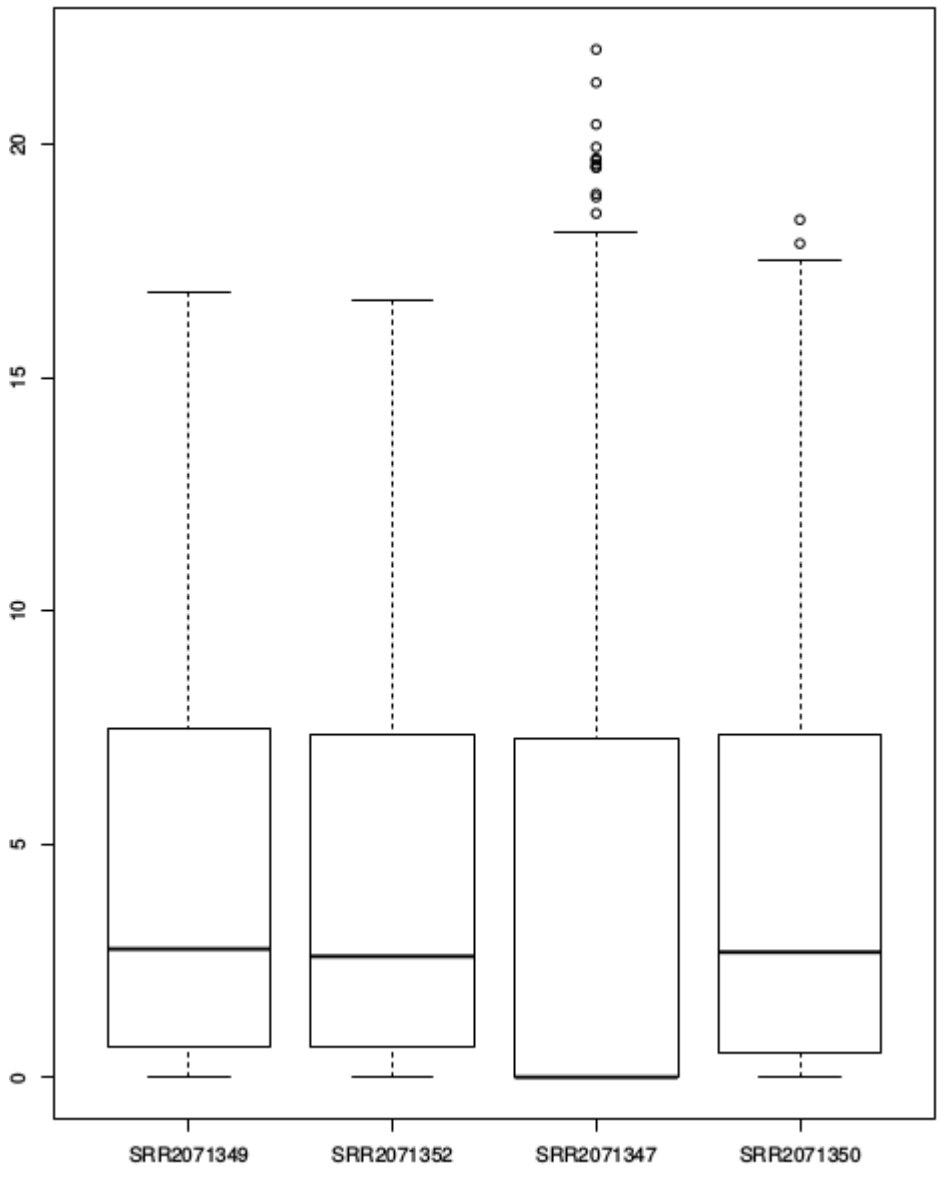
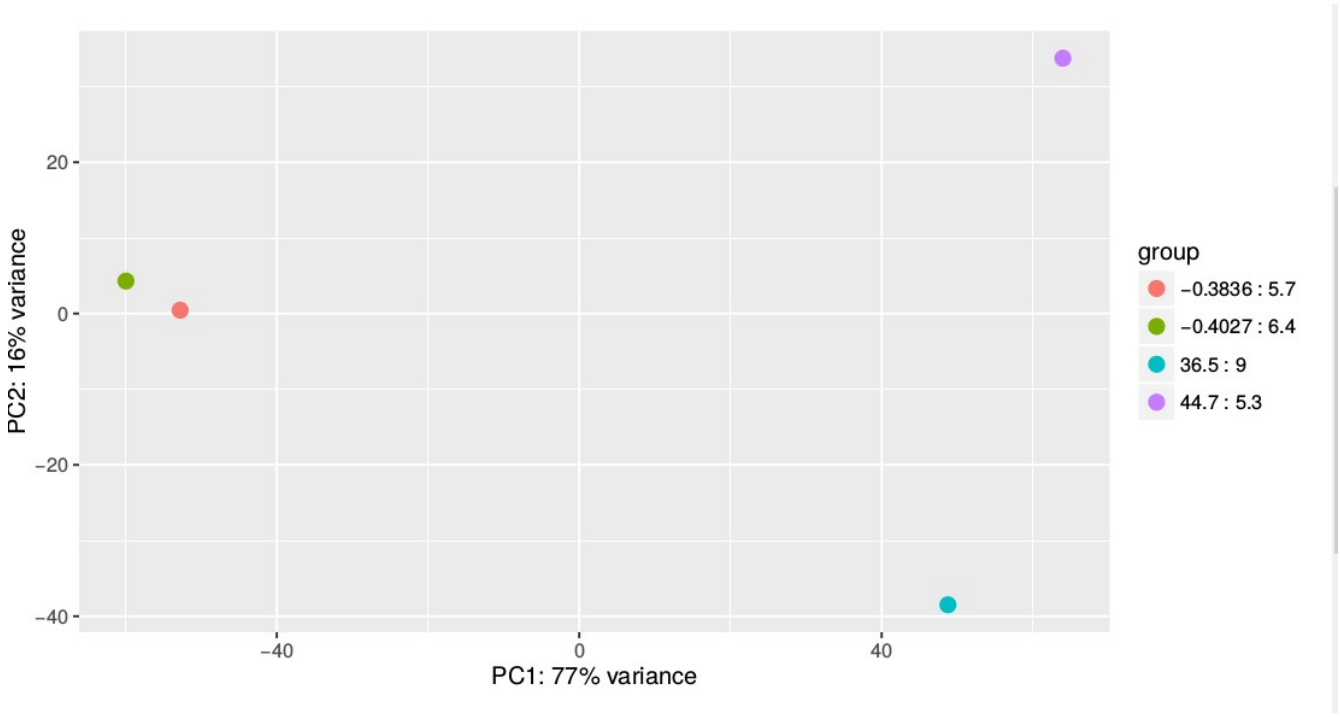
I used DESeq2 package to do the exploratory analysis. On the PCA plot, the fetal samples are on the same side so are the adult samples. The adult samples are very distant whereas the fetal samples are grouped together.

```
library("DESeq2")

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

(ddsMat <- DESeqDataSetFromMatrix(countData = countdata,
                                  colData = coldata,
  design = ~ Age + RIN))

rs <- rowSums(counts(dds))

boxplot(log2(counts(dds)[rs > 0,] + 1))

  rld <- rlog(dds, blind=FALSE)

plotPCA(rld, intgroup = c("Age", "RIN"))
```




20
0
−20
−40
PC2: 16% variance
−40
0
40
PC1: 77% variance
group
−0.3836 : 5.7
−0.4027 : 6.4
36.5 : 9
44.7 : 5.3