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

Data <- read.table("REBiofilm.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, 2.2), 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 <- Data

model<-lm(OD ~ Trt.1, data= mydata); #summary(model); # Anova(model, type="II")

marginal=lsmeans(model, ~ Trt.1); #pairs(marginal, adjust="fdr")

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

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

**stats::t.test**(mydata $OD ~ mydata $Trt, p.adj="BH", var.equal=F) #Welch’s T test

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

**stats::t.test**(mydata $OD ~ mydata $Trt, p.adj="BH", var.equal=F) #Welch’s T test

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, 2.0), 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 <- Data

model<-lm(Biofilm ~ Trt.1, data= mydata); #summary(model); # Anova(model, type="II")

marginal=lsmeans(model, ~ Trt.1); #pairs(marginal, adjust="fdr")

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

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

**stats::t.test**(mydata $ Biofilm ~ mydata $Trt, p.adj="BH", var.equal=F) #Welch’s T test

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

**stats::t.test**(mydata $ Biofilm ~ mydata $Trt, p.adj="BH", var.equal=F) #Welch’s T test

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

####################DDS root exudates#########################################

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

pGrowth.DDS <- **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, 2.2), 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.DDS

library(car); library(lsmeans); library(multcomp)  
mydata <- Data

model<-lm(OD ~ Trt.1, data= mydata); #summary(model); # Anova(model, type="II")

marginal=lsmeans(model, ~ Trt.1); #pairs(marginal, adjust="fdr")

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

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

**stats::t.test**(mydata $OD ~ mydata $Trt, p.adj="BH", var.equal=F) #Welch’s T test

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

**stats::t.test**(mydata $OD ~ mydata $Trt, p.adj="BH", var.equal=F) #Welch’s T test

pBiofilm.DDS <- **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, 2.0), 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.DDS

library(car); library(lsmeans); library(multcomp)  
mydata <- Data

model<-lm(Biofilm ~ Trt.1, data= mydata); #summary(model); # Anova(model, type="II")

marginal=lsmeans(model, ~ Trt.1); #pairs(marginal, adjust="fdr")

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

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

**stats::t.test**(mydata $ Biofilm ~ mydata $Trt, p.adj="BH", var.equal=F) #Welch’s T test

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

**stats::t.test**(mydata $ Biofilm ~ mydata $Trt, p.adj="BH", var.equal=F) #Welch’s T test

pGrowth.0 <- pGrowth +coord\_cartesian(ylim = c(0.8, 2.2))

pBiofilm.0 <- pBiofilm +coord\_cartesian(ylim = c(0.6, 1.85))

pGrowth.DDS.0 <- pGrowth.DDS +coord\_cartesian(ylim = c(0.8, 2.2))

pBiofilm.DDS.0 <- pBiofilm.DDS +coord\_cartesian(ylim = c(0.6, 1.85))

**ggarrange**(pGrowth.0, pBiofilm.0, pGrowth.DDS.0, pBiofilm.DDS.0, ncol=4, nrow=1, align="hv", legend="none" )