

Import file guidelines - 7900

1 - General information

Import files should contain a list of Quantification Cycle (**Cq**) values. Depending on the instrument software that generates the data, Cq values may have alternative names such as Ct, Cp, or TOP. Cq is the official abbreviation in the Real-time PCR Data Markup Language (more info on <http://www.rdml.org>).

The qbase^{PLUS} calculation engine is based on Cq values. Sigmoidal amplification curve data are not supported.

Import file formats can be either a tab delimited text file (.txt), a comma or semicolon separated value file (.csv) or a Microsoft Excel file (.xls). Microsoft Excel 2007 (.xlsx), OpenOffice.org Calc (.ods) and proprietary or binary instrument files are not supported.

In qbase^{PLUS}, there are character restrictions on sample, target and run names. Only the following characters are allowed: all alphanumerical characters (0-9, a-z, A-Z), space, _, -, \$, #, :, ^, . and the greek letter mu (μ). **Illegal characters** such as brackets and slashes should be removed or replaced.

2 - 7900

These guidelines are based on a specific instrument - software (version) combination. The described procedures may not be suitable for other software versions (e.g. new upgrades) but the described file format allows you to verify compliance of your data files with qbase^{PLUS}. See below for a list of supported instruments and software (versions).

Instruments: Applied Biosystems - 7900HT

Software: Sequence Detection Systems (SDS) 2.3

3 - Generating 7900 export files

Step 1: Open your data file in the SDS software and analyze it according to your needs.

Step 2: Click *File - Export* and export Results Table as tab delimited text (*.txt) file (Figure 1).

