

Submission 1_PBX

2025-07-13

Install packages & read data & local setting

```
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    3.5.2      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
```

```
#set path
setwd('/Users/stanpaw/Desktop/Data science 101/Submission 1')
#read data
metadata <- read.csv("QBS103_GSE157103_series_matrix-1.csv")
gene_exp_raw <- read.csv("QBS103_GSE157103_genes.csv")
#check data
glimpse(metadata)
```

```
## Rows: 126
## Columns: 25
## $ participant_id      <chr> "COVID_01_39y_male_NonICU", "C~
## $ geo_accession       <chr> "GSM4753021", "GSM4753022", "G~
## $ status              <chr> "Public on Aug 29 2020", "Publ~
## $ X.Sample_submission_date <chr> "Aug 28 2020", "Aug 28 2020", ~
## $ last_update_date    <chr> "Aug 29 2020", "Aug 29 2020", ~
## $ type                <chr> "SRA", "SRA", "SRA", "SRA", "S~
## $ channel_count       <int> 1, 1, 1, 1, 1, 1, 1, 1, 1, ~
## $ source_name_ch1     <chr> "Leukocytes from whole blood",~
## $ organism_ch1        <chr> "Homo sapiens", "Homo sapiens"~
## $ disease_status      <chr> "disease state: COVID-19", "di~
## $ age                 <chr> "39", "63", "33", "49", "49", ~
## $ sex                 <chr> " male", " male", " male", " m~
## $ icu_status          <chr> " no", " no", " no", " no", " ~
## $ apacheii            <chr> "15", " unknown", " unknown", ~
## $ charlson_score      <int> 0, 2, 2, 1, 1, 1, 7, 7, 2, 1, ~
## $ mechanical_ventilation <chr> " yes", " no", " no", " no", "~
## $ ventilator.free_days <int> 0, 28, 28, 28, 23, 28, 28, 0, ~
## $ hospital.free_days_post_45_day_followup <int> 0, 39, 18, 39, 27, 36, 42, 0, ~
```

```
## $ ferritin.ng.ml. <chr> "946", "1060", "1335", "583", ~
## $ crp.mg.l. <chr> "73.1", " unknown", "53.2", "2~
## $ ddimer.mg.l_feu. <chr> "1.3", "1.03", "1.48", "1.32",~
## $ procalcitonin.ng.ml.. <chr> "36", "0.37", "0.07", "0.98", ~
## $ lactate.mmol.l. <chr> "0.9", " unknown", " unknown",~
## $ fibrinogen <chr> "513", "unknown", "513", "949"~
## $ sofa <chr> "8", " unknown", " unknown", "~
```

```
glimpse(gene_exp_raw)
```

```
## Rows: 100
## Columns: 127
## $ X <chr> "A1BG", "A1CF", "A2M", "A2ML1", "A3GALT2~
## $ COVID_01_39y_male_NonICU <dbl> 0.49, 0.00, 0.21, 0.04, 0.07, 0.00, 0.03~
## $ COVID_02_63y_male_NonICU <dbl> 0.29, 0.00, 0.14, 0.00, 0.00, 0.00, 0.05~
## $ COVID_03_33y_male_NonICU <dbl> 0.26, 0.00, 0.03, 0.02, 0.00, 0.00, 0.07~
## $ COVID_04_49y_male_NonICU <dbl> 0.45, 0.01, 0.09, 0.07, 0.00, 0.00, 0.00~
## $ COVID_05_49y_male_NonICU <dbl> 0.17, 0.00, 0.00, 0.05, 0.07, 0.00, 0.00~
## $ COVID_06_.y_male_NonICU <dbl> 0.21, 0.00, 0.08, 0.04, 0.00, 0.00, 0.03~
## $ COVID_07_38y_female_NonICU <dbl> 0.49, 0.01, 0.23, 0.03, 0.07, 0.00, 0.00~
## $ COVID_08_78y_male_ICU <dbl> 0.12, 0.00, 0.08, 0.01, 0.00, 0.00, 0.00~
## $ COVID_09_64y_female_ICU <dbl> 0.51, 0.01, 0.88, 0.02, 0.79, 0.00, 0.00~
## $ COVID_10_62y_male_ICU <dbl> 0.10, 0.00, 0.13, 0.01, 0.15, 0.00, 0.12~
## $ COVID_11_52y_female_NonICU <dbl> 0.38, 0.02, 0.47, 0.03, 0.08, 0.00, 0.00~
## $ COVID_12_50y_male_ICU <dbl> 0.45, 0.00, 0.16, 0.00, 1.75, 0.00, 0.00~
## $ COVID_13_37y_male_NonICU <dbl> 0.18, 0.00, 0.07, 0.01, 0.00, 0.00, 0.00~
## $ COVID_14_55y_male_ICU <dbl> 0.23, 0.00, 0.22, 0.04, 0.93, 0.00, 0.07~
## $ COVID_15_68y_male_ICU <dbl> 0.42, 0.00, 0.07, 0.00, 0.15, 0.03, 0.00~
## $ COVID_16_48y_male_NonICU <dbl> 0.41, 0.01, 0.58, 0.00, 0.19, 0.00, 0.00~
## $ COVID_17_54y_male_NonICU <dbl> 0.63, 0.02, 0.15, 0.02, 0.00, 0.00, 0.05~
## $ COVID_18_70y_female_NonICU <dbl> 0.47, 0.00, 0.30, 0.02, 0.06, 0.03, 0.03~
## $ COVID_19_51y_male_NonICU <dbl> 0.33, 0.02, 0.11, 0.02, 0.00, 0.00, 0.04~
## $ COVID_20_62y_male_ICU <dbl> 0.32, 0.00, 0.07, 0.00, 0.22, 0.00, 0.00~
## $ COVID_21_66y_male_ICU <dbl> 0.18, 0.00, 0.00, 0.00, 0.37, 0.03, 0.00~
## $ COVID_22_43y_male_ICU <dbl> 0.09, 0.00, 0.06, 0.00, 0.06, 0.00, 0.06~
## $ COVID_23_76y_male_ICU <dbl> 0.18, 0.01, 0.03, 0.00, 0.07, 0.03, 0.04~
## $ COVID_24_55y_male_ICU <dbl> 0.22, 0.01, 0.11, 0.02, 0.15, 0.00, 0.00~
## $ COVID_25_55y_male_ICU <dbl> 0.29, 0.00, 0.09, 0.03, 0.00, 0.00, 0.06~
## $ COVID_26_41y_female_ICU <dbl> 0.42, 0.00, 0.18, 0.00, 0.87, 0.00, 0.00~
## $ COVID_27_71y_female_ICU <dbl> 0.16, 0.01, 0.23, 0.01, 0.18, 0.00, 0.00~
## $ COVID_28_63y_male_ICU <dbl> 0.18, 0.00, 0.18, 0.05, 0.45, 0.00, 0.00~
## $ COVID_29_63y_female_ICU <dbl> 0.35, 0.00, 0.03, 0.03, 0.15, 0.03, 0.08~
## $ COVID_30_54y_male_ICU <dbl> 0.23, 0.00, 0.11, 0.01, 0.00, 0.00, 0.03~
## $ COVID_31_50y_male_ICU <dbl> 0.15, 0.00, 0.47, 0.00, 0.00, 0.03, 0.00~
## $ COVID_32_72y_male_ICU <dbl> 0.34, 0.01, 0.04, 0.00, 0.29, 0.00, 0.04~
## $ COVID_33_81y_male_NonICU <dbl> 0.35, 0.00, 0.30, 0.06, 0.26, 0.00, 0.00~
## $ COVID_34_64y_female_NonICU <dbl> 0.36, 0.00, 0.11, 0.00, 0.12, 0.00, 0.00~
## $ COVID_35_58y_female_NonICU <dbl> 0.26, 0.00, 0.51, 0.02, 0.16, 0.00, 0.00~
## $ COVID_36_68y_male_NonICU <dbl> 0.18, 0.01, 0.09, 0.00, 0.08, 0.00, 0.00~
## $ COVID_37_87y_male_NonICU <dbl> 0.20, 0.00, 0.09, 0.07, 0.31, 0.00, 0.00~
## $ COVID_38_68y_male_ICU <dbl> 0.29, 0.00, 0.10, 0.02, 0.35, 0.00, 0.00~
## $ COVID_39_80y_female_ICU <dbl> 0.19, 0.00, 0.27, 0.00, 0.00, 0.07, 0.00~
## $ COVID_40_66y_male_ICU <dbl> 0.22, 0.00, 0.17, 0.00, 0.08, 0.00, 0.00~
## $ COVID_41_74y_male_ICU <dbl> 0.19, 0.00, 0.14, 0.00, 0.19, 0.00, 0.00~
```

