

GLM models of the effects of MHC-I functional divergence on lifetime fitness in great reed warblers (*Acrocephalus arundinaceus*)

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This document presents the R code and output from the GLM models behind the results on the effects of MHC-I functional divergence on fitness in adult great reed warblers reported in the paper:

Roved J., Hansson B., Tarka M., Hasselquist D., & Westerdahl H. (2019). MHC-I functional divergence is positively associated with life span and fitness in male great reed warblers: support for the divergent allele advantage hypothesis. *Molecular Ecology*.

The data set is available at the datadryad.org repository, the link is specified in the paper mentioned above.

Note: The variable names employed in the models stem from our original analyses. The names of the corresponding variables in the data set that is publicly available at the repository are given below:

LifeSpan = Life span

ToSucLife_1014 = Lifetime no. fledglings (excluding unsuccessful first time breeders)

RecruLife_1014 = Lifetime no. recruiting offspring (excluding unsuccessful first time breeders)

Total.no.alleles = No. MHC-I alleles

PdistPBR = P-distance PBR

PdistPSS = P-distance PSS

Subset the data.

```
data.males <- subset(data, Sex=="male")
data.females <- subset(data, Sex=="female")
```

Load R packages.

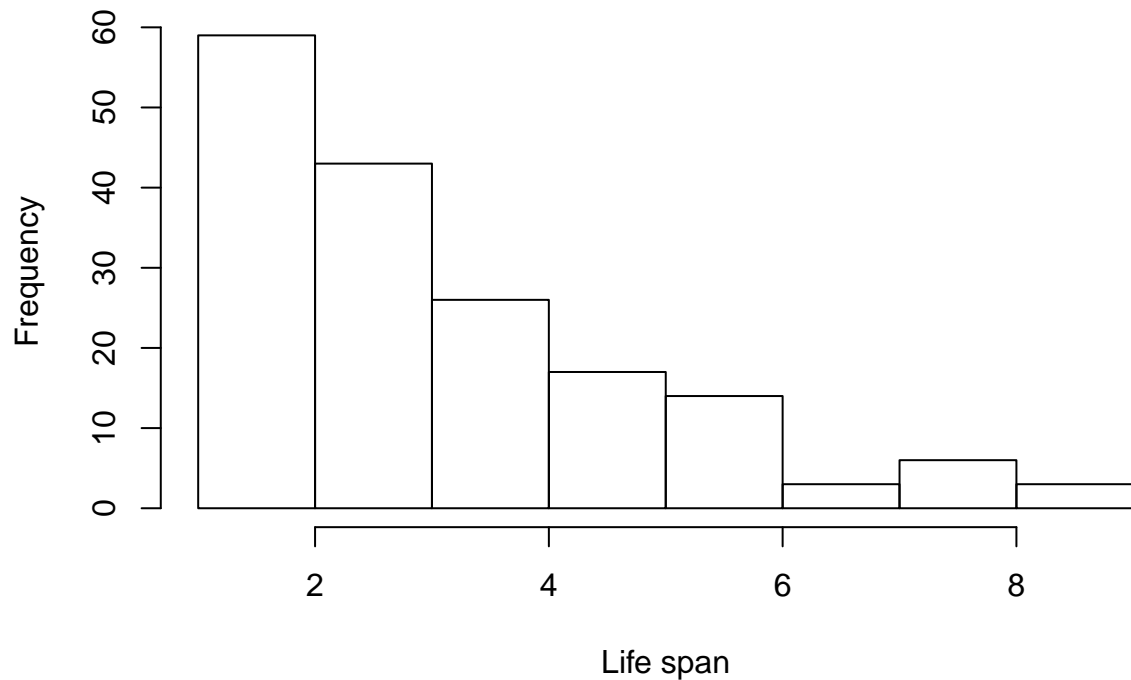
```
library(MASS)
```

Investigating the distribution of the fitness variables

We exclude samples for which we have no genetic data and unsuccessful first time breeders (by only selecting samples that have a value in the variables PdistPBR and ToSucLife_1014).

Life span

```
hist(data$LifeSpan[!is.na(data$PdistPBR)&!is.na(data$ToSucLife_1014)],main="",xlab="Life span",ylab="Fr
```



```
mean(data$LifeSpan[!is.na(data$PdistPBR)&!is.na(data$ToSucLife_1014)])
```

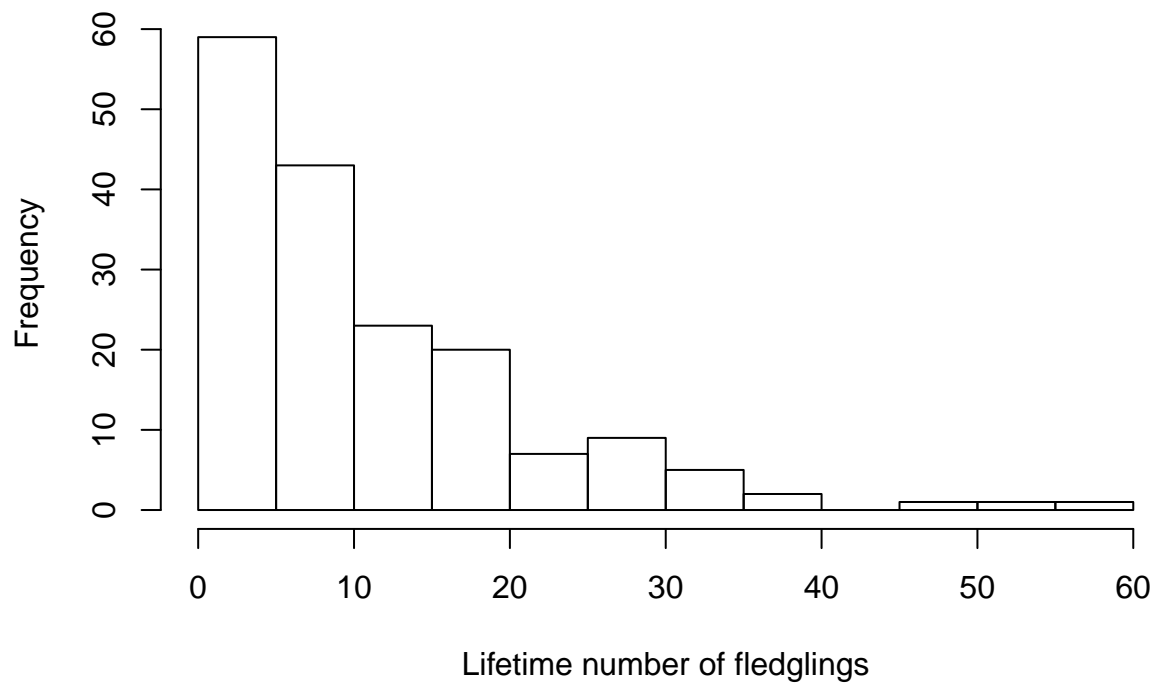
```
## [1] 3.473684
```

```
(sd(data$LifeSpan[!is.na(data$PdistPBR)&!is.na(data$ToSucLife_1014)]))^2
```

```
## [1] 3.603715
```

Lifetime number of fledglings

```
hist(data$ToSucLife_1014[!is.na(data$PdistPBR)&!is.na(data$ToSucLife_1014)],main="",xlab="Lifetime number of fledglings")
```



```
mean(data$ToSucLife_1014[!is.na(data$PdistPBR)&!is.na(data$ToSucLife_1014)])
```

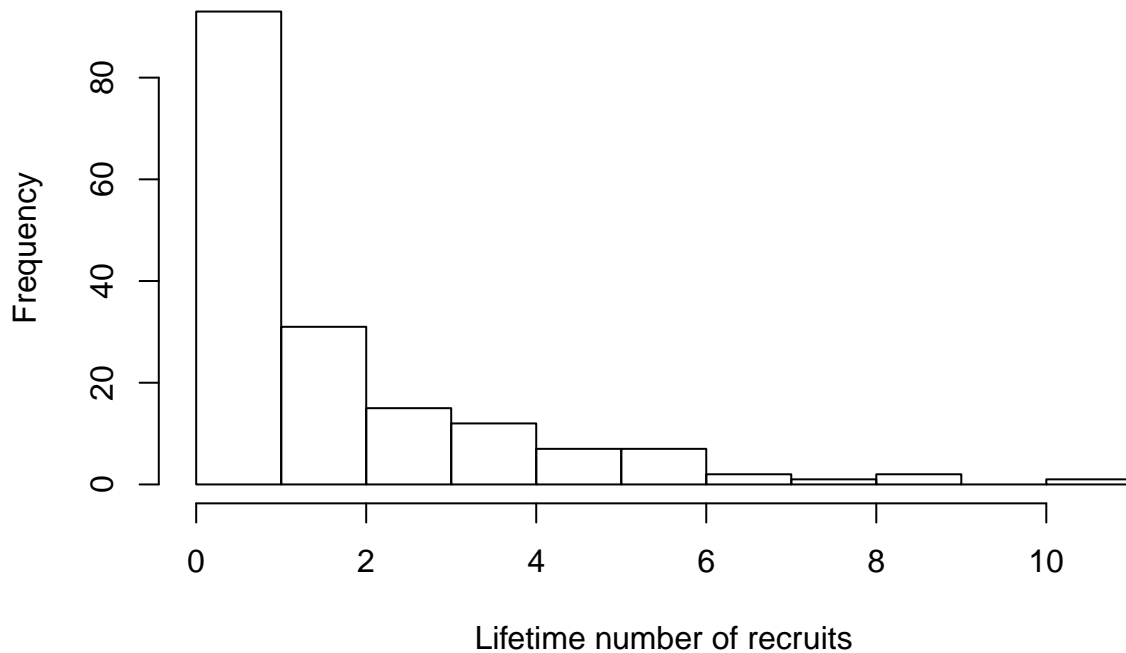
```
## [1] 12.05263
```

```
(sd(data$ToSucLife_1014[!is.na(data$PdistPBR)&!is.na(data$ToSucLife_1014)]))^2
```

```
## [1] 99.45015
```

Lifetime number of recruits

```
hist(data$RecruLife_1014[!is.na(data$PdistPBR)&!is.na(data$ToSucLife_1014)],main="",xlab="Lifetime number of recruits",ylab="Frequency")
```



```
mean(data$RecruLife_1014[!is.na(data$PdistPBR)&!is.na(data$ToSucLife_1014)])
```

```
## [1] 1.900585
```

```
(sd(data$RecruLife_1014[!is.na(data$PdistPBR)&!is.na(data$ToSucLife_1014)]))^2
```

```
## [1] 4.395941
```

Life span, lifetime number of fledglings, and lifetime number of recruits all appear to follow negative binomial distributions.

For the GLM models, we have estimated the overdispersion parameter of the negative binomial distributions using a maximum likelihood based method (kfit function) presented in [Michael J Crawley, The R Book, Wiley, 2007].

Function to test for overdispersion in GLM models using Pearson residuals (courtesy of Ben Bolker).

```
overdisp_fun <- function(model) {
  rdf <- df.residual(model)
  rp <- residuals(model,type="pearson")
  Pearson.chisq <- sum(rp^2)
  pratt <- Pearson.chisq/rdf
  pval <- pchisq(Pearson.chisq, df=rdf, lower.tail=FALSE)
```

```
c(chisq=Pearson.chisq,ratio=prat,rdf=rdf,p=pval)
}
```

Modeling the effects of MHC-I functional divergence on life span

GLM of life span on total number of alleles and P-distance PBR in males only

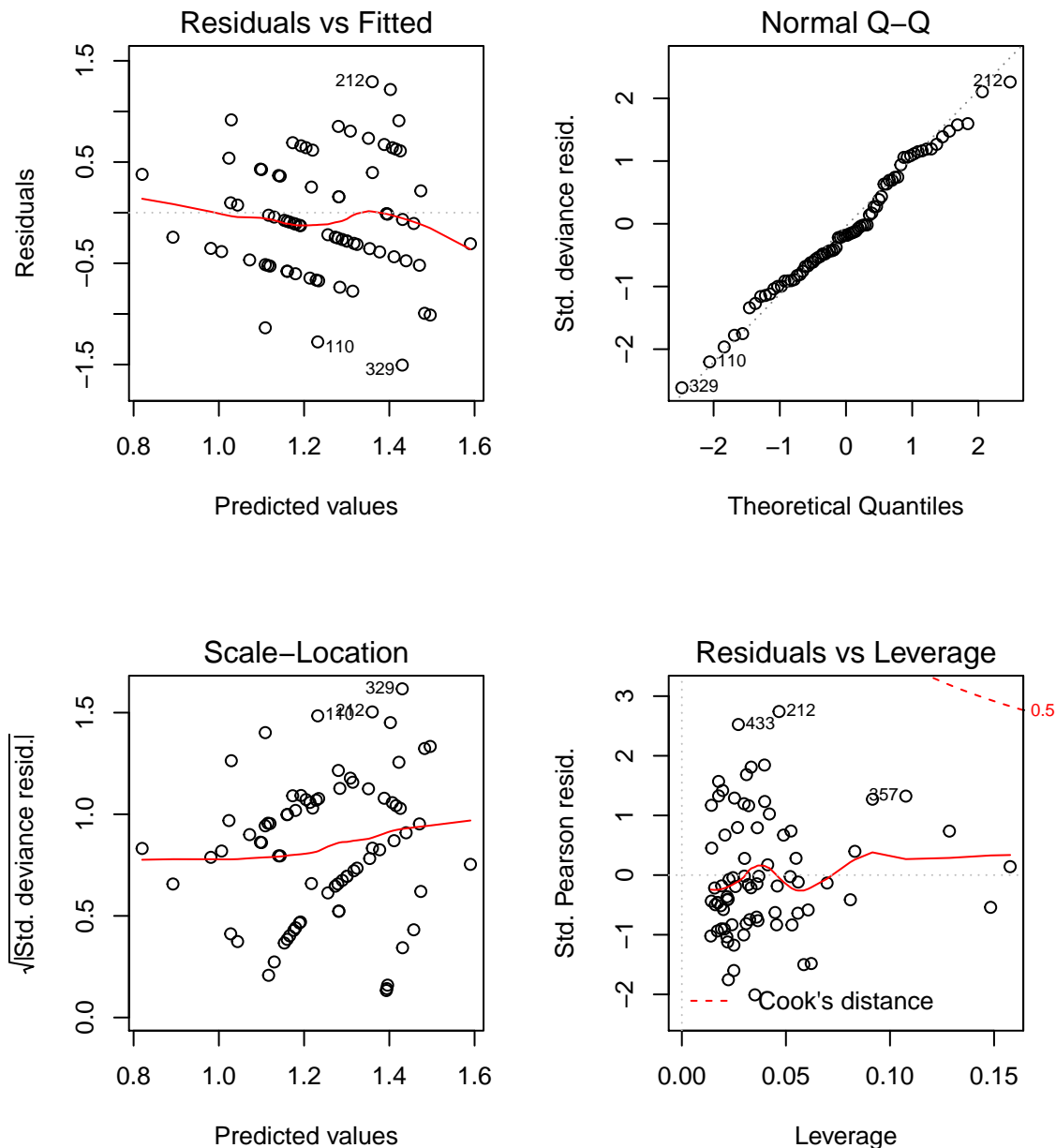
```
fm1_PBR <- glm(LifeSpan~Total.no.alleles+PdistPBR,negative.binomial(theta=5.14632,link="log"),data=data)
s1_PBR <- summary(fm1_PBR)
s1_PBR
```

```
##
## Call:
## glm(formula = LifeSpan ~ Total.no.alleles + PdistPBR, family = negative.binomial(theta = 5.14632,
##      link = "log"), data = data.males[!is.na(PdistPBR) & !is.na(ToSucLife_1014),
##      ])
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -1.5050  -0.4432  -0.1066   0.3828   1.2933
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    -2.76368     1.30462  -2.118  0.03755 *
## Total.no.alleles  0.02781     0.01811   1.535  0.12902
## PdistPBR        11.66330     3.67272   3.176  0.00219 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for Negative Binomial(5.1463) family taken to be 0.3432786)
##
##      Null deviance: 28.754  on 75  degrees of freedom
## Residual deviance: 25.249  on 73  degrees of freedom
## AIC: 303.35
##
## Number of Fisher Scoring iterations: 4
```

```
overdisp_fun(fm1_PBR)
```

```
##      chisq      ratio      rdf      p
## 25.0593297  0.3432785 73.0000000 1.0000000
```

```
par(mfrow=c(2,2))
plot(fm1_PBR)
```



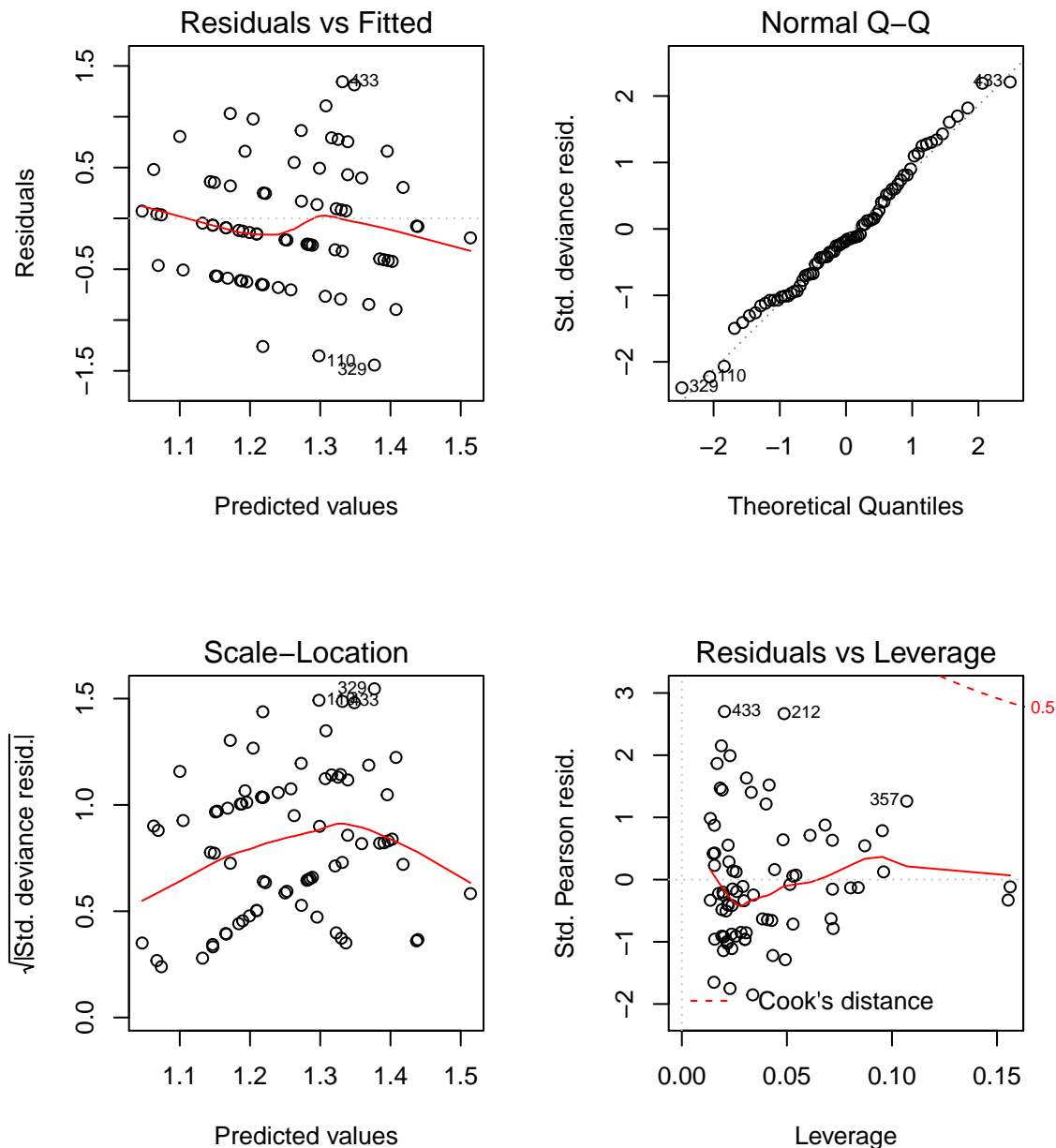
GLM of life span on total number of alleles and P-distance PSS in males only

```
fm1_PSS <- glm(LifeSpan~Total.no.alleles+PdistPSS,negative.binomial(theta=5.14632,link="log"),data=data)
s1_PSS <- summary(fm1_PSS)
s1_PSS
```

```
##
## Call:
## glm(formula = LifeSpan ~ Total.no.alleles + PdistPSS, family = negative.binomial(theta = 5.14632,
##   link = "log"), data = data.males[!is.na(PdistPSS) & !is.na(ToSucLife_1014),
##   ])
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -1.4432  -0.4743  -0.1057   0.3282   1.3444
##
```

```
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)   -2.31280    1.75402  -1.319   0.1914
## Total.no.alleles 0.02288    0.02022   1.132   0.2615
## PdistPSS       9.01796    4.32516   2.085   0.0406 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for Negative Binomial(5.1463) family taken to be 0.3774148)
##
##      Null deviance: 28.754  on 75  degrees of freedom
## Residual deviance: 27.094  on 73  degrees of freedom
## AIC: 305.19
##
## Number of Fisher Scoring iterations: 4
overdisp_fun(fm1_PSS)

##      chisq      ratio      rdf      p
## 27.5512777 0.3774148 73.0000000 0.9999997
par(mfrow=c(2,2))
plot(fm1_PSS)
```



