3. Exploration Gene - PCA

Fay

2022-10-05

Import data

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

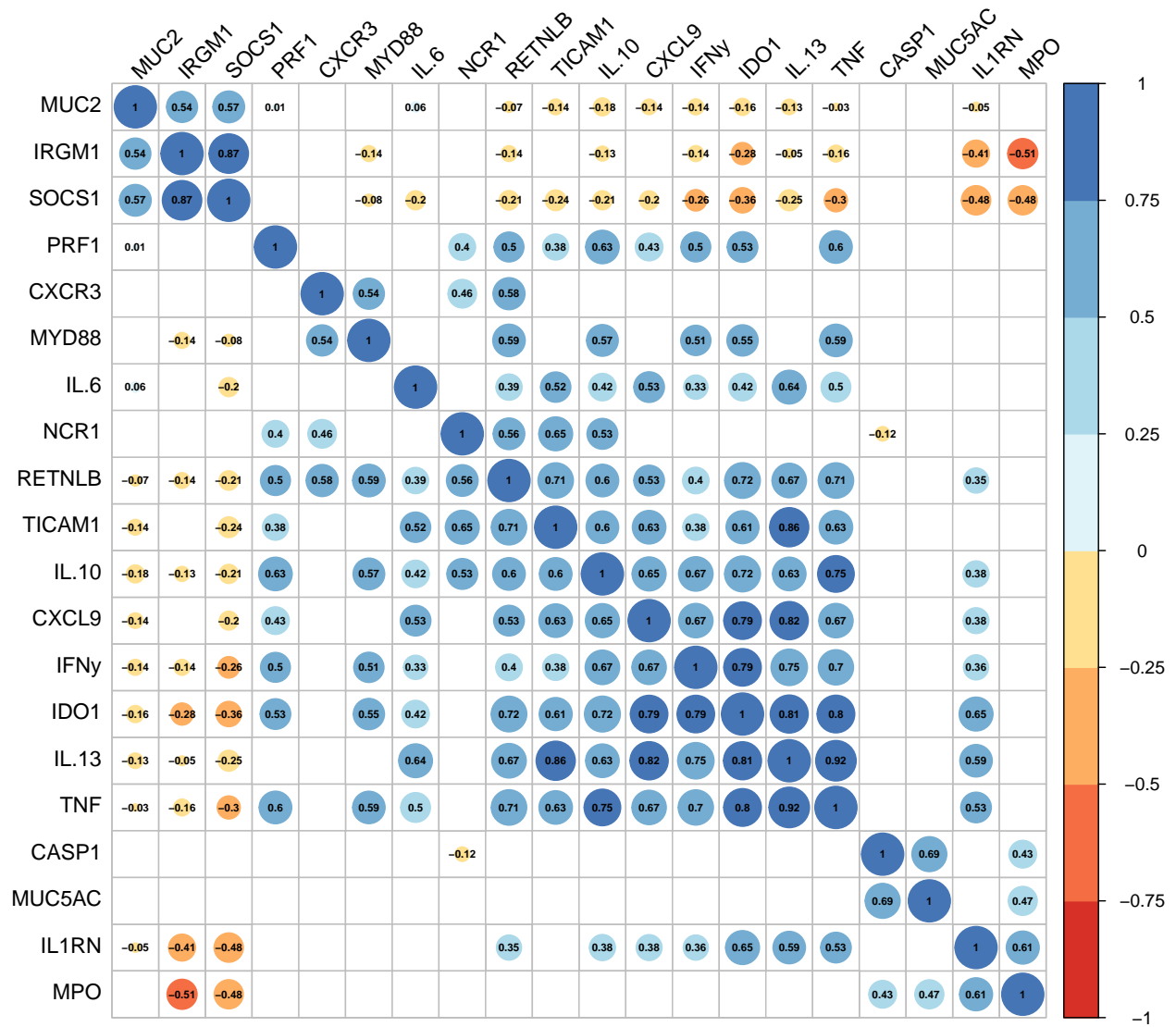## Vectors for selecting genes

```
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")
```
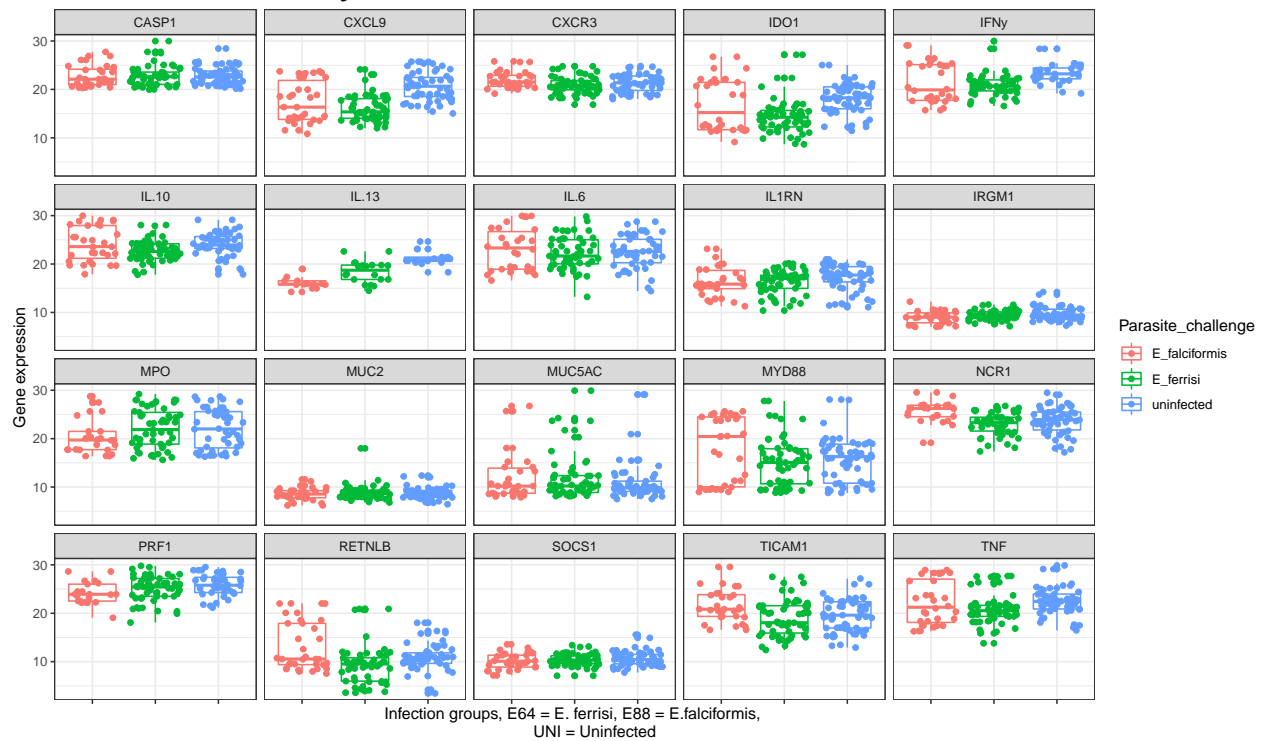
Lab data

