Exercise 8

Your Name

11 Dec 2015

```
genes <- read.delim("gene.description.txt")
subjects <- read.delim("cancer.patients.txt")
evals <- read.delim("gene.expression.txt",stringsAsFactors = FALSE)
```

```
chr8Genes <- genes[genes$Chromosome=="chr8",]
head(chr8Genes)
```

```
##                          probe HUGO.gene.symbol Chromosome     Start
## Contig29827_RC Contig29827_RC            FUT10       chr8  33228344
## NM_003046           NM_003046           SLC7A2       chr8  17396286
## Contig55940_RC Contig55940_RC            CYHR1       chr8 145675315
## NM_004133           NM_004133            HNF4G       chr8  76452203
## NM_004374           NM_004374            COX6C       chr8 100890223
## AF052142             AF052142            NCALD       chr8 102698770
```

```
chr8GenesOrd <-chr8Genes[order(chr8Genes$Start),]
head(chr8GenesOrd)
```

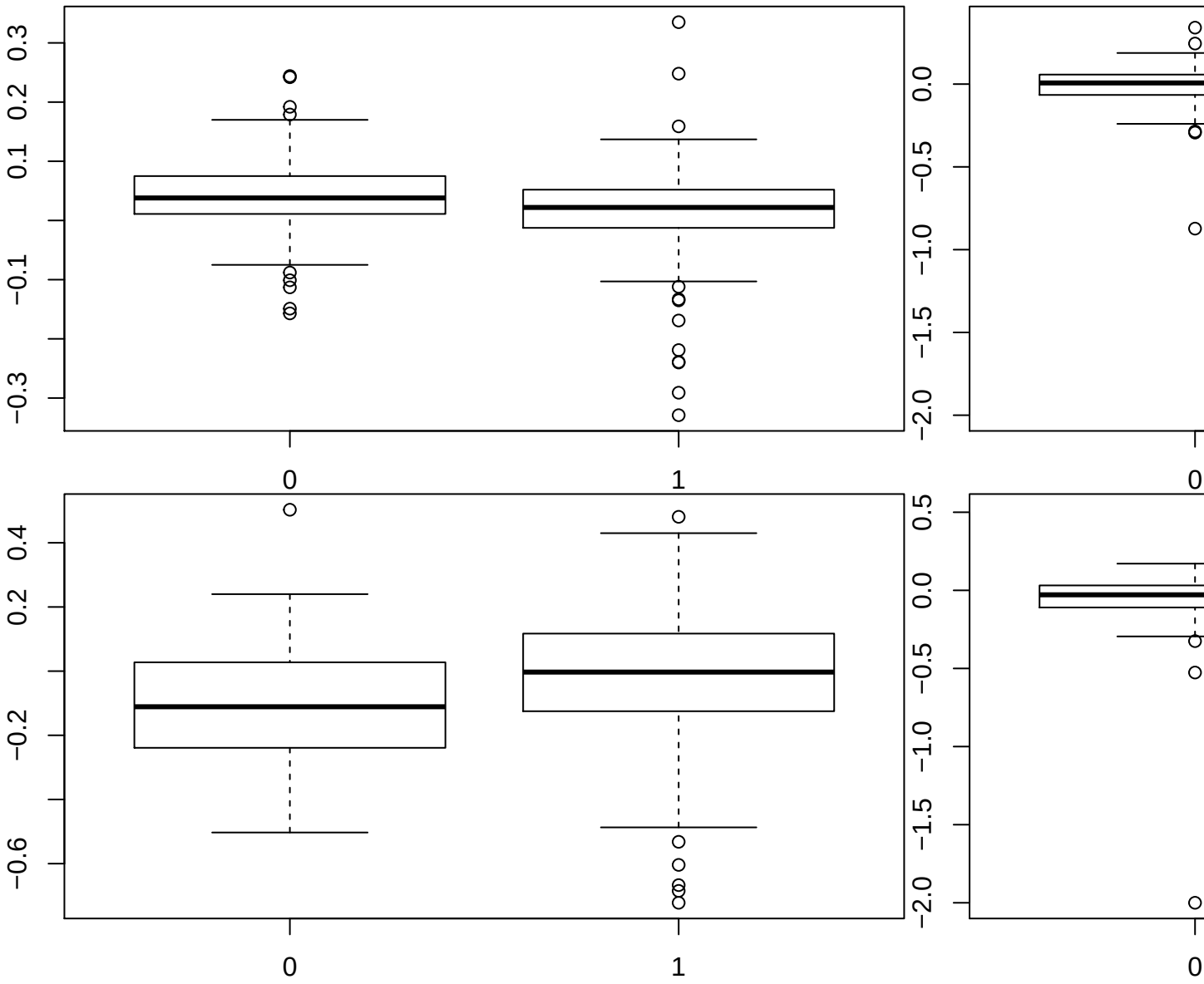
```
##                          probe HUGO.gene.symbol Chromosome    Start
## NM_004745           NM_004745           DLGAP2       chr8  1449569
## NM_018941           NM_018941             CLN8       chr8  1711870
## AL117604             AL117604             DLC1       chr8 12940872
## NM_003046           NM_003046           SLC7A2       chr8 17396286
## Contig58301_RC Contig58301_RC           SLC7A2       chr8 17396286
## NM_000662           NM_000662             NAT1       chr8 18067618
```

