

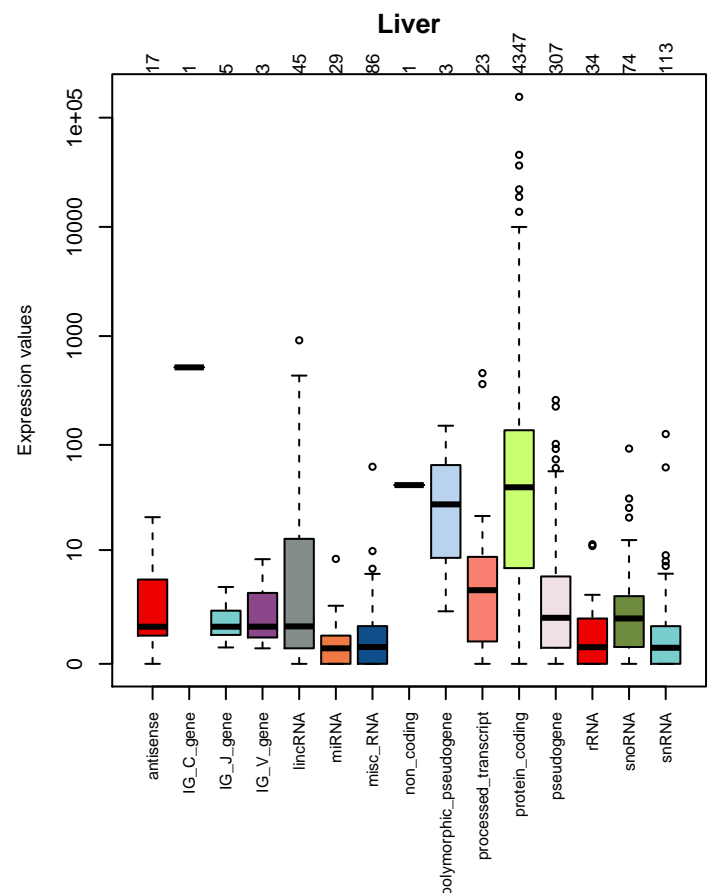
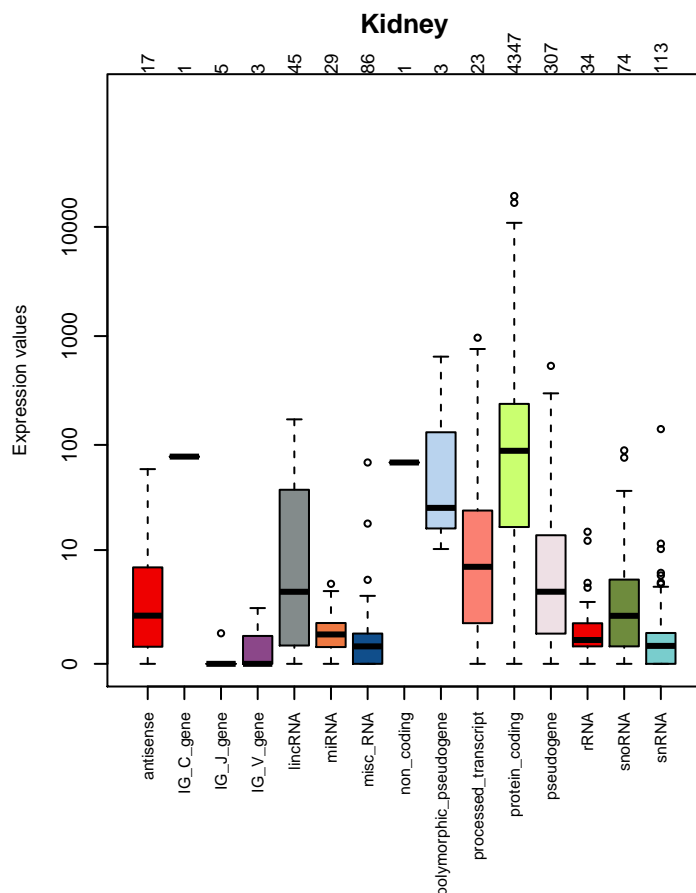