Correlations between the genes

Corrplot of correlations - Laboratory gene expression data

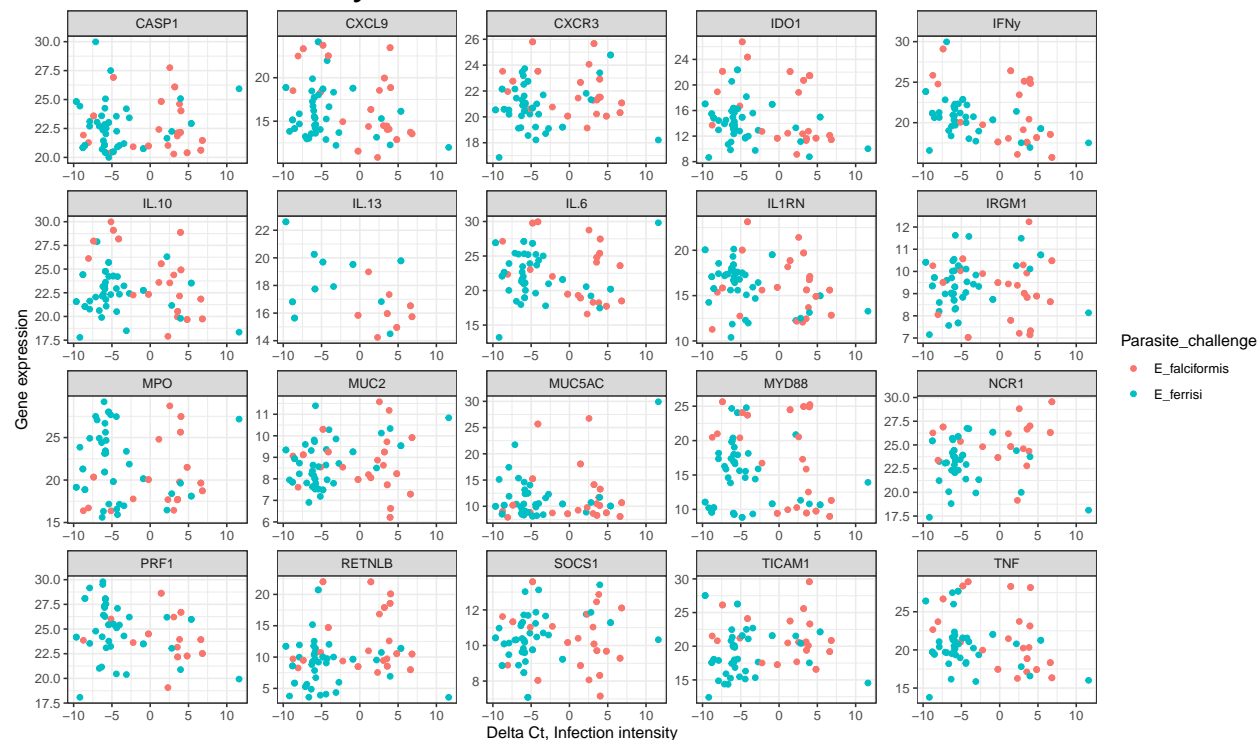Here is a corrplot of the correlations between the genes.

