My_Graphs Part 2

2024-08-07

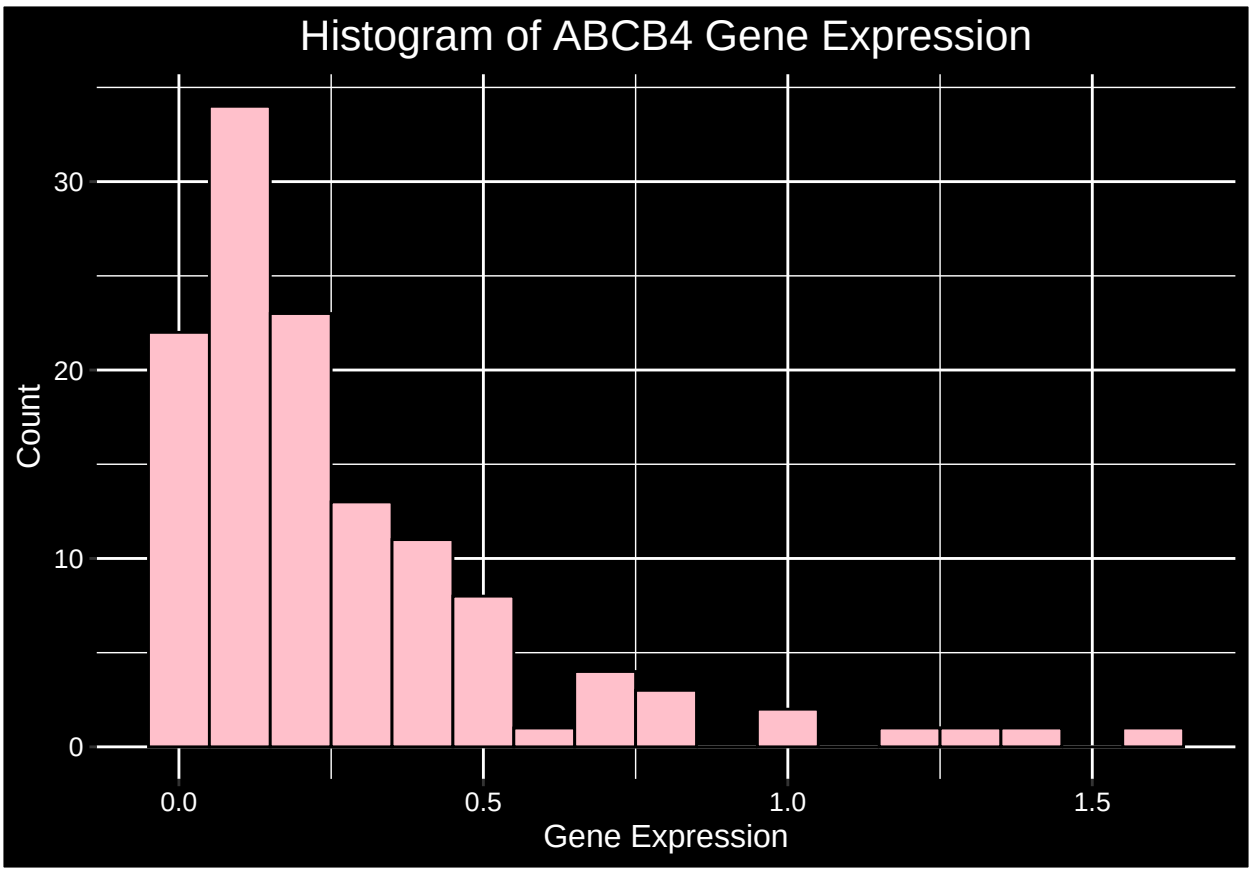
```
library(tidyverse)
```

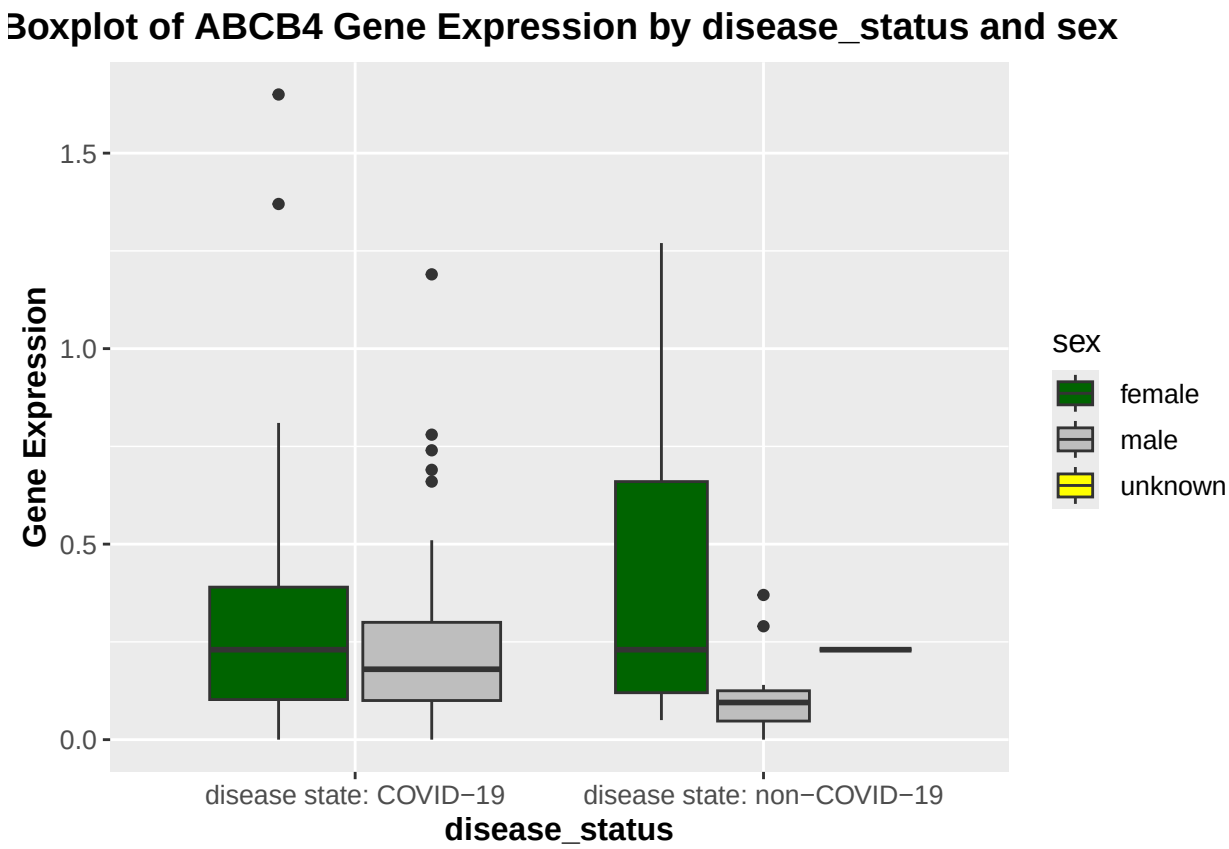
```
## -- Attaching core tidyverse packages ------------------------ tidyverse 2.0.0 --
## v dplyr     1.1.4     v readr     2.1.5
## v forcats   1.0.0     v stringr   1.5.1
## v ggplot2   3.5.1     v tibble    3.2.1
## v lubridate 1.9.3     v tidyr     1.3.1
## v purrr     1.0.2
## -- Conflicts ------------------------------------------ tidyverse_conflicts() --
## x dplyr::filter() masks stats::filter()
## x dplyr::lag()    masks stats::lag()
## i Use the conflicted package (<http://conflicted.r-lib.org/>) to force all conflicts to become errors
```

