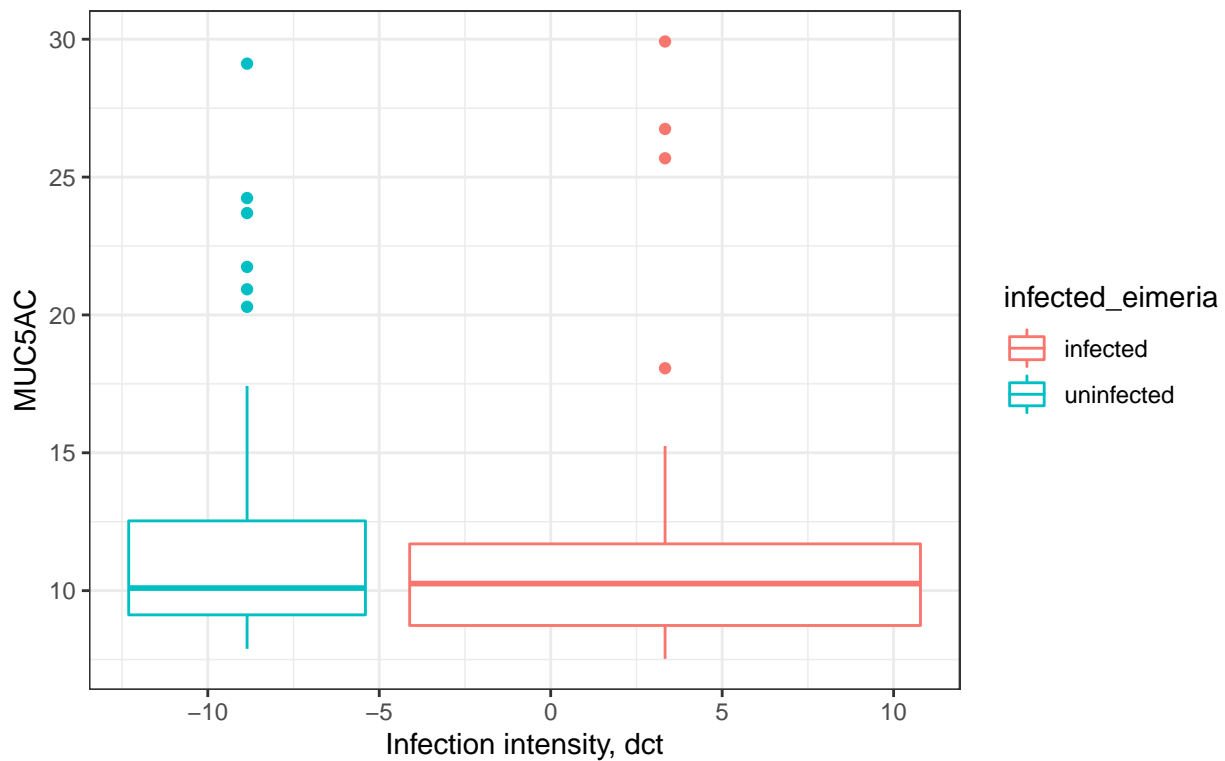
Immune gene expression against infection intensity in field samples



```
ggplot(lab, aes(x = delta, y = MUC5AC, color = infected_eimeria)) +
  geom_boxplot() +
  labs(x = "Infection intensity, dct",
       title = "Immune gene expression against infection intensity in lab
infections") +
  theme_bw()
```

Warning: Removed 6 rows containing missing values (stat_boxplot).

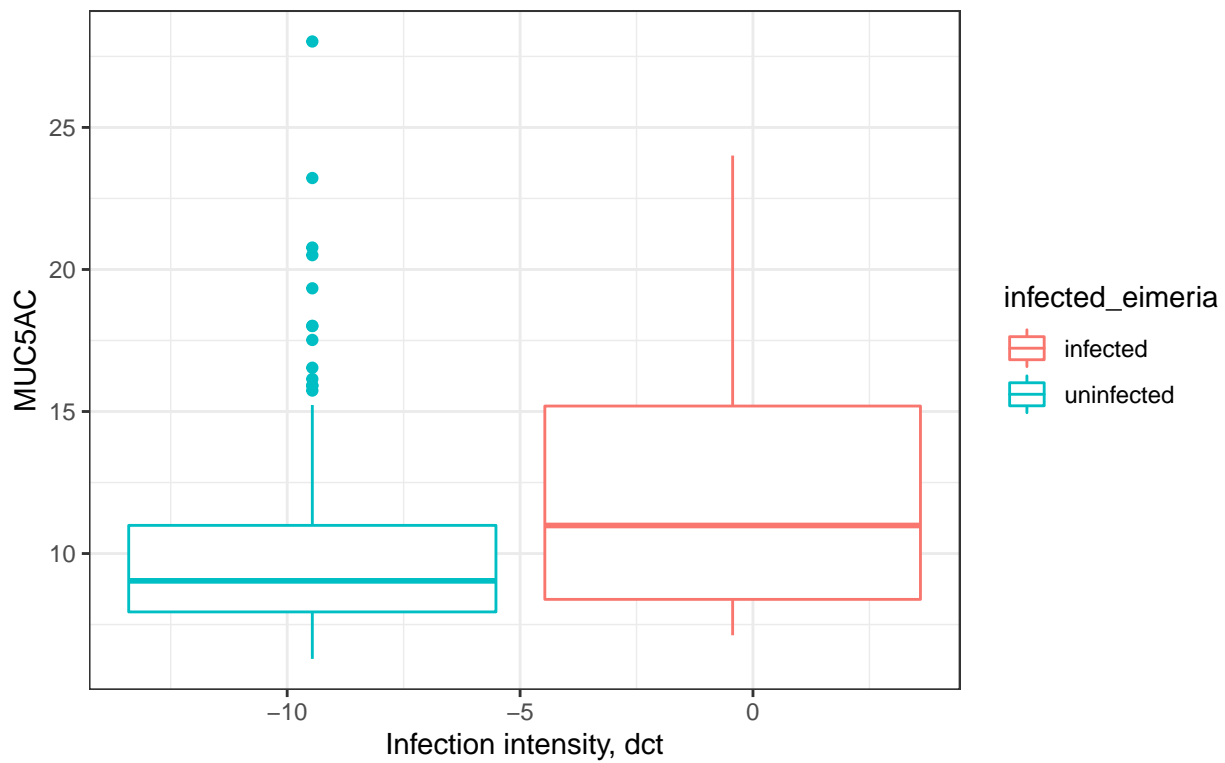
Immune gene expression against infection intensity in lab infections



```
ggplot(field, aes(x = delta_ct_cewe_MminusE, y = MUC5AC,
                  color = infected_eimeria)) +
  geom_boxplot() +
  labs(x = "Infection intensity, dct",
       title = "Immune gene expression against infection intensity in field
               samples") +
  theme_bw()
```

Warning: Removed 154 rows containing missing values (stat_boxplot).

Immune gene expression against infection intensity in field samples

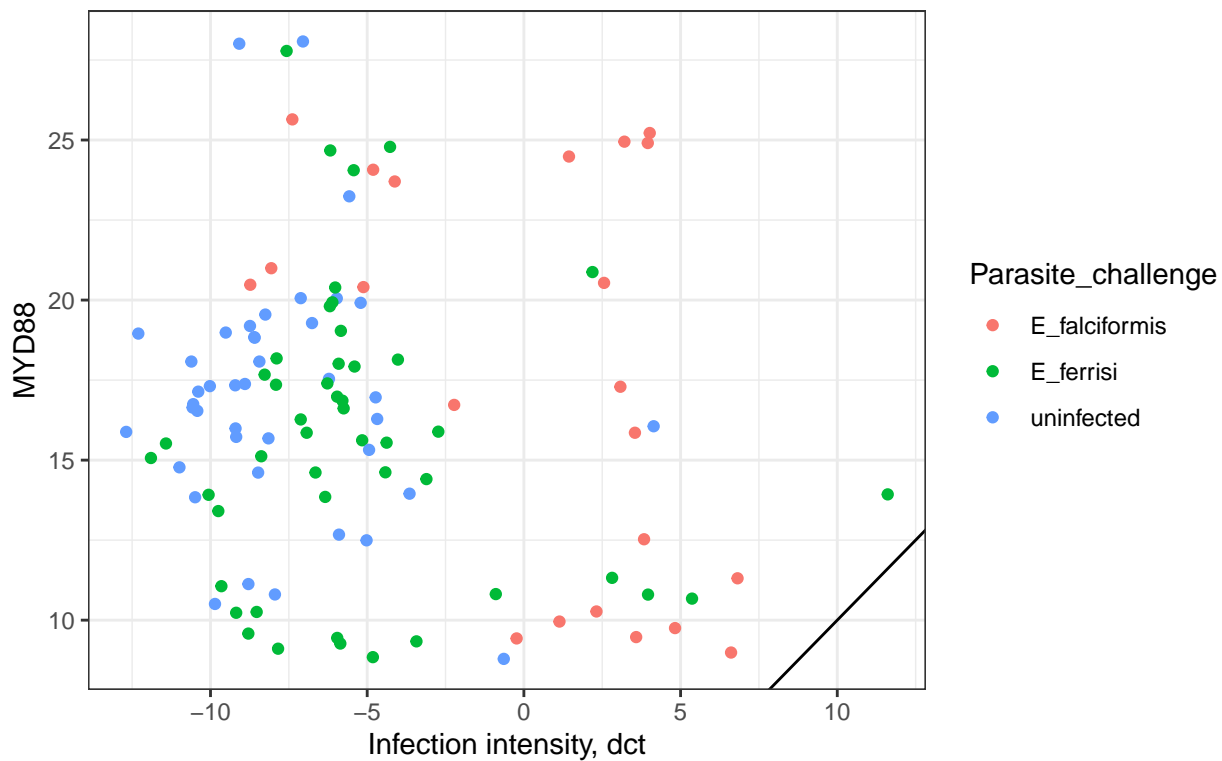


14. MYD88

```
ggplot(lab, aes(x = delta, y = MYD88, color = Parasite_challenge)) +
  geom_jitter() +
  geom_abline() +
  labs(x = "Infection intensity, dct",
       title = "Immune gene expression against infection intensity
in lab infections") +
  theme_bw()
```

Warning: Removed 6 rows containing missing values (geom_point).

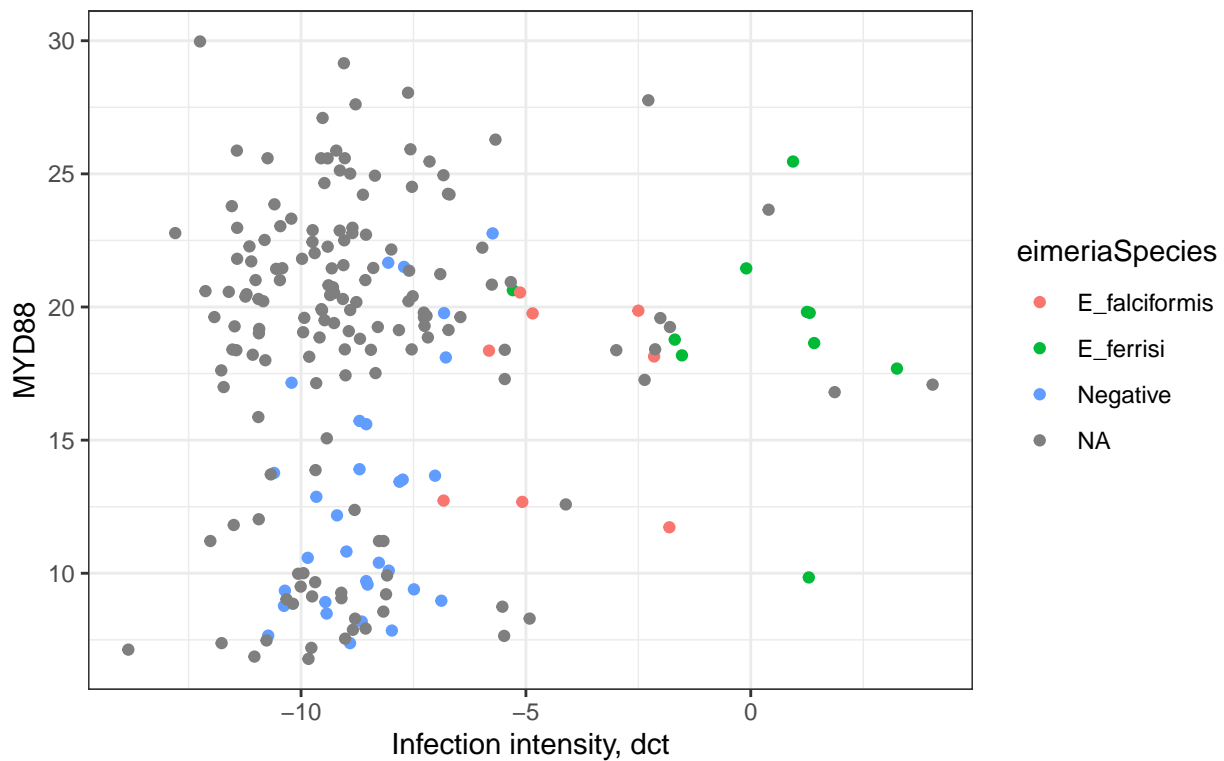
Immune gene expression against infection intensity in lab infections



```
ggplot(field, aes(x = delta_ct_cewe_MminusE, y = MYD88, color = eimeriaSpecies)) +
  geom_jitter() +
  geom_abline() +
  labs(x = "Infection intensity, dct",
       title = "Immune gene expression against infection intensity in field
       samples") +
  theme_bw()
```

Warning: Removed 154 rows containing missing values (geom_point).