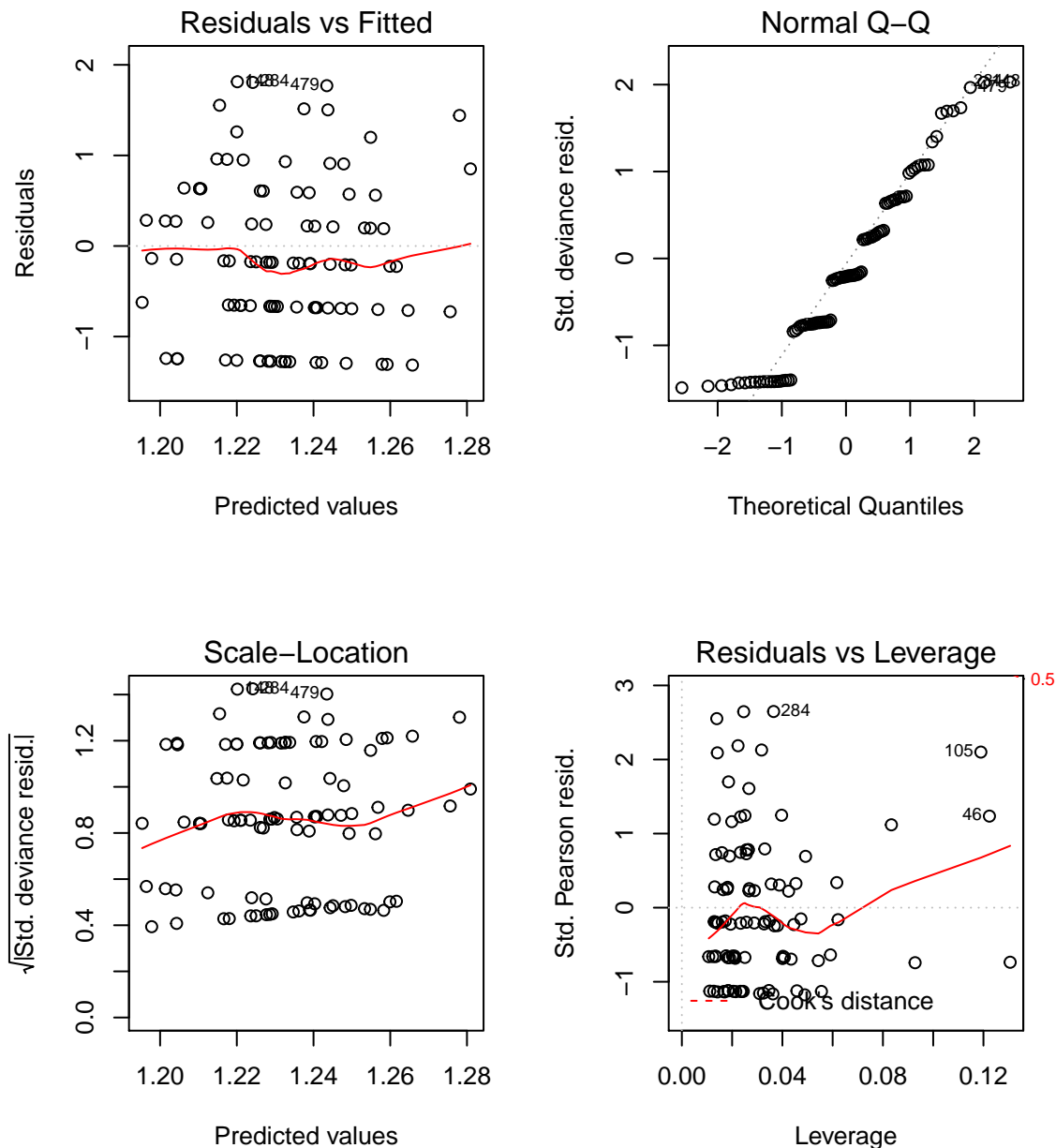
GLM of life span on total number of alleles and P-distance PBR in females only

```
fm2_PBR <- glm(LifeSpan~Total.no.alleles+PdistPBR,negative.binomial(theta=5.14632,link="log"),data=data)
s2_PBR <- summary(fm2_PBR)
s2_PBR
```

```
##
## Call:
## glm(formula = LifeSpan ~ Total.no.alleles + PdistPBR, family = negative.binomial(theta = 5.14632,
##   link = "log"), data = data.females[!is.na(PdistPBR) & !is.na(ToSucLife_1014),
##   ])
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -1.3148  -0.6869  -0.1884   0.5797   1.8134
##
```

```
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)    1.264632   1.786757   0.708   0.481
## Total.no.alleles 0.005697   0.022879   0.249   0.804
## PdistPBR      -0.346263   5.370565  -0.064   0.949
##
## (Dispersion parameter for Negative Binomial(5.1463) family taken to be 0.8213017)
##
##      Null deviance: 72.819  on 94  degrees of freedom
## Residual deviance: 72.750  on 92  degrees of freedom
## AIC: 404.93
##
## Number of Fisher Scoring iterations: 4
overdisp_fun(fm2_PBR)

##      chisq      ratio      rdf      p
## 75.5597338  0.8213015 92.0000000 0.8930381
par(mfrow=c(2,2))
plot(fm2_PBR)
```

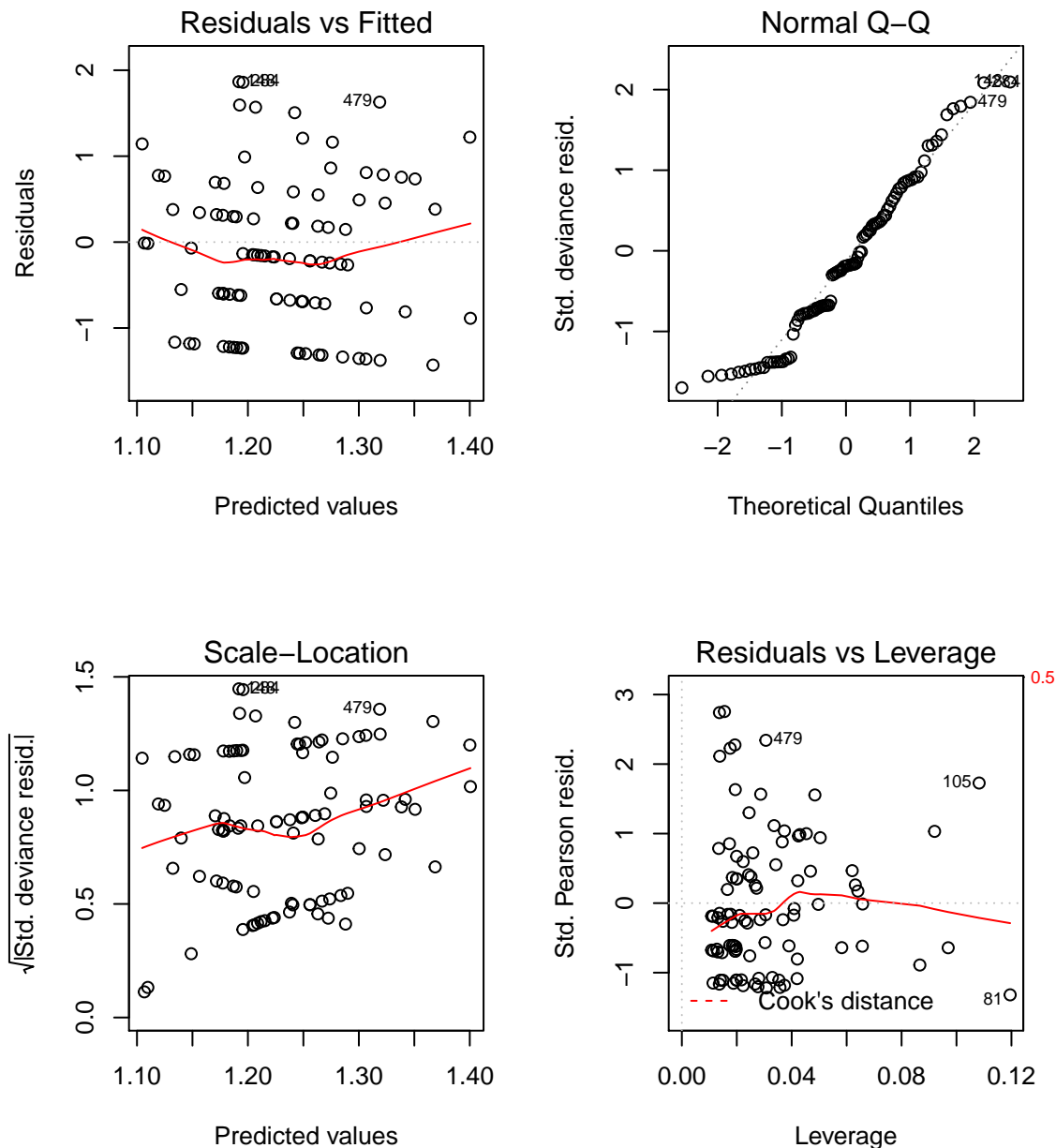
GLM of life span on total number of alleles and P-distance PSS in females only

```
fm2_PSS <- glm(LifeSpan~Total.no.alleles+PdistPSS,negative.binomial(theta=5.14632,link="log"),data=data)
s2_PSS <- summary(fm2_PSS)
s2_PSS
```

```
##
## Call:
## glm(formula = LifeSpan ~ Total.no.alleles + PdistPSS, family = negative.binomial(theta = 5.14632,
##   link = "log"), data = data.females[!is.na(PdistPSS) & !is.na(ToSucLife_1014),
##   ])
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -1.4313  -0.6993  -0.1710   0.4724   1.8661
##
```

```
## Coefficients:
##           Estimate Std. Error t value Pr(>|t|)
## (Intercept)   3.179939   2.035643   1.562   0.122
## Total.no.alleles -0.001591   0.022660  -0.070   0.944
## PdistPSS      -5.357085   5.362257  -0.999   0.320
##
## (Dispersion parameter for Negative Binomial(5.1463) family taken to be 0.8063923)
##
##      Null deviance: 72.819  on 94  degrees of freedom
## Residual deviance: 71.945  on 92  degrees of freedom
## AIC: 404.13
##
## Number of Fisher Scoring iterations: 4
overdisp_fun(fm2_PSS)

##      chisq      ratio      rdf      p
## 74.1880032  0.8063913 92.0000000 0.9129155
par(mfrow=c(2,2))
plot(fm2_PSS)
```



GLM of life span on total number of alleles and P-distance PBR in both sexes

```
fm3_PBR <- glm(LifeSpan~Total.no.alleles+PdistPBR+Sex+Total.no.alleles:Sex+PdistPBR:Sex,negative.binomial)
s3_PBR <- summary(fm3_PBR)
s3_PBR
```

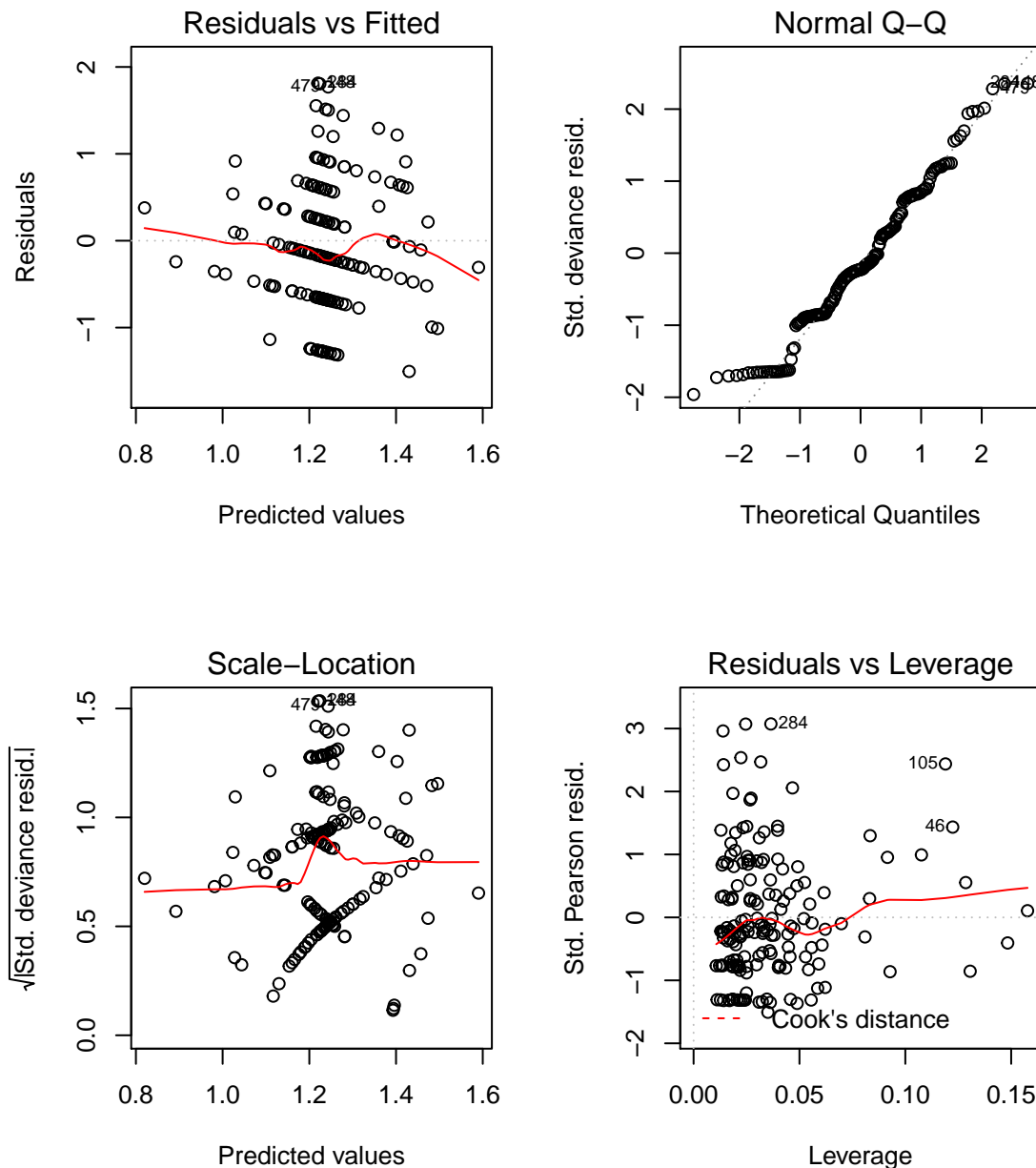
```
##
## Call:
## glm(formula = LifeSpan ~ Total.no.alleles + PdistPBR + Sex +
##     Total.no.alleles:Sex + PdistPBR:Sex, family = negative.binomial(theta = 5.14632,
##     link = "log"), data = data[!is.na(PdistPBR) & !is.na(ToSucLife_1014),
##     ])
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -1.5050  -0.6573  -0.1750   0.4280   1.8134
```

```
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      1.264632   1.539616   0.821   0.4126
## Total.no.alleles  0.005697   0.019714   0.289   0.7730
## PdistPBR         -0.346263   4.627717  -0.075   0.9404
## Sexmale          -4.028310   2.322488  -1.734   0.0847 .
## Total.no.alleles:Sexmale 0.022109   0.031166   0.709   0.4791
## PdistPBR:Sexmale   12.009561   6.736310   1.783   0.0765 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for Negative Binomial(5.1463) family taken to be 0.6098127)
##
##      Null deviance: 101.638  on 170  degrees of freedom
## Residual deviance:  97.999  on 165  degrees of freedom
## AIC: 708.28
##
## Number of Fisher Scoring iterations: 4

overdisp_fun(fm3_PBR)

##      chisq      ratio      rdf      p
## 100.6190635  0.6098125 165.0000000  0.9999804

par(mfrow=c(2,2))
plot(fm3_PBR)
```



GLM of life span on total number of alleles and P-distance PSS in both sexes

```
fm3_PSS <- glm(LifeSpan~Total.no.alleles+PdistPSS+Sex+Total.no.alleles:Sex+PdistPSS:Sex,negative.binomial)
s3_PSS <- summary(fm3_PSS)
s3_PSS
```

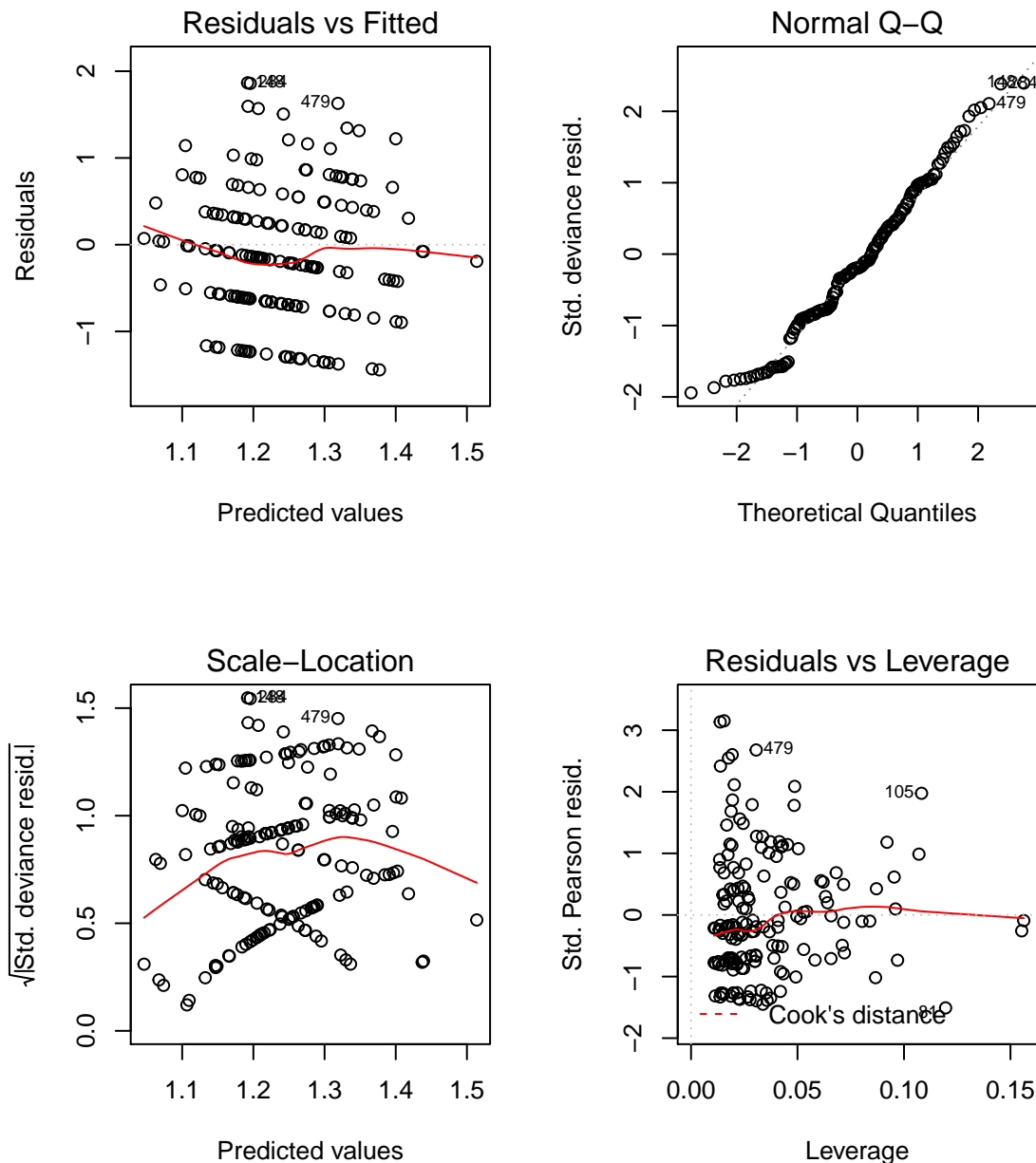
```
##
## Call:
## glm(formula = LifeSpan ~ Total.no.alleles + PdistPSS + Sex +
##       Total.no.alleles:Sex + PdistPSS:Sex, family = negative.binomial(theta = 5.14632,
##       link = "log"), data = data[!is.na(PdistPSS) & !is.na(ToSucLife_1014),
##       ])
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -1.4432  -0.6218  -0.1523   0.3805   1.8661
```

```
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      3.179939   1.780045   1.786  0.0759 .
## Total.no.alleles -0.001591   0.019815  -0.080  0.9361
## PdistPSS         -5.357085   4.688965  -1.142  0.2549
## Sexmale          -5.492737   2.862678  -1.919  0.0567 .
## Total.no.alleles:Sexmale 0.024473   0.032567   0.751  0.4534
## PdistPSS:Sexmale   14.375044   7.249065   1.983  0.0490 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for Negative Binomial(5.1463) family taken to be 0.6166023)
##
##      Null deviance: 101.638  on 170  degrees of freedom
## Residual deviance:  99.039  on 165  degrees of freedom
## AIC: 709.32
##
## Number of Fisher Scoring iterations: 4

overdisp_fun(fm3_PSS)

##      chisq      ratio      rdf      p
## 101.7392809  0.6166017 165.0000000  0.9999717

par(mfrow=c(2,2))
plot(fm3_PSS)
```



