Assigment 3 - Aman kumar - 17025

Nef (Negative Regulatory Factor) is a small 27 35 kDa protein that is coded by the HIV genome.This gene performs several different tasks during infection. However, despite being studied for more than two decades, it was not known how this protein increases the infectivity of new virus particles released from the cell. In the year 2015, two groups of scientists independently solved this 20 year old mystery and shed light on a pair of new genes that could restrict HIV in absence of the Nef protein (Rosa et al. 2015; Usami et al. 2015).

I have use this following paper to replicate results from the paper:

Rosa A, Chande A, Ziglio S, De Sanctis V, Bertorelli R, Goh SL, McCauley SM, Nowosielska A, Antonarakis SE, Luban J, et al. 2015. HIV 1 Nef promotes infection by excluding SERINC5 from virion incorporation. Nature 526:212—217.217.

They measured infectivity ratio of these same cell lines with Nef+ and Nef HIV. Using this data, they looked at correlations between expression levels of each gene with the infectivity ratio's. Genes whose expression level showed a strong correlation with the infectivity ratio were chosen as candidate genes that were involved in restricting the virus in the absence of the Nef gene . Further experimental validation of these candidate genes lead to interesting new discovery that.

```
getwd()
```

```
## [1] "D:/IISER BHOPAL/SEM 8/DSE 401/Assignment 3"
```

```
#setwd("D:/IISER BHOPAL/SEM 8/DSE 401/Assignment 3")
#getwd()
```

Loading the libraries

```
#install.packages("psych")
```

```
library(tidyverse)
library(dplyr)
library(tidyr)
library(Hmisc)
library(ggplot2)
library(psych)
library(factoextra)
library(devtools)
```

Reading files

Loading Read-count files

```
load_htseq <- list.files(pattern = "*.htseq")
all_samples <- lapply(load_htseq, read.delim, header=F)
all_samples <- as.data.frame(all_samples)
colnames(all_samples)<- c("MT4","MT4_count","HSB2","HSB2_count","HT1080","HT1080_count","RAJI",
"RAJI_count","CEM SS","CEM SS_count","DAUDI","DAUDI_count","C8166","C8166_count","RAMOS","RAMOS_
count","IMR90","IMR90_count","CEM_A_301","CEM_A_301_count","CEM_X_174","CEM_X_174_count","WI38",
"WI38_count","JURKAT_E6.1","JURKAT_E6.1_count","bl41","bl41_count","Jurkat_tag","Jurkat_tag_coun
t")
```

Extracting only count columns

```
samples <- all_samples[c(1, seq(2, 30, 2))]
colnames(samples)[1] <- c("Gene_ID")
```

Loading Inactivity ratio file

```
infect <- read.delim("infect.txt", sep="\t", header= F)
colnames(infect) <- c("accession_id", "infectivity_ratio", "cell_lines")
infect <- arrange(infect,accession_id)
```

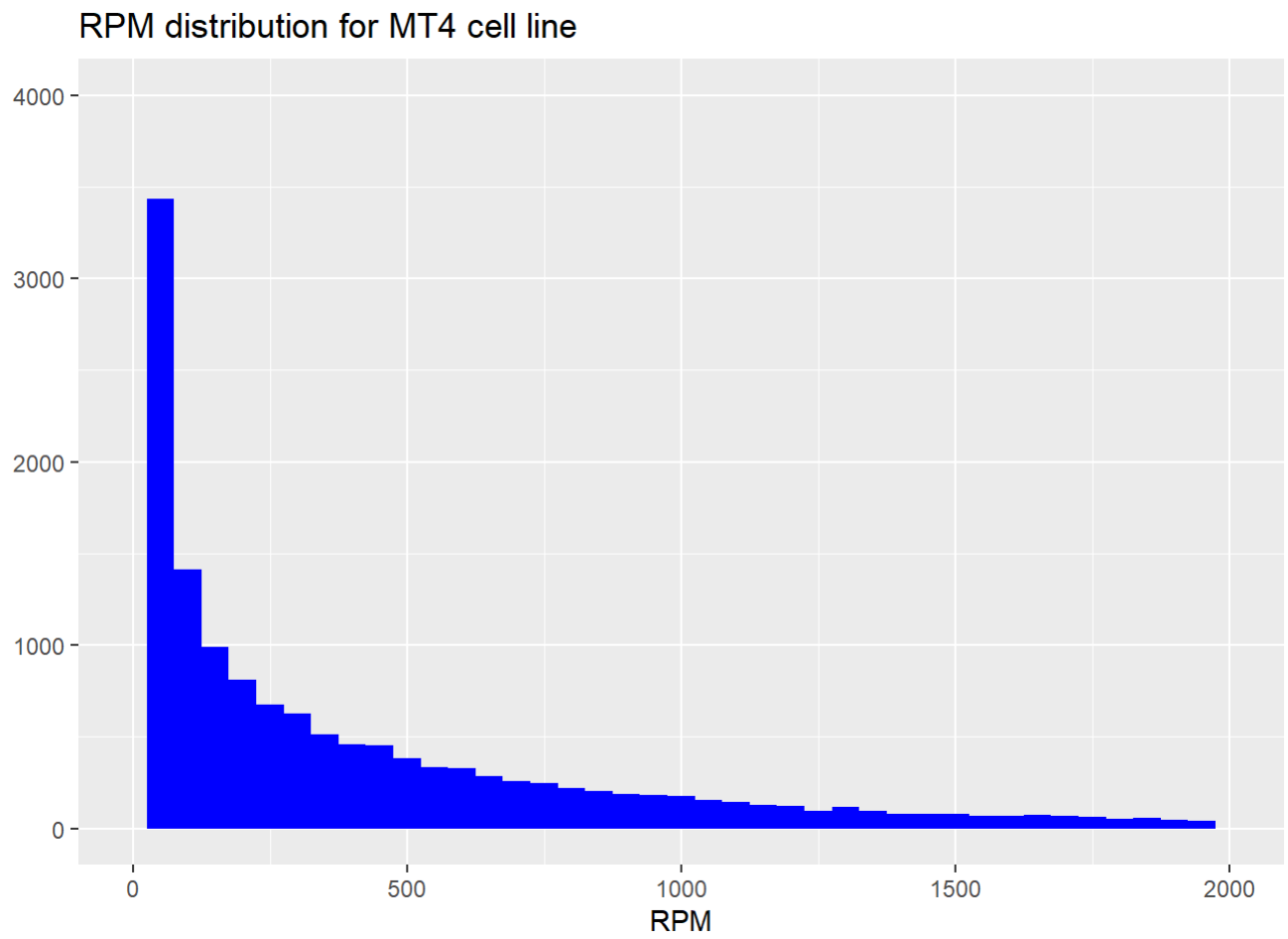
Data Visualization

```
MT4 = read.delim("SRR2166624.htseq", header=F)
MT4 <- MT4[MT4$V2 != 0,]
MT4 <- MT4[-c(58303, 58304, 58305, 58306, 58307),]
```

```
qplot(MT4$V2,
      geom="histogram",
      binwidth = 50,
      main = "RPM distribution for MT4 cell line",
      xlab = "RPM",
      fill=I("blue"),
      xlim=c(0,2000),
      ylim=c(0,4000))
```

```
## Warning: Removed 1291 rows containing non-finite values (stat_bin).
```

```
## Warning: Removed 2 rows containing missing values (geom_bar).
```

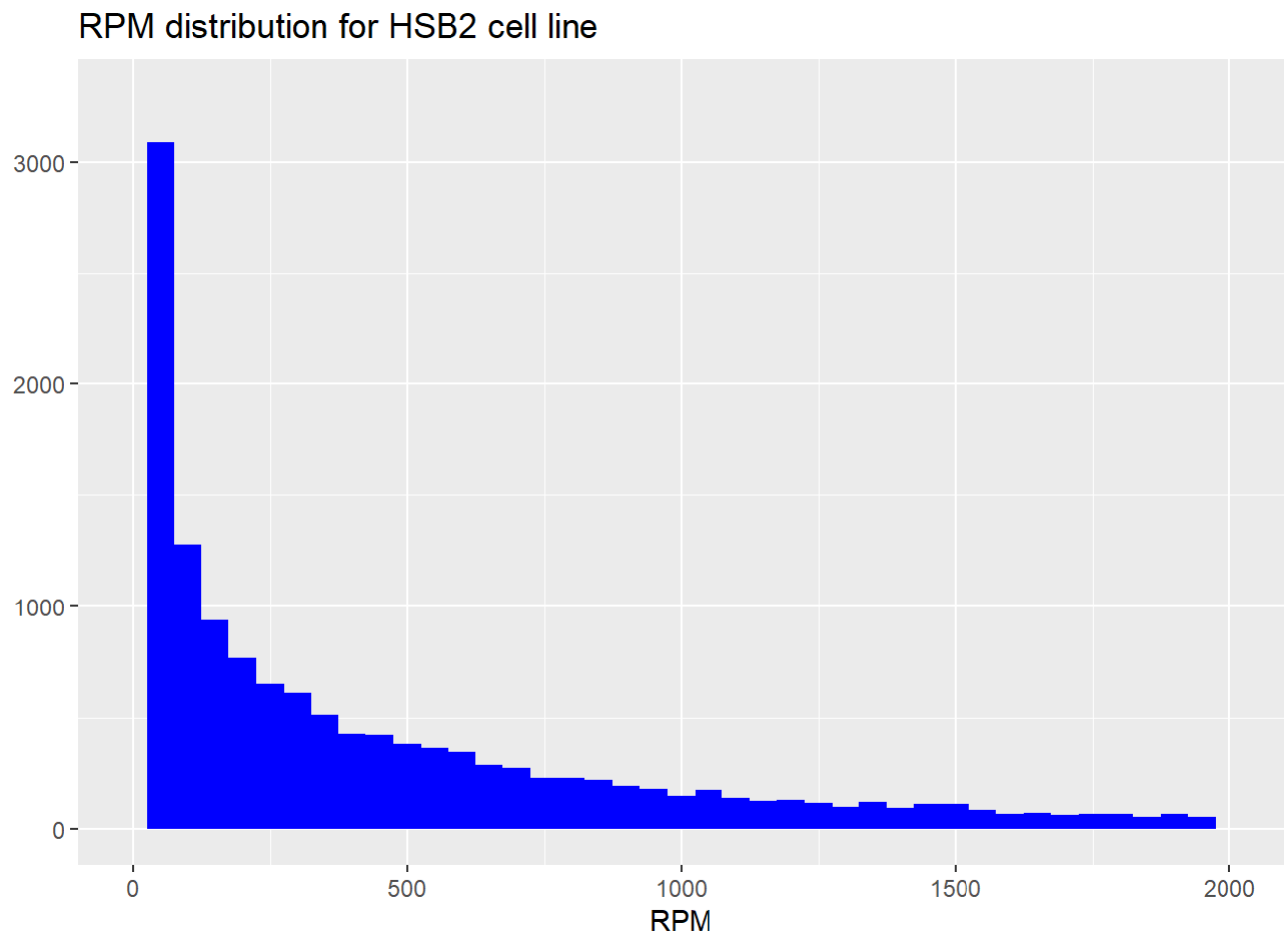



```
HSB2 = read.delim("SRR2166625.htseq", header=F)
HSB2 <- HSB2[HSB2$V2 != 0,]
```

```
qplot(HSB2$V2,
      geom="histogram",
      binwidth = 50,
      main = "RPM distribution for HSB2 cell line",
      xlab = "RPM",
      fill=I("blue"),
      xlim=c(0,2000),
      ylim=c(0,3300))
```

```
## Warning: Removed 1380 rows containing non-finite values (stat_bin).
```

```
## Warning: Removed 2 rows containing missing values (geom_bar).
```

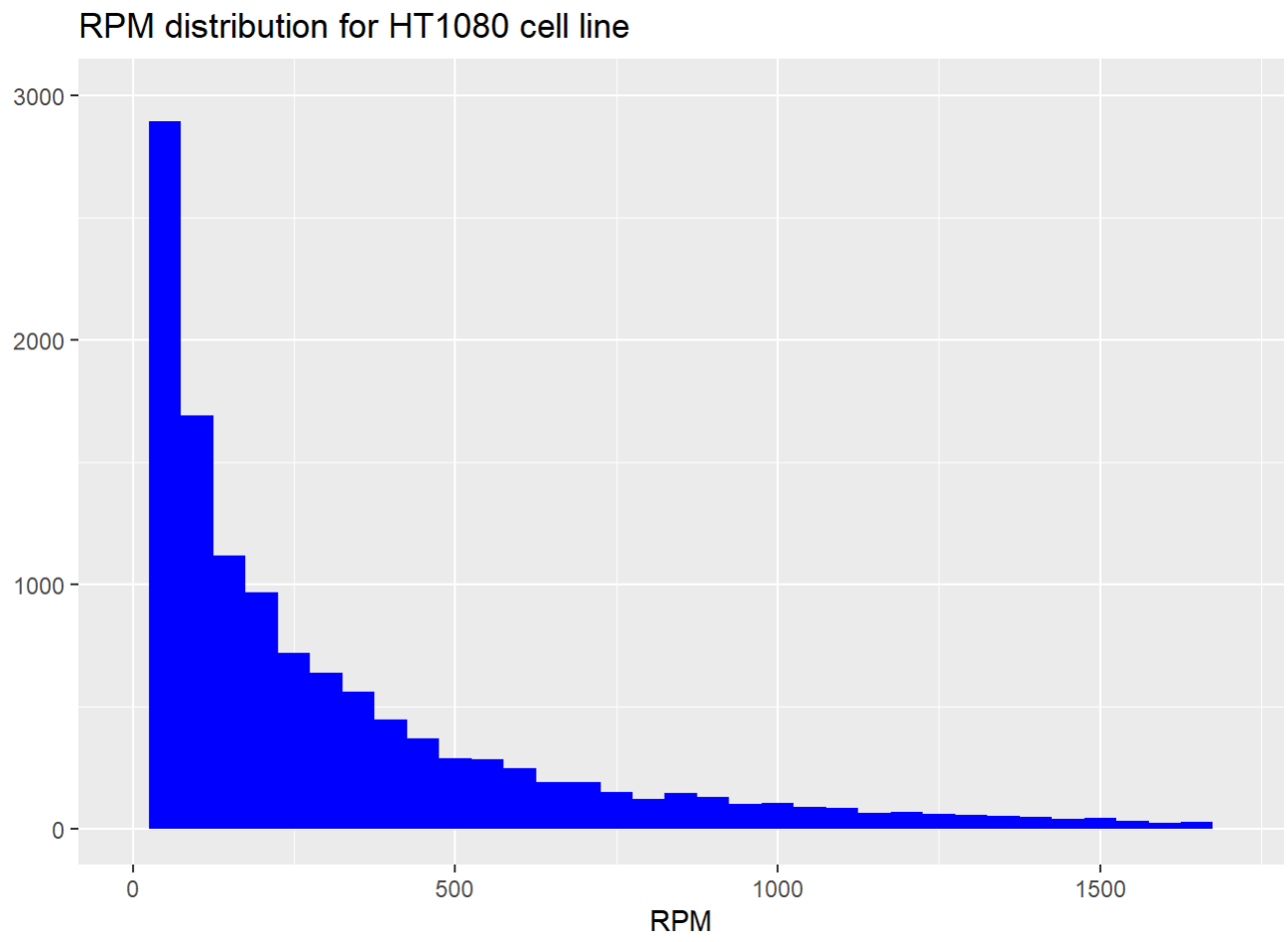



```
HT1080 = read.delim("SRR2166626.htseq", header=F)
HT1080 <- HT1080[HT1080$V2 != 0,]
```

```
qplot(HT1080$V2,
      geom="histogram",
      binwidth = 50,
      main = "RPM distribution for HT1080 cell line",
      xlab = "RPM",
      fill=I("blue"),
      xlim=c(0,1700),
      ylim=c(0,3000))
```

```
## Warning: Removed 688 rows containing non-finite values (stat_bin).
```

```
## Warning: Removed 2 rows containing missing values (geom_bar).
```