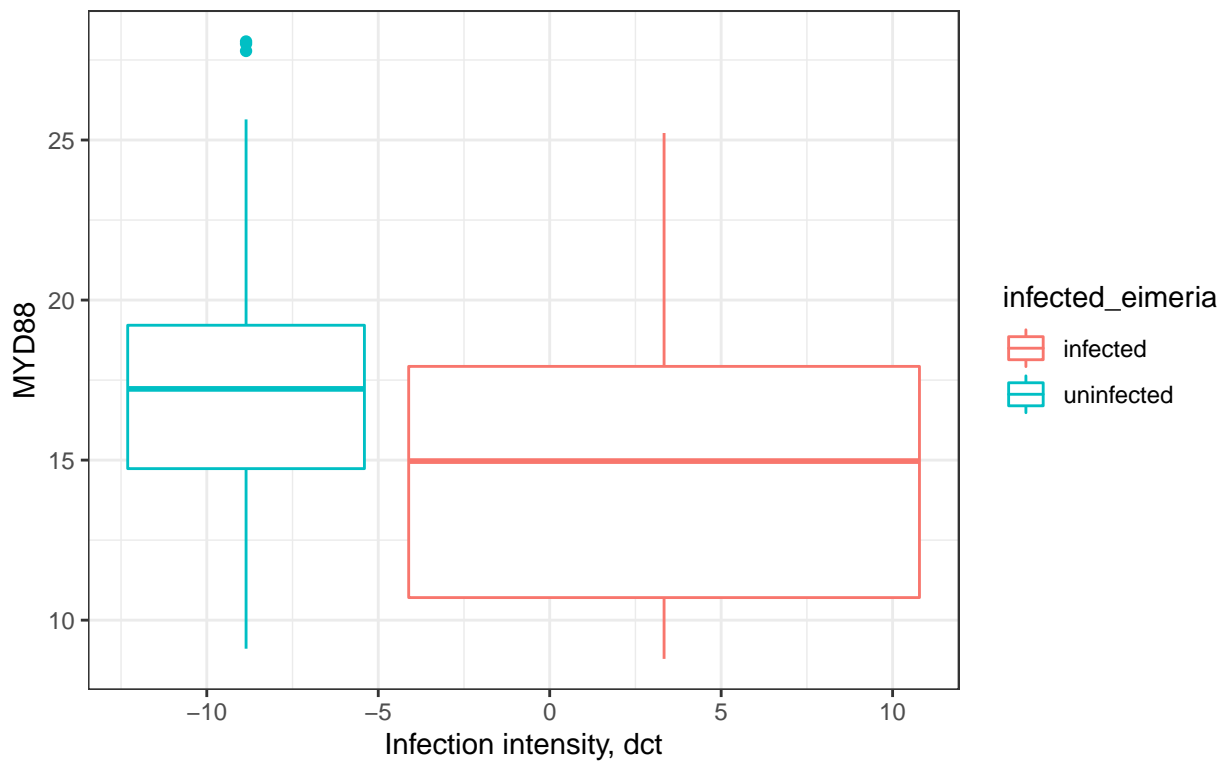
Immune gene expression against infection intensity in field samples



```
ggplot(lab, aes(x = delta, y = MYD88, color = infected_eimeria)) +
  geom_boxplot() +
  labs(x = "Infection intensity, dct",
       title = "Immune gene expression against infection intensity in lab
infections") +
  theme_bw()
```

```
## Warning: Removed 6 rows containing missing values (stat_boxplot).
```

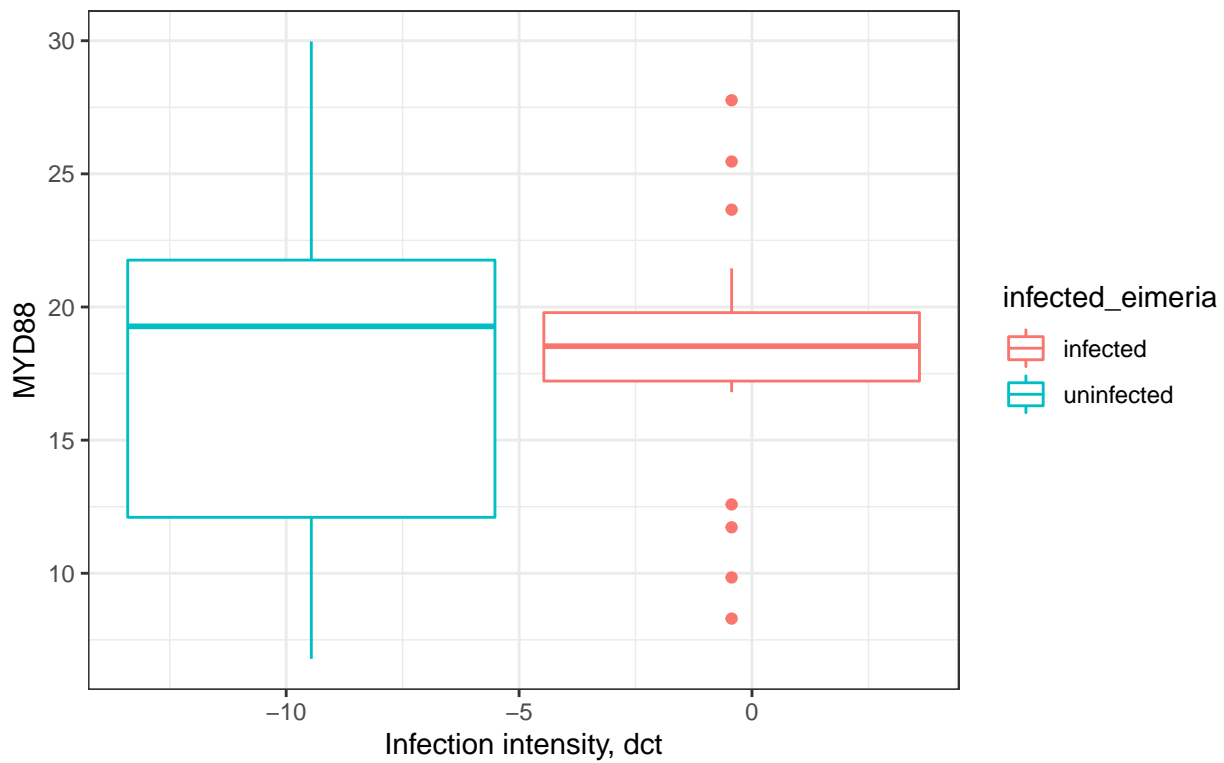
Immune gene expression against infection intensity in lab infections



```
ggplot(field, aes(x = delta_ct_cewe_MminusE, y = MYD88,  
                  color = infected_eimeria)) +  
  geom_boxplot() +  
  labs(x = "Infection intensity, dct",  
       title = "Immune gene expression against infection intensity in field  
samples") +  
  theme_bw()
```

Warning: Removed 154 rows containing missing values (stat_boxplot).

Immune gene expression against infection intensity in field samples



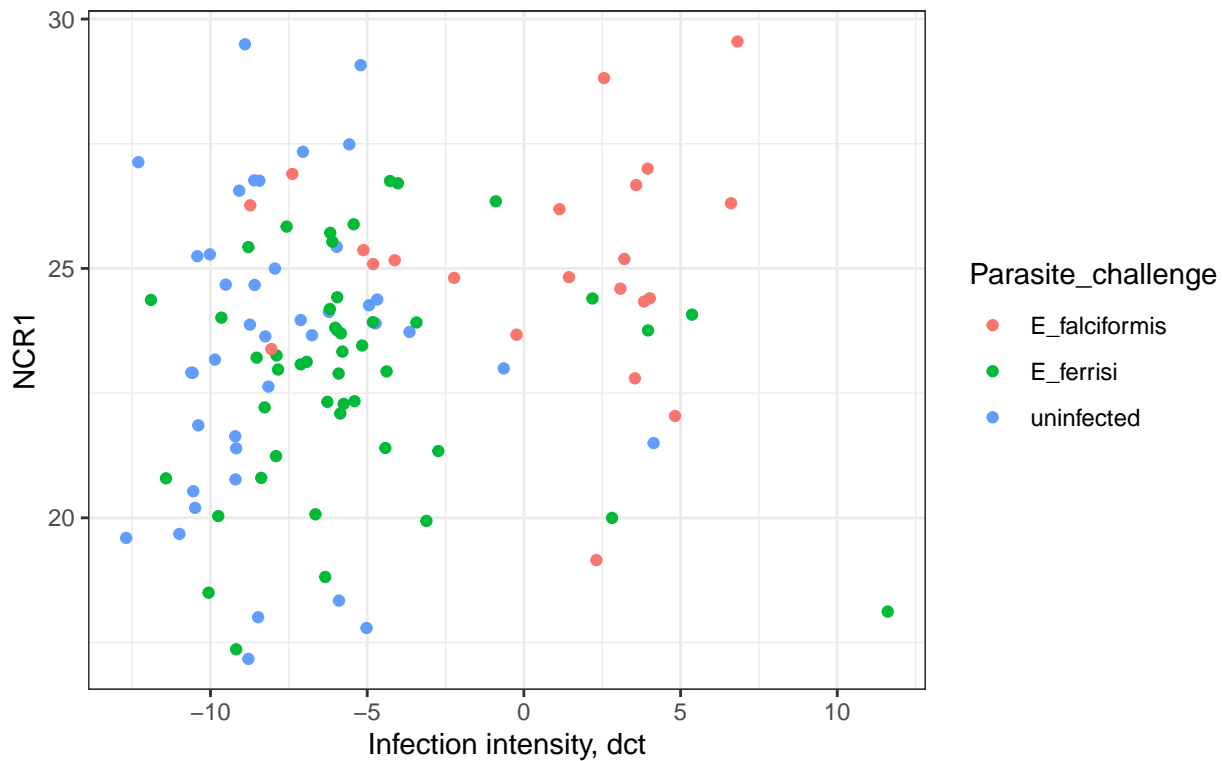
15.

NCR1

```
ggplot(lab, aes(x = delta, y = NCR1, color = Parasite_challenge)) +
  geom_jitter() +
  geom_abline() +
  labs(x = "Infection intensity, dct",
       title = "Immune gene expression against infection intensity
in lab infections") +
  theme_bw()
```

Warning: Removed 6 rows containing missing values (geom_point).

