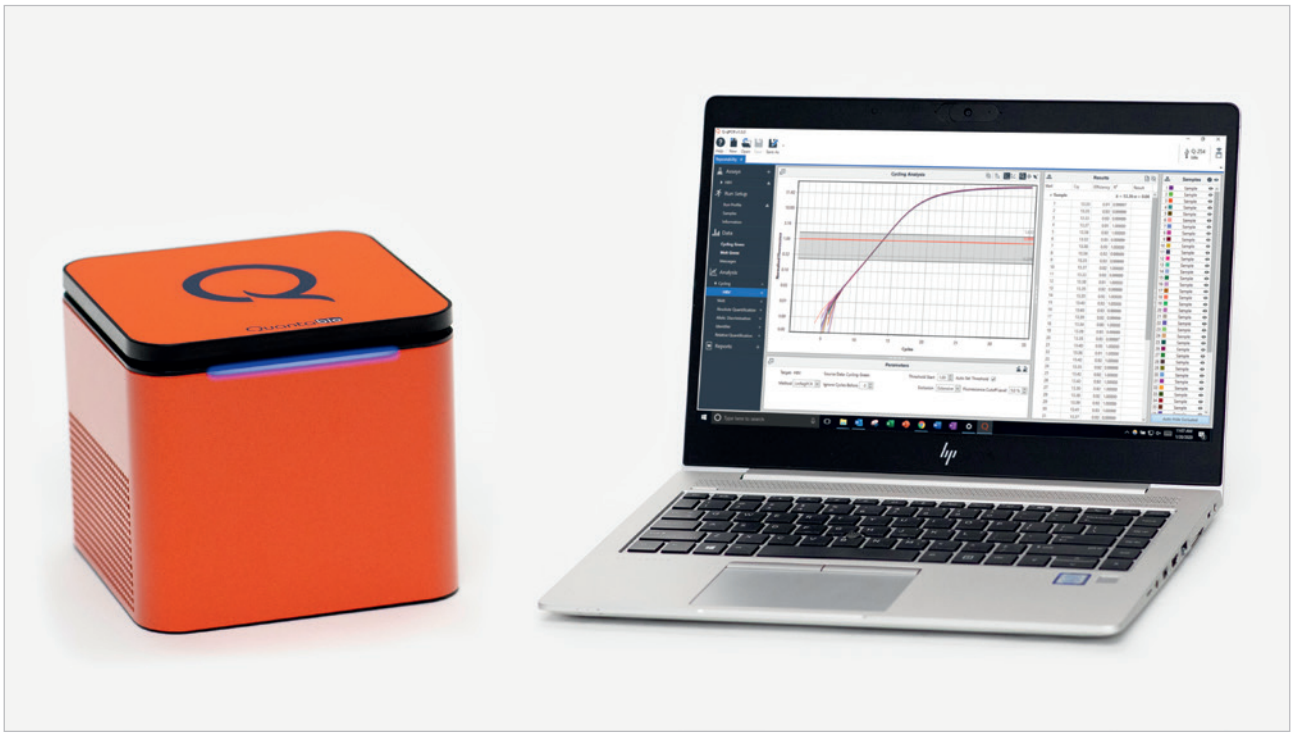
Q-qPCR Software

Simple, powerful qPCR analysis



DESCRIPTION:

Q-qPCR is the next generation analysis software for the Q cycler packed with intelligent features. The intuitive interface and advanced automated statistical analysis are designed to make life easier while meeting MIQE specifications. Results with detailed analysis are available as soon as your run has completed. With unlimited user licenses, you can use the software on any PC anywhere, anytime.