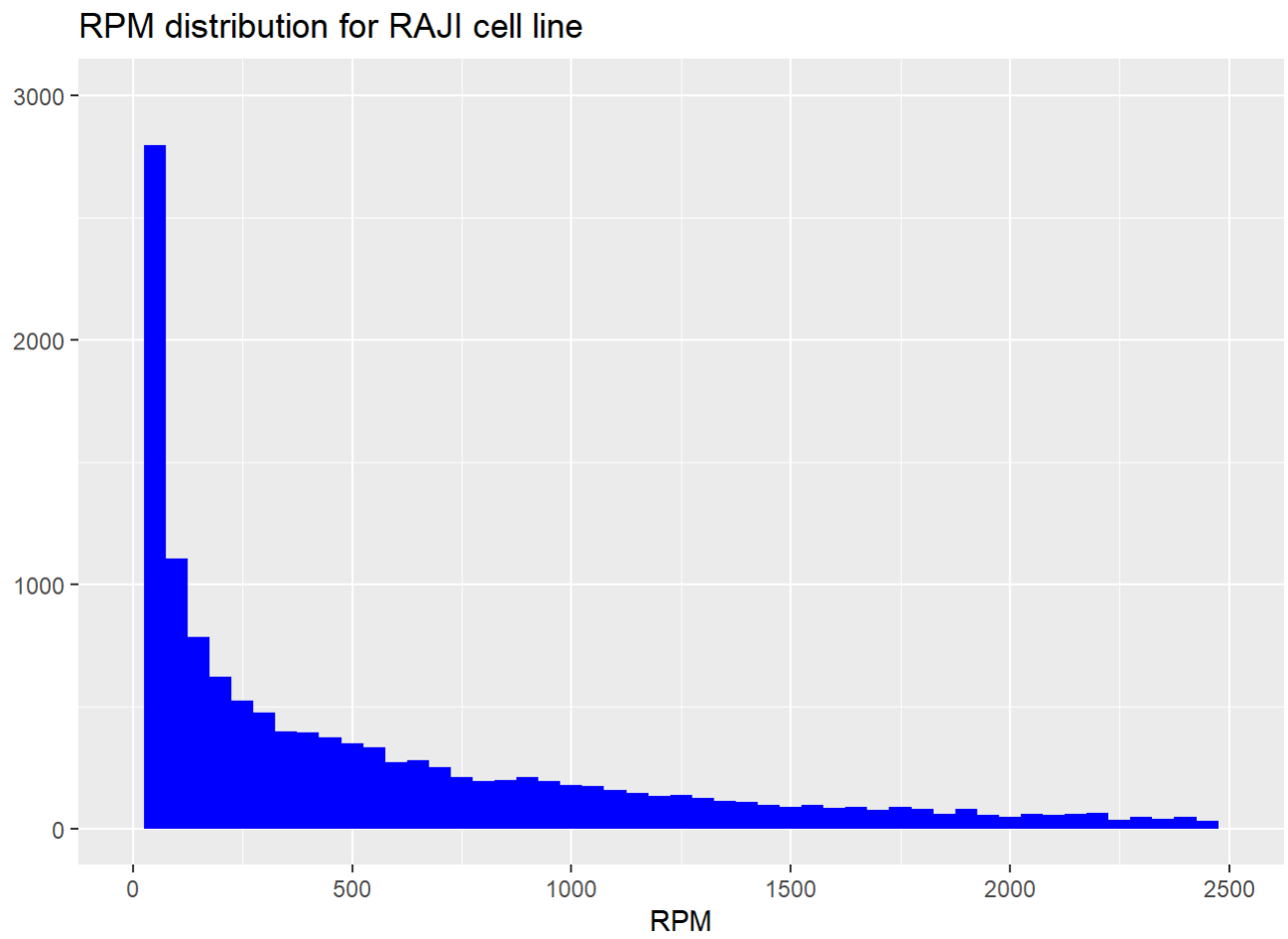



```
RAJI = read.delim("SRR2166627.htseq", header=F)
RAJI <- RAJI[RAJI$V2 != 0,]
```

```
qplot(RAJI$V2,
      geom="histogram",
      binwidth = 50,
      main = "RPM distribution for RAJI cell line",
      xlab = "RPM",
      fill=I("blue"),
      xlim=c(0,2500),
      ylim=c(0,3000))
```

```
## Warning: Removed 1486 rows containing non-finite values (stat_bin).
```

```
## Warning: Removed 2 rows containing missing values (geom_bar).
```

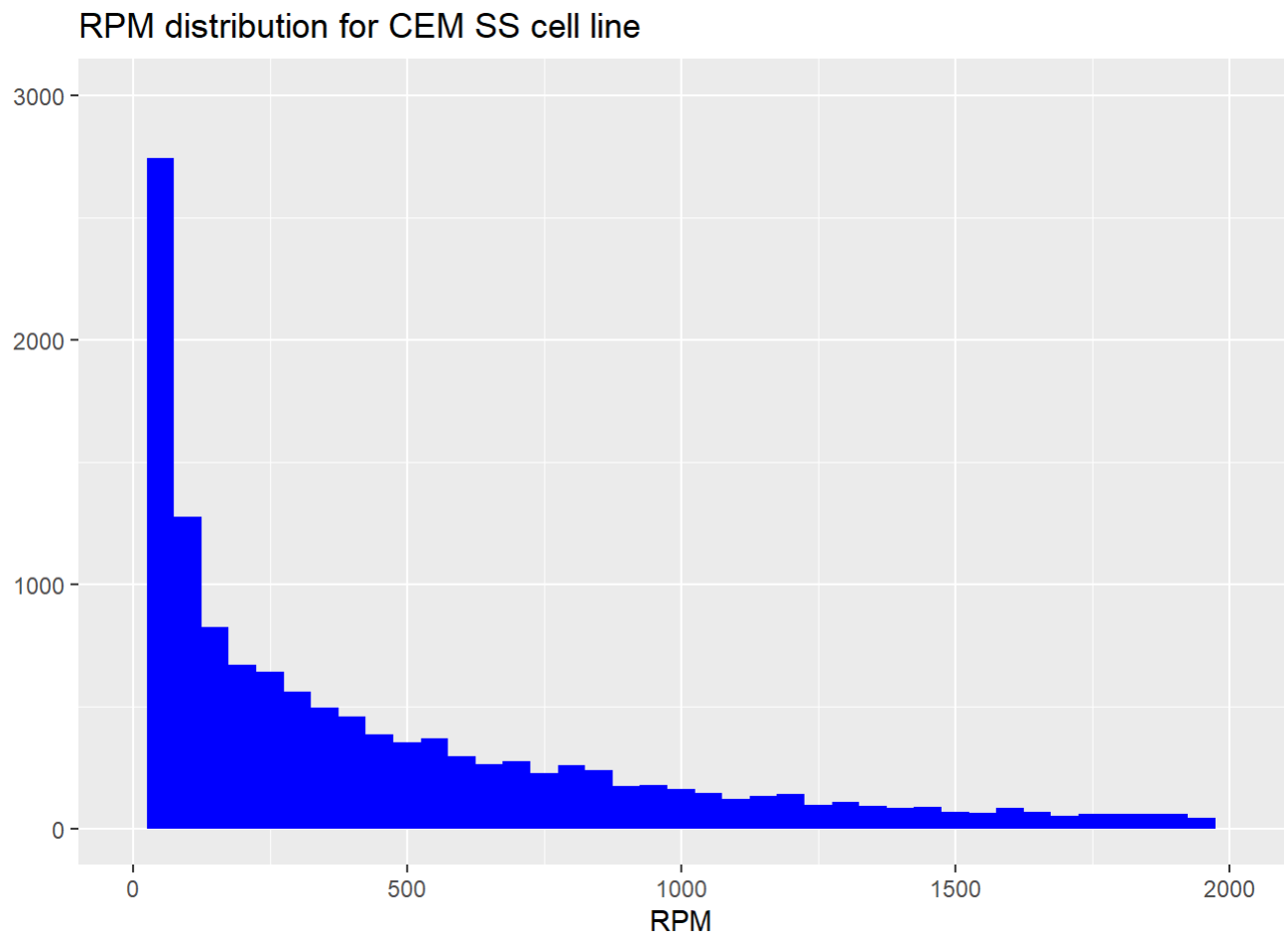



```
cell_line = read.delim("SRR2166628.htseq", header=F)
cell_line <- cell_line[cell_line$V2 != 0,]
```

```
qplot(cell_line$V2,
      geom="histogram",
      binwidth = 50,
      main = "RPM distribution for CEM SS cell line",
      xlab = "RPM",
      fill=I("blue"),
      xlim=c(0,2000),
      ylim=c(0,3000))
```

```
## Warning: Removed 1155 rows containing non-finite values (stat_bin).
```

```
## Warning: Removed 2 rows containing missing values (geom_bar).
```

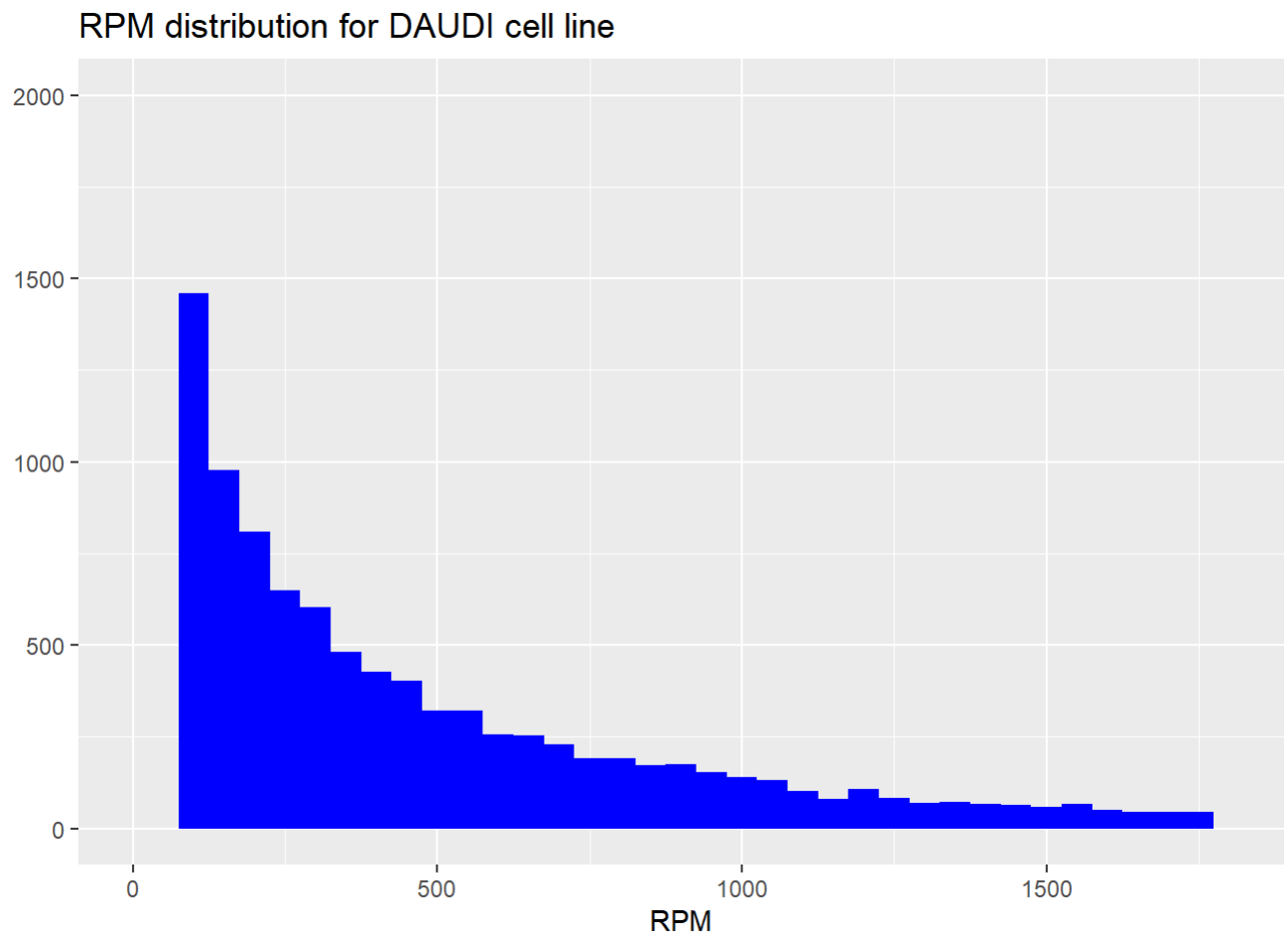



```
cell_line = read.delim("SRR2166629.htseq", header=F)
cell_line <- cell_line[cell_line$V2 != 0,]
```

```
qplot(cell_line$V2,
      geom="histogram",
      binwidth = 50,
      main = "RPM distribution for DAUDI cell line",
      xlab = "RPM",
      fill=I("blue"),
      xlim=c(0,1800),
      ylim=c(0,2000))
```

```
## Warning: Removed 1070 rows containing non-finite values (stat_bin).
```

```
## Warning: Removed 3 rows containing missing values (geom_bar).
```

