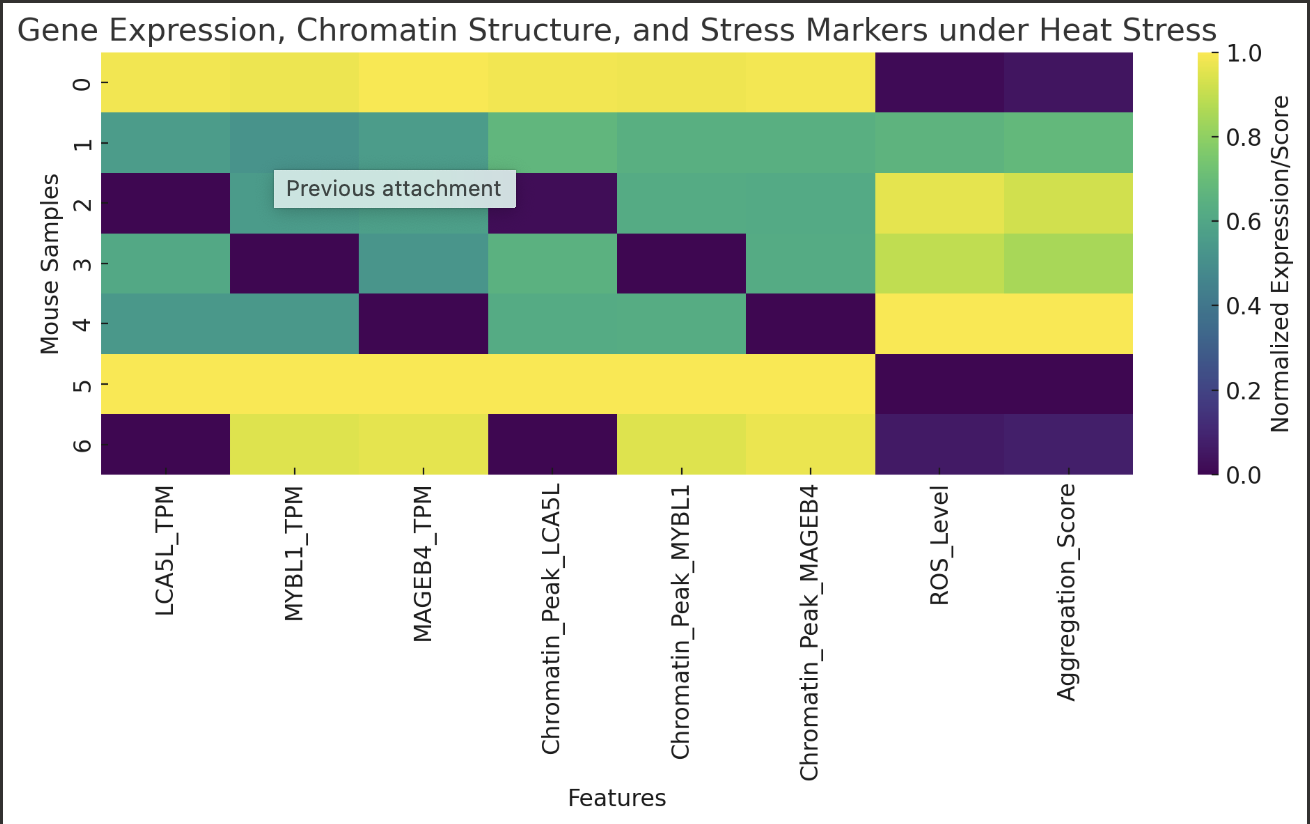
Data Generated from ChatGpt

Graph that was Generated

install.packages("readxl")

install.packages("pheatmap")

# Load necessary libraries

library(readxl)

library(pheatmap)

# Load the data

data <- read\_excel("Heat\_Stress\_Spermatogenesis\_Data.xlsx")

# Select relevant columns for heatmap

heatmap\_data <- data[, c("LCA5L\_TPM", "MYBL1\_TPM", "MAGEB4\_TPM",

"Chromatin\_Peak\_LCA5L", "Chromatin\_Peak\_MYBL1", "Chromatin\_Peak\_MAGEB4",

"ROS\_Level", "Aggregation\_Score")]

# Normalize data (min-max scaling)

normalize <- function(x) {(x - min(x)) / (max(x) - min(x))}

normalized\_data <- as.data.frame(lapply(heatmap\_data, normalize))

# Set row names to Mouse\_ID or Genotype for easier interpretation

rownames(normalized\_data) <- paste(data$Mouse\_ID, data$Genotype, data$Condition, sep = "\_")

# Create the heatmap

pheatmap(normalized\_data,

cluster\_rows = TRUE,

cluster\_cols = TRUE,

color = colorRampPalette(c("navy", "white", "firebrick3"))(50),

main = "Heatmap: Gene Expression, Chromatin State, and Stress Markers")

Code Ran