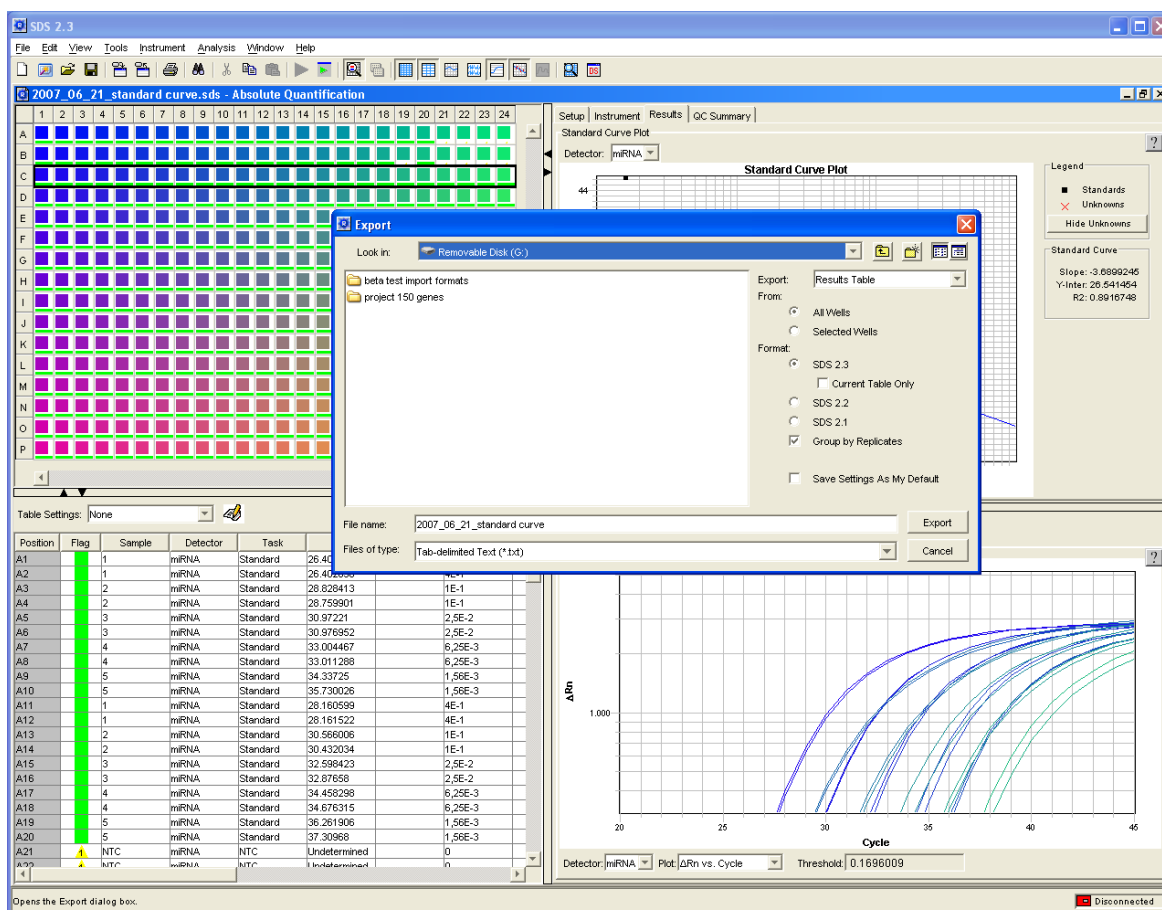


Figure 1

4 - 7900 data table format

The 7900 data table format depends on the software version being used, as well as the choice for absolute or relative quantification. Note that absolute quantification files can also be analyzed in qbase^{PLUS} to achieve relative quantification.

The absolute quantification files can hold data from a single run only. The first few rows contain general information about the run. This information is disregarded during import into qbase^{PLUS}. Next, there should be one or multiple data blocks starting with a row with the following column headers:

- Well ID > Well
- Sample name > Sample Name
- Target name > Detector Name
- Reporter column to extract multi-color run files into separate runs
- Sample type > Task
- Cq value > Ct
- Quantity value > Quantity

The relative quantification files can hold data from multiple runs combined into a single experiment. The first few rows contain general information about the run. This information is disregarded during import into qbase^{PLUS}. Next, there should be a row with the following column headers:

- The second column, PlateID (SDS2.2) or Plate (SDS 2.3), is used to recognize the different runs in the relative quantification file. The plate names will be taken over by qbase^{PLUS} as run names.

- Well ID > Well (SDS 2.2) or Pos (SDS 2.3)
- Sample name > Sample
- Target name > Detector
- Cq value > Ct

Three different example files can be [found](#) in the support section of the Biogazelle website. [7900AQ-ExampleFile.xls](#) is an example of an export file from an absolute quantification run. [7900RQ2.2-ExampleFile.xls](#) and [7900RQ2.3-ExampleFile.xls](#) are examples of export files from a relative quantification study - SDS versions 2.2 and 2.3 respectively.

5 - Import 7900 run files into qbase^{PLUS}




- Step 1:** Open the experiment () in which the run(s) need to be imported by double clicking it in the Project Explorer tree or by using the *Load experiment* option in the experiment context menu.
- Step 2:** Start the import wizard by clicking the *Import* button () in the command bar, select *import run* and click *next*. Alternatively, right click on runs () and select *Import runs ...* from the context menu (Figure 2).



Figure 2

- Step 3:** Select the experiment in which the run needs to be imported in the top part of the import wizard window. By default the active experiment is already selected. Browse for the file(s) to be imported by clicking the *Browse* button and select the correct 7900 file format from the *File type* drop down list (Figure 3). Optionally, the run name can be altered in the *Run name* text box.

Import Run

Import Biogazelle qBasePlus run data

Select experiment :

- ▼ Demo project 1
 - Demo experiment 1
 - Tutorials

Import File :

Separator :

File Type :

Run Name :

[Help on available import file formats](#)

Figure 3

Note - Runs can only be imported into loaded (open) experiments. Closed (unloaded) experiments are not available for selection.

Note - Simultaneous (batch) import of multiple files, as selected in the *Browse* window, is only available for fully licensed customers or users with a temporary demo license. Users with a free license can only import runs one by one.

Step 4: Click *Finish* to complete the import run wizard. You will see that the imported runs are added to your experiment. An individual window is opened for every imported run to allow editing of sample and target information. In addition, the sample and target list is automatically updated with the sample and target names that are included in the imported runs.