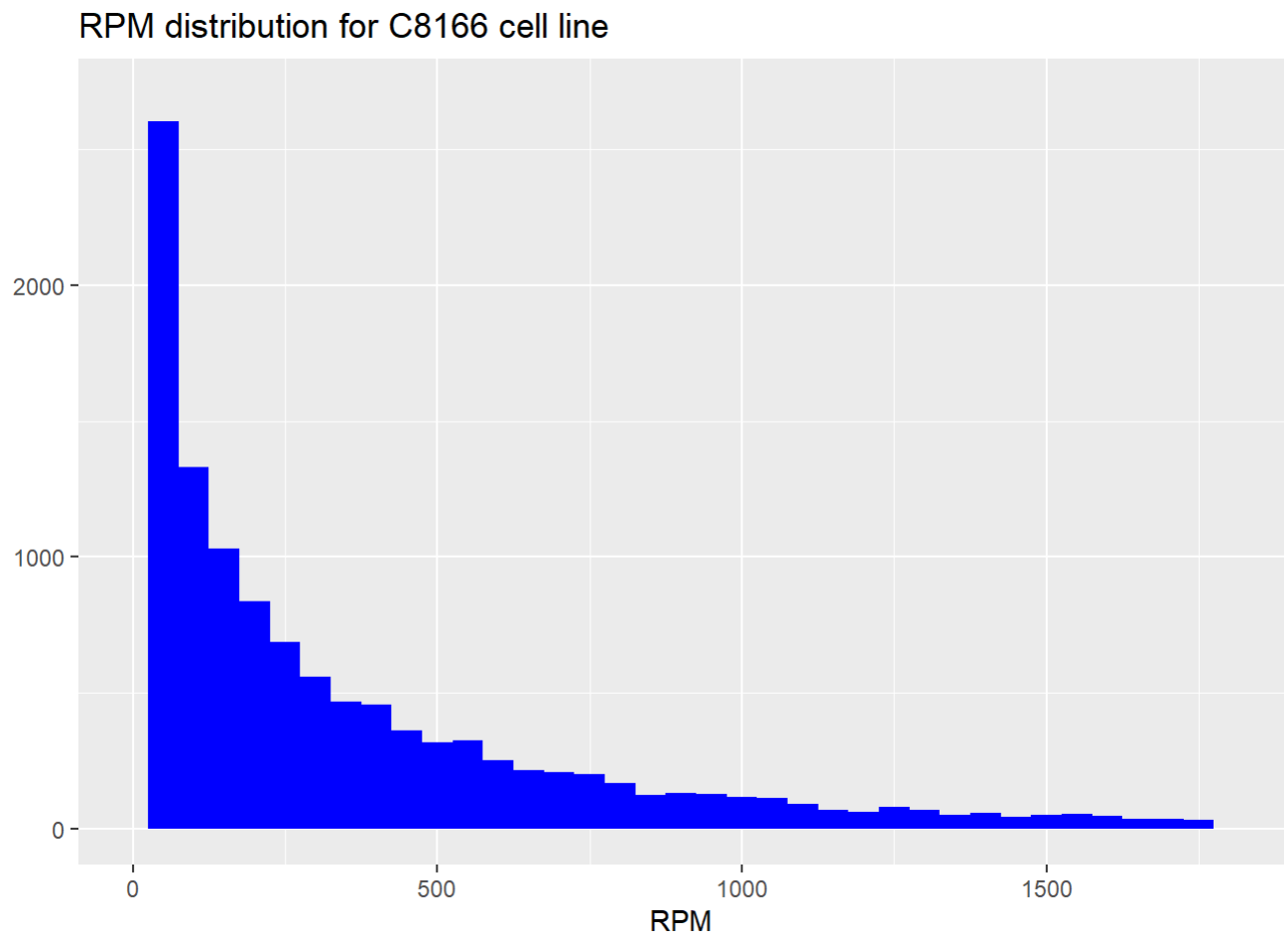



```
cell_line = read.delim("SRR2166630.htseq", header=F)
cell_line <- cell_line[cell_line$V2 != 0,]
```

```
qplot(cell_line$V2,
      geom="histogram",
      binwidth = 50,
      main = "RPM distribution for C8166 cell line",
      xlab = "RPM",
      fill=I("blue"),
      xlim=c(0,1800),
      ylim=c(0,2700))
```

```
## Warning: Removed 874 rows containing non-finite values (stat_bin).
```

```
## Warning: Removed 2 rows containing missing values (geom_bar).
```

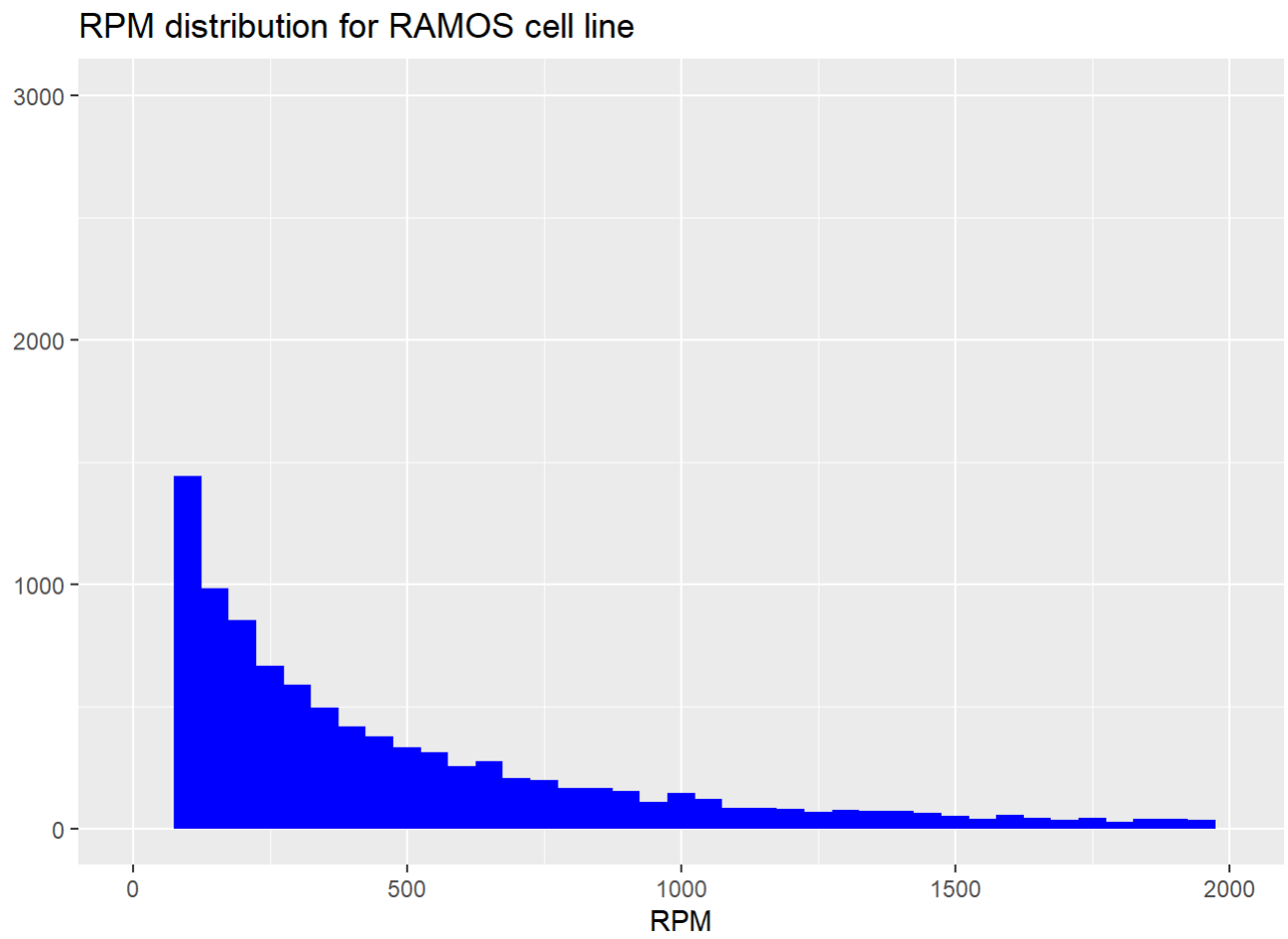



```
cell_line = read.delim("SRR2166631.htseq", header=F)
cell_line <- cell_line[cell_line$V2 != 0,]
```

```
qplot(cell_line$V2,
      geom="histogram",
      binwidth = 50,
      main = "RPM distribution for RAMOS cell line",
      xlab = "RPM",
      fill=I("blue"),
      xlim=c(0,2000),
      ylim=c(0,3000))
```

```
## Warning: Removed 779 rows containing non-finite values (stat_bin).
```

```
## Warning: Removed 3 rows containing missing values (geom_bar).
```

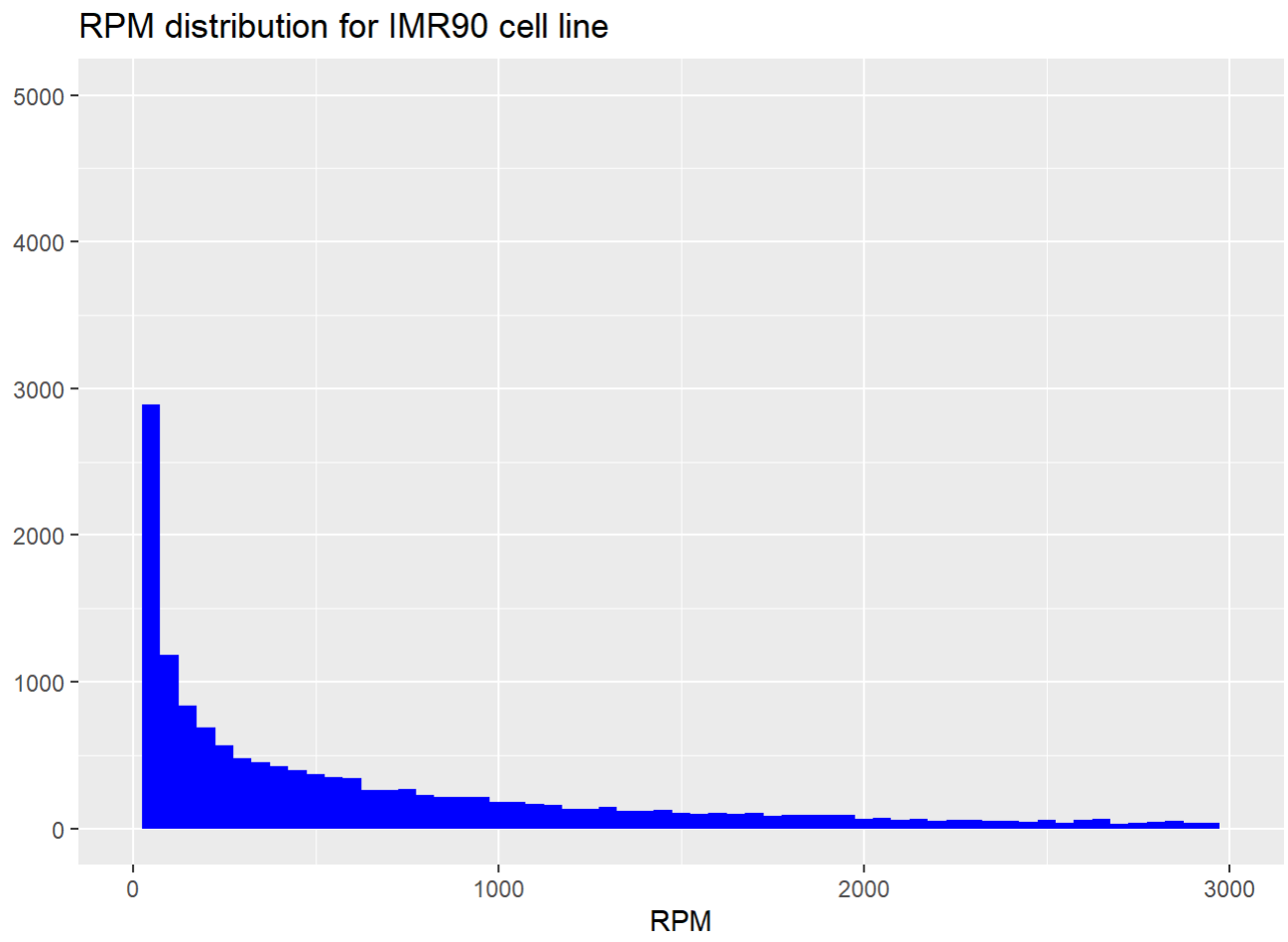



```
cell_line = read.delim("SRR2166632.htseq", header=F)
cell_line <- cell_line[cell_line$V2 != 0,]
```

```
qplot(cell_line$V2,
      geom="histogram",
      binwidth = 50,
      main = "RPM distribution for IMR90 cell line",
      xlab = "RPM",
      fill=I("blue"),
      xlim=c(0,3000),
      ylim=c(0,5000))
```

```
## Warning: Removed 1715 rows containing non-finite values (stat_bin).
```

```
## Warning: Removed 2 rows containing missing values (geom_bar).
```