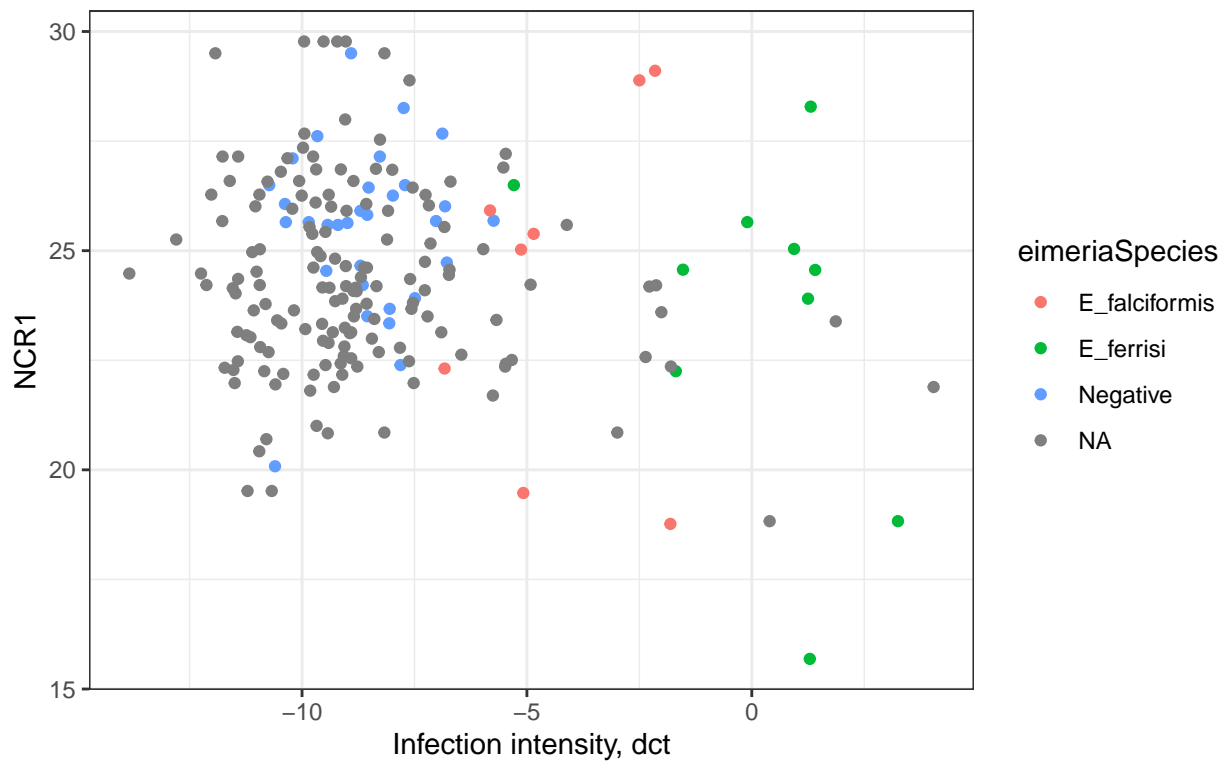
Immune gene expression against infection intensity in lab infections



```
ggplot(field, aes(x = delta_ct_cewe_MminusE, y = NCR1, color = eimeriaSpecies)) +
  geom_jitter() +
  geom_abline() +
  labs(x = "Infection intensity, dct",
       title = "Immune gene expression against infection intensity in field
samples") +
  theme_bw()
```

Warning: Removed 154 rows containing missing values (geom_point).

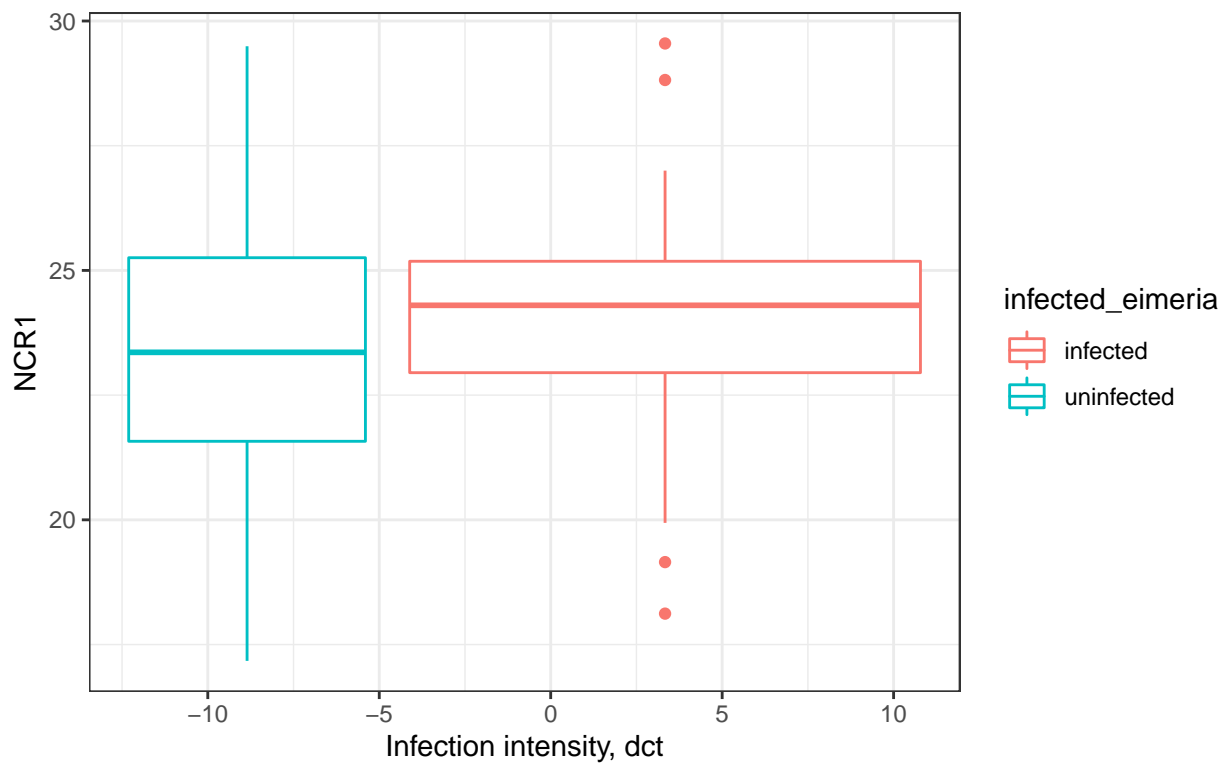
Immune gene expression against infection intensity in field samples



```
ggplot(lab, aes(x = delta, y = NCR1, color = infected_eimeria)) +
  geom_boxplot() +
  labs(x = "Infection intensity, dct",
       title = "Immune gene expression against infection intensity in lab
infections") +
  theme_bw()
```

Warning: Removed 6 rows containing missing values (stat_boxplot).

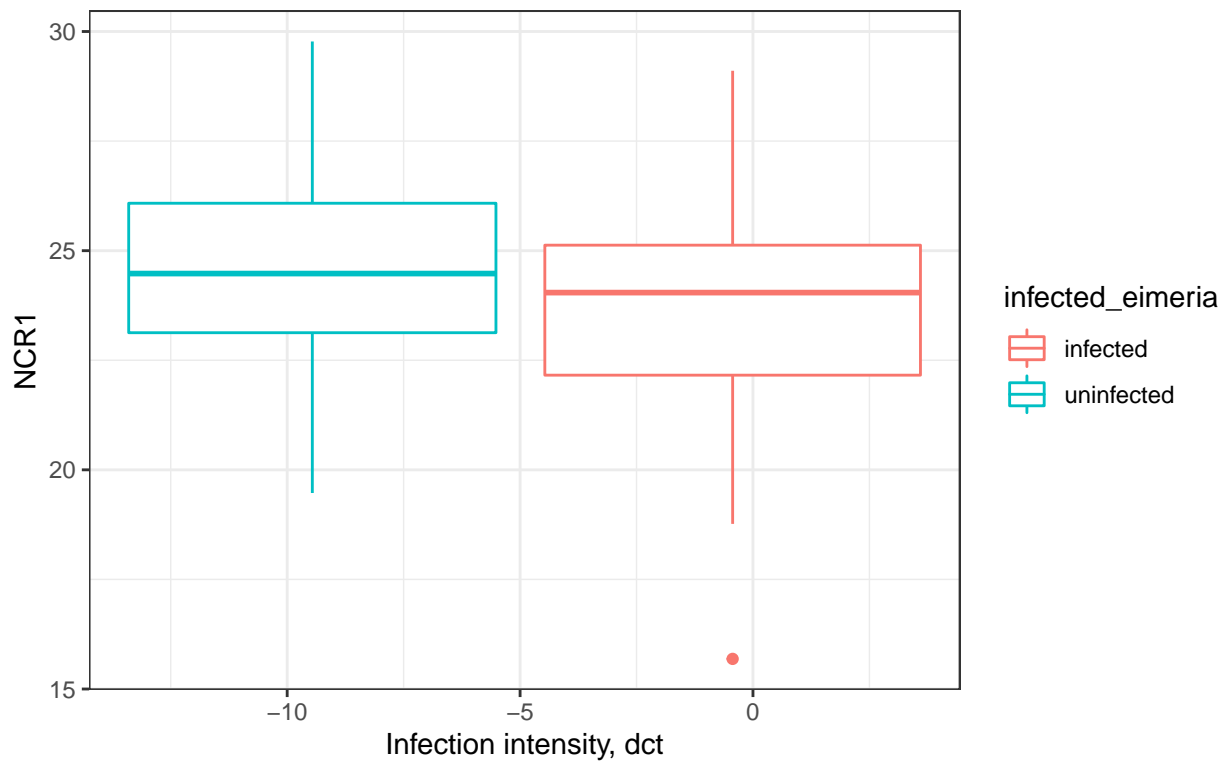
Immune gene expression against infection intensity in lab infections



```
ggplot(field, aes(x = delta_ct_cewe_MminusE, y = NCR1,  
                  color = infected_eimeria)) +  
  geom_boxplot() +  
  labs(x = "Infection intensity, dct",  
        title = "Immune gene expression against infection intensity in field  
samples") +  
  theme_bw()
```

Warning: Removed 154 rows containing missing values (stat_boxplot).

Immune gene expression against infection intensity in field samples

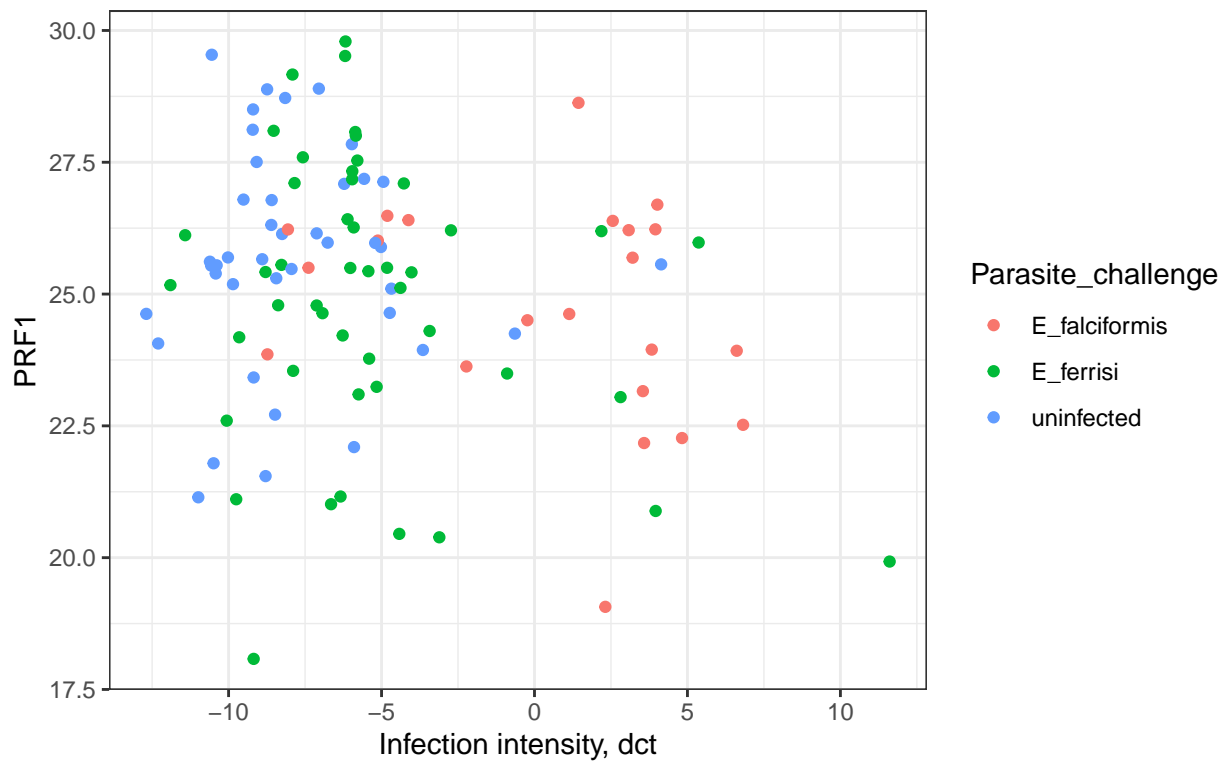


16. PRF1

```
ggplot(lab, aes(x = delta, y = PRF1, color = Parasite_challenge)) +
  geom_jitter() +
  geom_abline() +
  labs(x = "Infection intensity, dct",
       title = "Immune gene expression against infection intensity
in lab infections") +
  theme_bw()
```

Warning: Removed 6 rows containing missing values (geom_point).