Software Highlights

- **Fast and Powerful Analysis** – advanced algorithms support a variety of methods
- **Project Feature** – seamlessly combines multiple runs into one analysis
- **Intuitive Sample Editor** – allows samples to be annotated before, during or after a run
- **Smart Sample Selector** – makes it easier to view or hide samples from analysis
- **Freedom and Flexibility** – analyzes results on any PC with unlimited licenses
- **Simple Analysis** – automated calculation and results reporting with a few mouse clicks
- **Quick Results** – copies or exports publication-ready figures in seconds

Project

Take advantage of Q's superior temperature uniformity and consistent run-to-run performance to improve the throughput of your data analysis. The project feature enables multiple runs from multiple instruments to be combined into one analysis. Up to 10 runs can be combined per project allowing up to 480 samples to be analyzed at once.

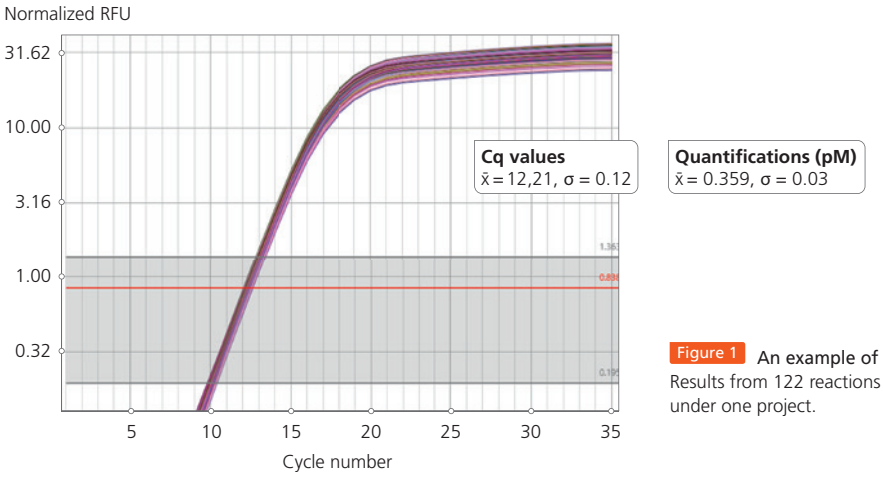


Figure 1 **An example of high repeatability of data generated on the Q.** Results from 122 reactions across multiple runs were combined and analyzed under one project.

Absolute Quantification

Absolute Quantification allows you to quantify the unknown concentration of a sample using a standard curve generated with samples of a known quantity. The concentration of each unknown sample is automatically calculated and reported in the Sample Results Table. The standard curve generated from a previous experiment can be imported and used as part of the absolution quantification analysis.

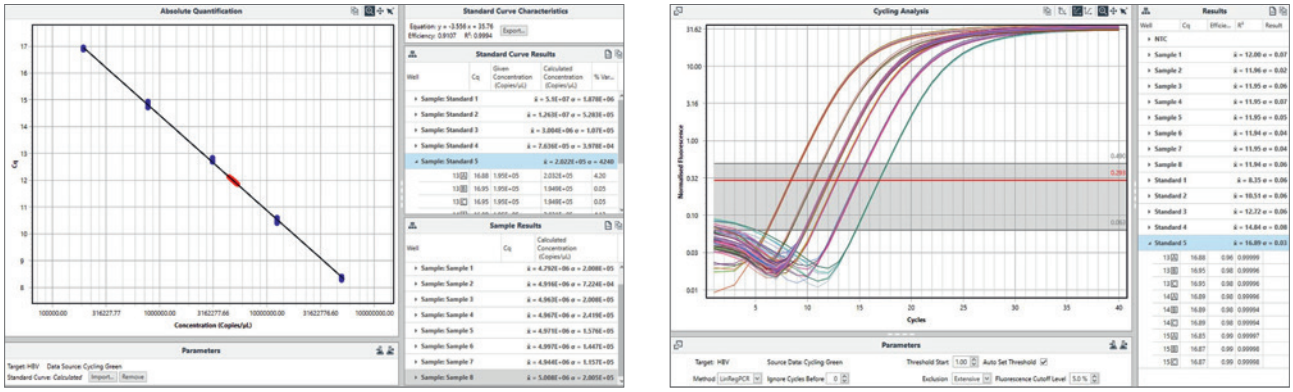


Figure 2 **Standard curve and cycling analysis of the Absolute Quantification module.** In this example, a five-point (blue dot) standard curve of 91% efficiency is used to determine viral loads in patients. Unknown samples are represented as red dots. The Cycling Analysis Results Table displays the mean and standard deviation of the Cq values for sample and standard replicates.

