Thomas Muamar

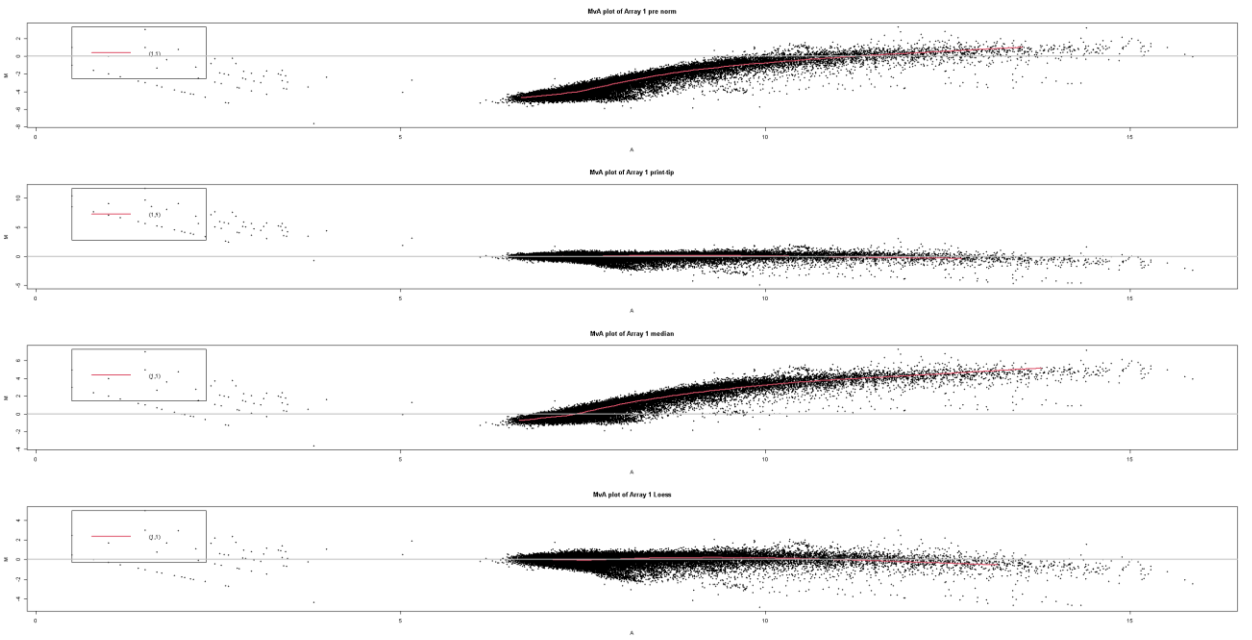
HW #2

1.

```
        dir.path <- “C:\\Users\\thomas\\Documents\\Data”
cy <- read.GenePix(path=dir.path, name.Gf = "F532 Median",name.Gb ="B532 Median", name.Rf = "F635
Median", name.Rb = "B635 Median",name.W ="Flags")
```

2.

```
        printtip1 <- maNorm(cy[,1], norm ="p", span=0.45)
        printtip2 <- maNorm(cy[,2], norm ="p", span=0.45)
        printtip3 <- maNorm(cy[,3], norm ="p", span=0.45)
        printtip4 <- maNorm(cy[,4], norm ="p", span=0.45)

        median1 <-maNorm(cy[,1], norm="median", span=0.45)
        median2 <-maNorm(cy[,2], norm="median", span=0.45)
        median3 <-maNorm(cy[,3], norm="median", span=0.45)
        median4 <-maNorm(cy[,4], norm="median", span=0.45)

        loess1 <-maNorm(cy[,1], norm="loess", span=0.45)
        loess2 <-maNorm(cy[,2], norm="loess", span=0.45)
        loess3 <-maNorm(cy[,3], norm="loess", span=0.45)
        loess4 <-maNorm(cy[,4], norm="loess", span=0.45)

        par(mfrow=c(4,1))
        maPlot(cy[,1], main = "MvA plot of Array 1 pre norm")
        maPlot(printtip1, main = "MvA plot of Array 1 print-tip")
        maPlot(median1, main = "MvA plot of Array 1 median")
        maPlot(loess1, main = "MvA plot of Array 1 Loess")

        par(mfrow=c(4,1))
        maPlot(cy[,2], main = "MvA plot of Array 2 pre norm")
        maPlot(printtip2, main = "MvA plot of Array 2 print-tip")
        maPlot(median2, main = "MvA plot of Array 2 median")
        maPlot(loess2, main = "MvA plot of Array 2 Loess")

        par(mfrow=c(4,1))
        maPlot(cy[,3], main = "MvA plot of Array 3 pre norm")
        maPlot(printtip3, main = "MvA plot of Array 3 print-tip")
        maPlot(median3, main = "MvA plot of Array 3 median")
        maPlot(loess3, main = "MvA plot of Array 3 Loess")

        par(mfrow=c(4,1))
        maPlot(cy[,4], main = "MvA plot of Array 4 pre norm")
        maPlot(printtip4, main = "MvA plot of Array 4 print-tip")
        maPlot(median4, main = "MvA plot of Array 4 median")
        maPlot(loess4, main = "MvA plot of Array 4 Loess")
```