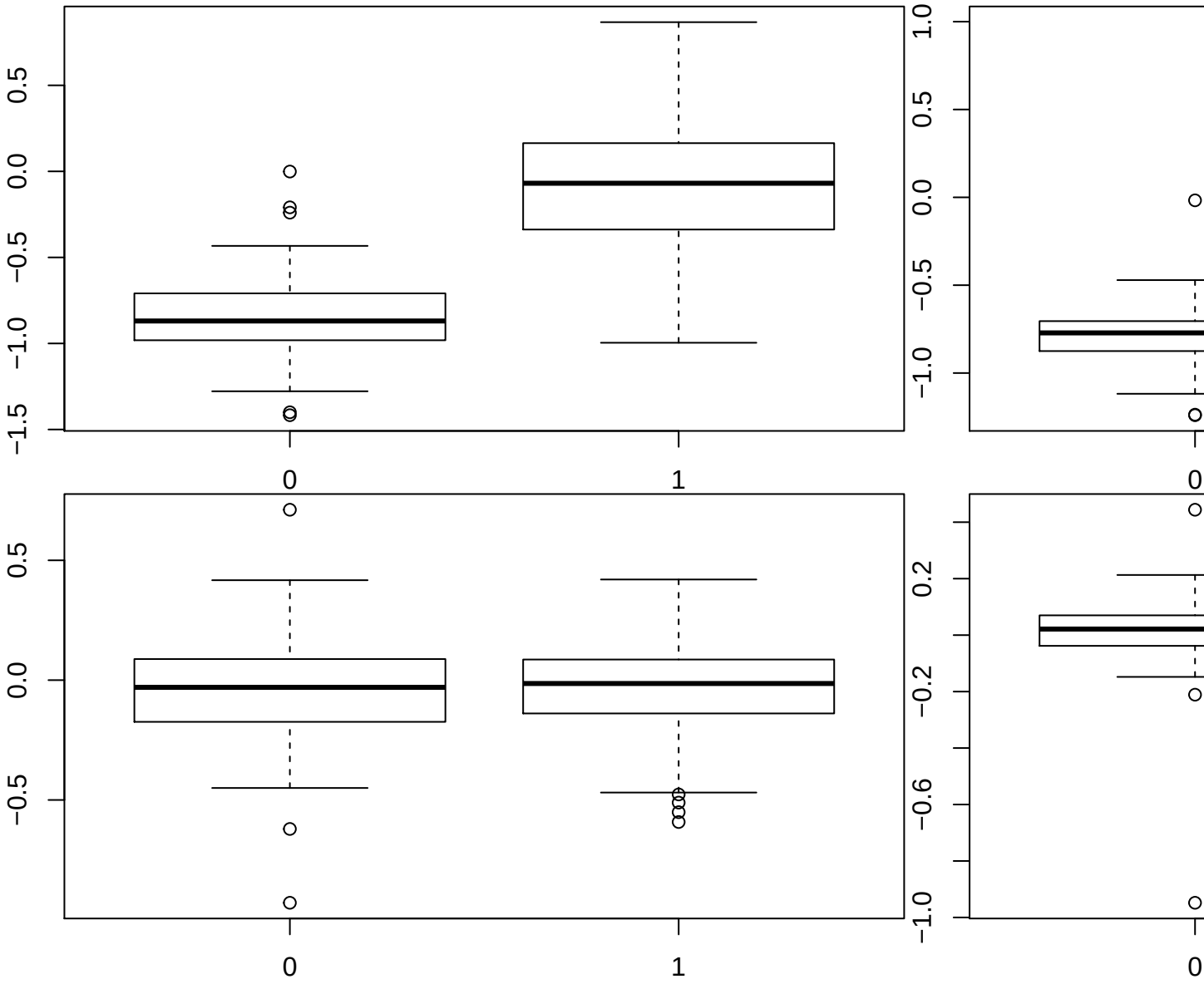
```
chr8Expression <- evals[match(chr8GenesOrd$probe,rownames(evals)),]
```