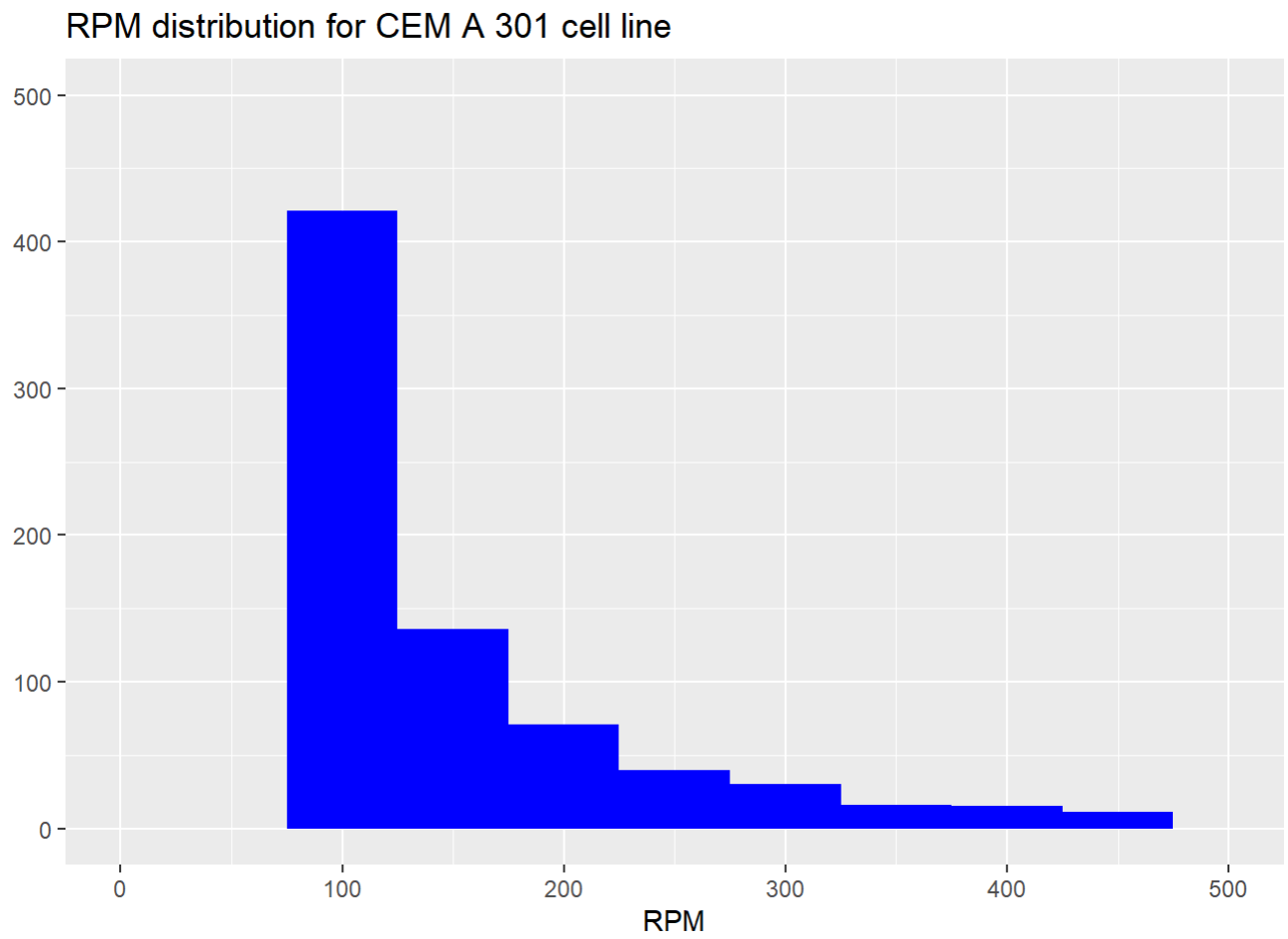



```
cell_line = read.delim("SRR2166633.htseq", header=F)
cell_line <- cell_line[cell_line$V2 != 0,]
```

```
qplot(cell_line$V2,
      geom="histogram",
      binwidth = 50,
      main = "RPM distribution for CEM A 301 cell line",
      xlab = "RPM",
      fill=I("blue"),
      xlim=c(0,500),
      ylim=c(0,500))
```

```
## Warning: Removed 43 rows containing non-finite values (stat_bin).
```

```
## Warning: Removed 3 rows containing missing values (geom_bar).
```

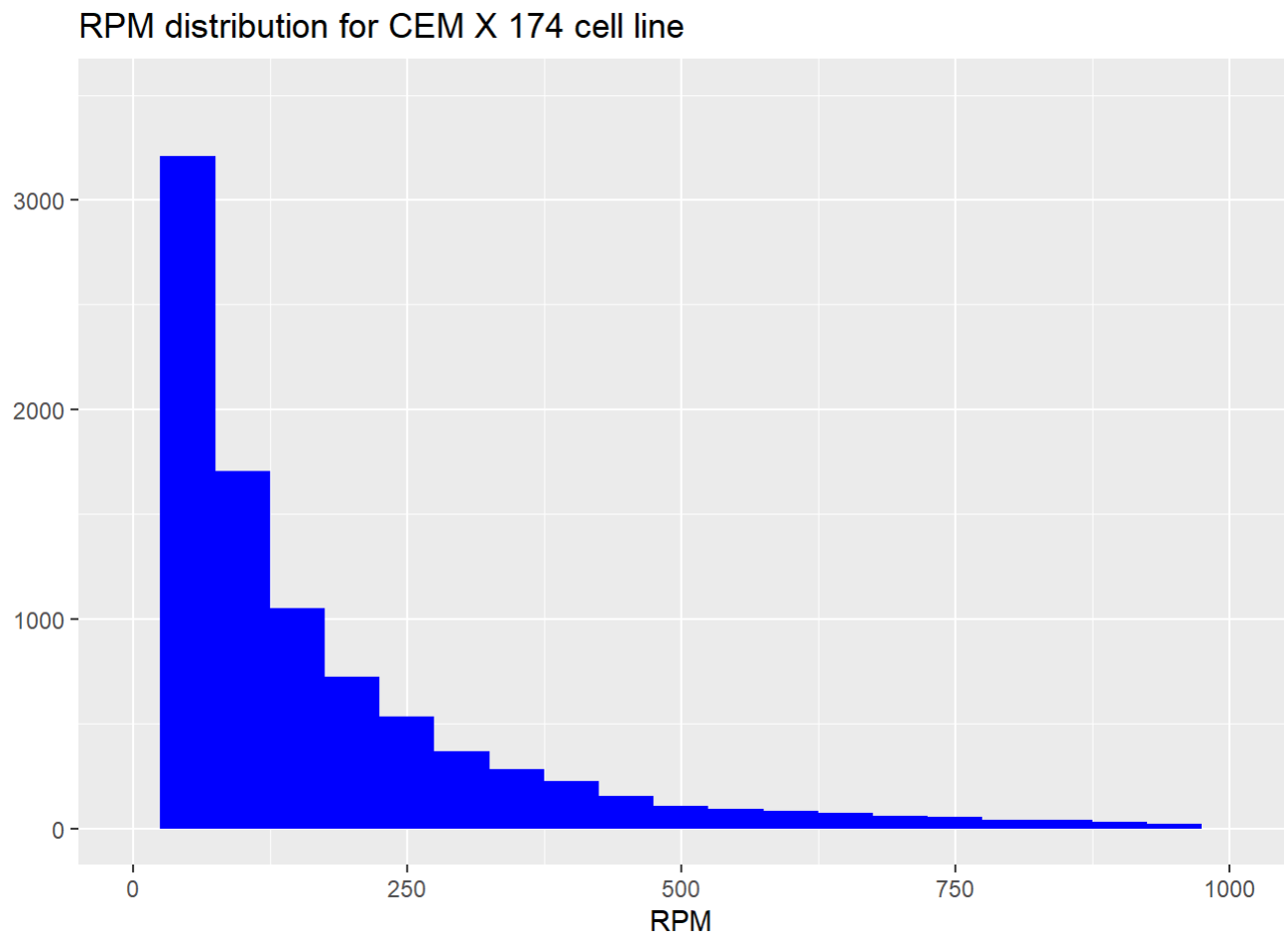



```
cell_line = read.delim("SRR2166634.htseq", header=F)
cell_line <- cell_line[cell_line$V2 != 0,]
```

```
qplot(cell_line$V2,
      geom="histogram",
      binwidth = 50,
      main = "RPM distribution for CEM X 174 cell line",
      xlab = "RPM",
      fill=I("blue"),
      xlim=c(0,1000),
      ylim=c(0,3500))
```

```
## Warning: Removed 392 rows containing non-finite values (stat_bin).
```

```
## Warning: Removed 2 rows containing missing values (geom_bar).
```

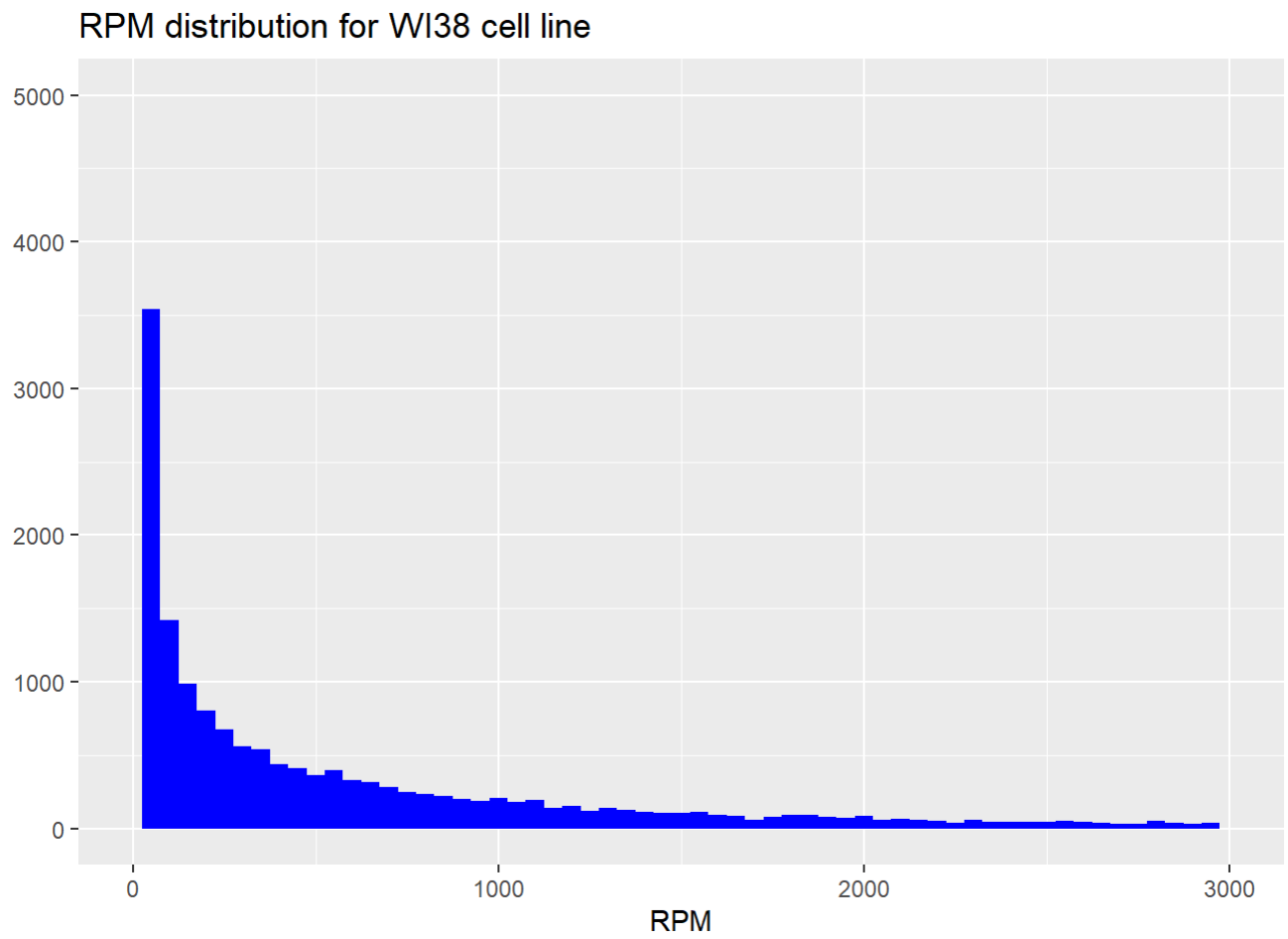



```
cell_line = read.delim("SRR2166635.htseq", header=F)
cell_line <- cell_line[cell_line$V2 != 0,]
```

```
qplot(cell_line$V2,
      geom="histogram",
      binwidth = 50,
      main = "RPM distribution for WI38 cell line",
      xlab = "RPM",
      fill=I("blue"),
      xlim=c(0,3000),
      ylim=c(0,5000))
```

```
## Warning: Removed 1471 rows containing non-finite values (stat_bin).
```

```
## Warning: Removed 2 rows containing missing values (geom_bar).
```

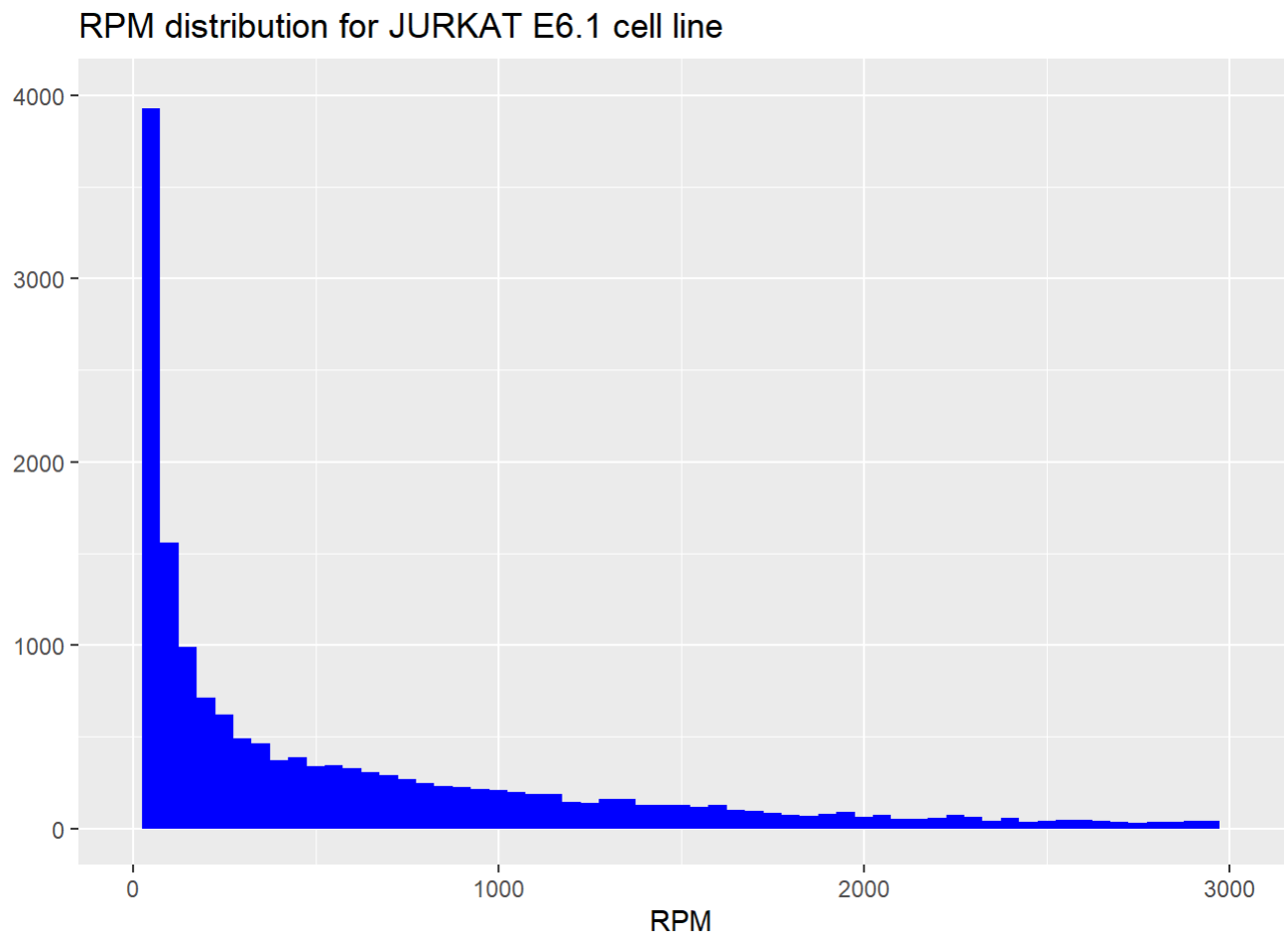



```
cell_line = read.delim("SRR2166636.htseq", header=F)
cell_line <- cell_line[cell_line$V2 != 0,]
```

```
qplot(cell_line$V2,
      geom="histogram",
      binwidth = 50,
      main = "RPM distribution for JURKAT E6.1 cell line",
      xlab = "RPM",
      fill=I("blue"),
      xlim=c(0,3000),
      ylim=c(0,4000))
```

```
## Warning: Removed 1361 rows containing non-finite values (stat_bin).
```

```
## Warning: Removed 2 rows containing missing values (geom_bar).
```

