Quality Control of Expression Data
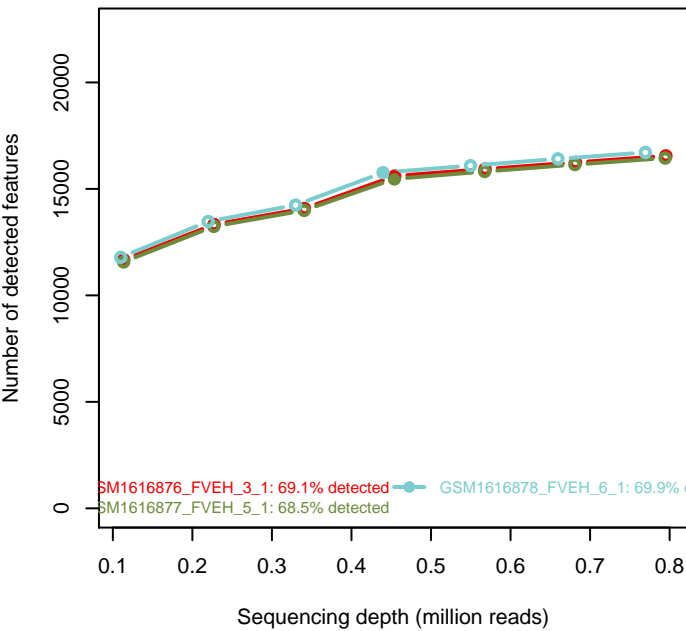
Generated by NOISeq on 23 Feb 2016, 23:46:50

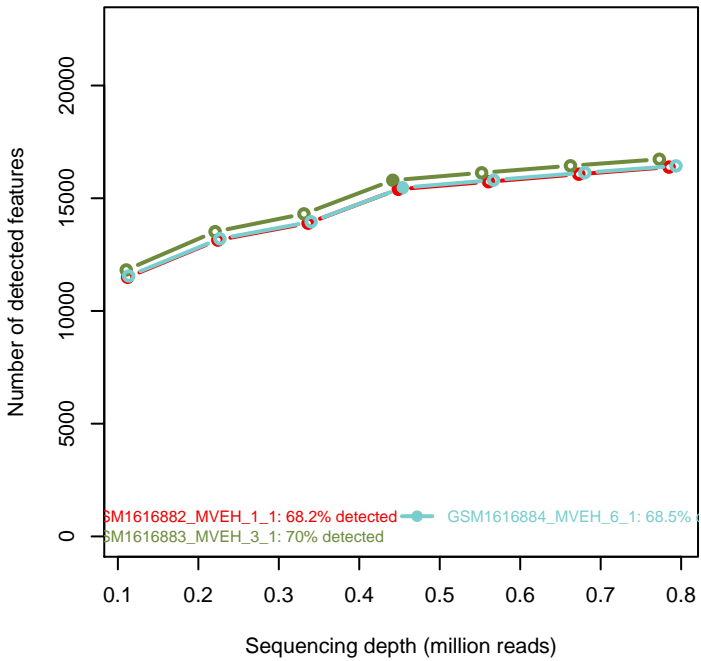## Content

Plot	Description
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

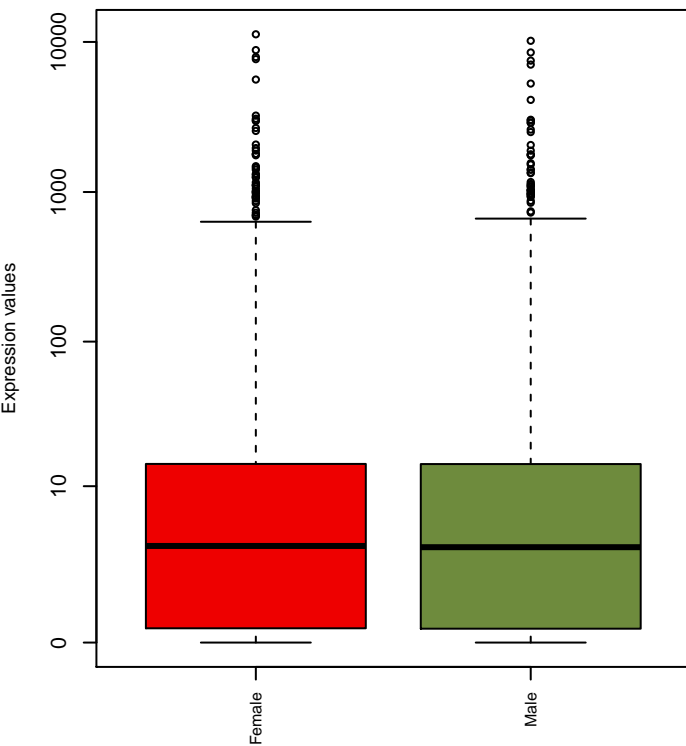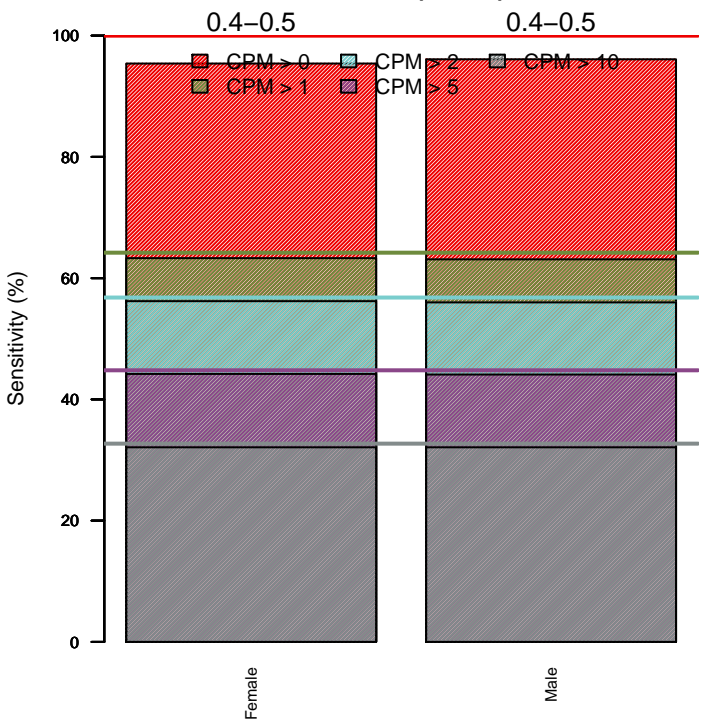## GLOBAL (22569)