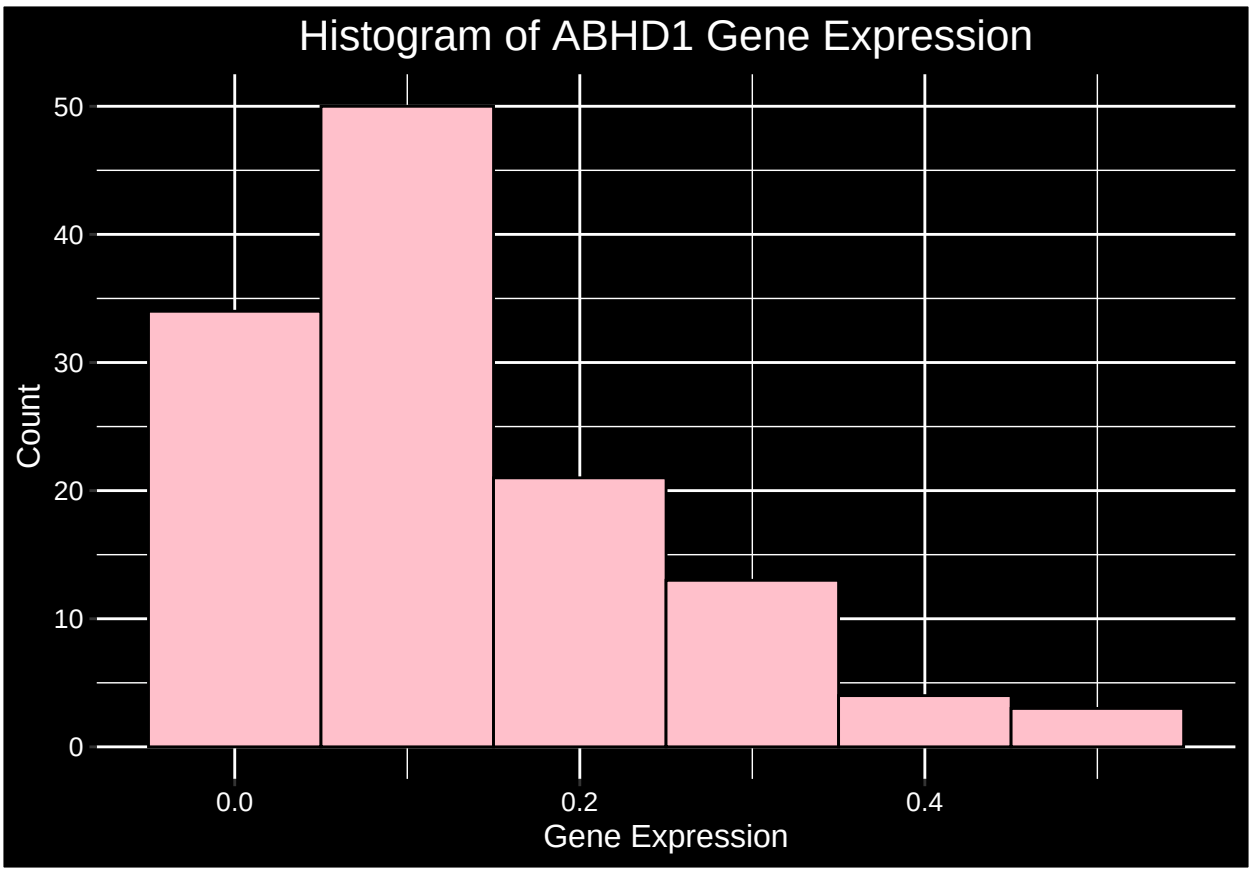
```
#cannot call within function, must call outside
gene_express_df <- read.csv("C:/Users/casha/Downloads/QBS103_GSE157103_genes.csv", row.names = 1)
metadata_df <- read.csv("C:/Users/casha/Downloads/QBS103_GSE157103_series_matrix.csv")

#establish function per parametes
#https://www.dataquest.io/blog/write-functions-in-r/
gene_plots <- function(data_frame, name_genes, continuous_covariate,  categorical_covariate_one, categor

# How to create a for loop in R-Studio:https://www.geeksforgeeks.org/for-loop-in-r/
  for (gene in name_genes) {
    gene_expression <- data_frame %>%
      rownames_to_column("gene") %>% #rows to columns
      filter(gene == !!gene) %>% #ONLY INCLUDE what matches the gene we're asking for

#wide format to long format
      pivot_longer(cols = -gene, names_to = "participant_id", values_to = "expression") %>%
      select(-gene)

  # Merge expression data with metadata
    merged_df <- gene_expression %>%
#https://www.datacamp.com/tutorial/merging-data-r: How to merge 2 datasets in R
      merge(metadata_df, by = "participant_id")




# Histogram
    histogram <- ggplot(merged_df, aes(x = expression)) + #define histogram
#https://www.datacamp.com/tutorial/make-histogram-basic-r
      geom_histogram(binwidth = 0.1, fill = "pink", color = "black") + #binwidth is how wide we want ea
      labs(
```