## \$ COVID_42_21y_female_ICU	<dbl> 0.24, 0.01, 0.33, 0.01, 0.39, 0.00, 0.00~
## \$ COVID_43_83y_female_ICU	<dbl> 0.29, 0.00, 0.00, 0.00, 0.11, 0.00, 0.00~
## \$ COVID_44_46y_male_ICU	<dbl> 0.22, 0.00, 0.14, 0.00, 0.00, 0.04, 0.00~
## \$ COVID_45_62y_female_ICU	<dbl> 0.14, 0.00, 0.15, 0.03, 0.19, 0.00, 0.00~
## \$ COVID_46_62y_male_ICU	<dbl> 0.53, 0.01, 0.10, 0.00, 0.06, 0.00, 0.00~
## \$ COVID_47_78y_male_ICU	<dbl> 0.08, 0.01, 0.04, 0.03, 0.60, 0.00, 0.00~
## \$ COVID_48_72y_female_ICU	<dbl> 0.19, 0.00, 0.06, 0.01, 0.23, 0.06, 0.02~
## \$ COVID_49_73y_male_ICU	<dbl> 0.48, 0.00, 0.09, 0.03, 0.00, 0.00, 0.00~
## \$ COVID_50_37y_male_ICU	<dbl> 0.08, 0.00, 0.01, 0.00, 0.00, 0.72, 0.00~
## \$ COVID_51_58y_female_NonICU	<dbl> 0.21, 0.00, 0.13, 0.00, 0.00, 0.00, 0.00~
## \$ COVID_52_71y_male_NonICU	<dbl> 0.25, 0.01, 0.00, 0.03, 0.00, 0.00, 0.00~
## \$ COVID_53_35y_female_NonICU	<dbl> 0.25, 0.00, 0.64, 0.10, 0.00, 0.00, 0.00~
## \$ COVID_55_62y_female_ICU	<dbl> 0.09, 0.00, 0.09, 0.01, 0.00, 0.00, 0.03~
## \$ COVID_56_33y_female_NonICU	<dbl> 0.28, 0.00, 0.16, 0.09, 0.23, 0.00, 0.00~
## \$ COVID_57_30y_female_NonICU	<dbl> 0.42, 0.00, 0.27, 0.01, 0.19, 0.05, 0.00~
## \$ COVID_58_62y_male_NonICU	<dbl> 0.39, 0.00, 0.08, 0.00, 0.00, 0.00, 0.00~
## \$ COVID_59_55y_male_NonICU	<dbl> 0.33, 0.00, 0.10, 0.00, 0.07, 0.00, 0.00~
## \$ COVID_60_49y_male_NonICU	<dbl> 0.22, 0.00, 0.14, 0.00, 0.00, 0.02, 0.00~
## \$ COVID_61_54y_female_NonICU	<dbl> 0.25, 0.00, 0.10, 0.03, 0.13, 0.00, 0.00~
## \$ COVID_62_78y_female_ICU	<dbl> 0.21, 0.00, 0.04, 0.00, 0.05, 0.00, 0.00~
## \$ COVID_63_39y_female_ICU	<dbl> 0.29, 0.00, 0.01, 0.00, 0.14, 0.00, 0.00~
## \$ COVID_64_65y_male_ICU	<dbl> 0.38, 0.01, 0.04, 0.02, 0.56, 0.00, 0.04~
## \$ COVID_65_84y_male_NonICU	<dbl> 0.40, 0.01, 0.07, 0.00, 0.58, 0.00, 0.00~
## \$ COVID_66_66y_female_NonICU	<dbl> 0.64, 0.00, 0.00, 0.00, 0.00, 0.00, 0.00~
## \$ COVID_67_57y_male_ICU	<dbl> 0.37, 0.00, 0.35, 0.00, 0.00, 0.00, 0.00~
## \$ COVID_68_79y_male_ICU	<dbl> 0.58, 0.00, 0.15, 0.01, 0.00, 0.05, 0.00~
## \$ COVID_69_77y_female_NonICU	<dbl> 0.52, 0.00, 0.29, 0.02, 0.00, 0.00, 0.00~
## \$ COVID_70_81y_male_NonICU	<dbl> 0.27, 0.00, 0.07, 0.00, 0.00, 0.06, 0.00~
## \$ COVID_71_37y_male_ICU	<dbl> 0.07, 0.01, 0.12, 0.01, 0.00, 0.00, 0.19~
## \$ COVID_72_50y_female_NonICU	<dbl> 0.52, 0.00, 0.10, 0.01, 0.00, 0.00, 0.00~
## \$ COVID_73_82y_male_NonICU	<dbl> 0.46, 0.01, 0.02, 0.02, 0.17, 0.04, 0.04~
## \$ COVID_74_55y_female_ICU	<dbl> 0.24, 0.00, 0.12, 0.02, 0.26, 0.00, 0.13~
## \$ COVID_75_55y_male_NonICU	<dbl> 0.23, 0.01, 0.14, 0.00, 0.00, 0.00, 0.00~
## \$ COVID_76_73y_female_ICU	<dbl> 0.17, 0.00, 0.09, 0.01, 0.04, 0.00, 0.04~
## \$ COVID_77_55y_female_ICU	<dbl> 0.05, 0.00, 0.01, 0.00, 0.00, 0.00, 0.00~
## \$ COVID_78_80y_male_NonICU	<dbl> 0.19, 0.00, 0.20, 0.00, 0.00, 0.00, 0.00~
## \$ COVID_79_27y_male_NonICU	<dbl> 0.08, 0.01, 0.03, 0.00, 0.00, 0.00, 0.03~
## \$ COVID_80_71y_male_ICU	<dbl> 0.28, 0.00, 0.05, 0.00, 0.05, 0.00, 0.00~
## \$ COVID_82_67y_male_NonICU	<dbl> 0.39, 0.01, 0.10, 0.00, 0.00, 0.00, 0.00~
## \$ COVID_83_85y_female_NonICU	<dbl> 0.47, 0.00, 0.18, 0.05, 0.00, 0.00, 0.00~
## \$ COVID_84_75y_female_NonICU	<dbl> 0.35, 0.00, 0.03, 0.00, 0.17, 0.00, 0.03~
## \$ COVID_85_62y_male_ICU	<dbl> 0.29, 0.00, 0.04, 0.00, 0.00, 0.00, 0.00~
## \$ COVID_86_52y_female_NonICU	<dbl> 0.60, 0.00, 0.27, 0.02, 0.00, 0.00, 0.00~
## \$ COVID_87_61y_male_ICU	<dbl> 0.65, 0.00, 0.15, 0.00, 0.00, 0.00, 0.00~
## \$ COVID_89_90y_female_NonICU	<dbl> 0.20, 0.00, 0.07, 0.03, 0.14, 0.00, 0.00~
## \$ COVID_90_86y_female_NonICU	<dbl> 0.40, 0.00, 0.05, 0.01, 0.31, 0.02, 0.00~
## \$ COVID_91_29y_female_NonICU	<dbl> 0.60, 0.00, 0.03, 0.02, 0.05, 0.00, 0.05~
## \$ COVID_92_82y_female_ICU	<dbl> 0.34, 0.00, 0.02, 0.04, 0.58, 0.00, 0.06~
## \$ COVID_93_81y_female_ICU	<dbl> 0.37, 0.00, 0.11, 0.00, 0.05, 0.00, 0.00~
## \$ COVID_94_24y_female_NonICU	<dbl> 0.81, 0.00, 0.17, 0.02, 0.00, 0.06, 0.00~
## \$ COVID_95_49y_male_NonICU	<dbl> 0.37, 0.01, 0.20, 0.02, 0.15, 0.00, 0.00~
## \$ COVID_96_51y_male_NonICU	<dbl> 1.61, 0.00, 0.02, 0.00, 0.00, 0.00, 0.00~
## \$ COVID_97_76y_male_ICU	<dbl> 0.19, 0.00, 0.02, 0.05, 0.12, 0.03, 0.00~
## \$ COVID_98_81y_male_NonICU	<dbl> 0.78, 0.00, 0.26, 0.00, 0.37, 0.00, 0.02~

```
## $ COVID_99_71y_male_ICU <dbl> 0.33, 0.00, 0.02, 0.00, 0.04, 0.00, 0.00~
## $ COVID_100_74y_female_NonICU <dbl> 0.30, 0.00, 0.09, 0.00, 0.04, 0.00, 0.02~
## $ COVID_101_58y_male_ICU <dbl> 0.33, 0.00, 0.11, 0.03, 0.05, 0.00, 0.00~
## $ COVID_102_84y_male_NonICU <dbl> 0.12, 0.00, 0.01, 0.01, 0.00, 0.07, 0.00~
## $ COVID_103_83y_male_NonICU <dbl> 0.20, 0.00, 0.03, 0.03, 0.04, 0.00, 0.00~
## $ NONCOVID_01_54y_female_NonICU <dbl> 0.89, 0.00, 0.04, 0.00, 0.00, 0.00, 0.00~
## $ NONCOVID_02_65y_male_ICU <dbl> 0.32, 0.00, 0.01, 0.00, 0.04, 0.00, 0.00~
## $ NONCOVID_03_65y_male_ICU <dbl> 0.44, 0.00, 0.05, 0.02, 0.04, 0.00, 0.00~
## $ NONCOVID_04_90y_male_NonICU <dbl> 0.21, 0.00, 0.05, 0.00, 0.21, 0.00, 0.00~
## $ NONCOVID_05_83y_female_NonICU <dbl> 0.31, 0.00, 0.01, 0.01, 0.00, 0.00, 0.00~
## $ NONCOVID_06_75y_female_ICU <dbl> 0.89, 0.00, 0.14, 0.01, 0.00, 0.06, 0.00~
## $ NONCOVID_07_50y_male_ICU <dbl> 0.45, 0.00, 0.07, 0.02, 0.00, 0.00, 0.00~
## $ NONCOVID_08_53y_female_ICU <dbl> 0.47, 0.01, 0.04, 0.00, 0.15, 0.00, 0.00~
## $ NONCOVID_09_49y_female_NonICU <dbl> 0.40, 0.00, 0.04, 0.00, 0.00, 0.00, 0.05~
## $ NONCOVID_10_67y_male_ICU <dbl> 0.33, 0.00, 0.05, 0.01, 0.23, 0.08, 0.00~
## $ NONCOVID_11_58y_female_NonICU <dbl> 0.58, 0.00, 0.03, 0.00, 0.00, 0.00, 0.00~
## $ NONCOVID_12_82y_male_ICU <dbl> 0.12, 0.00, 0.02, 0.00, 0.00, 0.02, 0.00~
## $ NONCOVID_13_65y_male_ICU <dbl> 0.31, 0.00, 0.04, 0.01, 0.32, 0.02, 0.00~
## $ NONCOVID_14_75y_female_ICU <dbl> 0.16, 0.00, 0.08, 0.00, 0.05, 0.02, 0.00~
## $ NONCOVID_15_83y_unknown_ICU <dbl> 0.59, 0.00, 0.03, 0.04, 0.00, 0.19, 0.00~
## $ NONCOVID_16_40y_female_ICU <dbl> 0.34, 0.00, 0.07, 0.00, 0.13, 0.00, 0.00~
## $ NONCOVID_17_84y_female_ICU <dbl> 0.37, 0.00, 0.07, 0.01, 0.18, 0.00, 0.00~
## $ NONCOVID_18_88y_male_ICU <dbl> 0.33, 0.00, 0.06, 0.00, 0.00, 0.00, 0.00~
## $ NONCOVID_19_66y_female_ICU <dbl> 0.25, 0.00, 0.11, 0.00, 0.04, 0.03, 0.00~
## $ NONCOVID_20_62y_female_ICU <dbl> 0.20, 0.00, 0.01, 0.02, 0.00, 0.07, 0.03~
## $ NONCOVID_21_71y_male_NonICU <dbl> 0.40, 0.00, 0.04, 0.02, 0.00, 0.00, 0.00~
## $ NONCOVID_22_63y_male_NonICU <dbl> 0.30, 0.00, 0.02, 0.02, 0.00, 0.00, 0.00~
## $ NONCOVID_23_42y_female_NonICU <dbl> 0.70, 0.00, 0.02, 0.01, 0.00, 0.00, 0.00~
## $ NONCOVID_24_32y_female_NonICU <dbl> 0.75, 0.00, 0.27, 0.00, 0.06, 0.00, 0.00~
## $ NONCOVID_25_62y_male_NonICU <dbl> 2.80, 0.00, 0.04, 0.00, 0.00, 0.00, 0.00~
## $ NONCOVID_26_36y_male_ICU <dbl> 0.22, 0.00, 0.28, 0.00, 0.00, 0.00, 0.00~
```

