Quality Control of Expression Data
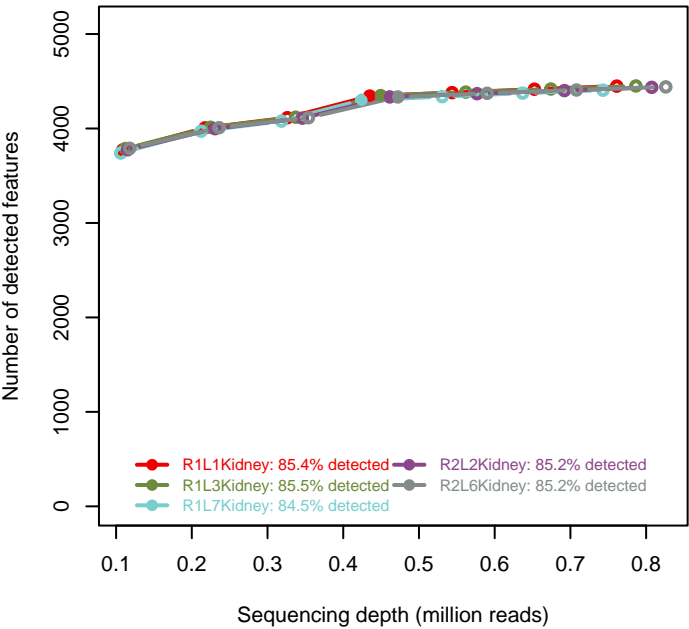
Generated by NOISeq on 28 fev 2023, 10:05:30

Content
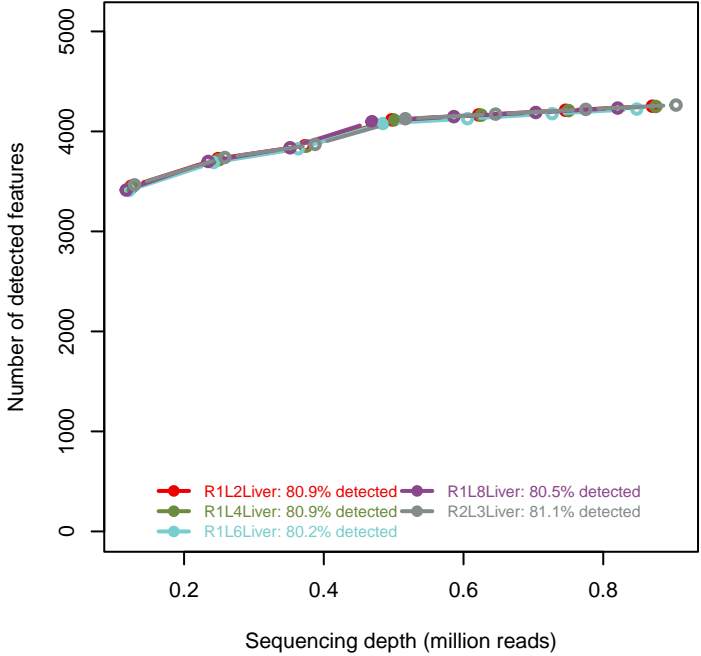
Plot	Description
Biotype detection	Plot not available. Biotypes information was not provided.
Biotype expression	Plot not available. Biotypes information was not provided.
Saturation	Number of detected genes (counts > 0) per sample across different sequencing depths
Expression boxplot	Distribution of 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

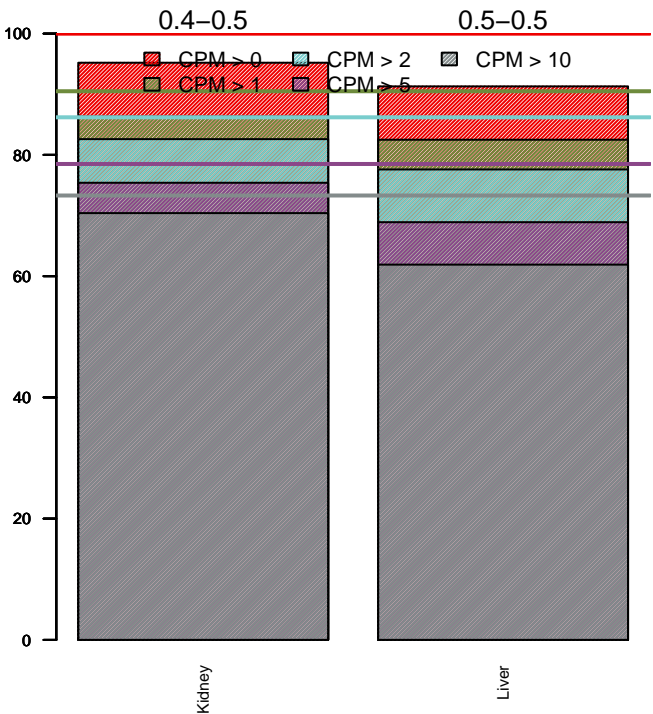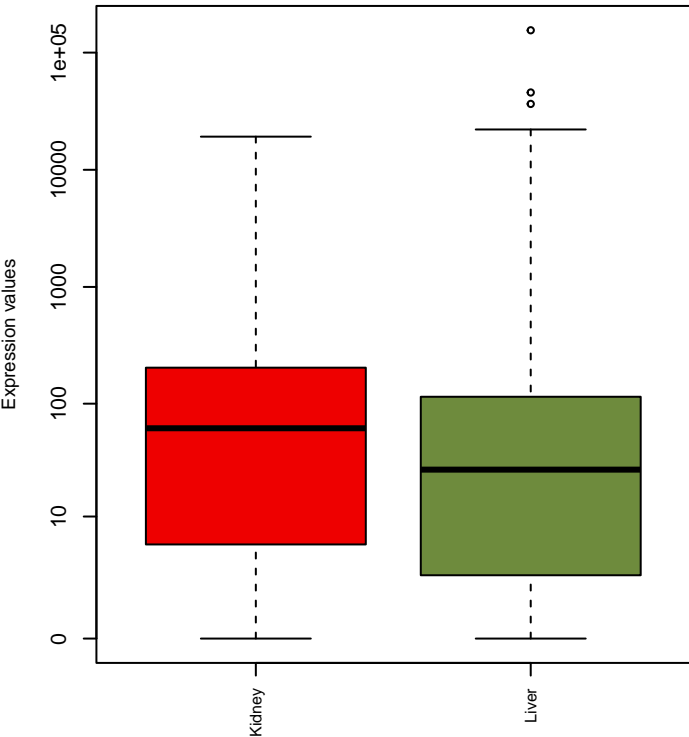## GLOBAL (5088)