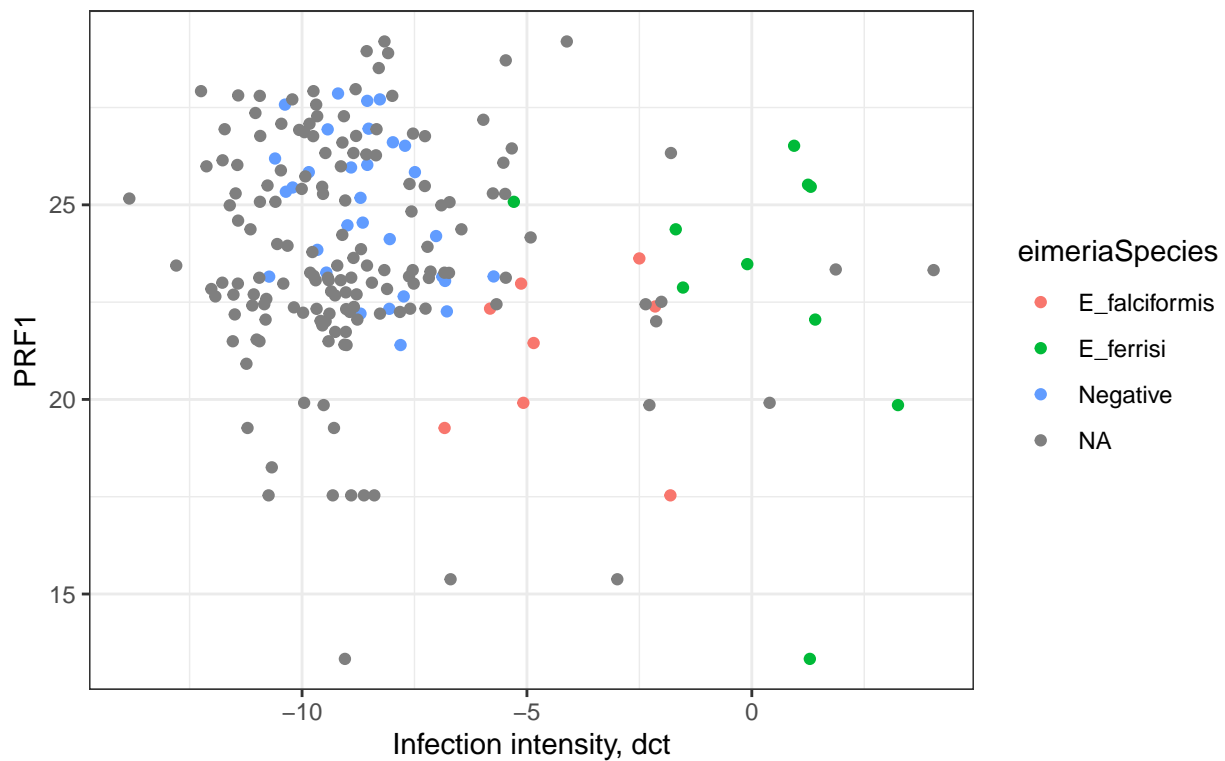
Immune gene expression against infection intensity in lab infections



```
ggplot(field, aes(x = delta_ct_cewe_MminusE, y = PRF1, color = eimeriaSpecies)) +
  geom_jitter() +
  geom_abline() +
  labs(x = "Infection intensity, dct",
       title = "Immune gene expression against infection intensity in field
               samples") +
  theme_bw()
```

Warning: Removed 154 rows containing missing values (geom_point).

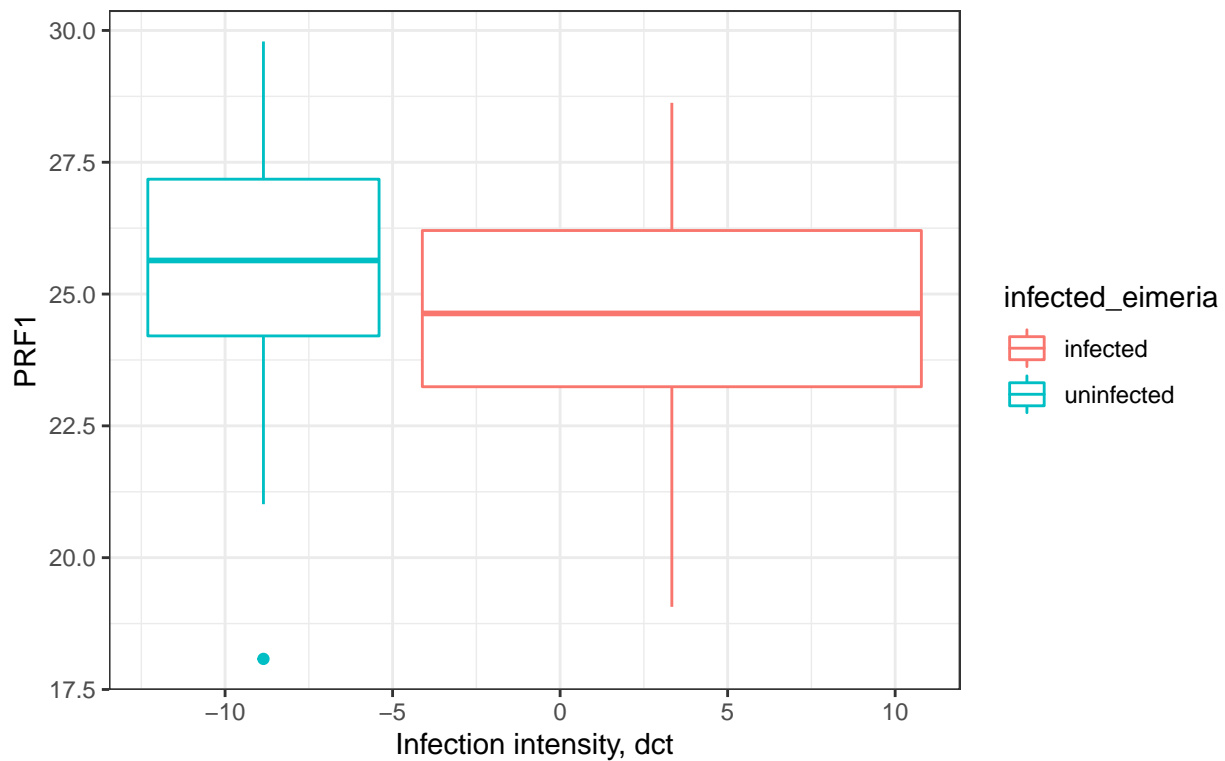
Immune gene expression against infection intensity in field samples



```
ggplot(lab, aes(x = delta, y = PRF1, color = infected_eimeria)) +
  geom_boxplot() +
  labs(x = "Infection intensity, dct",
       title = "Immune gene expression against infection intensity in lab
infections") +
  theme_bw()
```

Warning: Removed 6 rows containing missing values (stat_boxplot).

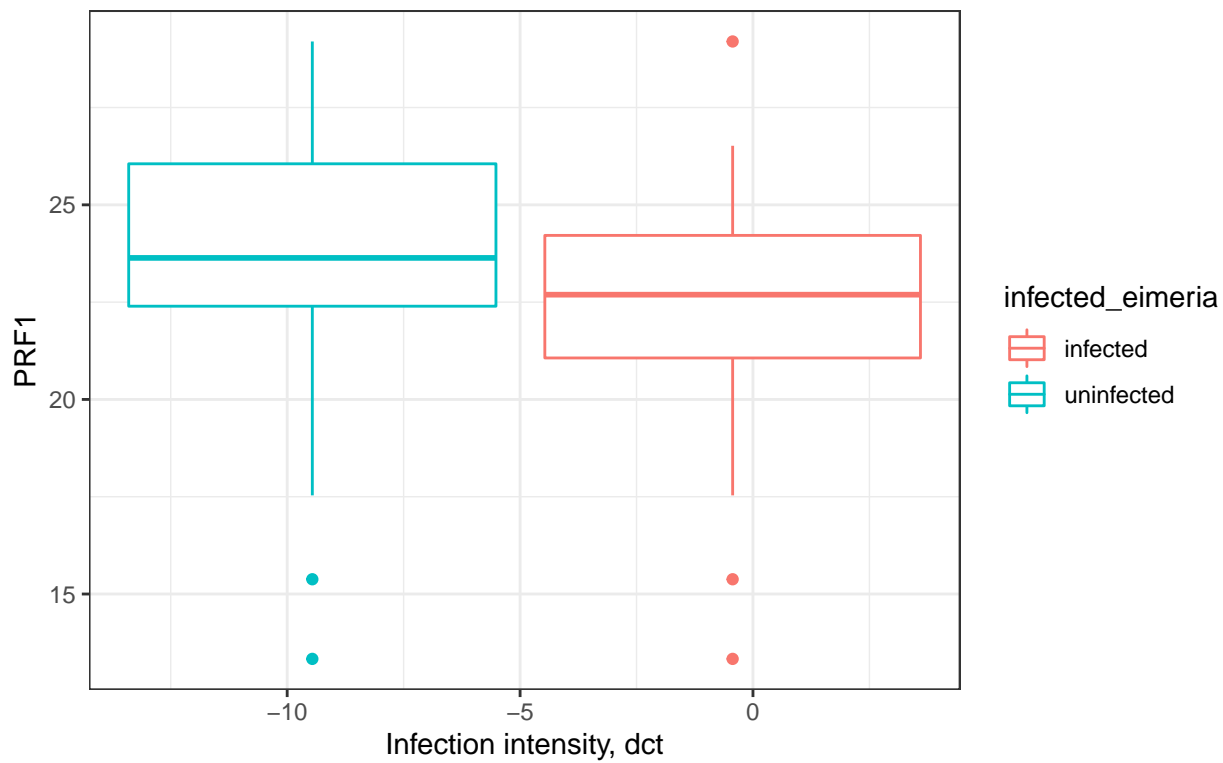
Immune gene expression against infection intensity in lab infections



```
ggplot(field, aes(x = delta_ct_cewe_MminusE, y = PRF1,
                  color = infected_eimeria)) +
  geom_boxplot() +
  labs(x = "Infection intensity, dct",
       title = "Immune gene expression against infection intensity in field
               samples") +
  theme_bw()
```

Warning: Removed 154 rows containing missing values (stat_boxplot).

Immune gene expression against infection intensity in field samples

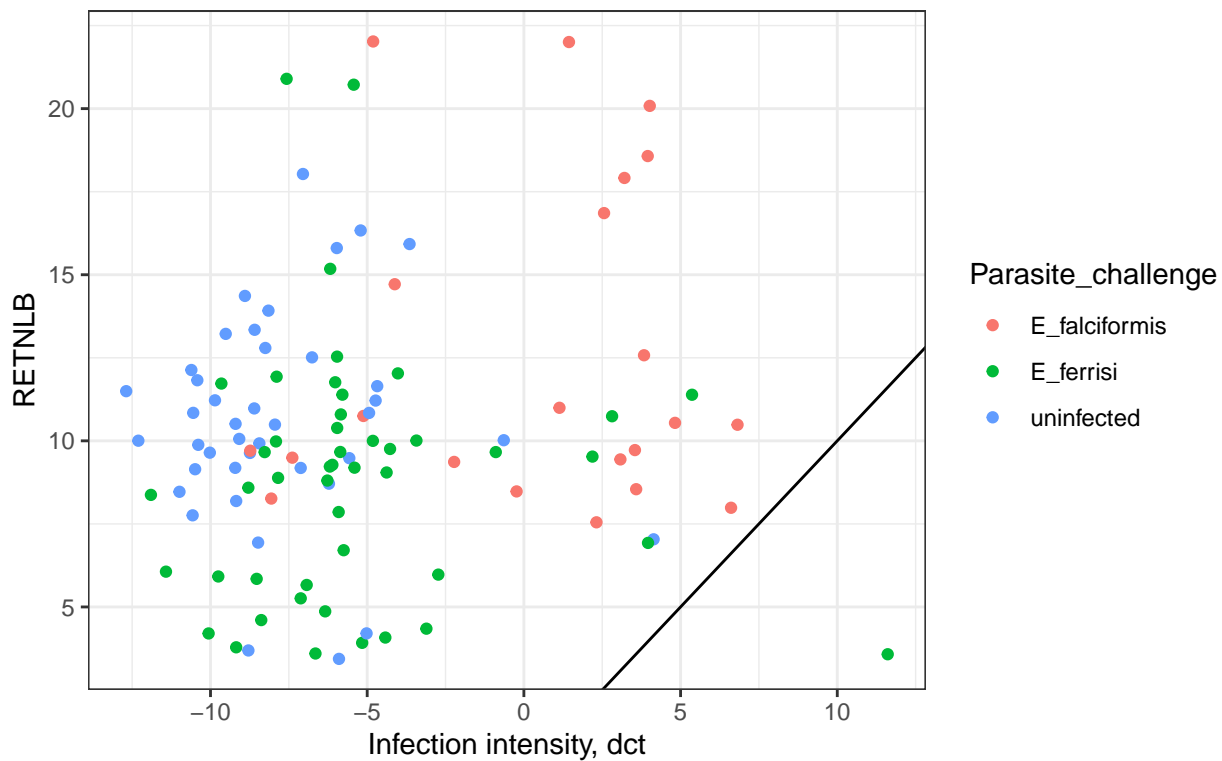


17. RETNLB

```
ggplot(lab, aes(x = delta, y = RETNLB, color = Parasite_challenge)) +
  geom_jitter() +
  geom_abline() +
  labs(x = "Infection intensity, dct",
       title = "Immune gene expression against infection intensity
in lab infections") +
  theme_bw()
```

Warning: Removed 6 rows containing missing values (geom_point).

