

I used Dseq package for my analysis :

282 genes were diferentially expressed at alpha = 0.05

```
library("DESeq2")
```

```
dds <- DESeqDataSet(se, design = ~ age + RIN)
```

```
dds <- DESeq(dds)
```

```
res <- results(dds)
```

```
res.05 <- results(dds, alpha=.05)
```

```
table(res.05$padj < .05)
```

FALSE TRUE

6459 282



