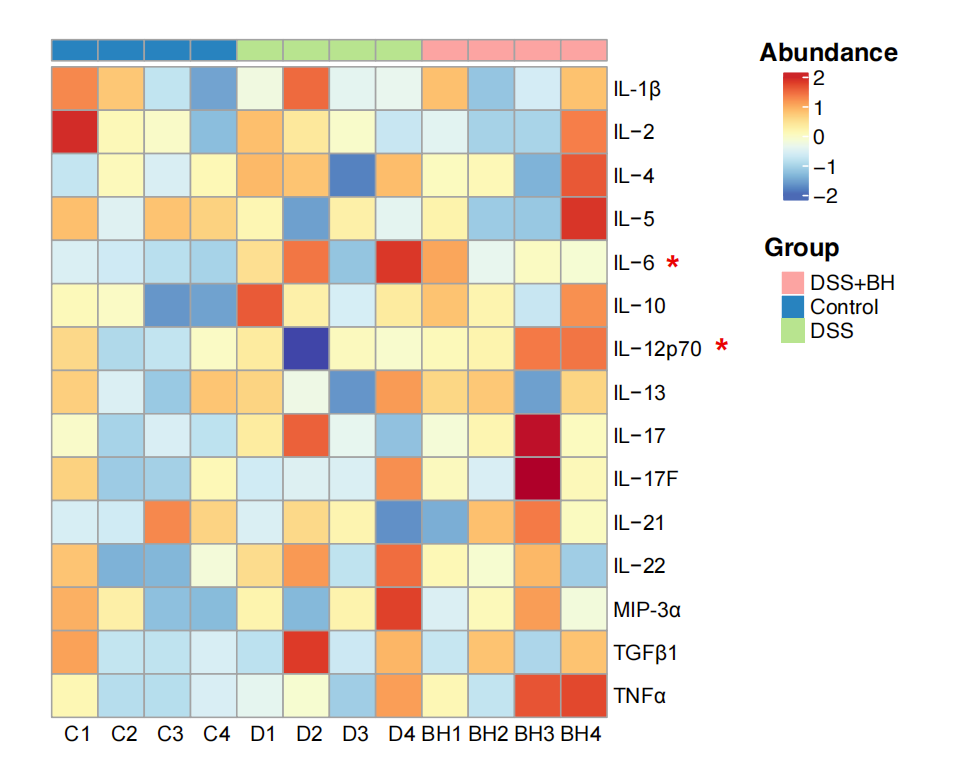
Fig3b



表格：metabolism\_factor.csv

使用软件：R

使用代码：

library(ComplexHeatmap)

library(grid)

factor<-read.csv("metabolism\_factor.csv",header=T,row.names=1)

factor<-log10(factor)

factor<-as.matrix(factor)

groupcolor<-c("#1F79B4","#B2DF8A","#33A02C")

names(groupcolor)<-c("C","D","BH")