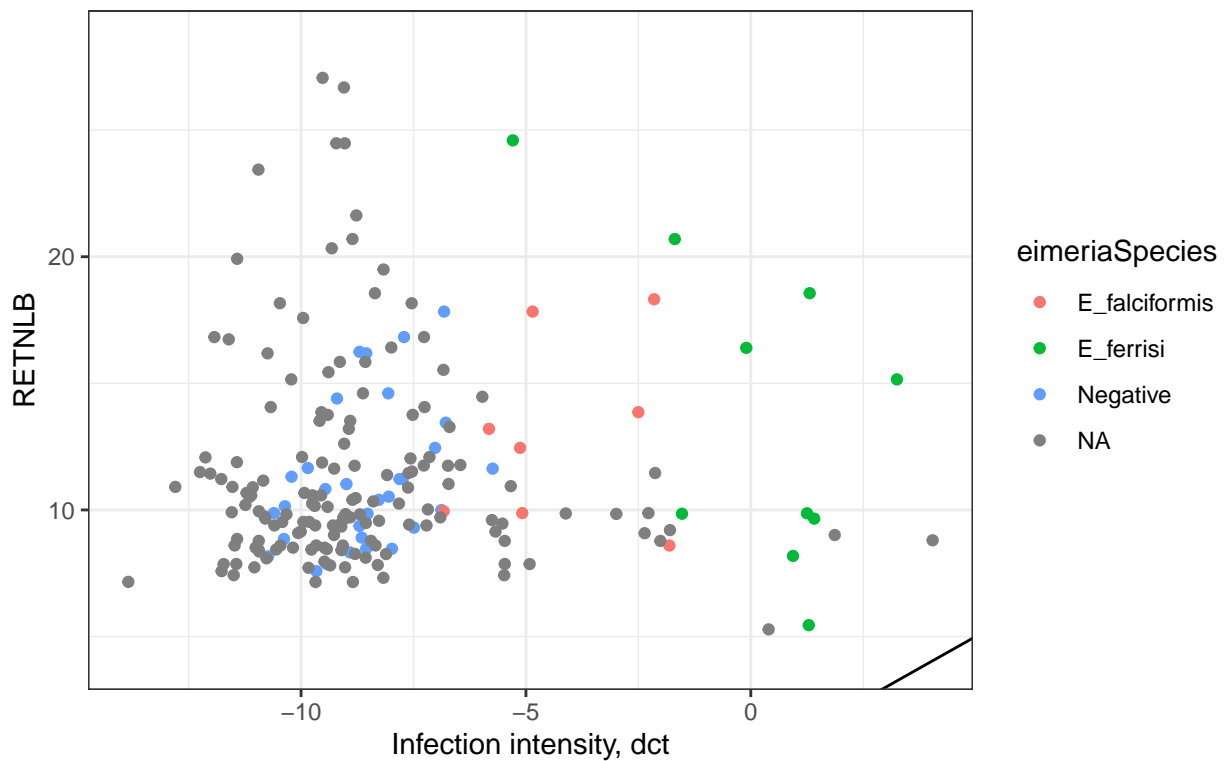
Immune gene expression against infection intensity in lab infections



```
ggplot(field, aes(x = delta_ct_cewe_MminusE, y = RETNLB, color = eimeriaSpecies)) +
  geom_jitter() +
  geom_abline() +
  labs(x = "Infection intensity, dct",
       title = "Immune gene expression against infection intensity in field
               samples") +
  theme_bw()
```

Warning: Removed 154 rows containing missing values (geom_point).

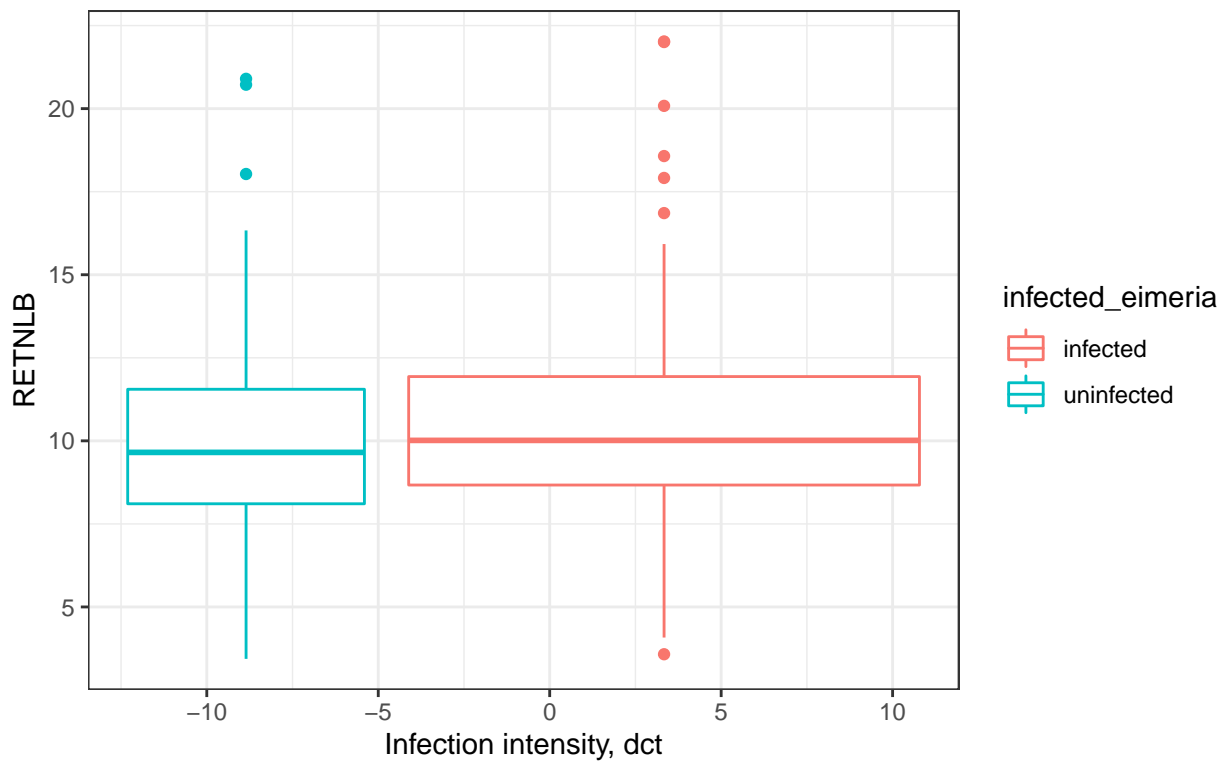
Immune gene expression against infection intensity in field samples



```
ggplot(lab, aes(x = delta, y = RETNLB, color = infected_eimeria)) +
  geom_boxplot() +
  labs(x = "Infection intensity, dct",
       title = "Immune gene expression against infection intensity in lab
infections") +
  theme_bw()
```

Warning: Removed 6 rows containing missing values (stat_boxplot).

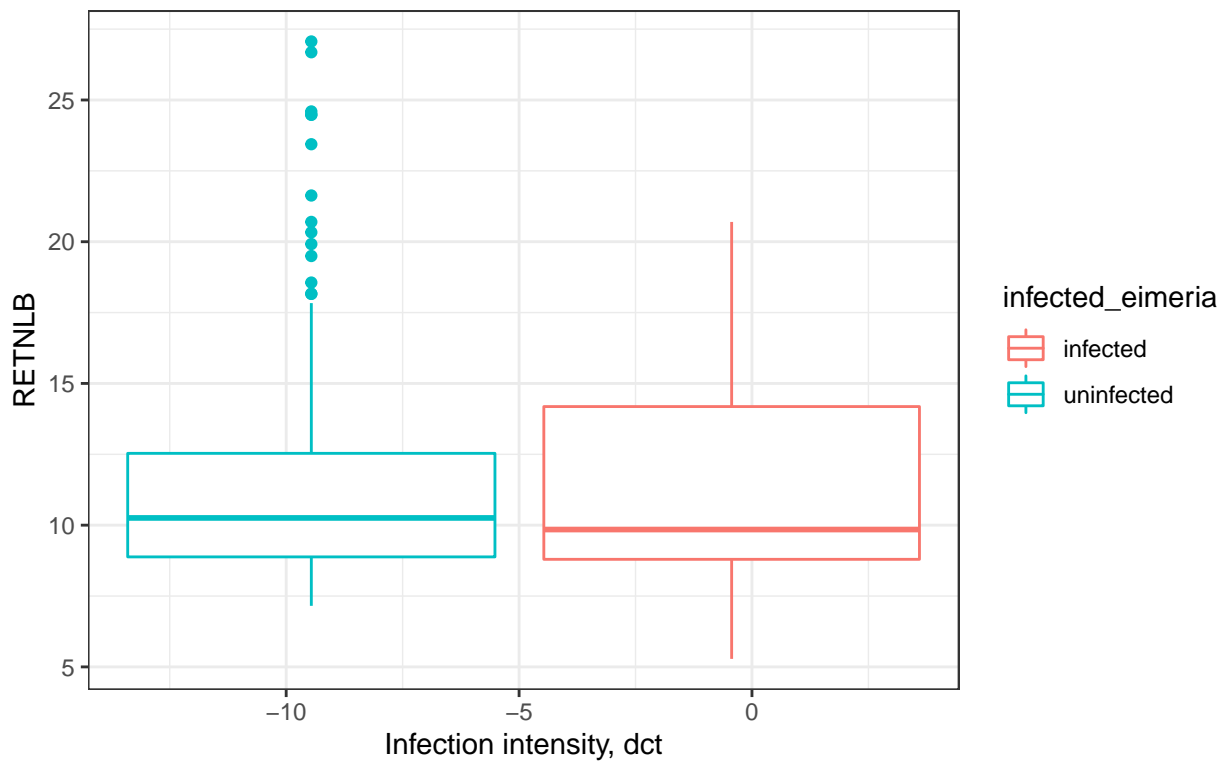
Immune gene expression against infection intensity in lab infections



```
ggplot(field, aes(x = delta_ct_cewe_MminusE, y = RETNLB,
                  color = infected_eimeria)) +
  geom_boxplot() +
  labs(x = "Infection intensity, dct",
       title = "Immune gene expression against infection intensity in field
samples") +
  theme_bw()
```

Warning: Removed 154 rows containing missing values (stat_boxplot).

