1. Done
2. mydata <- read.table("sle_b_cell.txt", header=T, row.names=1)

```
> mydata <- read.table("sle_b_cell.txt", header=T, row.names=1)
> length(mydata)
[1] 26
> dim(mydata)
[1] 34853    26
>
```

3. dim(mydata) produced 34853 and 26.
4. Mydata (prints the samples to the screen)

5. x <- c(mydata['control.1')]
   y <- (mydata['sle.2'])
   plot(x[,1],y[,1],xlab='Normal B cell sample',ylab='SLE B cell sample',main='E B cell sample vs. Normal B cell sample - all probsets')
   grid(col = "grey")
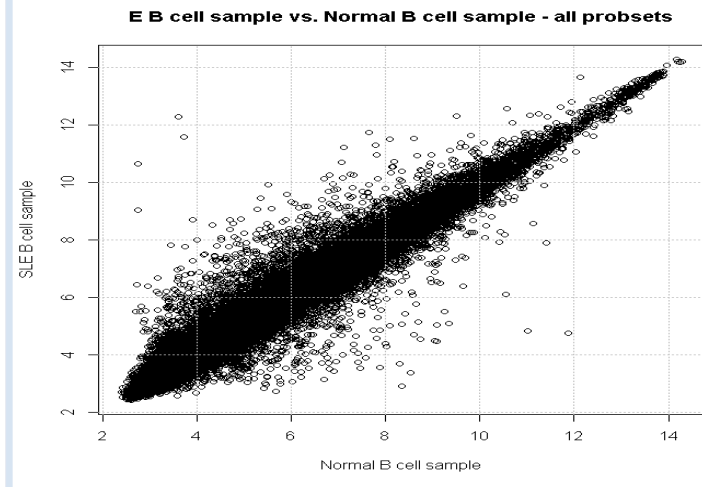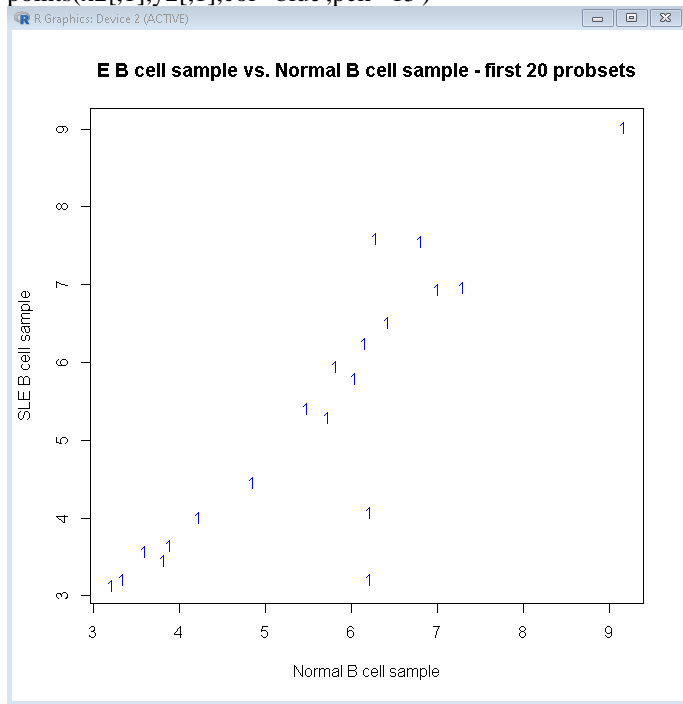
6.
```
y2 <- data.frame(y = y[,1][1:20])
x2 <- data.frame(x = x[,1][1:20])
plot(x2[,1],y2[,1],type='n',xlab='Normal B cell sample',ylab='SLE B cell sample',main='E B cell sample vs.
Normal B cell sample - first 20 probsets')
points(x2[,1],y2[,1],col='blue',pch='15')
```


7.
```
df <- data.frame(mydata)
x.numeric = as.numeric(df['211881_x_at', ])
plot(1:26,x.numeric,type ='n', xlab ='sample indices', ylab='intensities', main = 'gene profile plot of
211881_x_at')
lines(1:26,x.numeric,col='blue')
grid(col ='grey')
```

gene profile plot of 211881_x_at
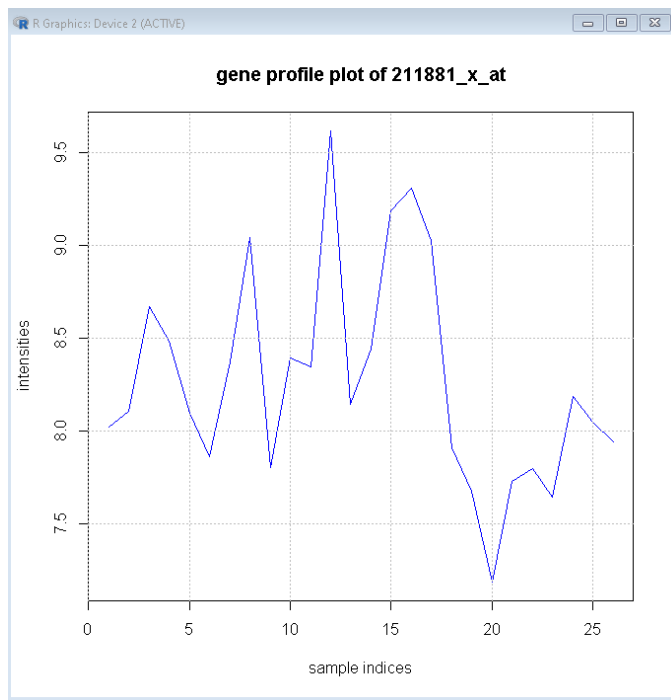
8. f <- data.frame(x.numeric,c(rep("SLE",17),rep("Control",9)))
   colnames(f) <- c('expression', 'sample')
   box <- ggplot(f,aes(x=sample,y=expression,fill=sample))+
   ggtitle("gene profile across conditions")+
   geom_boxplot()