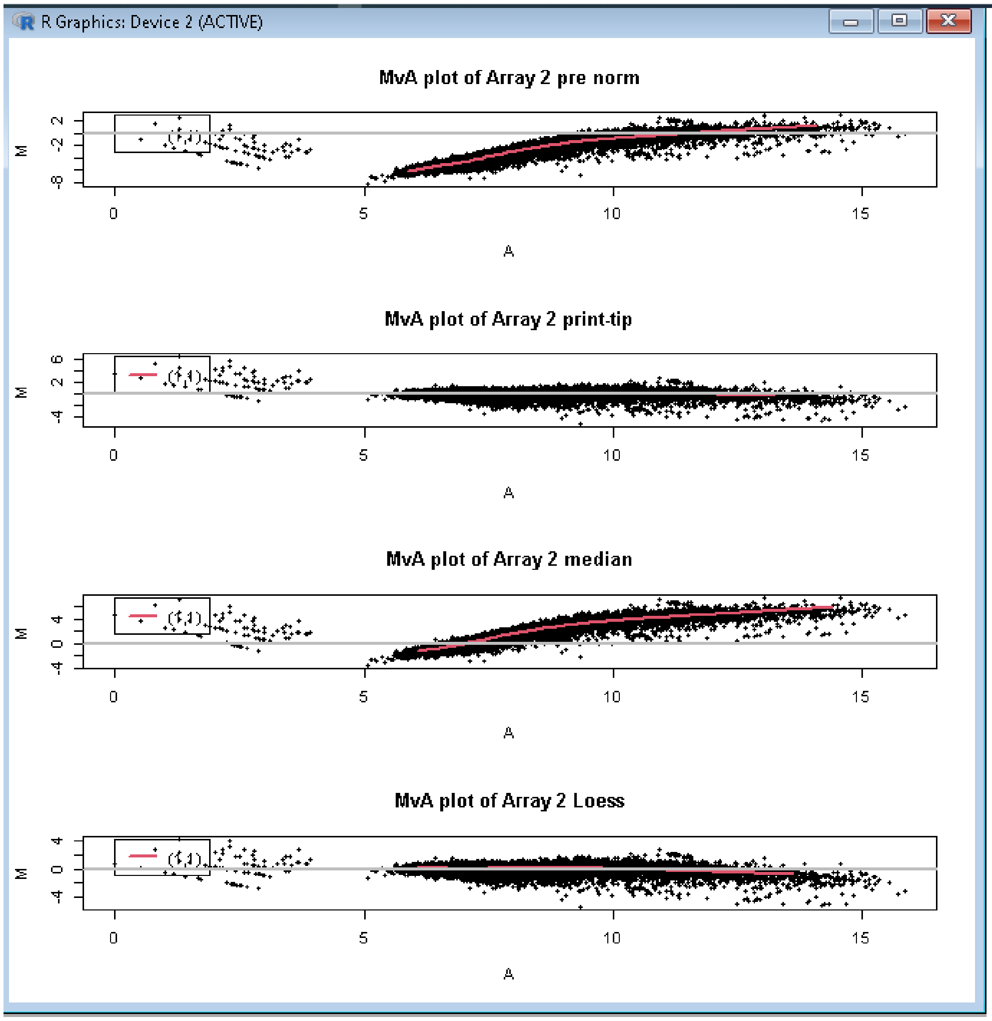


MvA plot of Array 1 pre norm

MvA plot of Array 1 print-tip

MvA plot of Array 1 median

MvA plot of Array 1 Loess

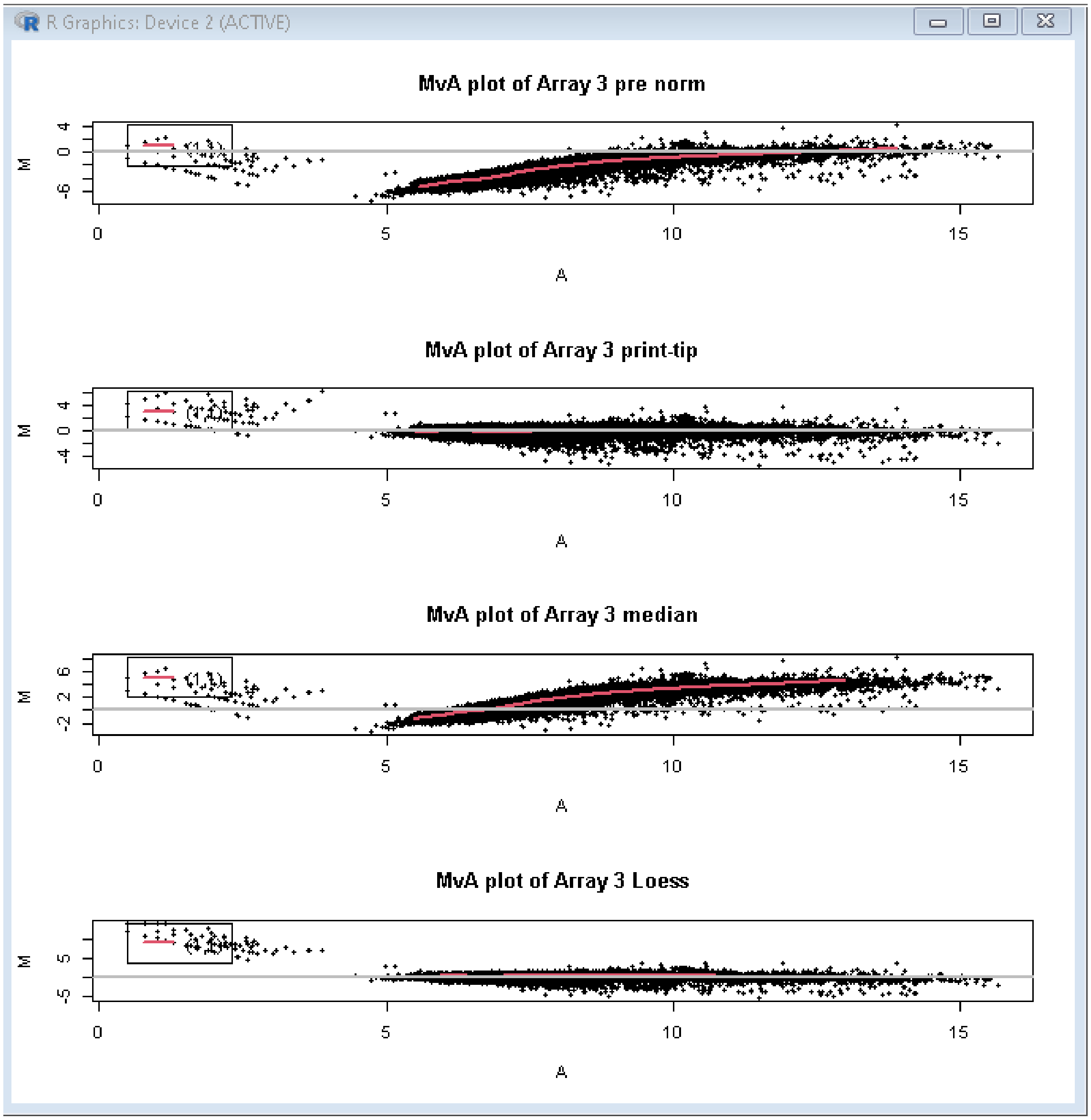


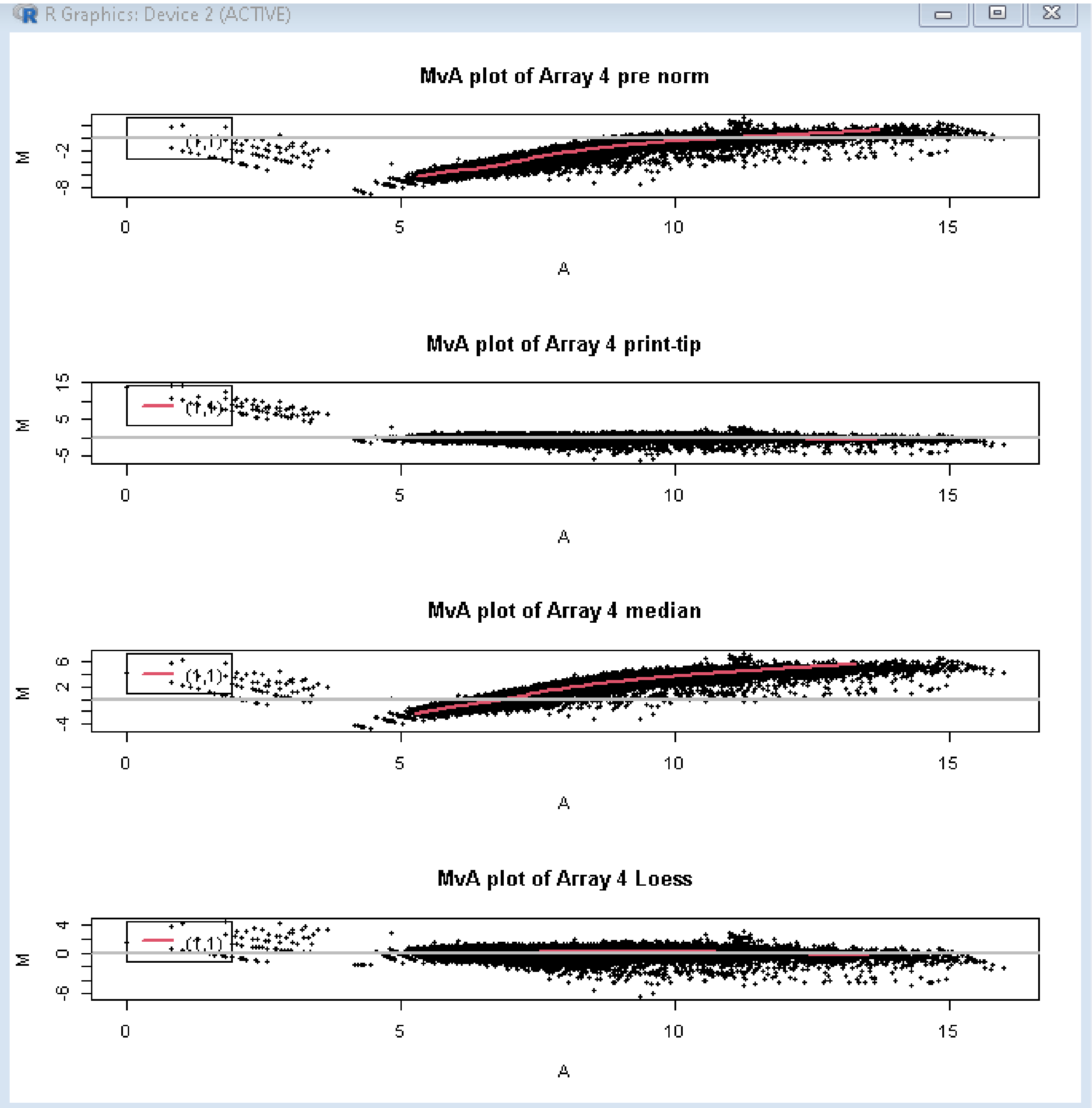
MvA plot of Array 2 pre norm

MvA plot of Array 2 print-tip

MvA plot of Array 2 median

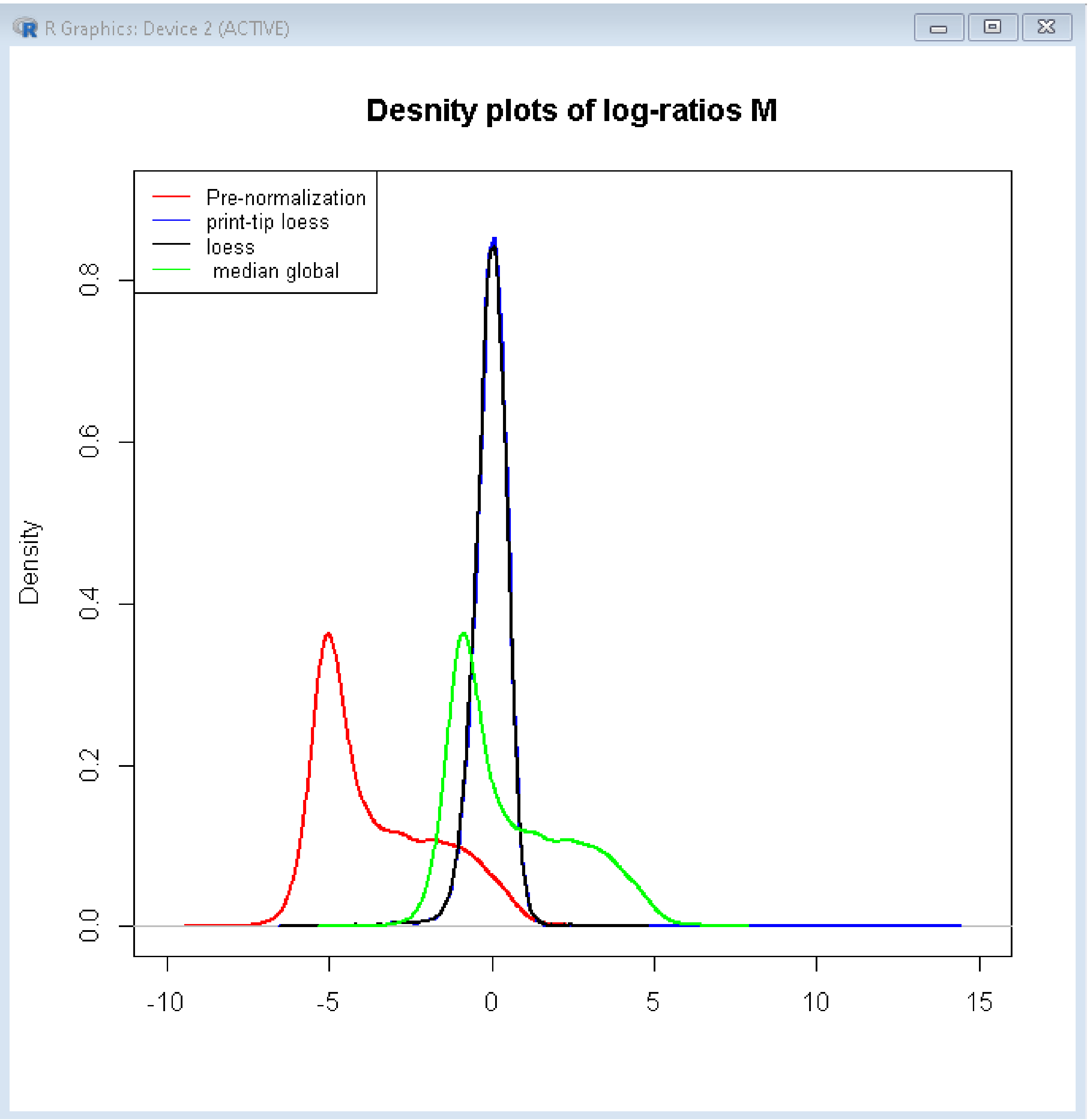
MvA plot of Array 2 Loess


R Graphics: Device 2 (ACTIVE)
MvA plot of Array 3 pre norm
M
4
0
-6
(1,1)
0
5
10
15
A
MvA plot of Array 3 print-tip
M
4
0
-4
(1,1)
0
5
10
15
A
MvA plot of Array 3 median
M
6
2
-2
(1,1)
0
5
10
15
A
MvA plot of Array 3 Loess
M
5
-5
(1,1)
0
5
10
15
A


