```
#Script used for the manuscript "Antioxidant supplementation slows
#telomere shortening in free-living white stork chicks" by Javier Pineda-
Pampliega,
#Amparo Herrera-Dueñas, Ellis Mulder, José I. Aguirre, Ursula Höfle, Simon
Verhulst.

library(Matrix)
library(lme4)
library(lmerTest)


#######Table 1: Oxidative Stress

table<-Supplementary material_Datasheet1_Table oxidative stress.csv

table$CHICK<-as.factor(table$CHICK)


#TOCOPHEROL

model_TOCOPHEROL<-lmer(TOCOPHEROL~TREATMENT+AGE+TREATMENT:AGE+(1|NEST/
CHICK),data=table,na.action=na.omit)
plot(residuals(model_TOCOPHEROL))
anova(model_TOCOPHEROL)
summary(model_TOCOPHEROL)

model_TOCOPHEROL_2<-lmer(TOCOPHEROL~TREATMENT+AGE+(1|NEST/
CHICK),data=table,na.action=na.omit)
plot(residuals(model_TOCOPHEROL_2))
anova(model_TOCOPHEROL_2)
summary(model_TOCOPHEROL_2)

#MDA

model_MDA<-lmer(MDA~TREATMENT+AGE+TREATMENT:AGE+(1|NEST/
CHICK),data=table,na.action=na.omit)
plot(residuals(model_MDA))
anova(model_MDA)
summary(model_MDA)

model_MDA_2<-lmer(MDA~TREATMENT+AGE+(1|NEST/CHICK),data=table,na.action=na.omit)
plot(residuals(model_MDA_2))
anova(model_MDA_2)
summary(model_MDA_2)

#TAC

model_TAC<-lmer(TAC~TREATMENT+AGE+TREATMENT:AGE+(1|NEST/
CHICK),data=table,na.action=na.omit)
plot(residuals(model_TAC))
anova(model_TAC)
summary(model_TAC)

model_TAC_2<-lmer(TAC~TREATMENT+AGE+(1|NEST/CHICK),data=table,na.action=na.omit)
plot(residuals(model_TAC_2))
anova(model_TAC_2)
```

```
model_FULL<-
lmer(Average~AGE+TREATMENT+SEX+HATCH_ORDER+MASS+AGE:TREATMENT+AGE:HATCH_ORDER+AGE
NEST/CHICK)+(1|GEL),data=table,na.action=na.omit)
plot(residuals(model_FULL))
anova(model_FULL)
summary(model_FULL)

model_FULL<-
lmer(Average~AGE+TREATMENT+SEX+HATCH_ORDER+MASS+AGE:HATCH_ORDER+AGE:TREATMENT+AGE
NEST/CHICK)+(1|GEL),data=table,na.action=na.omit)
plot(residuals(model_FULL))
anova(model_FULL)
summary(model_FULL)

model_FULL<-
lmer(Average~AGE+TREATMENT+SEX+HATCH_ORDER+MASS+AGE:HATCH_ORDER+AGE:MASS+(1|NEST/
CHICK)+(1|GEL),data=table,na.action=na.omit)
plot(residuals(model_FULL))
anova(model_FULL)
summary(model_FULL)

model_FULL<-lmer(Average~AGE+TREATMENT+SEX+HATCH_ORDER+MASS+AGE:HATCH_ORDER+(1|
NEST/CHICK)+(1|GEL),data=table,na.action=na.omit)
plot(residuals(model_FULL))
anova(model_FULL)
summary(model_FULL)

model_FULL<-lmer(Average~AGE+TREATMENT+SEX+HATCH_ORDER+MASS+(1|NEST/CHICK)+(1|
GEL),data=table,na.action=na.omit)
plot(residuals(model_FULL))
anova(model_FULL)
summary(model_FULL)

model_FULL<-lmer(Average~AGE+TREATMENT+SEX+HATCH_ORDER+(1|NEST/CHICK)+(1|
GEL),data=table,na.action=na.omit)
plot(residuals(model_FULL))
anova(model_FULL)
summary(model_FULL)

model_FULL<-lmer(Average~AGE+TREATMENT+HATCH_ORDER+(1|NEST/CHICK)+(1|
GEL),data=table,na.action=na.omit)
plot(residuals(model_FULL))