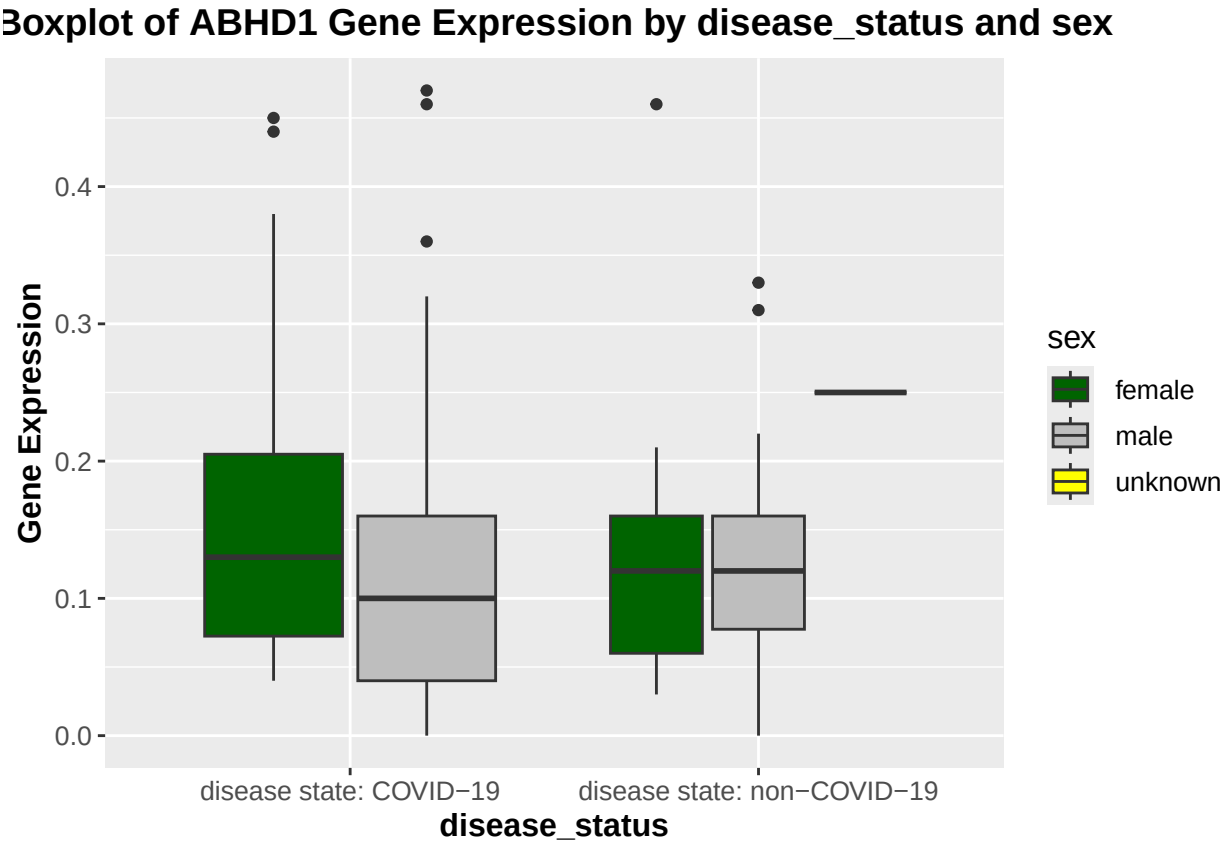
```
        title = paste("Histogram of", gene, "Gene Expression"),
        x = "Gene Expression",
        y = "Count" #number which falls within THIS level of gene expression
      ) +
      theme(
        plot.background = element_rect(fill = "black"),
        panel.background = element_rect(fill = "black"),
        text = element_text(size = 12, color = "white"),
        plot.title = element_text(hjust = 0.5, size = 16, color = "white"),
        axis.text = element_text(color = "white") #changes the color of the numbers on gridlines
  )

    print(histogram)




# Boxplot
    boxplot <- ggplot(merged_df, aes(x = .data[[categorical_covariate_one]], y = expression, fill = .da
      geom_boxplot() +
#Define colors: Have to use three colors because sex is female, male, and unknown
      scale_fill_manual(values = c('darkgreen', 'grey', 'yellow')) +
      labs(
        title = paste("Boxplot of", gene, "Gene Expression by", categorical_covariate_one, "and", categ
        x = categorical_covariate_one,
        y = "Gene Expression"
      ) +
      theme(
        text = element_text(size = 12),
        plot.title = element_text(hjust = 0.5, face = "bold", size = 14),
        axis.title = element_text(face = "bold")
  )

    print(boxplot)
  }
} #MAKE SURE TO CLOSE BRACKET OR FUNCTION WILL NOT RUN
```