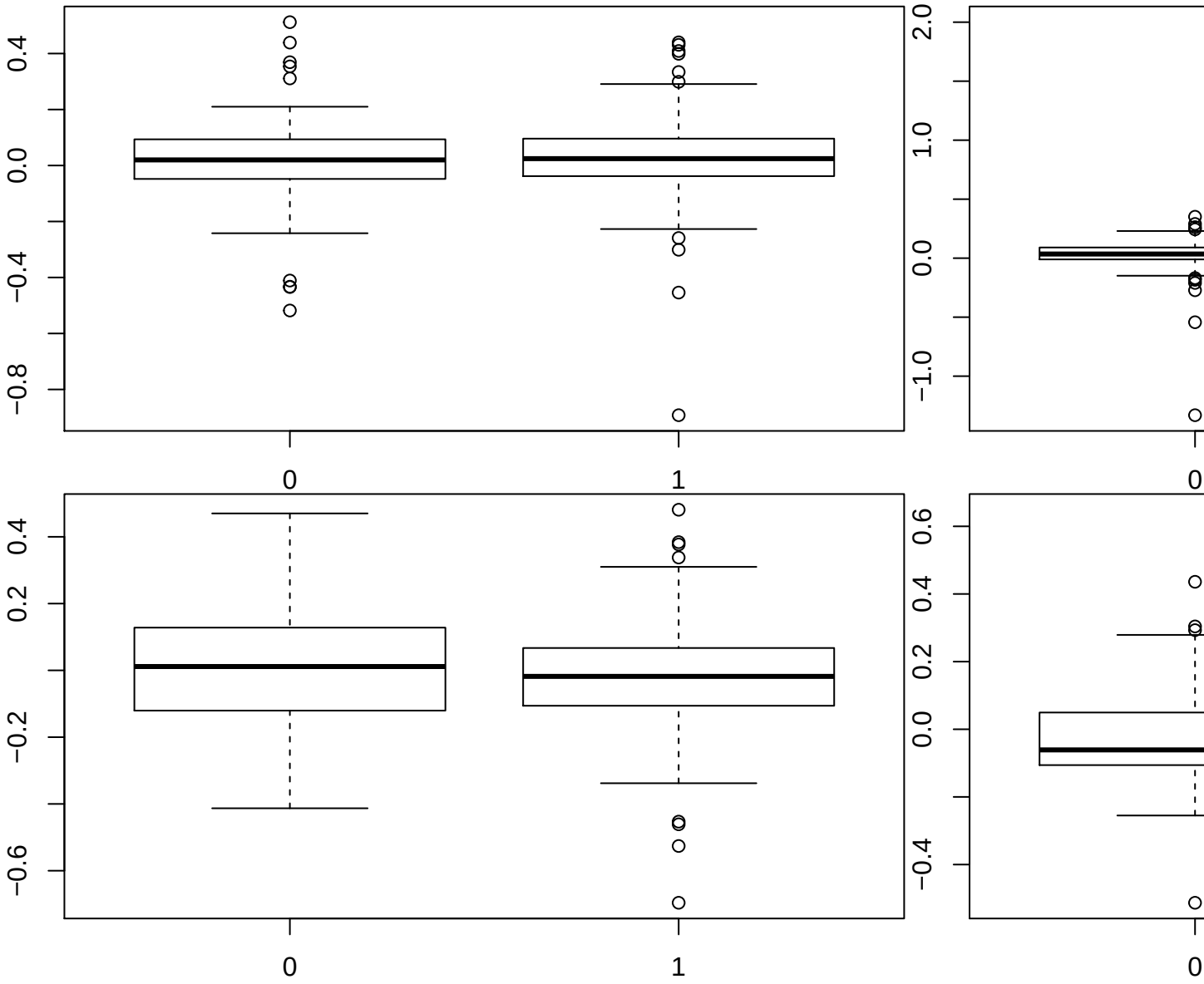
```
stats <- NULL
for (i in 1:18) {
   tmp <- t.test(as.numeric(chr8Expression[i,])~factor(subjects$er))
   stats[i] <- tmp$statistic
}
stats
```

