limits<-floor(max(max(matrixCorr,na.rm = T),-1\*min(matrixCorr,na.rm = T))\*10)/10

bk <- c(seq(-1\*limits,-0.01,by=0.01),seq(0,limits,by=0.01))

c<-c(colorRampPalette(colors = c("blue","white"))(length(bk)/2),colorRampPalette(colors = c("white","red"))(length(bk)/2))

pheatmap(allr,color = c,display\_numbers = matrix(ifelse(allq < 0.001, "\*\*", ifelse(allq < 0.01, "\*", ifelse(allq < 0.05, "+", ""))), nrow(allq)),cellwidth = 7, cellheight = 7, fontsize\_row = 7, fontsize\_col = 7,breaks=bk,annotation\_row = annotation\_row,border=FALSE,width = 13, height = 11, units = 'in',dpi=600,filename = "all.png")

pheatmap(all,scale = "row",color = c,annotation\_col = annotation\_col,annotation\_row = annotation\_row,annotation\_colors=annotation\_colors,show\_colnames=F,cluster\_col=FALSE,breaks=0.01\*bk,cellwidth = 3, cellheight = 10, fontsize\_row = 10, fontsize\_col = 10,border=FALSE,filename = "all.png")

自定注释信息的颜色列表

ann\_colors = list( Time = c("white", "firebrick"), CellType = c(CT1 = "#1B9E77", CT2 = "#D95F02"), GeneClass = c(Path1 = "#7570B3", Path2 = "#E7298A", Path3 = "#66A61E") )