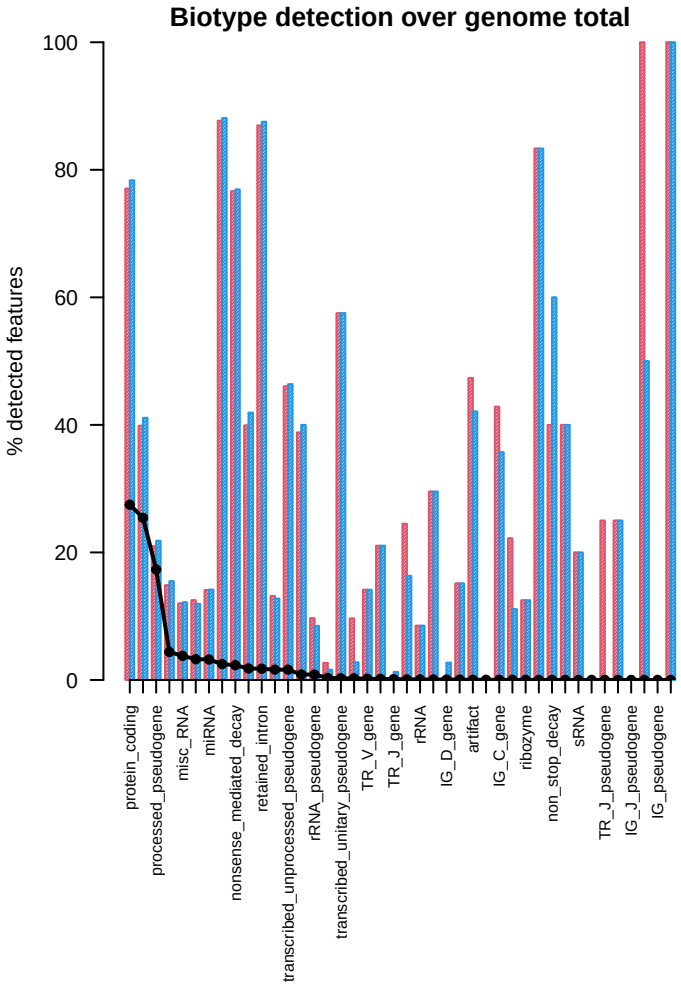
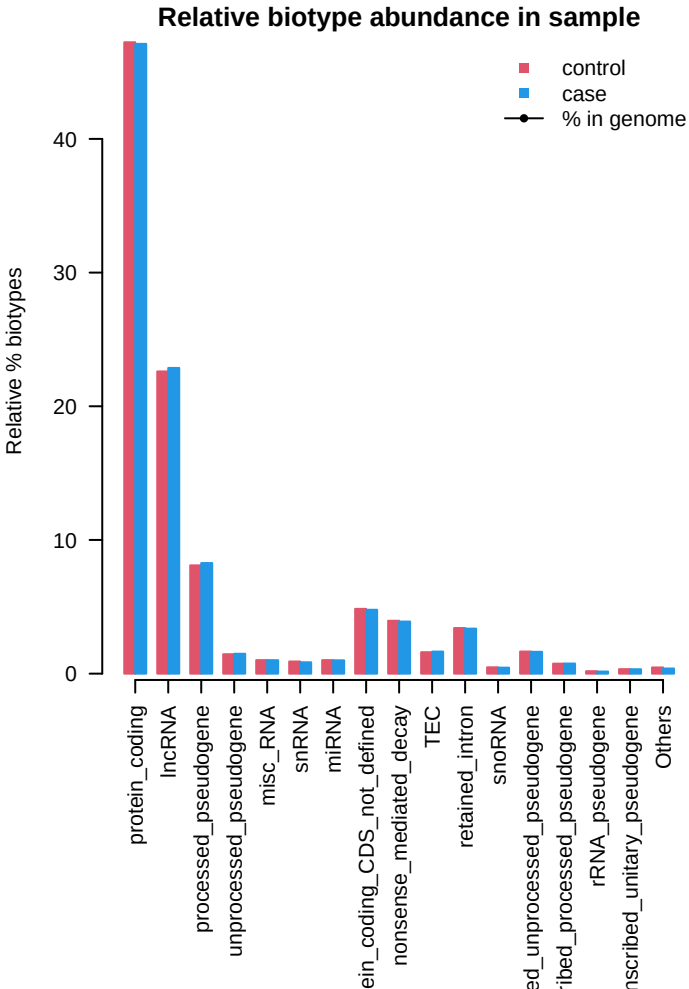
Quality Control of Expression Data