Number of detected features vs. Sequencing depth (million reads)

SM1616876_FVEH_3_1: 69.1% detected —●— GSM1616878_FVEH_6_1: 69.9%
SM1616877_FVEH_5_1: 68.5% detected

GLOBAL (22569)

Number of detected features vs. Sequencing depth (million reads)

SM1616882_MVEH_1_1: 68.2% detected —●— GSM1616884_MVEH_6_1: 68.5%
SM1616883_MVEH_3_1: 70% detected

GLOBAL (22569)

Expression values — Female, Male

GLOBAL (22569)

0.4−0.5   0.4−0.5

Sensitivity (%) — Female, Male

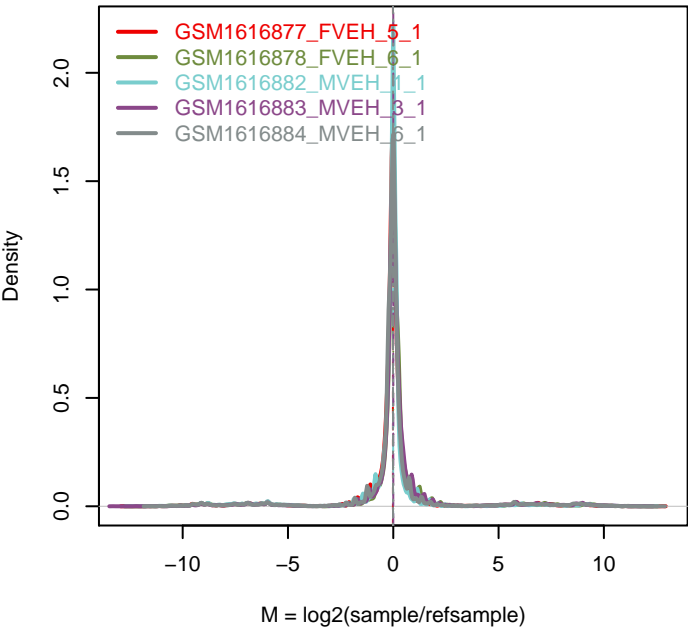CPM > 0   CPM > 2   CPM > 10
CPM > 1   CPM > 5

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

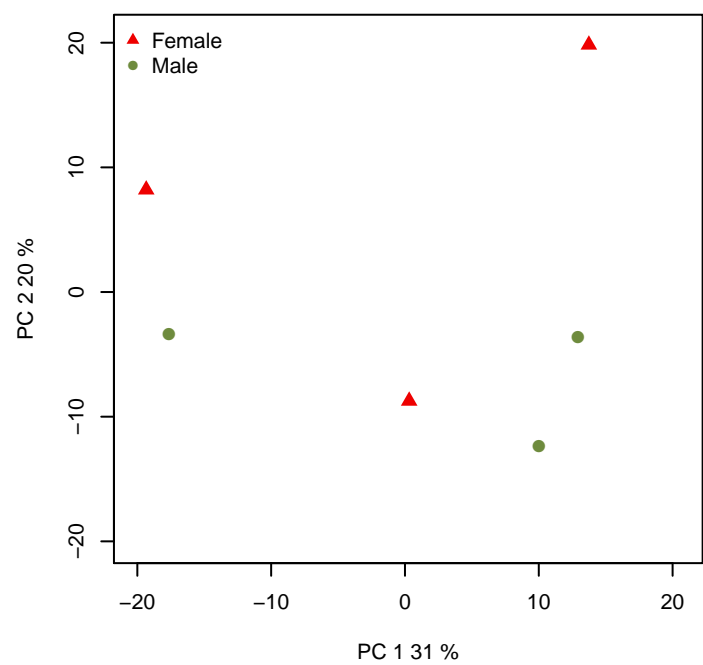

Confidence intervals for median of M values

Sample	0.5%	99.5%	Diagnostic Test
GSM1616877_FVEH_5_1	−0.022	−0.0099	FAILED
GSM1616878_FVEH_6_1	0	0	PASSED
GSM1616882_MVEH_1_1	−0.0108	−0.0018	FAILED
GSM1616883_MVEH_3_1	0	0	PASSED
GSM1616884_MVEH_6_1	−0.0161	−0.0055	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