

Figure S1. Heat map of differentially expressed genes (Log 10 transformed count data) between treatments (infection with *Argulus foliaceous* and control) of two inbred strains of *Kryptolebias marmoratus* (R and Dan).
Figure S2. Enriched gene ontology (GO) classifications at Level: GO ALL, for all differentially expressed genes (from results of EdgeR glm analysis), P<0.1.
Figure S3. Individual Ct values for 9 target immune-related genes. Four groups were analysed using RT-qPCR: two lines - R (green) and DAN (blue), as well as two treatments - infected (dark) and control (light).
**Figure S4.** Generalized Linear Model with Quasi-Likelihood Test for the analysis of differential gene expression in *Kryptolebias marmoratus* as a function of treatment (infection or control) and selfing line (DAN and R).

```r
targets <- readTargets("label_file_24.txt")
x <- read.delim("o_samples_input_matrix2", row.names=1, stringsAsFactors=FALSE)
head(x)
dim(x) #check no. sequences and sample columns
colSums(x) #reads per sample
colSums(x) / 1e06 #reads in millions
table(rowSums(x)) [1:30] # output no. sequences with low counts (from 0-30)
Treatment <- factor(targets$treat, levels=c("Sham", "Infected"))
Strain <- factor(targets$strain, levels=c("D", "R"))
y = DGEList(counts=x[,1:8])
keep <- rowSums(cpm(y)>1) >= 4
y <- y[keep, , keep.lib.sizes=FALSE]
y = calcNormFactors(y)
design2 <- model.matrix(~Treatment * Strain, data=targets)
y <- estimateGLMCommonDisp(y, design2, verbose=TRUE)
y <- estimateGLMTrendedDisp(y, design2)
y <- estimateGLMTagwiseDisp(y, design2)
fit <- glmQLFit(y, design2)
colnames(design2)
[1] "(Intercept)" "TreatmentInfected" "StrainR"
[4] "TreatmentInfected:StrainR"

qlf <- glmQLFTest(fit, coef=2:4)
tab <- topTags(qlf, n=67824)
FDR <- p.adjust(qlf$table$PValue, method="BH")
is.de <- decideTestsDGE(qlf)
```
Figure S5. Comparison among models of gene expression in *Kryptolebias marmoratus* as a function of treatment (infection or control) and selfing line (DAN and R), including and excluding individual (ID) as a random factor. (a) All nine immune-related genes targeted for qPCR (*MHC1uka, MHC2dab, Fgg, IRGF1, C7, cxcl11.8, Cd4-1, Lect2 and Ahsa1b*) (b) target immune-related identified as DE in qPCR analyses (*MHC2dab, Fgg, cxcl11.8, Cd4-1, IRGF1*)

(a)  
> m1 <- lmer(Gexpress~Line+Infect+(1|ID))
> m2 <- lmer(Gexpress~Line*Infect+(1|ID))
> m3 <- lm(Gexpress~Line*Infect)
> m4 <- lm(Gexpress~Line+Infect)
> anova(m1,m2,m3,m4)
refitting model(s) with ML (instead of REML)
Data: NULL
Models:
  m4: Gexpress ~ Line + Infect
  m1: Gexpress ~ Line + Infect + (1 | ID)
  m3: Gexpress ~ Line * Infect
  m2: Gexpress ~ Line * Infect + (1 | ID)
                 Df   AIC    BIC  logLik deviance  Chisq Chi Df Pr(>Chisq)
  m4  4 1047.4 1063.7 -519.72   1039.4  3.8410      1    0.05001 .
  m1  5 1045.6 1065.9 -517.80   1035.6  3.8410      1    0.05001 .
  m3  5 1047.8 1068.2 -518.90   1037.8  0.0000      0     1.00000
  m2  6 1046.4 1070.8 -517.22   1034.4  3.3645      1    0.06662 .
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Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(b)  
> m1 <- lmer(Gexpress~Line*Infect+(1|ID))
> m2 <- lmer(Gexpress~Line+Infect+(1|ID))
> m3 <- lm(Gexpress~Line+Infect)
> m4 <- lm(Gexpress~Line*Infect)
> anova(m1,m2,m3,m4)
refitting model(s) with ML (instead of REML)
Data: NULL
Models:
  m3: Gexpress ~ Line + Infect
  m2: Gexpress ~ Line + Infect + (1 | ID)
  m4: Gexpress ~ Line * Infect
  m1: Gexpress ~ Line * Infect + (1 | ID)
                 Df   AIC    BIC  logLik deviance  Chisq Chi Df Pr(>Chisq)
  m4  4  511.08  523.60 -251.54   503.08
  m1  5  513.08  528.73 -251.54   503.08 0.0000      1          1
  m3  5  511.97  527.62 -250.99   501.97 1.1084      0 <2e-16 ***
  m2  6  513.97  532.75 -250.99   501.97 0.0000      1          1
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Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1