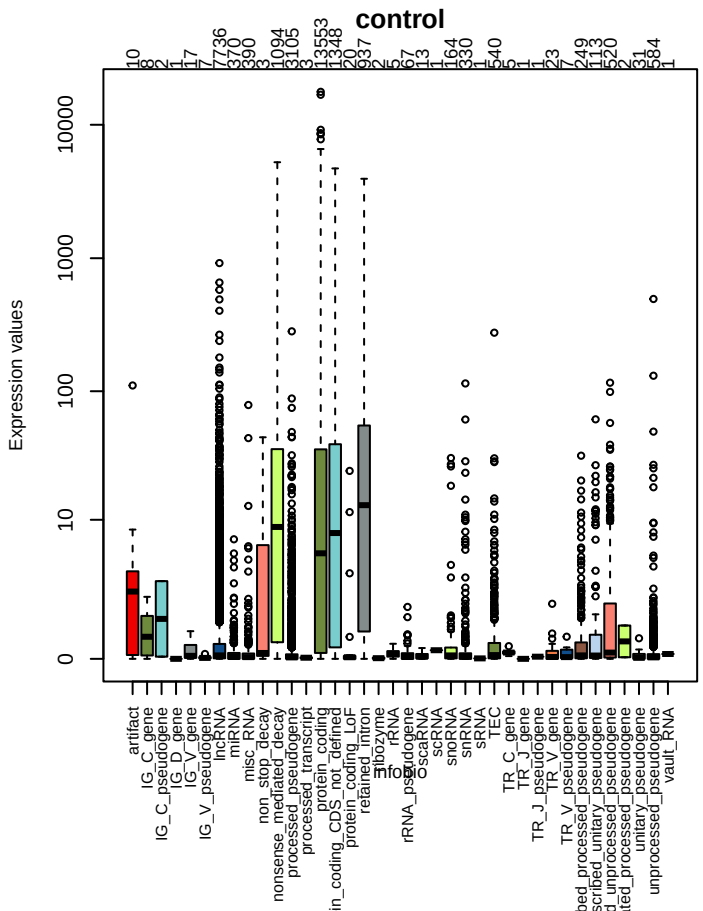
Generated by NOISeq on 28 Jan 2024, 15:25:29

