

## features

qbase<sup>PLUS</sup>



Easy . Fast . Reliable .

## Quantification models

- delta-delta-Cq (no efficiency correction, normalization with a single reference gene)
- Pfaffl model (efficiency correction, normalization with a single reference gene)
- qbase model (efficiency correction & multi-gene normalization)

## Normalization

- no normalization
- one reference gene
- multiple reference genes
- global mean [premium license only]
- global mean on common targets [premium license only]
- custom value
- inter-run calibration on normalized relative quantities (highest flexibility, fewest calculations)

## Efficiency correction

- one amplification efficiency for all assays in the experiment
- assay specific amplification efficiencies
- assay and run specific amplification efficiencies
  
- manually entered efficiency values or calculated from standard dilution series
- calculation and propagation of the error on the estimated amplification efficiency (e.g.  $95.4\% \pm 2.3\%$ )

## Error propagation

Uncertainties on the following levels are measured and propagated

- PCR replicates
- amplification efficiency values
- normalization factors
- inter-run calibration factors

## Data import

- specific importers for over 25 real-time PCR instruments
- batch import of multiple run files
- support for ABI relative quantification studies with data from multiple runs
- generic formats (simple & qbase)
- RDML compatibility

## Data management

- store data in hierarchical organization of projects and experiments
- unlimited number of experiments and runs per experiment
- experiments store raw Cq values, annotations and settings
- exchange of analyzed projects and experiments with colleagues
- export of publication-ready RDML files

## MIQE compliancy

- sample information
- assay information
- RDML compatibility

## The qbase<sup>PLUS</sup> feeling

- easy to use, fast and reliable
- instant calculations (no start or calculate button)
- from Cq tables to results in 24 seconds
- advanced window management
- alert bar with warnings and tips

## Quality control

- detect and exclude bad data to improve result quality
- replicate variability
- negative controls
- positive controls
- reference gene stability (geNorm M value & coefficient of variation on the normalized relative quantities of reference genes)
- normalization factor variability
- automatic data-exclusion for large experiments

## Run annotation

- taken over from instrument files
- custom editing of run (plate) layout in visual run editor
- import of sample and target name and property list
- exchange of run layouts (well annotation) between runs

## Analysis modules

- geNorm<sup>PLUS</sup>
- advanced copy number analysis [premium license only]
- statistics [premium license only]

## Graphs

- single target bar chart (with sample grouping based on sample properties)
- correlation plot
- multi-target bar chart
- normalization factor bar chart
- standard curves
- geNorm<sup>PLUS</sup> graphs
- copy number bar chart

## Platform independent

- Windows, Mac and Linux
- 32-bit and 64-bit

## Trust

- based on peer-reviewed and proven geNorm<sup>TM</sup> and qbase<sup>TM</sup> technology
- developed by Jo Vandesompele and Jan Hellemans with a +10 year track record on qPCR innovations