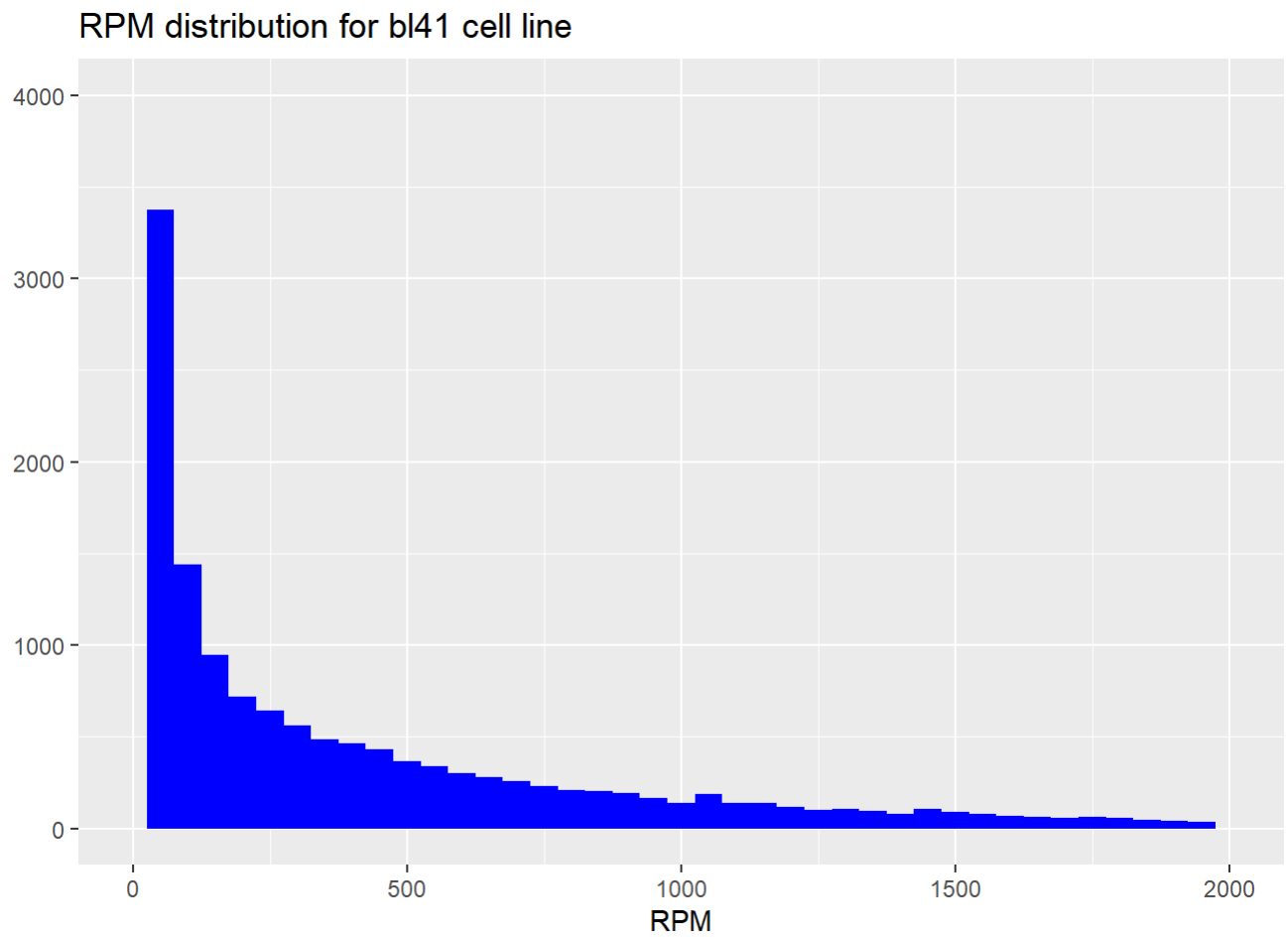



```
cell_line = read.delim("SRR2166637.htseq", header=F)
cell_line <- cell_line[cell_line$V2 != 0,]
```

```
qplot(cell_line$V2,
      geom="histogram",
      binwidth = 50,
      main = "RPM distribution for bl41 cell line",
      xlab = "RPM",
      fill=I("blue"),
      xlim=c(0,2000),
      ylim=c(0,4000))
```

```
## Warning: Removed 1273 rows containing non-finite values (stat_bin).
```

```
## Warning: Removed 2 rows containing missing values (geom_bar).
```

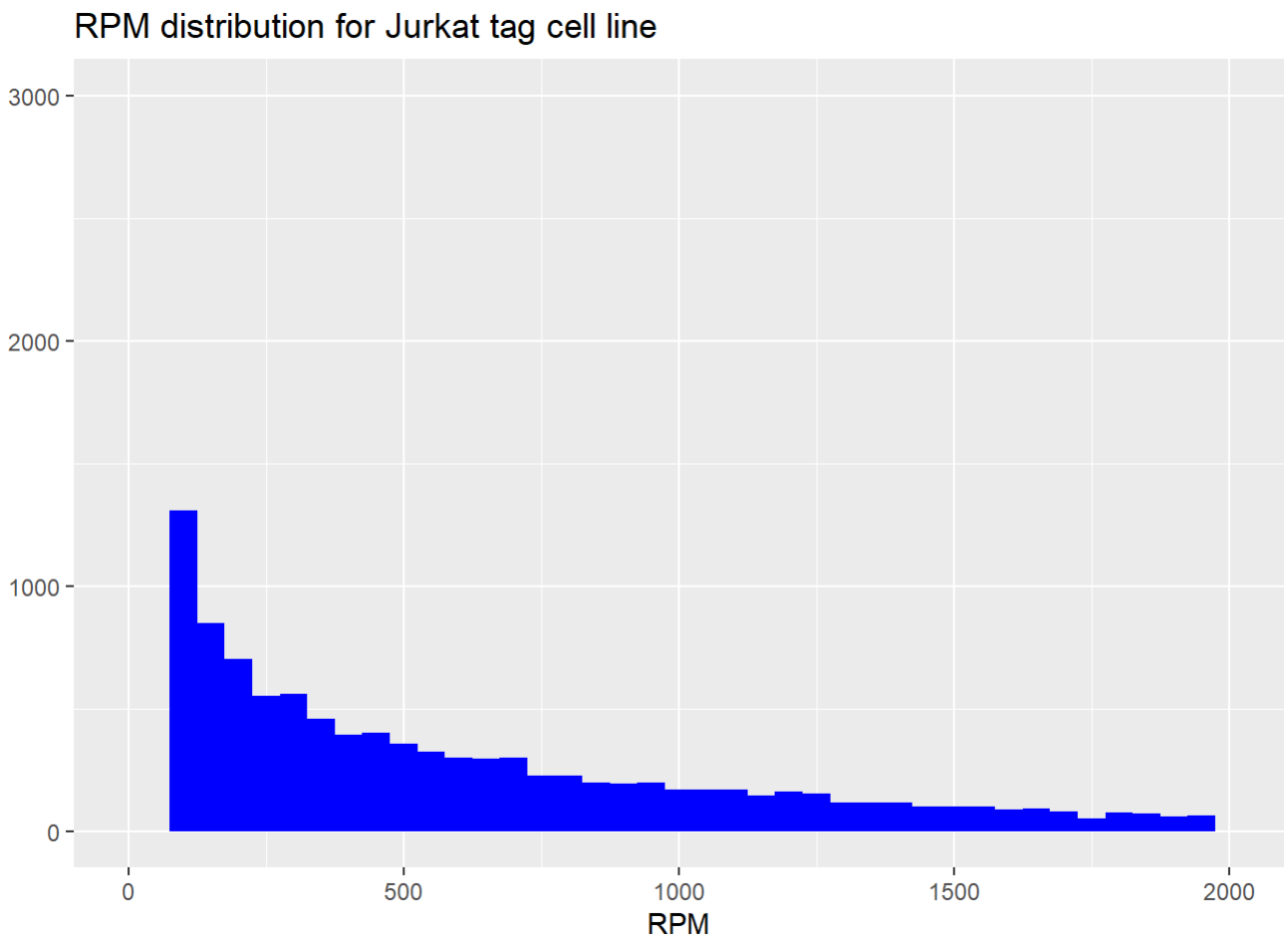



```
cell_line = read.delim("SRR2166638.htseq", header=F)
cell_line <- cell_line[cell_line$V2 != 0,]
```

```
qplot(cell_line$V2,
      geom="histogram",
      binwidth = 50,
      main = "RPM distribution for Jurkat tag cell line",
      xlab = "RPM",
      fill=I("blue"),
      xlim=c(0,2000),
      ylim=c(0,3000))
```

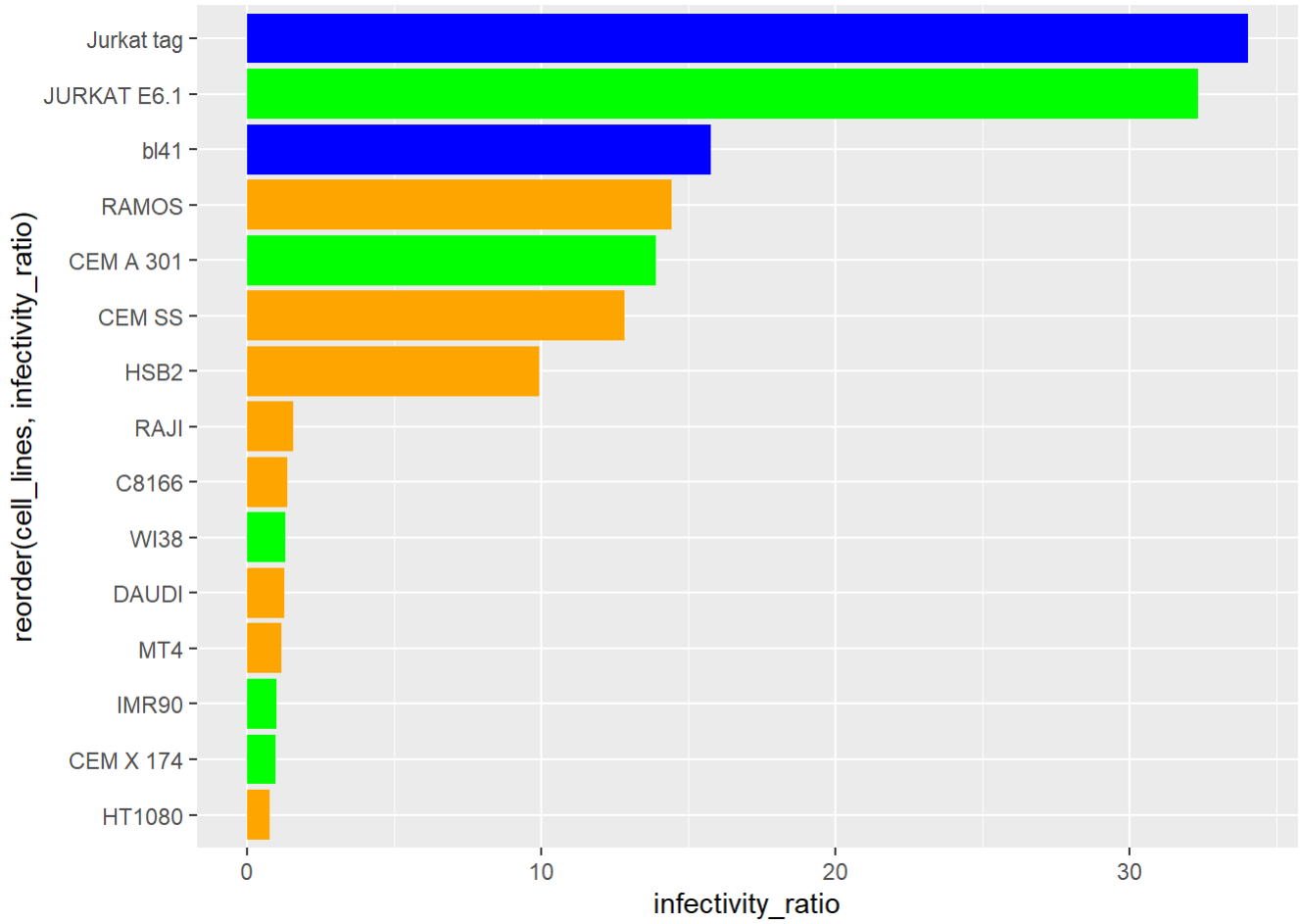
```
## Warning: Removed 1933 rows containing non-finite values (stat_bin).
```

```
## Warning: Removed 3 rows containing missing values (geom_bar).
```



