

qPCR Data used for comparison of curve analysis methods.

This Zip archive contains the raw fluorescence data, and the analysis results, as described in the paper of Ruijter et al, Methods 2012 (<http://dx.doi.org/10.1016/j.ymeth.2012.08.011>).

The following data can be found in this collection:

Main Folder: Datasets

Subfolder: Biomarker\_set

This folder contains 4 Excel files, each with 16 sheets. These sheets contain the raw fluorescence data of 16 genes (row per gene, column per cycle format).

These data originally come from the Vermeulen et al (Lancet Oncology 2009) paper.

File: Technical\_datasets.xls

This Excel file contains 4 sheets:

annotation

94\_replicates\_4\_dilutions\_set

380\_replicates-set

competimer\_set

The description of the latter 3 sheets can be found in the annotation sheet

Main Folder: Analysis results

Subfolder: biomarker\_set\_results

This folder contains 10 Excel files, each with the analysis results obtained with each of the curve analysis methods. The information per analysis method may differ. Each Excel file starts with a read\_me sheet describing the handling of the results file and the definition of missing values.

Subfolder: technical\_sets\_results

This folder contains 3 Excel files: one per technical data set. Each of the files contains a results sheet per curve analysis method and a read\_me sheet describing data handling and missing value definitions.

Main Folder: analysis\_template

This folder contains an Excel file with 6 sheets:

readme:

This sheet explain the calculations done in the next 3 sheets

bias\_and\_deviat\_from\_regres

added\_or\_reduced\_variation

detectable\_difference

These sheets show the calculation of the performance parameters based on dilution series as illustrated in Fig 1 of the Methods paper.

Target\_Quantities: F0 values obtained by the different curve analysis methods

Cq\_values: Cq values determined by the curve analysis methods

Jan Ruijter, 19-09-2012