QBS103_Final_Project

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Importing packages

```
## -- 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   3.5.2     v tibble    3.3.0
## v lubridate 1.9.4     v tidyr     1.3.1
## v purrr     1.0.4
## -- 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
##
## Attaching package: 'reshape2'
##
##
## The following object is masked from 'package:tidyr':
##
##     smiths
##
##
##
## Attaching package: 'kableExtra'
##
##
## The following object is masked from 'package:dplyr':
##
##     group_rows
```

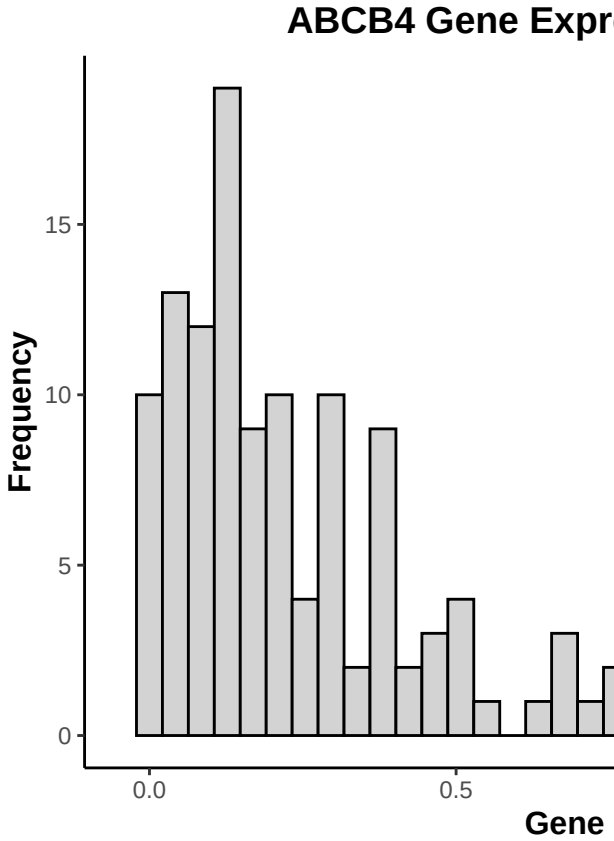
Importing and tidying data

```
## New names:
## Rows: 100 Columns: 127
## -- Column specification
## -------------------------------------------------------- Delimiter: "," chr
## (1): ...1 dbl (126): COVID_01_39y_male_NonICU, COVID_02_63y_male_NonICU,
## COVID_03_33y_...
## i Use `spec()` to retrieve the full column specification for this data. i
## Specify the column types or set `show_col_types = FALSE` to quiet this message.
## Rows: 126 Columns: 25
## -- Column specification
```

