######## cancer normal ###########

library(ComplexHeatmap)

library(circlize)

data <- read.table("C:/Users/lenovo/Desktop/final\_",sep=",",header=TRUE,row.names=1)

mat = as.matrix(data[, grep("s", colnames(data))])

mat\_scaled = t(apply(mat, 1, scale))

type = gsub("s\\d+\_", "", colnames(mat))

ha = HeatmapAnnotation(df = data.frame(type = type), col = list(type = c("Cancer" = "pink", "Normal" = "cyan")))

Heatmap(mat\_scaled, cluster\_columns = FALSE, show\_row\_dend = FALSE, name = "methylation", km = 5, col = colorRamp2(c(-2, 0, 2), c("dark green", "white", "red")),

top\_annotation = ha, top\_annotation\_height = unit(4, "mm"),

show\_row\_names = TRUE, row\_names\_side = "left", row\_names\_gp = gpar(fontsize = 1.2), show\_column\_names = FALSE, ) +

Heatmap(data$ROC, name = "ROC", width = unit(5, "mm"), col = colorRamp2(c(1.0, 0.8), c("dark blue", "light blue")))

############## early v/s late #############

library(ComplexHeatmap)

library(circlize)

data <- read.table("C:/Users/lenovo/Desktop/final\_",sep=",",header=TRUE,row.names=1)

mat = as.matrix(data[, grep("s", colnames(data))])

mat\_scaled = t(apply(mat, 1, scale))

type = gsub("s\\d+\_", "", colnames(mat))

ha = HeatmapAnnotation(df = data.frame(type = type), col = list(type = c("Early\_stage" = "pink", "Late\_stage" = "cyan")))

Heatmap(mat\_scaled, cluster\_columns = FALSE, show\_row\_dend = FALSE, name = "Methylation", km = 5, col = colorRamp2(c(-2, 0, 2), c("dark green", "white", "red")),

top\_annotation = ha, top\_annotation\_height = unit(4, "mm"),

show\_row\_names = TRUE, row\_names\_side = "left", row\_names\_gp = gpar(fontsize = 8.5), show\_column\_names = FALSE, ) +

Heatmap(data$ROC, name = "ROC", width = unit(5, "mm"), col = colorRamp2(c(0.7, 0.65, 0.6), c("magenta4", " magenta3", " linen")))

Input matrix header should be like this

Gene\_symbol,s1\_Normal,s2\_Normal,s3\_Normal,s4\_Normal,s5\_Normal,s6\_Normal,s7\_Normal,s8\_Normal,s9\_Normal,s10\_Normal,s11\_Normal,s12\_Normal,s13\_Normal,s14\_Normal,s15\_Normal,s16\_Normal,s17\_Normal,s18\_Normal,s19\_Normal,s20\_Normal,s21\_Normal,s22\_Normal,s23\_Normal,s24\_Normal,s25\_Normal,s26\_Normal,s27\_Normal,s28\_Normal,s29\_Normal,s30\_Normal,s31\_Normal,s32\_Normal,s33\_Normal,s34\_Normal,s35\_Normal,s36\_Normal,s37\_Normal,s38\_Normal,s39\_Normal,s40\_Normal,s41\_Normal,s42\_Normal,s43\_Normal,s44\_Normal,s45\_Normal,s46\_Normal,s47\_Normal

######## cancer normal ###########

library(ComplexHeatmap)

library(circlize)

data <- read.table("C:/Users/lenovo/Desktop/final\_",sep=",",header=TRUE,row.names=1)

mat = as.matrix(data[, grep("s", colnames(data))])

mat\_scaled = t(apply(mat, 1, scale))

type = gsub("s\\d+\_", "", colnames(mat))

ha = HeatmapAnnotation(df = data.frame(Sample\_type = type), col = list(type = c("Cancer" = "pink", "Normal" = "megenta")))

## Heatmap(mat\_scaled,top\_annotation = ha, cluster\_columns = FALSE, cluster\_rows = FALSE, show\_row\_dend = FALSE, name = "expression", show\_row\_names = TRUE, row\_names\_side = "left", row\_names\_gp = gpar(fontsize = 10), show\_column\_names = FALSE )+ Heatmap(data$ROC, name = "ROC", width = unit(5, "mm"),)

Heatmap(mat\_scaled,top\_annotation = ha, cluster\_columns = FALSE, cluster\_rows = FALSE, show\_row\_dend = FALSE, name = "Expression", show\_row\_names = TRUE, col = colorRamp2(c(-2, 0, 2), c("dark green", "light yellow", "red")), row\_names\_side = "left", row\_names\_gp = gpar(fontsize = 10), show\_column\_names = FALSE )+

Heatmap(data$ROC, name = "ROC", width = unit(5, "mm"),)

Heatmap(mat\_scaled,top\_annotation = ha, cluster\_columns = FALSE, cluster\_rows = FALSE, show\_row\_dend = FALSE, name = "Expression", show\_row\_names = TRUE, col = colorRamp2(c(-2, 0, 2), c("dark green", "white", "red")), row\_names\_side = "left", row\_names\_gp = gpar(fontsize = 10), show\_column\_names = FALSE )+

Heatmap(data$ROC, name = "ROC", width = unit(5, "mm"),)