############Plotting for FOL abundance in tomato rhizosphere soils and root tissues ##############

library (ggplot2); library(ggpubr)

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

Data$FOL <- log10 (Data$FOL/10)

p.FOL <- **ggplot**(Data, aes(x=Cultivar, y=FOL) ) +

**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="FOL abundance (log10 copies/g soil)") +

theme\_bw() +

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

p.FOL

p.FOL.0 <- p.FOL +coord\_cartesian(ylim = c(2.5, 4.5))

p.FOL.0

Data$FOLroot <- log10 (Data$FOLroot/10)

p.FOLroot <- **ggplot**(Data, aes(x=Cultivar, y=FOLroot) ) +

**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="FOL abundance (log10 copies/g DW)") +

theme\_bw() +

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

p.FOLroot

p.FOLroot.0 <- p.FOLroot +coord\_cartesian(ylim = c(2.5, 4.5))

p.FOLroot.0

**ggarrange**(p.FOL.0, p.FOLroot.0, ncol=2, nrow=1, align="hv", legend="none" )

library (dplyr); mdata <- **filter**(Data, Trt=="Local")

**stats::t.test**(mdata $FOL ~ mdata $Cultivar, p.adj="BH", var.equal=F)

**stats::t.test**(mdata $FOLroot ~ mdata $Cultivar, p.adj="BH", var.equal=F)