R Graphics: Device 2 (ACTIVE)
MvA plot of Array 4 pre norm
M
-8
-2
0
5
10
15
A
(1,1)
MvA plot of Array 4 print-tip
M
-5
5
15
0
5
10
15
A
(1,1)
MvA plot of Array 4 median
M
-4
2
6
0
5
10
15
A
(1,1)
MvA plot of Array 4 Loess
M
-6
0
4
0
5
10
15
A
(1,1)

3.

```
logratio4 <- maM(cy[,4])
ar4<-na.omit(logratio4)
median4log <- na.omit(maM(median4))
printtip4log <- na.omit(maM(printtip4))
loess4log <- na.omit(maM(loess4))

plot(density(ar4), lwd = 2, xlab = "",col = "red", xlim = c(-10, 15), ylim = c(0, 0.9),main ="Desnity plots of log-ratios M")
lines(density(printtip4log), col = "blue", lwd = 2)
lines(density(loess4log), col = "black", lwd = 2)
lines(density(median4log), col = "green", lwd = 2)

legend("topleft", legend = c("Pre-normalization","print-tip loess", "loess"," median global" ),
col=c("red", "blue", "black", "green" ), lty=1, cex=0.8)
```



4. Looking through all the plots it seems like print-tip loess is the most preferred for this data set. Loess and print tip loess seem to produce almost similar normalized results, but I believe print-tip loess shows to be the better out of the two.

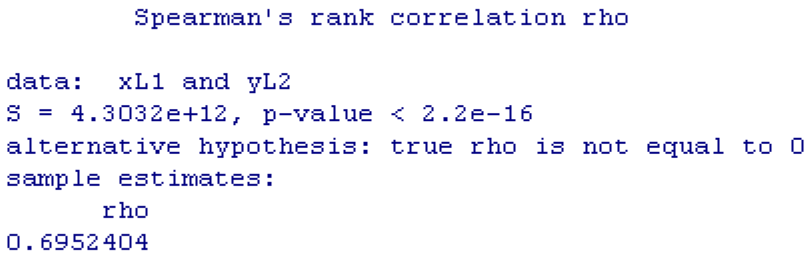
5.

```
for(i in 1:4){
  name <- paste("sample", i, sep = ".")
  bg <- maRb(cy[,i])
  fg <- maRf(cy[,i])
  diff <- fg - bg
  diff[diff < 0] <- NA
  assign(name, log2(diff))
}
```

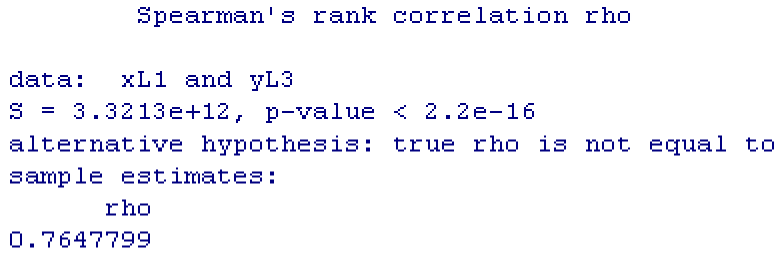
```
#Data separated for each array:
data.median1  <- apply(sample.1, 2,median, na.rm = T)
data.median2  <- apply(sample.2, 2, median, na.rm = T)
data.median3  <- apply(sample.3, 2, median, na.rm = T)
data.median4  <- apply(sample.4, 2, median, na.rm = T)

data.norm1 <- sweep(sample.1, 2, data.median1)
data.norm2 <- sweep(sample.2, 2, data.median2)
data.norm3 <- sweep(sample.3, 2, data.median3)
data.norm4 <- sweep(sample.4, 2, data.median4)

#matrix for all 4 arrays together:
data.prenorm <- cbind(sample.1, sample.2, sample.3, sample.4)
data.median  <- apply(data.prenorm, 2, median, na.rm = T)
data.norm    <- sweep(data.prenorm, 2, data.median)

colnames(data.norm) <- c("Array 1", "Array 2", "Array 3", "Array 4")
```

6.

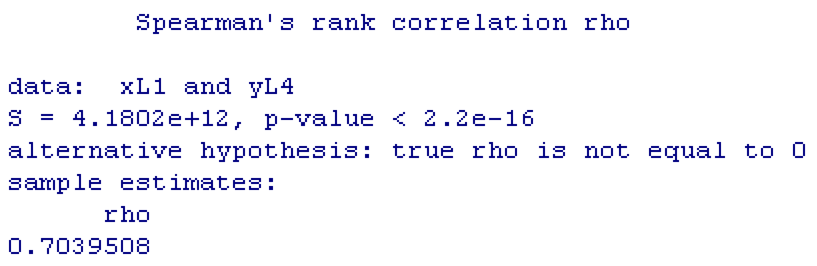
```
yL1<- na.omit(data.loess2[,1])
yL2<- na.omit(data.loess2[,2])
yL3<- na.omit(data.loess2[,3])
yL4<- na.omit(data.loess2[,4])

xL1<- na.omit(data.loess2[,1])
xL2<- na.omit(data.loess2[,2])
xL3<- na.omit(data.loess2[,3])
xL4<- na.omit(data.loess2[,4])

corr1 <- cor.test(x=xL1, y=yL2, method ="spearman",exact=FALSE)
corr2 <- cor.test(x=xL1, y=yL3, method ="spearman",exact=FALSE)
corr3 <- cor.test(x=xL1, y=yL4, method ="spearman",exact=FALSE)
corr4<- cor.test(x=xL2, y=yL3, method ="spearman",exact=FALSE)
corr5 <- cor.test(x=xL2, y=yL4, method ="spearman",exact=FALSE)
corr6 <- cor.test(x=xL3, y=yL4, method ="spearman",exact=FALSE)
```



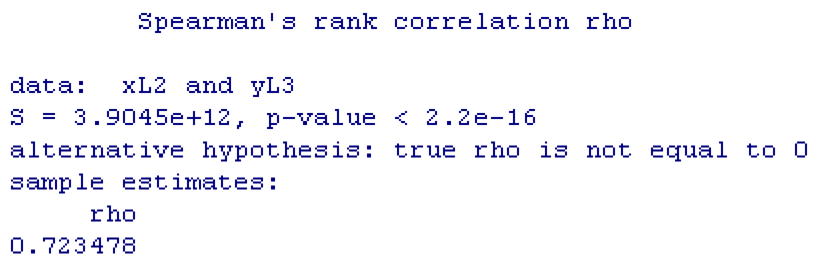
```
         Spearman's rank correlation rho

data:  xL1 and yL2
S = 4.3032e+12, p-value < 2.2e-16
alternative hypothesis: true rho is not equal to 0
sample estimates:
      rho
0.6952404
```



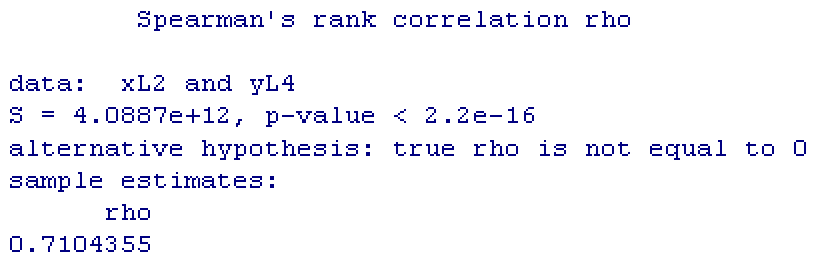
```
         Spearman's rank correlation rho

data:  xL1 and yL3
S = 3.3213e+12, p-value < 2.2e-16
alternative hypothesis: true rho is not equal to
sample estimates:
      rho
0.7647799
```



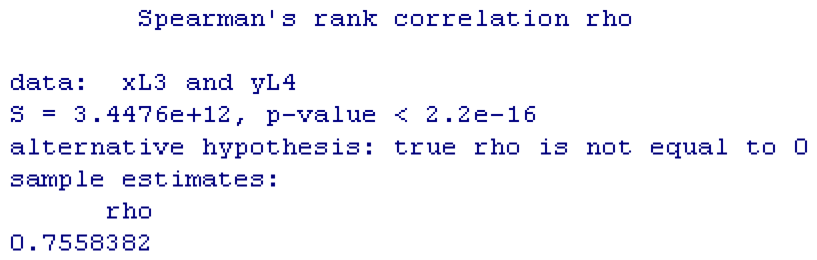
```
        Spearman's rank correlation rho

data:  xL1 and yL4
S = 4.1802e+12, p-value < 2.2e-16
alternative hypothesis: true rho is not equal to 0
sample estimates:
      rho
0.7039508
```



```
        Spearman's rank correlation rho

data:  xL2 and yL3
S = 3.9045e+12, p-value < 2.2e-16
alternative hypothesis: true rho is not equal to 0
sample estimates:
     rho
0.723478
```



