

# Quality Control of Expression Data

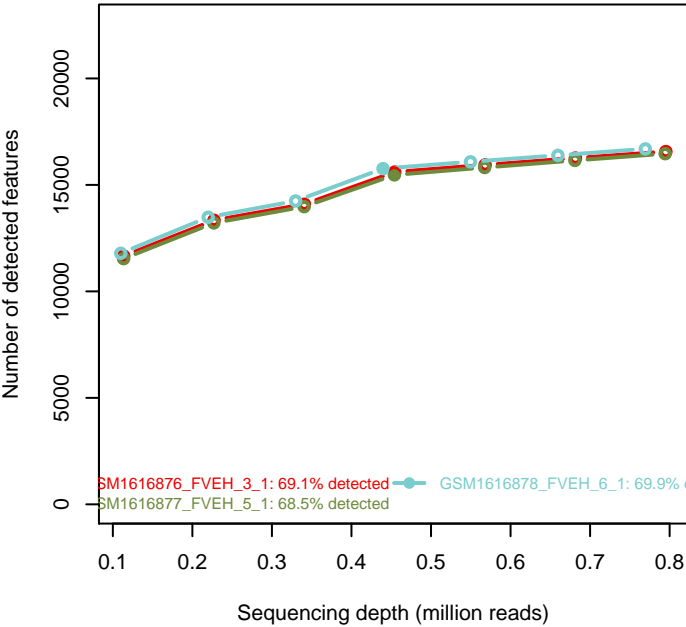
Generated by NOISeq on 24 Feb 2016, 08:18:51

## Content

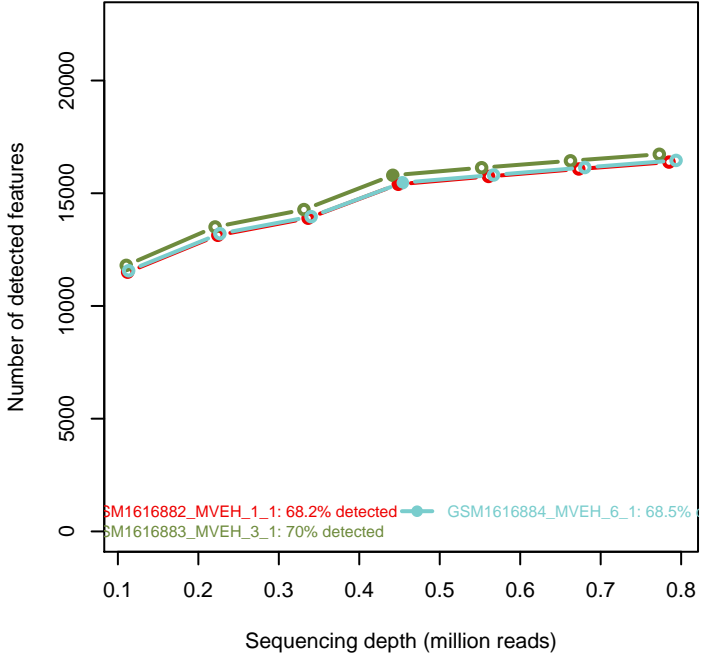
<i>Plot</i>	<i>Description</i>
<b>Biotype detection</b>	Plot not available. Biotypes information was not provided.
<b>Biotype expression</b>	Plot not available. Biotypes information was not provided.
<b>Saturation</b>	Number of detected genes (counts > 0) per sample across different sequencing depths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

# Sequencing depth & Expression quantification

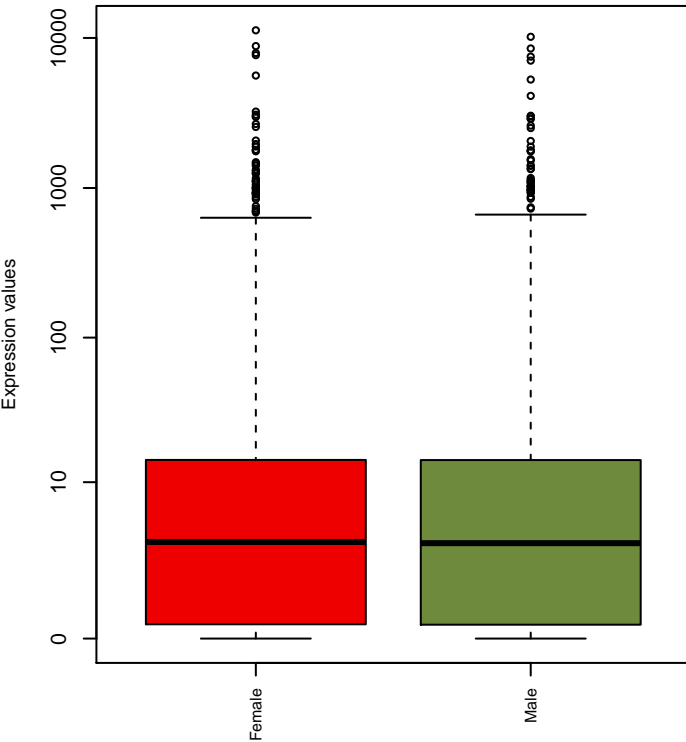
GLOBAL (22569)