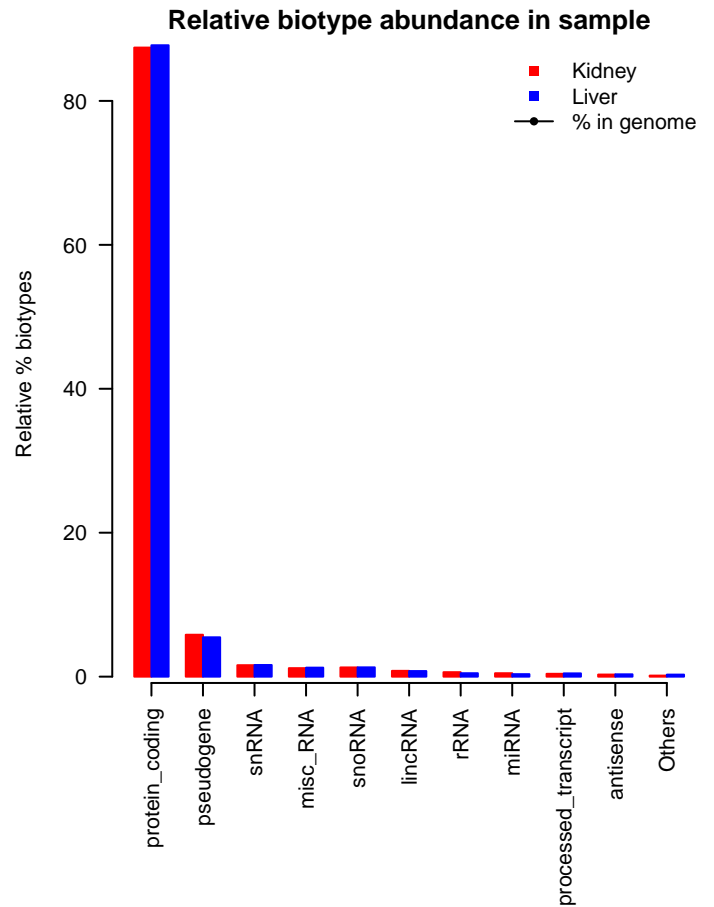
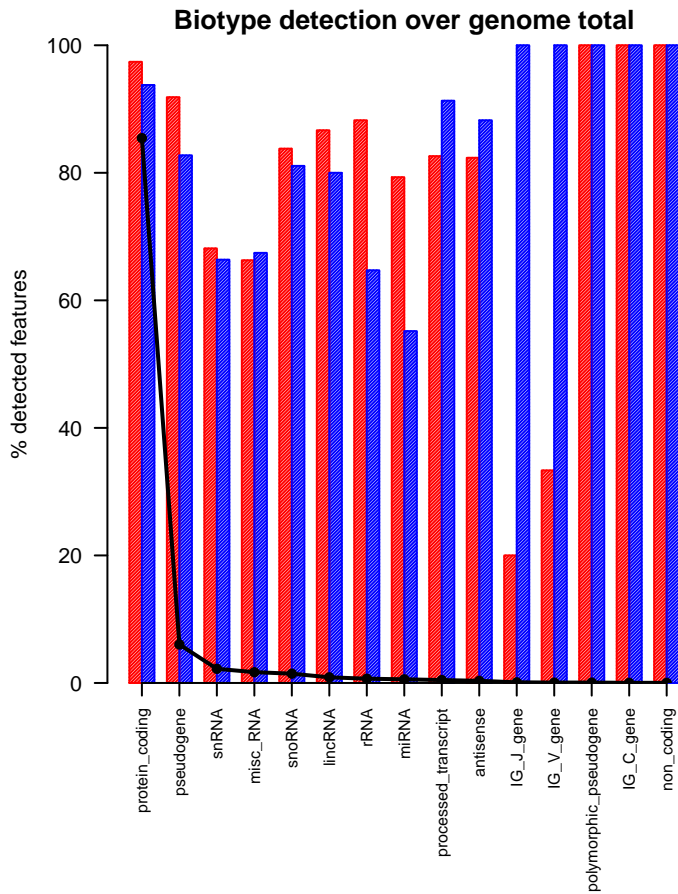
Quality Control of Expression Data

