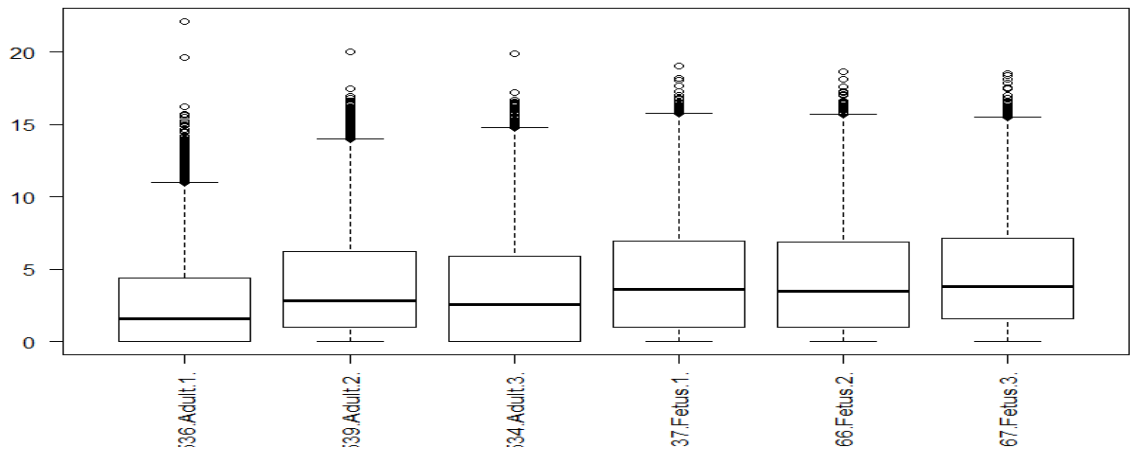
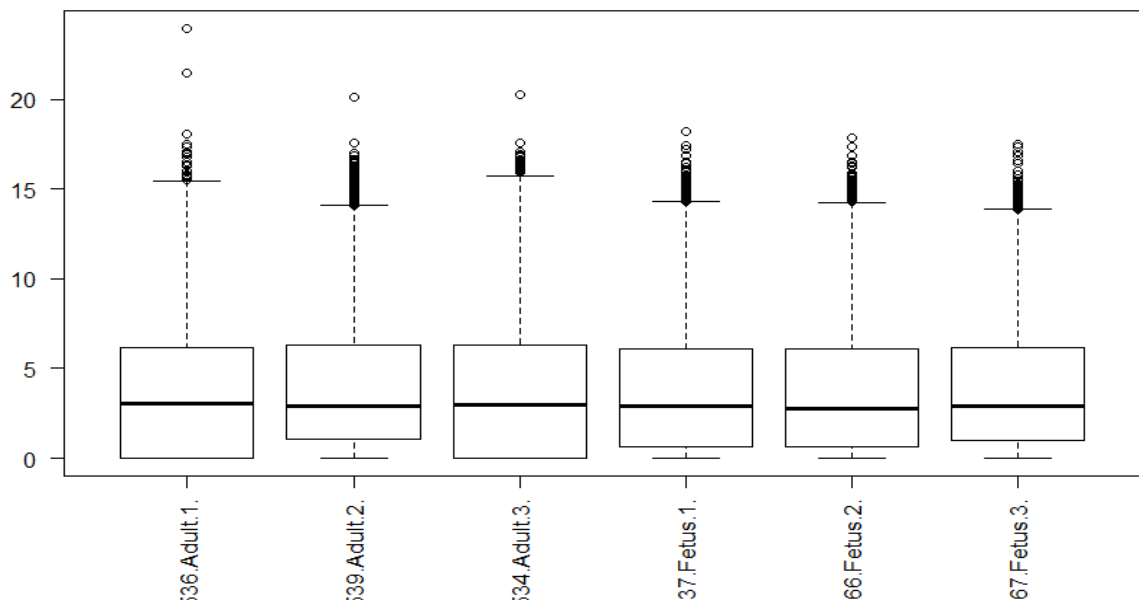


I used the DESeq2 package to perform exploratory analysis. The counts and phenotype data were combined into a DESeq2 summarised dataset. Box plots were constructed for counts data and DESeq2 median ratio normalisation was performed. PCA plot was made using plotPCA function. Adult and fetal groups clustered separately, but there was an outlier in the fetal group.

BOX PLOT BEFORE NORMALIZATION



BOX PLOT AFTER NORMALIZATION



PCA plot