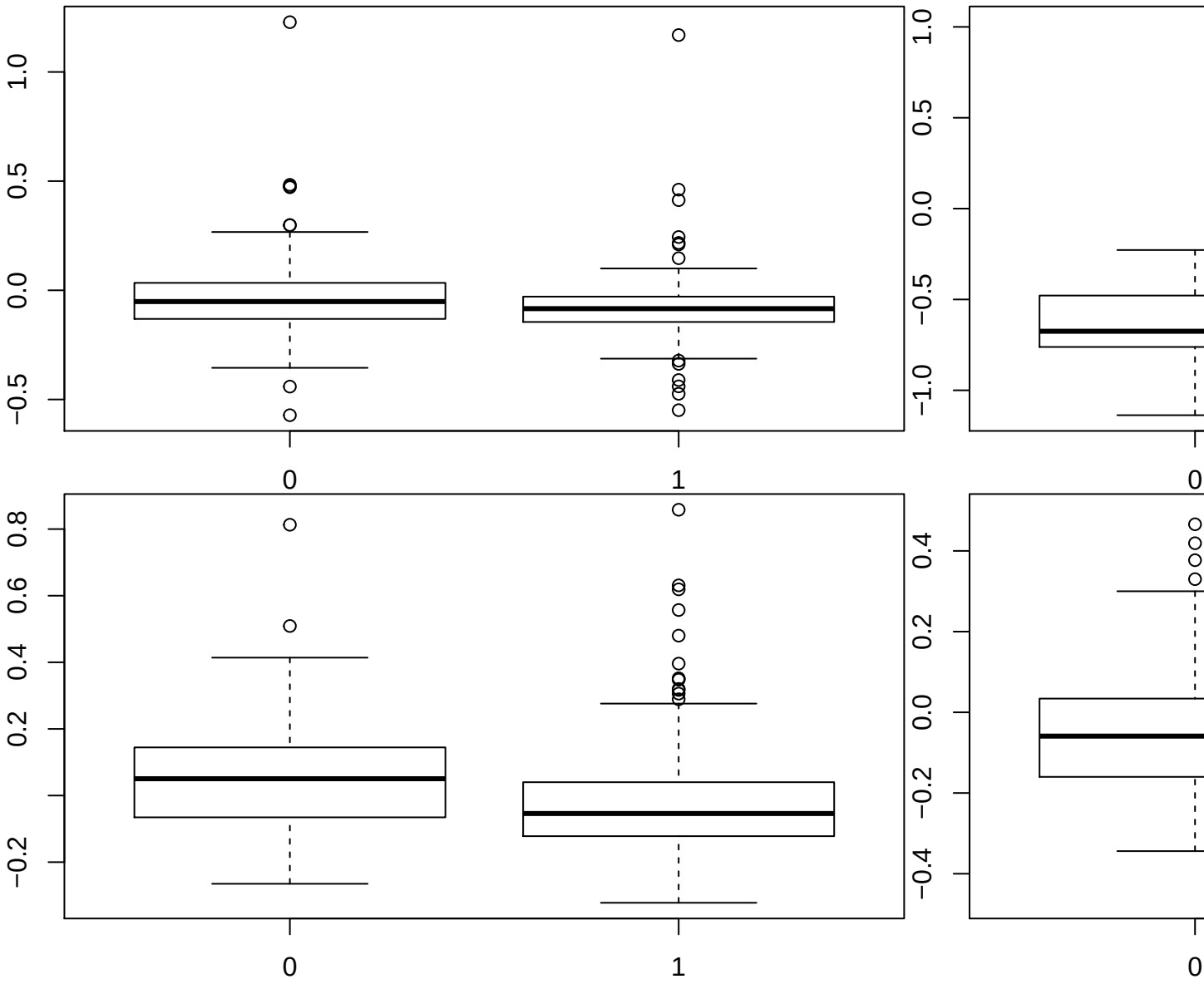
```
##  [1]   2.82013658  -1.17690895  -4.13585382  -4.13091555 -21.31987149
##  [6] -22.75125389  -0.07762344  -0.31208547  -0.25965200  -1.26131422
## [11]   1.10895279  -0.60803759   2.10413818 -14.84693045   3.81036285
## [16]  -3.11648774   8.09996889  -5.94711662
```