Work with the gene expression data

```
#working with rows & columns
gene_exp_t <- gene_exp_raw %>%
  column_to_rownames(var = "X") %>% #change the 1st columnname to rowname
  t() %>% #transpose the data frame
  as.data.frame()

gene_exp_t <- gene_exp_t %>%
  rownames_to_column(var="participant_id")

glimpse(gene_exp_t)
```

```
## Rows: 126
## Columns: 101
## $ participant_id <chr> "COVID_01_39y_male_NonICU", "COVID_02_63y_male_NonICU",~
## $ A1BG <dbl> 0.49, 0.29, 0.26, 0.45, 0.17, 0.21, 0.49, 0.12, 0.51, 0~
## $ A1CF <dbl> 0.00, 0.00, 0.00, 0.01, 0.00, 0.00, 0.01, 0.00, 0.01, 0~
## $ A2M <dbl> 0.21, 0.14, 0.03, 0.09, 0.00, 0.08, 0.23, 0.08, 0.88, 0~
## $ A2ML1 <dbl> 0.04, 0.00, 0.02, 0.07, 0.05, 0.04, 0.03, 0.01, 0.02, 0~
## $ A3GALT2 <dbl> 0.07, 0.00, 0.00, 0.00, 0.07, 0.00, 0.07, 0.00, 0.79, 0~
```

