

## **Table S1**

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## Script S1. R Scripts for statistical analysis

```
library(QuantPsyc)
library(boot)
library(car)
library(ggplot2)
library(devtools)
source_gist("524eade46135f6348140")
library(gdata)
library(phia)
library(nlme)
library(lme4)
library(lsmmeans)
library(compute.es);
library(Hmisc);
library(multcomp);
library(pastecs);
library(reshape);
library(WRS)
library(outliers)

#Install packages before running library() commands

#1. Correlation analyses for Supplementary Figs. S1, S2.

data <- read.csv("DATAFILE.csv", header = TRUE) #Read datafile into memory, file contains data for
all treatments & time-points

shapiro.test(data$VARIABLE) # Testing for normality

cor.test(data$VARIABLE1,data$VARIABLE2, use = "complete.obs", method = "pearson") #Pearson's
correlation analysis, where <VARIABLE1> and <VARIABLE2> are the column-headings of interest.

#2. Multivariate analysis of variance for Figs. 2B, C, D.

data <- read.csv("PostPreconditioningRaw.csv", header = TRUE) #Read datafile into memory, file
contains rawdata for post-preconditioning anemones ("PostPreconditioningRaw" worksheet)
```

```
leveneTest(VARIABLE ~ Treatment, data = data) # Homogeneity of variance test, repeat for each variable.
```

```
tapply(data$VARIABLE, data$VARIABLE, shapiro.test) # Testing for normality, repeat for each variable.
```

```
#Run the first MANOVA analysis - Raw data
```

```
multimod <- manova(cbind(log10(P.R), SymDensity, DR, Pgross, HostCS, sqrt(HostNQO), HostSDH, sqrt(HostCCO), SymCS, SymSDH, HostSOD) ~ Treatment, data = data)
```

```
summary(multimod, test = "Pillai")
```

```
summary.aov(multimod)
```

```
#Run the second MANOVA analysis - mETC complex activities normalised to CS activity.
```

```
multimod <- manova(cbind(HostSDH.CS, HostNQO.CS, HostCCO.CS, 1/sqrt(SymSDH.CS)) ~ Treatment, data = data)
```

```
summary(multimod, test = "Pillai")
```

```
summary.aov(multimod)
```

