library (stringr); library (vegan); library(reshape2); library (ggplot2); library(ggpubr)

myData.0 <- read.table("Rec.VOCDDS.txt", row.names=1, sep="\t", header=T, blank.lines.skip=F, check.names=F)

myData <- myData.0

myData$Pse <- log10(myData.0$Pse)

p.PseAb <- **ggplot**(myData, aes(x= **factor**(Trt, levels=c('CKVOC', 'VOC', 'CKDDS', 'DDS')), y= Pse, 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, 10), expand=c(0, 0.0001)) +

labs(x=NULL, y="Pseudomonas sp. (log10 copies g−1 soil)") +

theme\_bw() +

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

p.PseAb

( p.PseAb.0 <- p.PseAb +coord\_cartesian(ylim = c(6, 8.5)) )

library(car); library(multcompView); library(lsmeans); library(multcomp); library (dplyr)

mydata <- myData

model<-lm(Pse ~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$Bac <- log10(myData$Bac)

p.BacAb <- **ggplot**(myData, aes(x= **factor**(Trt, levels=c('CKVOC', 'VOC', 'CKDDS', 'DDS')), y= Bac, 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, 10), expand=c(0, 0.0001)) +

labs(x=NULL, y="Bacillus sp. (log10 copies g−1 soil)") +

theme\_bw() +

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

p.BacAb

( p.BacAb.0 <- p.BacAb +coord\_cartesian(ylim = c(6, 8.5)) )

library(car); library(multcompView); library(lsmeans); library(multcomp); library (dplyr)

mydata <- myData

model<-lm(Bac~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)

Biomass.bar <- **ggplot**(myData, aes(x= **factor**(Trt, levels=c('CKVOC', 'VOC', 'CKDDS', 'DDS')), y=Biomass, 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, 6.2), expand=c(0, 0.0001))+

labs(x=NULL, y="Plant dry biomass (g/plant)")+

theme\_bw() +

theme(panel.grid=element\_blank(), axis.text=element\_text(size=9, color="black"), legend.position="none", axis.title=element\_text(size=12) )

Biomass.bar

library(car); library(multcompView); library(lsmeans); library(multcomp); library (dplyr)

mydata <- myData

model<-lm(Biomass ~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**(Biomass.bar, p.PseAb.0, p.BacAb.0, ncol=3, nrow=1, align="hv", legend="none" )