############## Plotting the root colonization of Sm12 as affected by FOL and its metabolites#########

library(ggplot2); library(ggpubr)

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

Recruit$CFU <- log10(Recruit$CFU)

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

**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.split

(pRecruit.split.0 <- pRecruit.split +coord\_cartesian(ylim = c(5, 7.5)) )

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="none", reversed=T)