Modeling the effects of MHC-I functional divergence on lifetime number of fledgings

GLM of lifetime number of fledgings on total number of alleles and P-distance PBR in males only

```
fm4_PBR <- glm(ToSucLife_1014~Total.no.alleles+PdistPBR,negative.binomial(theta=1.656555,link="log"),data=s4_PBR)
s4_PBR <- summary(fm4_PBR)
s4_PBR
```

```
##
```

```
## Call:
```

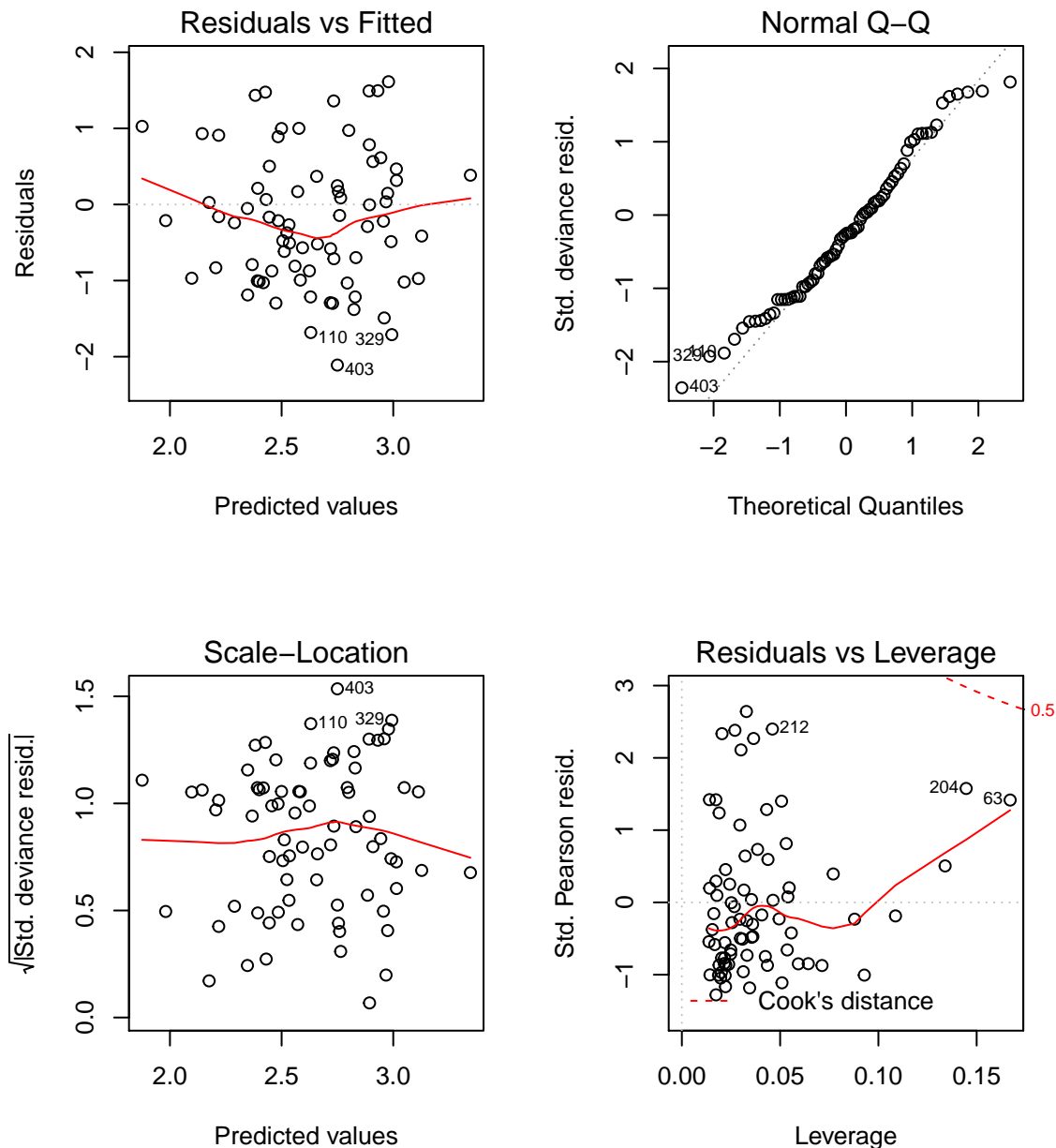
```
## glm(formula = ToSucLife_1014 ~ Total.no.alleles + PdistPBR, family = negative.binomial(theta = 1.656555, link = "log"), data = s4_PBR)
```

```

##      link = "log"), data = data.males[!is.na(PdistPBR) & !is.na(ToSucLife_1014),
##      ])
##
## Deviance Residuals:
##      Min        1Q    Median        3Q        Max
## -2.1104   -0.8979   -0.2296    0.3733    1.6130
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)   -4.77799     2.36035   -2.024  0.04660 *
## Total.no.alleles  0.04216     0.03285    1.283  0.20344
## PdistPBR       21.95219     6.66919    3.292  0.00154 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for Negative Binomial(1.6566) family taken to be 0.8162788)
##
##      Null deviance: 71.194  on 75  degrees of freedom
## Residual deviance: 61.065  on 73  degrees of freedom
## AIC: 548.69
##
## Number of Fisher Scoring iterations: 5
overdisp_fun(fm4_PBR)

##      chisq      ratio      rdf      p
## 59.5882720  0.8162777 73.0000000 0.8708043
par(mfrow=c(2,2))
plot(fm4_PBR)

```

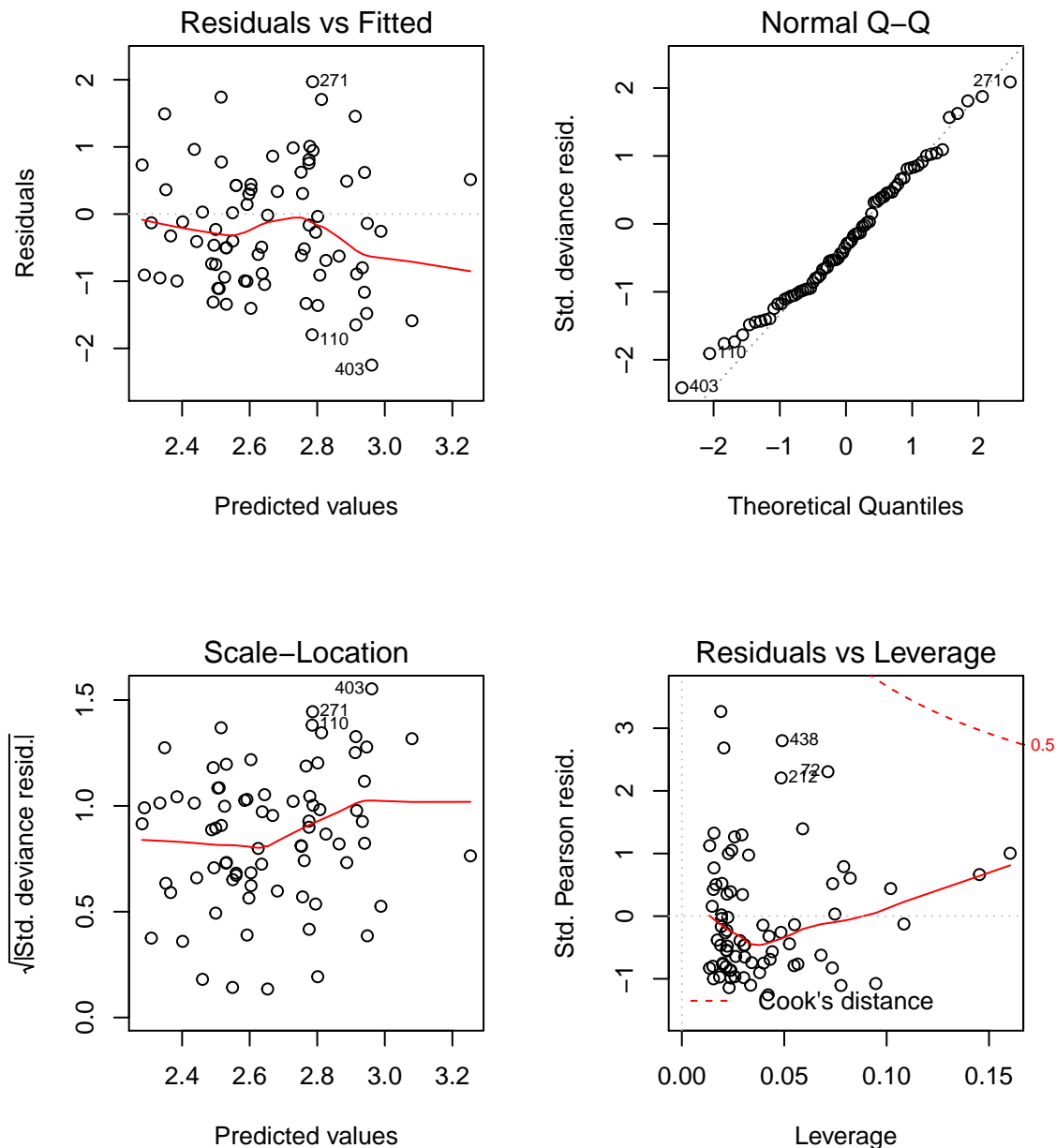
GLM of lifetime number of fledgings on total number of alleles and P-distance PSS in males only

```
fm4_PSS <- glm(ToSucLife_1014~Total.no.alleles+PdistPSS,negative.binomial(theta=1.656555,link="log"),data=males)
s4_PSS <- summary(fm4_PSS)
s4_PSS
```

```
##
## Call:
## glm(formula = ToSucLife_1014 ~ Total.no.alleles + PdistPSS, family = negative.binomial(theta = 1.656555, link = "log"), data = data.males[!is.na(PdistPSS) & !is.na(ToSucLife_1014)],
##      )
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -2.2487  -0.9171  -0.2981   0.4302   1.9706
```

```
##
## Coefficients:
##           Estimate Std. Error t value Pr(>|t|)
## (Intercept)   -3.72706     3.21410  -1.160   0.2500
## Total.no.alleles  0.02535     0.03699   0.685   0.4953
## PdistPSS       16.73262     7.94661   2.106   0.0387 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for Negative Binomial(1.6566) family taken to be 0.9075688)
##
##      Null deviance: 71.194  on 75  degrees of freedom
## Residual deviance: 66.568  on 73  degrees of freedom
## AIC: 554.19
##
## Number of Fisher Scoring iterations: 6
overdisp_fun(fm4_PSS)

##      chisq      ratio      rdf      p
## 66.2526731  0.9075709 73.0000000 0.6988037
par(mfrow=c(2,2))
plot(fm4_PSS)
```



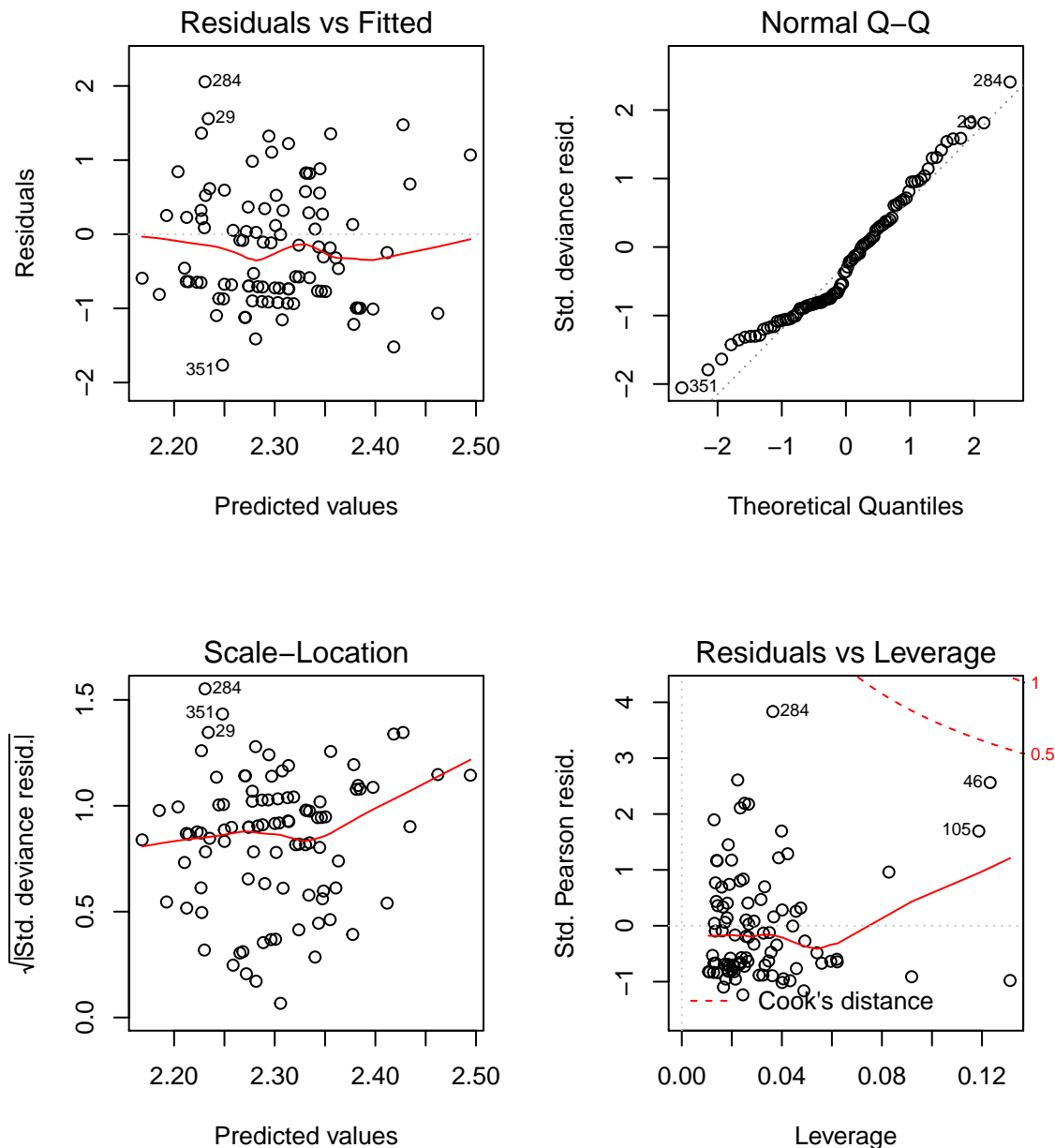
GLM of lifetime number of fledgings on total number of alleles and P-distance PBR in females only

```
fm5_PBR <- glm(ToSucLife_1014~Total.no.alleles+PdistPBR,negative.binomial(theta=1.656555,link="log"),data=females)
s5_PBR <- summary(fm5_PBR)
s5_PBR
```

```
##
## Call:
## glm(formula = ToSucLife_1014 ~ Total.no.alleles + PdistPBR, family = negative.binomial(theta = 1.656555, link = "log"), data = data.females[!is.na(PdistPBR) & !is.na(ToSucLife_1014)],
##      )
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -1.7646  -0.7670  -0.3059   0.3335   2.0569
```

```
##
## Coefficients:
##           Estimate Std. Error t value Pr(>|t|)
## (Intercept)    3.19732    2.06239   1.550   0.125
## Total.no.alleles 0.01181    0.02644   0.447   0.656
## PdistPBR      -3.38634    6.19942  -0.546   0.586
##
## (Dispersion parameter for Negative Binomial(1.6566) family taken to be 0.7562186)
##
##      Null deviance: 63.653  on 94  degrees of freedom
## Residual deviance: 63.063  on 92  degrees of freedom
## AIC: 618.72
##
## Number of Fisher Scoring iterations: 6
overdisp_fun(fm5_PBR)

##      chisq      ratio      rdf      p
## 69.5720925  0.7562184 92.0000000 0.9608471
par(mfrow=c(2,2))
plot(fm5_PBR)
```



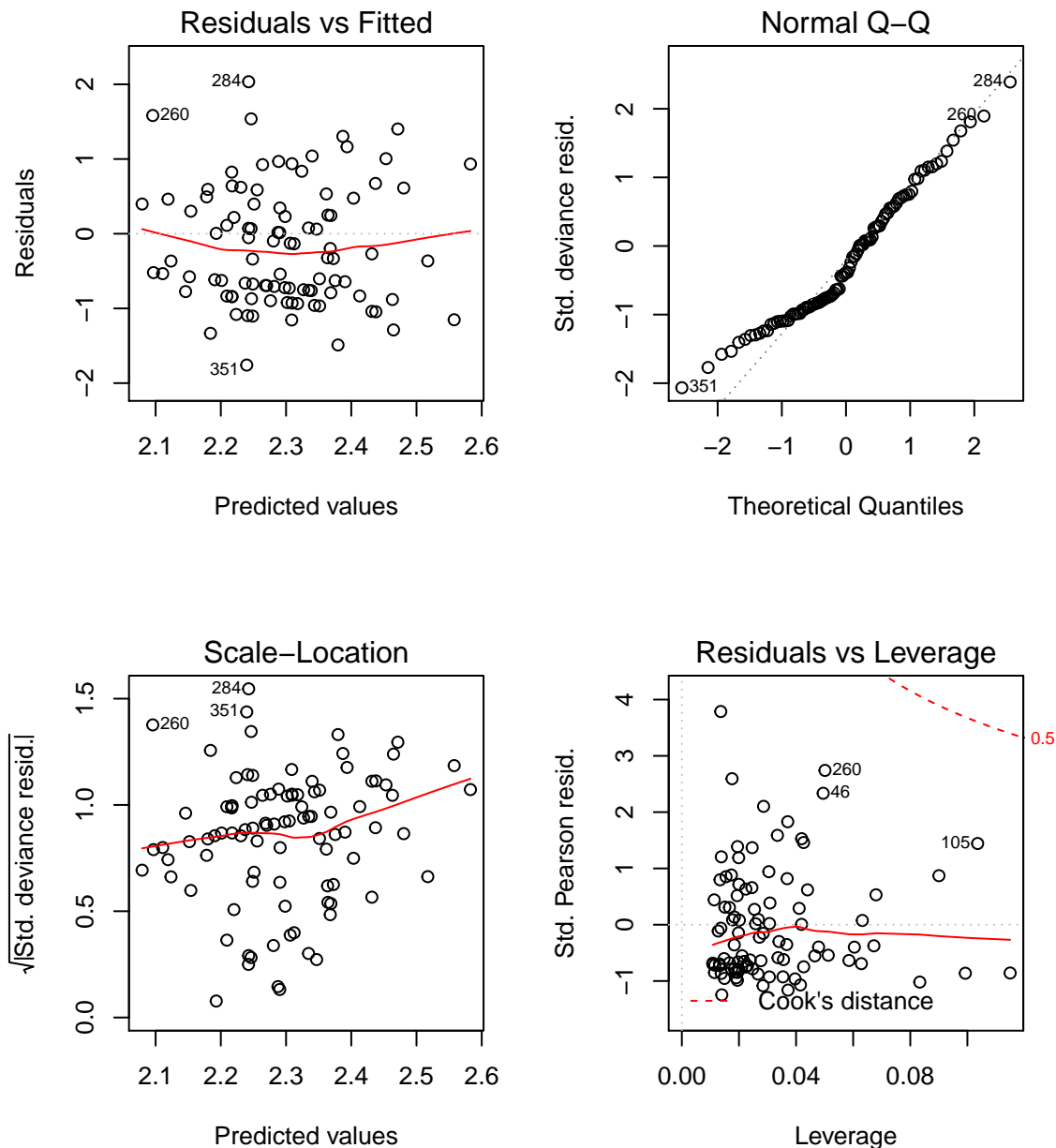
GLM of lifetime number of fledgings on total number of alleles and P-distance PSS in females only

```
fm5_PSS <- glm(ToSucLife_1014~Total.no.alleles+PdistPSS,negative.binomial(theta=1.656555,link="log"),data=females)
s5_PSS <- summary(fm5_PSS)
s5_PSS
```

```
##
## Call:
## glm(formula = ToSucLife_1014 ~ Total.no.alleles + PdistPSS, family = negative.binomial(theta = 1.656555, link = "log"), data = data.females[!is.na(PdistPSS) & !is.na(ToSucLife_1014),])
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -1.7586  -0.7825  -0.3324   0.4298   2.0345
```

```
##
## Coefficients:
##           Estimate Std. Error t value Pr(>|t|)
## (Intercept)    5.08582    2.35264   2.162  0.0332 *
## Total.no.alleles 0.00407    0.02605   0.156  0.8762
## PdistPSS       -7.90094    6.19254  -1.276  0.2052
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for Negative Binomial(1.6566) family taken to be 0.7343895)
##
##      Null deviance: 63.653  on 94  degrees of freedom
## Residual deviance: 62.076  on 92  degrees of freedom
## AIC: 617.73
##
## Number of Fisher Scoring iterations: 5
overdisp_fun(fm5_PSS)

##      chisq      ratio      rdf      p
## 67.5638913  0.7343901 92.0000000  0.9738731
par(mfrow=c(2,2))
plot(fm5_PSS)
```



