相对丰度堆叠图（单个样本）

##需要的包

library(ggplot2)

library(ggprism)

library(dplyr)

library(plyr)

library(ggpubr)

library (reshape2)

library(tidyverse)

library(ggsci)

##数据准备：

①不同处理土壤样品的微生物组成数据，包括【物种丰度信息，分类单元信息】

②样本分组数据

##读入数据

##物种组成数据

sep <- read.csv("C:/Users/hp/Desktop/daotian/all\_bin\_coverm.csv", header=T,

row.names = 1, stringsAsFactors = TRUE,comment.char="",quote = "")

tax <- read.csv("C:/Users/hp/Desktop/daotian/all\_bin\_gtdbtk\_tax\_7904.csv", header=T,

row.names = 1,comment.char="",stringsAsFactors = TRUE,quote = "")

##检查数据格式

head(sep)

head(tax)

##配色

col <- pal\_d3("category20")(20)

col2 <- pal\_d3("category20",alpha = 0.5)(20)

mypal <- c(col,col2[-8])

my\_col <- c(#5196d5', '#F28E2F', '#E15759', '#76B7B2', '#59A14F', '#BAB0AC', '#FF9DA7', '#9C755F', '#B07AA1', '#86BCB6', '#79706E', '#D37295', '#A0D6EC', '#D4A6C8', '#8CD17D', '#EDC948' )

my\_col1 <- c('#5196d5', '#F28E2F', '#E15759', '#76B7B2', # 主类

'#59A14F', '#BAB0AC', '#FF9DA7', '#9C755F',

'#B07AA1', '#86BCB6', '#79706E', '#D37295', # 次类

'#A0D6EC', '#D4A6C8', '#8CD17D', '#EDC948' # 含纹理的次类

)

##目上的

order <- sep %>%

group\_by(tax$Order) %>%

summarise\_all(sum)

colnames(order)[1] <- "Order"

row\_sums <- rowSums(order[,-1])

order <- cbind(order, Total = row\_sums)

order <- order[order(order$Total, decreasing = TRUE),]

order <- order[,-ncol(order)]

other <- order[16:nrow(order),]

rownames(other) <- other[,1]

other <- other[,-1]

col\_sum <- colSums(other)

other <- rbind(other, Others = col\_sum)

others <- cbind(Order = "Others", other[nrow(other),])

order1 <- rbind(order[1:15,], others)

order\_LONG <- order1 %>%

gather(key = "Samples", value = "abun", -Order)

#### 相对丰度堆叠图（Order）

ggplot() +

geom\_bar(data = order\_LONG, aes(x = Samples, weight = abun, fill = reorder(Order, -abun)),

position = "fill", width = 0.5) +

scale\_fill\_manual(values = my\_col1) +

scale\_y\_continuous(expand = c(0, 0),