Relative Quantification

The Q-qPCR software uses up-to-date statistical methods to analyze differences in gene expression in a given sample group relative to a control group. Three different methods are available for relative quantification analysis: REST (Relative Expression Software Tool), ΔΔCt and ΔCt. All the necessary calculation and statistics are carried out effortlessly within the software. Data is reported both numerically and graphically.

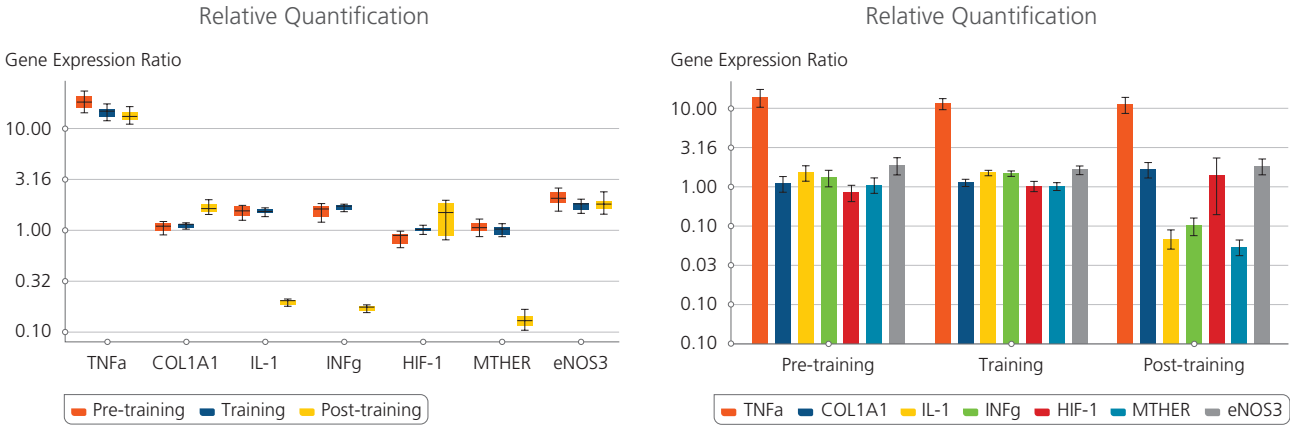


Figure 3 **Gene expression ratios are graphed as Box and Whisker plots or Bar charts depending on the method chosen.** Box and Whisker plots are only used for the REST method while Bar charts are used for the ΔΔCt and ΔCt methods. The graphs can be displayed with either the genes or treatment groups being labelled on the X-axis.

Melt Analysis

Melt analysis can be used as a quality control for cycling analysis by checking for non-specific products or amplicon contamination. It can also be used to genotype samples based on the differences in melt temperature between alleles. Chemistries compatible for melt analysis include intercalating dyes, FRET dual hybridization probes, Plexor and molecular beacons. Melt peaks can be inverted to accommodate the different chemistry types.