anova(model_FULL)
summary(model_FULL)

model_FULL<-lmer(Average~AGE+TREATMENT+(1|NEST/CHICK)+(1|
GEL),data=table,na.action=na.omit)
plot(residuals(model_FULL))
anova(model_FULL)
summary(model_FULL)


#######Table S1: Telomeres (Percentiles)

table<-Supplementary material_Datasheet_2_Table telomeres.csv
```

```
model_FULL<-
lmer(Percentile_10~AGE+TREATMENT+SEX+HATCH_ORDER+MASS+AGE:SEX+AGE:MASS+(1|NEST/
CHICK)+(1|GEL),data=table,na.action=na.omit)
plot(residuals(model_FULL))
anova(model_FULL)
summary(model_FULL)

model_FULL<-lmer(Percentile_10~AGE+TREATMENT+SEX+HATCH_ORDER+MASS+AGE:SEX+(1|
NEST/CHICK)+(1|GEL),data=table,na.action=na.omit)
plot(residuals(model_FULL))
anova(model_FULL)
summary(model_FULL)

model_FULL<-lmer(Percentile_10~AGE+TREATMENT+SEX+HATCH_ORDER+MASS+(1|NEST/CHICK)
+(1|GEL),data=table,na.action=na.omit)
plot(residuals(model_FULL))
anova(model_FULL)
summary(model_FULL)

model_FULL<-lmer(Percentile_10~AGE+TREATMENT+SEX+HATCH_ORDER+(1|NEST/CHICK)+(1|
GEL),data=table,na.action=na.omit)
plot(residuals(model_FULL))
anova(model_FULL)
summary(model_FULL)

model_FULL<-lmer(Percentile_10~AGE+TREATMENT+HATCH_ORDER+(1|NEST/CHICK)+(1|
GEL),data=table,na.action=na.omit)
plot(residuals(model_FULL))
anova(model_FULL)
summary(model_FULL)

model_FULL<-lmer(Percentile_10~AGE+TREATMENT+(1|NEST/CHICK)+(1|
GEL),data=table,na.action=na.omit)
plot(residuals(model_FULL))
anova(model_FULL)
summary(model_FULL)


#Percentile 20-------------------------------------------------------------

model_FULL<-
lmer(Percentile_20~AGE+TREATMENT+SEX+HATCH_ORDER+MASS+AGE:TREATMENT+AGE:HATCH_ORD
NEST/CHICK)+(1|GEL),data=table,na.action=na.omit)
plot(residuals(model_FULL))
anova(model_FULL)
summary(model_FULL)

model_FULL<-
lmer(Percentile_20~AGE+TREATMENT+SEX+HATCH_ORDER+MASS+AGE:HATCH_ORDER+AGE:SEX+AGE
NEST/CHICK)+(1|GEL),data=table,na.action=na.omit)
plot(residuals(model_FULL))
anova(model_FULL)
summary(model_FULL)

model_FULL<-
```

```
plot(residuals(model_FULL))
anova(model_FULL)
summary(model_FULL)

model_FULL<-lmer(Percentile_20~AGE+TREATMENT+HATCH_ORDER+(1|NEST/CHICK)+(1|
GEL),data=table,na.action=na.omit)
plot(residuals(model_FULL))
anova(model_FULL)
summary(model_FULL)

model_FULL<-lmer(Percentile_20~AGE+TREATMENT+(1|NEST/CHICK)+(1|
GEL),data=table,na.action=na.omit)
plot(residuals(model_FULL))
anova(model_FULL)
summary(model_FULL)

#Percentile 30-------------------------------------------------------------

model_FULL<-
lmer(Percentile_30~AGE+TREATMENT+SEX+HATCH_ORDER+MASS+AGE:TREATMENT+AGE:HATCH_ORD
NEST/CHICK)+(1|GEL),data=table,na.action=na.omit)
plot(residuals(model_FULL))
anova(model_FULL)
summary(model_FULL)

model_FULL<-
lmer(Percentile_30~AGE+TREATMENT+SEX+HATCH_ORDER+MASS+AGE:HATCH_ORDER+AGE:TREATME