- R1L1Kidney: 85.4% detected
- R1L3Kidney: 85.5% detected
- R1L7Kidney: 84.5% detected
- R2L2Kidney: 85.2% detected
- R2L6Kidney: 85.2% detected

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

GLOBAL (5088)

- R1L2Liver: 80.9% detected
- R1L4Liver: 80.9% detected
- R1L6Liver: 80.2% detected
- R1L8Liver: 80.5% detected
- R2L3Liver: 81.1% detected

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

GLOBAL (5088)

Expression values for Kidney and Liver

0.4−0.5   0.5−0.5

- CPM > 0
- CPM > 1
- CPM > 2
- CPM > 5
- CPM > 10
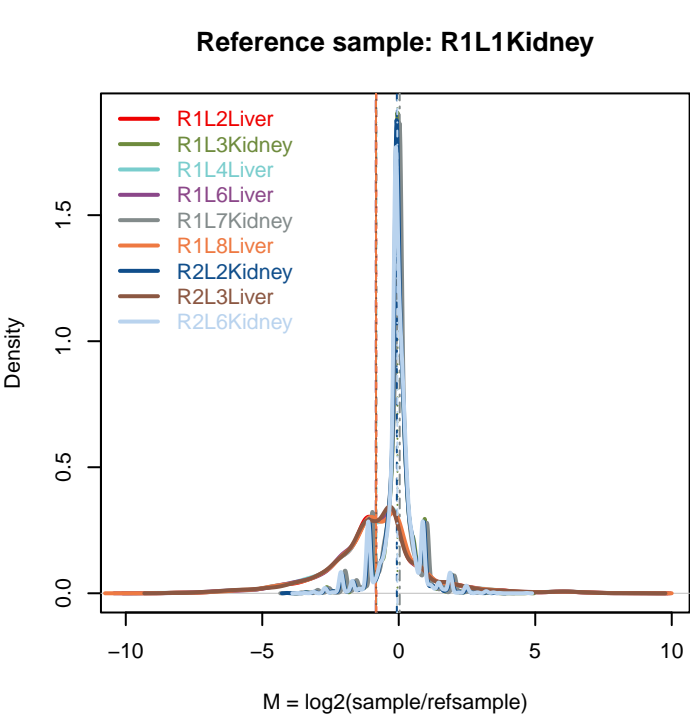
Sequencing bias detection

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: R1L1Kidney

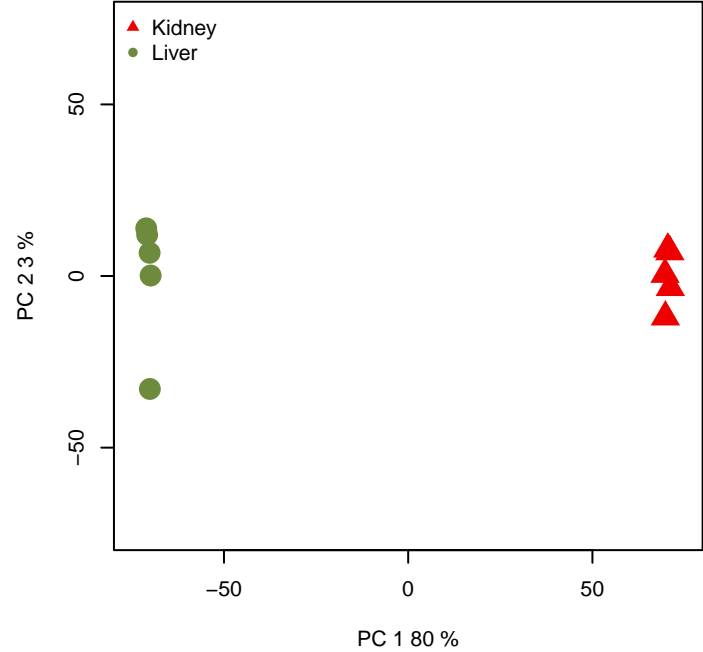### Confidence intervals for median of M values

Sample	0.28%	99.72%	Diagnostic Test
R1L2Liver	−0.8995	−0.7703	FAILED
R1L3Kidney	−0.0472	−0.0472	FAILED
R1L4Liver	−0.8796	−0.7579	FAILED
R1L6Liver	−0.9166	−0.7604	FAILED
R1L7Kidney	0.0348	0.0348	FAILED
R1L8Liver	−0.9033	−0.7581	FAILED
R2L2Kidney	−0.085	−0.0459	FAILED
R2L3Liver	−0.8783	−0.7473	FAILED
R2L6Kidney	−0.0699	−0.038	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