### #3. Linear Mixed Model Analyses for data in Fig. 3, 4, 5, 6B

```
data <- read.csv("HeatExptFvFm.csv", header = TRUE) #Read datafile into memory, file contains raw Fv/Fm data for anemones during acute heating experiment ("HeatExptFvFm" worksheet)
```

```
data$Day <- as.factor(data$Day) #Set numeric "Day" column as factor
```

```
tapply(data$FvFm, data$Day:data$Treatment, shapiro.test) #Test for normality
```

```
leveneTest(FvFm ~ Day*Treatment, data = data) #Test for homogeneity of variance
```

```
baseline <- lme(FvFm ~ 1, random = ~1 | Bowl/Day, data = data, method = "ML", na.action = na.exclude) #Create baseline model, random effect of replicate only, Day defined as within-subjects factor.
```

```
dayM <- update(baseline, .~. + Day)
```

```
treatmentM <- update(dayM, .~. + Treatment)
```

```
day_treatment <- update(treatmentM, .~. + Day:Treatment)
```

```
anova(baseline, dayM, treatmentM, day_treatment) #Test model fits
```

```
#Run exploratory analysis on model residuals. Plot histogram of residuals to confirm normal distribution.
```

```
plot(day_treatment)
```

```
plot(day_treatment, SOD1 ~ fitted(.) | Treatment, abline = c(0,1))
```

```
qqnorm(day_treatment,~resid(.)|Day)

qqnorm(day_treatment,~resid(.)|Treatment)

hist((resid(day_treatment) - mean(resid(day_treatment), na.rm=T)) / sd(resid(day_treatment),
na.rm=T), freq=F); curve(dnorm, add = TRUE)

anova(day_treatment) #Get ANOVA table for best-fitting model (lowest AIC value), assuming
residuals are normally distributed.

summary(glht(day_treatment, lsm(pairwise ~ Treatment|Day, adjust="tukey"))) #Post hoc pairwise
comparisons.

data <- read.csv("HeatExpt.csv", header = TRUE) #Read datafile into memory, file contains raw data
for anemones during acute heating experiment ("HeatExptFvFm" worksheet)

#Repeat the Linear Mixed Model analyses for each variable of interest.


