

Quality Control of Expression Data

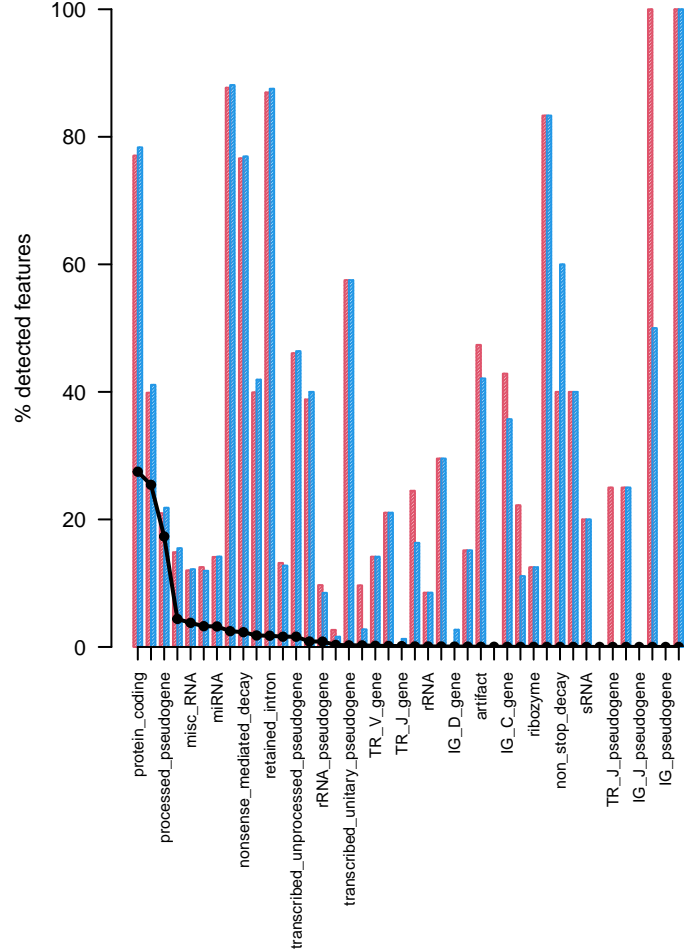
Generated by NOISeq on 28 Jan 2024, 15:24:54