NEST/CHICK)+(1|GEL),data=table,na.action=na.omit)
plot(residuals(model_FULL))
anova(model_FULL)
summary(model_FULL)

model_FULL<-
lmer(Percentile_30~AGE+TREATMENT+SEX+HATCH_ORDER+MASS+AGE:HATCH_ORDER+AGE:MASS+(1
NEST/CHICK)+(1|GEL),data=table,na.action=na.omit)
plot(residuals(model_FULL))
anova(model_FULL)
summary(model_FULL)

model_FULL<-lmer(Percentile_30~AGE+TREATMENT+SEX+HATCH_ORDER+MASS+AGE:MASS+(1|
NEST/CHICK)+(1|GEL),data=table,na.action=na.omit)
plot(residuals(model_FULL))
anova(model_FULL)
summary(model_FULL)

model_FULL<-lmer(Percentile_30~AGE+TREATMENT+SEX+HATCH_ORDER+MASS+(1|NEST/CHICK)
+(1|GEL),data=table,na.action=na.omit)
plot(residuals(model_FULL))
anova(model_FULL)
summary(model_FULL)

model_FULL<-lmer(Percentile_30~AGE+TREATMENT+SEX+HATCH_ORDER+(1|NEST/CHICK)+(1|
GEL),data=table,na.action=na.omit)
plot(residuals(model_FULL))
anova(model_FULL)
summary(model_FULL)
```

```
plot(residuals(model_FULL))
anova(model_FULL)
summary(model_FULL)

model_FULL<-
lmer(Percentile_40~AGE+TREATMENT+SEX+HATCH_ORDER+MASS+AGE:HATCH_ORDER+AGE:TREATME
NEST/CHICK)+(1|GEL),data=table,na.action=na.omit)
plot(residuals(model_FULL))
anova(model_FULL)
summary(model_FULL)

model_FULL<-
lmer(Percentile_40~AGE+TREATMENT+SEX+HATCH_ORDER+MASS+AGE:HATCH_ORDER+AGE:TREATME
NEST/CHICK)+(1|GEL),data=table,na.action=na.omit)
plot(residuals(model_FULL))
anova(model_FULL)
summary(model_FULL)

model_FULL<-
lmer(Percentile_40~AGE+TREATMENT+SEX+HATCH_ORDER+MASS+AGE:TREATMENT+(1|NEST/
CHICK)+(1|GEL),data=table,na.action=na.omit)
plot(residuals(model_FULL))
anova(model_FULL)
summary(model_FULL)

model_FULL<-lmer(Percentile_40~AGE+TREATMENT+SEX+HATCH_ORDER+MASS+(1|NEST/CHICK)
+(1|GEL),data=table,na.action=na.omit)
plot(residuals(model_FULL))
anova(model_FULL)
summary(model_FULL)

model_FULL<-lmer(Percentile_40~AGE+TREATMENT+SEX+HATCH_ORDER+(1|NEST/CHICK)+(1|
GEL),data=table,na.action=na.omit)
plot(residuals(model_FULL))
anova(model_FULL)
summary(model_FULL)

model_FULL<-lmer(Percentile_40~AGE+TREATMENT+SEX+(1|NEST/CHICK)+(1|
GEL),data=table,na.action=na.omit)
plot(residuals(model_FULL))
anova(model_FULL)
summary(model_FULL)

model_FULL<-lmer(Percentile_40~AGE+TREATMENT+(1|NEST/CHICK)+(1|
GEL),data=table,na.action=na.omit)
plot(residuals(model_FULL))
anova(model_FULL)
summary(model_FULL)


#Percentile 50------------------------------------------------------------

model_FULL<-
lmer(Percentile_50~AGE+TREATMENT+SEX+HATCH_ORDER+MASS+AGE:TREATMENT+AGE:HATCH_ORD
NEST/CHICK)+(1|GEL),data=table,na.action=na.omit)
plot(residuals(model_FULL))
```

```
summary(model_FULL)

model_FULL<-lmer(Percentile_50~AGE+TREATMENT+SEX+HATCH_ORDER+MASS+(1|NEST/CHICK)
+(1|GEL),data=table,na.action=na.omit)
plot(residuals(model_FULL))
anova(model_FULL)
summary(model_FULL)

