

Quality Control of Expression Data

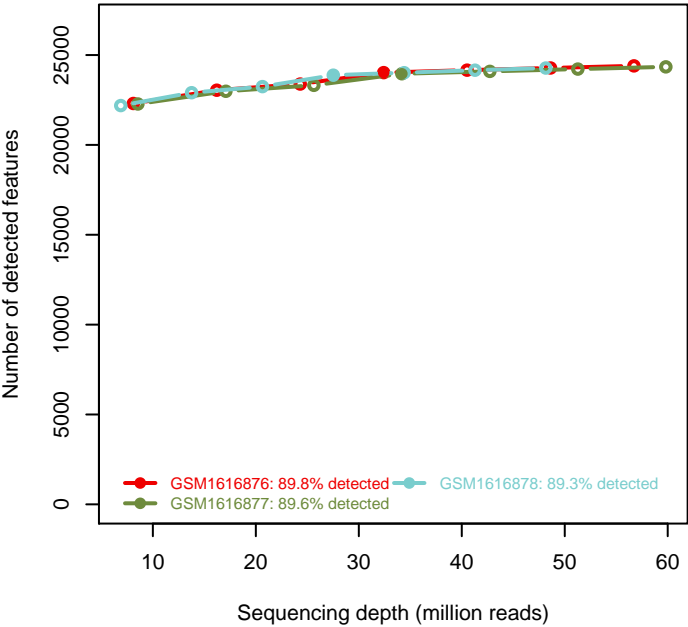
Generated by NOISeq on 14 Mar 2016, 03:17:33

Content

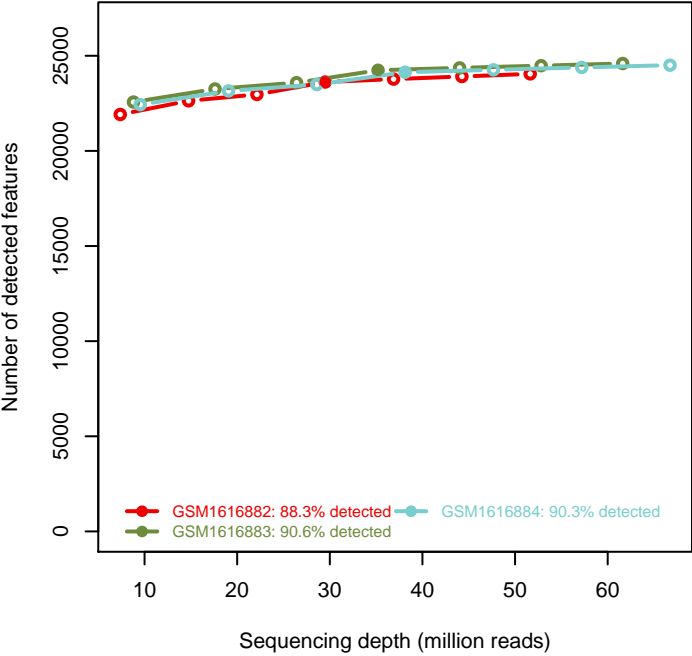
| <i>Plot</i> | <i>Description</i> |
|-----------------------------|---|
| Biotype detection | Plot not available. Biotypes information was not provided. |
| Biotype expression | Plot not available. Biotypes information was not provided. |
| Saturation | Number of detected genes (counts > 0) per sample across different sequencing depths |
| Expression boxplot | Distribution of gene counts per million (all biotypes) in each sample/condition |
| Expression barplot | Percentage of genes with >0, >1, >2, >5 or >10 counts per million in each sample/condition. |
| Length bias | Plot not available. Gene length was not provided. |
| GC content bias | Plot not available. Gene GC content was not provided. |
| RNA composition bias | Density plots of log fold changes (M) between pairs of samples. Confidence intervals for the median of M values. |
| Exploratory PCA | Principal Component Analysis score plots for PC1 vs PC2, and PC1 vs PC3. |

Sequencing depth & Expression quantification

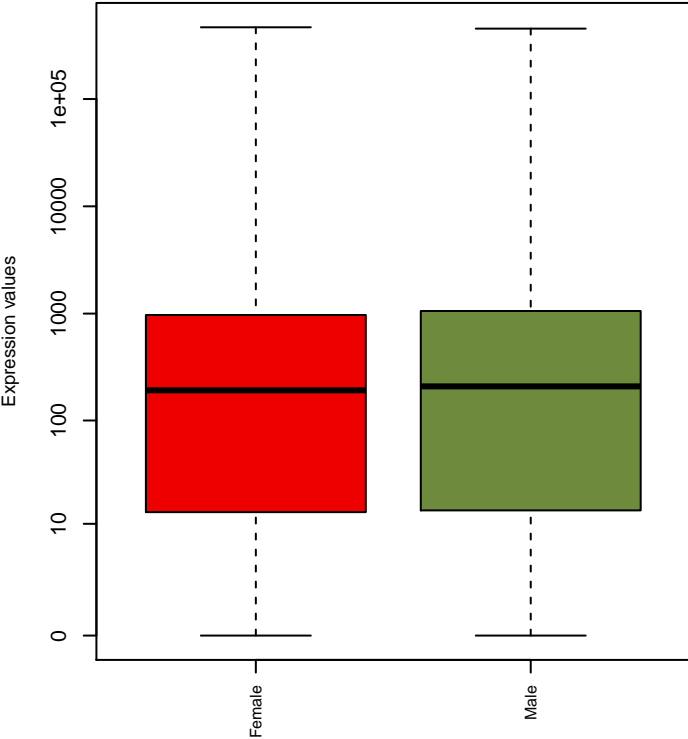
GLOBAL (26743)