Immune gene expression against infection intensity in field samples

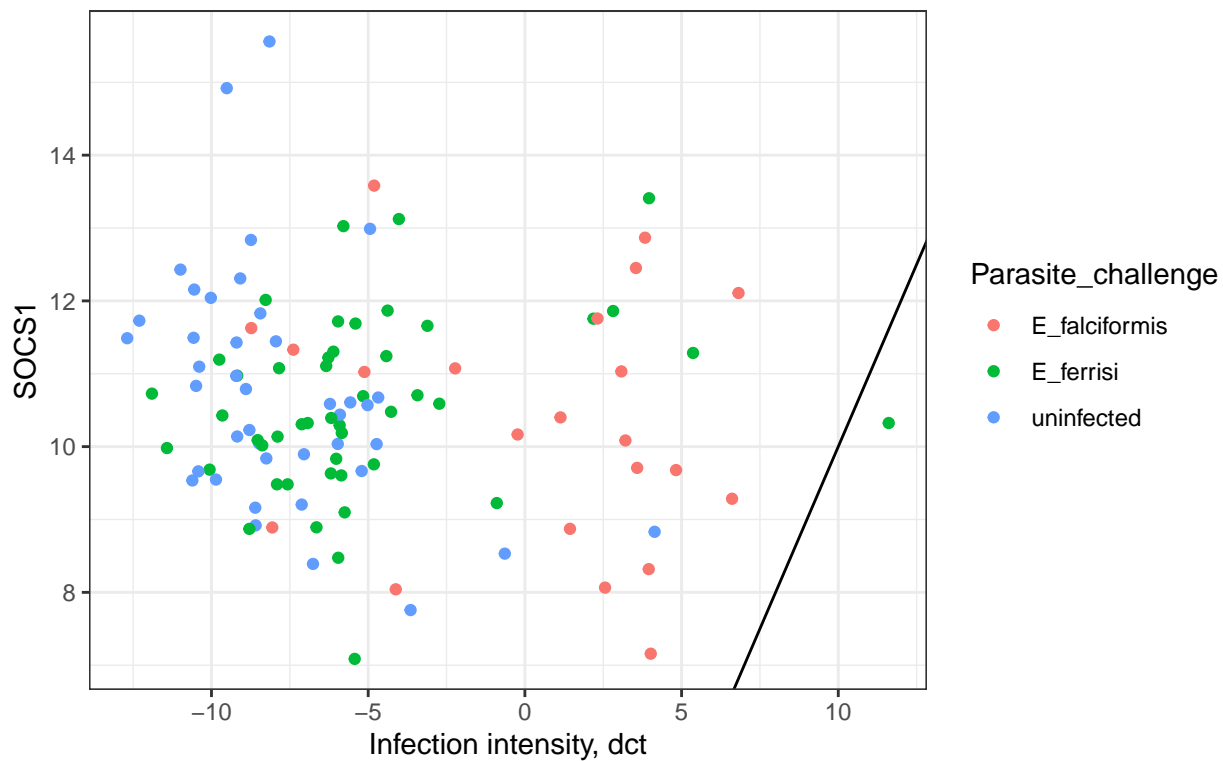


18. SOCS1

```
ggplot(lab, aes(x = delta, y = SOCS1, color = Parasite_challenge)) +
  geom_jitter() +
  geom_abline() +
  labs(x = "Infection intensity, dct",
       title = "Immune gene expression against infection intensity
               in lab infections") +
  theme_bw()
```

Warning: Removed 6 rows containing missing values (geom_point).

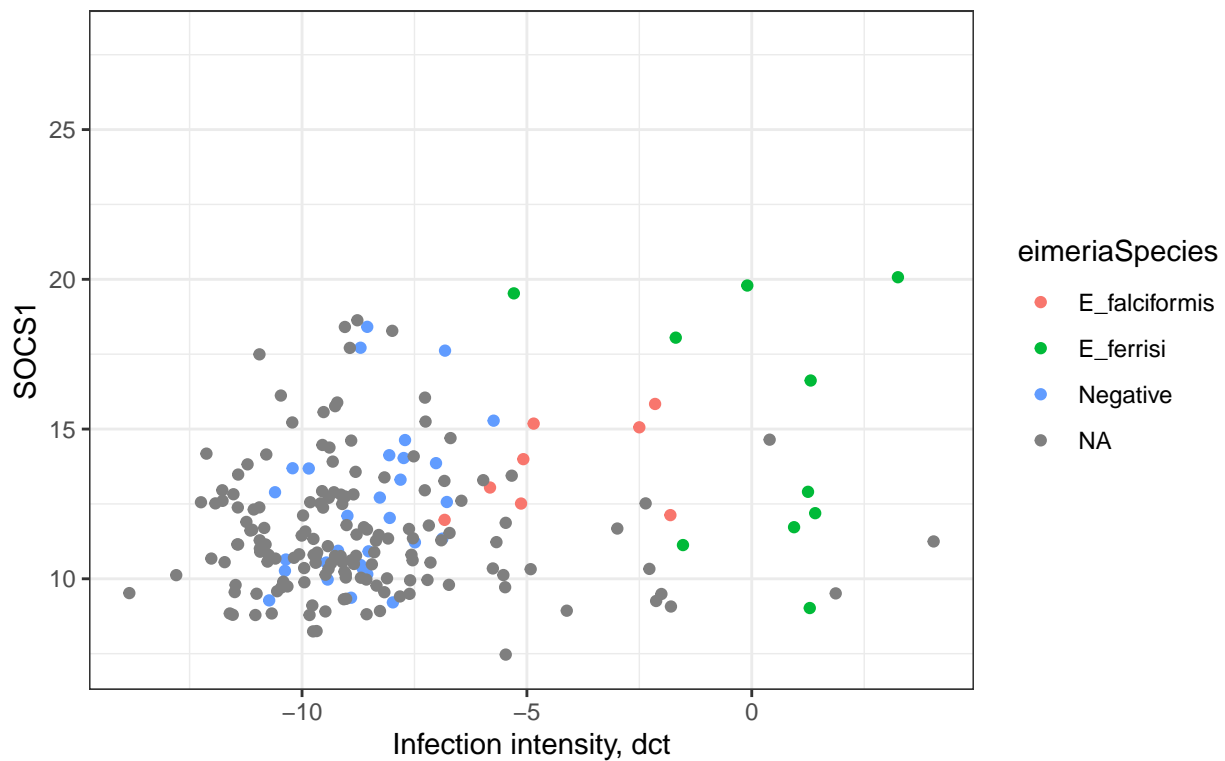
Immune gene expression against infection intensity in lab infections



```
ggplot(field, aes(x = delta_ct_cewe_MminusE, y = SOCS1, color = eimeriaSpecies)) +
  geom_jitter() +
  geom_abline() +
  labs(x = "Infection intensity, dct",
       title = "Immune gene expression against infection intensity in field
       samples") +
  theme_bw()
```

Warning: Removed 154 rows containing missing values (geom_point).

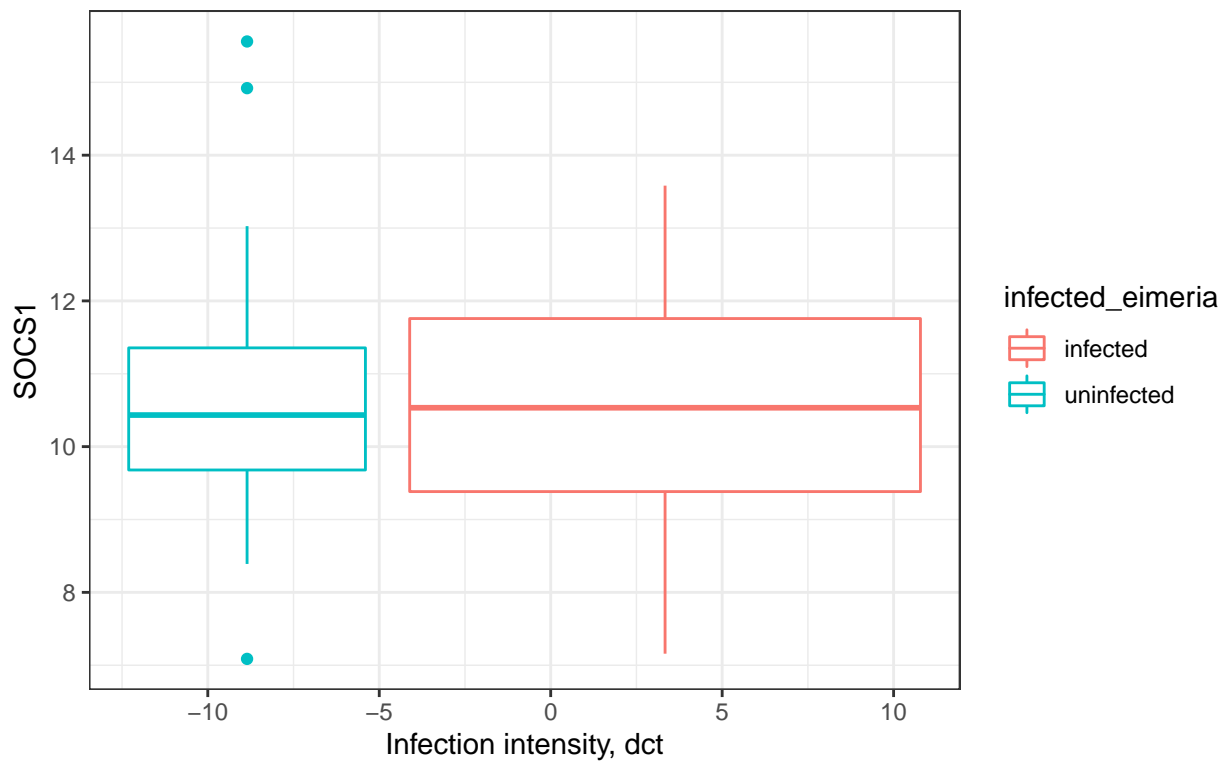
Immune gene expression against infection intensity in field samples



```
ggplot(lab, aes(x = delta, y = SOCS1, color = infected_eimeria)) +
  geom_boxplot() +
  labs(x = "Infection intensity, dct",
       title = "Immune gene expression against infection intensity in lab
infections") +
  theme_bw()
```

Warning: Removed 6 rows containing missing values (stat_boxplot).

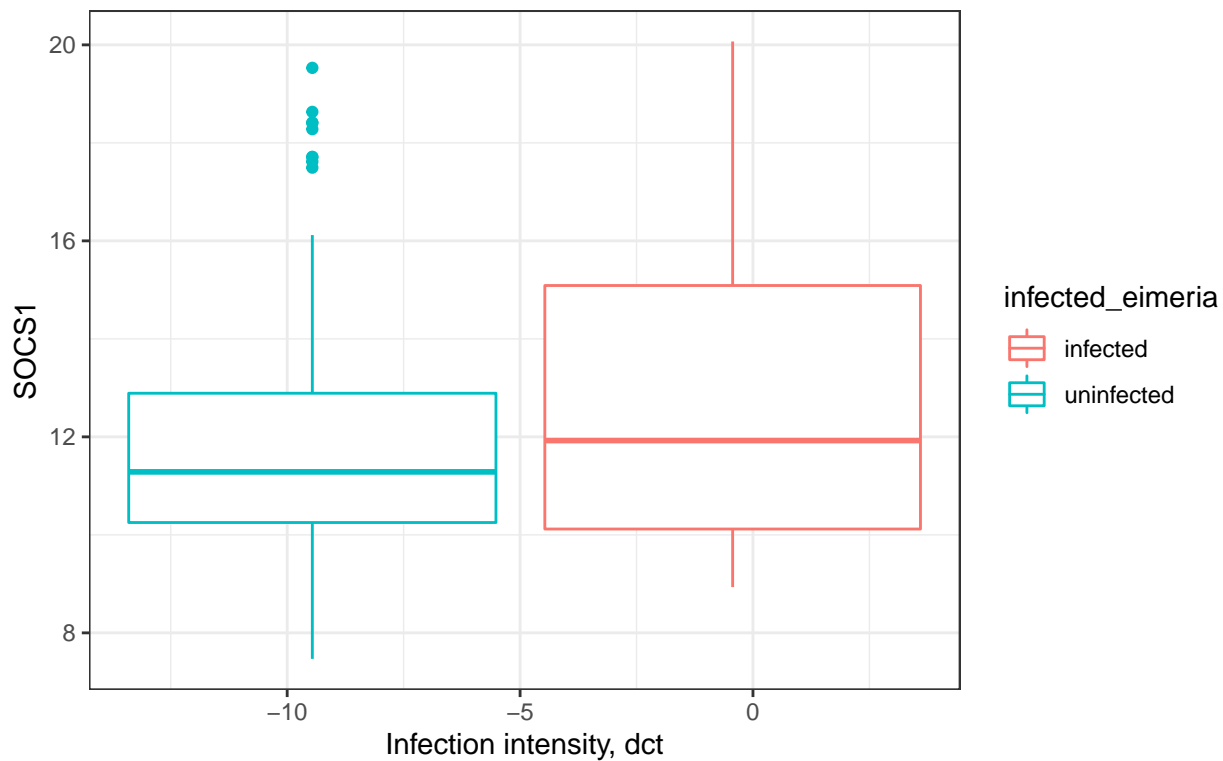
Immune gene expression against infection intensity in lab infections



```
ggplot(field, aes(x = delta_ct_cewe_MminusE, y = SOCS1,
                  color = infected_eimeria)) +
  geom_boxplot() +
  labs(x = "Infection intensity, dct",
       title = "Immune gene expression against infection intensity in field
               samples") +
  theme_bw()
```

Warning: Removed 154 rows containing missing values (stat_boxplot).