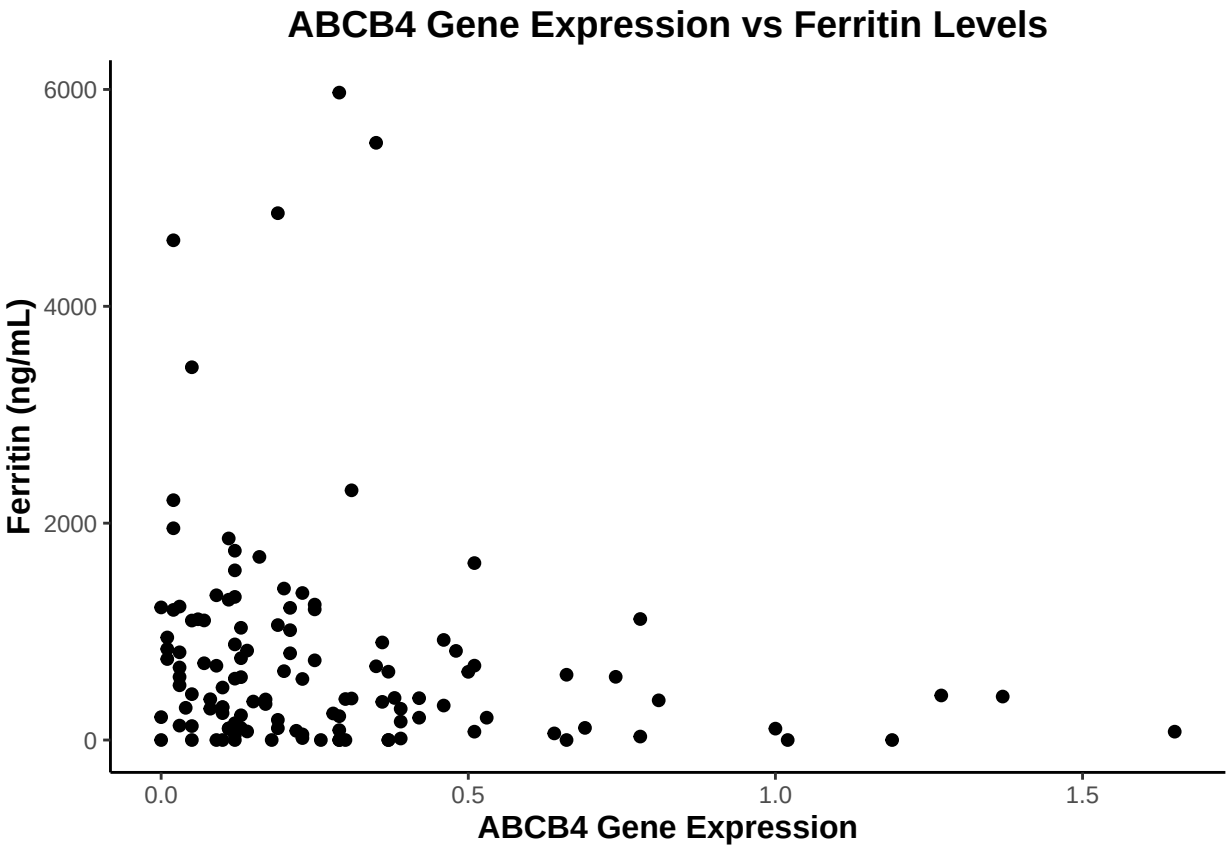
```
## ------------------------------------------------------- Delimiter: "," chr
## (21): participant_id, geo_accession, status, !Sample_submission_date, la... dbl
## (4): channel_count, charlson_score, ventilator-free_days, hospital-free...
## i Use `spec()` to retrieve the full column specification for this data. i
## Specify the column types or set `show_col_types = FALSE` to quiet this message.
## * `` -> `...1`
```

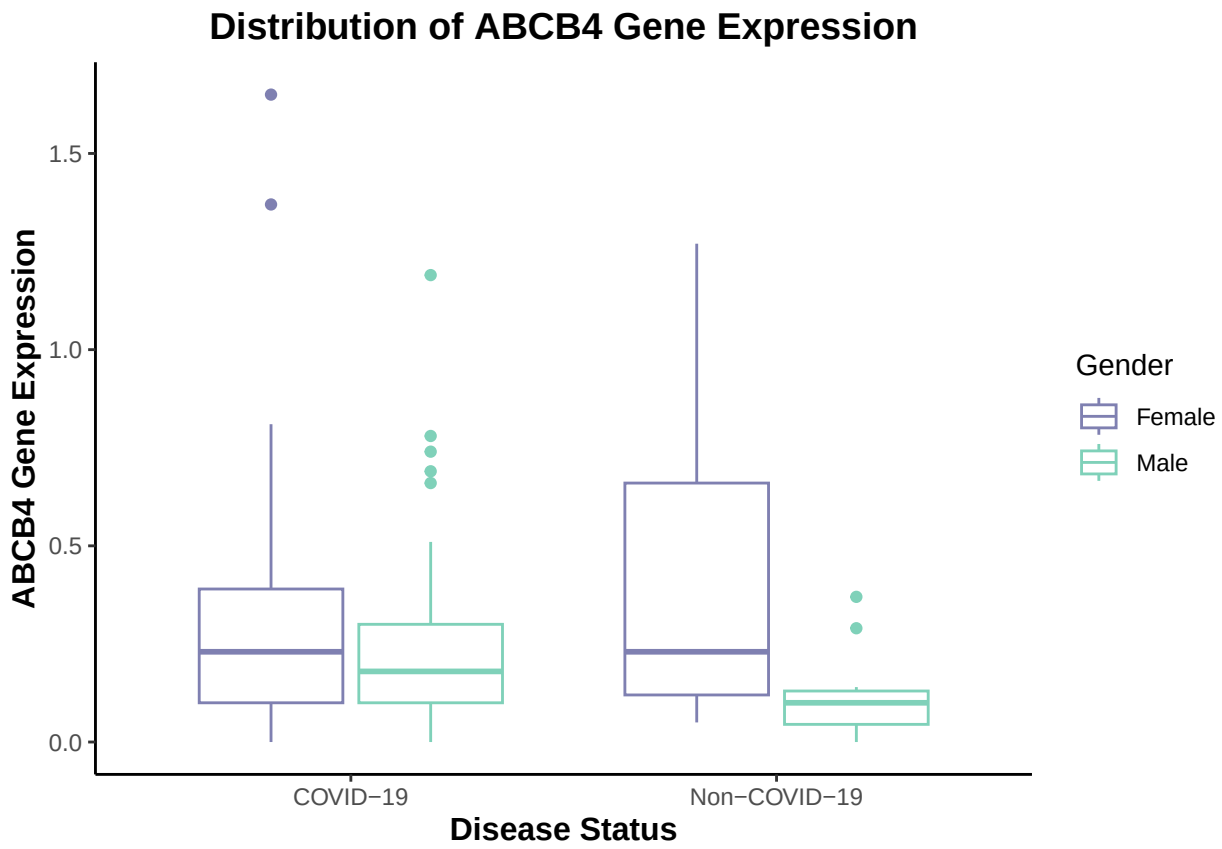
```
## Warning: NAs introduced by coercion
```