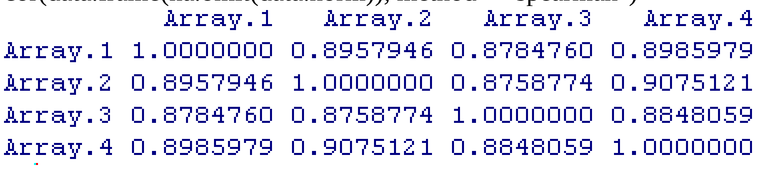
```
        Spearman's rank correlation rho

data:  xL2 and yL4
S = 4.0887e+12, p-value < 2.2e-16
alternative hypothesis: true rho is not equal to 0
sample estimates:
      rho
0.7104355
```



```
        Spearman's rank correlation rho

data:  xL3 and yL4
S = 3.4476e+12, p-value < 2.2e-16
alternative hypothesis: true rho is not equal to 0
sample estimates:
      rho
0.7558382
```

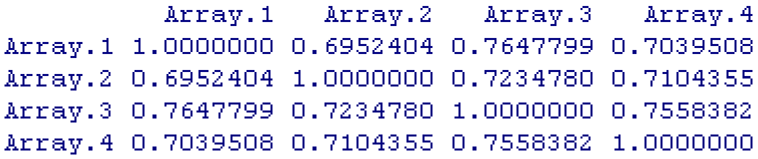
```
y1 <- data.norm[,1]
y2 <- data.norm[,2]
y3 <- data.norm[,3]
y4 <- data.norm[,4]

x1 <- data.norm[,1]
x2 <- data.norm[,2]
x3 <- data.norm[,3]
x4 <- data.norm[,4]

corr <- cor.test(x=x2, y=y2, method ="spearman",exact=FALSE)
```

```
cor(data.frame(na.omit(data.norm)), method = "spearman")
```



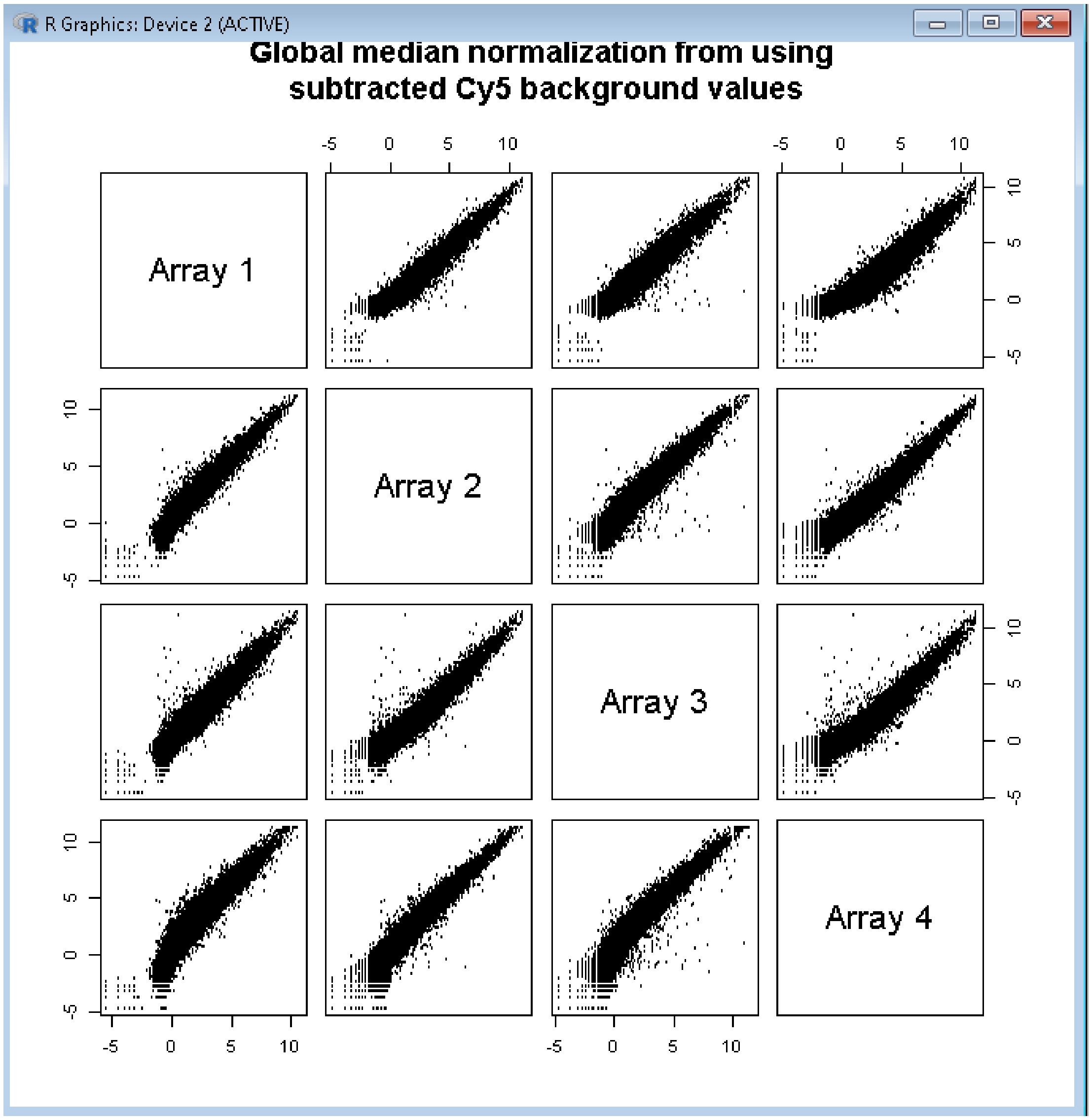
```
          Array.1   Array.2   Array.3   Array.4
Array.1 1.0000000 0.8957946 0.8784760 0.8985979
Array.2 0.8957946 1.0000000 0.8758774 0.9075121
Array.3 0.8784760 0.8758774 1.0000000 0.8848059
Array.4 0.8985979 0.9075121 0.8848059 1.0000000
```

```
data.loess <- cbind(loess1, loess2, loess3, loess4)
data.loess2 <- data.matrix(data.loess)
colnames(data.loess2) <- c("Array 1", "Array 2", "Array 3", "Array 4")
cor(data.frame(data.loess2),method = "spearman")
```

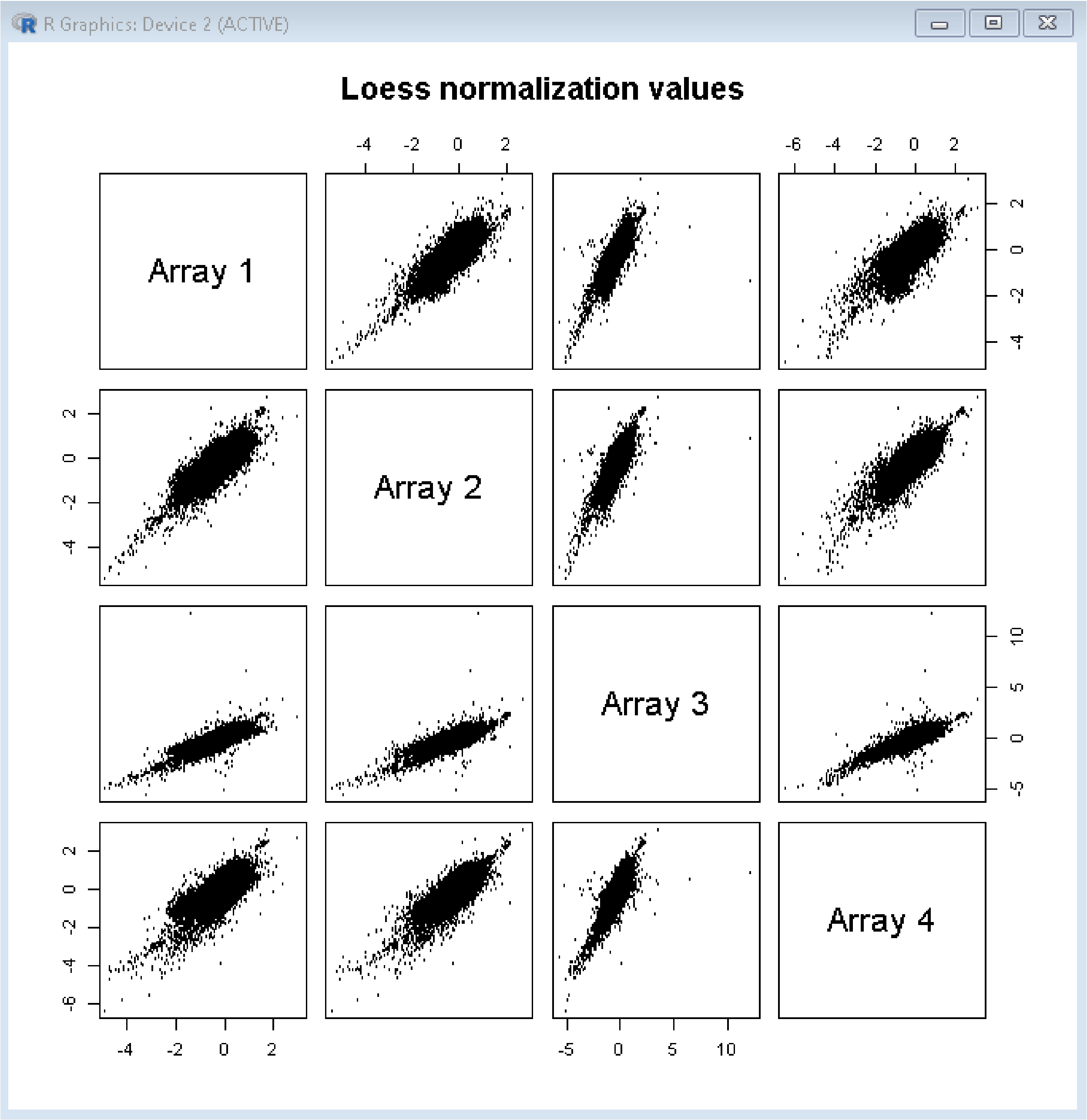


```
          Array.1   Array.2   Array.3   Array.4
Array.1 1.0000000 0.6952404 0.7647799 0.7039508
Array.2 0.6952404 1.0000000 0.7234780 0.7104355
Array.3 0.7647799 0.7234780 1.0000000 0.7558382
Array.4 0.7039508 0.7104355 0.7558382 1.0000000
```

```
pairs(data.norm, pch=21,col=1,main="Global median normalization from using\n subtracted Cy5 background
values",cex=0.4)
```