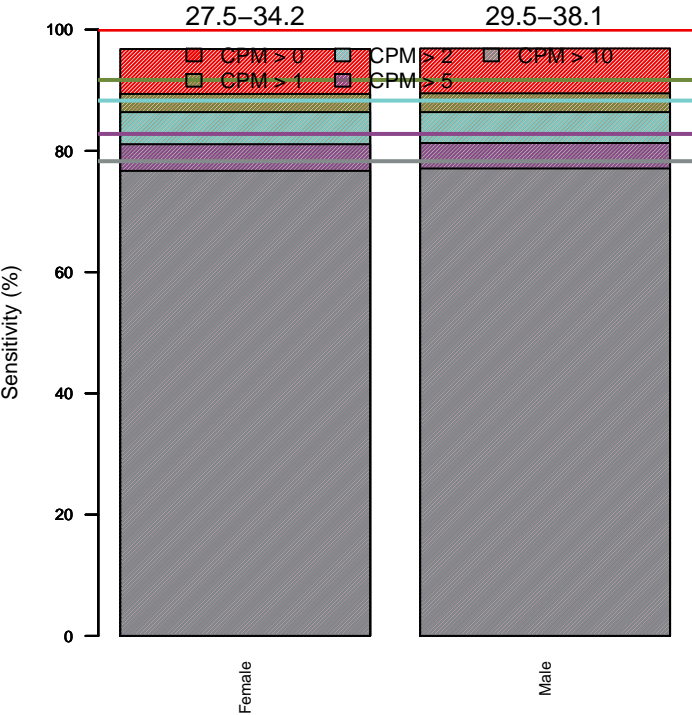
GLOBAL (26743)



GLOBAL (26743)



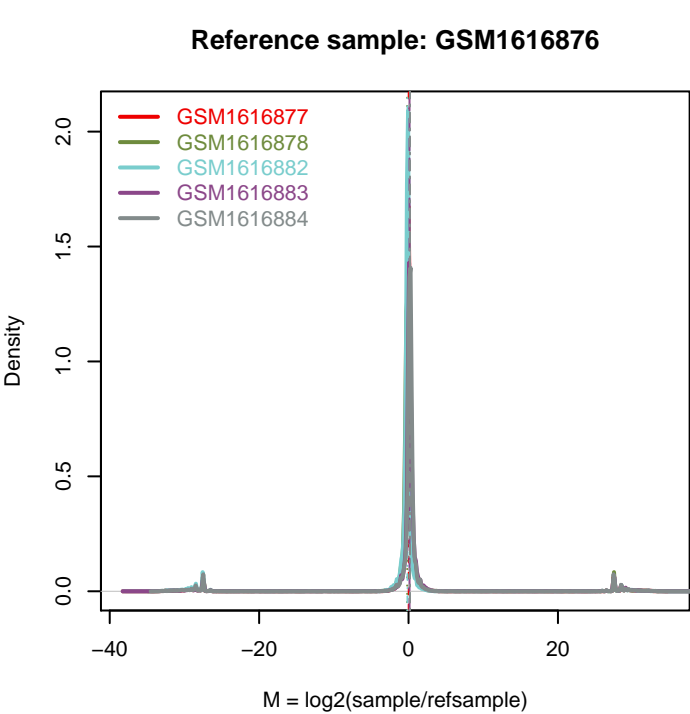
GLOBAL (26743)



Sequencing bias detection

Diagnostic plot for differences in RNA composition

FAILED. There is a pair of samples with significantly different RNA composition
Normalization for correcting this bias is required.



Confidence intervals for median of M values

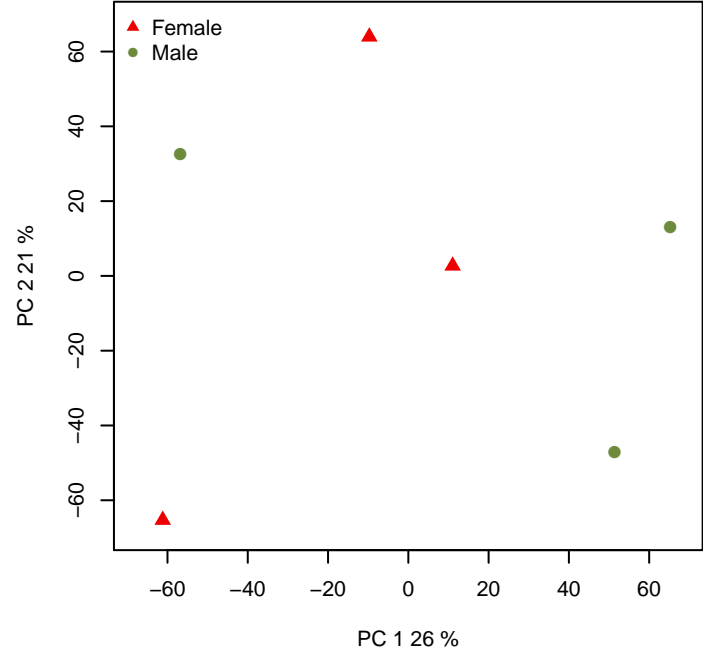
| Sample | 0.5% | 99.5% | Diagnostic Test |
|------------|---------|---------|-----------------|
| GSM1616877 | 0.019 | 0.0312 | FAILED |
| GSM1616878 | -0.1895 | -0.1766 | FAILED |
| GSM1616882 | -0.147 | -0.1354 | FAILED |
| GSM1616883 | 0.1254 | 0.1391 | FAILED |
| GSM1616884 | 0.1871 | 0.198 | FAILED |

Exploratory PCA

Use this plot to see if samples are clustered according to the experimental design.

Use ARSyNseq function to correct potential batch effects.

Scores



Scores