## \$ A4GALT	<dbl> 0.00, 0.00, 0.00, 0.00, 0.00, 0.00, 0.00, 0.00, 0.00, 0~
## \$ A4GNT	<dbl> 0.03, 0.05, 0.07, 0.00, 0.00, 0.03, 0.00, 0.00, 0.00, 0~
## \$ AAAS	<dbl> 18.92, 18.68, 13.85, 22.11, 8.45, 19.60, 28.59, 10.50, ~
## \$ AACS	<dbl> 4.07, 3.00, 1.83, 4.22, 1.17, 3.15, 4.24, 2.10, 4.86, 2~
## \$ AADAC	<dbl> 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0~
## \$ AADACL2	<dbl> 0.00, 0.00, 0.00, 0.00, 0.00, 0.01, 0.00, 0.00, 0.00, 0~
## \$ AADACL3	<dbl> 0.00, 0.06, 0.00, 0.00, 0.00, 0.00, 0.00, 0.00, 0.00, 0~
## \$ AADACL4	<dbl> 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0~
## \$ AADAT	<dbl> 0.00, 0.00, 0.00, 0.00, 0.03, 0.00, 0.03, 0.06, 0.00, 0~
## \$ AAGAB	<dbl> 22.93, 21.69, 18.27, 26.69, 17.02, 17.50, 26.28, 13.91, ~
## \$ AAK1	<dbl> 7.12, 6.46, 3.92, 8.74, 7.26, 6.65, 12.78, 3.82, 6.23, ~
## \$ AAMDC	<dbl> 17.19, 13.06, 13.35, 17.53, 10.14, 12.98, 12.62, 9.06, ~
## \$ AAMP	<dbl> 61.08, 54.54, 25.19, 67.95, 18.29, 45.09, 51.35, 20.41, ~
## \$ AANAT	<dbl> 0.31, 0.00, 0.65, 0.08, 1.02, 0.12, 0.13, 0.13, 0.85, 0~
## \$ AAR2	<dbl> 21.59, 19.22, 8.72, 20.83, 7.46, 13.60, 23.90, 8.18, 13~
## \$ AARD	<dbl> 0.18, 0.08, 0.05, 0.03, 0.10, 0.09, 0.12, 0.06, 0.09, 0~
## \$ AARS1	<dbl> 13.52, 13.91, 5.60, 15.34, 6.29, 13.70, 29.47, 4.97, 27~
## \$ AARS2	<dbl> 2.43, 2.15, 1.08, 2.69, 0.55, 2.21, 4.35, 1.06, 2.72, 2~
## \$ AARSD1	<dbl> 9.63, 11.80, 4.04, 14.61, 5.32, 11.30, 21.09, 4.32, 10.~
## \$ AASDH	<dbl> 6.38, 4.83, 2.76, 8.23, 5.23, 4.91, 8.90, 4.57, 4.60, 4~
## \$ AASDHPPT	<dbl> 19.45, 12.14, 7.64, 18.94, 11.54, 14.16, 23.49, 10.08, ~
## \$ AASS	<dbl> 0.21, 0.42, 0.04, 0.41, 0.21, 0.26, 0.63, 0.09, 0.17, 0~
## \$ AATF	<dbl> 45.83, 39.37, 42.35, 41.92, 30.56, 36.30, 44.16, 31.81, ~
## \$ AATK	<dbl> 5.60, 9.79, 5.34, 4.73, 1.50, 7.52, 4.16, 5.62, 12.09, ~
## \$ ABAT	<dbl> 9.63, 10.36, 4.59, 11.02, 4.42, 7.04, 12.02, 7.26, 10.3~
## \$ ABCA1	<dbl> 32.30, 15.84, 34.38, 14.24, 18.39, 3.64, 14.66, 5.34, 2~
## \$ ABCA10	<dbl> 0.32, 0.37, 0.29, 0.31, 0.19, 0.22, 0.55, 0.12, 0.29, 0~
## \$ ABCA12	<dbl> 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0~
## \$ ABCA13	<dbl> 0.49, 3.36, 0.26, 0.13, 0.16, 0.97, 0.23, 6.62, 1.29, 8~
## \$ ABCA2	<dbl> 8.47, 9.49, 14.24, 6.37, 5.90, 6.18, 9.16, 5.85, 15.72, ~
## \$ ABCA3	<dbl> 0.37, 0.71, 0.17, 0.94, 0.17, 0.43, 0.75, 0.17, 0.56, 0~
## \$ ABCA4	<dbl> 0.01, 0.00, 0.00, 0.00, 0.00, 0.00, 0.00, 0.00, 0.00, 0~
## \$ ABCA5	<dbl> 1.86, 2.81, 2.17, 2.94, 1.38, 1.89, 3.60, 2.78, 2.29, 2~
## \$ ABCA6	<dbl> 0.19, 0.11, 0.07, 0.02, 0.03, 0.03, 0.05, 0.10, 0.03, 0~
## \$ ABCA7	<dbl> 39.31, 30.42, 54.85, 18.91, 23.28, 23.43, 30.95, 27.47, ~
## \$ ABCA8	<dbl> 0.00, 0.00, 0.00, 0.01, 0.00, 0.00, 0.00, 0.00, 0.00, 0~
## \$ ABCA9	<dbl> 0.27, 0.20, 0.33, 0.30, 0.21, 0.15, 0.23, 0.15, 0.20, 0~
## \$ ABCB1	<dbl> 1.61, 1.68, 0.59, 3.14, 1.66, 1.92, 4.20, 0.33, 1.41, 1~
## \$ ABCB10	<dbl> 15.59, 10.98, 4.04, 10.00, 5.69, 9.33, 15.09, 9.94, 9.0~
## \$ ABCB11	<dbl> 0.38, 0.25, 0.14, 0.18, 0.07, 0.12, 0.18, 0.05, 0.25, 0~
## \$ ABCB4	<dbl> 0.01, 0.19, 0.09, 0.74, 0.21, 0.26, 0.81, 0.07, 0.35, 0~
## \$ ABCB5	<dbl> 0.04, 0.04, 0.15, 0.11, 0.04, 0.06, 0.11, 0.04, 0.07, 0~
## \$ ABCB6	<dbl> 2.77, 2.52, 3.14, 2.11, 1.14, 2.08, 3.99, 2.57, 4.76, 2~
## \$ ABCB7	<dbl> 6.42, 5.80, 2.59, 7.42, 3.40, 4.87, 7.33, 3.58, 5.55, 3~
## \$ ABCB8	<dbl> 2.95, 2.35, 1.57, 2.71, 0.71, 2.41, 3.51, 0.72, 2.51, 1~
## \$ ABCB9	<dbl> 0.20, 0.51, 0.05, 0.31, 0.12, 0.75, 1.11, 0.26, 4.04, 0~
## \$ ABCC1	<dbl> 11.20, 9.39, 4.74, 13.05, 4.29, 8.45, 12.24, 4.61, 8.65~
## \$ ABCC10	<dbl> 8.85, 4.46, 4.08, 5.75, 1.91, 3.88, 7.33, 3.21, 5.87, 4~
## \$ ABCC11	<dbl> 0.04, 0.01, 0.09, 0.02, 0.02, 0.00, 0.02, 0.09, 0.42, 0~
## \$ ABCC12	<dbl> 0.00, 0.00, 0.00, 0.01, 0.00, 0.00, 0.00, 0.00, 0.01, 0~
## \$ ABCC2	<dbl> 1.65, 1.31, 1.72, 1.55, 2.56, 0.85, 1.57, 1.37, 3.28, 1~
## \$ ABCC3	<dbl> 7.19, 16.21, 1.44, 11.11, 3.13, 4.94, 5.34, 3.87, 7.84, ~
## \$ ABCC4	<dbl> 5.96, 4.49, 0.58, 4.09, 7.37, 4.12, 8.10, 4.59, 13.45, ~
## \$ ABCC5	<dbl> 14.83, 22.21, 13.02, 17.49, 5.53, 14.04, 23.46, 11.86, ~

```