Bar Plot

```
ggplot(data = infect, aes(x= reorder(cell_lines, infectivity_ratio), y= infectivity_ratio))+geom
_bar(stat = "identity", fill=c("orange", "orange", "orange", "orange", "orange", "orange", "oran
ge", "orange", "green", "green", "green", "green", "green", "blue", "blue" ))+ coord_flip()
```



Normalizing the datasets

Here we are making function to convert reads into normal reads per million

```
Normaliser <- function(x){
  x/(sum(x)/1000000)
}
```

Using the above function in our samples dataset

```
samples[,2:16] <- lapply(samples[,2:16], Normaliser)
```

Dividing data into 6 subsets for better computation

```
sample_1 <- samples[1:10000,]
sample_2 <- samples[10001:20000,]
sample_3 <- samples[20001: 30000,]
sample_4 <- samples[30001: 40000,]
sample_5 <- samples [40001: 50000,]
sample_6 <- samples [50001: 58307,]
```

re-defing data

transposing the datasets

```
sample_t_1 <- as.data.frame(t(sample_1))
names(sample_t_1) <- sample_t_1[1,]
sample_t_1 <- sample_t_1[-1,]

sample_t_2 <- as.data.frame(t(sample_2))
names(sample_t_2) <- sample_t_2[1,]
sample_t_2 <- sample_t_2[-1,]

sample_t_3 <- as.data.frame(t(sample_3))
names(sample_t_3) <- sample_t_3[1,]
sample_t_3 <- sample_t_3[-1,]

sample_t_4 <- as.data.frame(t(sample_4))
names(sample_t_4) <- sample_t_4[1,]
sample_t_4 <- sample_t_4[-1,]

sample_t_5 <- as.data.frame(t(sample_5))
names(sample_t_5) <- sample_t_5[1,]
sample_t_5 <- sample_t_5[-1,]

sample_t_6 <- as.data.frame(t(sample_6))
names(sample_t_6) <- sample_t_6[1,]
sample_t_6 <- sample_t_6[-1,]
```

```
sample_t_1_infect <- data.frame(infect$infectivity_ratio ,sample_t_1)
sample_t_2_infect <- data.frame(infect$infectivity_ratio ,sample_t_2)
sample_t_3_infect <- data.frame(infect$infectivity_ratio ,sample_t_3)
sample_t_4_infect <- data.frame(infect$infectivity_ratio ,sample_t_4)
sample_t_5_infect <- data.frame(infect$infectivity_ratio ,sample_t_5)
sample_t_6_infect <- data.frame(infect$infectivity_ratio ,sample_t_6)
```

creating data frame which will use in doing correlation test

```
samples_t <- as.data.frame(t(samples))
names(samples_t) <- samples_t[1,]
samples_t <- samples_t[-1,]

samples_infect <- data.frame(infect$infectivity_ratio ,samples_t)
```

correlation test

```
i <- c()
cor_e <- c()
cor_p <- c()

for (i in 2:58308)
{
  m = cor.test(samples_infect[,1],as.numeric(samples_infect[,i]),method = 'spearman', use = 'pai
rwise.complete.obs',p.adjust.methods = "fdr", exact = F)
  cor_e[i-1] = m$estimate
  cor_p[i-1] = m$p.value
}

cor_test <- data.frame(Gene = colnames(samples_infect[,2:58308]),
                           cor_value = cor_e,
                           p_value = cor_p
                           )

cor_test <- na.omit(cor_test)

#cor_test
```

subseting genes of interest

```
gene_of_interest <- na.omit(cor_test[cor_test$cor_value > 0.7 & cor_test$p_value < 0.01 ,])
gene_of_interest
```

```
##                  Gene cor_value      p_value
## 14    ENSG00000001561 0.7035714 3.424337e-03
## 181   ENSG00000007350 0.7453940 1.424820e-03
## 196   ENSG00000007952 0.8357143 1.044469e-04
## 355   ENSG00000015133 0.7035714 3.424337e-03
## 631   ENSG00000047662 0.7035714 3.424337e-03
## 654   ENSG00000049167 0.7321429 1.912964e-03
## 772   ENSG00000057468 0.7107143 2.978995e-03
## 913   ENSG00000065060 0.7035714 3.424337e-03
## 923   ENSG00000065328 0.7464286 1.391411e-03
## 944   ENSG00000065675 0.7214286 2.398868e-03
## 1110  ENSG00000070388 0.7063350 3.246150e-03
## 1120  ENSG00000070601 0.7456984 1.414923e-03
## 1185  ENSG00000072201 0.7035714 3.424337e-03
## 1349  ENSG00000076555 0.7178571 2.581165e-03
## 1359  ENSG00000076864 0.7642857 9.073101e-04
## 1504  ENSG00000080644 0.8321429 1.190282e-04
## 1519  ENSG00000081019 0.7107143 2.978995e-03
## 1695  ENSG00000086475 0.7607143 9.911286e-04
## 1760  ENSG00000088035 0.7142857 2.774384e-03
## 1808  ENSG00000089022 0.7285714 2.065210e-03
## 1996  ENSG00000093072 0.7204347 2.448527e-03
## 2142  ENSG00000099954 0.7077479 3.157952e-03
## 2180  ENSG00000100077 0.7464286 1.391411e-03
## 2191  ENSG00000100104 0.7142857 2.774384e-03
## 2321  ENSG00000100473 0.7178571 2.581165e-03
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## 56622 ENSG00000280194 0.7357143 1.769869e-03
## 56688 ENSG00000280277 0.7566879 1.093031e-03
## 57045 ENSG00000281852 0.7332989 1.865664e-03
## 57082 ENSG00000282080 0.7356708 1.771556e-03
## 57104 ENSG00000282277 0.7058578 3.276374e-03
## 57494 ENSG00000283414 0.7204347 2.448527e-03
## 57886 ENSG00000284070 0.7204347 2.448527e-03
## 58127 ENSG00000284543 0.7598615 1.012041e-03
## 58177 ENSG00000284621 0.8315466 1.216184e-04
## 58294 ENSG00000284740 0.7828421 5.589454e-04
```

correlation test

```
i <- c()
cor_e <- c()
cor_p <- c()

for (i in 2:58308)
{
  m = cor.test(samples_infect[,1],as.numeric(samples_infect[,i]),method = 'pearson', use = 'pair
wise.complete.obs',p.adjust.methods = "fdr", exact = F)
  cor_e[i-1] = m$estimate
  cor_p[i-1] = m$p.value
}

cor_test <- data.frame(Gene = colnames(samples_infect[,2:58308]),
                           cor_value = cor_e,
                           p_value = cor_p
                           )

#cor_test
```

subseting genes of interest

```
gene_of_interest <- na.omit(cor_test[cor_test$cor_value > 0.9 & cor_test$p_value < 0.01 ,])
gene_of_interest
```

```
##                  Gene cor_value      p_value
## 9778  ENSG00000154537 0.9254256 7.705474e-07
## 10269 ENSG00000158813 0.9019888 4.296749e-06
## 11315 ENSG00000164300 0.9194246 1.255658e-06
## 13429 ENSG00000172995 0.9005775 4.698709e-06
## 29794 ENSG00000230830 0.9046848 3.608298e-06
## 36137 ENSG00000241537 0.9190814 1.289741e-06
## 46552 ENSG00000260966 0.9006792 4.668736e-06
## 47792 ENSG00000263818 0.9107026 2.396988e-06
## 50568 ENSG00000269802 0.9172384 1.486291e-06
## 51770 ENSG00000271776 0.9030633 4.010310e-06
```

SERINC5

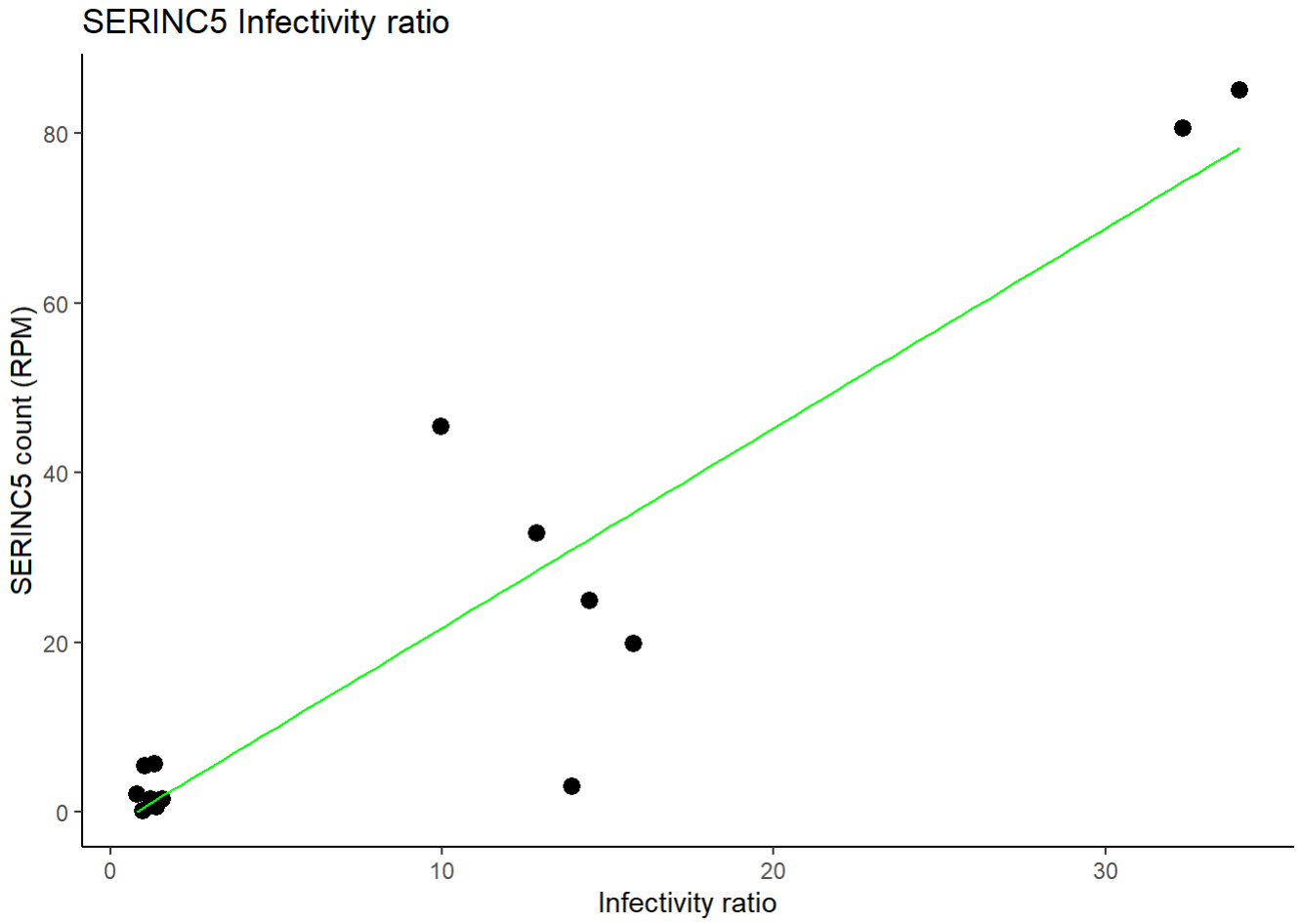
To recreate the results from the paper, we need to look at the correlation value SERINC5
Ensemble ID of **SERINC5** is ENSG00000164300 and from the table above, we can see that it has a correlation value of 0.91.

Now we replicate he Figure 1-d from the paper…

```
Serinc5 <- samples_infect[, colnames(samples_infect) == c("infect.infectivity_ratio", "ENSG00000
164300")]
```

```
ggplot(data = Serinc5, aes(infect.infectivity_ratio, as.numeric(ENSG00000164300), size= 1.0))+
geom_point(pch=20)+
geom_smooth(method = "lm", se=F, col="green", size=0.5)+
xlab("Infectivity ratio")+
ylab("SERINC5 count (RPM)")+
ggtitle("SERINC5 Infectivity ratio")+
geom_smooth(method = "lm", se=F, col="green", size=0.5)+
theme_classic()+
theme(legend.position = "none")
```

```
## `geom_smooth()` using formula 'y ~ x'
## `geom_smooth()` using formula 'y ~ x'
```

