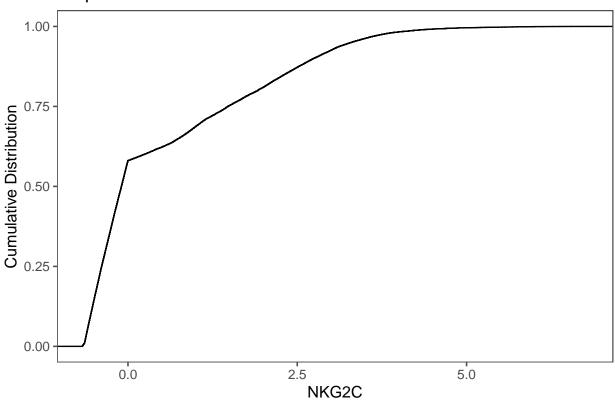
## library(tidyverse) ## -- Attaching packages ------- tidyverse 1.3.2 --## v ggplot2 3.3.6 v purrr 0.3.4 ## v tibble 3.1.8 1.0.10 v dplyr ## v tidyr 1.2.1 v stringr 1.4.1 2.1.3 ## v readr v forcats 0.5.2 ## -- Conflicts ---------- tidyverse\_conflicts() --## x dplyr::filter() masks stats::filter() ## x dplyr::lag() masks stats::lag() library(ggthemes) #1.) data <- read.csv("cytof\_one\_experiment.csv")</pre> #2.) #ECDF ggplot(data, aes(x=NKG2C)) +stat\_ecdf() + ggtitle("Empirical Cumulative Distribution Function of NKG2C") +

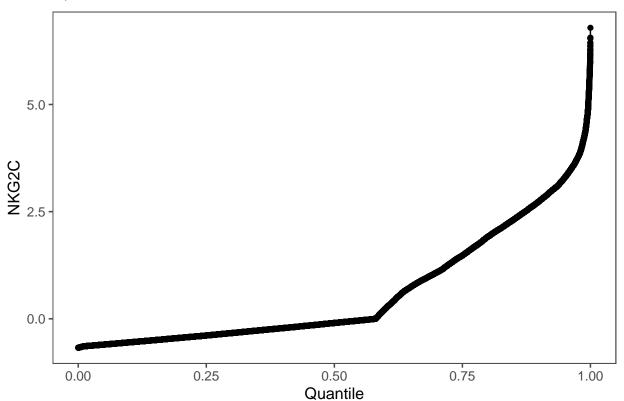
## Empirical Cumulative Distribution Function of NKG2C

ylab("Cumulative Distribution") +

xlab("NKG2C") +
theme\_few()



## Quantile Plot of NKG2C

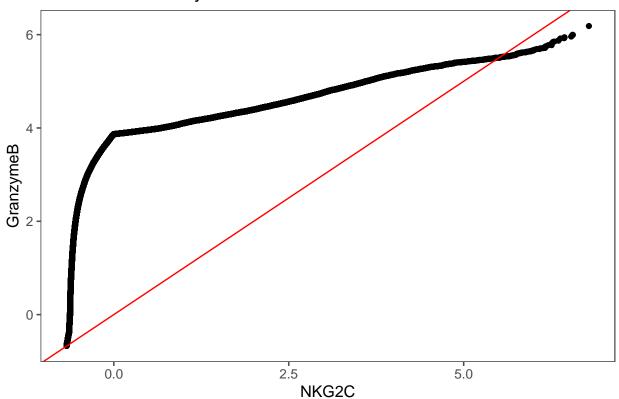


The two above plots show the univariate distribution of NKG2C. A substantial chunk of NKG2C's density occurs at values 0 and below; the median value (.50 quantile) is less than zero. Additionally, there is a constant accumulation of density from NKG2C=0 to NKG2C=3. This is evidenced by a linear line on the ECDF plot between these two points. Finally, the vast majority of NKG2C values are less than 5 as the ECDF plot has almost reached a value of 1 by this point.

```
#3.)
qq.df <- as.data.frame(qqplot(data$NKG2C, data$GranzymeB, plot.it = FALSE))
ggplot(qq.df, aes(x=x, y=y)) +
    geom_point() +
    geom_abline(slope=1, intercept=0, col="red") +
    ggtitle("Q-Q Plot of GranzymeB vs. NKG2C")+
    ylab("GranzymeB") +</pre>
```

xlab("NKG2C") +
theme\_few()

## Q-Q Plot of GranzymeB vs. NKG2C



Across the vast majority of quantiles, GranzymeB takes on greater values than NKG2C as the Q-Q plot line is above the identity line. It is only at the lowest and highest quantiles that NKG2C takes on greater values than GranzymeB (where the Q-Q plot line falls below the identity line). This is due to the univariate distribution of NKG2C explored above, where a majority of the density was clumped at values equal to or slightly less than 0.