#4. Multiple regression analyses testing the effect of treatment on the relationship between host
NQO and host CCO (Fig. 6A)

data <- read.csv("HeatExpt.csv", header = TRUE) #Read datafile into memory, file contains raw data
for anemones during acute heating experiment ("HeatExpt" worksheet)

#Subset treatment groups data

preconditioned <- subset(data, Treatment == "PC") #Select data for preconditioned anemones

control <- subset(data, Treatment == "CT") #Select data for control anemones

naive <- subset(data, Treatment == "NV") #Select data for naive anemones

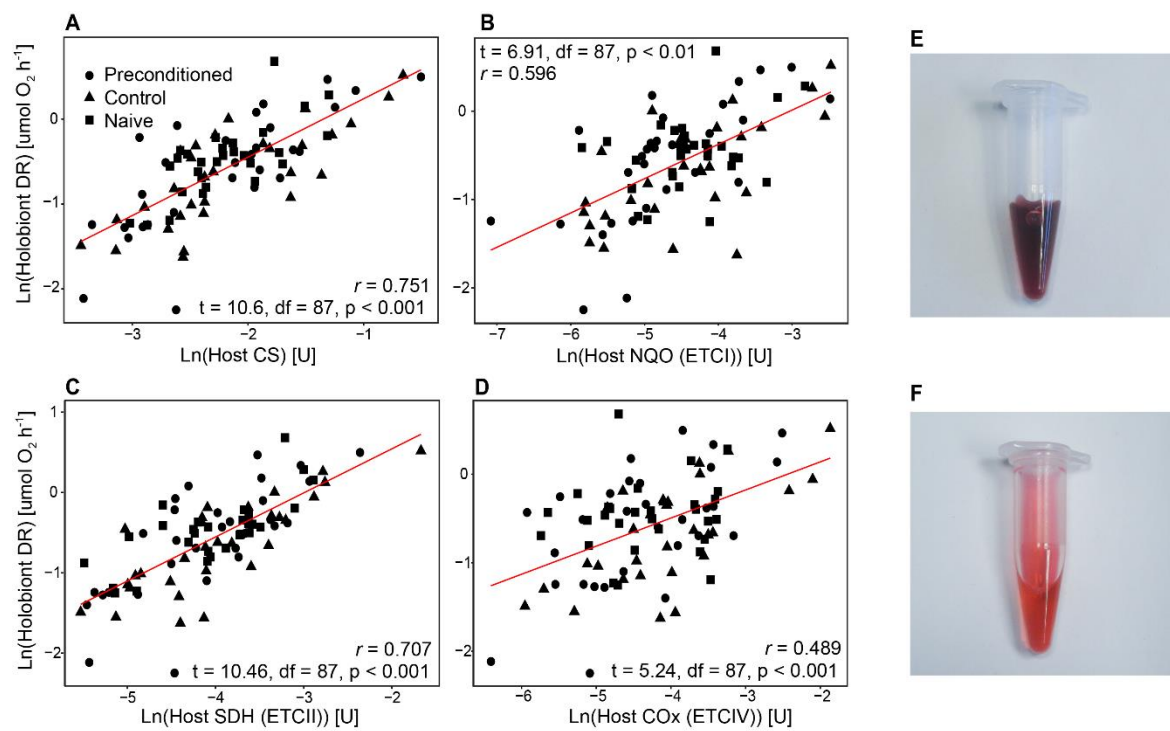
#Pearson's correlation analyses for Host NQO / Host CCO activity for each treatment group.

cor.test(preconditioned$HostNQO, preconditioned$HostCCO, use = "complete.obs", method =
"pearson")

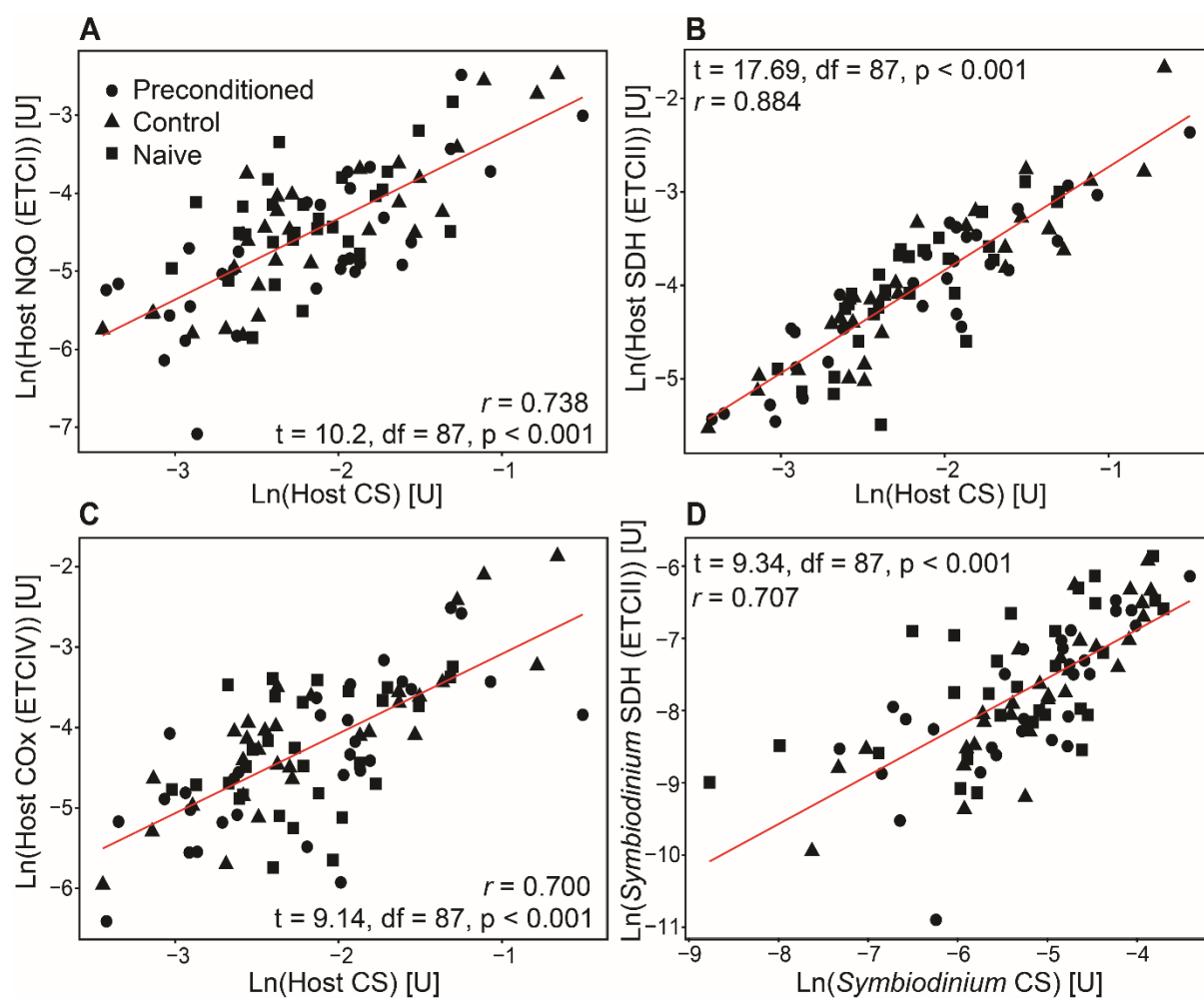
#Linear regression analyses of HostNQO and Treatment as predictors of Host CCO

regression <- lm(HostCCO ~ HostNQO + Treatment + HostNQO*Treatment, data = data, na.action =
na.exclude)

anova(regression)
```



**Fig. S1.** Pearson's correlation analysis of the relationship between holobiont dark respiration (DR) and host (A) citrate synthase (CS) activity, (B) NADH:coenzyme Q oxidoreductase (NQO) activity, (C) succinate dehydrogenase (SDH) activity, and (D) cytochrome *c* oxidase (COx) activity in *Exaiptasia pallida* anemones. All data are natural log-transformed. Panel E) Oxidised (brown) and (F) reduced (pink) cytochrome *c* (1 mM in 20 mM KPi buffer, pH 7.0).



**Fig. S2.** Pearson's correlation analysis of the relationship between host citrate synthase (CS) activity and (A) NADH:coenzyme Q oxidoreductase (NQO) activity, (B) succinate dehydrogenase (SDH) activity, and (C) cytochrome *c* oxidase (COx) activity. Panel D) Relationship between *Symbiodinium* CS and SDH activities. All data are natural log-transformed.