model_FULL<-lmer(Percentile_50~AGE+TREATMENT+SEX+HATCH_ORDER+(1|NEST/CHICK)+(1|
GEL),data=table,na.action=na.omit)
plot(residuals(model_FULL))
anova(model_FULL)
summary(model_FULL)

model_FULL<-lmer(Percentile_50~AGE+TREATMENT+HATCH_ORDER+(1|NEST/CHICK)+(1|
GEL),data=table,na.action=na.omit)
plot(residuals(model_FULL))
anova(model_FULL)
summary(model_FULL)

model_FULL<-lmer(Percentile_50~AGE+TREATMENT+(1|NEST/CHICK)+(1|
GEL),data=table,na.action=na.omit)
plot(residuals(model_FULL))
anova(model_FULL)
summary(model_FULL)

#Percentile 60-------------------------------------------------------------

model_FULL<-
lmer(Percentile_60~AGE+TREATMENT+SEX+HATCH_ORDER+MASS+AGE:TREATMENT+AGE:HATCH_ORD
NEST/CHICK)+(1|GEL),data=table,na.action=na.omit)
plot(residuals(model_FULL))
anova(model_FULL)
summary(model_FULL)

model_FULL<-
lmer(Percentile_60~AGE+TREATMENT+SEX+HATCH_ORDER+MASS+AGE:HATCH_ORDER+AGE:TREATME
NEST/CHICK)+(1|GEL),data=table,na.action=na.omit)
plot(residuals(model_FULL))
anova(model_FULL)
summary(model_FULL)

model_FULL<-
lmer(Percentile_60~AGE+TREATMENT+SEX+HATCH_ORDER+MASS+AGE:HATCH_ORDER+AGE:TREATME
NEST/CHICK)+(1|GEL),data=table,na.action=na.omit)
plot(residuals(model_FULL))
anova(model_FULL)
summary(model_FULL)

model_FULL<-
lmer(Percentile_60~AGE+TREATMENT+SEX+HATCH_ORDER+MASS+AGE:TREATMENT+(1|NEST/
CHICK)+(1|GEL),data=table,na.action=na.omit)
plot(residuals(model_FULL))
anova(model_FULL)
summary(model_FULL)
```

```
plot(residuals(model_FULL))
anova(model_FULL)
summary(model_FULL)

#Percentile 70--------------------------------------------------------------

model_FULL<-
lmer(Percentile_70~AGE+TREATMENT+SEX+HATCH_ORDER+MASS+AGE:TREATMENT+AGE:HATCH_ORD
NEST/CHICK)+(1|GEL),data=table,na.action=na.omit)
plot(residuals(model_FULL))
anova(model_FULL)
summary(model_FULL)

model_FULL<-
lmer(Percentile_70~AGE+TREATMENT+SEX+HATCH_ORDER+MASS+AGE:HATCH_ORDER+AGE:TREATME
NEST/CHICK)+(1|GEL),data=table,na.action=na.omit)
plot(residuals(model_FULL))
anova(model_FULL)
summary(model_FULL)

model_FULL<-
lmer(Percentile_70~AGE+TREATMENT+SEX+HATCH_ORDER+MASS+AGE:SEX+AGE:TREATMENT+(1|
NEST/CHICK)+(1|GEL),data=table,na.action=na.omit)
plot(residuals(model_FULL))
anova(model_FULL)
summary(model_FULL)

model_FULL<-
lmer(Percentile_70~AGE+TREATMENT+SEX+HATCH_ORDER+MASS+AGE:TREATMENT+(1|NEST/
CHICK)+(1|GEL),data=table,na.action=na.omit)
plot(residuals(model_FULL))
anova(model_FULL)
summary(model_FULL)

model_FULL<-lmer(Percentile_70~AGE+TREATMENT+SEX+HATCH_ORDER+MASS+(1|NEST/CHICK)
+(1|GEL),data=table,na.action=na.omit)
plot(residuals(model_FULL))
anova(model_FULL)
summary(model_FULL)

model_FULL<-lmer(Percentile_70~AGE+TREATMENT+MASS+HATCH_ORDER+(1|NEST/CHICK)+(1|
GEL),data=table,na.action=na.omit)
plot(residuals(model_FULL))
anova(model_FULL)