Content

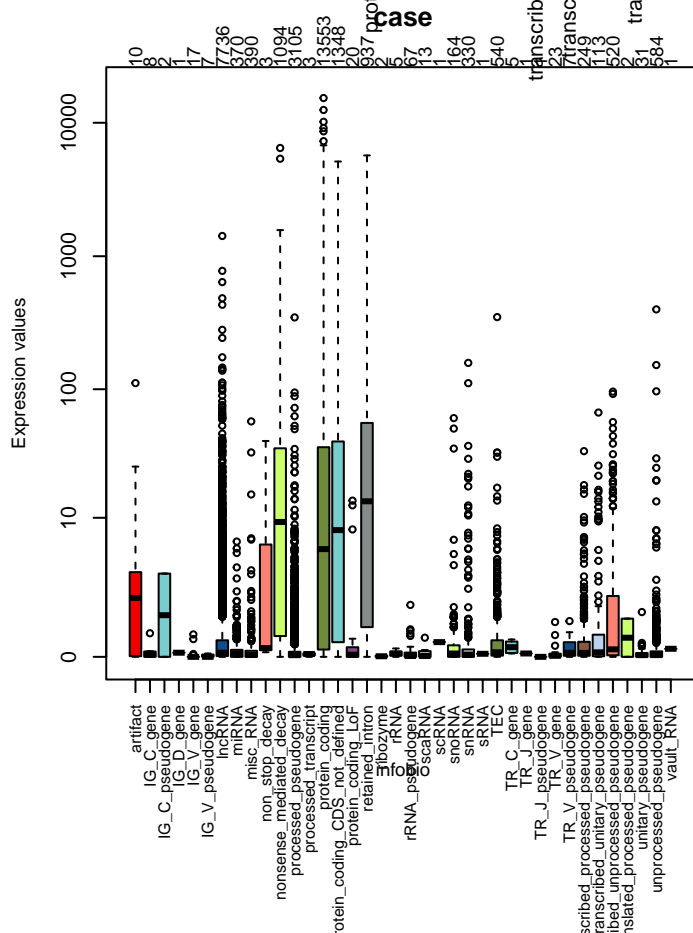
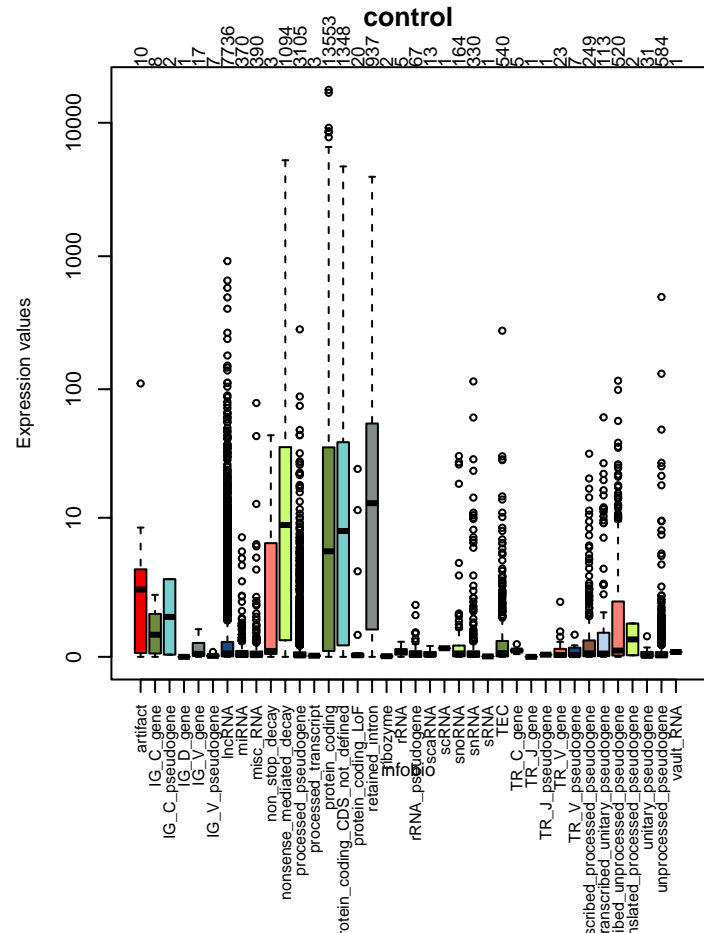
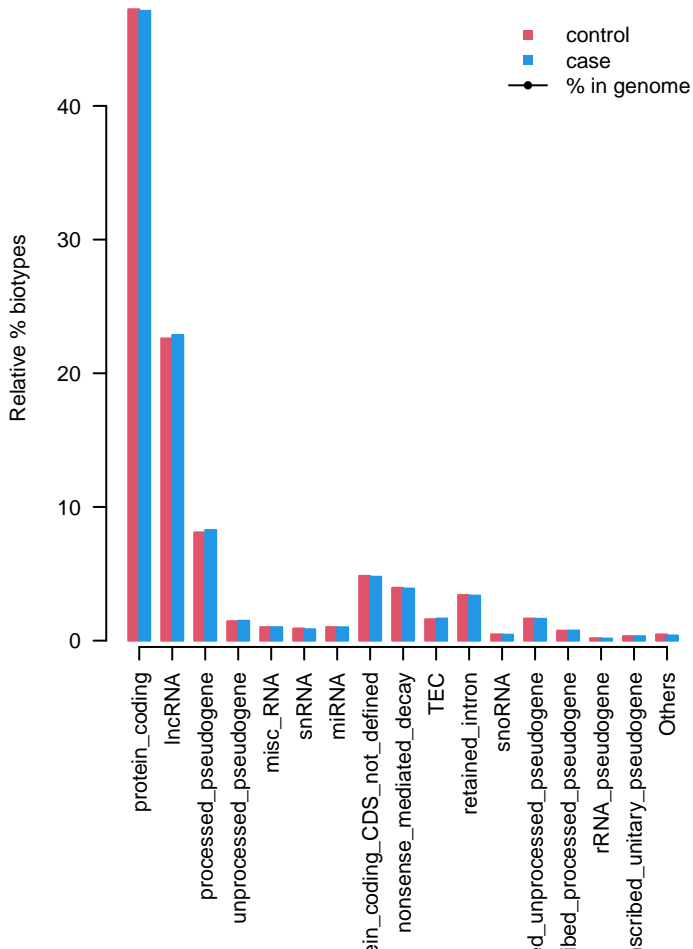
<i>Plot</i>	<i>Description</i>
Biotype detection	Biotype abundance in the genome with %genes detected (counts > 0) in the sample/condition. Biotype abundance within the sample/condition.
Biotype expression	Distribution of gene counts per million per biotype in sample/condition (only genes with counts > 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.
Exploratory PCA	Principal Component Analysis score plots for PC1 vs PC2, and PC1 vs PC3.

