Case Study 2

I made this case study to show similarities between Banana and Apples genes.
The scientific names for banana and apple are Musa Balbisiana, Malus Baccata.
I used seqinr package.

(R) Code

```
r_from_f <-function(f,df1,df2){return  (sqrt(f/(f+(df1/df2))))}
comp_plt <- function(seq1,seq2){
par(mfrow=c(1,2))    # set the plotting area into a 1*2 array
barplot(table(seq1),col=1:4)
barplot(table(seq2),col=1:4)}
library(seqinr)
banana <- read.fasta("Musa balbisiana.fasta")
apple <- read.fasta("Malus baccata.fasta")
apple_seq <- apple$NC_045389.1
banana_seq <- banana$NC_045389.1
table(banana)
table(apple)
var.test(table(banana),table(apple))
r_from_f(1.086,3,3)
comp_plt(banana,apple)
```

Output

1) R-statistics which show correlation between both genes.

```
banana
    a     c     g     t
53291 31544 30768 53900
apple
    a     c     g     t
50114 29831 28673 51406


        F test to compare two variances

data:  table(banana) and table(apple)
F = 1.086, num df = 3, denom df = 3, p-value = 0.9475
alternative hypothesis: true ratio of variances is not equal to 1
95 percent confidence interval:
  0.07034135 16.76715105
sample estimates:
ratio of variances
         1.086013

[1] 0.7215356
```

2) Plot show distribution of 4 nucleotides.
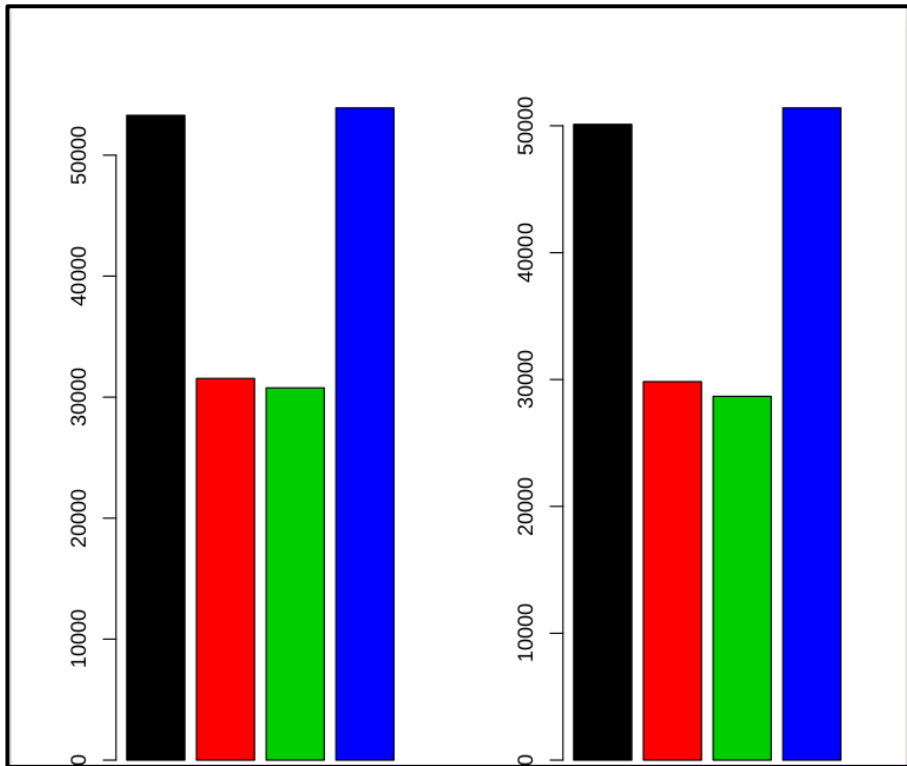
Conclusion

Study show that both genes are similar.