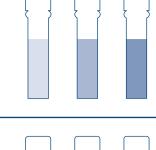


RNA quantification and analysis

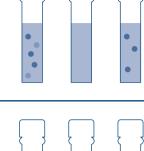
Tools and Methods

The four key parameters that characterize an RNA sample

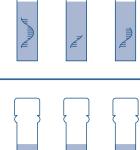
Size



Quantity
Is there enough RNA to assay?

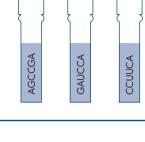


Purity Is the RNA free of contaminants?



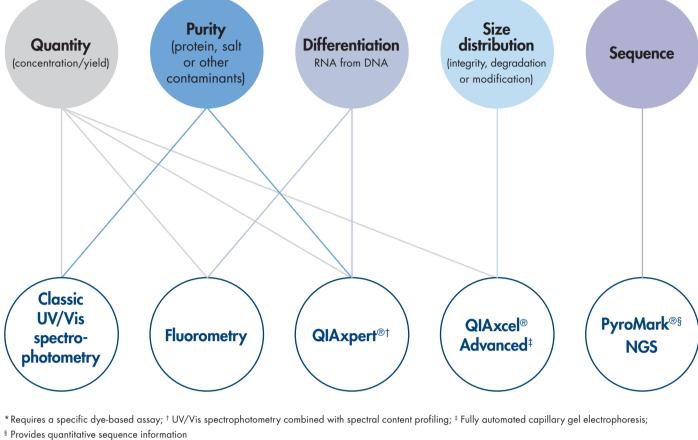
Is the RNA degraded?

Sequence



Is this the right sequence?

Choosing the right technology for RNA sample assessment



RNA concentration $(\mu g/ml) =$ 40 μ g/ml x A_{260} x dilution factor

RNA quantity and purity

Note: 1 OD260 Unit = 40 µg/ml for ssRNA, based

Concentration

on a standard 1 cm path length and neutral pH Total RNA yield (μg) = concentration x volume of sample (ml)

QIAGEN solution for nucleic acid quantification

Lower value indicates protein contaminants.

Pure RNA has an A_{260}/A_{280} ratio of 1.8–2.0.

Purity

Pure RNA has an A_{260}/A_{230} ratio of >1.8. Lower value indicates salt and other contaminants.

RNA purity

and possible sample contaminants. Pure sample of RNA

Up to 16 samples in less than 2 minutes 6.01 2 µl sample

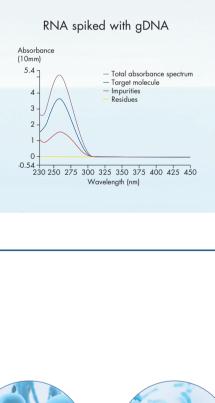
consumption

Rapid analyses via touchscreen

The QIAxpert spectrophotometer provides a detailed insight into your sample's quantity and purity by analyzing your nucleic acid with spectral content profiling. This proprietary analysis feature lets you differentiate between DNA, RNA







Human

Size (kb)

1.9

5.0

2.0

1.0

rRNA

285

Plant

Size (kb)

1.9

3.7

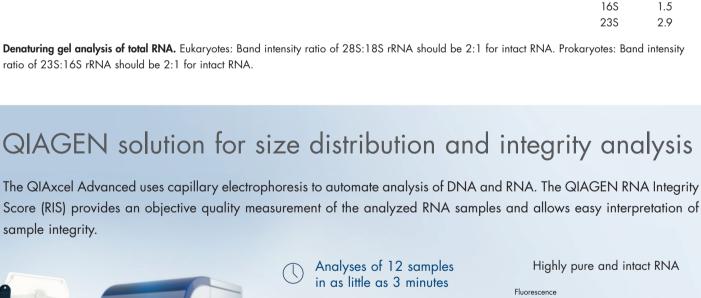
rRNA

25S

0.601 230 250 275 300 325 350 375 400 425 450

Bacteria Yeast Mouse **rRNA** Size (kb) Size (kb) Size (kb) **rRNA** rRNA

2.0 **18**S **18**S 235 2.9 26S 3.8 285



Unattended analysis of up to 96 samples

Resolution down to 3-5 bp

Library

construction &

for fragments <500 bp

Reliable detection with sensitivity down to 0.1 ng/µl

1.9

4.7

amplification

Pyrosequencing is a unique detection technology that enables rapid and accurate quantification of sequence variation.

Process 24–96 samples

Various analysis modes

RNA sequencing (RNA-seq) is a method of investigating the transcriptome of an organism using next-generation deepsequencing techniques. The RNA content of a sample is directly sequenced after appropriate library construction, providing an in-depth analysis of the transcriptome. Transcriptomic analyses may be validated using an independent technique, for example, quantitative PCR (qPCR).

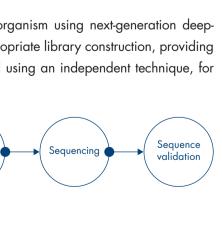
RNA sequence

cDNA

synthesis

RNA

sample



Time (min)

guantification

Adapter

ligation

The PyroMark systems are widely used for quality control and verification and validation of NGS results.

CIACEN

PyroMark Q48 Autopre

QIAGEN solution for sequence verification



Find out more about RNA sample analysis at www.qiagen.com/RNASampleQC.

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