#################FA Transplant disease################

library (ggplot2)

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

p.DI.FD.FA <- **ggplot**(Data.FD, aes(x= **factor**(Cultivar, levels=c('D72', 'Z19')) , y=FA.DI,

fill=**factor**(Trt, levels=c('D72-Control', 'D72-Sys', 'Z19-Control', 'Z19-Sys')) )) +

**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") +

# geom\_jitter(color="grey30", position=position\_jitter(0.20), size=2, alpha=1) +

# facet\_wrap ( .~ **factor**(Cultivar, levels=c('D72', 'Z19')), scales = "free", nrow =1) +

scale\_y\_continuous (limits=c(0, 100), expand=c(0, 0.01)) +

scale\_fill\_manual(values = c("cyan", "cyan4", "chartreuse", "darkolivegreen"), guide= "none") +

labs(x=NULL, y="Disease severity") +

theme\_bw() +

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

p.DI.FD.FA

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

mydata <- Data.FD

model<-lm(FA.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)