a1<-read.csv("F:/RyuyanYUYING/Acexu/CEXU/1111111.csv", header=T) names(data)

ggplot(data=data, aes(x=term.description,y=observed.gene.count, fill=category)) + geom\_bar(stat="identity", width=0.8)

library(ggplot2)

GO\_term\_order=factor(as.integer(rownames(data)),labels=data$term.description)

#66C3A5 #FD8D62 #66C3A5

COLS <- c("#66C3A5", "#FD8D62", "#FD8D62")

ggplot(data=data1, aes(x=GO\_term\_order,y=observed.gene.count, fill=category)) +

geom\_bar(stat="identity", width=0.8) +

scale\_fill\_manual(values = COLS) + theme\_bw() + coord\_flip() +

xlab("GO term") + ylab("Num of Genes") +labs(title = "The Most Enriched GO Terms")+

theme(axis.text.x=element\_text(face = "bold", color="gray50",angle = 0,vjust = 1, hjust = 1))+

theme(axis.text.y=element\_text(size=6))