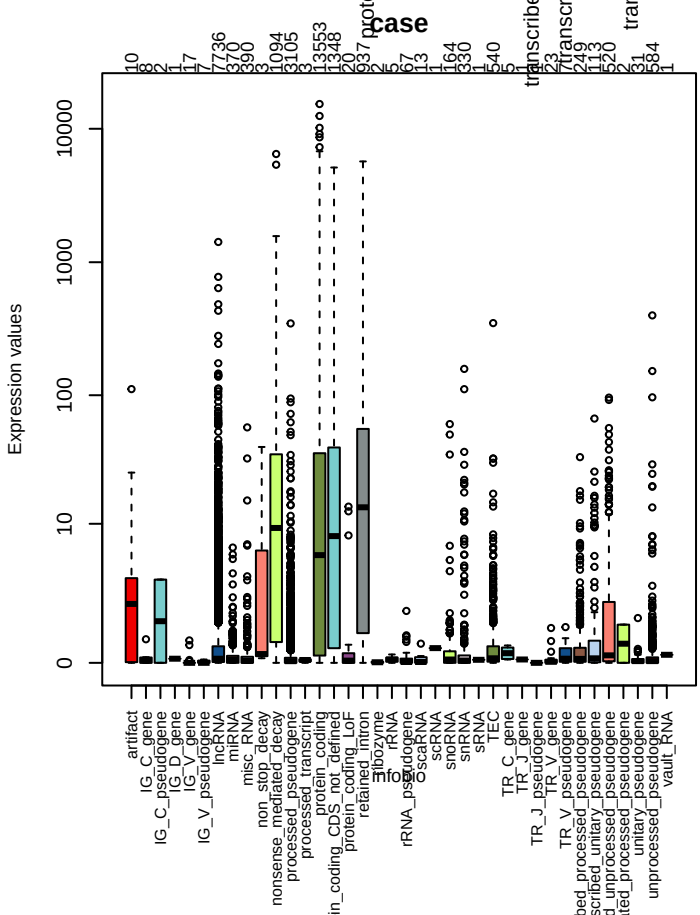
Content

Biotype detection

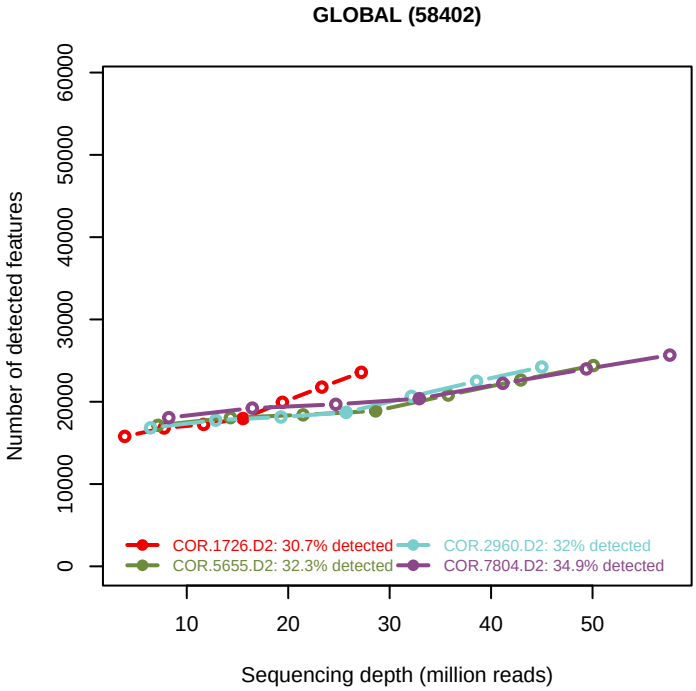


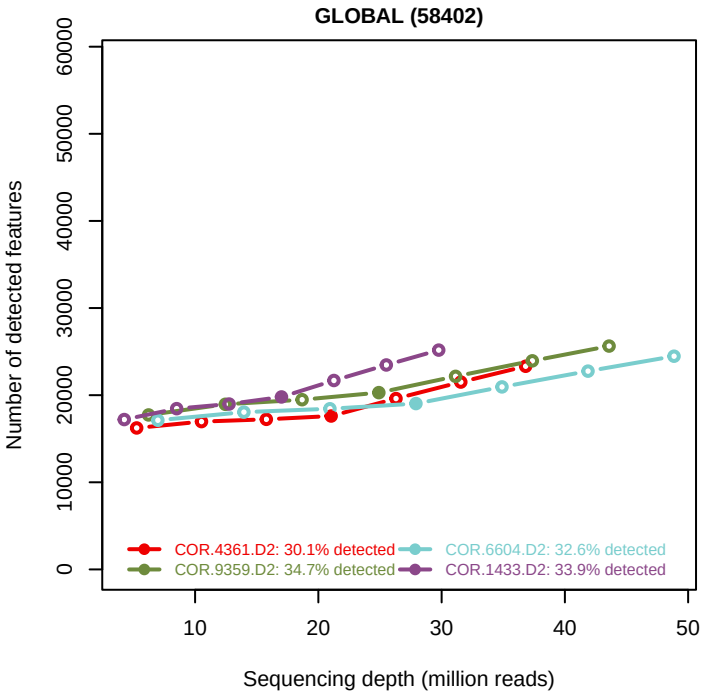


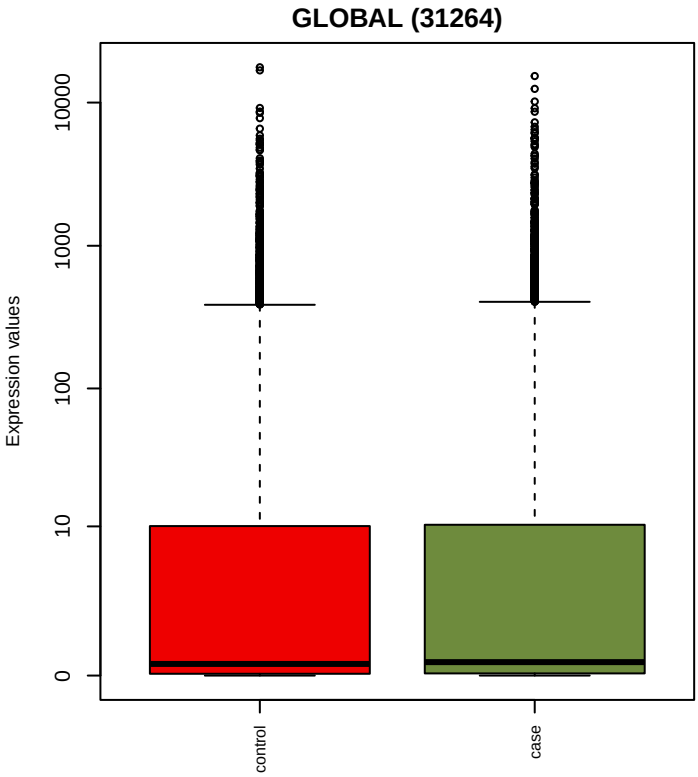


