####################Plotting properties of Δ*fub1* ########################

library(ggplot2); library(ggpubr); library (dplyr)

#####FA production of Δ*fub1* mutant#######

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

FA.Data $Time <- as.factor(FA.Data$Time)

Fub.FA <- **ggplot**(FA.Data, aes(x= Trt, y= FA )) + # fill = **factor**(Trt, levels= c('FOL', 'fub'))

**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, 105), expand=c(0, 0.0001) ) + # , breaks=seq(0, 9, 2)

facet\_wrap ( .~ **factor**(Time, levels=c('5', '10', '15')), scales = "fixed", nrow =1) +

labs(x=NULL, y="Fusaric acid content (ug/ml)")+

theme\_bw() +

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

Fub.FA

T.data <- FA.Data

T.data <- **filter**(T.data, Time =="15")

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

#######Disease forΔ*fub1*###########

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

Fub.DI <- **ggplot**(Data, aes(x= Cultivar, y= DI, fill = **factor**(Trt, levels= c('FOL', 'fub')) )) + #

**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, 85), expand=c(0, 0.0001) ) + # , breaks=seq(0, 9, 2)

labs(x=NULL, y="Fusarium wilt disease severity")+

theme\_bw() +

theme(panel.grid=element\_blank(),legend.title = element\_blank(),

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

Fub.DI

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

mydata <- Data

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

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

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

############Rhizosphere Sphingomonas sp. abundance###########

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

Data$Sph <- log10(Data$Sph)

fub.Sph <- **ggplot**(Data, aes(x= Cultivar, y=Sph, 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") +

labs(x=NULL, y="Sphingomonas sp. abundance (log10 copies/g soil)") +

theme\_bw() +

theme(panel.grid=element\_blank(),legend.title = element\_blank(),

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

fub.Sph

( fub.Sph.0 <- fub.Sph +coord\_cartesian(ylim = c(5, 8)) )

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

mydata <- Data

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

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

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

########## Sm12 abundance#########

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

Recruit$CFU <- log10(Recruit$CFU)

pRecruit.fub <- **ggplot**(Recruit, aes(x= Cultivar, y= CFU, fill = **factor**(Trt, levels= c('Control', 'FOL', 'fub') ) )) + #

**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") +

labs(x=NULL, y="Sm12 abundance (log10CFU/g soil)")+

theme\_bw() +

theme(panel.grid=element\_blank(),legend.title = element\_blank(),

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

pRecruit.fub

(pRecruit.fub.0 <- pRecruit.fub +coord\_cartesian(ylim = c(5, 8)) )

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

mydata <- Recruit

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

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

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

**ggarrange**(fub.Sph.0, pRecruit.fub.0, ncol=2, nrow=1, align = "hv", legend="none")