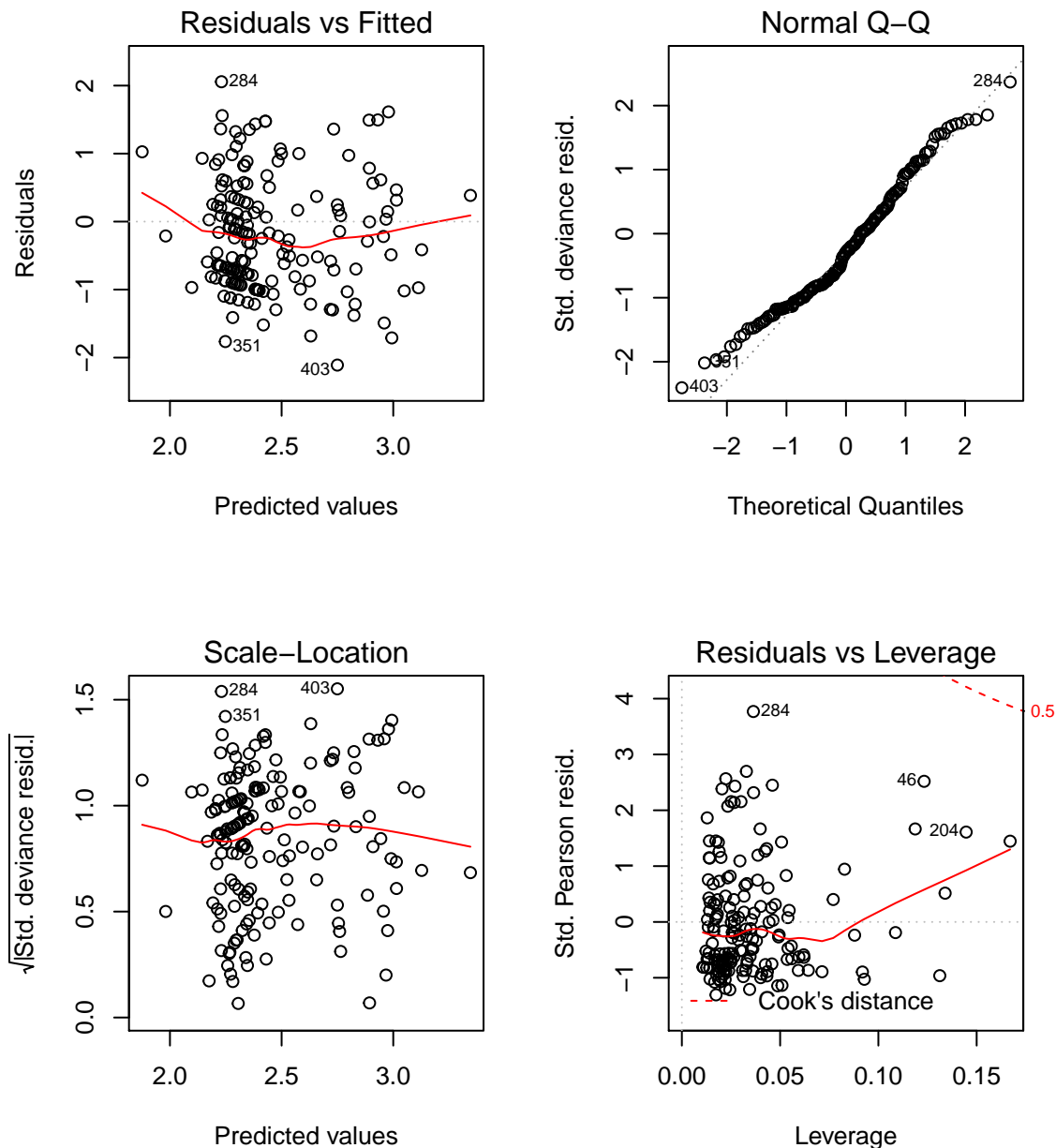
GLM of lifetime number of fledgings on total number of alleles and P-distance PBR in both sexes

```
fm6_PBR <- glm(ToSucLife_1014~Total.no.alleles+PdistPBR+Sex+Total.no.alleles:Sex+PdistPBR:Sex,negative.binomial(theta = 1.656555, link = "log"), data = data[!is.na(PdistPBR) & !is.na(ToSucLife_1014),])
s6_PBR <- summary(fm6_PBR)
s6_PBR
```

```
##
## Call:
## glm(formula = ToSucLife_1014 ~ Total.no.alleles + PdistPBR +
##      Sex + Total.no.alleles:Sex + PdistPBR:Sex, family = negative.binomial(theta = 1.656555,
##      link = "log"), data = data[!is.na(PdistPBR) & !is.na(ToSucLife_1014),
##      ])
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
```

```
## -2.1104 -0.8215 -0.2475 0.3559 2.0569
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      3.19732    2.09831   1.524  0.12948
## Total.no.alleles  0.01181    0.02690   0.439  0.66129
## PdistPBR        -3.38634    6.30739  -0.537  0.59207
## Sexmale          -7.97518    3.12179  -2.555  0.01153 *
## Total.no.alleles:Sexmale 0.03035    0.04194   0.724  0.47029
## PdistPBR:Sexmale  25.33822    9.07946   2.791  0.00588 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for Negative Binomial(1.6566) family taken to be 0.7827894)
##
##    Null deviance: 143.78  on 170  degrees of freedom
## Residual deviance: 124.13  on 165  degrees of freedom
## AIC: 1167.4
##
## Number of Fisher Scoring iterations: 6
overdisp_fun(fm6_PBR)

##          chisq          ratio          rdf          p
## 129.1602445    0.7827894 165.0000000    0.9821231
par(mfrow=c(2,2))
plot(fm6_PBR)
```

GLM of lifetime number of fledgings on total number of alleles and P-distance PSS in both sexes

```
fm6_PSS <- glm(ToSucLife_1014~Total.no.alleles+PdistPSS+Sex+Total.no.alleles:Sex+PdistPSS:Sex,negative.binomial(theta = 1.656555, link = "log"), data = data[!is.na(PdistPBR) & !is.na(ToSucLife_1014),])
s6_PSS <- summary(fm6_PSS)
s6_PSS
```

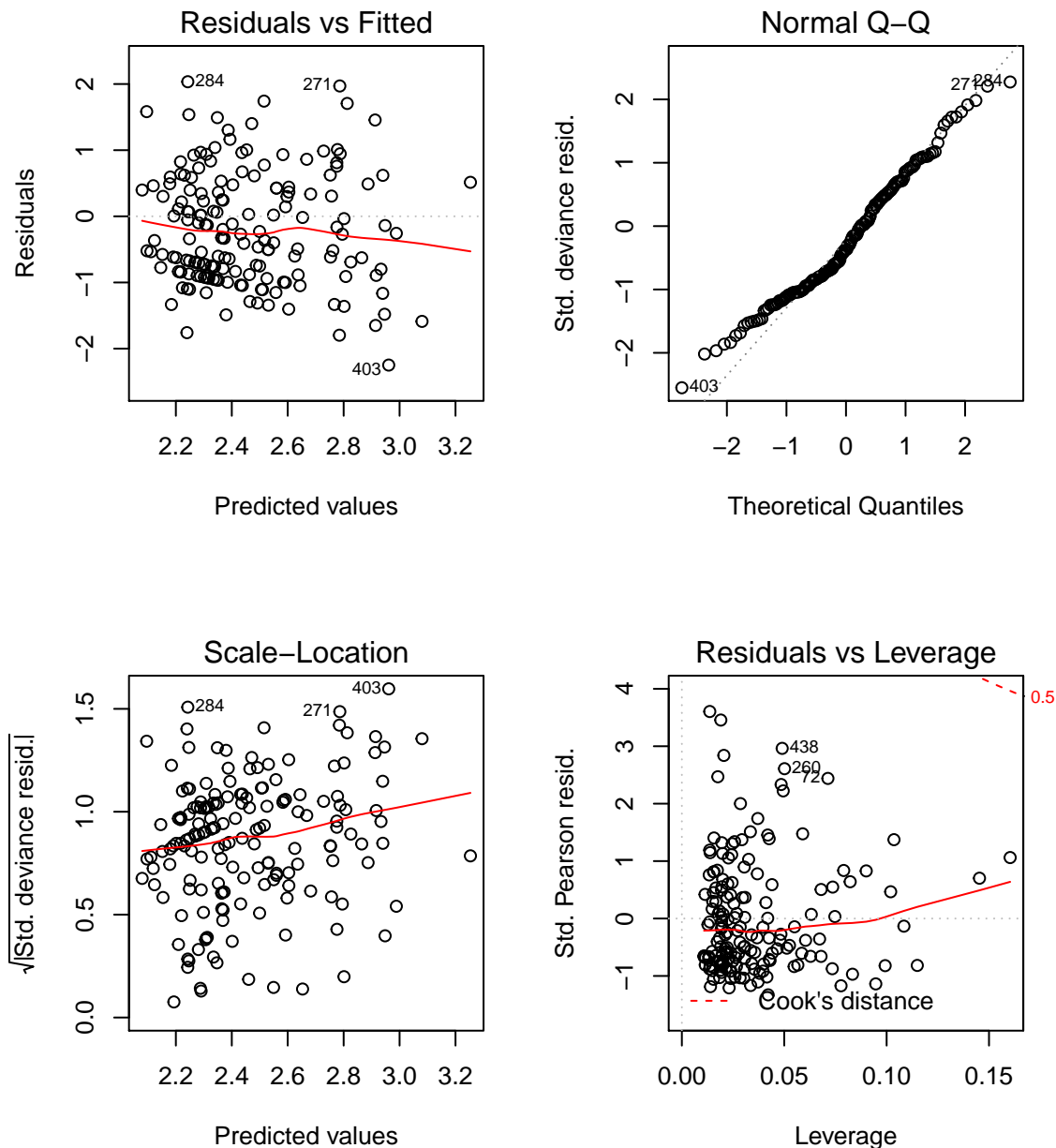
```
##
## Call:
## glm(formula = ToSucLife_1014 ~ Total.no.alleles + PdistPSS +
##     Sex + Total.no.alleles:Sex + PdistPSS:Sex, family = negative.binomial(theta = 1.656555,
##     link = "log"), data = data[!is.na(PdistPBR) & !is.na(ToSucLife_1014),
##     ])
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
```

```

## -2.2487 -0.8420 -0.3253 0.4339 2.0345
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      5.085983   2.472325   2.057  0.0412 *
## Total.no.alleles  0.004071   0.027371   0.149  0.8819
## PdistPSS         -7.901424   6.507563  -1.214  0.2264
## Sexmale          -8.813039   3.917111  -2.250  0.0258 *
## Total.no.alleles:Sexmale 0.021282   0.044408   0.479  0.6324
## PdistPSS:Sexmale  24.634040   9.938732   2.479  0.0142 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for Negative Binomial(1.6566) family taken to be 0.8110086)
##
##      Null deviance: 143.78  on 170  degrees of freedom
## Residual deviance: 128.64  on 165  degrees of freedom
## AIC: 1171.9
##
## Number of Fisher Scoring iterations: 6
overdisp_fun(fm6_PSS)

##      chisq      ratio      rdf      p
## 133.8165637  0.8110095 165.0000000  0.9641613
par(mfrow=c(2,2))
plot(fm6_PSS)

```



Modeling the effects of MHC-I functional divergence on lifetime number of recruits

GLM of lifetime number of recruits on total number of alleles and P-distance PBR in males only

```
fm7_PBR <- glm(RecruLife_1014~Total.no.alleles+PdistPBR,negative.binomial(theta=1.40551,link="log"),data=
s7_PBR <- summary(fm7_PBR)
s7_PBR
```

```
##
```

```
## Call:
```

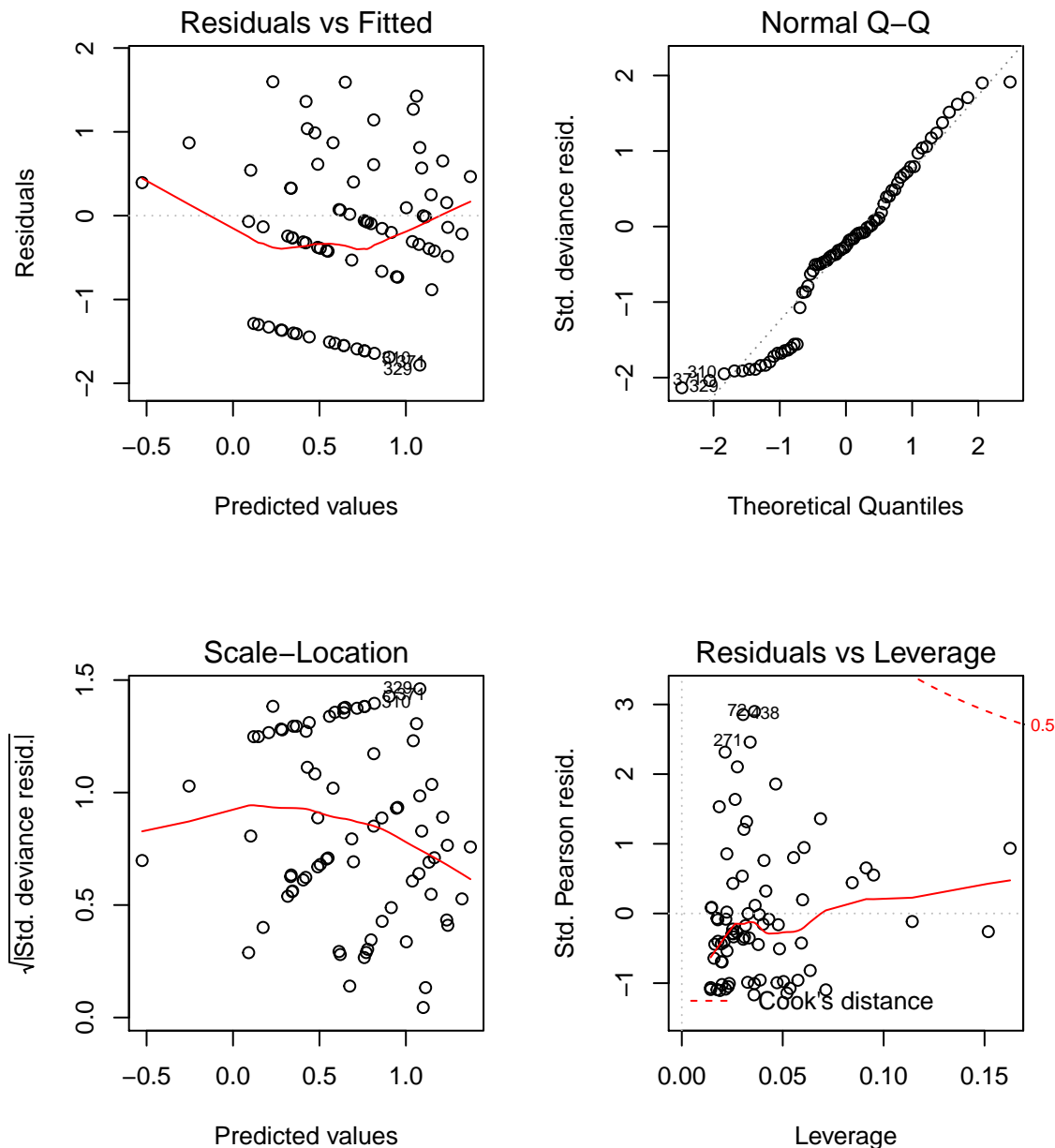
```
## glm(formula = RecruLife_1014 ~ Total.no.alleles + PdistPBR, family = negative.binomial(theta = 1.40551,
```

```

##      link = "log"), data = data.males[!is.na(PdistPBR) & !is.na(ToSucLife_1014),
##      ])
##
## Deviance Residuals:
##      Min        1Q      Median        3Q        Max
## -1.7826   -0.7714   -0.2091    0.3456    1.5977
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)   -9.69571     3.11922  -3.108  0.00268 **
## Total.no.alleles  0.09970     0.04266   2.337  0.02219 *
## PdistPBR       28.94496     8.73674   3.313  0.00144 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for Negative Binomial(1.4055) family taken to be 0.7232984)
##
##      Null deviance: 73.051  on 75  degrees of freedom
## Residual deviance: 64.076  on 73  degrees of freedom
## AIC: 290.62
##
## Number of Fisher Scoring iterations: 5
overdisp_fun(fm7_PBR)

##      chisq      ratio      rdf      p
## 52.8009289  0.7233004 73.0000000 0.9640887
par(mfrow=c(2,2))
plot(fm7_PBR)

```



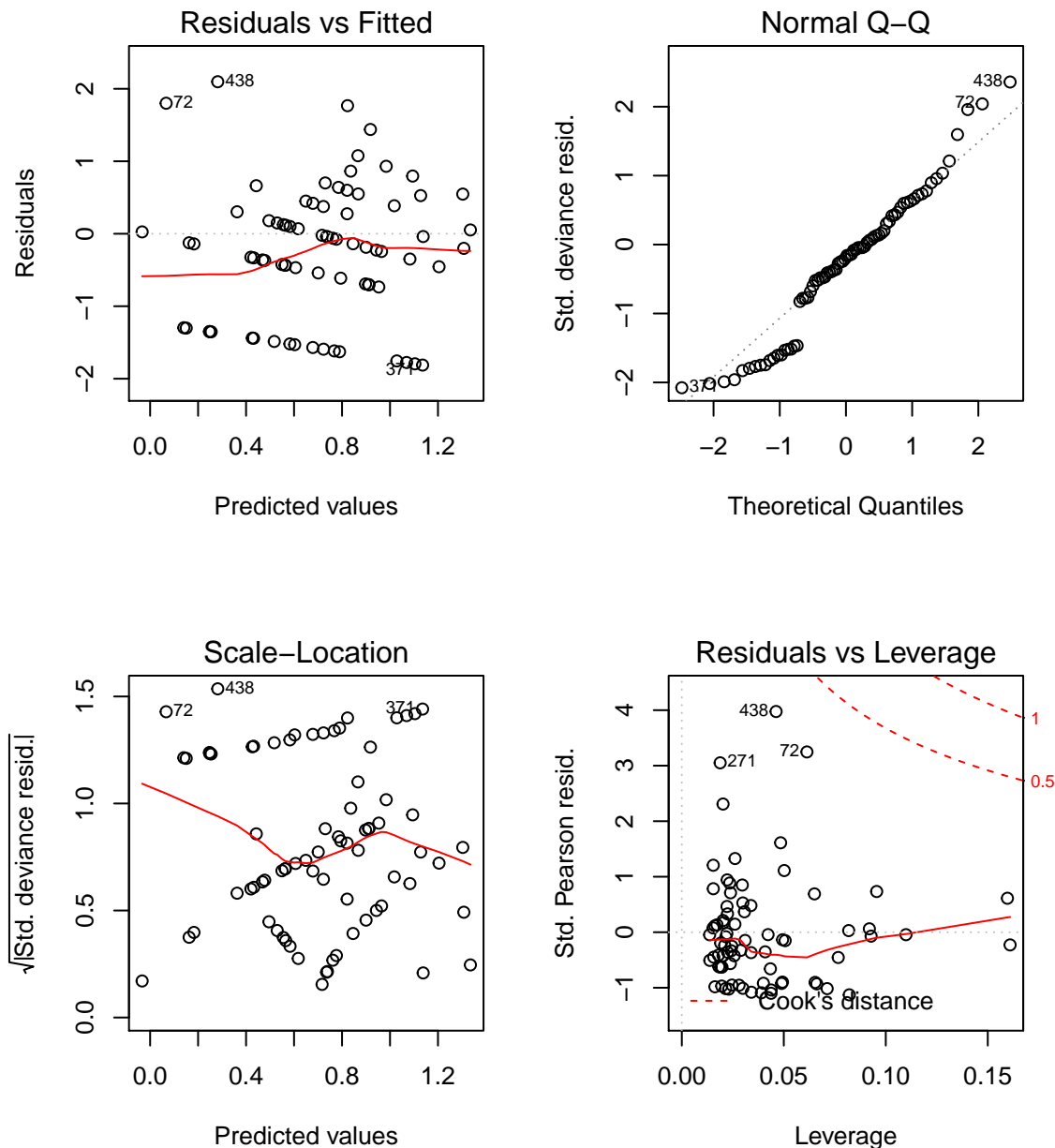
GLM of lifetime number of recruits on total number of alleles and P-distance PSS in males only

```
fm7_PSS <- glm(RecruLife_1014~Total.no.alleles+PdistPSS,negative.binomial(theta=1.40551,link="log"),data=
s7_PSS <- summary(fm7_PSS)
s7_PSS
```

```
##
## Call:
## glm(formula = RecruLife_1014 ~ Total.no.alleles + PdistPSS, family = negative.binomial(theta = 1.40551,
## link = "log"), data = data.males[!is.na(PdistPSS) & !is.na(ToSucLife_1014),
## ])
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -1.8120  -0.7114  -0.1635   0.3208   2.0971
```

```
##
## Coefficients:
##           Estimate Std. Error t value Pr(>|t|)
## (Intercept)  -10.26910     4.20981  -2.439   0.0171 *
## Total.no.alleles  0.09372     0.04826   1.942   0.0560 .
## PdistPSS       26.86065    10.33874   2.598   0.0113 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for Negative Binomial(1.4055) family taken to be 0.8291243)
##
##      Null deviance: 73.051  on 75  degrees of freedom
## Residual deviance: 67.128  on 73  degrees of freedom
## AIC: 293.67
##
## Number of Fisher Scoring iterations: 5
overdisp_fun(fm7_PSS)

##      chisq      ratio      rdf      p
## 60.5258756  0.8291216 73.0000000 0.8512463
par(mfrow=c(2,2))
plot(fm7_PSS)
```