Generated by NOISeq on 08 Jun 2015, 16:03:36

Content

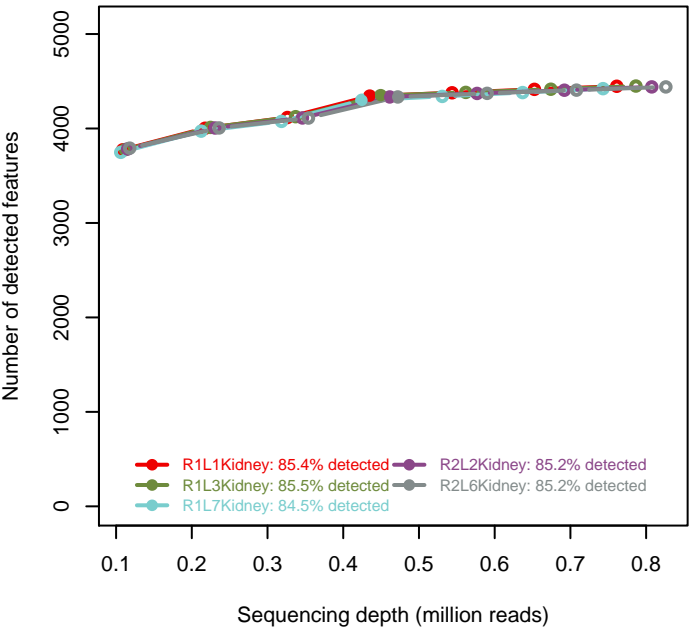
<i>Plot</i>	<i>Description</i>
Biotype detection	Biotype abundance in the genome with %genes detected (counts > 0) in the sample/condition. Biotype abundance within the sample/condition.
Biotype expression	Distribution of gene counts per million per biotype in sample/condition (only genes with counts > 0).
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	Mean gene expression per each length bin. Fitted curve and diagnostic test.
GC content bias	Mean gene expression per each GC content bin. Fitted curve and diagnostic test.
RNA composition bias	Density plots of log fold changes (M) between pairs of samples. Confidence intervals for the median of M values.

Biotype detection

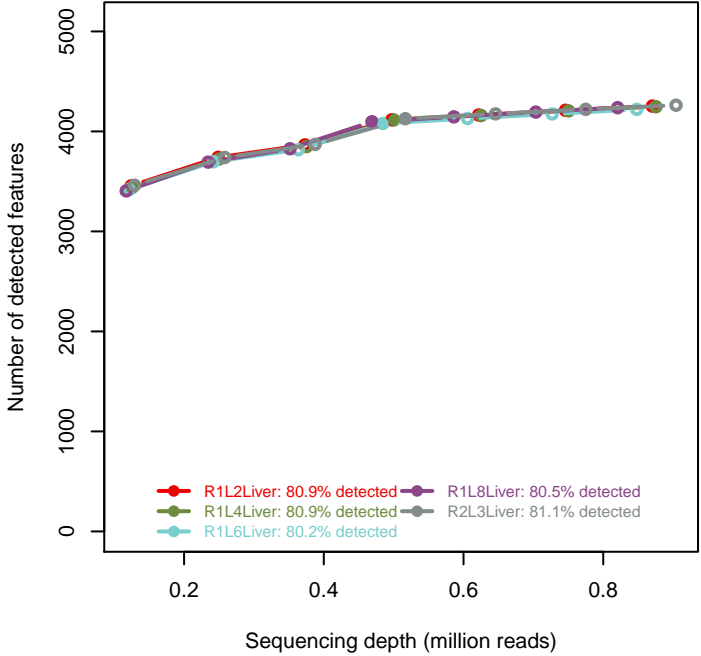


Sequencing depth & Expression quantification

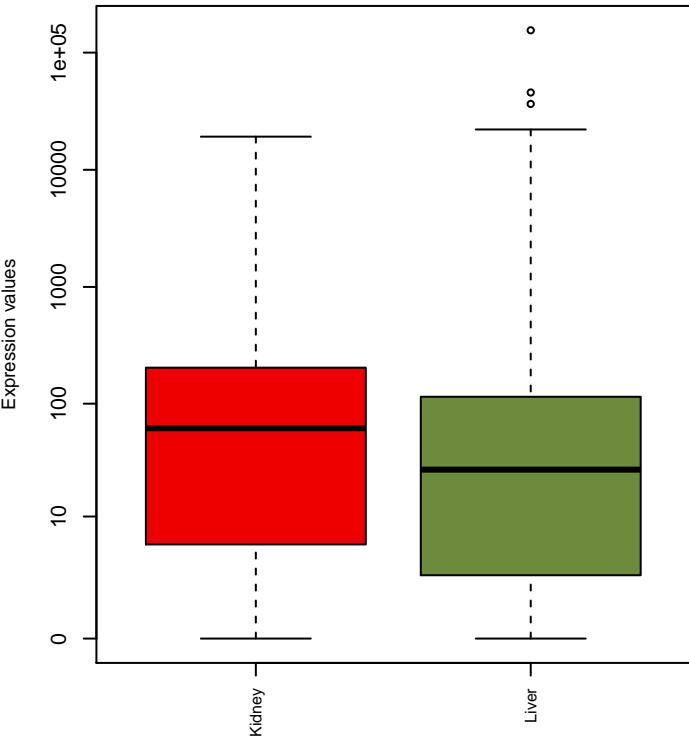
GLOBAL (5088)



