require("vegan"); library(ggplot2); library(ggpubr); library (readr); library(reshape2); library(car); library (dplyr)

Data <- read.table("DDSBiofilm.txt", row.names=1, sep="\t", header=T, blank.lines.skip=F, check.names=F)

pGrowth <- **ggplot**(Data, aes(x= Isolate, y=OD, fill= Trt )) +

**stat\_summary**(fun=mean, position=position\_dodge(), color="transparent", width=0.70, linewidth=0, geom="bar")+

**stat\_summary**(fun.data=mean\_se, geom="errorbar", position=position\_dodge(0.70),

width=0.40, linewidth=0.75, colour="black") +

scale\_y\_continuous (limits=c(0, 1.7), expand=c(0, 0.0001) ) + # , breaks=seq(0, 9, 2)

labs(x=NULL, y="Bacteria growth (OD600)")+

theme\_bw() +

theme(panel.grid=element\_blank(), axis.text=element\_text(size=9, color="black"), axis.title=element\_text(size=12) )

pGrowth

library(car); library(lsmeans); library(multcomp)

mydata <- **filter**(Data, Isolate =="RV33")

model<-lm(OD ~ Trt, data= mydata); #summary(model);

Anova(model, type="II")

marginal=lsmeans(model, ~ Trt); #pairs(marginal, adjust="fdr")

cld(marginal, alpha=0.05, Letters=letters, adjust="fdr", reversed=T)

mydata <- **filter**(Data, Isolate =="RV57")

model<-lm(OD ~ Trt, data= mydata); #summary(model);

Anova(model, type="II")

marginal=lsmeans(model, ~ Trt); #pairs(marginal, adjust="fdr")

cld(marginal, alpha=0.05, Letters=letters, adjust="fdr", reversed=T)

pBiofilm <- **ggplot**(Data, aes(x= Isolate, y= Biofilm, fill= Trt )) +

**stat\_summary**(fun=mean, position=position\_dodge(), color="transparent", width=0.70, linewidth=0, geom="bar")+

**stat\_summary**(fun.data=mean\_se, geom="errorbar", position=position\_dodge(0.70),

width=0.40, linewidth=0.75, colour="black") +

scale\_y\_continuous (limits=c(0, 1.25), expand=c(0, 0.0001) ) + # , breaks=seq(0, 9, 2)

labs(x=NULL, y="Biofilm formation (OD600)")+

theme\_bw() +

theme(panel.grid=element\_blank(), axis.text=element\_text(size=9, color="black"), axis.title=element\_text(size=12) )

pBiofilm

library(car); library(lsmeans); library(multcomp)

mydata <- **filter**(Data, Isolate =="RV33")

model<-lm(Biofilm ~ Trt, data= mydata); #summary(model);

Anova(model, type="II")

marginal=lsmeans(model, ~ Trt); #pairs(marginal, adjust="fdr")

cld(marginal, alpha=0.05, Letters=letters, adjust="fdr", reversed=T)

mydata <- **filter**(Data, Isolate =="RV57")

model<-lm(Biofilm ~ Trt, data= mydata); #summary(model);

Anova(model, type="II")

marginal=lsmeans(model, ~ Trt); #pairs(marginal, adjust="fdr")

cld(marginal, alpha=0.05, Letters=letters, adjust="fdr", reversed=T)

**ggarrange**(pGrowth, pBiofilm, ncol=2, nrow=1, align="hv", legend="none" )