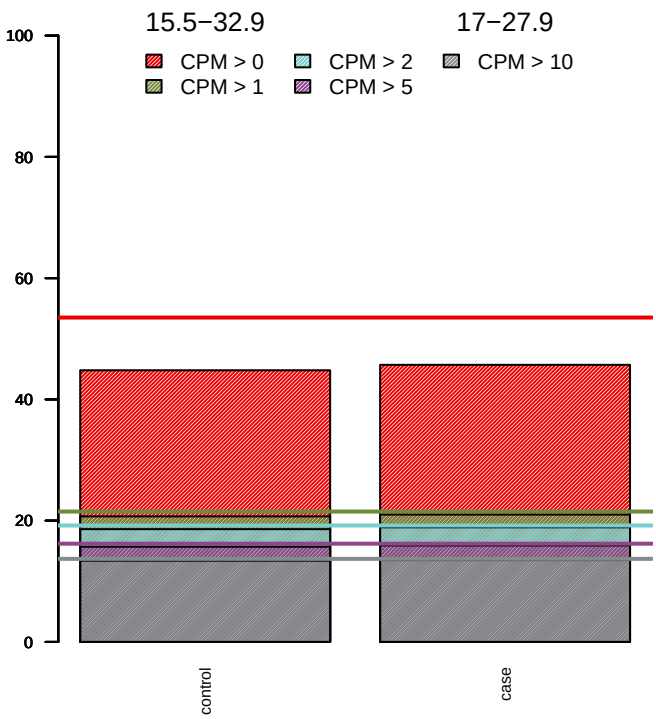


Sequencing depth & Expression quantification







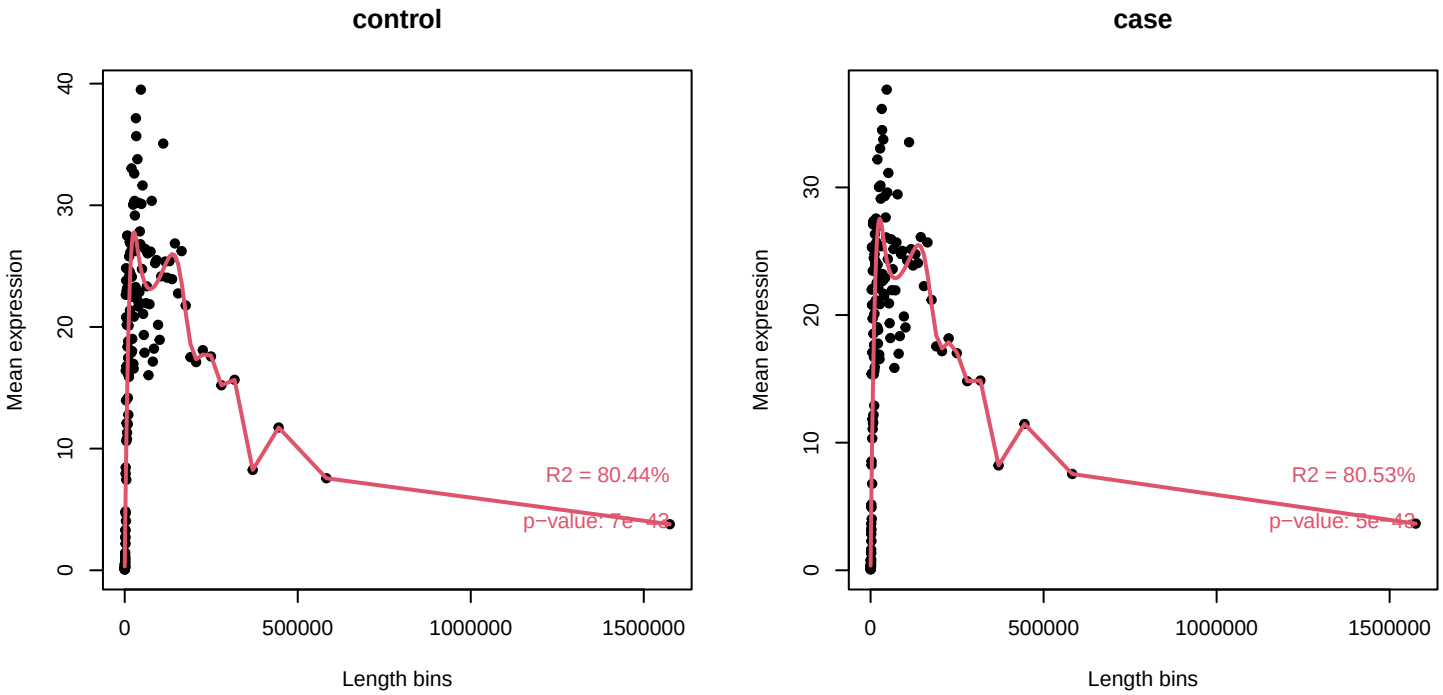


Sequencing bias detection

Diagnostic plot for feature length bias