R Graphics: Device 2 (ACTIVE)
Global median normalization from using
subtracted Cy5 background values
Array 1
Array 2
Array 3
Array 4
-5
0
5
10

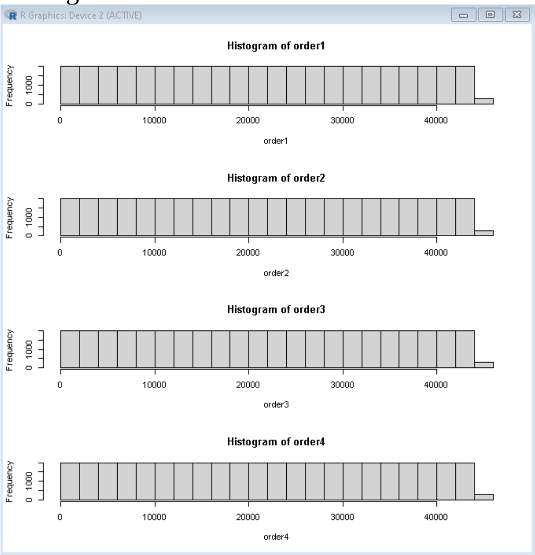
```
pairs(data.loess2, pch=21,col=1,main="Loess normalization values",cex=0.4)
```



7.

```
        for(i in 1:4){
          name <- paste("samp", i, sep = ".")
          bg <- maRb(cy[,i])
          fg <- maRf(cy[,i])
          diff <- fg - bg
          assign(name, diff)
        }
data.prelog <- cbind(samp.1, samp.2, samp.3, samp.4)
colnames(data.prelog) <- c("Array 1", "Array 2", "Array 3", "Array 4")

sorted <- apply(data.prelog, 2, sort)
meanValues1  <- rowMeans(data.frame(sorted[,1]),na.rm=T)
meanValues2  <- rowMeans(data.frame(sorted[,2]),na.rm=T)
```

```
meanValues3  <- rowMeans(data.frame(sorted[,3]),na.rm=T)
meanValues4  <- rowMeans(data.frame(sorted[,4]),na.rm=T)
data.meanValues <- cbind(meanValues1, meanValues2, meanValues3, meanValues4)

prelog1<- rank(data.prelog[,1], ties="first")
prelog2<- rank(data.prelog[,2], ties="first")
prelog3<- rank(data.prelog[,3], ties="first")
prelog4<- rank(data.prelog[,4], ties="first")

order1<- rank(data.meanValues[,1], ties="first")
order2 <- rank(data.meanValues[,2], ties="first")
order3 <- rank(data.meanValues[,3], ties="first")
order4 <- rank(data.meanValues[,4], ties="first")
data.order <- cbind(order1, order2, order3, order4)
#histogram distribution:
```

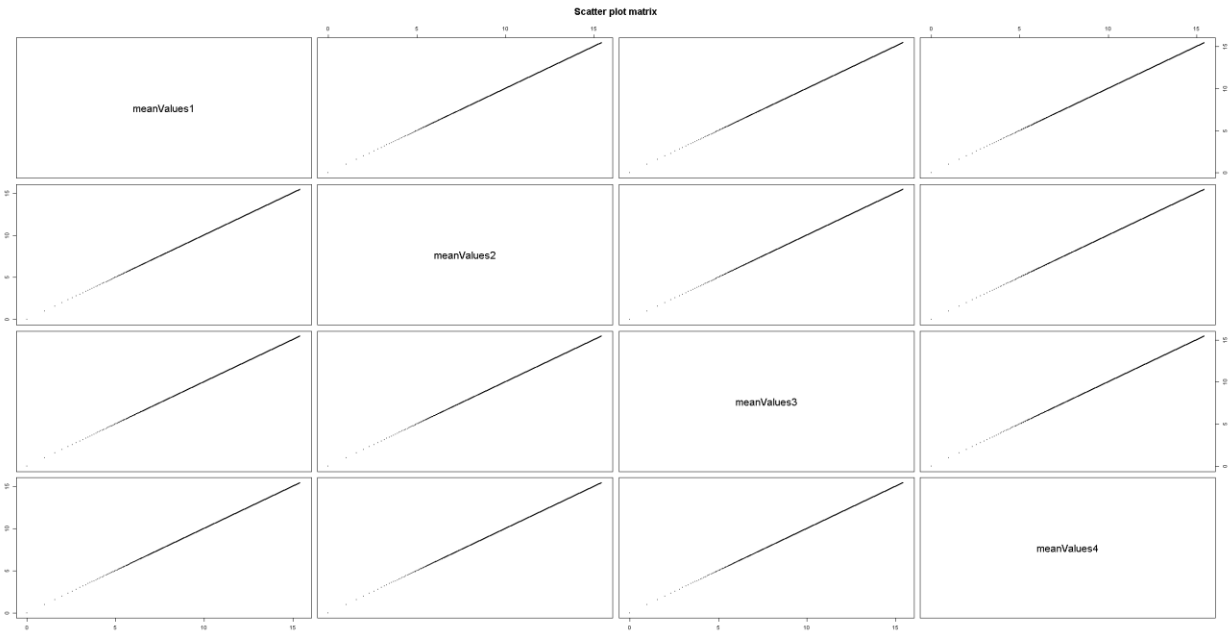


```
colnames(data.order) <- c("order1", "order2", "order 3", "order 4")
```

8.

```
> orderLog <- log2(data.order)
> cor(orderLog, method="spearman")
        order1 order2 order 3 order 4
order1       1      1       1       1
order2       1      1       1       1
order 3      1      1       1       1
order 4      1      1       1       1
```

```
pairs(orderLog, pch=21,col=1,main="Scatter plot matrix",cex=0.4)
```

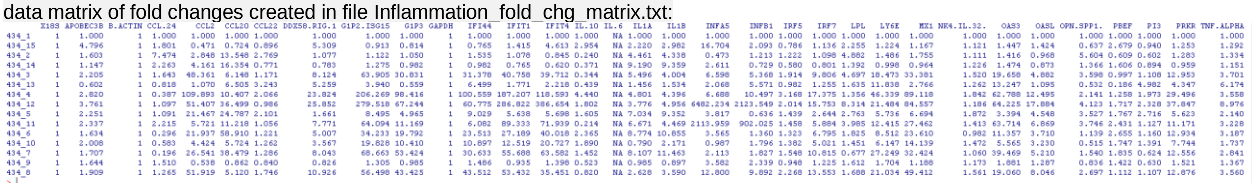


9. From looking at the data the normalization method that was the best is the quantile normalization method because when you see the spearman correlation numbers the datas are all normalized to each other. They are all at the value of 1.It means a perfect association between the ranks.
10.

```
f.parse <- function(path=getwd(), file="Inflammation_qRT-PCR.csv",out=out.fi) {
d <- read.table(paste(path,file,sep=""),skip=11,sep=",",header=T)
u <- as.character(unique(d$Name))
u <- u[u!=""]; u <- u[!is.na(u)];
ref <- unique(as.character(d$Name[d$Type=="Reference"]))
u <- unique(c(ref,u))
p <- unique(toupper(as.character(d$Name.1)))
p <- sort(setdiff(p,c("")))
mat <- matrix(0,nrow=length(u),ncol=length(p))
dimnames(mat) <- list(u,p)
for (i in 1:length(u)) {
print(paste(i,": ",u[i],sep=""))
tmp <- d[d$Name %in% u[i],c(1:3,6,9)]
g <- toupper(unique(as.character(tmp$Name.1)))
g <- sort(setdiff(g,c("",hg)))
for (j in 1:length(g)) {
v <- tmp[toupper(as.character(tmp$Name.1)) %in% g[j],5]
v <- v[v!=999]
v <- v[((v/mean(v))<1.5) & ((v/mean(v))>0.67)] #gene j vector
hv3 <- NULL
for (k in 1:length(hg)) { #housekeeping gene vector (each filtered by reps)
hv <- tmp[toupper(as.character(tmp$Name.1)) %in% hg[k],5]
hv <- hv[hv!=999]
hv3 <- c(hv3,hv[((hv/mean(hv))<1.5) & ((hv/mean(hv))>0.67)])
}
sv <- mean(as.numeric(v)) - mean(as.numeric(hv3)) #scaled value for gene j
if(i==1) { #reference sample only
mat[u[i],g[j]] <- sv
next
}
mat[u[i],g[j]] <- sv - mat[u[1],g[j]]
}
}
mat[1,][!is.na(mat[1,])] <- 0
fc <- 2^(-1 * mat)
write.table(t(c("Subject",dimnames(mat)[[2]])),paste(path,out,sep=""),quote=F,sep="\t",col.names=F,row.names=F)
write.table(round(fc,3),paste(path,out,sep=""),quote=F,sep="\t",append=T,col.names=F)
}
# run function
pa <- "C:/Users/thomas/Documents/Inflammation_"
```

