library (vegan); library (ggplot2); library (ggpubr); library(ggrepel); library (Hmisc); library (simba); library (readr)

design\_filter\_16s<- read.table("design\_filter\_16s.txt", row.names=1, sep="\t", header=T, blank.lines.skip=F, check.names=F)

tax\_filter\_16s<- read.table("tax\_filter\_16s.txt", row.names=1, sep="\t", header=T, blank.lines.skip=F, check.names=F)

otu\_filter\_16s <- read.table("otu\_filter\_16s.txt", row.names=1, sep="\t", header=T, blank.lines.skip=F, check.names=F)

dim (otu\_filter\_16s)

####Whole####

otu\_filter\_16s.dist<-**vegdist**(**decostand**(t(otu\_filter\_16s), "hellinger"), method="bray", diag=TRUE, upper=TRUE)

otu\_filter\_16s.dist <- as.matrix(otu\_filter\_16s.dist)

otu\_filter\_16s.dist\_up <- otu\_filter\_16s.dist

otu\_filter\_16s.dist\_up [**upper.tri**(otu\_filter\_16s.dist\_up, diag=T)] <-NA

otu\_filter\_16s.dist\_up <- as.data.frame(otu\_filter\_16s.dist\_up)

otu\_filter\_16s.dist\_up <- **liste** (otu\_filter\_16s.dist\_up)

otu\_filter\_16s.dist\_up <- otu\_filter\_16s.dist\_up [which(otu\_filter\_16s.dist\_up $we!= "NA"), ]

dist.Whole <- otu\_filter\_16s.dist\_up

dist.Whole$group <- "aaWhole"

data<- dist.Whole

n<- 1

data$NBX <- as.character (data$NBX); data$NBY <- as.character (data$NBY)

data$NBX <-substr(data$NBX, 1, nchar(data$NBX)-1)

data$NBY <-substr(data$NBY, 1, nchar(data$NBY)-1)

dataB <- data # [which(data$NBX != data$NBY), ]

dataB$Group <- paste(dataB $ NBX, dataB $ NBY, sep="-")

dataB <- dataB [dataB $ Group %in% c("CK-WD", "CK-CU", "CK-RE"),]

dataB$we <- dataB$we\*100

p.dis <- **ggplot**(dataB, aes(x= **factor**(Group, levels=c("CK-WD", "CK-CU", "CK-RE")), y=we)) +

# **stat\_summary**(fun=mean, position=position\_dodge(), color="transparent", width=0.70, size=0, geom="bar")+

# **stat\_summary**(fun.data=mean\_se, geom="errorbar", position=position\_dodge(0.70), width=0.40, size=0.75, colour="black") +

geom\_jitter(color="grey50", position=position\_jitter(0.20), size=1.5, alpha=1) +

**geom\_boxplot**(alpha=1, outlier.size=1, outlier.shape=1, size=1.25, width=0.5, fill=NA ) + #

# scale\_fill\_manual(values = c("cyan3", "dodgerblue")) +

scale\_y\_continuous (limits=c(20, 35), expand=c(0, 0.01))+

labs(x=NULL, y="Bray-Curtis distance dissimilarity (%)")+

theme\_bw() +

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

#stat\_compare\_means(label="p.signif", comparisons=combn(levels(as.factor(dataB$Group)), 2, simplify=FALSE, paired="wilcox.test" ))

p.dis

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

mydata <- dataB

model<-lm(we ~ Group, data= mydata); #summary(model); #Anova(model, type="II")

marginal=lsmeans(model, ~ Group); #pairs(marginal, adjust="fdr")

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