summary(model_FULL)

model_FULL<-lmer(Percentile_70~AGE+TREATMENT+HATCH_ORDER+(1|NEST/CHICK)+(1|
GEL),data=table,na.action=na.omit)
plot(residuals(model_FULL))
anova(model_FULL)
summary(model_FULL)

model_FULL<-lmer(Percentile_70~AGE+TREATMENT+(1|NEST/CHICK)+(1|
GEL),data=table,na.action=na.omit)
plot(residuals(model_FULL))
anova(model_FULL)
```

```
anova(model_FULL)
summary(model_FULL)

model_FULL<-
lmer(Percentile_80~AGE+TREATMENT+SEX+HATCH_ORDER+MASS+AGE:TREATMENT+(1|NEST/
CHICK)+(1|GEL),data=table,na.action=na.omit)
plot(residuals(model_FULL))
anova(model_FULL)
summary(model_FULL)

model_FULL<-lmer(Percentile_80~AGE+TREATMENT+SEX+HATCH_ORDER+MASS+(1|NEST/CHICK)
+(1|GEL),data=table,na.action=na.omit)
plot(residuals(model_FULL))
anova(model_FULL)
summary(model_FULL)

model_FULL<-lmer(Percentile_80~AGE+TREATMENT+MASS+HATCH_ORDER+(1|NEST/CHICK)+(1|
GEL),data=table,na.action=na.omit)
plot(residuals(model_FULL))
anova(model_FULL)
summary(model_FULL)

model_FULL<-lmer(Percentile_80~AGE+TREATMENT+HATCH_ORDER+(1|NEST/CHICK)+(1|
GEL),data=table,na.action=na.omit)
plot(residuals(model_FULL))
anova(model_FULL)
summary(model_FULL)

model_FULL<-lmer(Percentile_80~AGE+TREATMENT+(1|NEST/CHICK)+(1|
GEL),data=table,na.action=na.omit)
plot(residuals(model_FULL))
anova(model_FULL)
summary(model_FULL)

#Percentile 90--------------------------------------------------------------

model_FULL<-
lmer(Percentile_90~AGE+TREATMENT+SEX+HATCH_ORDER+MASS+AGE:TREATMENT+AGE:HATCH_ORD
NEST/CHICK)+(1|GEL),data=table,na.action=na.omit)
plot(residuals(model_FULL))
anova(model_FULL)
summary(model_FULL)

model_FULL<-
lmer(Percentile_90~AGE+TREATMENT+SEX+HATCH_ORDER+MASS+AGE:HATCH_ORDER+AGE:TREATME
NEST/CHICK)+(1|GEL),data=table,na.action=na.omit)
plot(residuals(model_FULL))
anova(model_FULL)
summary(model_FULL)

model_FULL<-
lmer(Percentile_90~AGE+TREATMENT+SEX+HATCH_ORDER+MASS+AGE:SEX+AGE:TREATMENT+(1|
NEST/CHICK)+(1|GEL),data=table,na.action=na.omit)
plot(residuals(model_FULL))
anova(model_FULL)
summary(model_FULL)
```

```
model_FULL<-lmer(Percentile_90~AGE+TREATMENT+HATCH_ORDER+(1|NEST/CHICK)+(1|
GEL),data=table,na.action=na.omit)
plot(residuals(model_FULL))
anova(model_FULL)
summary(model_FULL)

model_FULL<-lmer(Percentile_90~AGE+TREATMENT+(1|NEST/CHICK)+(1|
GEL),data=table,na.action=na.omit)
plot(residuals(model_FULL))
anova(model_FULL)
summary(model_FULL)


#######Table S2: Treatment and Mass/Size

table<-Supplementary material_Datasheet_2_Table telomeres.csv

table$CHICK<-as.factor(table$CHICK)
table$DAY<-as.factor(table$DAY)

model_MASS<-lmer(MASS~DAY+TREATMENT+TREATMENT:DAY+(1|NEST/
CHICK),data=table,na.action=na.omit)
plot(model_MASS)
anova(model_MASS)
summary(model_MASS)

model_MASS<-lmer(MASS~DAY+TREATMENT+(1|NEST/CHICK),data=table,na.action=na.omit)