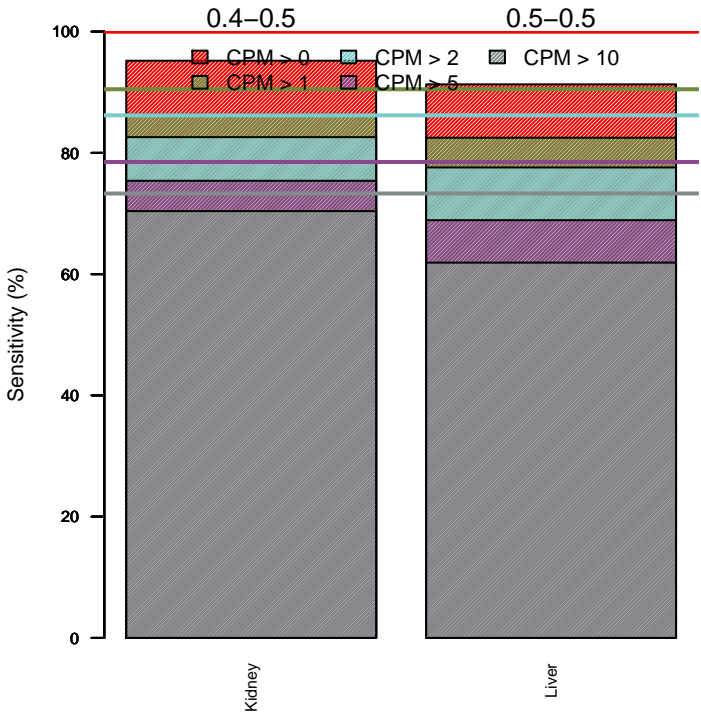
GLOBAL (5088)



GLOBAL (5088)



GLOBAL (5088)