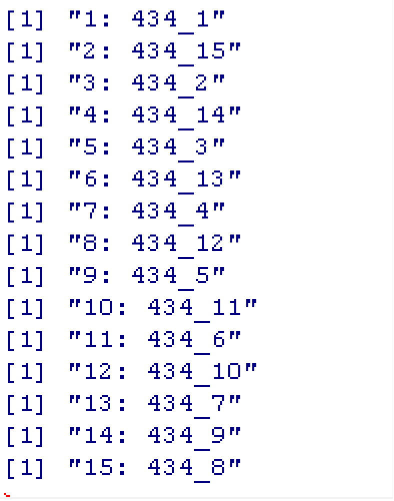
fi <- "qRT-PCR.csv"
out.fi <- "fold_chg_matrix.txt "
f.parse(pa,fi,out.fi)

patients<-read.delim("Inflammation_fold_chg_matrix.txt", header=T, row.names=1)
data matrix of fold changes created in file Inflammation_fold_chg_matrix.txt:

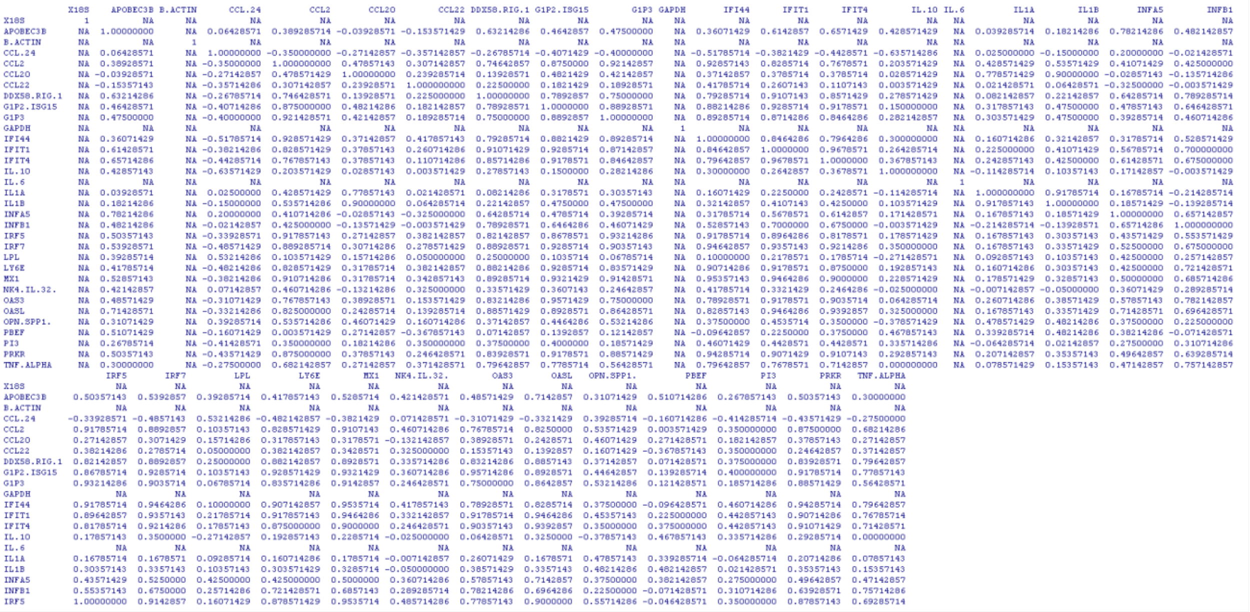


```
       X18S APOBEC3B B.ACTIN CCL.24    CCL2  CCL20 CCL22 DDX58.RIG.1 G1P2.ISG15   G1P3 GAPDH   IFI44   IFIT1   IFIT4 IL.10 IL.6  IL1A   IL1B    INFA5    INFB1  IRF5   IRF7   LPL   LY6E    MX1 NK4.IL.32.   OAS3   OASL OPN.SPP1.  PBEF   PI3   PRKR TNF.ALPHA
434_1     1    1.000       1  1.000   1.000  1.000 1.000       1.000      1.000  1.000     1   1.000   1.000   1.000 1.000   NA 1.000  1.000    1.000    1.000 1.000  1.000 1.000  1.000  1.000      1.000  1.000  1.000     1.000 1.000 1.000  1.000     1.000
434_15    1    4.796       1  1.801   0.471  0.724 0.896       5.309      0.913  0.814     1   0.765   1.415   4.613 2.954   NA 2.220  2.982   16.704    2.093 0.786  1.136 2.255  1.224  1.167      1.121  1.447  1.424     0.637 2.679 0.940  1.253     1.292
434_2     1    1.603       1  7.474   2.848 13.548 2.769       1.077      1.122  1.050     1   1.535   1.078   0.845 0.240   NA 4.461  4.338    0.473    1.213 1.222  1.098 4.882  1.486  1.755      1.111  1.416  0.968     5.604 0.609 0.602  1.283     1.334
434_14    1    1.147       1  2.263   4.161 16.354 0.771       0.783      1.275  0.982     1   0.982   0.765   0.620 0.371   NA 9.190  9.359    2.611    0.729 0.580  0.801 1.392  0.998  0.964      1.226  1.474  0.873     1.366 1.606 0.894  0.959     1.151
434_3     1    2.205       1  1.643  48.361  6.148 1.171       8.124     63.905 30.831     1  31.378  40.758  39.712 0.344   NA 5.496  4.004    6.598    5.368 1.914  9.806 4.697 18.473 33.381      1.520 19.658  4.882     3.598 0.997 1.108 12.953     3.701
434_13    1    0.602       1  0.818   1.070  6.505 3.243       5.259      3.940  0.559     1   6.499   1.771   2.218 0.439   NA 1.456  1.534    2.068    5.571 0.982  1.255 1.635 11.838  2.766      1.262 13.247  1.095     0.532 0.186 4.982  4.347     6.174
434_4     1    2.820       1  0.387 109.893 10.407 2.066      23.824    206.269 98.416     1 100.559 187.207 118.593 4.440   NA 4.801  4.396    6.688   10.497 3.168 17.375 1.356 46.339 89.118      1.842 62.788 12.495     2.141 1.258 1.973 29.496     3.558
434_12    1    3.761       1  1.097  51.407 36.499 0.986      25.852    279.518 67.244     1  60.775 286.822 386.654 1.802   NA 3.776  4.956 6482.234 2123.549 2.014 15.753 8.314 21.484 84.557      1.186 64.225 17.884     4.123 1.717 2.328 37.847     8.976
434_5     1    2.251       1  1.091  21.467 24.787 2.101       1.661      8.495  4.965     1   9.029   5.638   5.698 1.605   NA 7.034  9.352    3.817    0.636 1.439  2.644 2.763  5.736  6.694      1.872  3.394  4.548     3.527 1.767 2.716  5.623     2.140
434_11    1    2.337       1  2.215   5.721 11.218 1.056       7.771     64.094 11.169     1   6.082  89.333  71.939 0.214   NA 6.671  4.469 2113.959  902.025 1.458  5.884 3.985 12.415 27.462      1.413 63.714  6.869     3.746 2.431 1.127 11.171     3.228
434_6     1    1.634       1  0.296  21.937 58.910 1.221       5.007     34.233 19.792     1  23.513  27.189  40.018 2.365   NA 8.774 10.855    3.565    1.360 1.323  6.795 1.825  8.512 23.610      0.982 11.357  3.710     1.139 2.655 1.160 12.934     3.187
434_10    1    2.008       1  0.583   4.424  5.724 1.262       3.567     19.828 10.410     1  10.897  12.519  20.727 1.890   NA 0.790  2.171    0.987    1.796 1.382  5.021 1.451  6.147 14.139      1.472  5.565  3.230     0.515 1.747 1.391  7.744     1.737
434_7     1    1.707       1  0.196  26.541 38.479 1.286       8.043     68.663 53.424     1  30.633  55.688  63.582 1.452   NA 8.107 11.463    2.113    1.827 1.548 10.815 0.677 27.249 32.424      1.060 39.469  5.210     1.540 1.835 0.624 12.556     2.841
434_9     1    1.644       1  1.510   0.538  0.862 0.840       0.826      1.305  0.985     1   1.486   0.935   1.398 0.523   NA 0.985  0.897    3.582    2.339 0.948  1.225 1.612  1.704  1.188      1.173  1.881  1.287     0.836 1.422 0.630  1.521     1.367
434_8     1    1.909       1  1.265  51.919  5.120 1.746      10.926     56.498 43.425     1  43.512  53.432  35.451 0.820   NA 2.628  3.590   12.800    9.892 2.268 13.553 1.688 21.034 49.412      1.561 19.060  8.046     2.697 1.112 1.107 12.876     3.560
```

spearman<-cor(data.frame(patients),method="spearman")