## $ ABCC6      <dbl> 6.62, 5.87, 3.13, 3.37, 1.66, 3.96, 3.61, 6.19, 3.07, 3~
## $ ABCC8      <dbl> 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0~
## $ ABCC9      <dbl> 1.53, 1.89, 1.97, 2.82, 1.84, 1.37, 2.31, 1.24, 1.98, 1~
## $ ABCD1      <dbl> 11.26, 4.65, 5.83, 4.80, 1.93, 2.56, 3.96, 2.65, 4.35, ~
## $ ABCD2      <dbl> 1.55, 1.08, 0.39, 1.74, 0.59, 2.64, 5.25, 0.14, 1.55, 0~
## $ ABCD3      <dbl> 10.62, 11.23, 3.99, 12.38, 8.19, 8.52, 13.14, 10.82, 8.~
## $ ABCD4      <dbl> 11.19, 9.86, 7.83, 13.60, 5.43, 10.19, 12.96, 4.79, 8.9~
## $ ABCE1      <dbl> 14.09, 15.52, 4.50, 21.20, 7.16, 14.20, 28.46, 5.15, 19~
## $ ABCF1      <dbl> 24.40, 16.84, 7.89, 23.92, 12.33, 19.56, 28.37, 7.60, 1~
## $ ABCF2      <dbl> 8.77, 7.21, 3.12, 8.26, 2.76, 5.57, 11.28, 2.95, 6.56, ~
## $ 'ABCF2-H2BE1' <dbl> 11.67, 8.84, 3.06, 12.51, 4.72, 6.47, 13.61, 3.78, 10.5~
## $ ABCF3      <dbl> 23.37, 18.63, 11.57, 23.62, 9.86, 16.81, 25.96, 9.26, 2~
## $ ABCG1      <dbl> 32.76, 23.76, 41.14, 15.72, 9.43, 13.84, 14.96, 7.55, 7~
## $ ABCG2      <dbl> 0.17, 0.00, 0.15, 0.14, 0.03, 0.13, 0.05, 0.07, 0.00, 0~
## $ ABCG4      <dbl> 0.01, 0.07, 0.00, 0.00, 0.00, 0.00, 0.05, 0.00, 0.00, 0~
## $ ABCG5      <dbl> 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0~
## $ ABCG8      <dbl> 0.02, 0.01, 0.00, 0.04, 0.04, 0.00, 0.02, 0.02, 0.03, 0~
## $ ABHD1      <dbl> 0.04, 0.14, 0.00, 0.31, 0.04, 0.21, 0.38, 0.00, 0.05, 0~
## $ ABHD10     <dbl> 14.74, 10.57, 6.84, 16.73, 6.93, 10.02, 18.21, 8.30, 10~
## $ ABHD11     <dbl> 8.50, 8.85, 8.22, 9.64, 4.02, 6.51, 8.27, 4.15, 6.66, 6~
## $ ABHD12     <dbl> 14.66, 9.02, 4.84, 13.22, 3.36, 9.33, 13.35, 4.17, 10.7~
## $ ABHD12B    <dbl> 0.55, 1.18, 0.88, 0.68, 0.68, 0.48, 0.32, 0.59, 1.43, 0~
## $ ABHD13     <dbl> 15.58, 14.33, 9.97, 16.70, 21.02, 11.72, 16.37, 17.79, ~
## $ ABHD14A    <dbl> 6.89, 7.08, 2.12, 9.21, 1.95, 8.84, 13.20, 1.69, 8.89, ~
## $ 'ABHD14A-ACY1' <dbl> 0.00, 0.00, 0.00, 0.00, 0.00, 0.00, 0.17, 0.00, 0.00, 0~
## $ ABHD14B    <dbl> 18.53, 18.78, 7.63, 28.23, 6.49, 23.99, 36.75, 6.54, 15~
## $ ABHD15     <dbl> 6.82, 5.76, 2.41, 8.12, 2.26, 4.99, 8.38, 1.81, 4.43, 2~
## $ ABHD16A    <dbl> 77.48, 57.11, 77.73, 56.77, 63.66, 44.47, 57.29, 52.79, ~
## $ ABHD16B    <dbl> 0.29, 0.19, 0.08, 0.05, 0.04, 0.12, 0.18, 0.04, 0.32, 0~
## $ ABHD17A    <dbl> 13.79, 11.89, 6.88, 12.28, 4.11, 11.68, 12.89, 3.71, 9.~
## $ ABHD17B    <dbl> 8.78, 7.38, 5.59, 9.89, 6.64, 7.10, 11.82, 6.96, 9.58, ~
## $ ABHD17C    <dbl> 1.37, 3.34, 1.64, 1.24, 1.17, 2.52, 2.60, 2.73, 2.56, 4~
## $ ABHD18     <dbl> 6.93, 5.10, 4.06, 6.57, 7.94, 3.93, 7.49, 4.65, 6.46, 3~
## $ ABHD2      <dbl> 46.50, 63.70, 36.05, 54.52, 72.44, 45.66, 44.91, 38.54, ~
## $ ABHD3      <dbl> 73.51, 80.70, 113.96, 106.44, 190.95, 83.74, 121.66, 15~
## $ ABHD4      <dbl> 44.47, 44.43, 37.71, 41.75, 29.65, 34.00, 31.88, 35.22, ~
## $ ABHD5      <dbl> 60.14, 79.17, 77.50, 69.89, 51.39, 60.38, 41.47, 135.01~
## $ ABHD6      <dbl> 3.47, 4.54, 2.15, 7.84, 1.45, 4.30, 5.11, 5.93, 4.96, 2~
## $ ABHD8      <dbl> 3.27, 0.99, 2.59, 1.86, 1.11, 1.27, 2.22, 0.84, 2.72, 2~
## $ ABI1       <dbl> 75.36, 60.41, 61.63, 66.52, 79.84, 54.23, 66.89, 64.55, ~
## $ ABI2       <dbl> 3.22, 3.68, 0.67, 4.99, 2.12, 3.47, 5.82, 1.23, 2.57, 0~