Biotype detection

Biotype detection over genome total

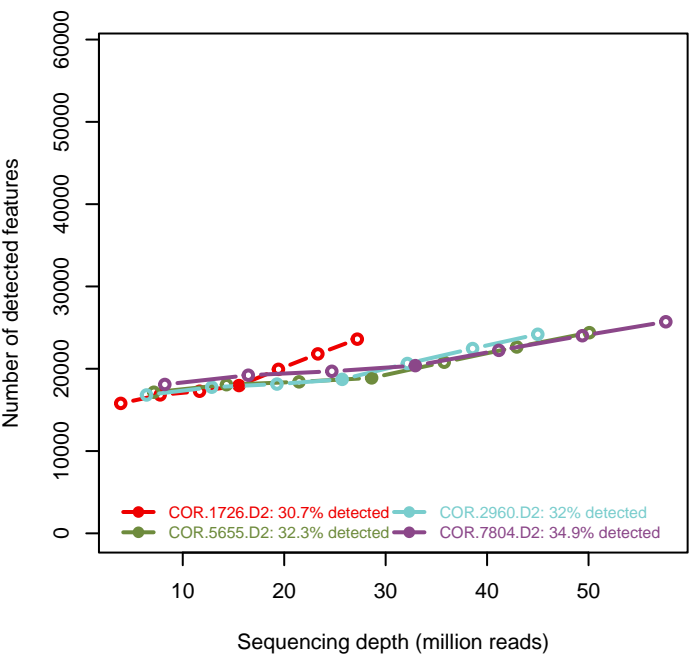


Relative biotype abundance in sample

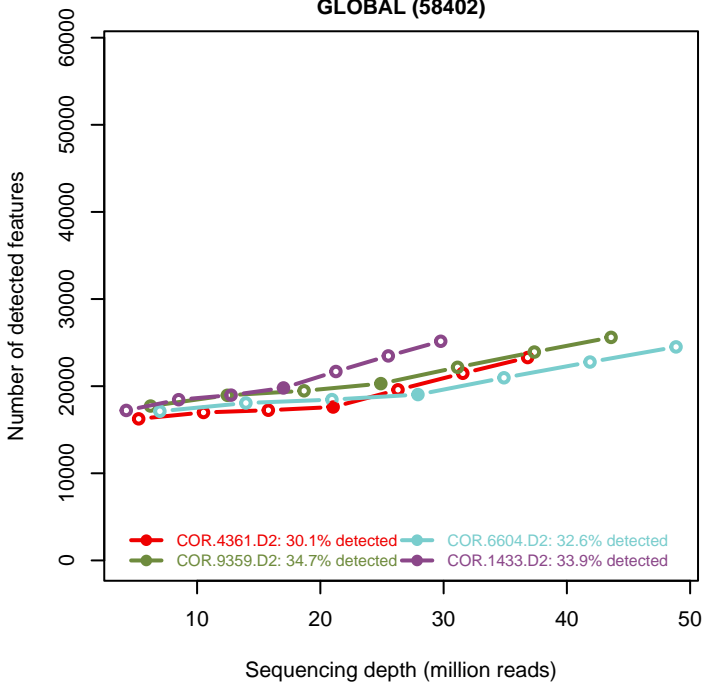


Sequencing depth & Expression quantification

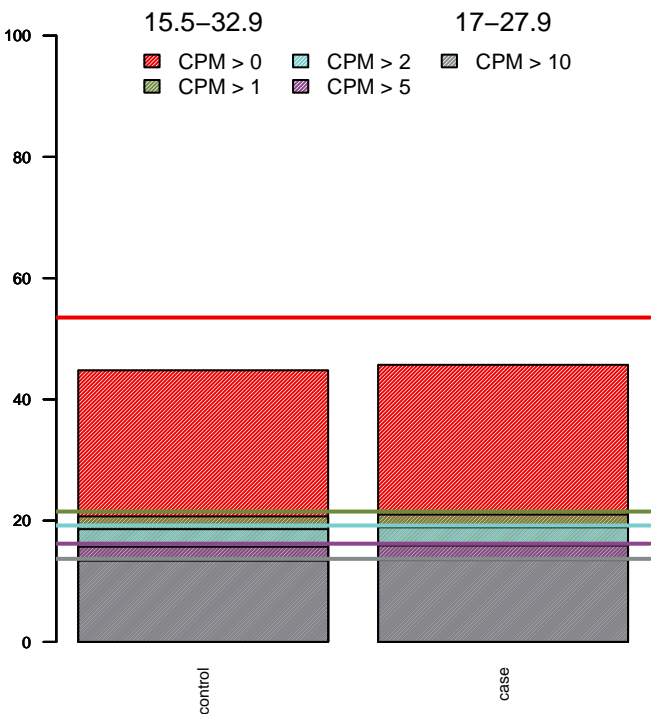
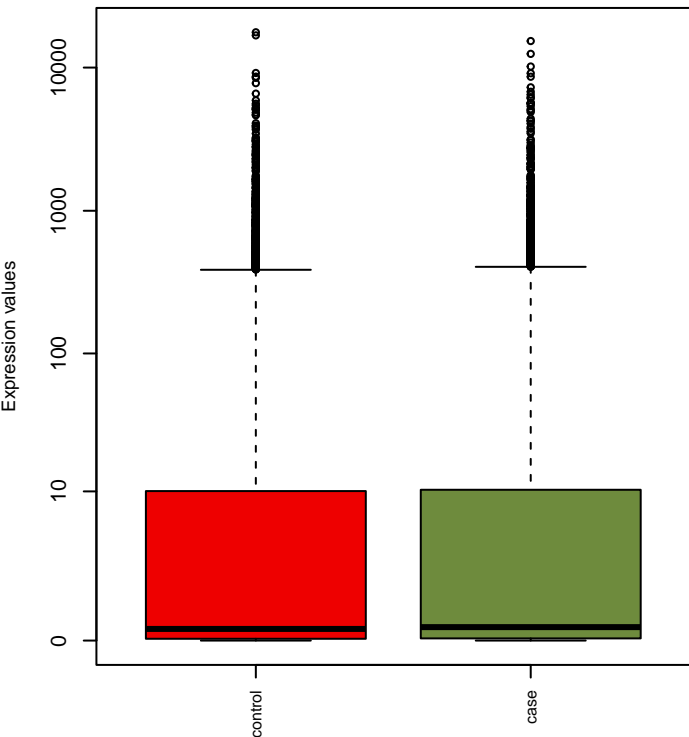
GLOBAL (58402)



GLOBAL (58402)



GLOBAL (31264)