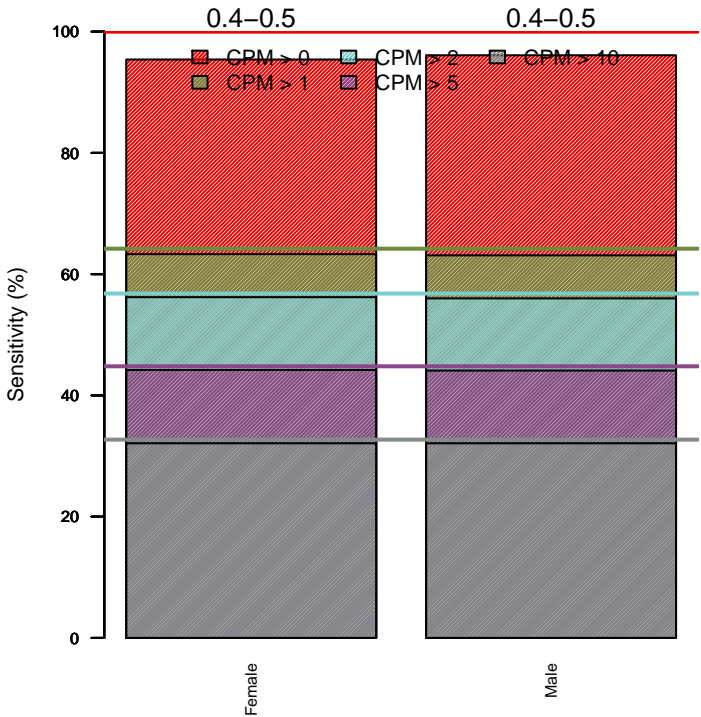
GLOBAL (22569)



GLOBAL (22569)



GLOBAL (22569)

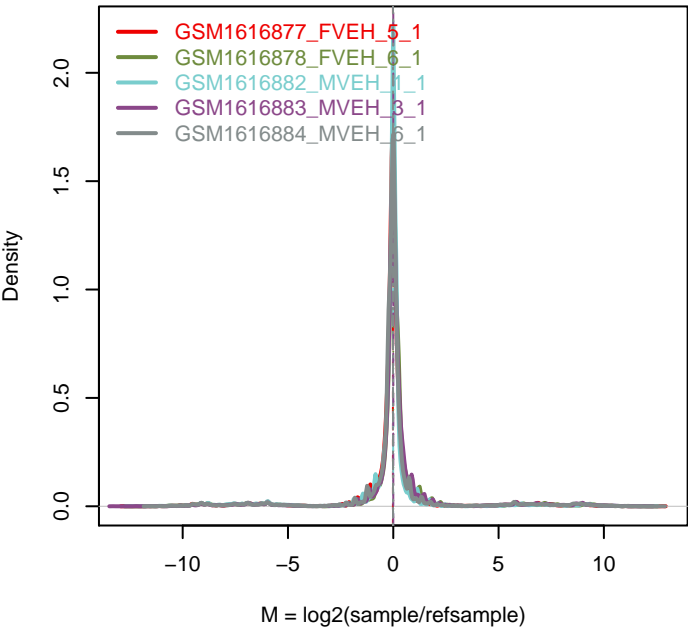


# Sequencing bias detection

## 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.

Reference sample: GSM1616876\_FVEH\_3\_1



Confidence intervals for median of M values

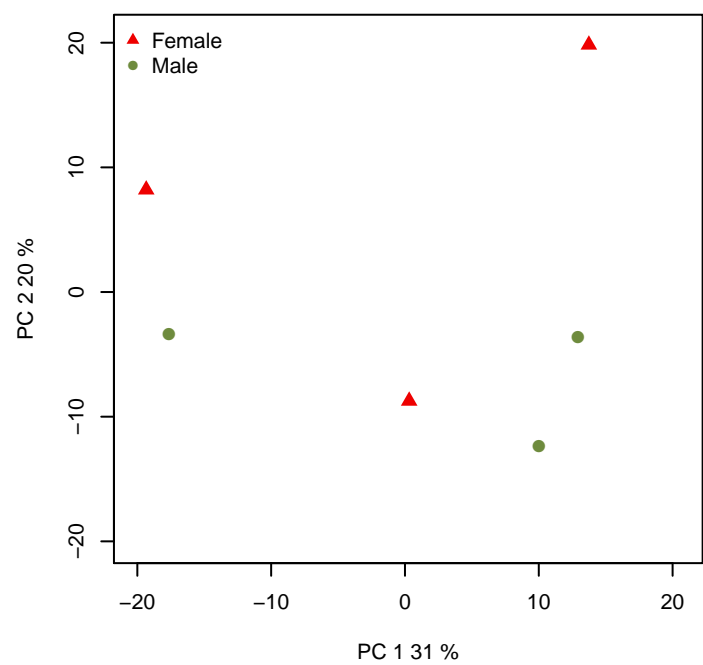
Sample	0.5%	99.5%	Diagnostic Test
GSM1616877_FVEH_5_1	-0.0226	-0.01	FAILED
GSM1616878_FVEH_6_1	0	0	PASSED
GSM1616882_MVEH_1_1	-0.0109	-0.0021	FAILED
GSM1616883_MVEH_3_1	0	0	PASSED
GSM1616884_MVEH_6_1	-0.0158	-0.0056	FAILED

# 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

