Quality Control of Expression Data

Generated by NOISeq on 28 mar 2023, 12:52:48

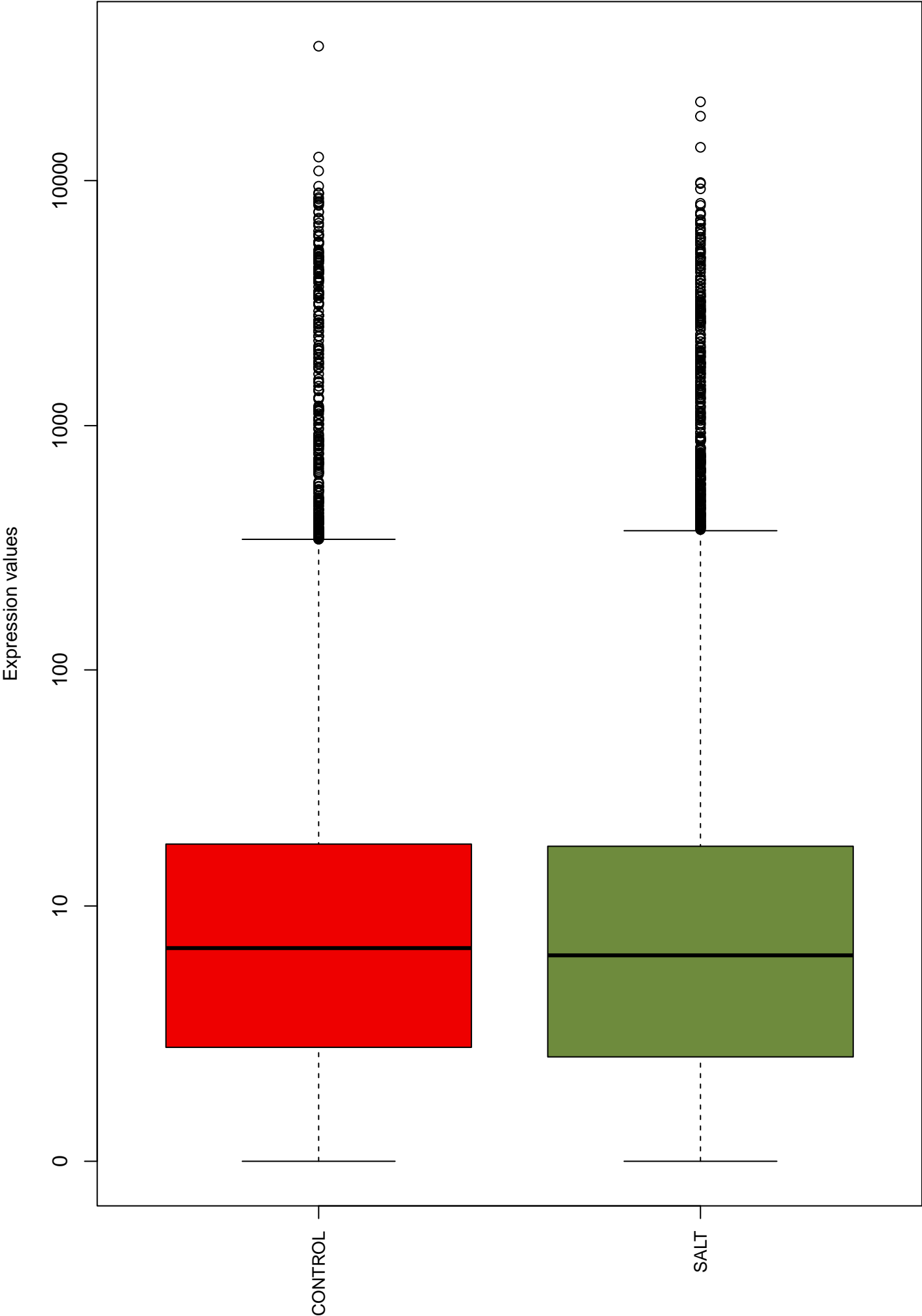