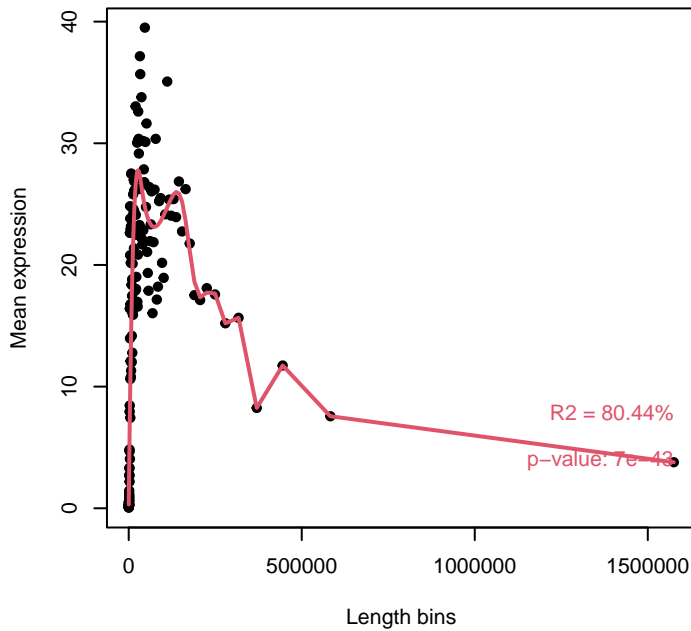
Sequencing bias detection

Diagnostic plot for feature length bias

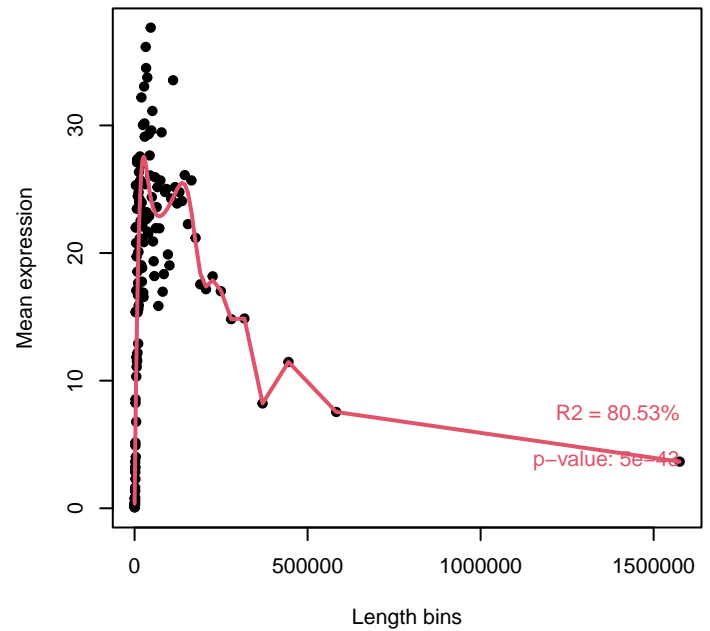
FAILED. At least one of the model p-values was lower than 0.05 and $R^2 > 70\%$.

Normalization for correcting length bias is recommended.

control



case



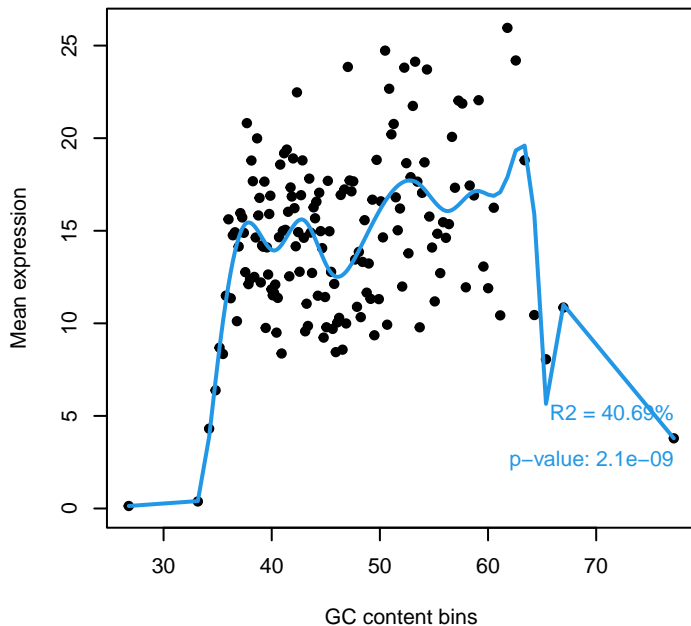
Diagnostic plot for GC content bias

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

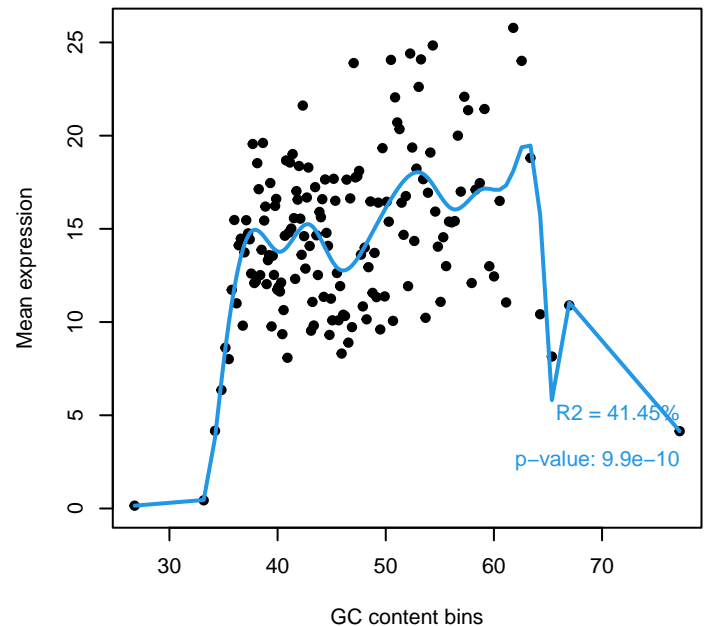
Normalization for correcting GC content bias could be advisable.