	MUC2	IRGM1	SOCS1	PRF1	CXCR3	MYD88	IL.6	NCR1	RETNLB	TICAM1	IL.10	CXCL9	IFNy	IDO1	IL.13	TNF	CASP1	MUC5AC	IL1RN	MPO
MUC2	1	0.54	0.57	0.01			0.06		-0.07	-0.14	-0.18	-0.14	-0.14	-0.16	-0.13	-0.03			-0.05	
IRGM1	0.54	1	0.87			-0.14			-0.14		-0.13		-0.14	-0.28	-0.05	-0.16			-0.41	-0.51
SOCS1	0.57	0.87	1			-0.08	-0.2		-0.21	-0.24	-0.21	-0.2	-0.26	-0.36	-0.25	-0.3			-0.48	-0.48
PRF1	0.01			1				0.4	0.5	0.38	0.63	0.43	0.5	0.53		0.6				
CXCR3					1	0.54		0.46	0.58											
MYD88		-0.14	-0.08		0.54	1			0.59		0.57		0.51	0.55		0.59				
IL.6	0.06		-0.2				1		0.39	0.52	0.42	0.53	0.33	0.42	0.64	0.5				
NCR1				0.4	0.46			1	0.56	0.65	0.53						-0.12			
RETNLB	-0.07	-0.14	-0.21	0.5	0.58	0.59	0.39	0.56	1	0.71	0.6	0.53	0.4	0.72	0.67	0.71			0.35	
TICAM1	-0.14		-0.24	0.38			0.52	0.65	0.71	1	0.6	0.63	0.38	0.61	0.86	0.63				
IL.10	-0.18	-0.13	-0.21	0.63		0.57	0.42	0.53	0.6	0.6	1	0.65	0.67	0.72	0.63	0.75			0.38	
CXCL9	-0.14		-0.2	0.43			0.53		0.53	0.63	0.65	1	0.67	0.79	0.82	0.67			0.38	
IFNy	-0.14	-0.14	-0.26	0.5		0.51	0.33	0.4		0.38	0.67	0.67	1	0.79	0.75	0.7			0.36	
IDO1	-0.16	-0.28	-0.36	0.53		0.55	0.42		0.72	0.61	0.72	0.79	0.79	1	0.81	0.8			0.65	
IL.13	-0.13	-0.05	-0.25				0.64		0.67	0.86	0.63	0.82	0.75	0.81	1	0.92			0.59	
TNF	-0.03	-0.16	-0.3	0.6		0.59	0.5		0.71	0.63	0.75	0.67	0.7	0.8	0.92	1			0.53	
CASP1								-0.12									1	0.69		0.43
MUC5AC																	0.69	1		0.47
IL1RN	-0.05	-0.41	-0.48					0.35			0.38	0.38	0.36	0.65	0.59	0.53			1	0.61
MPO		-0.51	-0.48														0.43	0.47	0.61	1

