library(pheatmap)#加载包

setwd("C:/Users/hao/Desktop/")#进入数据所在目录

data <- read.delim("WRKY-gene-expression.txt",header = T,row.names = 1)#数据一半为制表符分割,但是如果数据有空格分隔就会导致列数不对,用此函数导入

data <- as.matrix(data)#把数据转换为矩阵类型

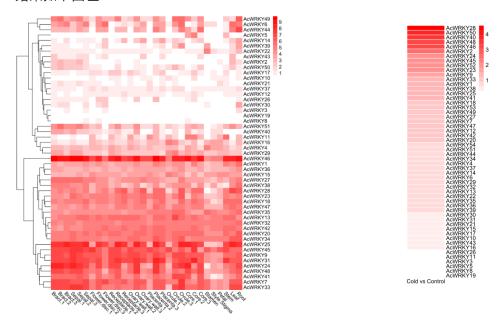
data <- log2(data+1)#对数据进行标准化处理,避免差异太大无法区分

pheatmap(data,cluster\_cols = FALSE,filename="expression.pdf",width = 9,height = 10,border=FALSE,legend\_breaks = c(1:15),

border\_color=NA,treeheight\_row = 80,margins = 5,clustering\_method = "average",angle\_col = "315",margins=5,

fontsize = 12,color = colorRampPalette(c("white","red"))(15))

## 结果如下图左:



dat <- read.delim("Cold-vs-Control-expression.txt",header = T,row.names = 1)

dat <- as.matrix(dat)

dat < - log2(dat+1)

 $pheatmap(dat,cluster\_cols = FALSE,filename="cold vs control.pdf",width = 5,height = 10,cluster\_rows = FALSE,border=FALSE,legend\_breaks = c(1:15),$ 

border\_color="white",cellwidth = 80,labels\_col =  $c("","","","Cold vs Control"),angle_col = "0",$ 

cellheight = 10,fontsize = 12,color = colorRampPalette(c("white","red"))(15)) #labels\_col = c("","","Cold vs Control"),为了只选取一列数据,原始数据有三列,没找到用一列数据绘制热图,所以把另外两列数据的表达量更改为零,即无颜色,然后将它们的名字不显示,最后得到上图右