## Content

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
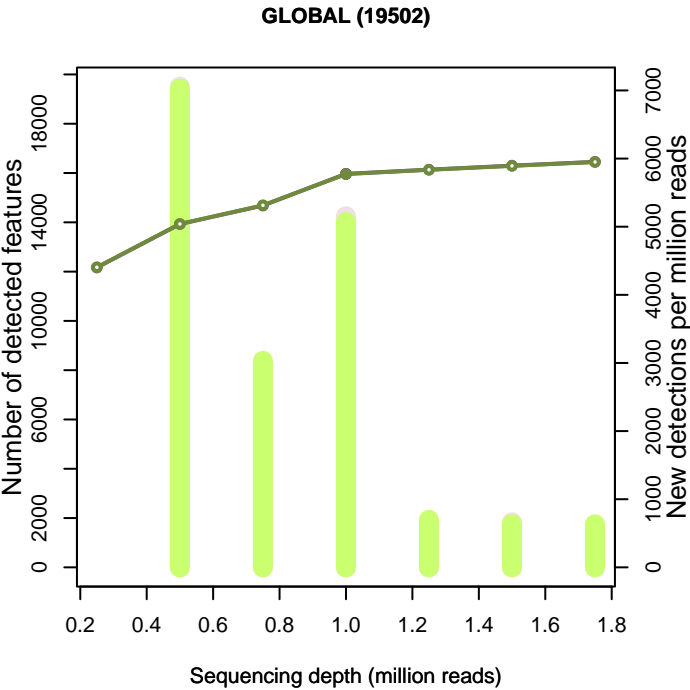
