

FA1

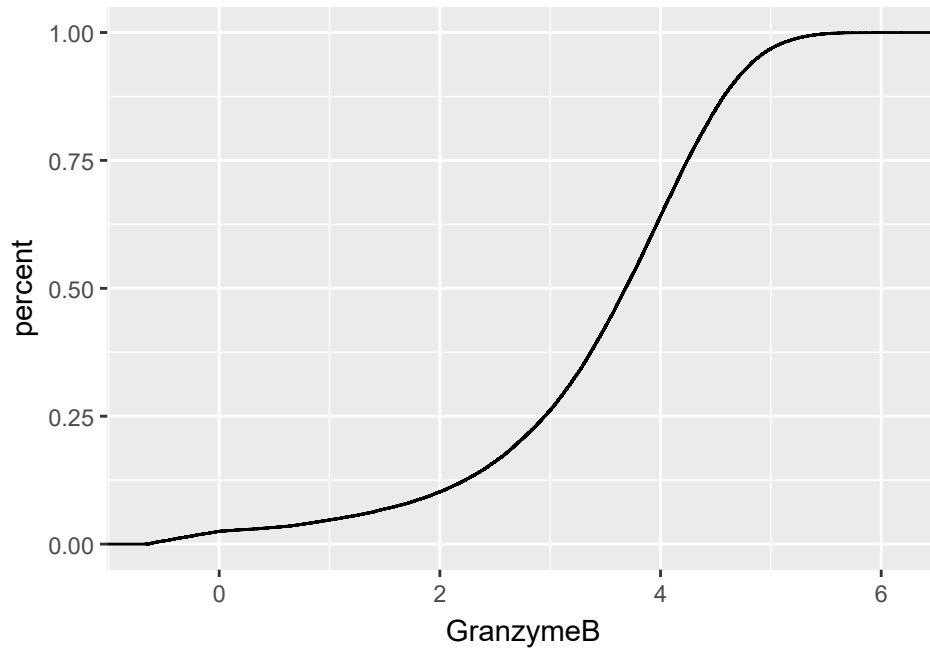
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```
library(ggplot2)
library(magrittr)
library(stringr)
library(gridExtra)
dataset <- read.csv("cytof_one_experiment.csv")

save(dataset, file="my_work_space.RData")
```

```
granzymeB <- dataset$GranzymeB
ggplot(dataset, aes(x = granzymeB)) + stat_ecdf() + xlab("GranzymeB") + ylab("percent")
```

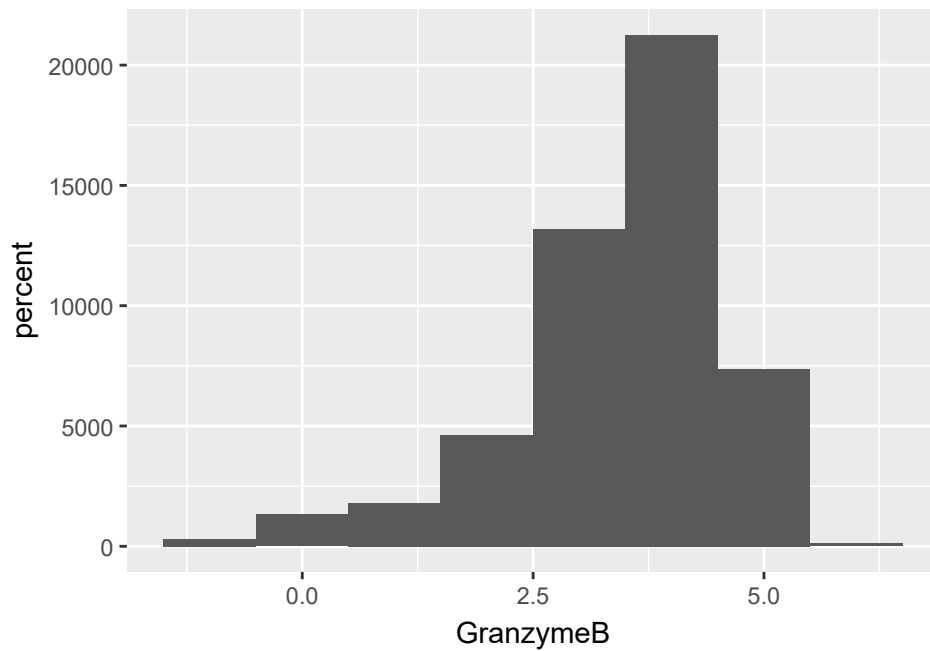
ECDF plot for GranzymeB



This plot shows a slow increase at lower values, sharp rise in the middle. This means that most of the values in this column are concentrated in the middle and less extreme lower values.

```
ggplot(dataset, aes(x = granzymeB)) + geom_histogram(binwidth = 1) +  
  xlab("GranzymeB") + ylab("percent")
```

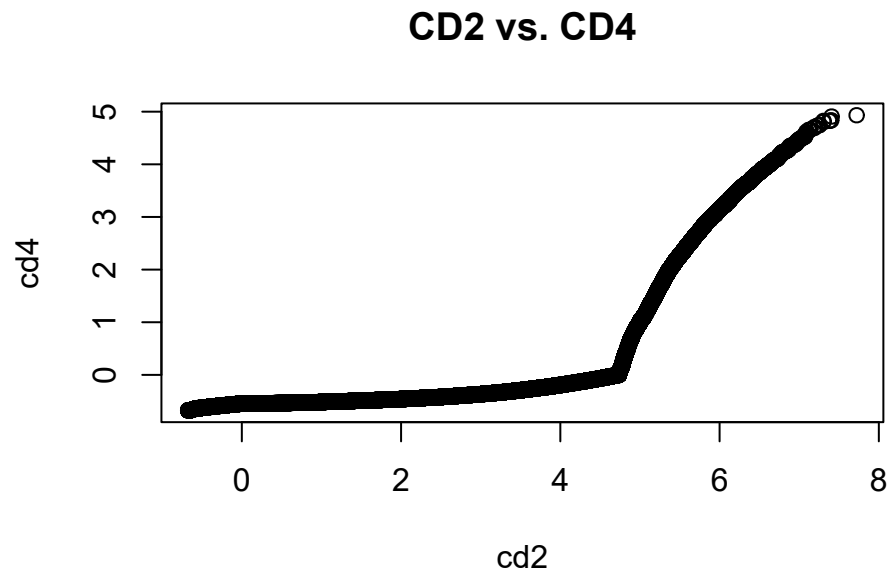
Histogram plot for GranzymeB



The histogram for granzymeB is skewed to the left which means that most of the values in this column are large and there are less lower values.

```
cd2 <- dataset$CD2  
cd4 <- dataset$CD4  
  
qqplot(cd2, cd4, main = "CD2 vs. CD4")
```

Q-Q plot for CD2 and CD4



This plot deviates significantly from a straight diagonal line which implies that the quantiles do not have a similar distribution. Towards the right, CD4 values increase sharply compared to CD2 which suggests that it is more skewed to the right.