Latex Table Generation. Code is commented to remove outputs.



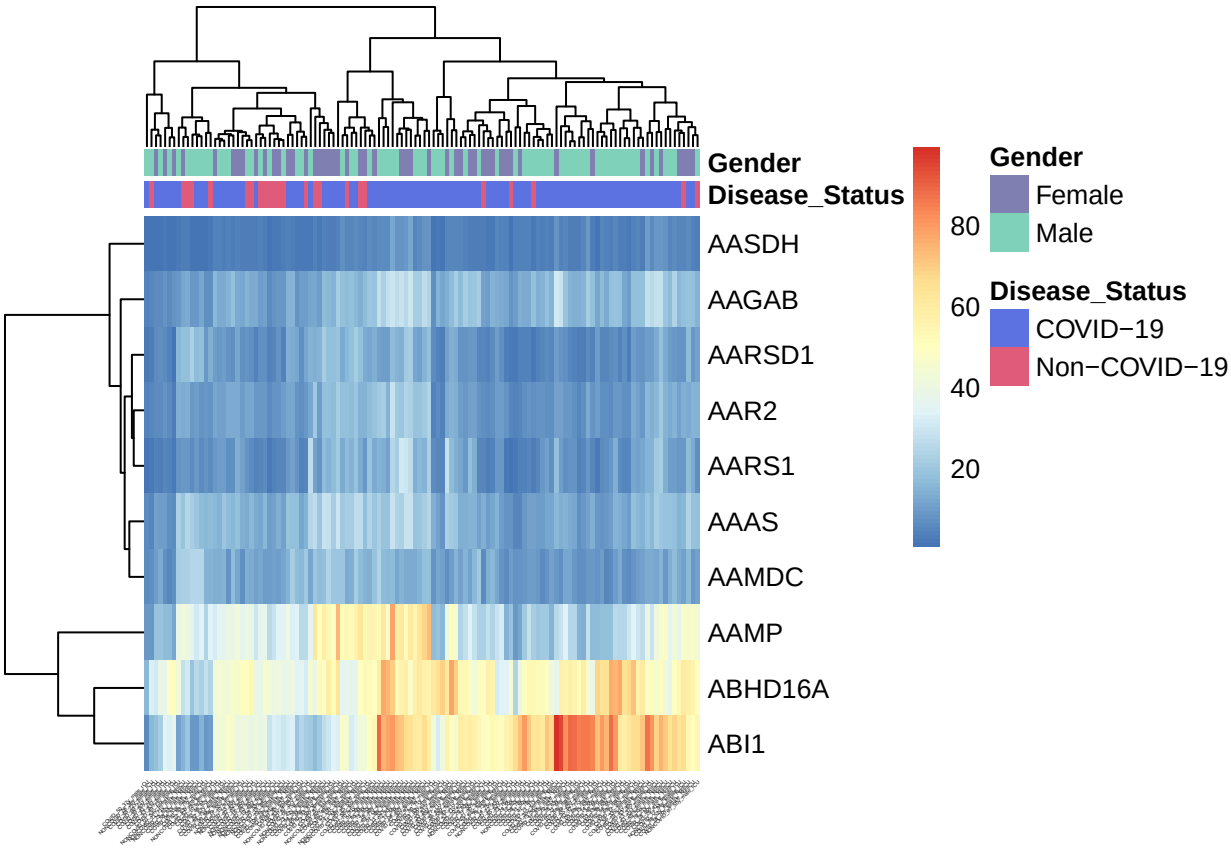
Histogram, scatterplot, and boxplot from submission 1 of gene ABCB4.