```

```

#combine gene expression & metadata
#common samples ID
common_ids <- intersect(metadata$participant_id, gene_exp_t$participant_id)
#filter data using these IDs
metadata_clean <- metadata %>% filter(participant_id %in% common_ids)
gene_expr_clean <- gene_exp_t %>% filter(participant_id %in% common_ids)

full_data <- left_join(metadata, gene_exp_t, by = "participant_id")
glimpse(full_data)

```

```

## Rows: 126
## Columns: 125

```

## \$ participant_id	<chr> "COVID_01_39y_male_NonICU", "C~
## \$ geo_accession	<chr> "GSM4753021", "GSM4753022", "G~
## \$ status	<chr> "Public on Aug 29 2020", "Publ~
## \$ X.Sample_submission_date	<chr> "Aug 28 2020", "Aug 28 2020", ~
## \$ last_update_date	<chr> "Aug 29 2020", "Aug 29 2020", ~
## \$ type	<chr> "SRA", "SRA", "SRA", "SRA", "S~
## \$ channel_count	<int> 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, ~
## \$ source_name_ch1	<chr> "Leukocytes from whole blood",~
## \$ organism_ch1	<chr> "Homo sapiens", "Homo sapiens"~
## \$ disease_status	<chr> "disease state: COVID-19", "di~
## \$ age	<chr> "39", "63", "33", "49", "49", ~
## \$ sex	<chr> " male", " male", " male", " m~
## \$ icu_status	<chr> " no", " no", " no", " no", " ~
## \$ apacheii	<chr> "15", " unknown", " unknown", ~
## \$ charlson_score	<int> 0, 2, 2, 1, 1, 1, 7, 7, 2, 1, ~
## \$ mechanical_ventilation	<chr> " yes", " no", " no", " no", "~
## \$ ventilator.free_days	<int> 0, 28, 28, 28, 23, 28, 28, 0, ~
## \$ hospital.free_days_post_45_day_followup	<int> 0, 39, 18, 39, 27, 36, 42, 0, ~
## \$ ferritin.ng.ml.	<chr> "946", "1060", "1335", "583", ~
## \$ crp.mg.l.	<chr> "73.1", " unknown", "53.2", "2~
## \$ ddimer.mg.l_feu.	<chr> "1.3", "1.03", "1.48", "1.32",~
## \$ procalcitonin.ng.ml..	<chr> "36", "0.37", "0.07", "0.98", ~
## \$ lactate.mmol.l.	<chr> "0.9", " unknown", " unknown",~
## \$ fibrinogen	<chr> "513", "unknown", "513", "949"~
## \$ sofa	<chr> "8", " unknown", " unknown", "~
## \$ A1BG	<dbl> 0.49, 0.29, 0.26, 0.45, 0.17, ~
## \$ A1CF	<dbl> 0.00, 0.00, 0.00, 0.01, 0.00, ~
## \$ A2M	<dbl> 0.21, 0.14, 0.03, 0.09, 0.00, ~
## \$ A2ML1	<dbl> 0.04, 0.00, 0.02, 0.07, 0.05, ~
## \$ A3GALT2	<dbl> 0.07, 0.00, 0.00, 0.00, 0.07, ~
## \$ A4GALT	<dbl> 0.00, 0.00, 0.00, 0.00, 0.00, ~
## \$ A4GNT	<dbl> 0.03, 0.05, 0.07, 0.00, 0.00, ~
## \$ AAAS	<dbl> 18.92, 18.68, 13.85, 22.11, 8.~
## \$ AACS	<dbl> 4.07, 3.00, 1.83, 4.22, 1.17, ~
## \$ AADAC	<dbl> 0, 0, 0, 0, 0, NA, 0, 0, 0, 0,~
## \$ AADACL2	<dbl> 0.00, 0.00, 0.00, 0.00, 0.00, ~
## \$ AADACL3	<dbl> 0.00, 0.06, 0.00, 0.00, 0.00, ~
## \$ AADACL4	<dbl> 0, 0, 0, 0, 0, NA, 0, 0, 0, 0,~
## \$ AADAT	<dbl> 0.00, 0.00, 0.00, 0.00, 0.03, ~
## \$ AAGAB	<dbl> 22.93, 21.69, 18.27, 26.69, 17~
## \$ AAK1	<dbl> 7.12, 6.46, 3.92, 8.74, 7.26, ~
## \$ AAMDC	<dbl> 17.19, 13.06, 13.35, 17.53, 10~
## \$ AAMP	<dbl> 61.08, 54.54, 25.19, 67.95, 18~
## \$ AANAT	<dbl> 0.31, 0.00, 0.65, 0.08, 1.02, ~
## \$ AAR2	<dbl> 21.59, 19.22, 8.72, 20.83, 7.4~
## \$ AARD	<dbl> 0.18, 0.08, 0.05, 0.03, 0.10, ~
## \$ AARS1	<dbl> 13.52, 13.91, 5.60, 15.34, 6.2~
## \$ AARS2	<dbl> 2.43, 2.15, 1.08, 2.69, 0.55, ~
## \$ AARSD1	<dbl> 9.63, 11.80, 4.04, 14.61, 5.32~
## \$ AASDH	<dbl> 6.38, 4.83, 2.76, 8.23, 5.23, ~
## \$ AASDHPPT	<dbl> 19.45, 12.14, 7.64, 18.94, 11.~
## \$ AASS	<dbl> 0.21, 0.42, 0.04, 0.41, 0.21, ~
## \$ AATF	<dbl> 45.83, 39.37, 42.35, 41.92, 30~
## \$ AATK	<dbl> 5.60, 9.79, 5.34, 4.73, 1.50, ~

## \$ ABAT	<dbl> 9.63, 10.36, 4.59, 11.02, 4.42~
## \$ ABCA1	<dbl> 32.30, 15.84, 34.38, 14.24, 18~
## \$ ABCA10	<dbl> 0.32, 0.37, 0.29, 0.31, 0.19, ~
## \$ ABCA12	<dbl> 0, 0, 0, 0, 0, NA, 0, 0, 0, 0,~
## \$ ABCA13	<dbl> 0.49, 3.36, 0.26, 0.13, 0.16, ~
## \$ ABCA2	<dbl> 8.47, 9.49, 14.24, 6.37, 5.90,~
## \$ ABCA3	<dbl> 0.37, 0.71, 0.17, 0.94, 0.17, ~
## \$ ABCA4	<dbl> 0.01, 0.00, 0.00, 0.00, 0.00, ~
## \$ ABCA5	<dbl> 1.86, 2.81, 2.17, 2.94, 1.38, ~
## \$ ABCA6	<dbl> 0.19, 0.11, 0.07, 0.02, 0.03, ~
## \$ ABCA7	<dbl> 39.31, 30.42, 54.85, 18.91, 23~
## \$ ABCA8	<dbl> 0.00, 0.00, 0.00, 0.01, 0.00, ~
## \$ ABCA9	<dbl> 0.27, 0.20, 0.33, 0.30, 0.21, ~
## \$ ABCB1	<dbl> 1.61, 1.68, 0.59, 3.14, 1.66, ~
## \$ ABCB10	<dbl> 15.59, 10.98, 4.04, 10.00, 5.6~
## \$ ABCB11	<dbl> 0.38, 0.25, 0.14, 0.18, 0.07, ~
## \$ ABCB4	<dbl> 0.01, 0.19, 0.09, 0.74, 0.21, ~
## \$ ABCB5	<dbl> 0.04, 0.04, 0.15, 0.11, 0.04, ~
## \$ ABCB6	<dbl> 2.77, 2.52, 3.14, 2.11, 1.14, ~
## \$ ABCB7	<dbl> 6.42, 5.80, 2.59, 7.42, 3.40, ~
## \$ ABCB8	<dbl> 2.95, 2.35, 1.57, 2.71, 0.71, ~
## \$ ABCB9	<dbl> 0.20, 0.51, 0.05, 0.31, 0.12, ~
## \$ ABCC1	<dbl> 11.20, 9.39, 4.74, 13.05, 4.29~
## \$ ABCC10	<dbl> 8.85, 4.46, 4.08, 5.75, 1.91, ~
## \$ ABCC11	<dbl> 0.04, 0.01, 0.09, 0.02, 0.02, ~
## \$ ABCC12	<dbl> 0.00, 0.00, 0.00, 0.01, 0.00, ~
## \$ ABCC2	<dbl> 1.65, 1.31, 1.72, 1.55, 2.56, ~
## \$ ABCC3	<dbl> 7.19, 16.21, 1.44, 11.11, 3.13~
## \$ ABCC4	<dbl> 5.96, 4.49, 0.58, 4.09, 7.37, ~
## \$ ABCC5	<dbl> 14.83, 22.21, 13.02, 17.49, 5.~
## \$ ABCC6	<dbl> 6.62, 5.87, 3.13, 3.37, 1.66, ~
## \$ ABCC8	<dbl> 0, 0, 0, 0, 0, NA, 0, 0, 0, 0,~
## \$ ABCC9	<dbl> 1.53, 1.89, 1.97, 2.82, 1.84, ~
## \$ ABCD1	<dbl> 11.26, 4.65, 5.83, 4.80, 1.93,~
## \$ ABCD2	<dbl> 1.55, 1.08, 0.39, 1.74, 0.59, ~
## \$ ABCD3	<dbl> 10.62, 11.23, 3.99, 12.38, 8.1~
## \$ ABCD4	<dbl> 11.19, 9.86, 7.83, 13.60, 5.43~
## \$ ABCE1	<dbl> 14.09, 15.52, 4.50, 21.20, 7.1~
## \$ ABCF1	<dbl> 24.40, 16.84, 7.89, 23.92, 12.~
## \$ ABCF2	<dbl> 8.77, 7.21, 3.12, 8.26, 2.76, ~
## \$ 'ABCF2-H2BE1'	<dbl> 11.67, 8.84, 3.06, 12.51, 4.72~
## \$ ABCF3	<dbl> 23.37, 18.63, 11.57, 23.62, 9.~
## \$ ABCG1	<dbl> 32.76, 23.76, 41.14, 15.72, 9.~
## \$ ABCG2	<dbl> 0.17, 0.00, 0.15, 0.14, 0.03, ~
## \$ ABCG4	<dbl> 0.01, 0.07, 0.00, 0.00, 0.00, ~
## \$ ABCG5	<dbl> 0, 0, 0, 0, 0, NA, 0, 0, 0, 0,~
## \$ ABCG8	<dbl> 0.02, 0.01, 0.00, 0.04, 0.04, ~
## \$ ABHD1	<dbl> 0.04, 0.14, 0.00, 0.31, 0.04, ~
## \$ ABHD10	<dbl> 14.74, 10.57, 6.84, 16.73, 6.9~
## \$ ABHD11	<dbl> 8.50, 8.85, 8.22, 9.64, 4.02, ~
## \$ ABHD12	<dbl> 14.66, 9.02, 4.84, 13.22, 3.36~
## \$ ABHD12B	<dbl> 0.55, 1.18, 0.88, 0.68, 0.68, ~
## \$ ABHD13	<dbl> 15.58, 14.33, 9.97, 16.70, 21.~
## \$ ABHD14A	<dbl> 6.89, 7.08, 2.12, 9.21, 1.95, ~


```
## $ 'ABHD14A-ACY1' <dbl> 0.00, 0.00, 0.00, 0.00, 0.00, ~
## $ ABHD14B <dbl> 18.53, 18.78, 7.63, 28.23, 6.4~
## $ ABHD15 <dbl> 6.82, 5.76, 2.41, 8.12, 2.26, ~
## $ ABHD16A <dbl> 77.48, 57.11, 77.73, 56.77, 63~
## $ ABHD16B <dbl> 0.29, 0.19, 0.08, 0.05, 0.04, ~
## $ ABHD17A <dbl> 13.79, 11.89, 6.88, 12.28, 4.1~
## $ ABHD17B <dbl> 8.78, 7.38, 5.59, 9.89, 6.64, ~
## $ ABHD17C <dbl> 1.37, 3.34, 1.64, 1.24, 1.17, ~
## $ ABHD18 <dbl> 6.93, 5.10, 4.06, 6.57, 7.94, ~
## $ ABHD2 <dbl> 46.50, 63.70, 36.05, 54.52, 72~
## $ ABHD3 <dbl> 73.51, 80.70, 113.96, 106.44, ~
## $ ABHD4 <dbl> 44.47, 44.43, 37.71, 41.75, 29~
## $ ABHD5 <dbl> 60.14, 79.17, 77.50, 69.89, 51~
## $ ABHD6 <dbl> 3.47, 4.54, 2.15, 7.84, 1.45, ~
## $ ABHD8 <dbl> 3.27, 0.99, 2.59, 1.86, 1.11, ~
## $ ABI1 <dbl> 75.36, 60.41, 61.63, 66.52, 79~
## $ ABI2 <dbl> 3.22, 3.68, 0.67, 4.99, 2.12, ~
```