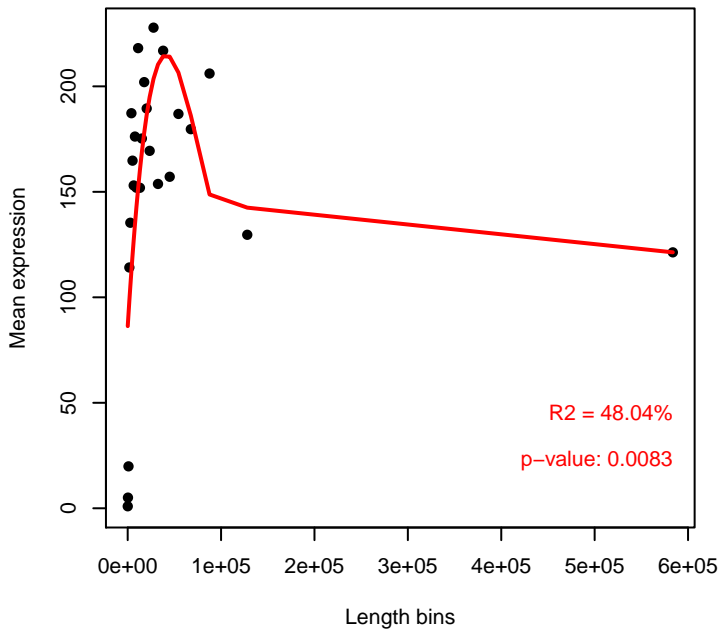
Sequencing bias detection

Diagnostic plot for feature length bias

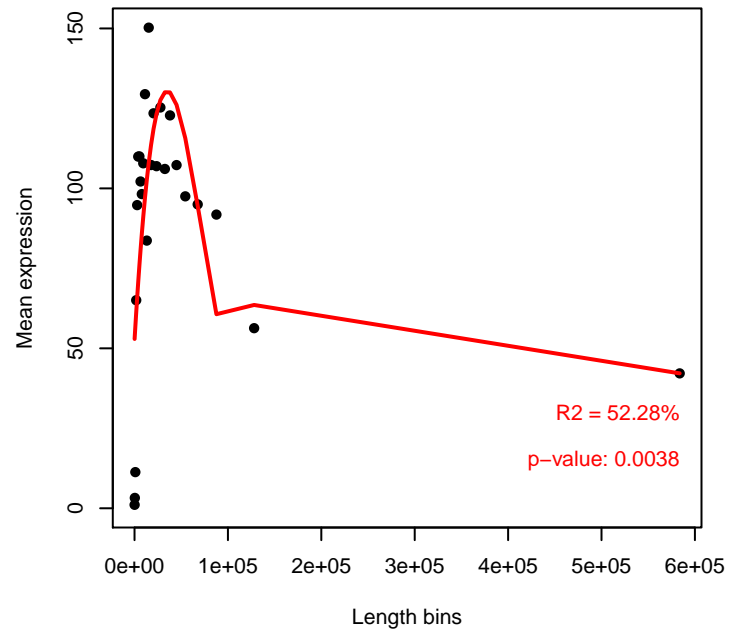
WARNING. At least one of the model p-values was lower than 0.05, but $R^2 < 70\%$ for at least one condition.

Normalization for correcting length bias could be advisable.
Please check in the plots below the strength of the relationship between length and expression.

Kidney



Liver

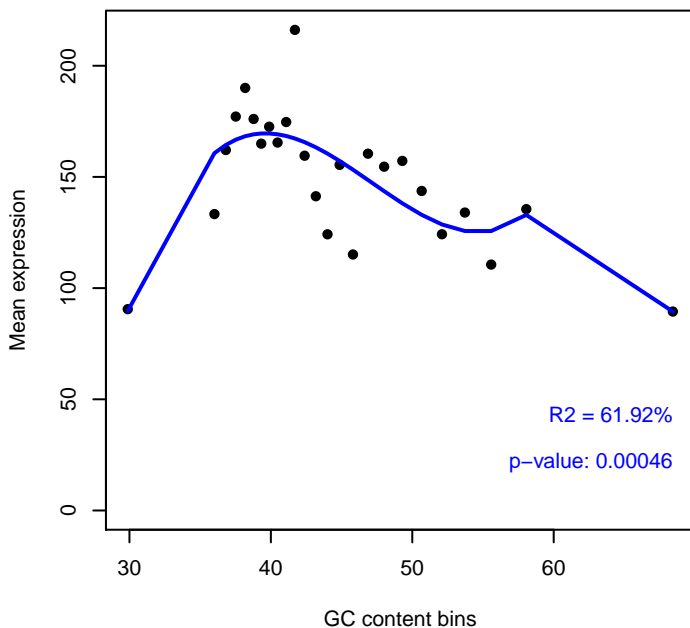


Diagnostic plot for GC content bias

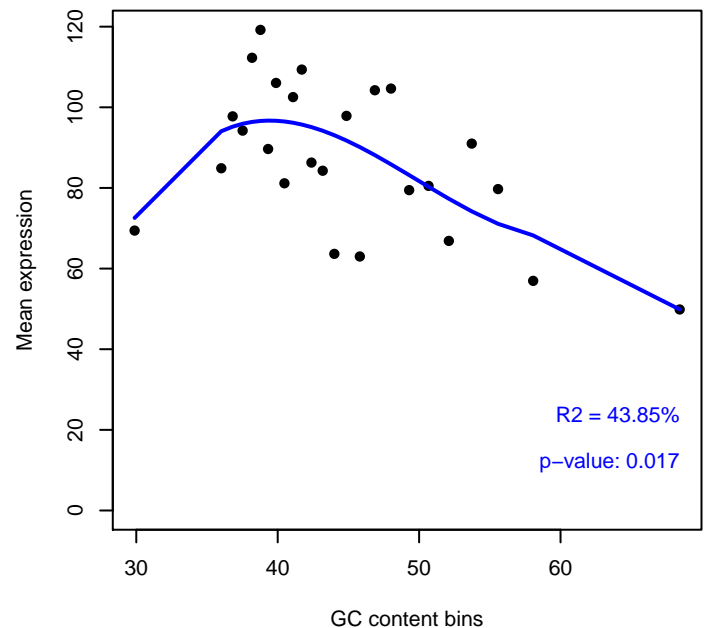
WARNING. At least one of the model p-values was lower than 0.05, but $R^2 < 70\%$ for at least one condition.

