#########Heatmap showing the changing patterns of bacterial genera altered by FOL and/or FA####

library(dplyr)

forMA.D72.FA<-read.table("forMA.D72.Genus.FA.txt", row.names=1, sep="\t", header=T, blank.lines.skip=F, check.names=F)

forMA.Z19.FA<-read.table("forMA.Z19.Genus.FA.txt", row.names=1, sep="\t", header=T, blank.lines.skip=F, check.names=F)

forMA.D72.FOL <-read.table("forMA.D72.Genus.txt", row.names=1, sep="\t", header=T, blank.lines.skip=F, check.names=F)

forMA.Z19.FOL <-read.table("forMA.Z19.Genus.txt", row.names=1, sep="\t", header=T, blank.lines.skip=F, check.names=F)

Pct <- 0.01; BM=50

D72.Sys\_En.FOL <- filter(forMA.D72.FOL, log2FoldChange>0&baseMean>BM & padj< Pct); dim (D72.Sys\_En.FOL)

D72.Sys\_De.FOL <- filter(forMA.D72.FOL, log2FoldChange<0&baseMean>BM & padj< Pct); dim (D72.Sys\_De.FOL)

Z19.Sys\_En.FOL <- filter(forMA.Z19.FOL, log2FoldChange>0&baseMean>BM & padj< Pct); dim (Z19.Sys\_En.FOL)

Z19.Sys\_De.FOL <- filter(forMA.Z19.FOL, log2FoldChange<0&baseMean>BM & padj< Pct); dim (Z19.Sys\_De.FOL)

Sys\_En.FOL = union( rownames(D72.Sys\_En.FOL), rownames(Z19.Sys\_En.FOL) )

Sys\_De.FOL = union( rownames(D72.Sys\_De.FOL), rownames(Z19.Sys\_De.FOL) )

De.En.All.FOL = union(Sys\_En.FOL, Sys\_De.FOL)

D72.Sys\_En.FA <- filter(forMA.D72.FA, log2FoldChange>0&baseMean>BM & padj< Pct); dim (D72.Sys\_En.FA)

D72.Sys\_De.FA <- filter(forMA.D72.FA, log2FoldChange<0&baseMean>BM & padj< Pct); dim (D72.Sys\_De.FA)

Z19.Sys\_En.FA <- filter(forMA.Z19.FA, log2FoldChange>0&baseMean>BM & padj< Pct); dim (Z19.Sys\_En.FA)

Z19.Sys\_De.FA <- filter(forMA.Z19.FA, log2FoldChange<0&baseMean>BM & padj< Pct); dim (Z19.Sys\_De.FA)

Sys\_En.FA = union( rownames(D72.Sys\_En.FA), rownames(Z19.Sys\_En.FA) )

Sys\_De.FA = union( rownames(D72.Sys\_De.FA), rownames(Z19.Sys\_De.FA) )

De.En.All.FA = union(Sys\_En.FA, Sys\_De.FA)

length(rownames(D72.Sys\_En.FOL))

length(rownames(D72.Sys\_En.FA))

length (intersect( rownames(D72.Sys\_En.FOL), rownames(D72.Sys\_En.FA) ) )

length(rownames(Z19.Sys\_En.FOL))

length(rownames(Z19.Sys\_En.FA))

length (intersect( rownames(Z19.Sys\_En.FOL), rownames(Z19.Sys\_En.FA) ) )

length(rownames(D72.Sys\_De.FOL))

length(rownames(D72.Sys\_De.FA))

length (intersect( rownames(D72.Sys\_De.FOL), rownames(D72.Sys\_De.FA) ) )

length(rownames(Z19.Sys\_De.FOL))

length(rownames(Z19.Sys\_De.FA))

length (intersect( rownames(Z19.Sys\_De.FOL), rownames(Z19.Sys\_De.FA) ) )

De.En.All = union(De.En.All.FOL, De.En.All.FA)

Cs = De.En.All

Heat.data <- forMA.D72.FOL [Cs, c("log2FoldChange", "padj") ]

colnames(Heat.data) <- c("FC.D72.FOL", "P.72")

Heat.data$ FC.Z19.FOL <- forMA.Z19.FOL [Cs, ]$ log2FoldChange

Heat.data$ FC.D72.FA <- forMA.D72.FA [Cs, ]$ log2FoldChange

Heat.data$ FC.Z19.FA <- forMA.Z19.FA [Cs, ]$ log2FoldChange

Heat.data <- Heat.data [ , -which(colnames(Heat.data) %in% c("P.72"))]

range(Heat.data)

library(pheatmap); library(RColorBrewer)

bk <- c(seq(-2.302, -0.1, by=0.01), seq(0,2.302,by=0.01))

pheatmap(Heat.data, clustering\_distance\_rows ="euclidean", # "euclidean", "maximum", "manhattan", "canberra", "binary" "minkowski"

clustering\_distance\_cols ="euclidean",

clustering\_method ="complete",

color=c(colorRampPalette(colors=c("dodgerblue2","white"))(length(bk)/2),colorRampPalette(colors=c("white","red3"))(length(bk)/2)),

legend\_breaks=seq(-2, 2, 1), breaks=bk,

fontsize=6, fontsize\_row=8)