FAILED. At least one of the model p−values was lower than 0.05 and R2 > 70%.

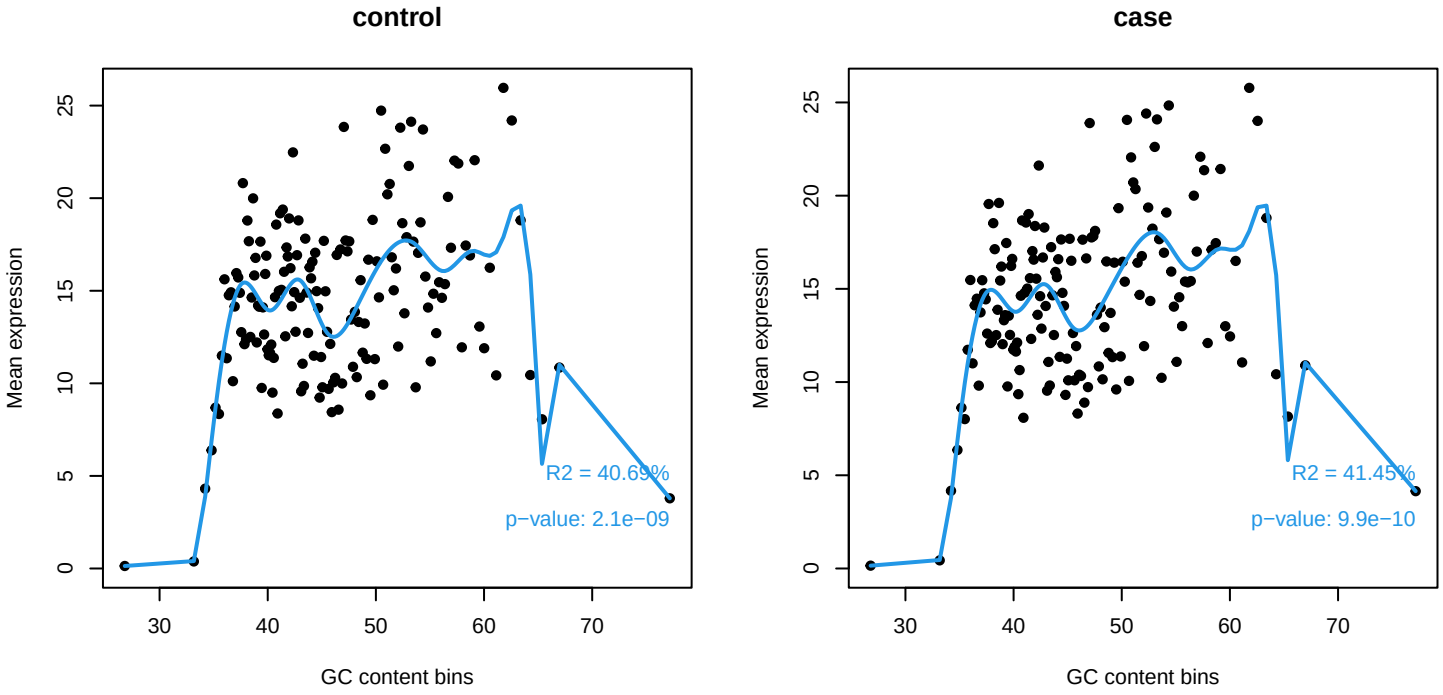
Normalization for correcting length bias is recommended.