plot(model_MASS)
anova(model_MASS)
summary(model_MASS)


model_TARSUS<-lmer(TARSUS~DAY+TREATMENT+TREATMENT:DAY+(1|NEST/
CHICK),data=table,na.action=na.omit)
plot(model_TARSUS)
anova(model_TARSUS)
summary(model_TARSUS)

model_TARSUS<-lmer(TARSUS~DAY+TREATMENT+(1|NEST/
CHICK),data=table,na.action=na.omit)
plot(model_TARSUS)
anova(model_TARSUS)
summary(model_TARSUS)



#######Table S3: Differences between percentiles

table<-Supplementary material_Datasheet_3_Table percentiles

table$CHICK<-as.factor(table$CHICK)
table$GEL<-as.factor(table$GEL)

model_Percentiles<-lmer(Telomeres~Percentiles+AGE+Percentiles:AGE+(1|NEST/CHICK/
Sample)+(1|GEL),data=table,na.action=na.omit)
plot(residuals(model_Percentiles))
```

```
table<-Supplementary material_Datasheet_2_Table telomeres

table$CHICK<-as.factor(table$CHICK)
table$GEL<-as.factor(table$GEL)
table$DAY<-as.factor(table$DAY)

table$TOCOPHEROL_transformed<-scale(table$TOCOPHEROL,center=TRUE,scale=TRUE)
table$MDA_transformed<-scale(table$MDA,center=TRUE,scale=TRUE)
table$TAC_transformed<-scale(table$TAC,center=TRUE,scale=TRUE)

OX_model_Average<-
lmer(Average~AGE+TOCOPHEROL_transformed+MDA_transformed+TAC_transformed+(1|GEL)
+(1|NEST/CHICK),data=table,na.action=na.omit)
plot(residuals(OX_model_Average))
anova(OX_model_Average)
summary(OX_model_Average)

#############################################################################
###PERCENTILE 10

OX_model_Percentile_10<-
lmer(Percentile_10~AGE+TOCOPHEROL_transformed+MDA_transformed+TAC_transformed+(1|
GEL)+(1|NEST/CHICK),data=table,na.action=na.omit)
plot(residuals(OX_model_Percentile_10))
anova(OX_model_Percentile_10)
summary(OX_model_Percentile_10)

#############################################################################
###PERCENTILE 20

OX_model_Percentile_20<-
lmer(Percentile_20~AGE+TOCOPHEROL_transformed+MDA_transformed+TAC_transformed+(1|
GEL)+(1|NEST/CHICK),data=table,na.action=na.omit)
plot(residuals(OX_model_Percentile_20))
anova(OX_model_Percentile_20)
summary(OX_model_Percentile_20)

#############################################################################
###PERCENTILE 30
OX_model_Percentile_30<-
lmer(Percentile_30~AGE+TOCOPHEROL_transformed+MDA_transformed+TAC_transformed+(1|
GEL)+(1|NEST/CHICK),data=table,na.action=na.omit)
plot(residuals(OX_model_Percentile_30))
anova(OX_model_Percentile_30)
summary(OX_model_Percentile_30)

#############################################################################
###PERCENTILE 40

OX_model_Percentile_40<-
lmer(Percentile_40~AGE+TOCOPHEROL_transformed+MDA_transformed+TAC_transformed+(1|
GEL)+(1|NEST/CHICK),data=table,na.action=na.omit)
plot(residuals(OX_model_Percentile_40))
anova(OX_model_Percentile_40)
summary(OX_model_Percentile_40)