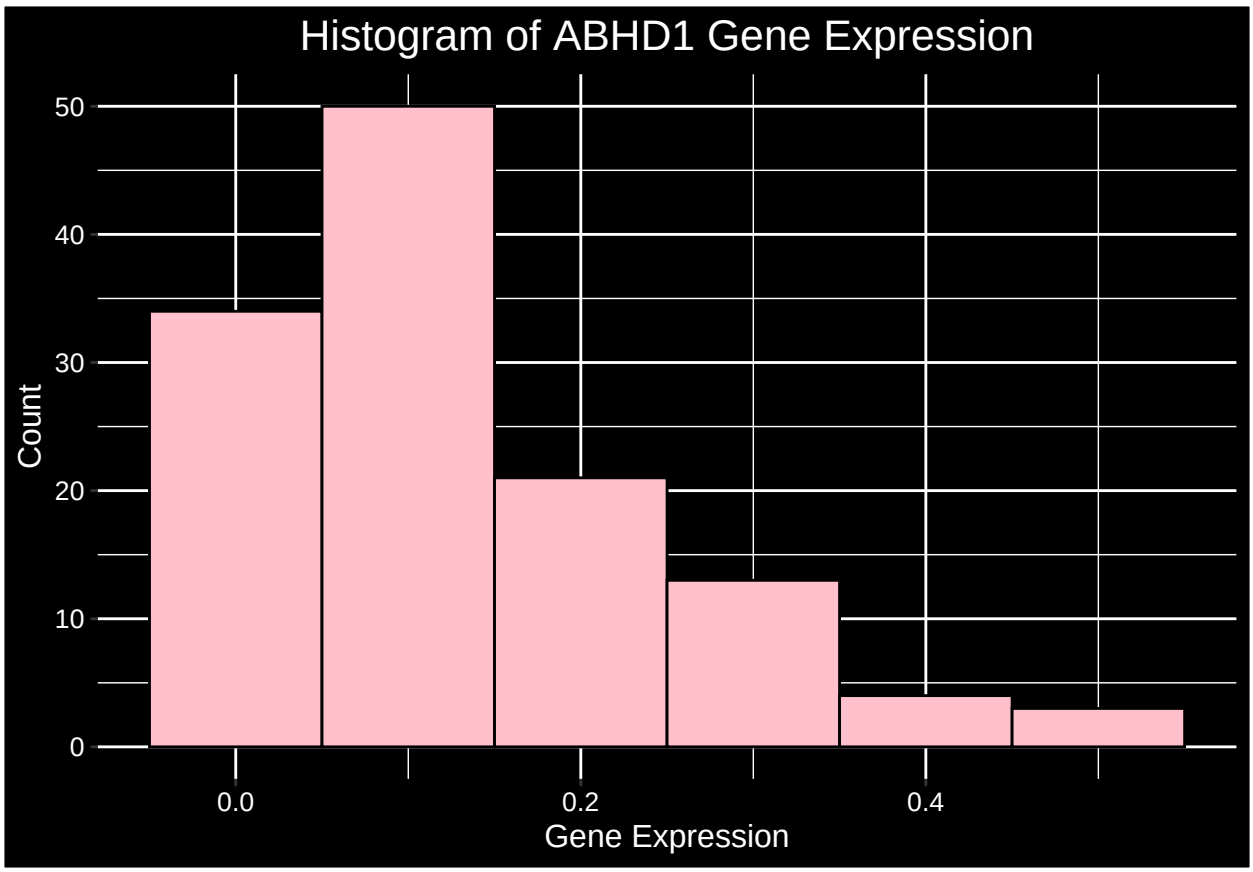
```
# Define the genes to plot
genes_want <- c("ABCB4", "ABHD1", "ABHD1")

# Call the function using original form of: "data_frame, name_genes, continuous_covariate, categorical_
gene_plots(gene_express_df, genes_want, "age", "disease_status", "sex")
```