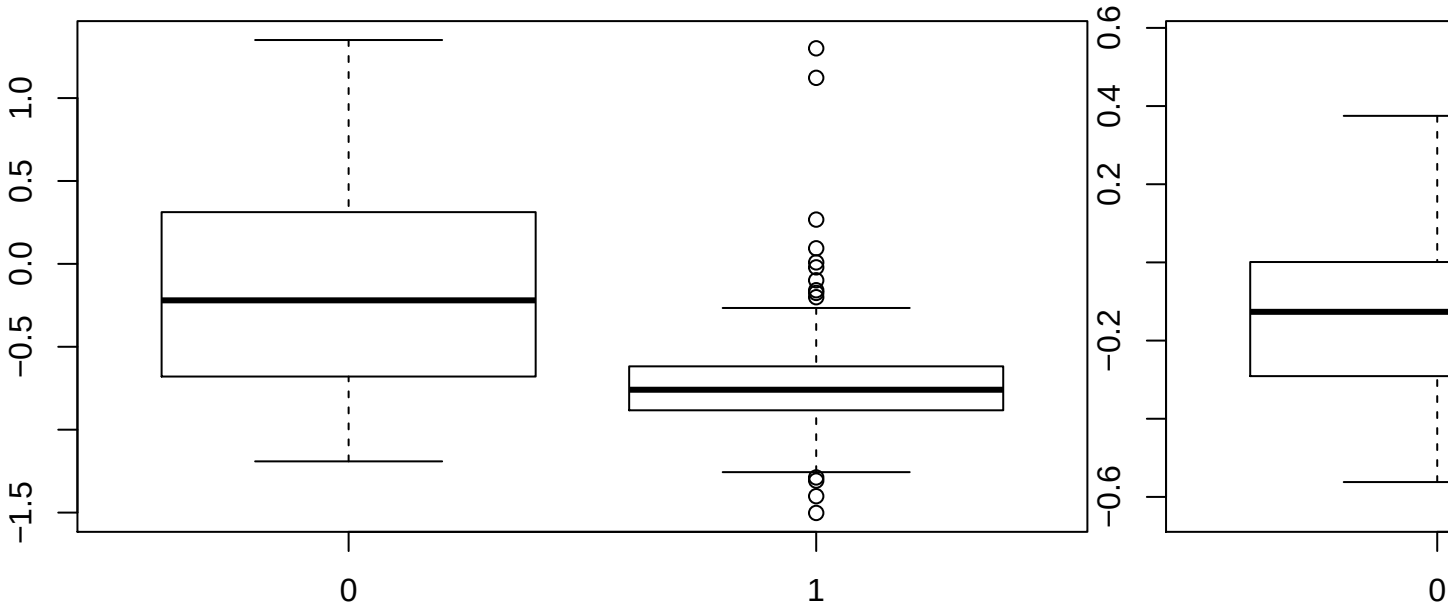
```
stats <- NULL
par(mfrow=c(1,1))
for (i in 1:18) {
   tmp <- t.test(as.numeric(chr8Expression[i,])~factor(subjects$er))
   boxplot(as.numeric(chr8Expression[i,])~factor(subjects$er))
   stats[i] <- tmp$statistic
}
```


0.3
0.2
0.1
−0.1
−0.3
0
1
0.0
−0.5
−1.0
−1.5
−2.0
0
0.4
0.2
−0.2
−0.6
0
1
0.5
0.0
−0.5
−1.0
−1.5
−2.0
0


0.5
0.0
−0.5
−1.0
−1.5
0
1
1.0
0.5
0.0
−0.5
−1.0
0
0.5
0.0
−0.5
0
1
0.2
−0.2
−0.6
−1.0
0


0.4
0.0
−0.4
−0.8
0
1
2.0
1.0
0.0
−1.0
0
0.4
0.2
−0.2
−0.6
0
1
0.6
0.4
0.2
0.0
−0.4
0


1.0
0.5
0.0
−0.5
0
1
1.0
0.5
0.0
−0.5
−1.0
0
0.8
0.6
0.4
0.2
−0.2
0
1
0.4
0.2
0.0
−0.2
−0.4
0




```
stats
```

```
##  [1]   2.82013658  -1.17690895  -4.13585382  -4.13091555 -21.31987149
##  [6] -22.75125389  -0.07762344  -0.31208547  -0.25965200  -1.26131422
## [11]   1.10895279  -0.60803759   2.10413818 -14.84693045   3.81036285
## [16]  -3.11648774   8.09996889  -5.94711662
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