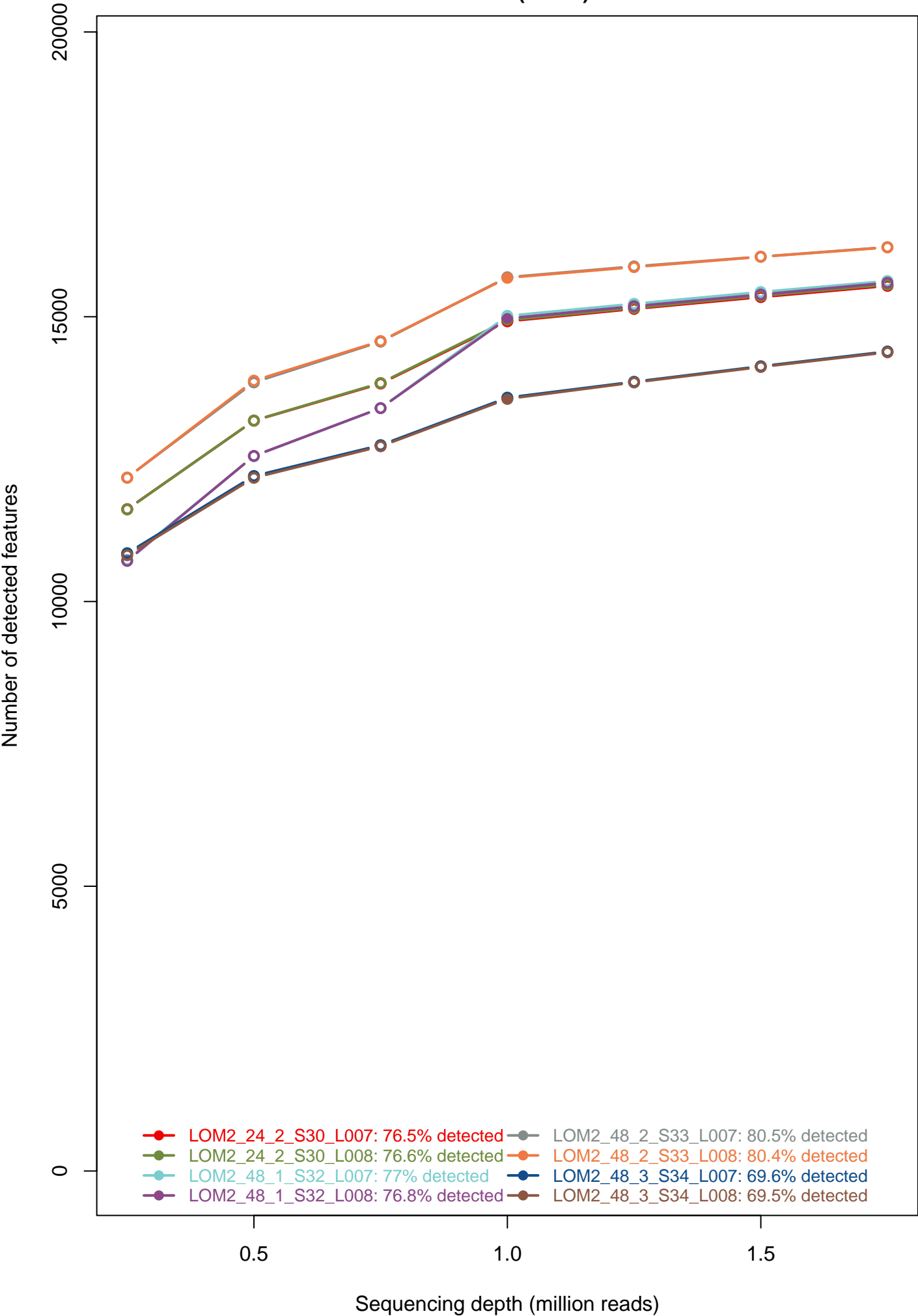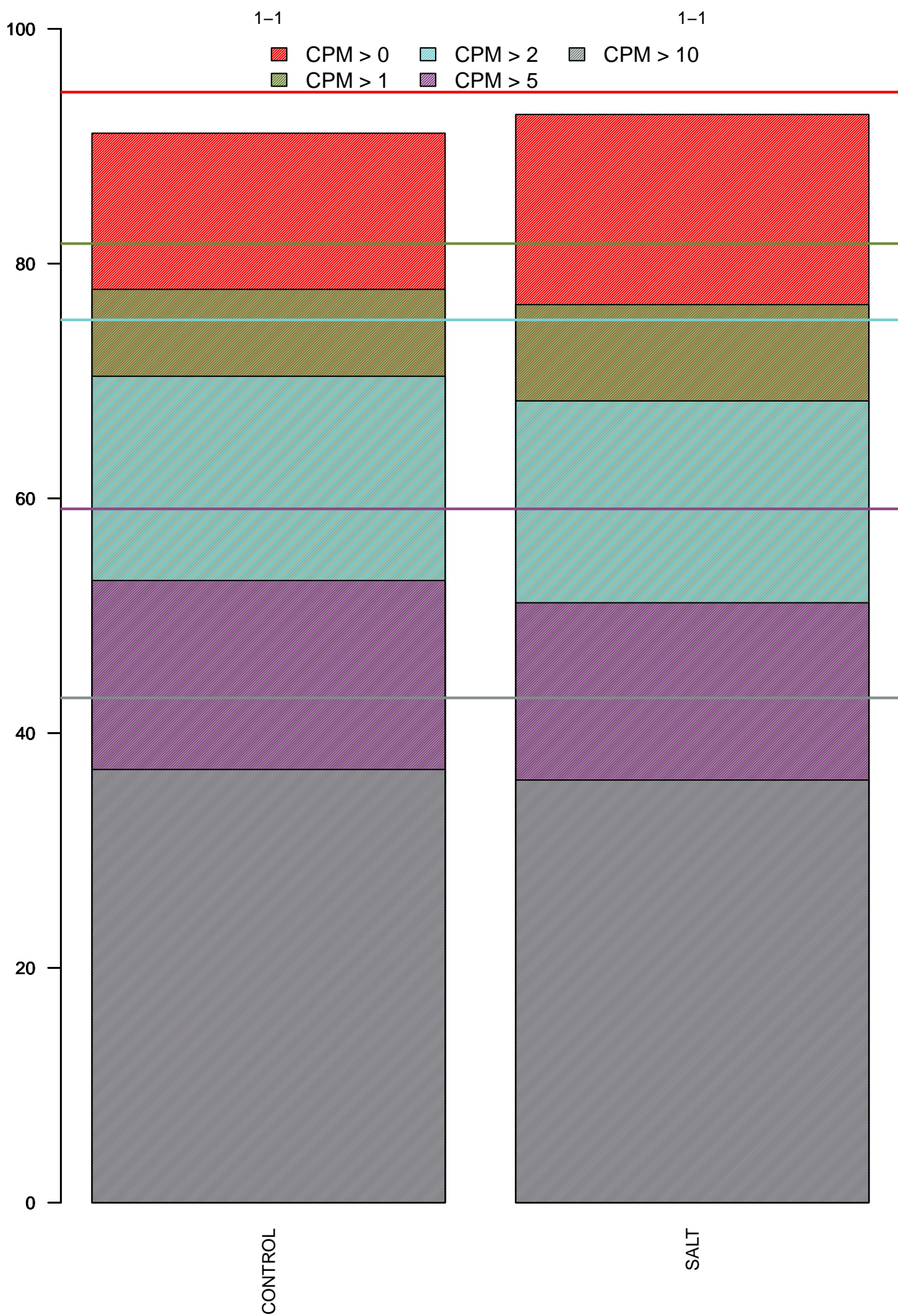## GLOBAL (19502)