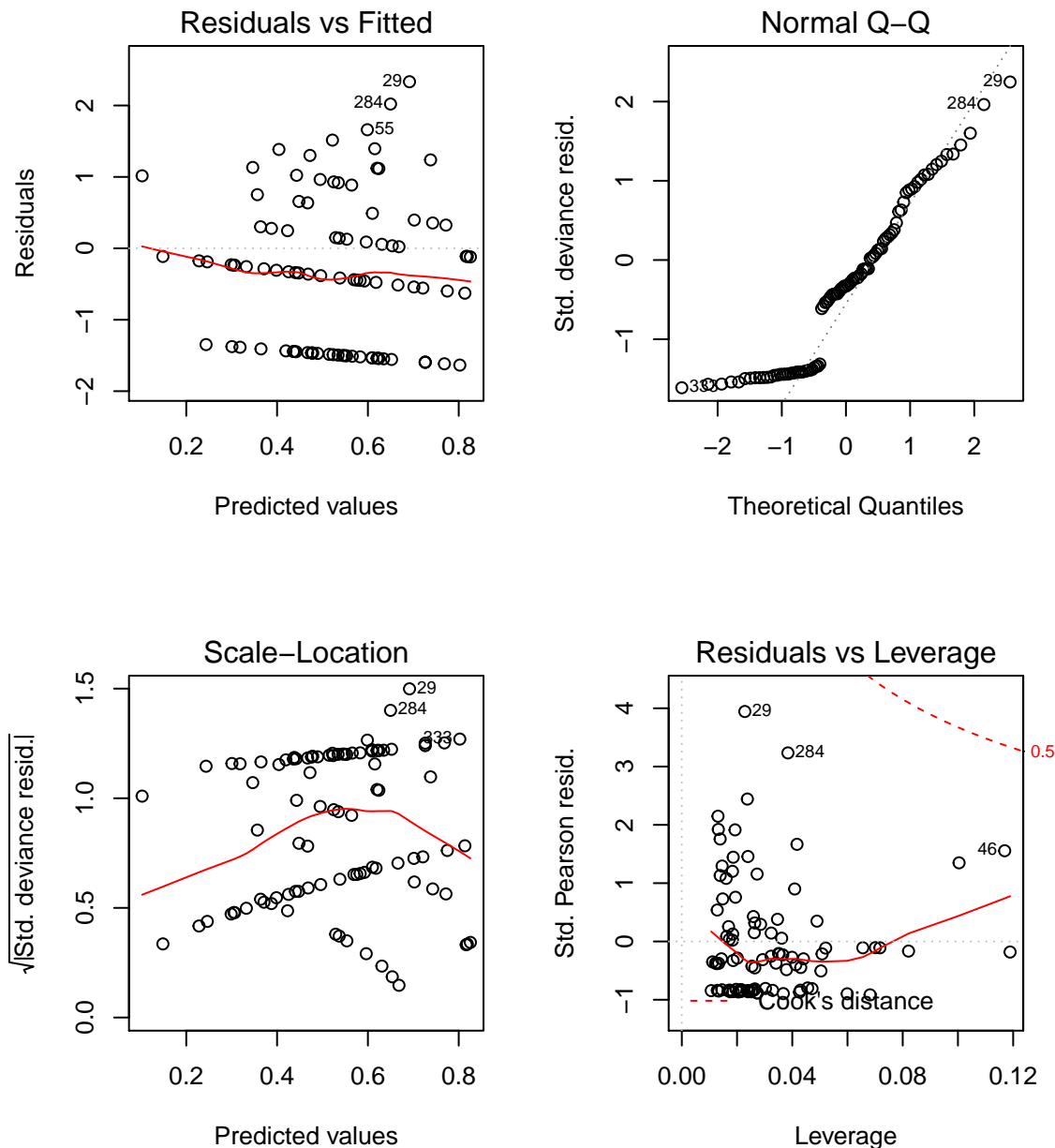
GLM of lifetime number of recruits on total number of alleles and P-distance PBR in females only

```
fm8_PBR <- glm(RecruLife_1014~Total.no.alleles+PdistPBR,negative.binomial(theta=1.40551,link="log"),data=females)
s8_PBR <- summary(fm8_PBR)
s8_PBR
```

```
##
## Call:
## glm(formula = RecruLife_1014 ~ Total.no.alleles + PdistPBR, family = negative.binomial(theta = 1.40551, link = "log"), data = data.females[!is.na(PdistPBR) & !is.na(ToSucLife_1014), ])
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -1.6347  -1.4625  -0.3396   0.3135   2.3327
```

```
##
## Coefficients:
##           Estimate Std. Error t value Pr(>|t|)
## (Intercept)  -0.53598    3.44587  -0.156   0.877
## Total.no.alleles -0.04161    0.04371  -0.952   0.344
## PdistPBR      5.22055   10.36608   0.504   0.616
##
## (Dispersion parameter for Negative Binomial(1.4055) family taken to be 1.102901)
##
##      Null deviance: 113.2  on 94  degrees of freedom
## Residual deviance: 111.5  on 92  degrees of freedom
## AIC: 345.37
##
## Number of Fisher Scoring iterations: 5
overdisp_fun(fm8_PBR)

##           chisq           ratio           rdf           p
## 101.4667300    1.1028992  92.0000000    0.2345127
par(mfrow=c(2,2))
plot(fm8_PBR)
```

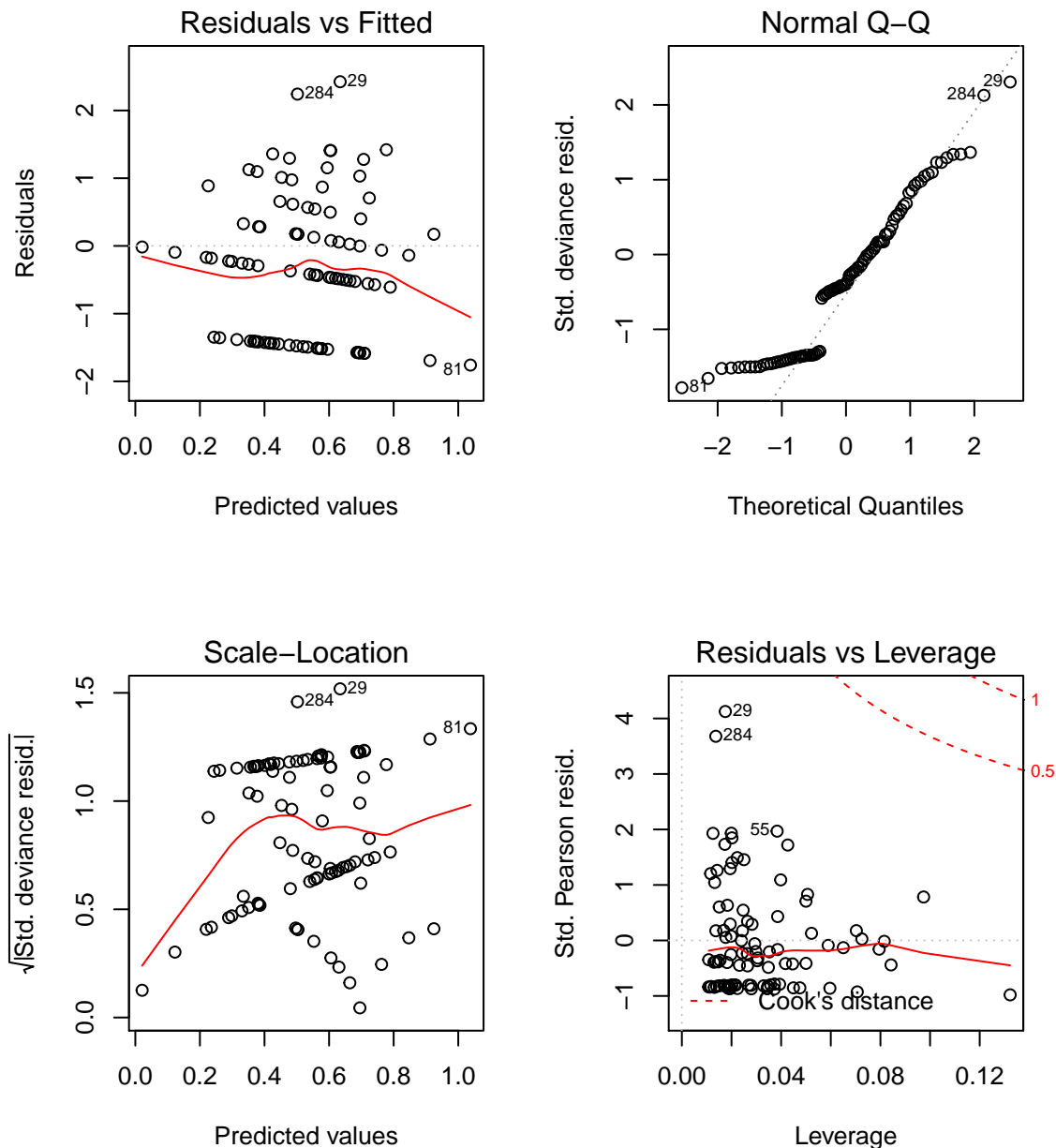
GLM of lifetime number of recruits on total number of alleles and P-distance PSS in females only

```
fm8_PSS <- glm(RecruLife_1014~Total.no.alleles+PdistPSS,negative.binomial(theta=1.40551,link="log"),data=
s8_PSS <- summary(fm8_PSS)
s8_PSS
```

```
##
## Call:
## glm(formula = RecruLife_1014 ~ Total.no.alleles + PdistPSS, family = negative.binomial(theta = 1.40551,
## link = "log"), data = data.females[!is.na(PdistPSS) & !is.na(ToSucLife_1014),
## ])
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -1.7596  -1.4213  -0.4168   0.3066   2.4245
```

```
##
## Coefficients:
##           Estimate Std. Error t value Pr(>|t|)
## (Intercept)    4.10393    3.92662   1.045   0.299
## Total.no.alleles -0.06025    0.04425  -1.362   0.177
## PdistPSS       -7.68950   10.33549  -0.744   0.459
##
## (Dispersion parameter for Negative Binomial(1.4055) family taken to be 1.125134)
##
##      Null deviance: 113.20  on 94  degrees of freedom
## Residual deviance: 111.23  on 92  degrees of freedom
## AIC: 345.1
##
## Number of Fisher Scoring iterations: 5
overdisp_fun(fm8_PSS)

##           chisq           ratio           rdf           p
## 103.5124441    1.1251353  92.0000000    0.1936933
par(mfrow=c(2,2))
plot(fm8_PSS)
```



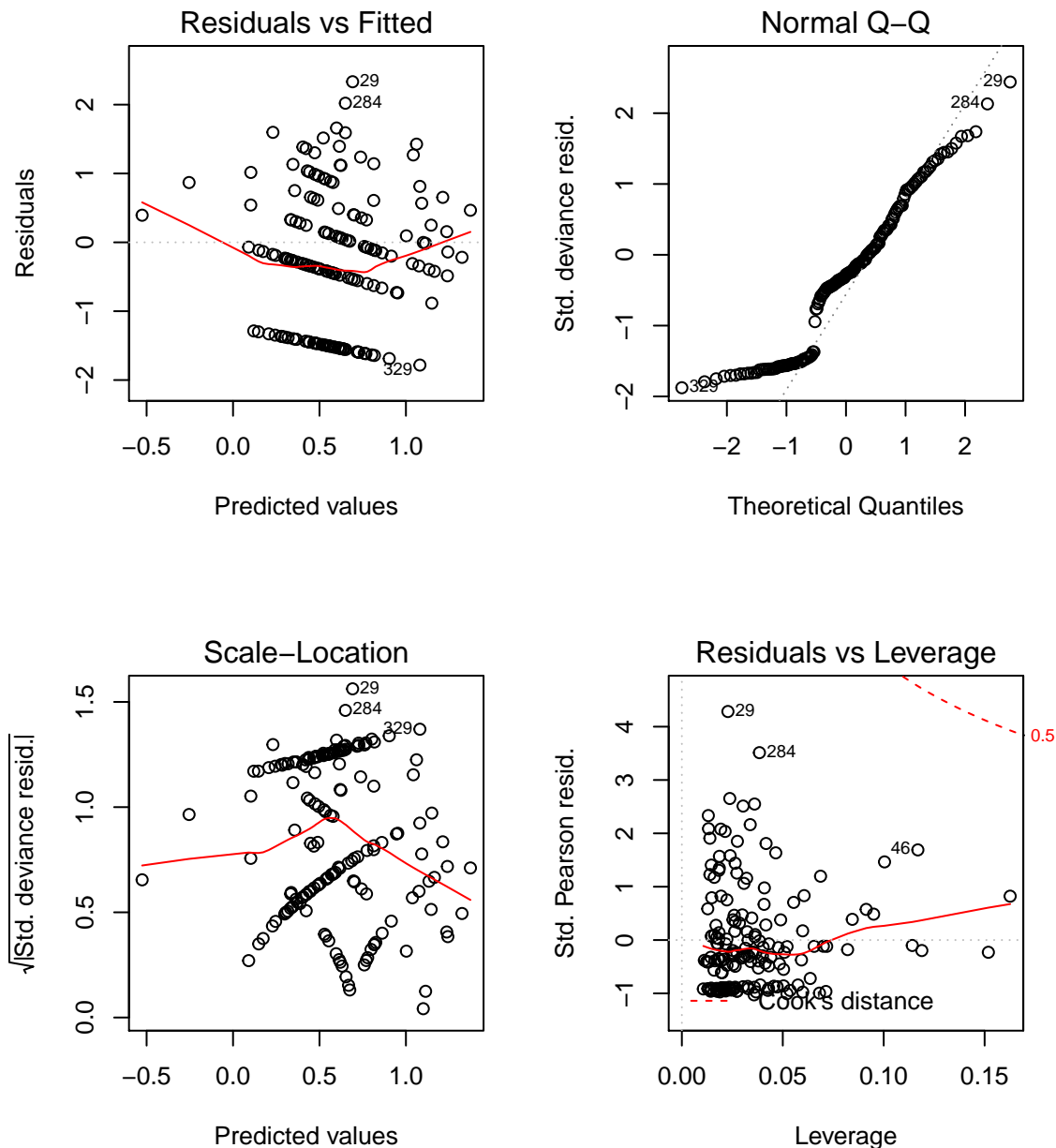
GLM of lifetime number of recruits on total number of alleles and P-distance PBR in both sexes

```
fm9_PBR <- glm(RecruLife_1014~Total.no.alleles+PdistPBR+Sex+Total.no.alleles:Sex+PdistPBR:Sex,negative.binomial(theta = 1.40551, link = "log"), data = data[!is.na(PdistPBR) & !is.na(ToSucLife_1014),])
s9_PBR <- summary(fm9_PBR)
s9_PBR
```

```
##
## Call:
## glm(formula = RecruLife_1014 ~ Total.no.alleles + PdistPBR +
##     Sex + Total.no.alleles:Sex + PdistPBR:Sex, family = negative.binomial(theta = 1.40551,
##     link = "log"), data = data[!is.na(PdistPBR) & !is.na(ToSucLife_1014),
##     ])
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
```

```
## -1.7826 -1.3926 -0.2654 0.3280 2.3327
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    -0.53598     3.17268  -0.169   0.8661
## Total.no.alleles -0.04161     0.04024  -1.034   0.3026
## PdistPBR        5.22055     9.54425   0.547   0.5851
## Sexmale        -9.15973     4.75842  -1.925   0.0560 .
## Total.no.alleles:Sexmale 0.14132     0.06303   2.242   0.0263 *
## PdistPBR:Sexmale  23.72440    13.77533   1.722   0.0869 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for Negative Binomial(1.4055) family taken to be 0.9349556)
##
##      Null deviance: 187.69  on 170  degrees of freedom
## Residual deviance: 175.58  on 165  degrees of freedom
## AIC: 635.99
##
## Number of Fisher Scoring iterations: 5
overdisp_fun(fm9_PBR)

##      chisq      ratio      rdf      p
## 154.2676589  0.9349555 165.0000000  0.7147116
par(mfrow=c(2,2))
plot(fm9_PBR)
```



GLM of lifetime number of recruits on total number of alleles and P-distance PSS in both sexes

```
fm9_PSS <- glm(RecruLife_1014~Total.no.alleles+PdistPSS+Sex+Total.no.alleles:Sex+PdistPSS:Sex,negative.binomial(theta = 1.40551, link = "log"), data = data[!is.na(PdistPSS) & !is.na(ToSucLife_1014),])
s9_PSS <- summary(fm9_PSS)
s9_PSS
```