```

```
anova(OX_model_Percentile_60)
summary(OX_model_Percentile_60)

##############################################################################
###PERCENTILE 70

OX_model_Percentile_70<-
lmer(Percentile_70~AGE+TOCOPHEROL_transformed+MDA_transformed+TAC_transformed+(1|
GEL)+(1|NEST/CHICK),data=table,na.action=na.omit)
plot(residuals(OX_model_Percentile_70))
anova(OX_model_Percentile_70)
summary(OX_model_Percentile_70)

##############################################################################
###PERCENTILE 80

OX_model_Percentile_80<-
lmer(Percentile_80~AGE+TOCOPHEROL_transformed+MDA_transformed+TAC_transformed+(1|
GEL)+(1|NEST/CHICK),data=table,na.action=na.omit)
plot(residuals(OX_model_Percentile_80))
anova(OX_model_Percentile_80)
summary(OX_model_Percentile_80)

##############################################################################
###PERCENTILE 90

OX_model_Percentile_90<-
lmer(Percentile_90~AGE+TOCOPHEROL_transformed+MDA_transformed+TAC_transformed+(1|
GEL)+(1|NEST/CHICK),data=table,na.action=na.omit)
plot(residuals(OX_model_Percentile_90))
anova(OX_model_Percentile_90)
summary(OX_model_Percentile_90)


#######Table S5:Analysis relation telomeres and mass

table<-Supplementary material_Datasheet_2_Table telomeres

table$CHICK<-as.factor(table$CHICK)
table$GEL<-as.factor(table$GEL)

model_Average_mass<-lmer(Average~MASS+AGE+MASS:AGE+(1|NEST/CHICK)+(1|
GEL),data=table,na.action=na.omit)
plot(residuals(model_Average_mass))
anova(model_Average_mass)
summary(model_Average_mass)

model_Average_mass_2<-lmer(Average~MASS+AGE+(1|NEST/CHICK)+(1|
GEL),data=table,na.action=na.omit)
plot(residuals(model_Average_mass_2))
anova(model_Average_mass_2)
summary(model_Average_mass_2)

##############################################################################
###PERCENTILE 10
```

```
model_Percentile_20_mass<-lmer(Percentile_20~MASS+AGE+MASS:AGE+(1|NEST/CHICK)+(1|
GEL),data=table,na.action=na.omit)
plot(residuals(model_Percentile_20_mass))
anova(model_Percentile_20_mass)
summary(model_Percentile_20_mass)

model_Percentile_20_mass_2<-lmer(Percentile_20~MASS+AGE+(1|NEST/CHICK)+(1|
GEL),data=table,na.action=na.omit)
plot(model_Percentile_20_mass_2)
anova(model_Percentile_20_mass_2)
summary(model_Percentile_20_mass_2)

##############################################################################
###PERCENTILE 30

model_Percentile_30_mass<-lmer(Percentile_30~MASS+AGE+MASS:AGE+(1|NEST/CHICK)+(1|
GEL),data=table,na.action=na.omit)
plot(residuals(model_Percentile_30_mass))
anova(model_Percentile_30_mass)
summary(model_Percentile_30_mass)

model_Percentile_30_mass_2<-lmer(Percentile_30~MASS+AGE+(1|NEST/CHICK)+(1|
GEL),data=table,na.action=na.omit)
plot(model_Percentile_30_mass_2)
anova(model_Percentile_30_mass_2)