Diagnostic plot for GC content bias

WARNING. At least one of the model p−values was lower than 0.05, but R2 < 70% for at least one condition.

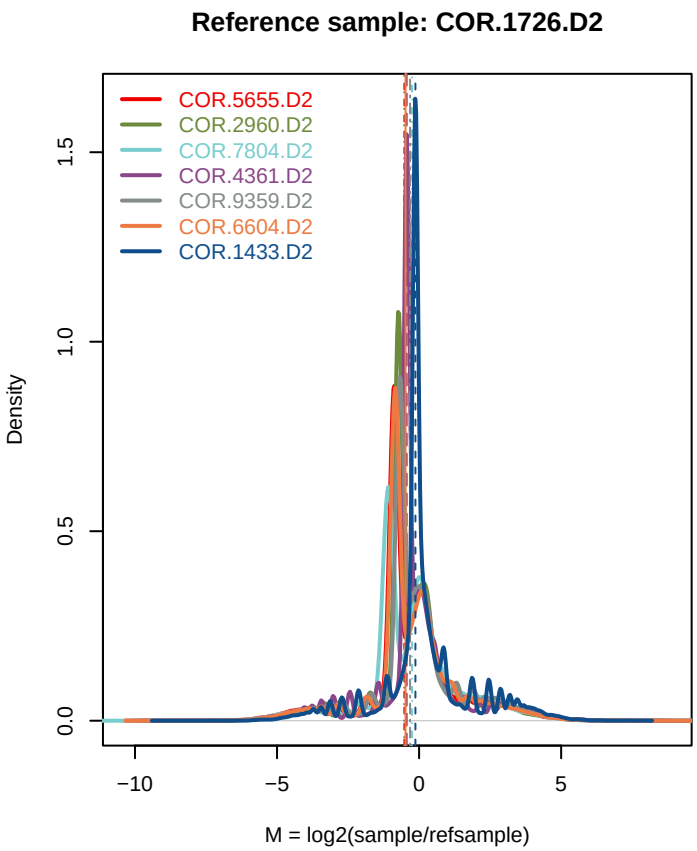
Normalization for correcting GC content bias could be advisable.
Plese check in the plots below the strength of the relationship between GC content and expression.



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.



Confidence intervals for median of M values

Sample	0.36%	99.64%	Diagnostic Test
COR.5655.D2	−0.5553	−0.4695	FAILED
COR.2960.D2	−0.574	−0.4728	FAILED
COR.7804.D2	−0.2766	−0.2192	FAILED
COR.4361.D2	−0.4365	−0.4365	FAILED
COR.9359.D2	−0.3413	−0.2914	FAILED
COR.6604.D2	−0.517	−0.4356	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.