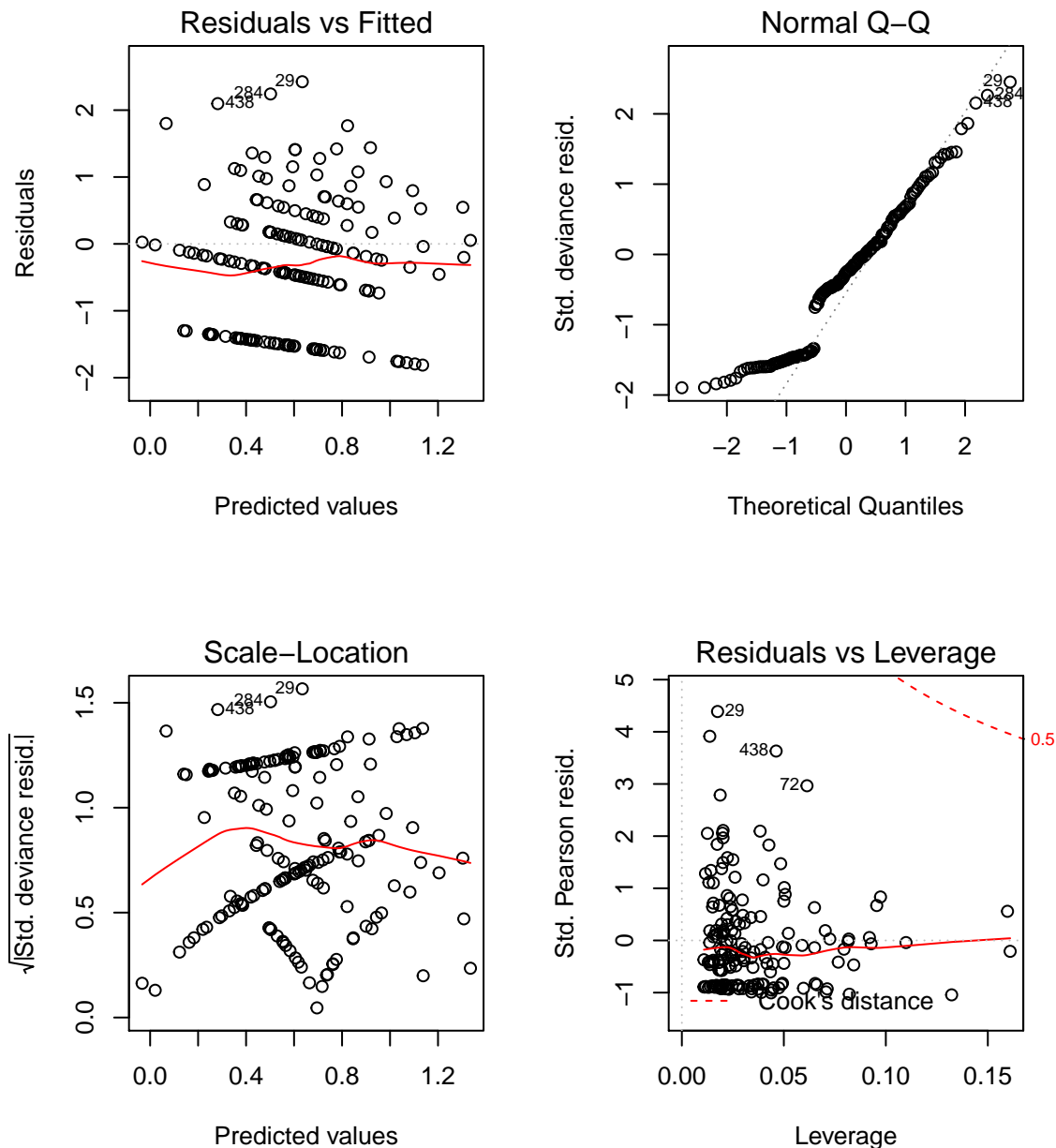
```
##
## Call:
## glm(formula = RecruLife_1014 ~ Total.no.alleles + PdistPSS +
##     Sex + Total.no.alleles:Sex + PdistPSS:Sex, family = negative.binomial(theta = 1.40551,
##     link = "log"), data = data[!is.na(PdistPSS) & !is.na(ToSucLife_1014),
##     ])
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
```

```

## -1.8120 -1.3934 -0.2542 0.3154 2.4245
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      4.10393    3.69103   1.112  0.2678
## Total.no.alleles -0.06025    0.04159  -1.449  0.1493
## PdistPSS         -7.68950    9.71538  -0.791  0.4298
## Sexmale          -14.37303    5.90543  -2.434  0.0160 *
## Total.no.alleles:Sexmale 0.15397    0.06725   2.290  0.0233 *
## PdistPSS:Sexmale   34.55016   14.91831   2.316  0.0218 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for Negative Binomial(1.4055) family taken to be 0.9941722)
##
##      Null deviance: 187.69  on 170  degrees of freedom
## Residual deviance: 178.36  on 165  degrees of freedom
## AIC: 638.77
##
## Number of Fisher Scoring iterations: 5
overdisp_fun(fm9_PSS)

##      chisq      ratio      rdf      p
## 164.0383197  0.9941716 165.0000000  0.5065083
par(mfrow=c(2,2))
plot(fm9_PSS)

```



Modeling the effects of MHC-I functional divergence on offspring fledging success

Linear model of lifetime number of fledgings on total number of alleles and P-distance PBR with lifespan as covariate in males only

```
fm10_PBR <- lm(ToSucLife_1014~LifeSpan+Total.no.alleles+PdistPBR,data=data.males[!is.na(PdistPBR)&!is.na(ToSucLife_1014)])
s10_PBR <- summary(fm10_PBR)
s10_PBR
```

```
##
## Call:
## lm(formula = ToSucLife_1014 ~ LifeSpan + Total.no.alleles + PdistPBR,
##     data = data.males[!is.na(PdistPBR) & !is.na(ToSucLife_1014)],
```

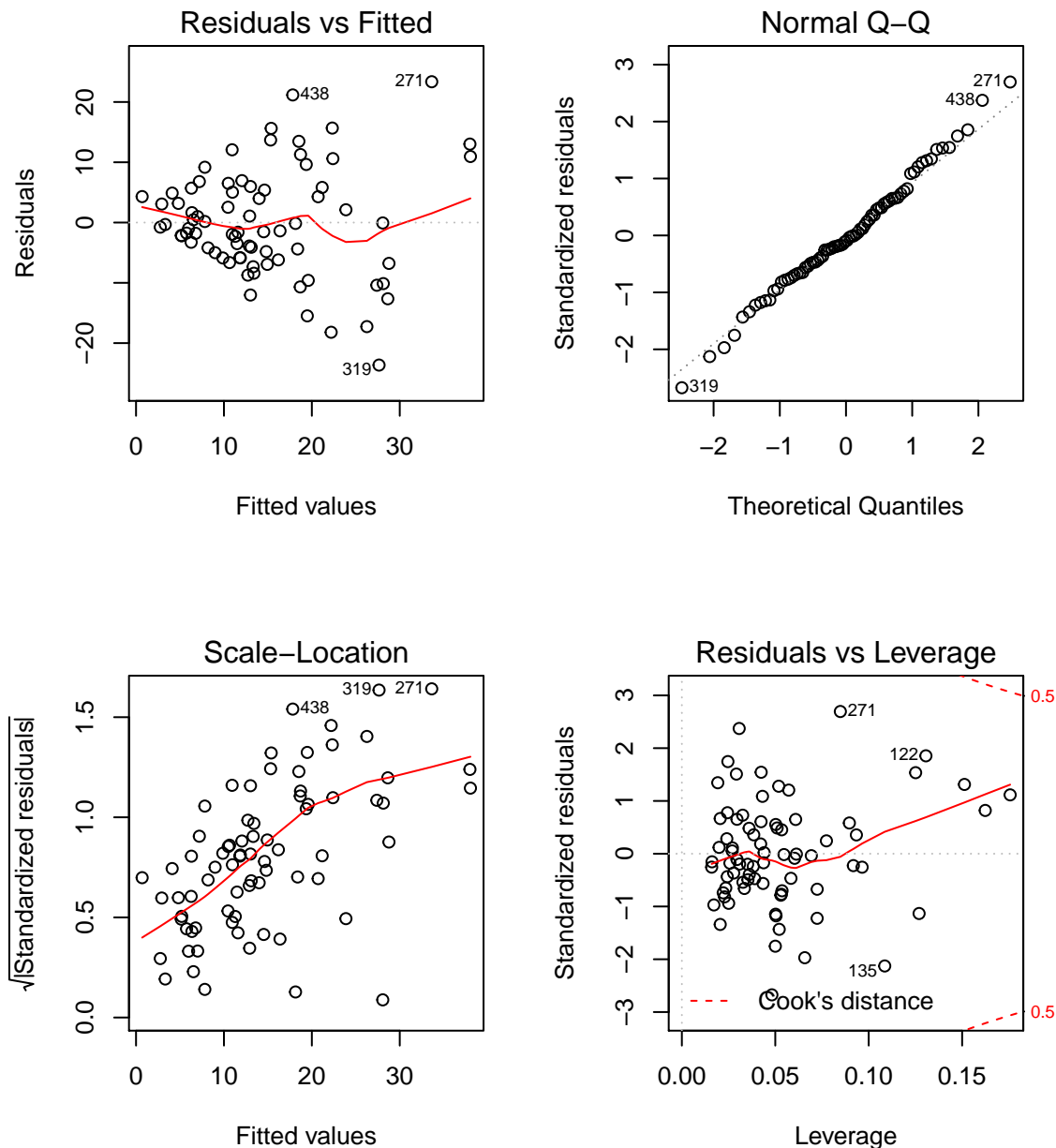
```
##      ])
```

## Residuals:					
	Min	1Q	Median	3Q	Max
##	-23.6438	-5.8328	-0.8704	5.4632	23.3595

## Coefficients:					
	Estimate	Std. Error	t value	Pr(> t)	
## (Intercept)	-52.5044	29.4221	-1.785	0.0786	.
## LifeSpan	4.7575	0.7195	6.612	5.68e-09	***
## Total.no.alleles	0.2099	0.4034	0.520	0.6044	
## PdistPBR	152.3550	85.6042	1.780	0.0793	.

```
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 9.061 on 72 degrees of freedom
## Multiple R-squared:  0.4644, Adjusted R-squared:  0.4421
## F-statistic: 20.81 on 3 and 72 DF,  p-value: 8.194e-10
```

```
par(mfrow=c(2,2))
plot(fm10_PBR)
```

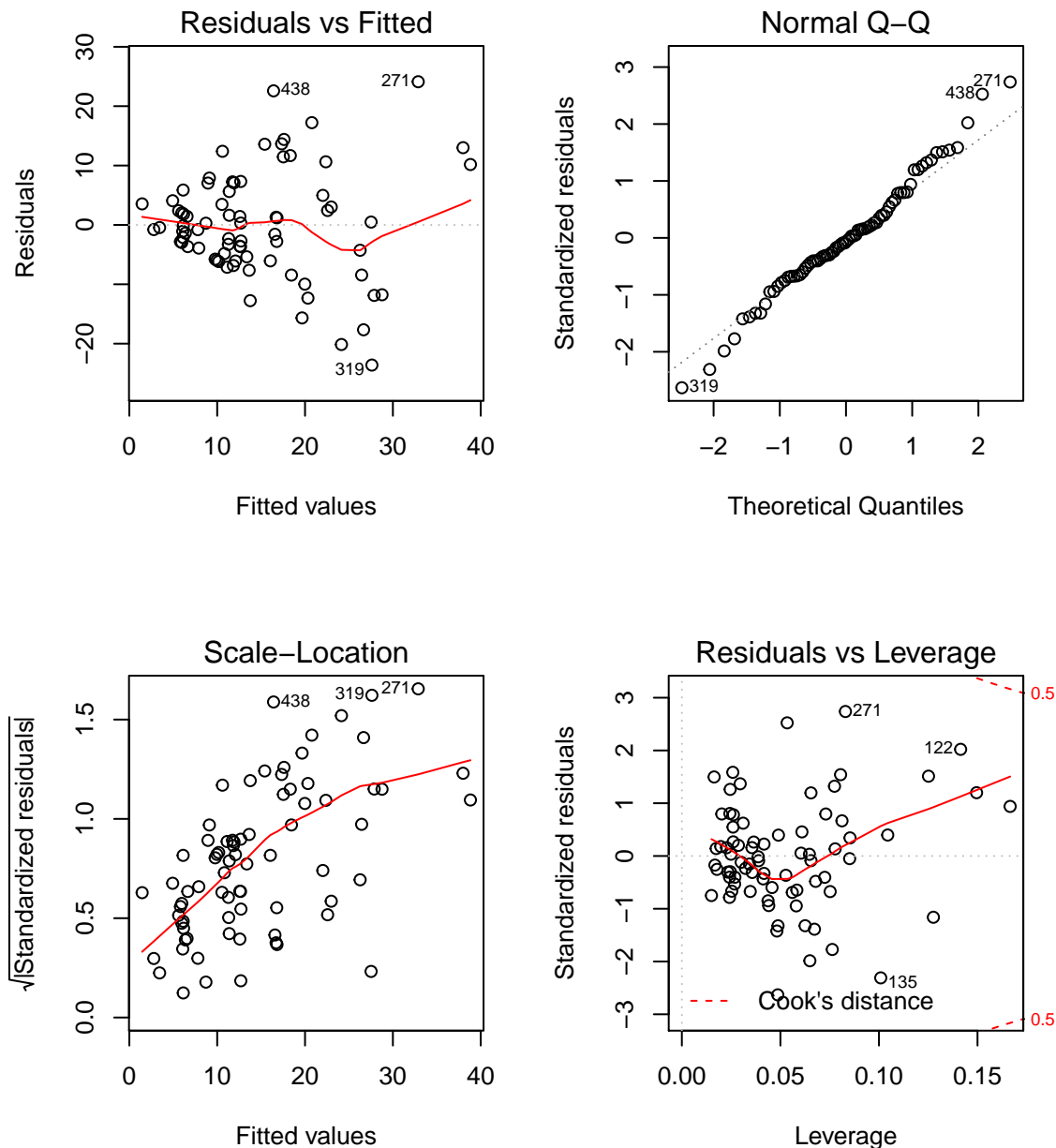
Linear model of lifetime number of fledgings on total number of alleles and P-distance PSS with lifespan as covariate in males only

```
fm10_PSS <- lm(ToSucLife_1014~LifeSpan+Total.no.alleles+PdistPSS,data=data.males[!is.na(PdistPSS)&!is.na(ToSucLife_1014)])
s10_PSS <- summary(fm10_PSS)
s10_PSS
```

```
##
## Call:
## lm(formula = ToSucLife_1014 ~ LifeSpan + Total.no.alleles + PdistPSS,
##     data = data.males[!is.na(PdistPSS) & !is.na(ToSucLife_1014),
##     ])
##
## Residuals:
```

##	Min	1Q	Median	3Q	Max
##	-23.6097	-5.4712	-0.6145	5.1370	24.1169

```
##
## Coefficients:
##           Estimate Std. Error t value Pr(>|t|)
## (Intercept)  -38.09164   38.25115  -0.996   0.323
## LifeSpan      5.02654    0.70723   7.107 7e-10 ***
## Total.no.alleles 0.07344    0.43684   0.168   0.867
## PdistPSS      94.07153   96.00763   0.980   0.330
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 9.198 on 72 degrees of freedom
## Multiple R-squared:  0.4482, Adjusted R-squared:  0.4252
## F-statistic: 19.49 on 3 and 72 DF,  p-value: 2.356e-09
par(mfrow=c(2,2))
plot(fm10_PSS)
```



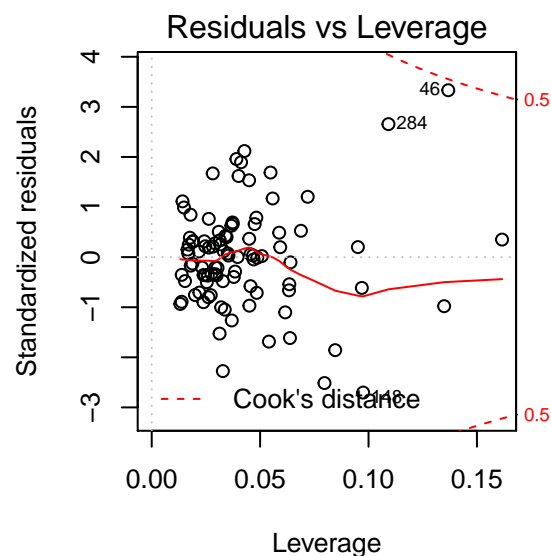
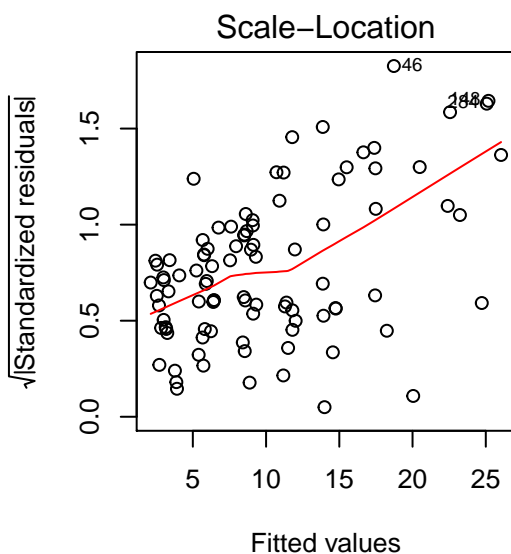
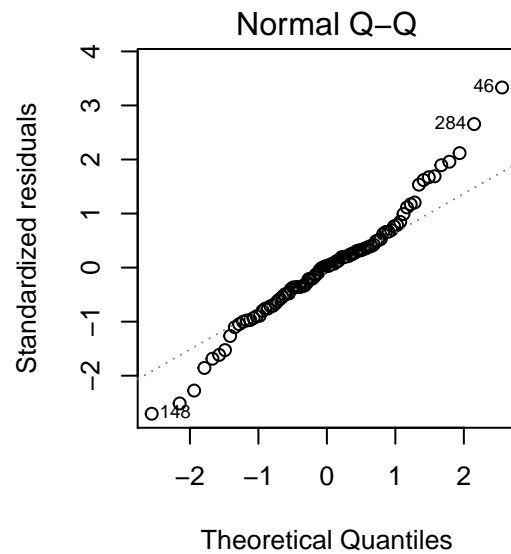
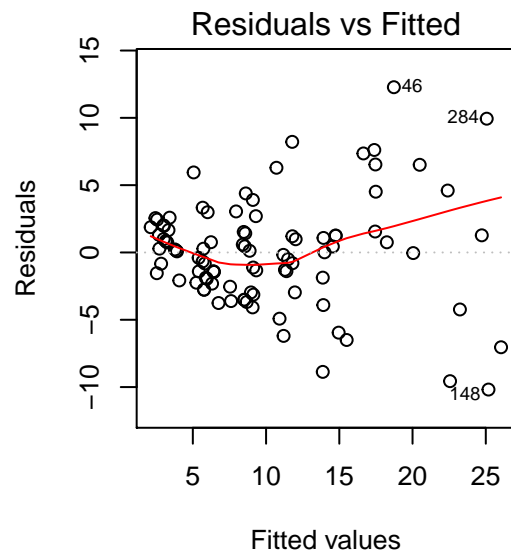
Linear model of lifetime number of fledgings on total number of alleles and P-distance PBR with lifespan as covariate in females only

```
fm11_PBR <- lm(ToSucLife_1014~LifeSpan+Total.no.alleles+PdistPBR,data=data.females[!is.na(PdistPBR)&!is.na(ToSucLife_1014)])
s11_PBR <- summary(fm11_PBR)
s11_PBR
```

```
##
## Call:
## lm(formula = ToSucLife_1014 ~ LifeSpan + Total.no.alleles + PdistPBR,
##     data = data.females[!is.na(PdistPBR) & !is.na(ToSucLife_1014),
##     ])
##
## Residuals:
```

	Min	1Q	Median	3Q	Max
	-10.1845	-2.1607	0.1229	1.6074	12.2748

```
##
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)    11.11888   11.25593   0.988   0.326
## LifeSpan        2.83950    0.19055  14.901 <2e-16 ***
## Total.no.alleles 0.06114    0.14379   0.425   0.672
## PdistPBR       -37.50437   33.77333  -1.110   0.270
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 3.965 on 91 degrees of freedom
## Multiple R-squared:  0.7121, Adjusted R-squared:  0.7026
## F-statistic: 75.02 on 3 and 91 DF,  p-value: < 2.2e-16
par(mfrow=c(2,2))
plot(fm11_PBR)
```