Choose variables

```
#check number of rows before start
nrow(full_data) == nrow(metadata)
```

```
## [1] TRUE
```

```
#check variables
names(full_data)
```

```
## [1] "participant_id"
## [2] "geo_accession"
## [3] "status"
## [4] "X.Sample_submission_date"
## [5] "last_update_date"
## [6] "type"
## [7] "channel_count"
## [8] "source_name_ch1"
## [9] "organism_ch1"
## [10] "disease_status"
## [11] "age"
## [12] "sex"
## [13] "icu_status"
## [14] "apacheii"
## [15] "charlson_score"
## [16] "mechanical_ventilation"
## [17] "ventilator.free_days"
## [18] "hospital.free_days_post_45_day_followup"
## [19] "ferritin.ng.ml."
## [20] "crp.mg.l."
## [21] "ddimer.mg.l_feu."
## [22] "procalcitonin.ng.ml.."
## [23] "lactate.mmol.l."
## [24] "fibrinogen"
## [25] "sofa"
```

[26] "A1BG"
[27] "A1CF"
[28] "A2M"
[29] "A2ML1"
[30] "A3GALT2"
[31] "A4GALT"
[32] "A4GNT"
[33] "AAAS"
[34] "AACS"
[35] "AADAC"
[36] "AADACL2"
[37] "AADACL3"
[38] "AADACL4"
[39] "AADAT"
[40] "AAGAB"
[41] "AAK1"
[42] "AAMDC"
[43] "AAMP"
[44] "AANAT"
[45] "AAR2"
[46] "AARD"
[47] "AARS1"
[48] "AARS2"
[49] "AARSD1"
[50] "AASDH"
[51] "AASDHPPT"
[52] "AASS"
[53] "AATF"
[54] "AATK"
[55] "ABAT"
[56] "ABCA1"
[57] "ABCA10"
[58] "ABCA12"
[59] "ABCA13"
[60] "ABCA2"
[61] "ABCA3"
[62] "ABCA4"
[63] "ABCA5"
[64] "ABCA6"
[65] "ABCA7"
[66] "ABCA8"
[67] "ABCA9"
[68] "ABCB1"
[69] "ABCB10"
[70] "ABCB11"
[71] "ABCB4"
[72] "ABCB5"
[73] "ABCB6"
[74] "ABCB7"
[75] "ABCB8"
[76] "ABCB9"
[77] "ABCC1"
[78] "ABCC10"
[79] "ABCC11"

```
## [80] "ABCC12"
## [81] "ABCC2"
## [82] "ABCC3"
## [83] "ABCC4"
## [84] "ABCC5"
## [85] "ABCC6"
## [86] "ABCC8"
## [87] "ABCC9"
## [88] "ABCD1"
## [89] "ABCD2"
## [90] "ABCD3"
## [91] "ABCD4"
## [92] "ABCE1"
## [93] "ABCF1"
## [94] "ABCF2"
## [95] "ABCF2-H2BE1"
## [96] "ABCF3"
## [97] "ABCG1"
## [98] "ABCG2"
## [99] "ABCG4"
## [100] "ABCG5"
## [101] "ABCG8"
## [102] "ABHD1"
## [103] "ABHD10"
## [104] "ABHD11"
## [105] "ABHD12"
## [106] "ABHD12B"
## [107] "ABHD13"
## [108] "ABHD14A"
## [109] "ABHD14A-ACY1"
## [110] "ABHD14B"
## [111] "ABHD15"
## [112] "ABHD16A"
## [113] "ABHD16B"
## [114] "ABHD17A"
## [115] "ABHD17B"
## [116] "ABHD17C"
## [117] "ABHD18"
## [118] "ABHD2"
## [119] "ABHD3"
## [120] "ABHD4"
## [121] "ABHD5"
## [122] "ABHD6"
## [123] "ABHD8"
## [124] "ABI1"
## [125] "ABI2"
```

```
'AAK1' %in% colnames(full_data)
```

```
## [1] TRUE
```

```
summary(full_data$AAK1)
```

```
##      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.     NA's
##      0.840   3.790   5.090   5.403   6.460   13.890        1
```

```
# change ferritin from char to num
full_data <- full_data %>%
  mutate(ferritin = as.numeric(`ferritin.ng.ml.`))
```

```
## Warning: There was 1 warning in 'mutate()'.
## i In argument: 'ferritin = as.numeric(ferritin.ng.ml.)'.
## Caused by warning:
## ! NAs introduced by coercion
```

```
summary(full_data$ferritin)
```

```
##      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.     NA's
##      14.0   222.0   573.0   833.5  1091.5  5971.0        16
```

```
summary(full_data$AAK1)
```

```
##      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.     NA's
##      0.840   3.790   5.090   5.403   6.460   13.890        1
```

```
summary(full_data$ferritin.ng.ml.)
```

```
##      Length      Class      Mode
##      126 character character
```

```
#check distribution of categorical covarities
table(full_data$sex, useNA = "always")
```

```
##
##      female      male unknown  <NA>
##         51         74         1      0
```