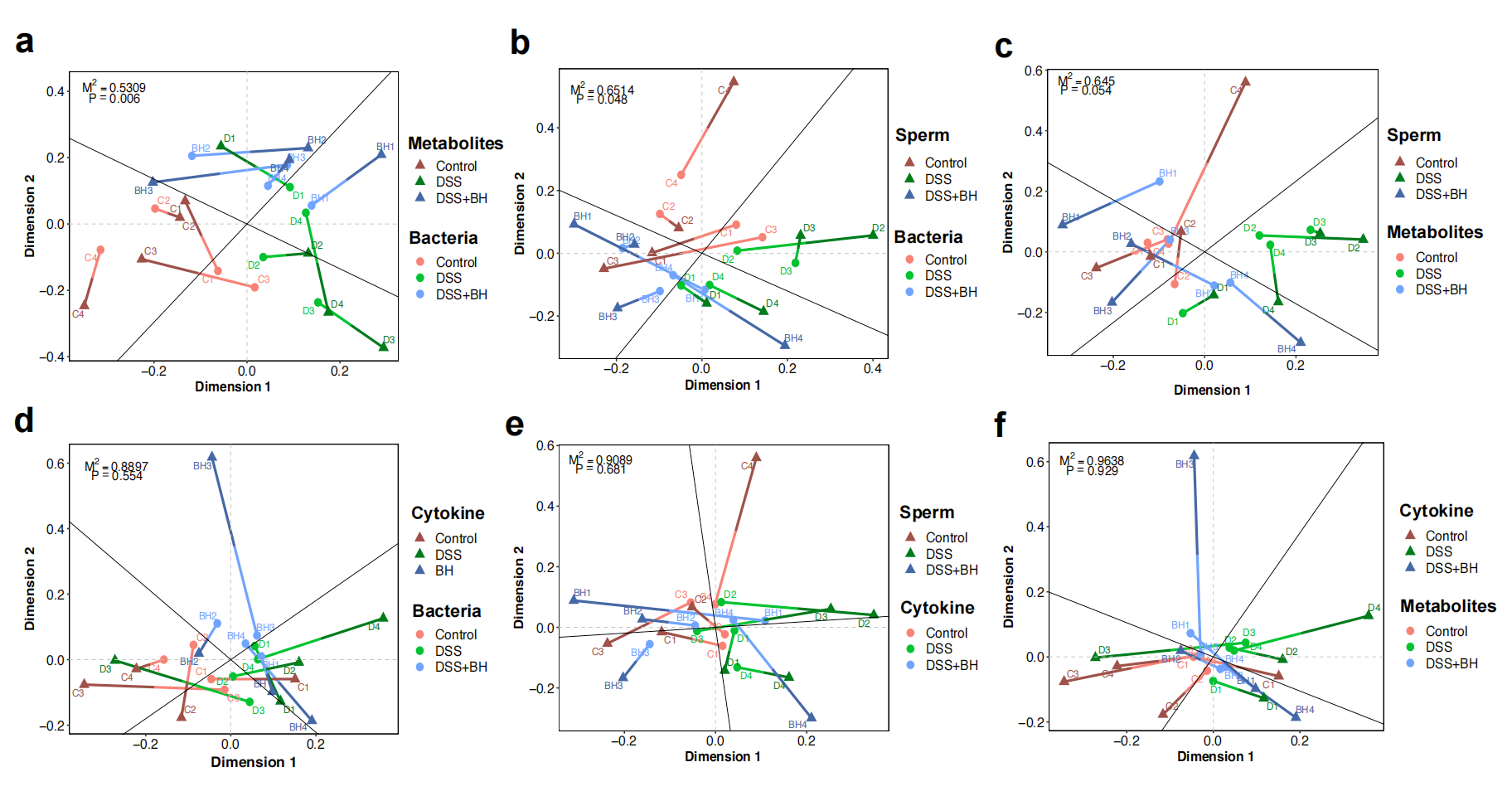
ann\_colors<-list(group=groupcolor)

ann\_colors=list(group=c(C="#1F79B4",D="#B2DF8A",BH="#33A02C"))

annotation\_col=data.frame(group=c(rep("C",4),rep("D",4),rep("BH",4)))

p3<-pheatmap(factor, scale="row", col=colorRampPalette(rev(brewer.pal(n = 11, name = "RdYlBu")))(20),annotation\_col=annotation\_col,annotation\_names\_col=F,cluster\_cols=FALSE,cluster\_rows=FALSE,annotation\_colors=ann\_colors)