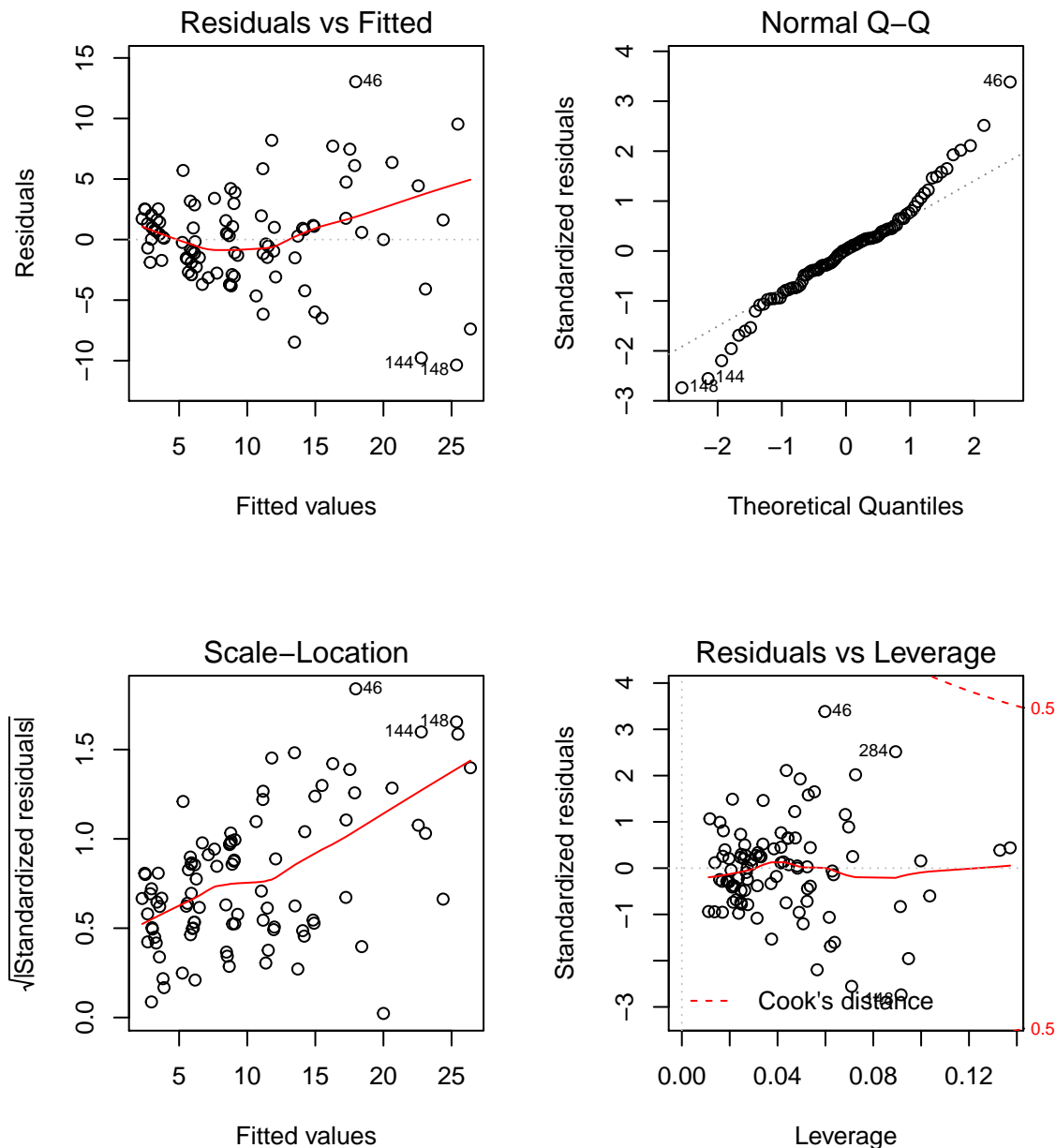
Linear model of lifetime number of fledgings on total number of alleles and P-distance PSS with lifespan as covariate in females only

```
fm11_PSS <- lm(ToSucLife_1014~LifeSpan+Total.no.alleles+PdistPSS,data=data.females[!is.na(PdistPSS)&!is.na(ToSucLife_1014)])
s11_PSS <- summary(fm11_PSS)
s11_PSS
```

```
##
## Call:
## lm(formula = ToSucLife_1014 ~ LifeSpan + Total.no.alleles + PdistPSS,
##     data = data.females[!is.na(PdistPSS) & !is.na(ToSucLife_1014),
##     ])
##
## Residuals:
```

	Min	1Q	Median	3Q	Max
	-10.3651	-2.0775	0.1081	1.6705	13.0347

```
##
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)    11.40047   13.17409   0.865   0.389
## LifeSpan        2.82151    0.19194  14.700 <2e-16 ***
## Total.no.alleles 0.06757    0.14389   0.470   0.640
## PdistPSS       -33.30141   34.45899  -0.966   0.336
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 3.971 on 91 degrees of freedom
## Multiple R-squared:  0.7111, Adjusted R-squared:  0.7016
## F-statistic: 74.68 on 3 and 91 DF,  p-value: < 2.2e-16
par(mfrow=c(2,2))
plot(fm11_PSS)
```

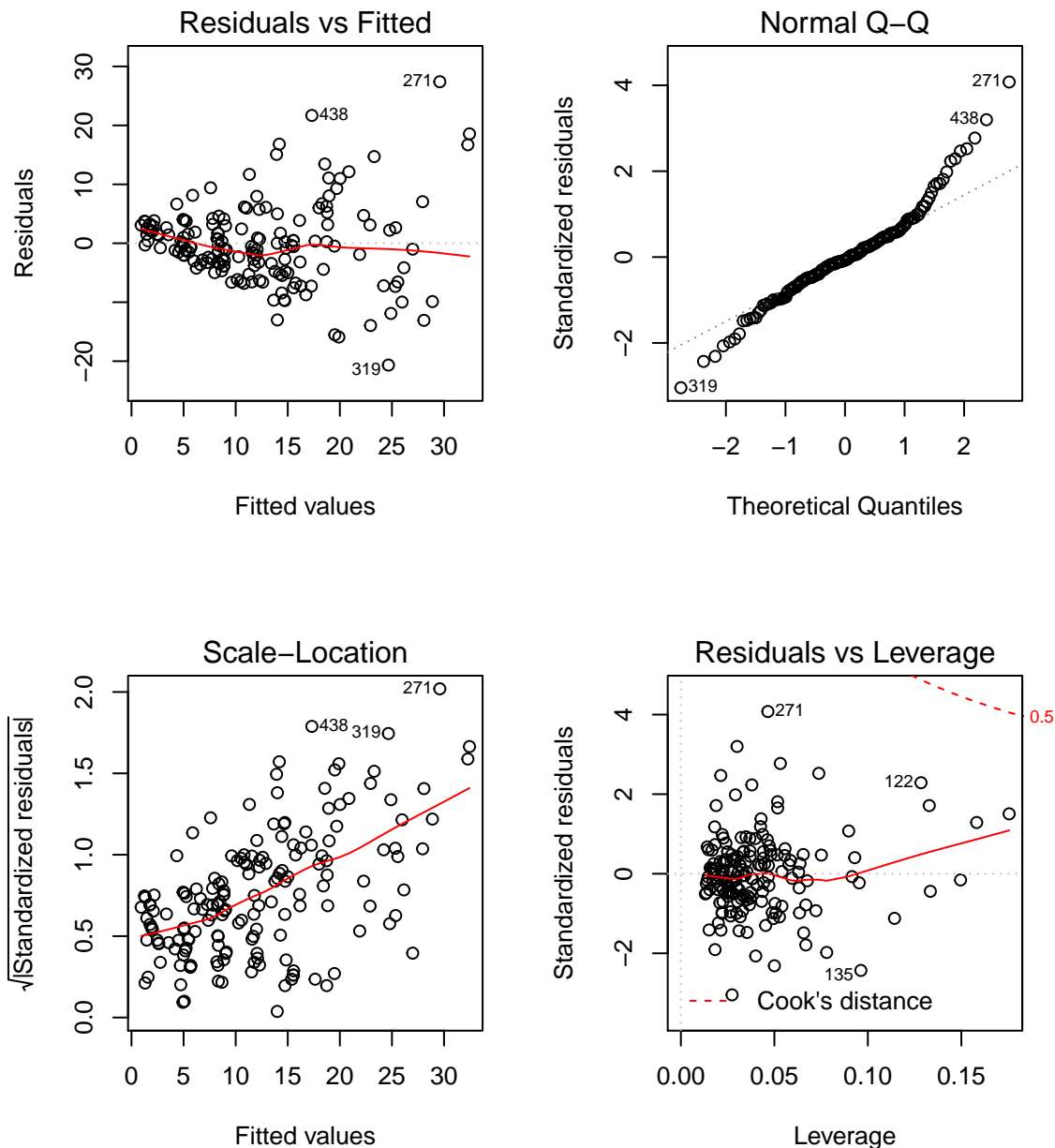


Linear model of lifetime number of fledgings on total number of alleles and P-distance PBR with lifespan as covariate in both sexes

```
fm12_PBR <- lm(ToSucLife_1014~LifeSpan+Total.no.alleles+PdistPBR+Sex+Total.no.alleles:Sex+PdistPBR:Sex,
s12_PBR <- summary(fm12_PBR)
s12_PBR
```

```
##
## Call:
## lm(formula = ToSucLife_1014 ~ LifeSpan + Total.no.alleles + PdistPBR +
##     Sex + Total.no.alleles:Sex + PdistPBR:Sex, data = data[!is.na(PdistPBR) &
##     !is.na(ToSucLife_1014), ])
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -20.6629  -3.5429  -0.4787   3.1341  27.4032
```

```
##
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)      9.26681   19.53120    0.474   0.6358
## LifeSpan         3.35383    0.28300   11.851 <2e-16 ***
## Total.no.alleles  0.05105    0.24961    0.205   0.8382
## PdistPBR        -36.79178   58.63195   -0.628   0.5312
## Sexmale         -76.15279   29.39188   -2.591   0.0104 *
## Total.no.alleles:Sexmale  0.29404    0.39225    0.750   0.4546
## PdistPBR:Sexmale  245.28201   85.58624    2.866   0.0047 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 6.883 on 164 degrees of freedom
## Multiple R-squared:  0.5405, Adjusted R-squared:  0.5236
## F-statistic: 32.15 on 6 and 164 DF,  p-value: < 2.2e-16
par(mfrow=c(2,2))
plot(fm12_PBR)
```

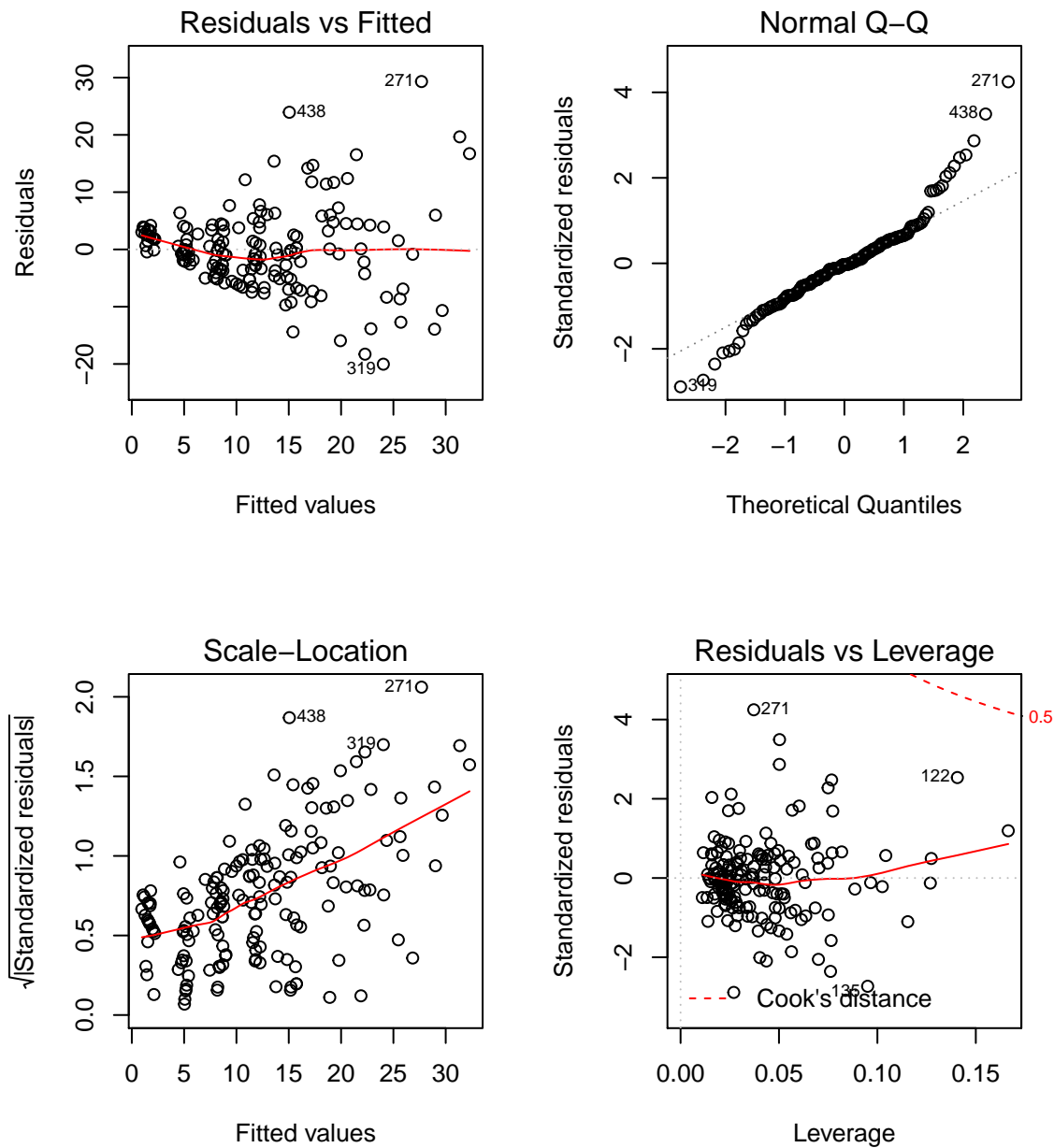



Linear model of lifetime number of fledgings on total number of alleles and P-distance PSS with lifespan as covariate in both sexes

```
fm12_PSS <- lm(ToSucLife_1014~LifeSpan+Total.no.alleles+PdistPSS+Sex+Total.no.alleles:Sex+PdistPSS:Sex,
s12_PSS <- summary(fm12_PSS)
s12_PSS
```

```
##
## Call:
## lm(formula = ToSucLife_1014 ~ LifeSpan + Total.no.alleles + PdistPSS +
##     Sex + Total.no.alleles:Sex + PdistPSS:Sex, data = data[!is.na(PdistPSS) &
##     !is.na(ToSucLife_1014), ])
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -20.0382  -3.5805  -0.2141   3.2492  29.3120
```

```
##
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)      4.96890   23.26213    0.214   0.831
## LifeSpan          3.44599    0.28785   11.971 <2e-16 ***
## Total.no.alleles  0.06869    0.25489    0.269   0.788
## PdistPSS         -21.42623   60.94379   -0.352   0.726
## Sexmale          -57.24369   37.35539   -1.532   0.127
## Total.no.alleles:Sexmale  0.13088    0.41867    0.313   0.755
## PdistPSS:Sexmale  165.45598   94.84718    1.744   0.083 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 7.034 on 164 degrees of freedom
## Multiple R-squared:  0.52, Adjusted R-squared:  0.5024
## F-statistic: 29.61 on 6 and 164 DF, p-value: < 2.2e-16
par(mfrow=c(2,2))
plot(fm12_PSS)
```



Modeling the effects of MHC-I functional divergence on offspring recruitment success

Linear model of lifetime number of recruits on total number of alleles and P-distance PBR with lifetime number of fledglings as covariate in males only

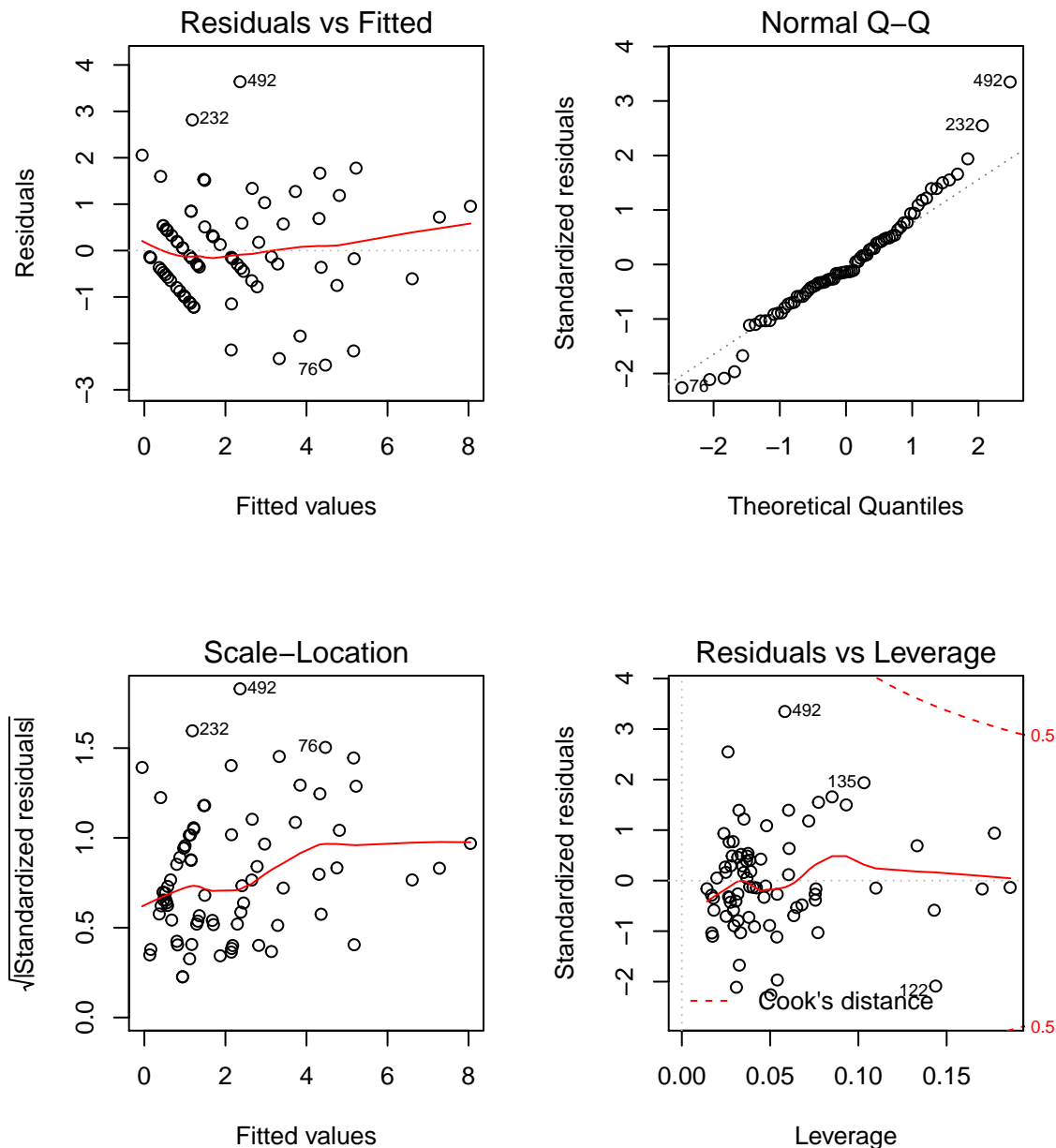
```
fm13_PBR <- lm(RecruLife_1014~ToSucLife_1014+Total.no.alleles+PdistPBR,data=data.males[!is.na(PdistPBR)])
s13_PBR <- summary(fm13_PBR)
s13_PBR
```

```
##
## Call:
## lm(formula = RecruLife_1014 ~ ToSucLife_1014 + Total.no.alleles +
```

```

##      PdistPBR, data = data.males[!is.na(PdistPBR) & !is.na(ToSucLife_1014),
##      ])
##
## Residuals:
##      Min        1Q      Median        3Q        Max
## -2.4679 -0.6180 -0.1508  0.5467  3.6382
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    -5.48675     3.70735  -1.480   0.1432
## ToSucLife_1014  0.13848     0.01149  12.054 <2e-16 ***
## Total.no.alleles 0.11761     0.04971   2.366  0.0207 *
## PdistPBR       12.80035    10.71313   1.195  0.2361
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.12 on 72 degrees of freedom
## Multiple R-squared:  0.7178, Adjusted R-squared:  0.706
## F-statistic: 61.04 on 3 and 72 DF,  p-value: < 2.2e-16
par(mfrow=c(2,2))
plot(fm13_PBR)