Please check in the plots below the strength of the relationship between GC content and expression.

control



case

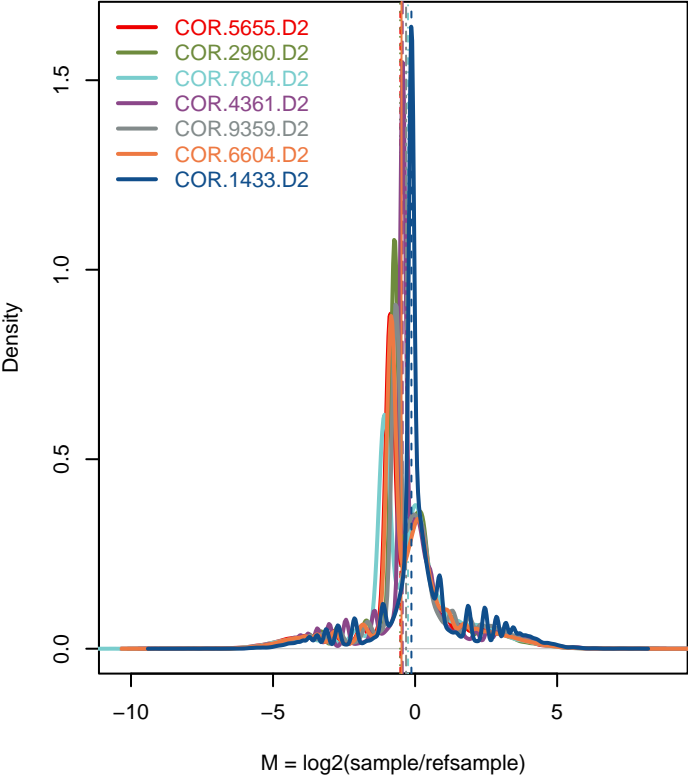


Diagnostic plot for differences in RNA composition

FAILED. There is a pair of samples with significantly different RNA composition

Normalization for correcting this bias is required.

Reference sample: COR.1726.D2



Confidence intervals for median of M values

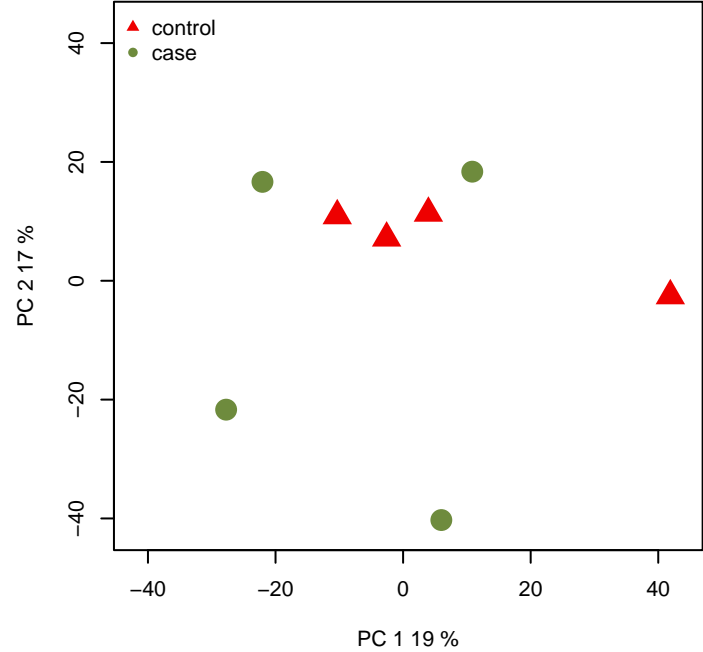
Sample	0.36%	99.64%	Diagnostic Test
COR.5655.D2	-0.5585	-0.4687	FAILED
COR.2960.D2	-0.5704	-0.477	FAILED
COR.7804.D2	-0.2763	-0.2203	FAILED
COR.4361.D2	-0.4365	-0.4365	FAILED
COR.9359.D2	-0.343	-0.2895	FAILED
COR.6604.D2	-0.5145	-0.4316	FAILED
COR.1433.D2	-0.1297	-0.1297	FAILED

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