Fig 6a-f



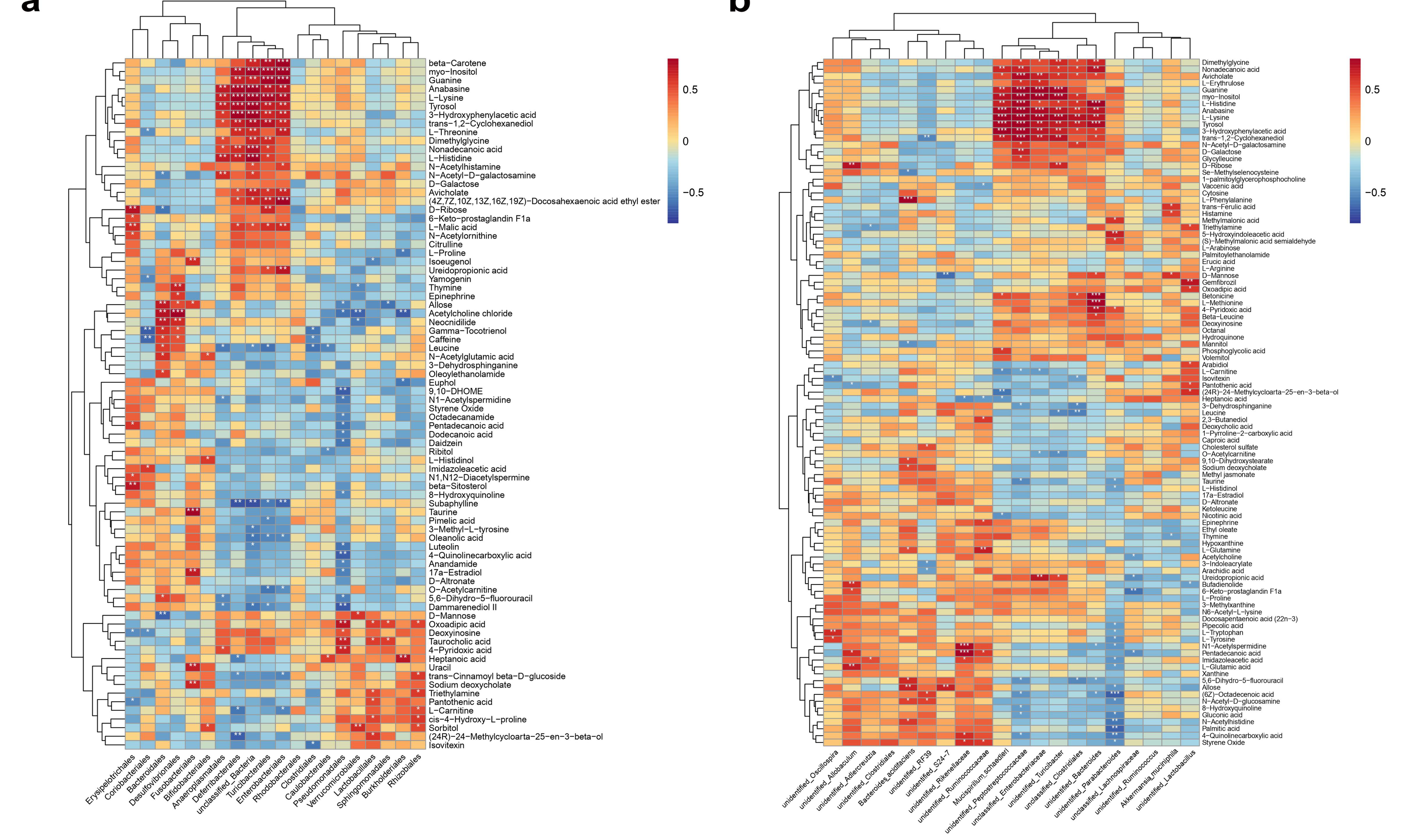
表格：mantel\_facor+metabolites+sperm.xlsx

mantel\_bacteria.xlsx

使用软件：R

绘图平台：<https://www.omicstudio.cn/tool>

Fig 6g-h



表格：cor\_metabolism.xlsx

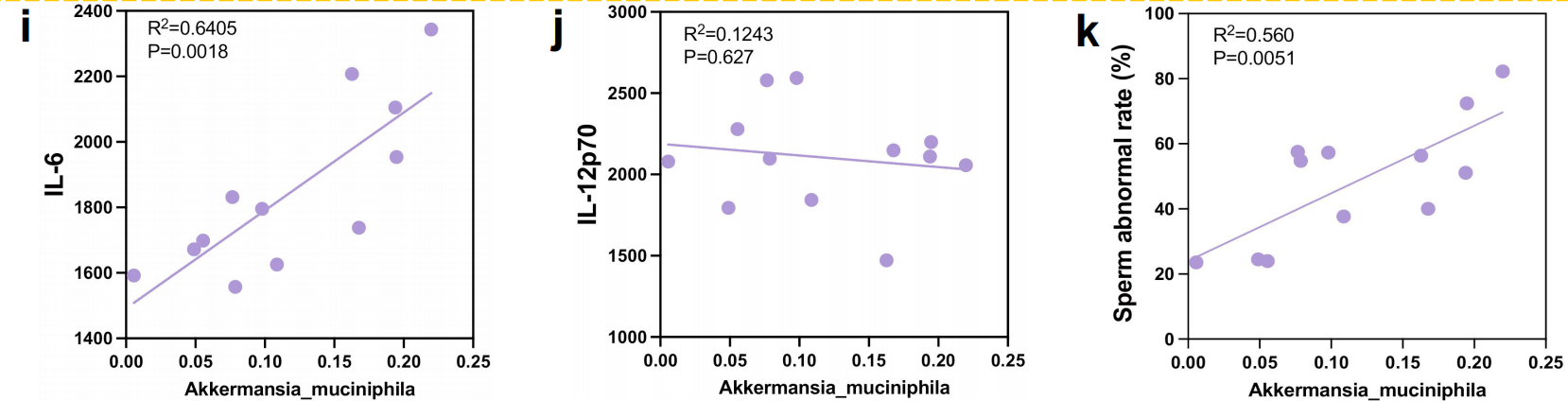
cor\_species.xlsx

cor\_order.xlsx

使用软件：R

绘图平台：<https://www.omicstudio.cn/tool>

Fig 6i-k



表格：correlation.xlsx

使用软件：graphpad prism9