```

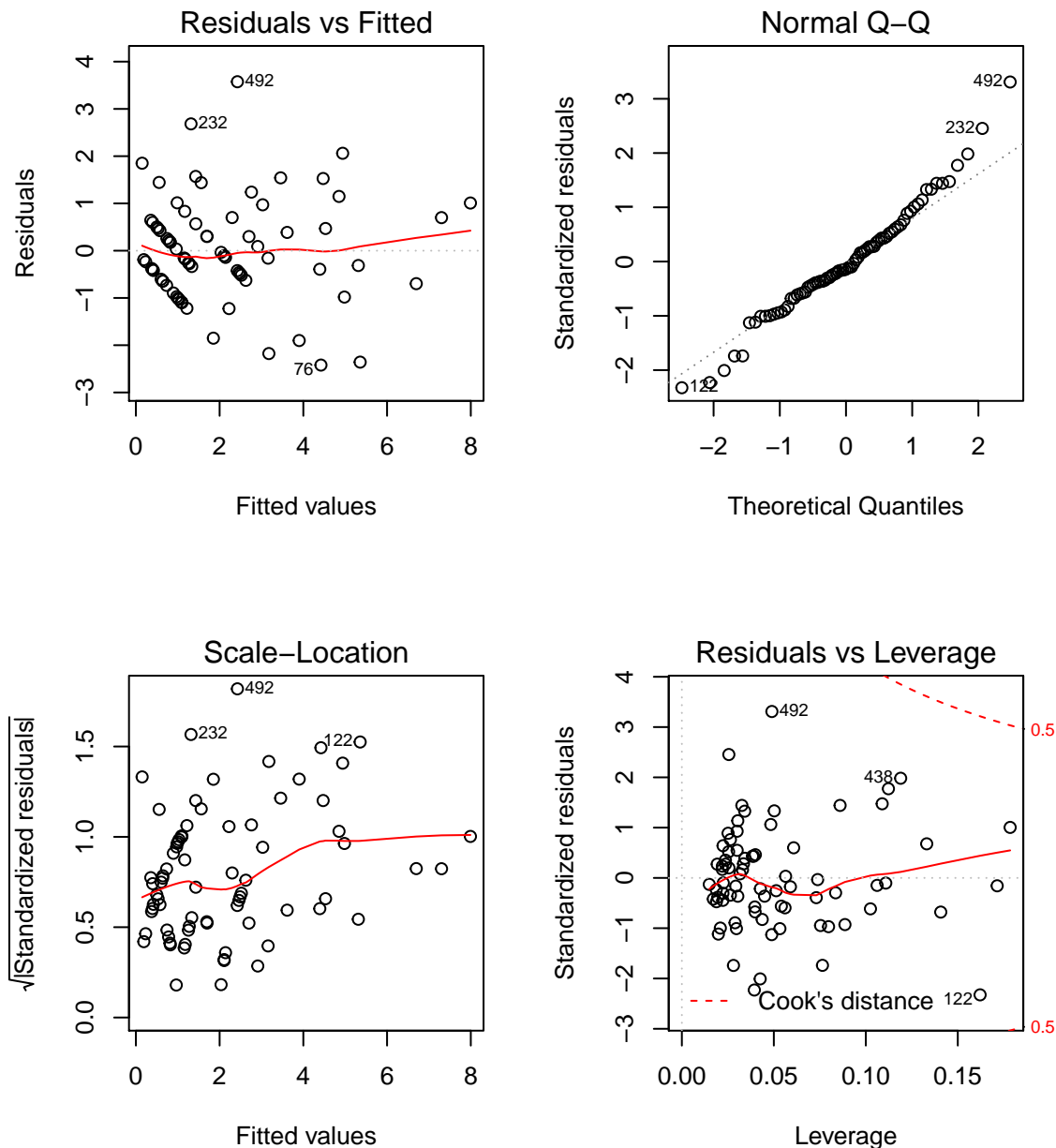


Linear model of lifetime number of recruits on total number of alleles and P-distance PSS with lifetime number of fledglings as covariate in males only

```
fm13_PSS <- lm(RecruLife_1014~ToSucLife_1014+Total.no.alleles+PdistPSS,data=data.males[!is.na(PdistPSS)])
s13_PSS <- summary(fm13_PSS)
s13_PSS
```

```
##
## Call:
## lm(formula = RecruLife_1014 ~ ToSucLife_1014 + Total.no.alleles +
##     PdistPSS, data = data.males[!is.na(PdistPSS) & !is.na(ToSucLife_1014),
##     ])
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -2.4205 -0.6302 -0.1484  0.5762  3.5749
```

```
##
## Coefficients:
##           Estimate Std. Error t value Pr(>|t|)
## (Intercept)   -9.13968    4.63216  -1.973  0.05232 .
## ToSucLife_1014  0.13900    0.01088  12.775 < 2e-16 ***
## Total.no.alleles 0.14205    0.05242   2.710  0.00841 **
## PdistPSS       20.22049   11.57660   1.747  0.08496 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.108 on 72 degrees of freedom
## Multiple R-squared:  0.7239, Adjusted R-squared:  0.7124
## F-statistic: 62.92 on 3 and 72 DF,  p-value: < 2.2e-16
par(mfrow=c(2,2))
plot(fm13_PSS)
```

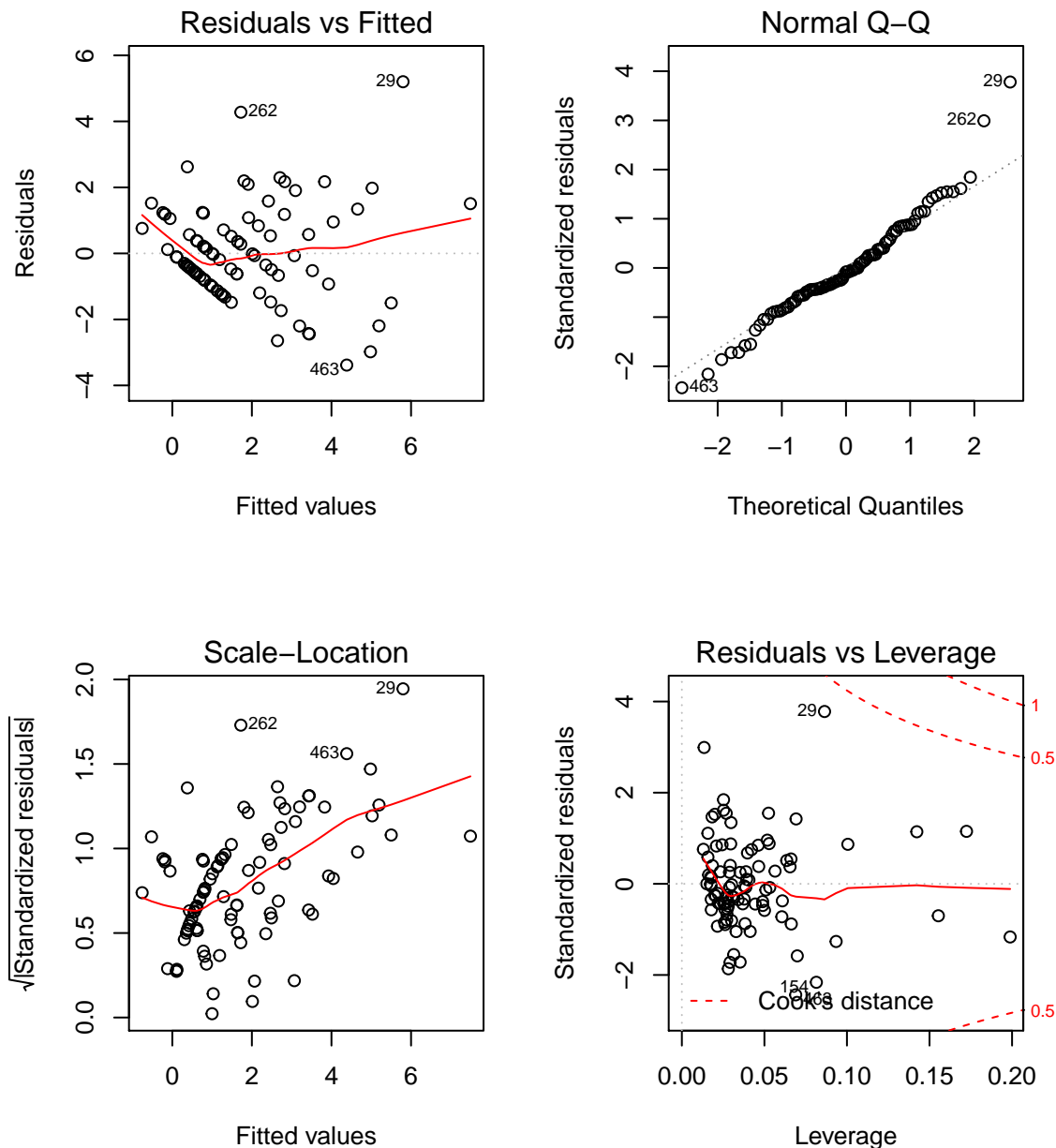


Linear model of lifetime number of recruits on total number of alleles and P-distance PBR with lifetime number of fledglings as covariate in females only

```
fm14_PBR <- lm(RecruLife_1014~ToSucLife_1014+Total.no.alleles+PdistPBR,data=data.females[!is.na(PdistPBR)])
s14_PBR <- summary(fm14_PBR)
s14_PBR
```

```
##
## Call:
## lm(formula = RecruLife_1014 ~ ToSucLife_1014 + Total.no.alleles +
##     PdistPBR, data = data.females[!is.na(PdistPBR) & !is.na(ToSucLife_1014),
##     ])
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -3.3836 -0.7834 -0.1138  0.7974  5.2017
```

```
##
## Coefficients:
##           Estimate Std. Error t value Pr(>|t|)
## (Intercept)   -5.31908     4.10214  -1.297    0.198
## ToSucLife_1014  0.21433     0.02052  10.446 <2e-16 ***
## Total.no.alleles -0.08760     0.05224  -1.677    0.097 .
## PdistPBR       19.49656    12.28996   1.586    0.116
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.439 on 91 degrees of freedom
## Multiple R-squared:  0.5521, Adjusted R-squared:  0.5373
## F-statistic: 37.39 on 3 and 91 DF,  p-value: 7.743e-16
par(mfrow=c(2,2))
plot(fm14_PBR)
```

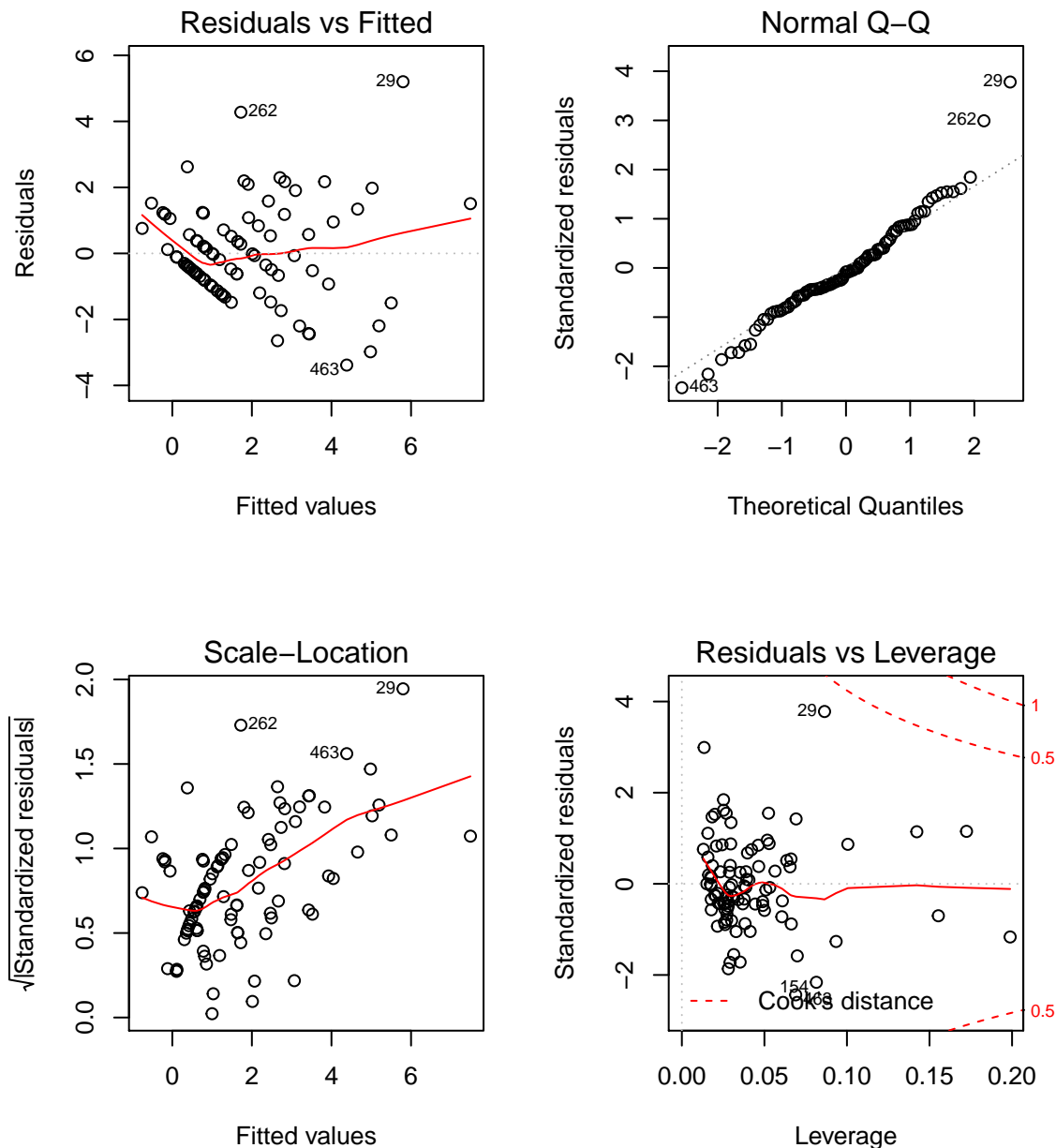



Linear model of lifetime number of recruits on total number of alleles and P-distance PSS with lifetime number of fledglings as covariate in females only

```
fm14_PSS <- lm(RecruLife_1014~ToSucLife_1014+Total.no.alleles+PdistPSS,data=data.females[!is.na(PdistPSS)])
s14_PSS <- summary(fm14_PSS)
s14_PSS
```

```
##
## Call:
## lm(formula = RecruLife_1014 ~ ToSucLife_1014 + Total.no.alleles +
##     PdistPSS, data = data.females[!is.na(PdistPSS) & !is.na(ToSucLife_1014),
##     ])
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -3.5868 -0.7087 -0.1396  0.7950  5.3625
```

```
##
## Coefficients:
##           Estimate Std. Error t value Pr(>|t|)
## (Intercept)   -1.52332     4.85235  -0.314   0.7543
## ToSucLife_1014  0.21371     0.02093  10.210 <2e-16 ***
## Total.no.alleles -0.10328     0.05280  -1.956   0.0535 .
## PdistPSS        6.92181    12.70041   0.545   0.5871
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.457 on 91 degrees of freedom
## Multiple R-squared:  0.5412, Adjusted R-squared:  0.5261
## F-statistic: 35.78 on 3 and 91 DF,  p-value: 2.288e-15
par(mfrow=c(2,2))
plot(fm14_PBR)
```

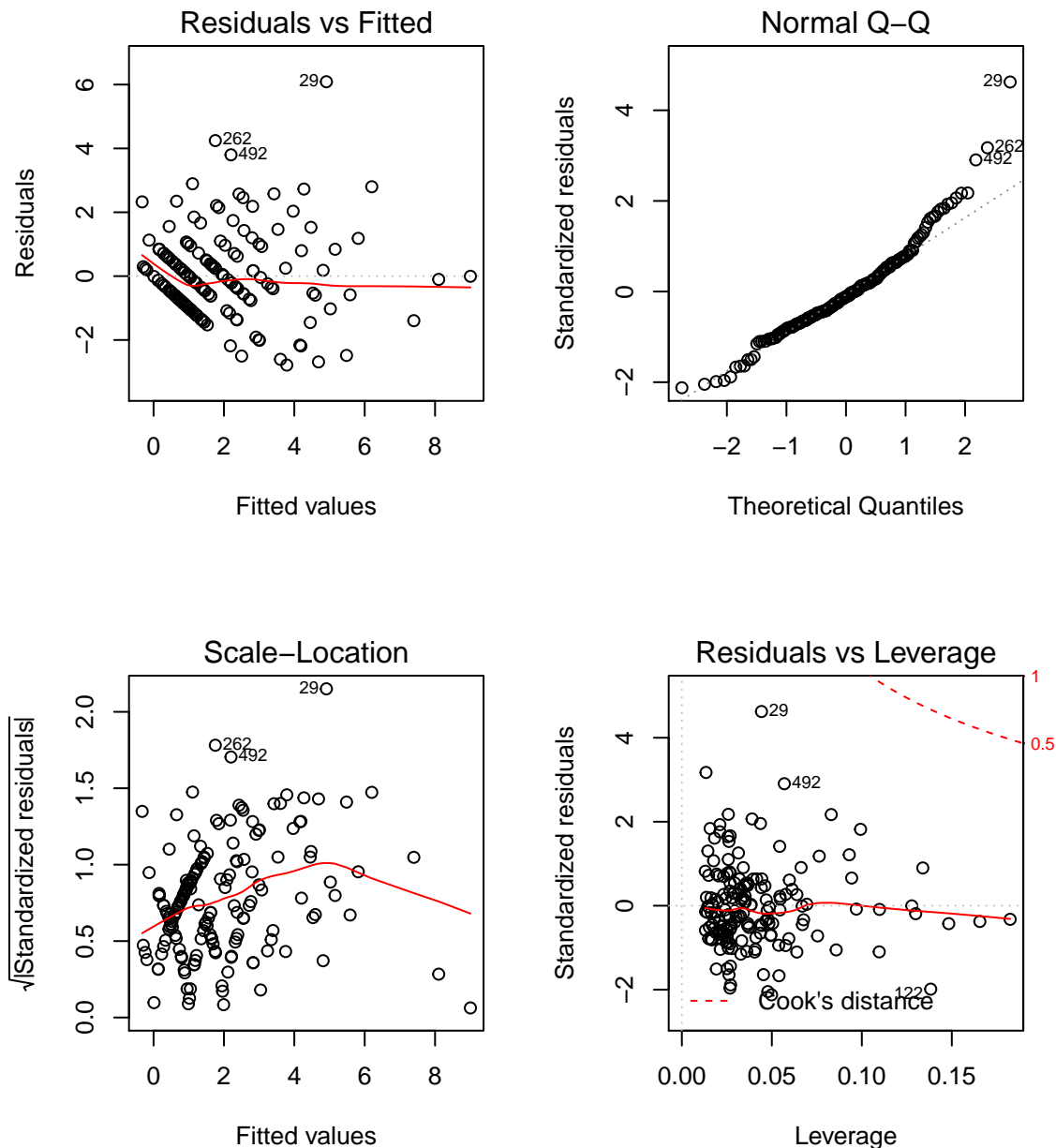


Linear model of lifetime number of recruits on total number of alleles and P-distance PBR with lifetime number of fledglings as covariate in both sexes

```
fm15_PBR <- lm(RecruLife_1014~ToSucLife_1014+Total.no.alleles+PdistPBR+Sex+Total.no.alleles:Sex+PdistPBR:Sex, data = data[!is.na(PdistPBR) & !is.na(ToSucLife_1014), ])
s15_PBR <- summary(fm15_PBR)
s15_PBR
```

```
##
## Call:
## lm(formula = RecruLife_1014 ~ ToSucLife_1014 + Total.no.alleles +
##     PdistPBR + Sex + Total.no.alleles:Sex + PdistPBR:Sex, data = data[!is.na(PdistPBR) &
##     !is.na(ToSucLife_1014), ])
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -2.7865 -0.8432 -0.1574  0.6730  6.0886
```

```
##
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)      -4.25247    3.82396  -1.112   0.2677
## ToSucLife_1014     0.16436    0.01121  14.656 <2e-16 ***
## Total.no.alleles  -0.08175    0.04885  -1.674   0.0961 .
## PdistPBR          17.42576   11.48167   1.518   0.1310
## Sexmale            1.38591    5.86322   0.236   0.8134
## Total.no.alleles:Sexmale 0.18208    0.07688   2.368   0.0190 *
## PdistPBR:Sexmale  -13.49193   17.13914  -0.787   0.4323
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.347 on 164 degrees of freedom
## Multiple R-squared:  0.602, Adjusted R-squared:  0.5874
## F-statistic: 41.34 on 6 and 164 DF,  p-value: < 2.2e-16
par(mfrow=c(2,2))
plot(fm15_PBR)
```



Linear model of lifetime number of recruits on total number of alleles and P-distance PSS with lifetime number of fledglings as covariate in both sexes

```
fm15_PSS <- lm(RecruLife_1014~ToSucLife_1014+Total.no.alleles+PdistPSS+Sex+Total.no.alleles:Sex+PdistPSS:Sex, data = data[!is.na(PdistPSS) & !is.na(ToSucLife_1014), ])
s15_PSS <- summary(fm15_PSS)
s15_PSS
```

```
##
## Call:
## lm(formula = RecruLife_1014 ~ ToSucLife_1014 + Total.no.alleles +
##     PdistPSS + Sex + Total.no.alleles:Sex + PdistPSS:Sex, data = data[!is.na(PdistPSS) &
##     !is.na(ToSucLife_1014), ])
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -2.9970 -0.8266 -0.1215  0.6371  6.2583
```

```
##
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)      0.53677    4.45724   0.120  0.90429
## ToSucLife_1014    0.16279    0.01097  14.846 < 2e-16 ***
## Total.no.alleles -0.10010    0.04900  -2.043  0.04268 *
## PdistPSS          2.49426   11.70647   0.213  0.83154
## Sexmale          -7.69698    7.22931  -1.065  0.28858
## Total.no.alleles:Sexmale 0.23085    0.08048   2.869  0.00467 **
## PdistPSS:Sexmale   11.70793   18.39705   0.636  0.52540
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.352 on 164 degrees of freedom
## Multiple R-squared:  0.5987, Adjusted R-squared:  0.5841
## F-statistic: 40.79 on 6 and 164 DF,  p-value: < 2.2e-16
par(mfrow=c(2,2))
plot(fm15_PSS)
```