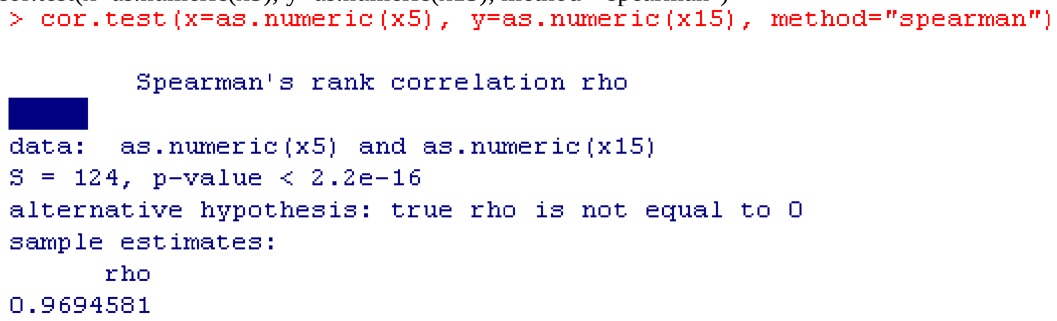
```
[1] "1: 434_1"
[1] "2: 434_15"
[1] "3: 434_2"
[1] "4: 434_14"
[1] "5: 434_3"
[1] "6: 434_13"
[1] "7: 434_4"
[1] "8: 434_12"
[1] "9: 434_5"
[1] "10: 434_11"
[1] "11: 434_6"
[1] "12: 434_10"
[1] "13: 434_7"
[1] "14: 434_9"
[1] "15: 434_8"
```



```
            X18S    APOBEC3B B.ACTIN      CCL.24         CCL2       CCL20        CCL22 DDX58.RIG.1 G1P2.ISG15        G1P3 GAPDH       IFI44      IFIT1      IFIT4        IL.10 IL.6         IL1A        IL1B       INFA5        INFB1
X18S           1          NA      NA          NA           NA          NA           NA          NA         NA          NA    NA          NA         NA         NA           NA   NA           NA          NA          NA           NA
APOBEC3B      NA  1.00000000      NA  0.06428571  0.389285714 -0.03928571 -0.153571429  0.63214286  0.4642857  0.47500000    NA  0.36071429  0.6142857  0.6571429  0.428571429   NA  0.039285714  0.18214286  0.78214286  0.482142857
B.ACTIN       NA          NA       1          NA           NA          NA           NA          NA         NA          NA    NA          NA         NA         NA           NA   NA           NA          NA          NA           NA
CCL.24        NA  0.06428571      NA  1.00000000 -0.350000000 -0.27142857 -0.357142857 -0.26785714 -0.4071429 -0.40000000    NA -0.51785714 -0.3821429 -0.4428571 -0.635714286   NA  0.025000000 -0.15000000  0.20000000 -0.021428571
CCL2          NA  0.38928571      NA -0.35000000  1.000000000  0.47857143  0.307142857  0.74642857  0.8750000  0.92142857    NA  0.92857143  0.8285714  0.7678571  0.203571429   NA  0.428571429  0.53571429  0.41071429  0.425000000
CCL20         NA -0.03928571      NA -0.27142857  0.478571429  1.00000000  0.239285714  0.13928571  0.4821429  0.42142857    NA  0.37142857  0.3785714  0.3785714  0.028571429   NA  0.778571429  0.90000000 -0.02857143 -0.135714286
CCL22         NA -0.15357143      NA -0.35714286  0.307142857  0.23928571  1.000000000  0.22500000  0.1821429  0.18928571    NA  0.41785714  0.2607143  0.1107143  0.003571429   NA  0.021428571  0.06428571 -0.32500000 -0.003571429
DDX58.RIG.1   NA  0.63214286      NA -0.26785714  0.746428571  0.13928571  0.225000000  1.00000000  0.7892857  0.75000000    NA  0.79285714  0.9107143  0.8571429  0.278571429   NA  0.082142857  0.22142857  0.64285714  0.789285714
G1P2.ISG15    NA  0.46428571      NA -0.40714286  0.875000000  0.48214286  0.182142857  0.78928571  1.0000000  0.88928571    NA  0.88214286  0.9285714  0.9178571  0.150000000   NA  0.317857143  0.47500000  0.47857143  0.646428571
G1P3          NA  0.47500000      NA -0.40000000  0.921428571  0.42142857  0.189285714  0.75000000  0.8892857  1.00000000    NA  0.89285714  0.8714286  0.8464286  0.282142857   NA  0.303571429  0.47500000  0.39285714  0.460714286
GAPDH         NA          NA      NA          NA           NA          NA           NA          NA         NA          NA     1          NA         NA         NA           NA   NA           NA          NA          NA           NA
IFI44         NA  0.36071429      NA -0.51785714  0.928571429  0.37142857  0.417857143  0.79285714  0.8821429  0.89285714    NA  1.00000000  0.8464286  0.7964286  0.300000000   NA  0.160714286  0.32142857  0.31785714  0.528571429
IFIT1         NA  0.61428571      NA -0.38214286  0.828571429  0.37857143  0.260714286  0.91071429  0.9285714  0.87142857    NA  0.84642857  1.0000000  0.9678571  0.264285714   NA  0.225000000  0.41071429  0.56785714  0.700000000
IFIT4         NA  0.65714286      NA -0.44285714  0.767857143  0.37857143  0.110714286  0.85714286  0.9178571  0.84642857    NA  0.79642857  0.9678571  1.0000000  0.367857143   NA  0.242857143  0.42500000  0.61428571  0.675000000
IL.10         NA  0.42857143      NA -0.63571429  0.203571429  0.02857143  0.003571429  0.27857143  0.1500000  0.28214286    NA  0.30000000  0.2642857  0.3678571  1.000000000   NA -0.114285714  0.10357143  0.17142857 -0.003571429
IL.6          NA          NA      NA          NA           NA          NA           NA          NA         NA          NA    NA          NA         NA         NA           NA    1           NA          NA          NA           NA
IL1A          NA  0.03928571      NA  0.02500000  0.428571429  0.77857143  0.021428571  0.08214286  0.3178571  0.30357143    NA  0.16071429  0.2250000  0.2428571 -0.114285714   NA  1.000000000  0.91785714  0.16785714 -0.214285714
IL1B          NA  0.18214286      NA -0.15000000  0.535714286  0.90000000  0.064285714  0.22142857  0.4750000  0.47500000    NA  0.32142857  0.4107143  0.4250000  0.103571429   NA  0.917857143  1.00000000  0.18571429 -0.139285714
INFA5         NA  0.78214286      NA  0.20000000  0.410714286 -0.02857143 -0.325000000  0.64285714  0.4785714  0.39285714    NA  0.31785714  0.5678571  0.6142857  0.171428571   NA  0.167857143  0.18571429  1.00000000  0.657142857
INFB1         NA  0.48214286      NA -0.02142857  0.425000000 -0.13571429 -0.003571429  0.78928571  0.6464286  0.46071429    NA  0.52857143  0.7000000  0.6750000 -0.003571429   NA -0.214285714 -0.13928571  0.65714286  1.000000000
IRF5          NA  0.50357143      NA -0.33928571  0.917857143  0.27142857  0.382142857  0.82142857  0.8678571  0.93214286    NA  0.91785714  0.8964286  0.8178571  0.178571429   NA  0.167857143  0.30357143  0.43571429  0.553571429
IRF7          NA  0.53928571      NA -0.48571429  0.889285714  0.30714286  0.278571429  0.88928571  0.9285714  0.90357143    NA  0.94642857  0.9357143  0.9214286  0.350000000   NA  0.167857143  0.33571429  0.52500000  0.675000000
LPL           NA  0.39285714      NA  0.53214286  0.103571429  0.15714286  0.050000000  0.25000000  0.1035714  0.06785714    NA  0.10000000  0.2178571  0.1785714 -0.271428571   NA  0.092857143  0.10357143  0.42500000  0.257142857
LY6E          NA  0.41785714      NA -0.48214286  0.828571429  0.31785714  0.382142857  0.88214286  0.9285714  0.83571429    NA  0.90714286  0.9178571  0.8750000  0.192857143   NA  0.160714286  0.30357143  0.42500000  0.721428571
MX1           NA  0.52857143      NA -0.38214286  0.910714286  0.31785714  0.342857143  0.89285714  0.9321429  0.91428571    NA  0.95357143  0.9464286  0.9000000  0.228571429   NA  0.178571429  0.32857143  0.50000000  0.685714286
NK4.IL.32.    NA  0.42142857      NA  0.07142857  0.460714286 -0.13214286  0.325000000  0.33571429  0.3607143  0.24642857    NA  0.41785714  0.3321429  0.2464286 -0.025000000   NA -0.007142857 -0.05000000  0.36071429  0.289285714
OAS3          NA  0.48571429      NA -0.31071429  0.767857143  0.38928571  0.153571429  0.83214286  0.9571429  0.75000000    NA  0.78928571  0.9178571  0.9035714  0.064285714   NA  0.260714286  0.38571429  0.57857143  0.782142857
OASL          NA  0.71428571      NA -0.33214286  0.825000000  0.24285714  0.139285714  0.88571429  0.8928571  0.86428571    NA  0.82857143  0.9464286  0.9392857  0.325000000   NA  0.167857143  0.33571429  0.71428571  0.696428571
OPN.SPP1.     NA  0.31071429      NA  0.39285714  0.535714286  0.46071429  0.160714286  0.37142857  0.4464286  0.53214286    NA  0.37500000  0.4535714  0.3500000 -0.378571429   NA  0.478571429  0.48214286  0.37500000  0.225000000
PBEF          NA  0.51071429      NA -0.16071429  0.003571429  0.27142857 -0.367857143  0.07142857  0.1392857  0.12142857    NA -0.09642857  0.2250000  0.3750000  0.467857143   NA  0.339285714  0.48214286  0.38214286 -0.071428571
PI3           NA  0.26785714      NA -0.41428571  0.350000000  0.18214286  0.350000000  0.37500000  0.4000000  0.18571429    NA  0.46071429  0.4428571  0.4428571  0.335714286   NA -0.064285714  0.02142857  0.27500000  0.310714286
PRKR          NA  0.50357143      NA -0.43571429  0.875000000  0.37857143  0.246428571  0.83928571  0.9178571  0.88571429    NA  0.94285714  0.9071429  0.9107143  0.292857143   NA  0.207142857  0.35357143  0.49642857  0.639285714
TNF.ALPHA     NA  0.30000000      NA -0.27500000  0.682142857  0.27142857  0.371428571  0.79642857  0.7785714  0.56428571    NA  0.79642857  0.7678571  0.7142857  0.000000000   NA  0.078571429  0.15357143  0.47142857  0.757142857
                   IRF5       IRF7         LPL         LY6E        MX1   NK4.IL.32.        OAS3       OASL   OPN.SPP1.         PBEF          PI3        PRKR   TNF.ALPHA
X18S                 NA         NA          NA           NA         NA           NA          NA         NA          NA           NA           NA          NA          NA
APOBEC3B     0.50357143  0.5392857  0.39285714  0.417857143  0.5285714  0.421428571  0.48571429  0.7142857  0.31071429  0.510714286  0.267857143  0.50357143  0.30000000
B.ACTIN              NA         NA          NA           NA         NA           NA          NA         NA          NA           NA           NA          NA          NA
CCL.24      -0.33928571 -0.4857143  0.53214286 -0.482142857 -0.3821429  0.071428571 -0.31071429 -0.3321429  0.39285714 -0.160714286 -0.414285714 -0.43571429 -0.27500000
CCL2         0.91785714  0.8892857  0.10357143  0.828571429  0.9107143  0.460714286  0.76785714  0.8250000  0.53571429  0.003571429  0.350000000  0.87500000  0.68214286
CCL20        0.27142857  0.3071429  0.15714286  0.317857143  0.3178571 -0.132142857  0.38928571  0.2428571  0.46071429  0.271428571  0.182142857  0.37857143  0.27142857
CCL22        0.38214286  0.2785714  0.05000000  0.382142857  0.3428571  0.325000000  0.15357143  0.1392857  0.16071429 -0.367857143  0.350000000  0.24642857  0.37142857
DDX58.RIG.1  0.82142857  0.8892857  0.25000000  0.882142857  0.8928571  0.335714286  0.83214286  0.8857143  0.37142857  0.071428571  0.375000000  0.83928571  0.79642857
G1P2.ISG15   0.86785714  0.9285714  0.10357143  0.928571429  0.9321429  0.360714286  0.95714286  0.8928571  0.44642857  0.139285714  0.400000000  0.91785714  0.77857143
G1P3         0.93214286  0.9035714  0.06785714  0.835714286  0.9142857  0.246428571  0.75000000  0.8642857  0.53214286  0.121428571  0.185714286  0.88571429  0.56428571
GAPDH                NA         NA          NA           NA         NA           NA          NA         NA          NA           NA           NA          NA          NA
IFI44        0.91785714  0.9464286  0.10000000  0.907142857  0.9535714  0.417857143  0.78928571  0.8285714  0.37500000 -0.096428571  0.460714286  0.94285714  0.79642857
IFIT1        0.89642857  0.9357143  0.21785714  0.917857143  0.9464286  0.332142857  0.91785714  0.9464286  0.45357143  0.225000000  0.442857143  0.90714286  0.76785714
IFIT4        0.81785714  0.9214286  0.17857143  0.875000000  0.9000000  0.246428571  0.90357143  0.9392857  0.35000000  0.375000000  0.442857143  0.91071429  0.71428571
IL.10        0.17857143  0.3500000 -0.27142857  0.192857143  0.2285714 -0.025000000  0.06428571  0.3250000 -0.37857143  0.467857143  0.335714286  0.29285714  0.00000000
IL.6                 NA         NA          NA           NA         NA           NA          NA         NA          NA           NA           NA          NA          NA
IL1A         0.16785714  0.1678571  0.09285714  0.160714286  0.1785714 -0.007142857  0.26071429  0.1678571  0.47857143  0.339285714 -0.064285714  0.20714286  0.07857143
IL1B         0.30357143  0.3357143  0.10357143  0.303571429  0.3285714 -0.050000000  0.38571429  0.3357143  0.48214286  0.482142857  0.021428571  0.35357143  0.15357143
INFA5        0.43571429  0.5250000  0.42500000  0.425000000  0.5000000  0.360714286  0.57857143  0.7142857  0.37500000  0.382142857  0.275000000  0.49642857  0.47142857
INFB1        0.55357143  0.6750000  0.25714286  0.721428571  0.6857143  0.289285714  0.78214286  0.6964286  0.22500000 -0.071428571  0.310714286  0.63928571  0.75714286
IRF5         1.00000000  0.9142857  0.16071429  0.878571429  0.9535714  0.485714286  0.77857143  0.9000000  0.55714286 -0.046428571  0.350000000  0.87857143  0.69285714
```