Gene expression in response to infection group, laboratory infections
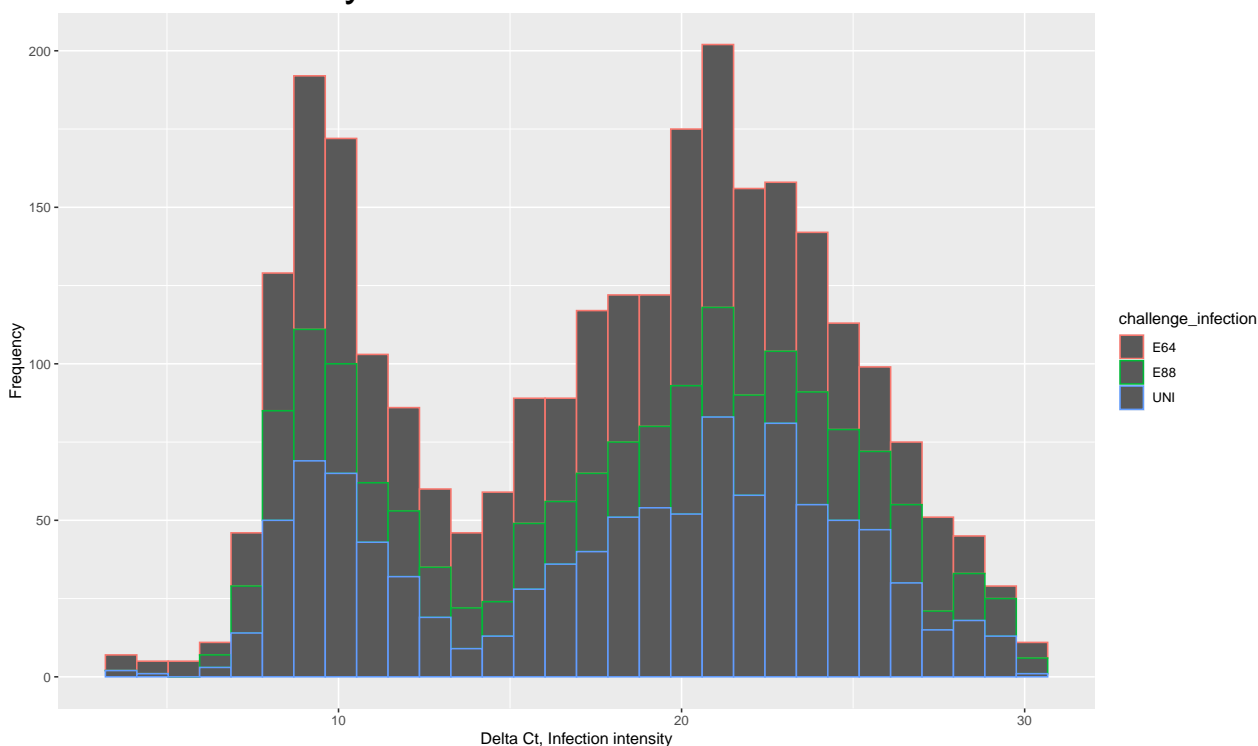


```
g %>%
    filter(!Parasite_challenge == "uninfected", MC.Eimeria == "TRUE") %>%
    ggplot(aes(x = delta_ct_cewe_MminusE, y = gene_expression,
               color = Parasite_challenge)) +
    geom_jitter() +
    facet_wrap(~ Gene, scales = "free") +
