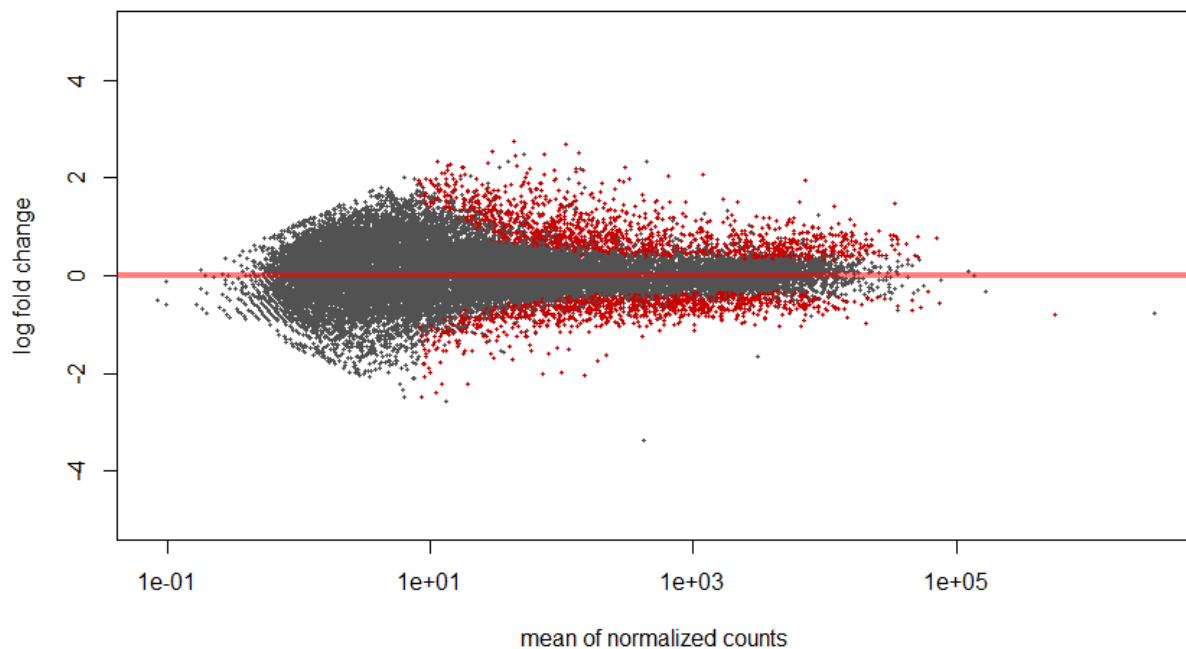


Differential gene expression analysis

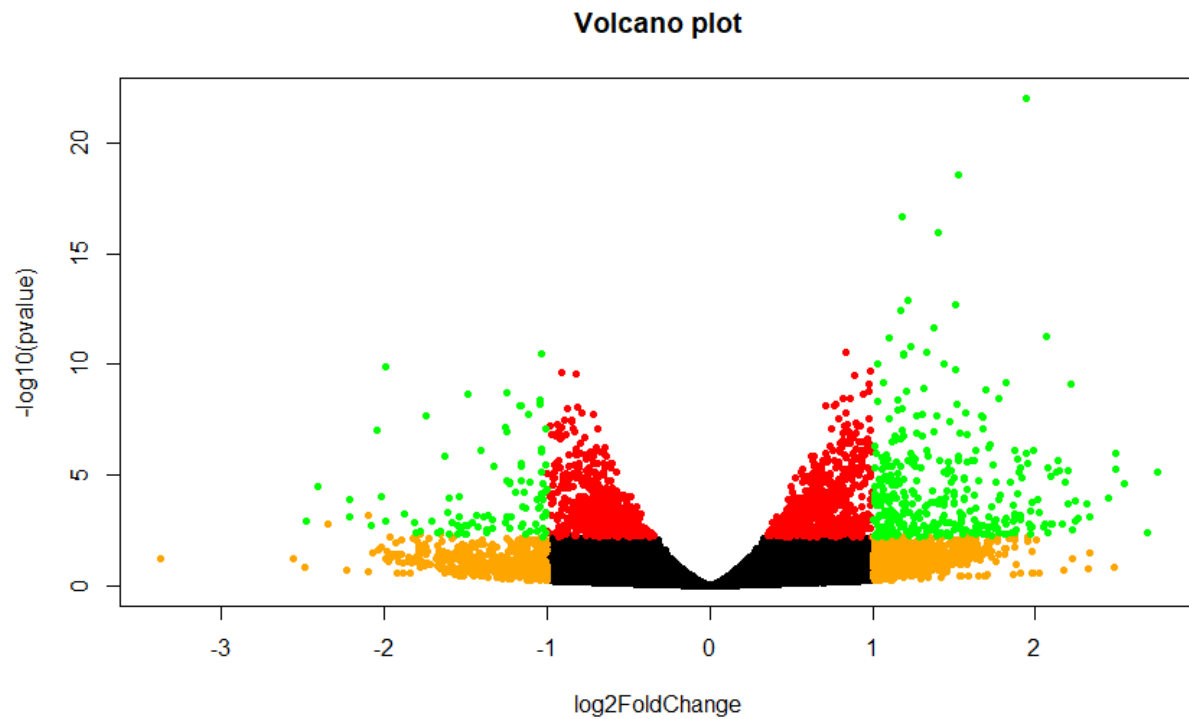
I used the DESeq2 package to perform the gene expression analysis

For the gene expression statistical analysis, adjusted p-value rather than p-value was used to subset up-regulated and down-regulated genes between fetal brain and adult brains samples. The reason for this is to adjust for multiple testing between the three fetal brain and three adult brains samples. $\text{padj} < 0.05$ and fold change > 1 or < -1 were selected for up-regulation and down-regulation, respectively.

346 genes were up-regulated and 92 were down-regulated



This is a MA plot where the red points indicate differentially expressed genes



This is a volcano plot where red points indicate genes having padj values less than 0.05, orange points indicate upregulated and downregulated genes and green points indicate a subset of both.