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).

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, level=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
 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