    theme_light() +
    labs(x = "Delta Ct, Infection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

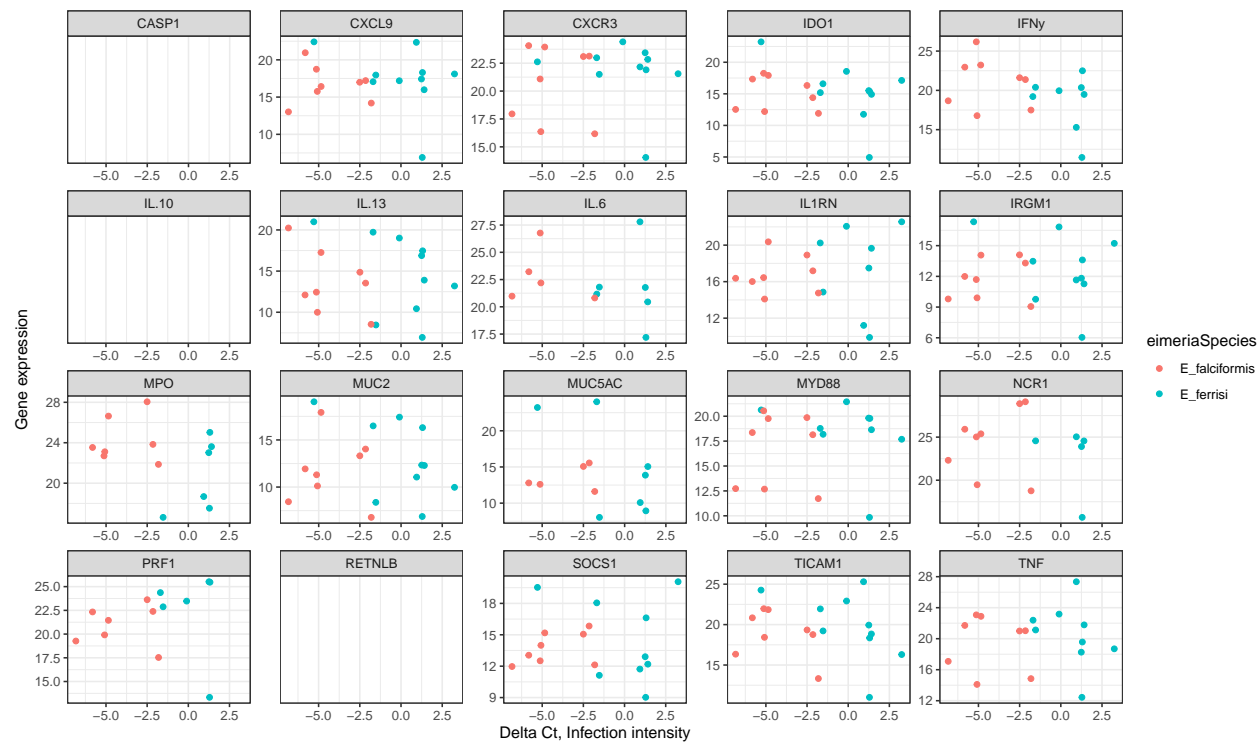Here is a corrplot of the correlations between the genes. I am using the non-normalized genes

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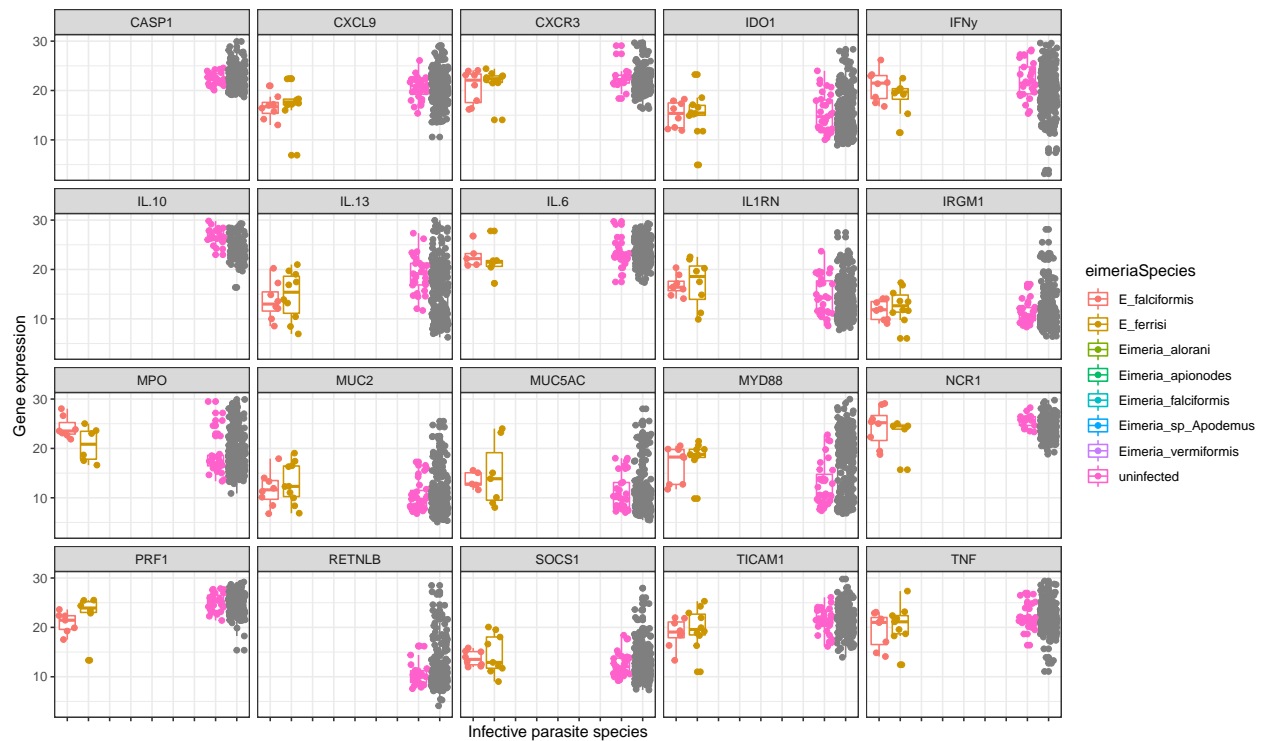