	Left axis	Right axis	%detected
LOM1_24_3_S37_L007			81.9
LOM1_24_3_S37_L008			81.8

GLOBAL (18457)

GLOBAL (19502)

Number of detected features

Sequencing depth (million reads)

LOM2_24_2_S30_L007: 76.5% detected
LOM2_24_2_S30_L008: 76.6% detected
LOM2_48_1_S32_L007: 77% detected
LOM2_48_1_S32_L008: 76.8% detected
LOM2_48_2_S33_L007: 80.5% detected
LOM2_48_2_S33_L008: 80.4% detected
LOM2_48_3_S34_L007: 69.6% detected
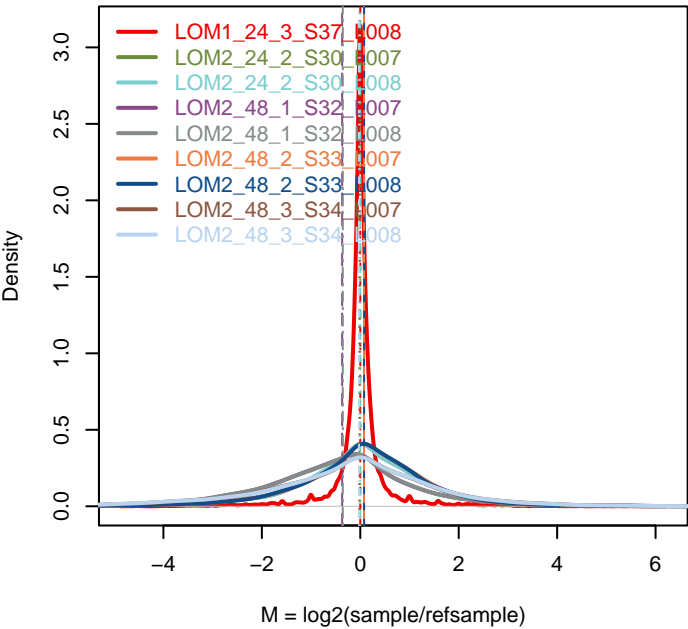LOM2_48_3_S34_L008: 69.5% detected

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: LOM1_24_3_S37_L007
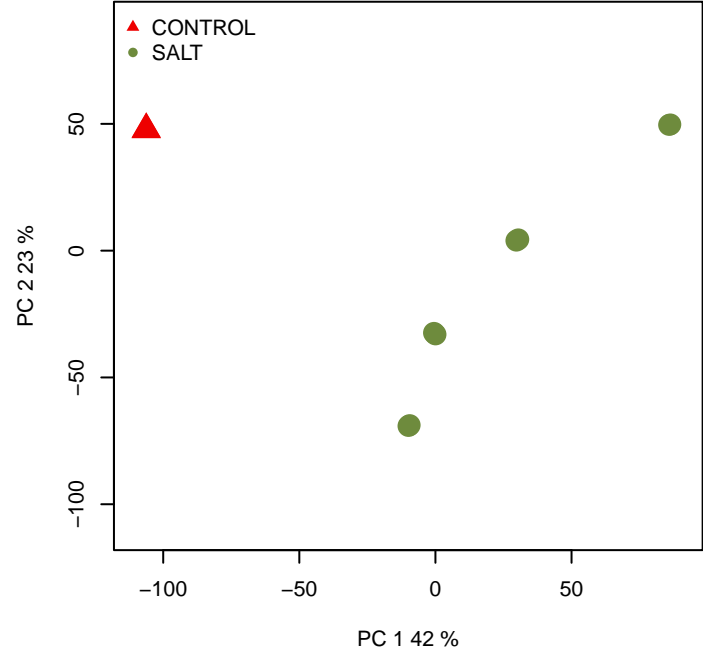

Confidence intervals for median of M values

Sample	0.28%	99.72%	Diagnostic Test
LOM1_24_3_S37_L008	−0.0018	0	FAILED
LOM2_24_2_S30_L007	0	0.0252	PASSED
LOM2_24_2_S30_L008	0	0.0238	PASSED
LOM2_48_1_S32_L007	−0.405	−0.3342	FAILED
LOM2_48_1_S32_L008	−0.3843	−0.3216	FAILED
LOM2_48_2_S33_L007	0.048	0.1088	FAILED
LOM2_48_2_S33_L008	0.051	0.1013	FAILED
LOM2_48_3_S34_L007	−0.0572	0	FAILED
LOM2_48_3_S34_L008	−0.0612	0	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