11. x1<-patients[1,]
    x3<-patients[3,]
    x2<-patients[2,]
    x4<-patients[4,]
    x5<-patients[5,]

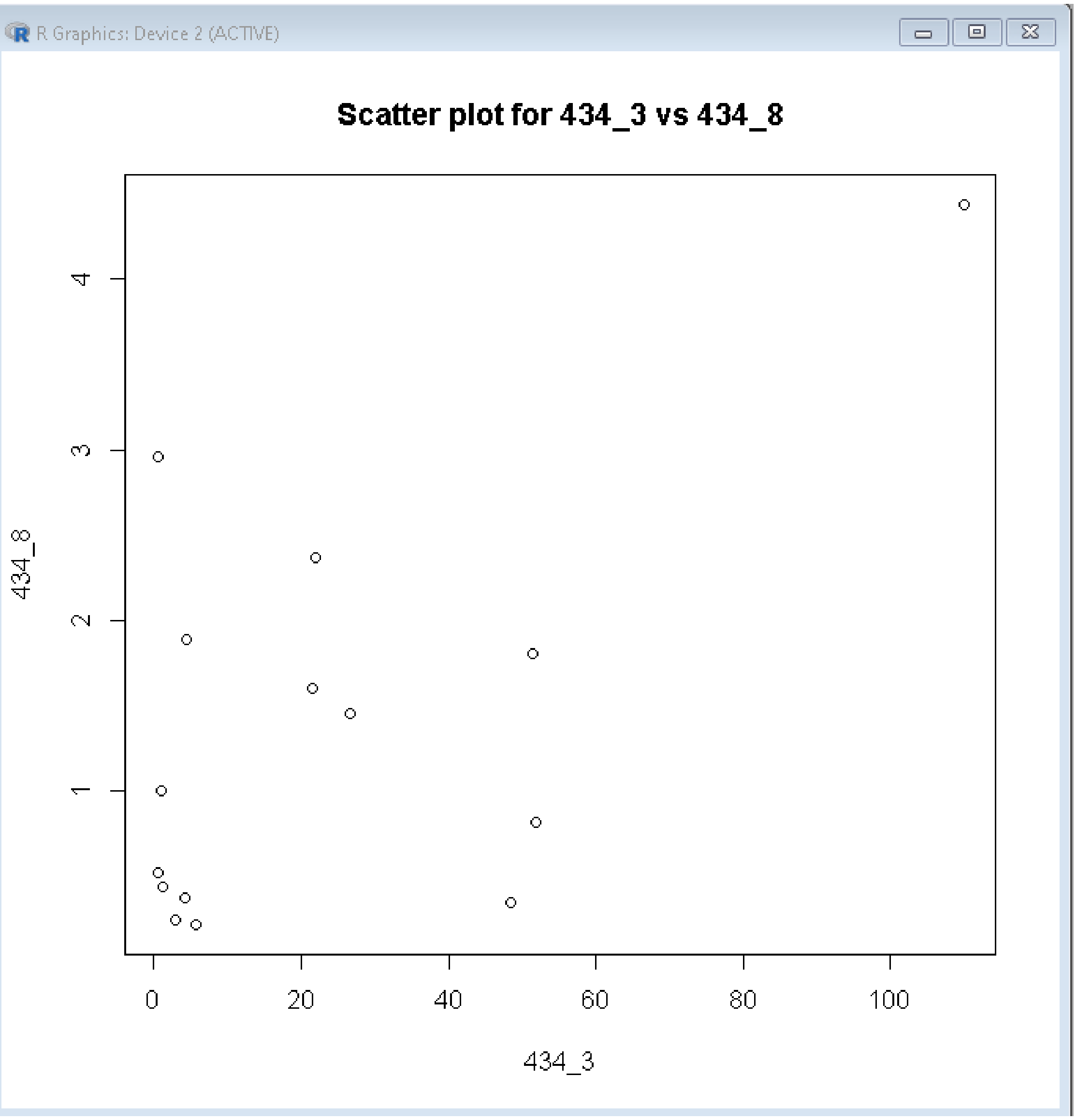
```
x6<-patients[6,]
x7<-patients[7,]
x8<-patients[8,]
x9<-patients[9,]
x10<-patients[10,]
x11<-patients[11,]
x12<-patients[12,]
x13<-patients[13,]
x14<-patients[14,]
x15<-patients[15,]
cor.test(x=as.numeric(x5), y=as.numeric(x15), method="spearman")
```



```
> cor.test(x=as.numeric(x5), y=as.numeric(x15), method="spearman")

        Spearman's rank correlation rho

data:  as.numeric(x5) and as.numeric(x15)
S = 124, p-value < 2.2e-16
alternative hypothesis: true rho is not equal to 0
sample estimates:
      rho
0.9694581
```

So the patients 434_3 and patient 434_8 were shown to be the most correlated.

```
plot(patient, main="Scatter plot for 434_3 vs 434_8")
```


R Graphics: Device 2 (ACTIVE)
Scatter plot for 434_3 vs 434_8
434_8
1
2
3
4
0
20
40
60
80
100
434_3