Immune gene expression against infection intensity in field samples

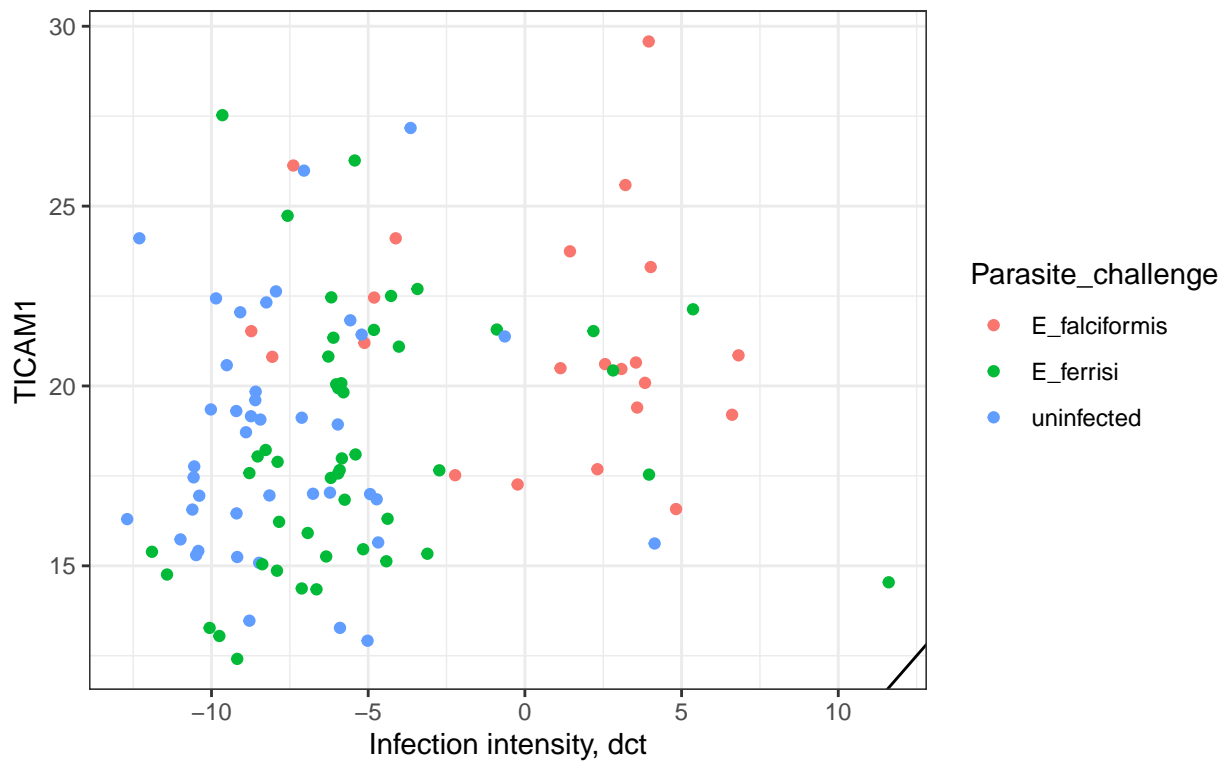


19. TICAM1

```
ggplot(lab, aes(x = delta, y = TICAM1, color = Parasite_challenge)) +
  geom_jitter() +
  geom_abline() +
  labs(x = "Infection intensity, dct",
       title = "Immune gene expression against infection intensity
in lab infections") +
  theme_bw()
```

Warning: Removed 6 rows containing missing values (geom_point).

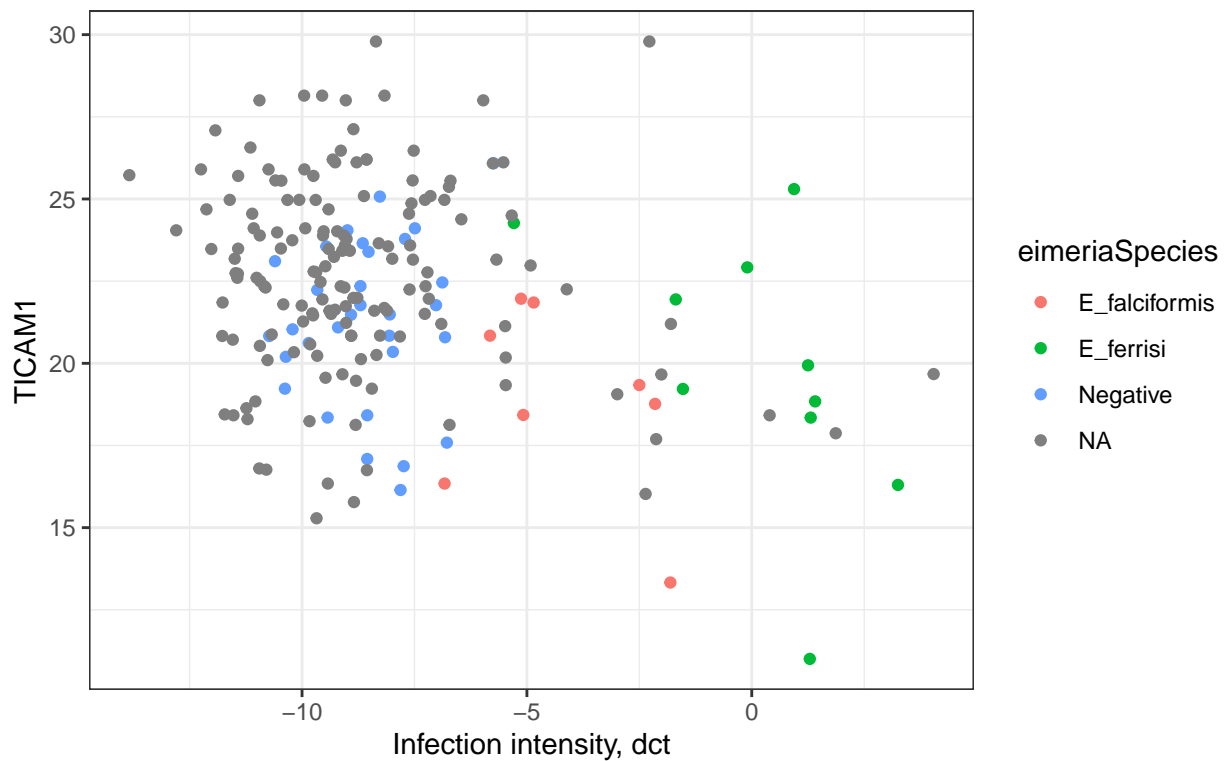
Immune gene expression against infection intensity in lab infections



```
ggplot(field, aes(x = delta_ct_cewe_MminusE, y = TICAM1, color = eimeriaSpecies)) +
  geom_jitter() +
  geom_abline() +
  labs(x = "Infection intensity, dct",
       title = "Immune gene expression against infection intensity in field
               samples") +
  theme_bw()
```

Warning: Removed 154 rows containing missing values (geom_point).

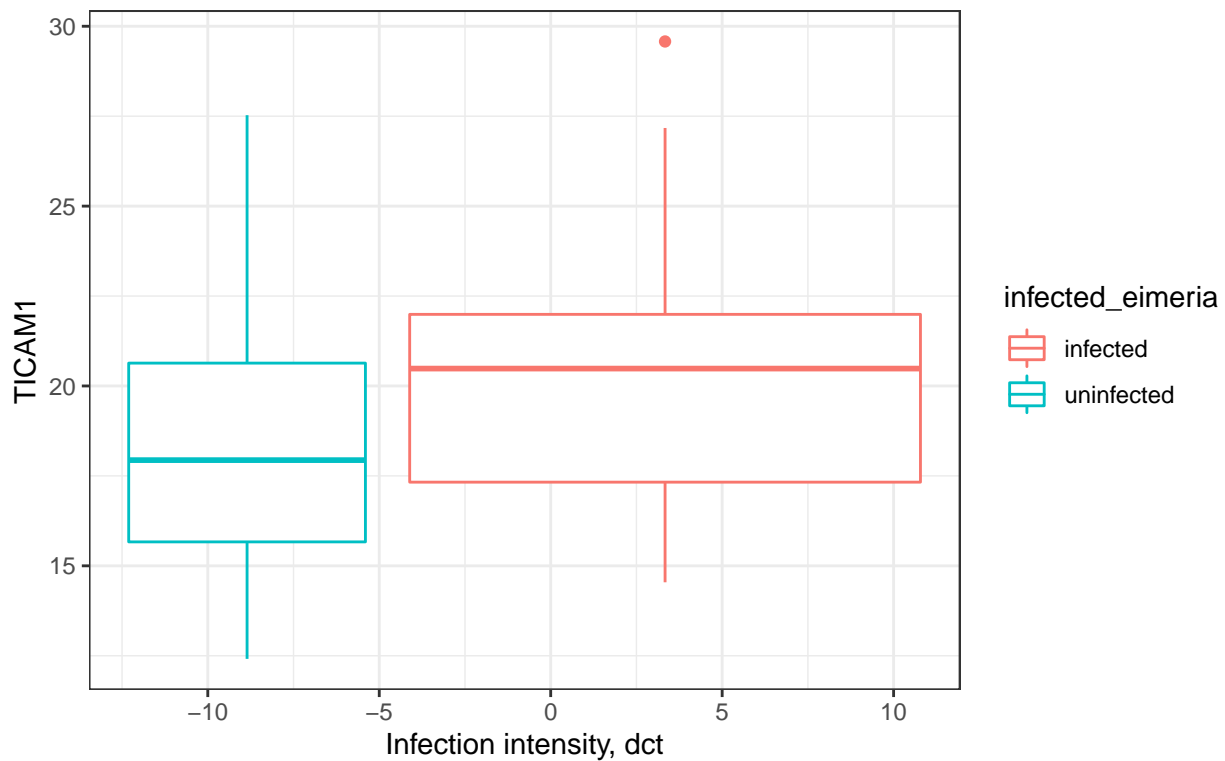
Immune gene expression against infection intensity in field samples



```
ggplot(lab, aes(x = delta, y = TICAM1, color = infected_eimeria)) +
  geom_boxplot() +
  labs(x = "Infection intensity, dct",
       title = "Immune gene expression against infection intensity in lab
infections") +
  theme_bw()
```

Warning: Removed 6 rows containing missing values (stat_boxplot).