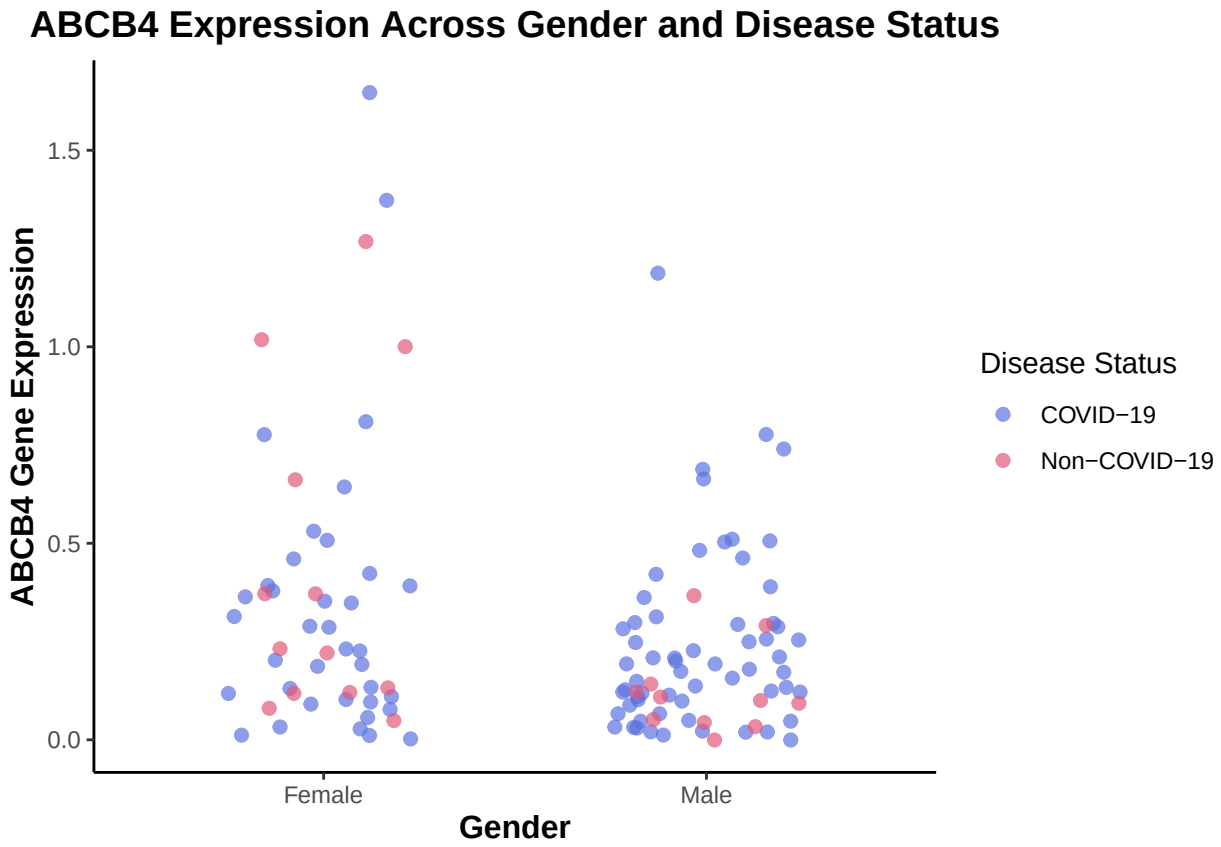

ABCB4 Gene Expression vs Ferritin Levels
Ferritin (ng/mL)
6000
4000
2000
0
0.0
0.5
1.0
1.5
ABCB4 Gene Expression



Heatmap of select genes

```
## Warning: Setting row names on a tibble is deprecated.
```


Gender
Disease_Status
AASDH
AAGAB
AARSD1
AAR2
AARS1
AAAS
AAMDC
AAMP
ABHD16A
ABI1
80
60
40
20
Gender
Female
Male
Disease_Status
COVID−19
Non−COVID−19


ABCB4 Expression Across Gender and Disease Status
ABCB4 Gene Expression
1.5
1.0
0.5
0.0
Female
Male
Gender
Disease Status
COVID−19
Non−COVID−19

Jitter plot