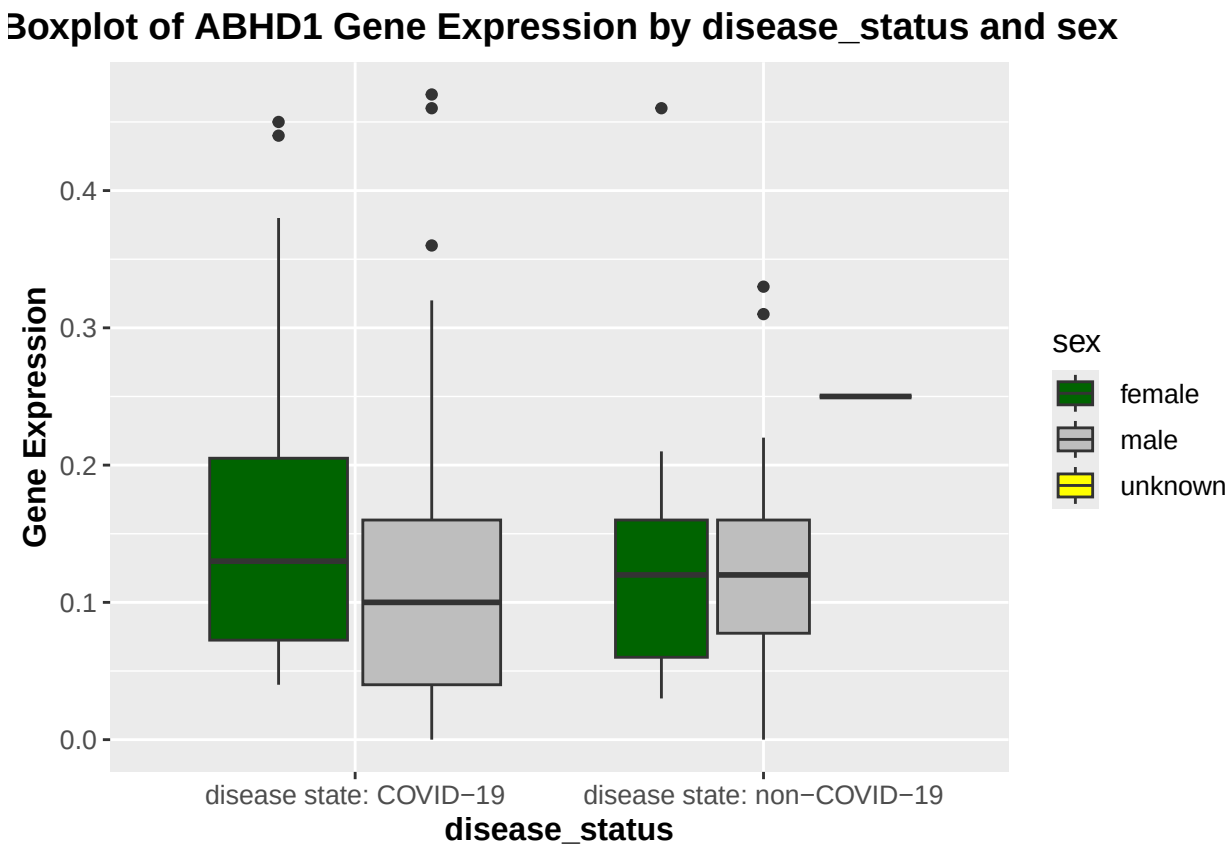

Histogram of ABCB4 Gene Expression
Count
30
20
10
0
0.0
0.5
1.0
1.5
Gene Expression


Boxplot of ABCB4 Gene Expression by disease_status and sex
Gene Expression
1.5
1.0
0.5
0.0
disease state: COVID−19
disease state: non−COVID−19
disease_status
sex
female
male
unknown


Histogram of ABHD1 Gene Expression
Count
50
40
30
20
10
0
0.0
0.2
0.4
Gene Expression


Boxplot of ABHD1 Gene Expression by disease_status and sex
Gene Expression
0.0
0.1
0.2
0.3
0.4
disease state: COVID−19
disease state: non−COVID−19
disease_status
sex
female
male
unknown


Histogram of ABHD1 Gene Expression
Count
50
40
30
20
10
0
0.0
0.2
0.4
Gene Expression


Boxplot of ABHD1 Gene Expression by disease_status and sex
Gene Expression
0.0
0.1
0.2
0.3
0.4
disease state: COVID−19
disease state: non−COVID−19
disease_status
sex
female
male
unknown