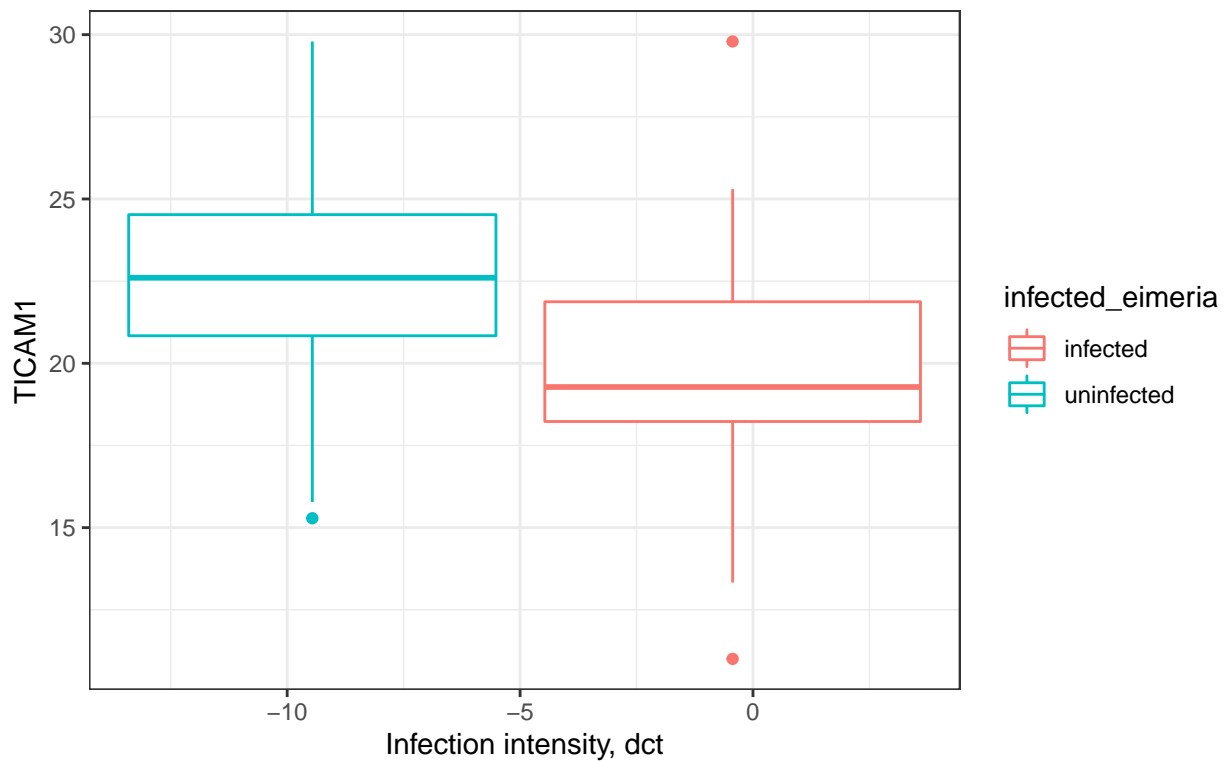
Immune gene expression against infection intensity in lab infections



```
ggplot(field, aes(x = delta_ct_cewe_MminusE, y = TICAM1,
                  color = infected_eimeria)) +
  geom_boxplot() +
  labs(x = "Infection intensity, dct",
       title = "Immune gene expression against infection intensity in field
samples") +
  theme_bw()
```

Warning: Removed 154 rows containing missing values (stat_boxplot).

Immune gene expression against infection intensity in field samples

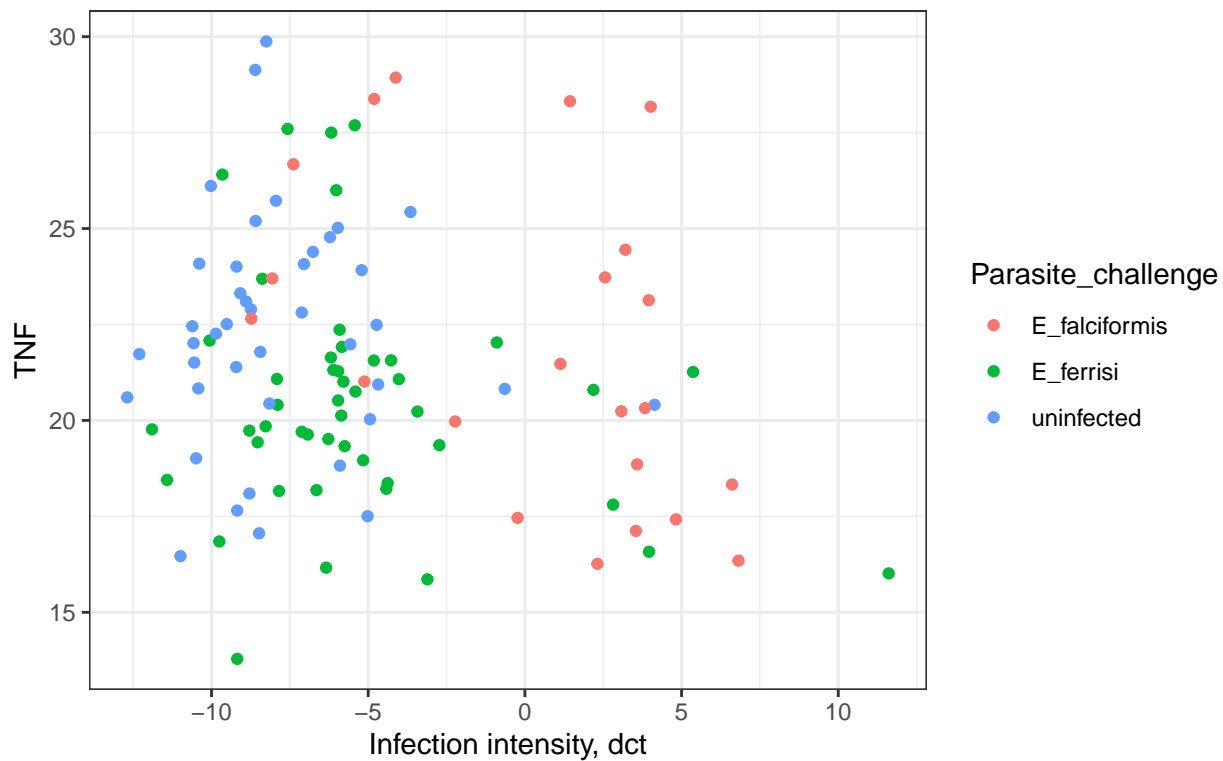


20. TNF

```
ggplot(lab, aes(x = delta, y = TNF, color = Parasite_challenge)) +
  geom_jitter() +
  geom_abline() +
  labs(x = "Infection intensity, dct",
       title = "Immune gene expression against infection intensity
in lab infections") +
  theme_bw()
```

Warning: Removed 6 rows containing missing values (geom_point).

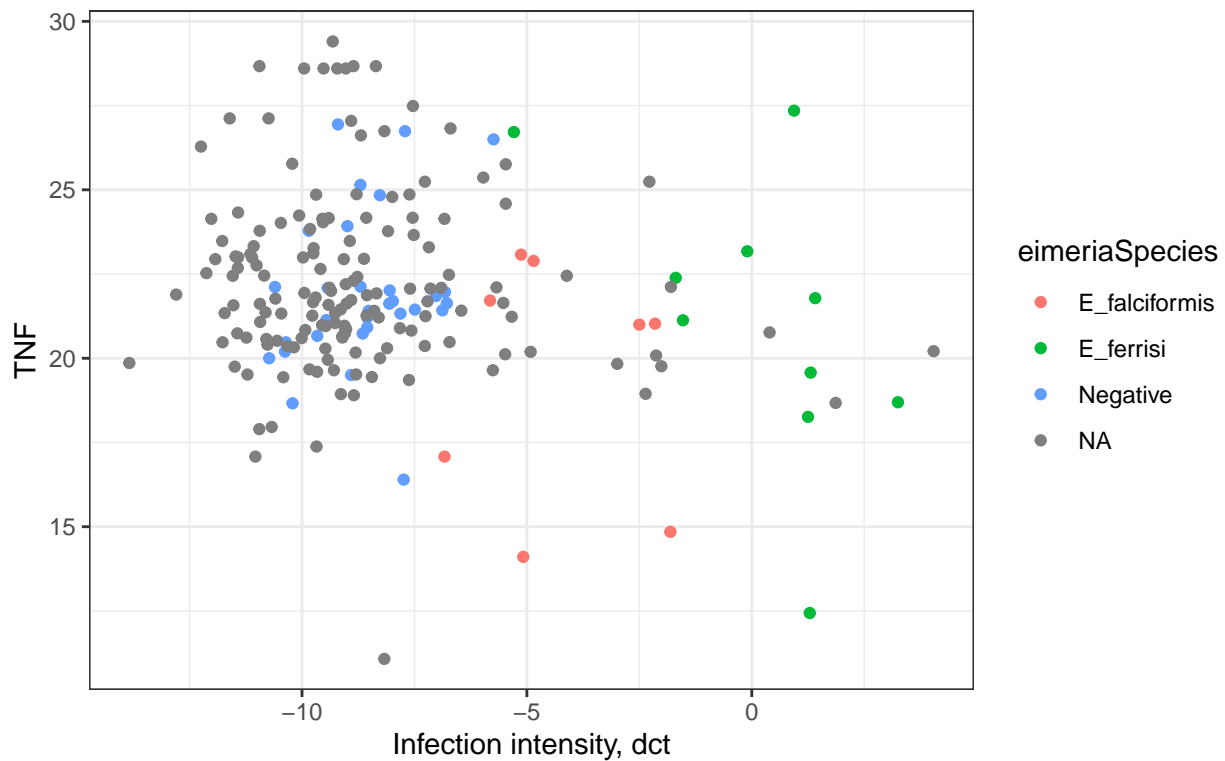
Immune gene expression against infection intensity in lab infections



```
ggplot(field, aes(x = delta_ct_cewe_MminusE, y = TNF, color = eimeriaSpecies)) +
  geom_jitter() +
  geom_abline() +
  labs(x = "Infection intensity, dct",
       title = "Immune gene expression against infection intensity in field
               samples") +
  theme_bw()
```

Warning: Removed 154 rows containing missing values (geom_point).

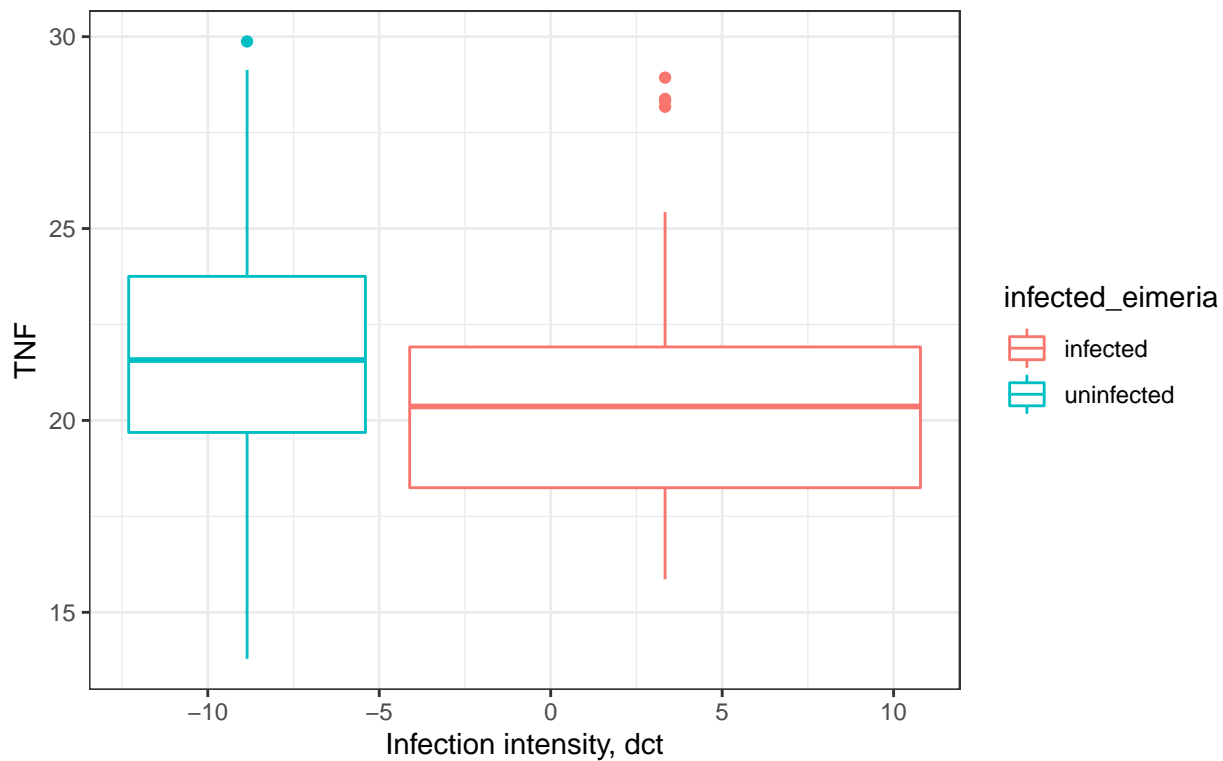
Immune gene expression against infection intensity in field samples



```
ggplot(lab, aes(x = delta, y = TNF, color = infected_eimeria)) +
  geom_boxplot() +
  labs(x = "Infection intensity, dct",
       title = "Immune gene expression against infection intensity in lab
infections") +
  theme_bw()
```

Warning: Removed 6 rows containing missing values (stat_boxplot).

Immune gene expression against infection intensity in lab infections



```
ggplot(field, aes(x = delta_ct_cewe_MminusE, y = TNF,
                  color = infected_eimeria)) +
  geom_boxplot() +
  labs(x = "Infection intensity, dct",
       title = "Immune gene expression against infection intensity in field
               samples") +
  theme_bw()
```

Warning: Removed 154 rows containing missing values (stat_boxplot).

Immune gene expression against infection intensity in field samples