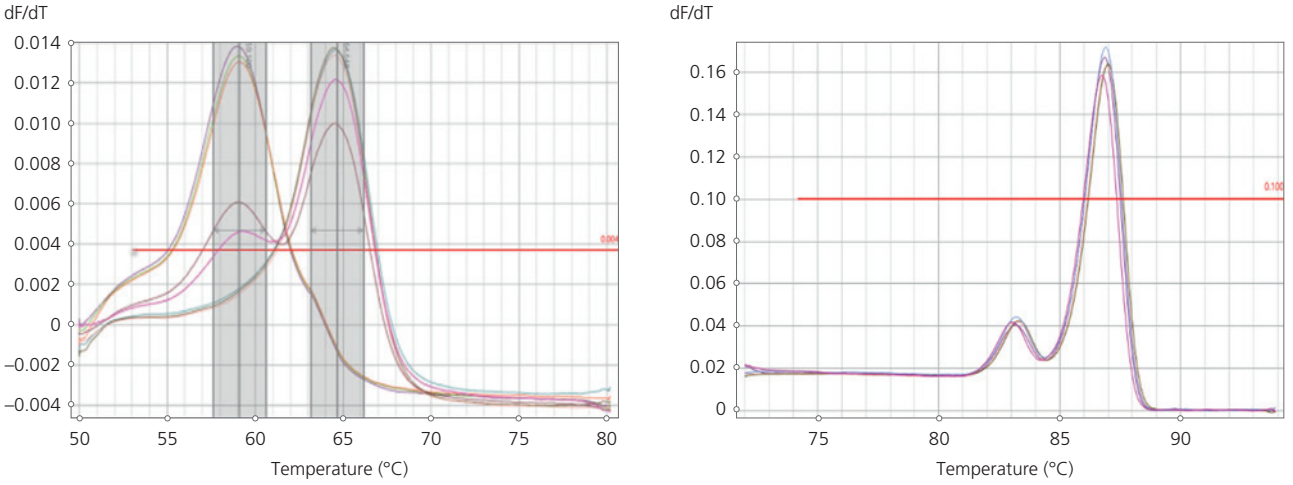


Figure 4 **The melt analysis displays first derivative curves where the peaks represent the melt temperature (Tm).** Samples can be classified into known genotypes by using the specific Tm values associated with each genotype. Melt analysis can also be used to identify non-specific PCR product as a quality control for cycling conditions.

High Resolution Melting (HRM)

The optional HRM analysis module characterizes DNA samples according to their dissociation behavior as they transition from double stranded DNA to single stranded DNA with increasing temperature. By using normalized melt curves, you can identify DNA sequence variants, including single base changes, insertion-deletions and base pair substitutions. A software key (sold separately) is required to activate the HRM analysis module.

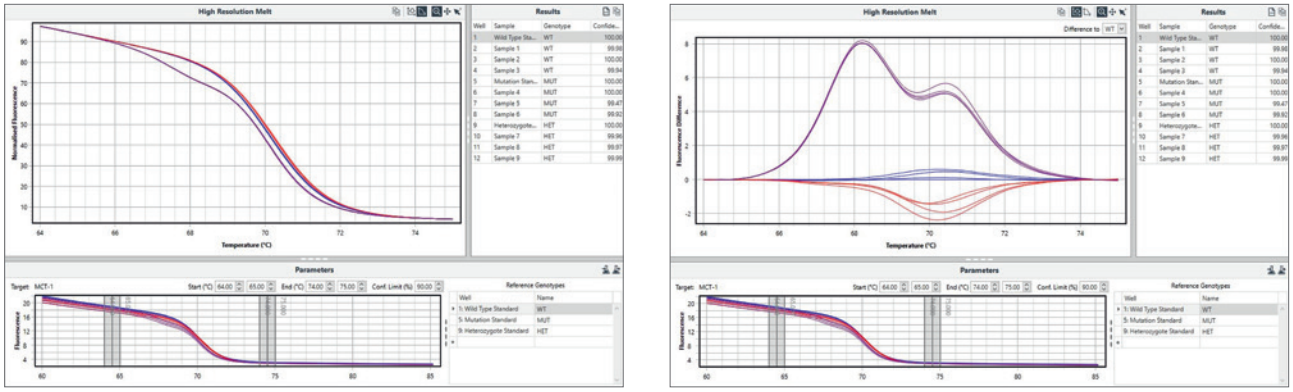


Figure 5 **Normalized melt curves and differences plots of the HRM analysis module.** Results are reported as a genotype along with a confidence percentage. Even the difficult A/T Class IV SNPs can be detected as shown by the example: A base allele (red), T base allele (blue), and the heterozygote (purple).