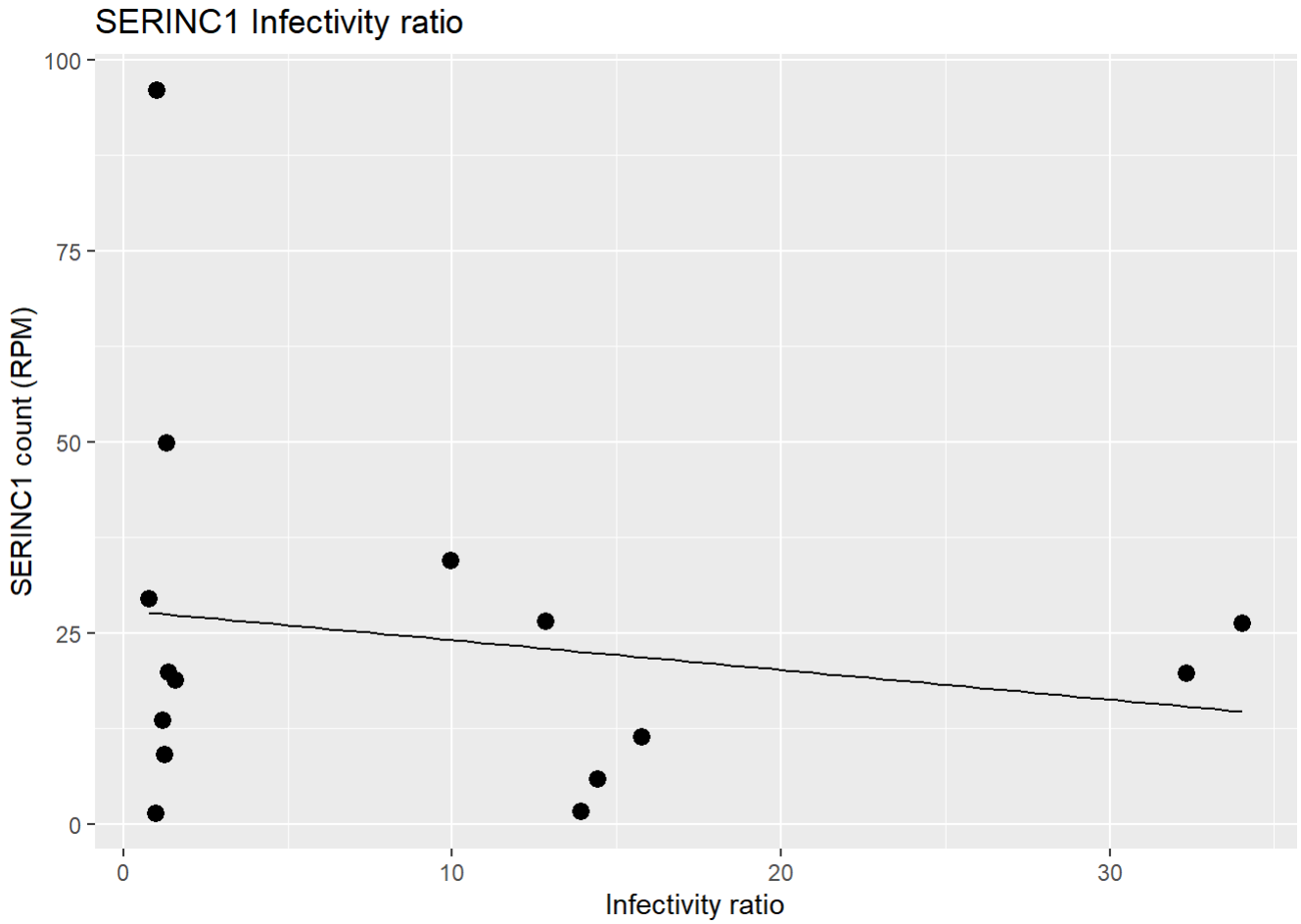


We can also plot the infectivity ratio vs. RPM graph for all the SERNIC genes

SERINC1 ENSG00000111897
SERINC2 ENSG00000168528
SERINC3 ENSG00000132824
SERINC4 ENSG00000184716
SERINC5 ENSG00000164300

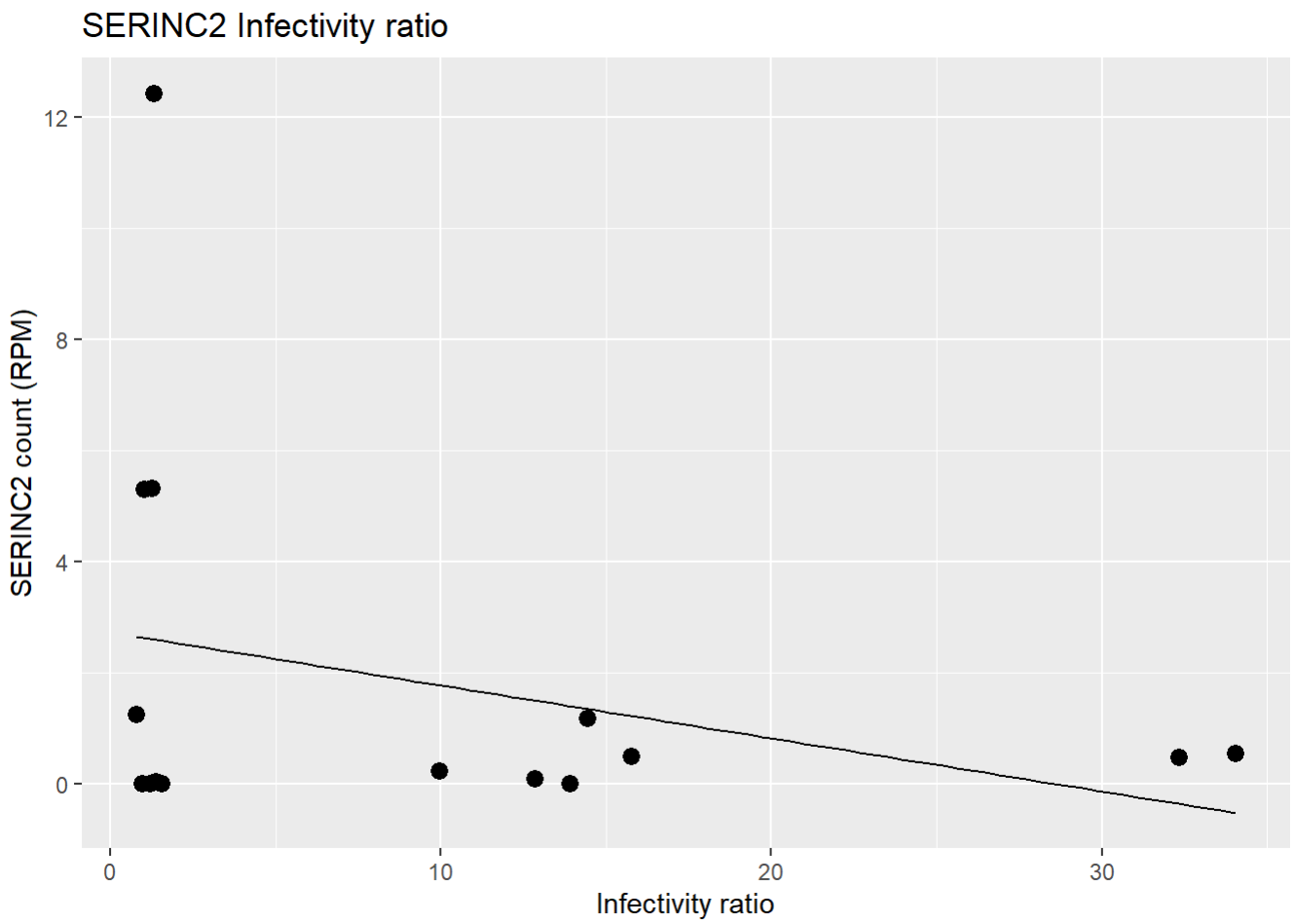
```
ggplot(data = samples_infect, aes(infect.infectivity_ratio, as.numeric(ENSG00000111897), size=
1.0))+
geom_point(pch=20, col="black")+
geom_smooth(method = "lm", se=F, col="black", size=0.5)+
xlab("Infectivity ratio")+
ylab("SERINC1 count (RPM)")+
ggtitle("SERINC1 Infectivity ratio")+
theme(legend.position = "none")
```

```
## `geom_smooth()` using formula 'y ~ x'
```



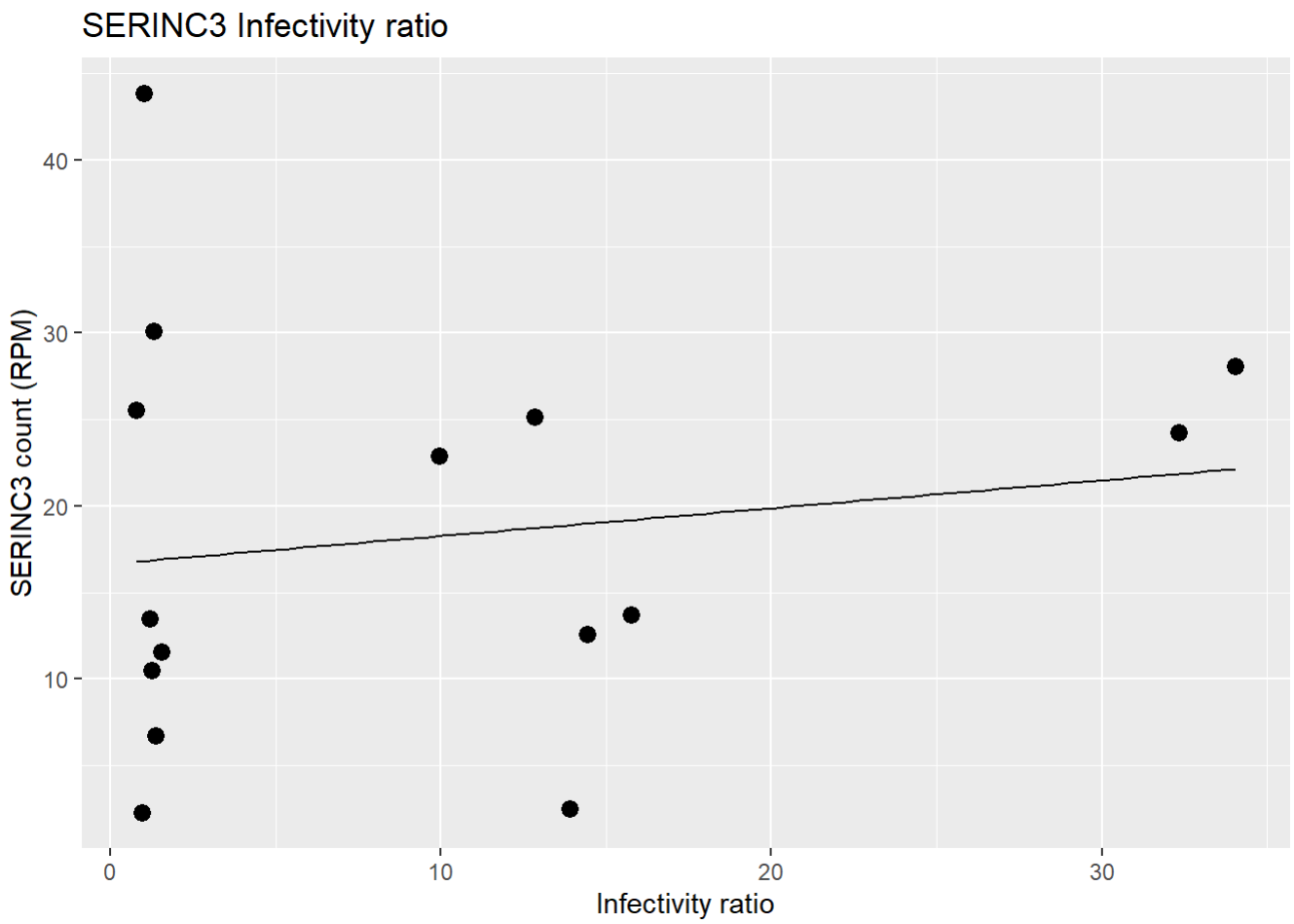

```
ggplot(data = samples_infect, aes(infect.infectivity_ratio, as.numeric(ENSG00000168528), size=
1.0))+
geom_point(pch=20, col="black")+
geom_smooth(method = "lm", se=F, col="black", size=0.5)+
xlab("Infectivity ratio")+
ylab("SERINC2 count (RPM)")+
ggtitle("SERINC2 Infectivity ratio")+
theme(legend.position = "none")
```

```
## `geom_smooth()` using formula 'y ~ x'
```



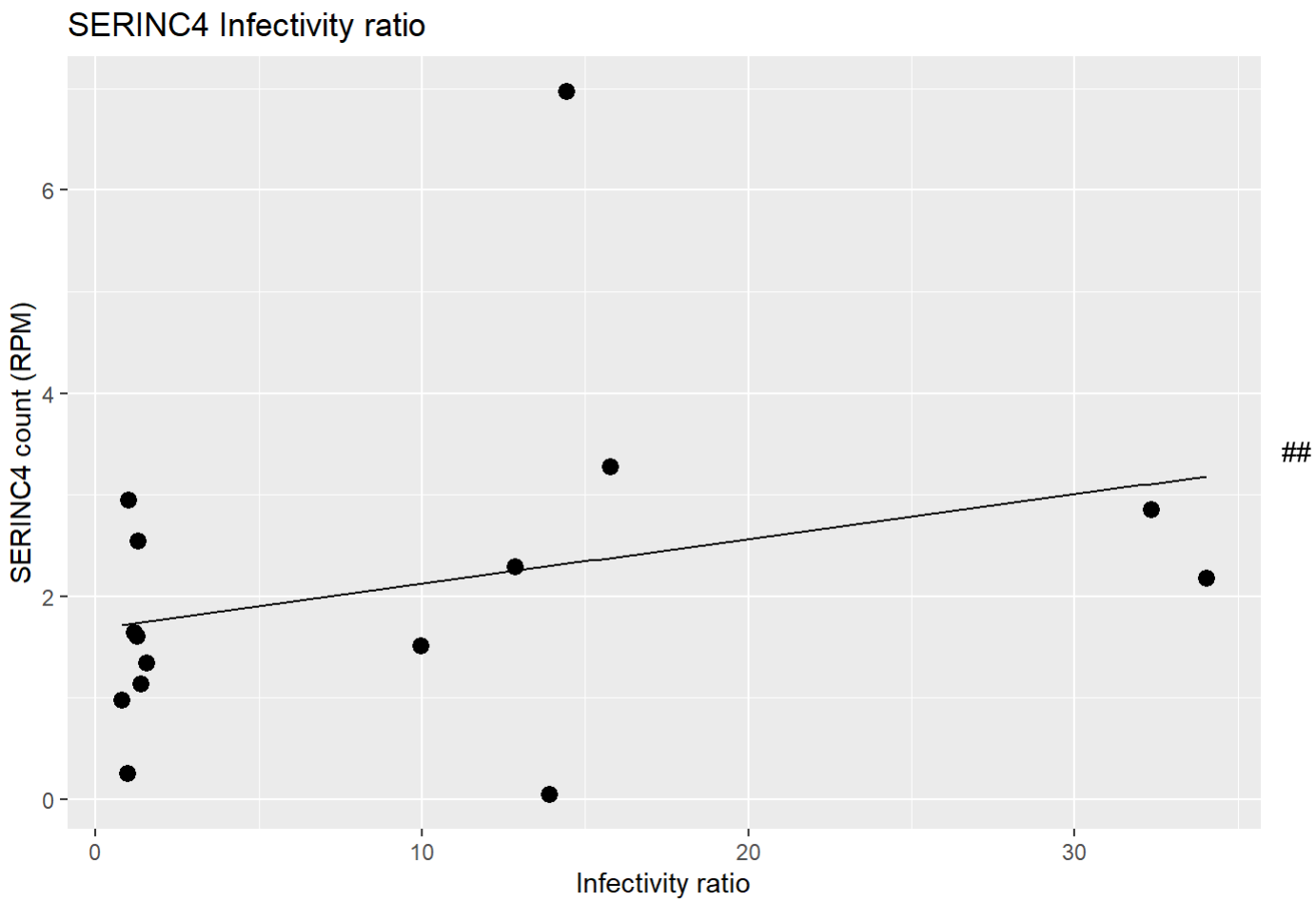

```
ggplot(data = samples_infect, aes(infect.infectivity_ratio, as.numeric(ENSG00000132824), size=
1.0))+
geom_point(pch=20, col="black")+
geom_smooth(method = "lm", se=F, col="black", size=0.5)+
xlab("Infectivity ratio")+
ylab("SERINC3 count (RPM)")+
ggtitle("SERINC3 Infectivity ratio")+
theme(legend.position = "none")
```

```
## `geom_smooth()` using formula 'y ~ x'
```




```
ggplot(data = samples_infect, aes(infect.infectivity_ratio, as.numeric(ENSG00000184716), size=
1.0))+
geom_point(pch=20, col="black")+
geom_smooth(method = "lm", se=F, col="black", size=0.5)+
xlab("Infectivity ratio")+
ylab("SERINC4 count (RPM)")+
ggtitle("SERINC4 Infectivity ratio")+
theme(legend.position = "none")
```

```
## `geom_smooth()` using formula 'y ~ x'
```