```
g %>%
    filter(!eimeriaSpecies == "uninfected", MC.Eimeria == "TRUE") %>%
    ggplot(aes(x = delta_ct_cewe_MminusE, y = gene_expression,
               color = eimeriaSpecies)) +
    geom_jitter() +
    facet_wrap(~ Gene, scales = "free") +
    theme_light() +
    labs(x = "Delta Ct, Infection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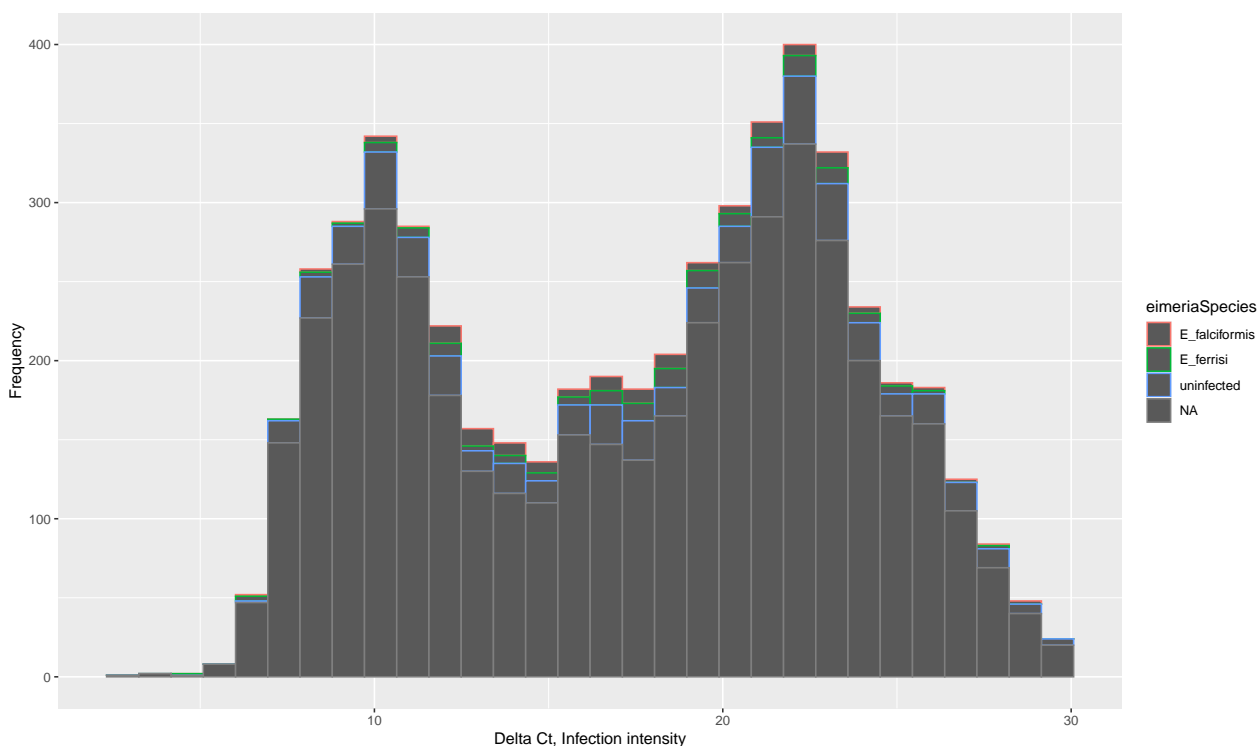
Gene expression correlations in lab and field data

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

Here is a corrplot of the correlations between the genes.