Normalization for correcting GC content bias could be advisable.
Please check in the plots below the strength of the relationship between GC content and expression.

Kidney



Liver

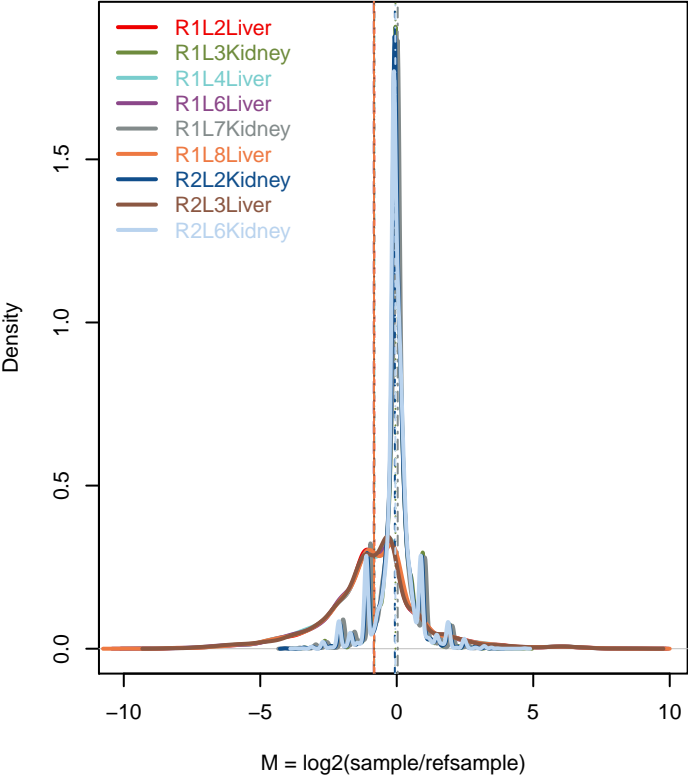


Diagnostic plot for differences in RNA composition

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

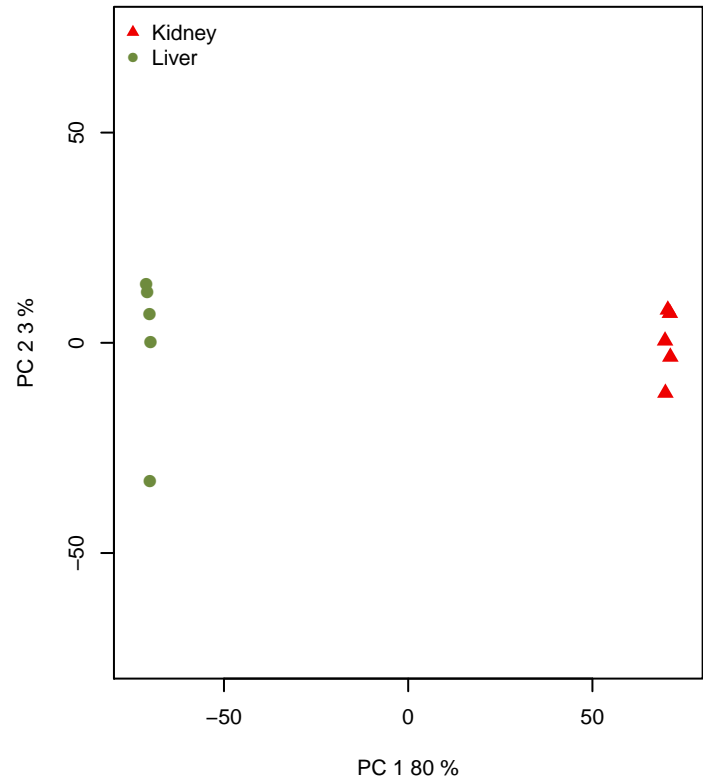
Sample	0.28%	99.72%	Diagnostic Test
R1L2Liver	-0.9043	-0.7642	FAILED
R1L3Kidney	-0.0472	-0.0472	FAILED
R1L4Liver	-0.8882	-0.7541	FAILED
R1L6Liver	-0.9162	-0.7556	FAILED
R1L7Kidney	0.0348	0.0348	FAILED
R1L8Liver	-0.9035	-0.7545	FAILED
R2L2Kidney	-0.085	-0.0469	FAILED
R2L3Liver	-0.8817	-0.7516	FAILED
R2L6Kidney	-0.0704	-0.0349	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