summary(model_Percentile_30_mass_2)ç

##############################################################################
###PERCENTILE 40

model_Percentile_40_mass<-lmer(Percentile_40~MASS+AGE+MASS:AGE+(1|NEST/CHICK)+(1|
GEL),data=table,na.action=na.omit)
plot(residuals(model_Percentile_40_mass))
anova(model_Percentile_40_mass)
summary(model_Percentile_40_mass)

model_Percentile_40_mass_2<-lmer(Percentile_40~MASS+AGE+(1|NEST/CHICK)+(1|
GEL),data=table,na.action=na.omit)
plot(model_Percentile_40_mass_2)
anova(model_Percentile_40_mass_2)
summary(model_Percentile_40_mass_2)

##############################################################################
###PERCENTILE 50

model_Percentile_50_mass<-lmer(Percentile_50~MASS+AGE+MASS:AGE+(1|NEST/CHICK)+(1|
GEL),data=table,na.action=na.omit)
plot(residuals(model_Percentile_50_mass))
anova(model_Percentile_50_mass)
summary(model_Percentile_50_mass)

model_Percentile_50_mass_2<-lmer(Percentile_50~MASS+AGE+(1|NEST/CHICK)+(1|
GEL),data=table,na.action=na.omit)
plot(model_Percentile_50_mass_2)
anova(model_Percentile_50_mass_2)
```

```
anova(model_Percentile_60_mass_2)
summary(model_Percentile_60_mass_2)

############################################################################
###PERCENTILE 70

model_Percentile_70_mass<-lmer(Percentile_70~MASS+AGE+MASS:AGE+(1|NEST/CHICK)+(1|
GEL),data=table,na.action=na.omit)
plot(residuals(model_Percentile_70_mass))
anova(model_Percentile_70_mass)
summary(model_Percentile_70_mass)

model_Percentile_70_mass_2<-lmer(Percentile_70~MASS+AGE+(1|NEST/CHICK)+(1|
GEL),data=table,na.action=na.omit)
plot(model_Percentile_70_mass_2)
anova(model_Percentile_70_mass_2)
summary(model_Percentile_70_mass_2)

############################################################################
###PERCENTILE 80

model_Percentile_80_mass<-lmer(Percentile_80~MASS+AGE+MASS:AGE+(1|NEST/CHICK)+(1|
GEL),data=table,na.action=na.omit)
plot(residuals(model_Percentile_80_mass))
anova(model_Percentile_80_mass)
summary(model_Percentile_80_mass)

model_Percentile_80_mass_2<-lmer(Percentile_80~MASS+AGE+(1|NEST/CHICK)+(1|
GEL),data=table,na.action=na.omit)
plot(model_Percentile_80_mass_2)
anova(model_Percentile_80_mass_2)
summary(model_Percentile_80_mass_2)

############################################################################
###PERCENTILE 90

model_Percentile_90_mass<-lmer(Percentile_90~MASS+AGE+MASS:AGE+(1|NEST/CHICK)+(1|
GEL),data=table,na.action=na.omit)
plot(residuals(model_Percentile_90_mass))
anova(model_Percentile_90_mass)
summary(model_Percentile_90_mass)

model_Percentile_90_mass_2<-lmer(Percentile_90~MASS+AGE+(1|NEST/CHICK)+(1|
GEL),data=table,na.action=na.omit)
plot(model_Percentile_90_mass_2)
anova(model_Percentile_90_mass_2)
summary(model_Percentile_90_mass_2)
```