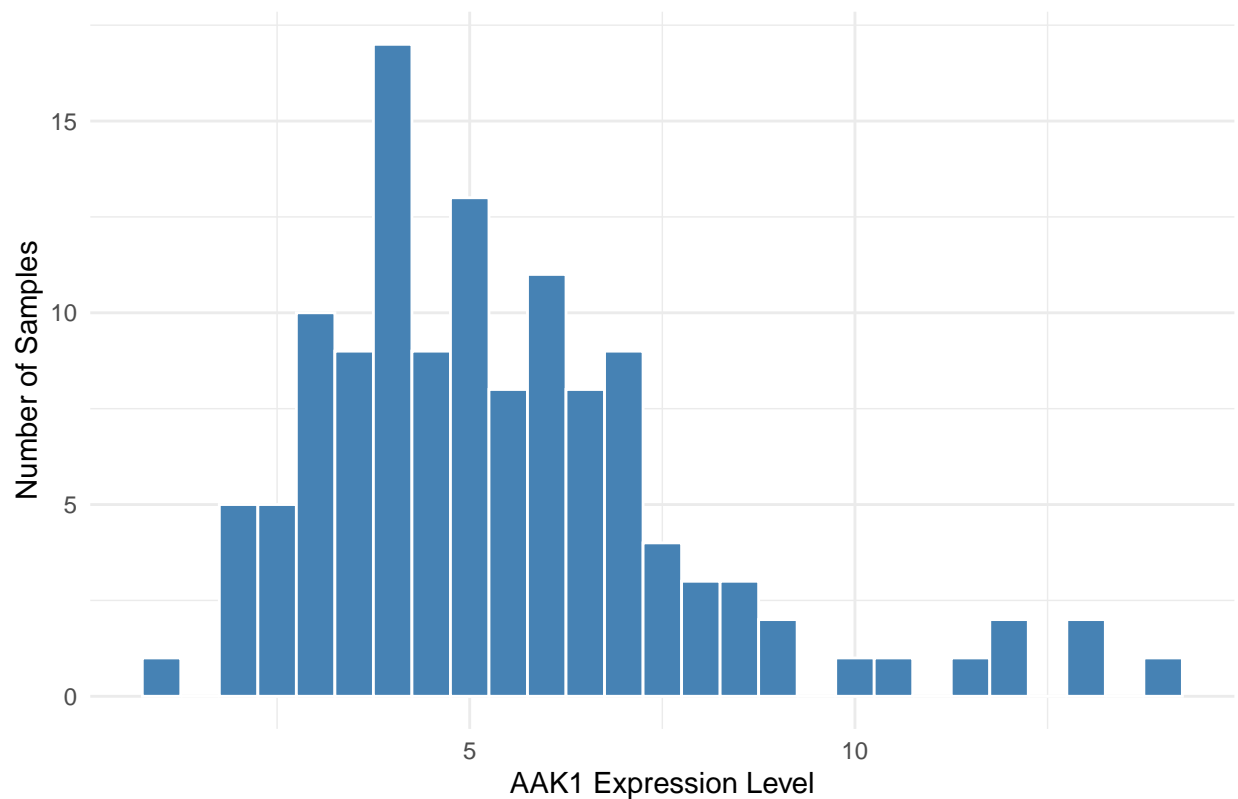
```
table(full_data$icu_status, useNA = "always")
```

```
##
##      no  yes <NA>
##      60  66    0
```

Graphs

```
#Histogram of AAK1 expression
ggplot(full_data, aes(x=AAK1))+
  geom_histogram(binwidth = 0.5, fill = 'steelblue', color = 'white', na.rm = TRUE) +
  labs(
    title = "Histogram of AAK1 Gene Expression",
    x = "AAK1 Expression Level",
    y = "Number of Samples"
  ) +
  theme_minimal()
```

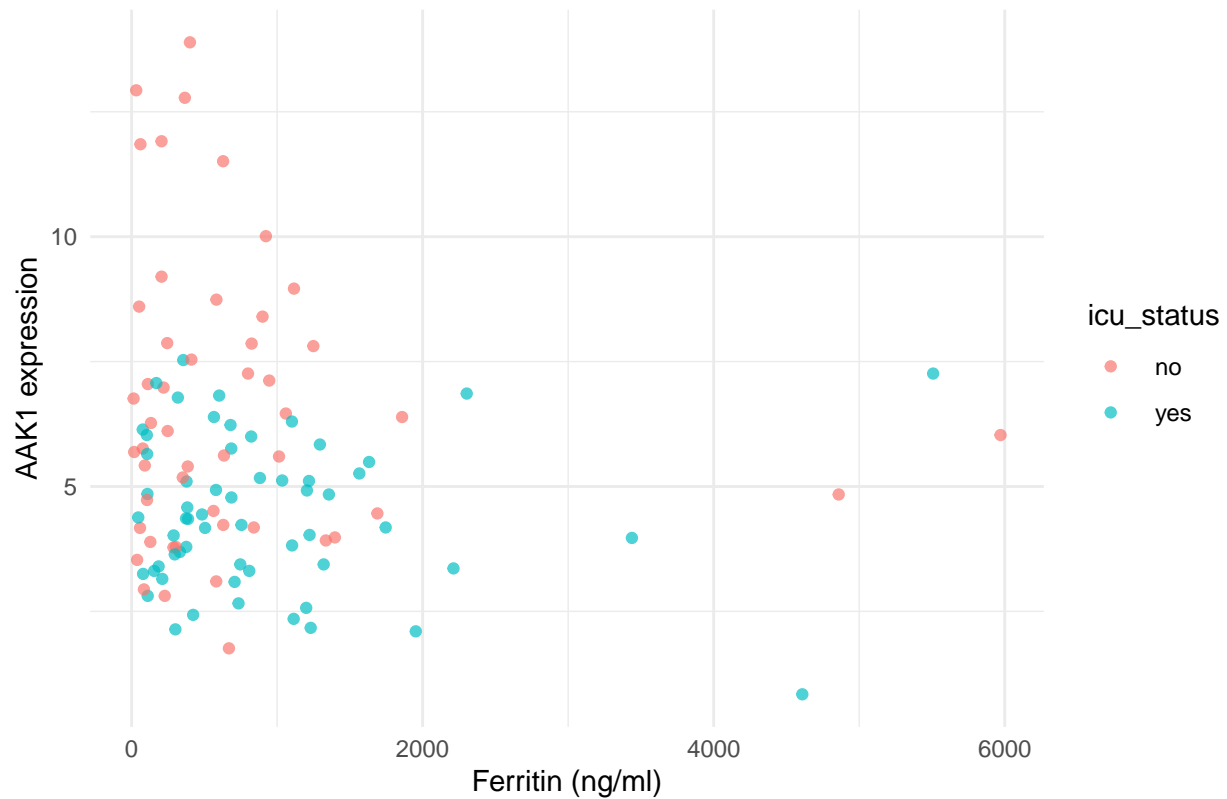
Histogram of AAK1 Gene Expression



```
#Scatter plots of AAK1 and Ferritin
ggplot(full_data, aes(x=ferritin, y=AAK1, color=icu_status)) +
  geom_point(alpha = 0.7) +
  labs(
    title = "Scatterplot: AAK1 Expression vs. Ferritin Level",
    x = "Ferritin (ng/ml)",
    y = "AAK1 expression"
  ) +
  theme_minimal()
```

```
## Warning: Removed 17 rows containing missing values or values outside the scale range
## ('geom_point()').
```

Scatterplot: AAK1 Expression vs. Ferritin Level



```
#Boxplot of AAK1 by Sex and ICU status
ggplot(full_data, aes(x = sex, y = AAK1, fill = icu_status)) +
  geom_boxplot() +
  labs(title = "AAK1 Expression by Sex and ICU Status",
       x = "Sex",
       y = "AAK1 Expression") +
  theme_minimal()
```

```
## Warning: Removed 1 row containing non-finite outside the scale range
## ('stat_boxplot()').
```