##

Next we find the genes with positive correlation as well as the genes with negative correlation

```
poscor <- cor_test[cor_test$cor_value >= 0.9 & cor_test$p_value <= 0.01,] # For positively corre
lated genes
posgenenames<- poscor$Gene
posgenes <- samples_infect[, posgenenames]
```

```
## Error in `[.data.frame`(samples_infect, , posgenenames): undefined columns selected
```

```
posgenes <- t(posgenes)
```

```
## Error in t(posgenes): object 'posgenes' not found
```

```
negcor <- cor_test[cor_test$cor_value <= -0.6 & cor_test$p_value <= 0.05,] #For negatively corre
lated genes
neggenenames<- negcor$Gene
neggenes <- samples_infect[, neggenenames]
```

```
## Error in `[.data.frame`(samples_infect, , neggenenames): undefined columns selected
```

```
neggenes <- t(neggenes)
```

```
## Error in t(neggenes): object 'neggenes' not found
```

```
head(poscor, n=11L)
```

```
##       Gene cor_value p_value
## NA    <NA>        NA      NA
## NA.1  <NA>        NA      NA
## NA.2  <NA>        NA      NA
## NA.3  <NA>        NA      NA
## NA.4  <NA>        NA      NA
## NA.5  <NA>        NA      NA
## NA.6  <NA>        NA      NA
## NA.7  <NA>        NA      NA
## NA.8  <NA>        NA      NA
## NA.9  <NA>        NA      NA
## NA.10 <NA>        NA      NA
```

```
head(negcor, n=12L)
```

```
##       Gene cor_value p_value
## NA    <NA>        NA      NA
## NA.1  <NA>        NA      NA
## NA.2  <NA>        NA      NA
## NA.3  <NA>        NA      NA
## NA.4  <NA>        NA      NA
## NA.5  <NA>        NA      NA
## NA.6  <NA>        NA      NA
## NA.7  <NA>        NA      NA
## NA.8  <NA>        NA      NA
## NA.9  <NA>        NA      NA
## NA.10 <NA>        NA      NA
## NA.11 <NA>        NA      NA
```

Our Hypothesis

The following genes might be able to block HIV as well… **SAMHD1 (ENSG00000101347): APOBEC3G (ENSG00000239713): MX2 (ENSG00000183486): TRIM5 (ENSG00000132256): Tethering (ENSG00000130303):** Blocs HIV Budding

Generating the data

```
SAMHD1 <- cor_test[cor_test$Gene=="ENSG00000101347",]
SAMHD1$cor_value
```

```
## [1] -0.4216684
```

```
APOBEC3G <- cor_test[cor_test$Gene=="ENSG00000239713",]
APOBEC3G$cor_value
```

```
## [1] -0.1196492
```

```
MX2 <- cor_test[cor_test$Gene=="ENSG00000183486",]
MX2$cor_value
```

```
## [1] 0.5551704
```

```
TRIM5 <- cor_test[cor_test$Gene=="ENSG00000132256",]
TRIM5$cor_value
```

```
## [1] -0.1989562
```

```
TETHERIN <- cor_test[cor_test$Gene=="ENSG00000130303",]
TETHERIN$cor_value
```

```
## [1] -0.2239895
```

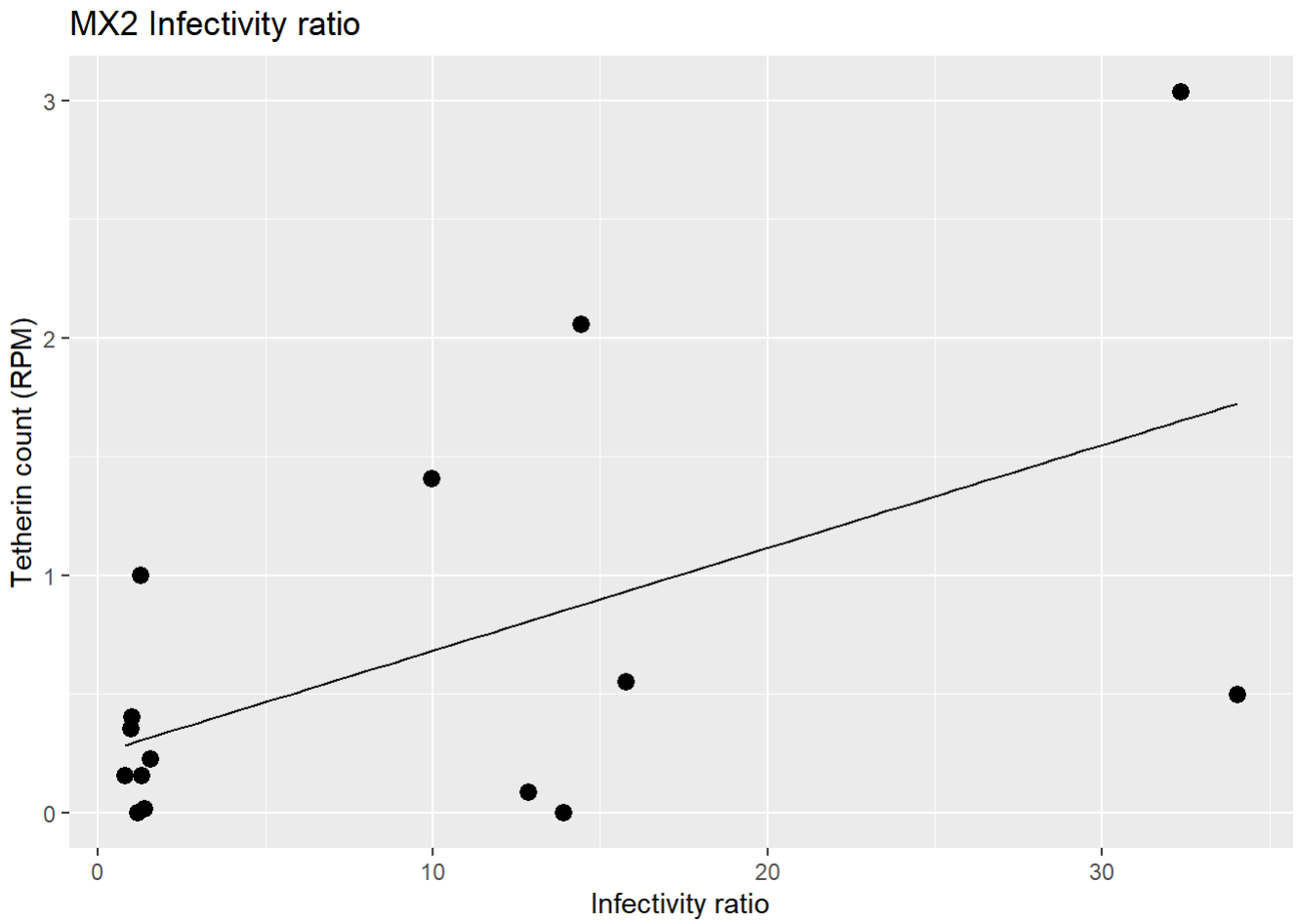
We only find significant correlation with MX2 so we plot its graph…

```
MX2 <- samples_infect[, colnames(samples_infect) == c("infect.infectivity_ratio", "ENSG000001834
86")]
```

Now Plotting

```
ggplot(data = MX2, aes(infect.infectivity_ratio, as.numeric(ENSG00000183486), size= 1.0))+
geom_point(pch=20)+
geom_smooth(method = "lm", se=F, col="black", size=0.5)+
xlab("Infectivity ratio")+
ylab("Tetherin count (RPM)")+
ggtitle("MX2 Infectivity ratio")+
geom_smooth(method = "lm", se=F, col="black", size=0.5)+
theme(legend.position = "none")
```

```
## `geom_smooth()` using formula 'y ~ x'
## `geom_smooth()` using formula 'y ~ x'
```



Upregulatd genes

```
head(poscor)
```

```
##      Gene cor_value p_value
## NA   <NA>        NA      NA
## NA.1 <NA>        NA      NA
## NA.2 <NA>        NA      NA
## NA.3 <NA>        NA      NA
## NA.4 <NA>        NA      NA
## NA.5 <NA>        NA      NA
```

Among the above genes we find the following genes to be of most importance during HIV attack

ENSG00000158813 EDA
ENSG00000269802 AC011491.3

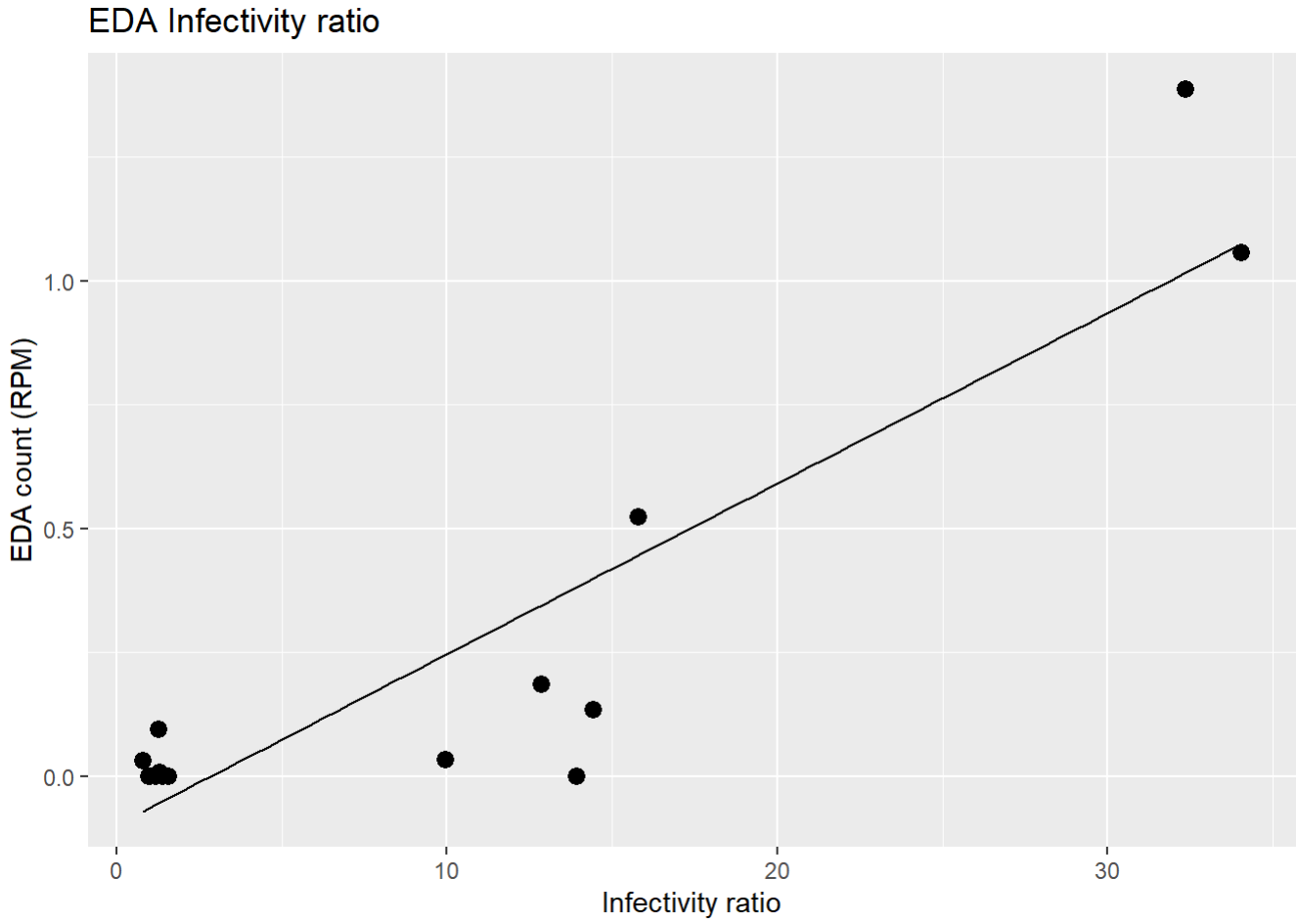
EDA [ENSG00000158813]

About EDA: The protein encoded by this gene is a type II membrane protein that can be cleaved by furin to produce a secreted form.
Hypothesis: Upon infection with HIV, envelope proteins are attached to cell membrane so the fully packaged HIV with capcid can go and attached to cell membrane and leave the cell to infect new cell. So it might be upregulating this gene in order to increase it's infectivity.

```
EDA <- samples_infect[, colnames(samples_infect) == c("infect.infectivity_ratio", "ENSG000001588
13")]
```

```
ggplot(data = EDA, aes(infect.infectivity_ratio, as.numeric(ENSG00000158813), size= 1.0))+
geom_point(pch=20)+
geom_smooth(method = "lm", se=F, col="black", size=0.5)+
xlab("Infectivity ratio")+
ylab("EDA count (RPM)")+
ggtitle("EDA Infectivity ratio")+
theme(legend.position = "none")
```

```
## `geom_smooth()` using formula 'y ~ x'
```



Down regulated genes

```
head(negcor)
```

```
##      Gene cor_value p_value
## NA   <NA>        NA      NA
## NA.1 <NA>        NA      NA
## NA.2 <NA>        NA      NA
## NA.3 <NA>        NA      NA
## NA.4 <NA>        NA      NA
## NA.5 <NA>        NA      NA
```

Among above negatively correlated genes we found PLXNB2 Gene (ENSG00000196576) most interesting.

```
PLXNB2 <- samples_infect[, colnames(samples_infect) == c("infect.infectivity_ratio", "ENSG000001
96576")]
```

Now Plotting

```
ggplot(data = PLXNB2, aes(infect.infectivity_ratio, as.numeric(ENSG00000196576), size= 1.0))+
geom_point(pch=20)+
geom_smooth(method = "lm", se=F, col="black", size=0.5)+
xlab("Infectivity ratio")+
ylab("PLXNB2 count (RPM)")+
ggtitle("PLXNB2 Infectivity ratio")+
theme(legend.position = "none")
```