

Import file guidelines –
7300, 7500 and 7500 FAST
SDS 1.3 and SDS 1.4

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Subject

This chapter explains how to create 7300, 7500 and 7500 FAST data files.

Summary

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 – 7300, 7500 and 7500 FAST

Software: Sequence Detection Systems (SDS) 1.3 and 1.4

General information

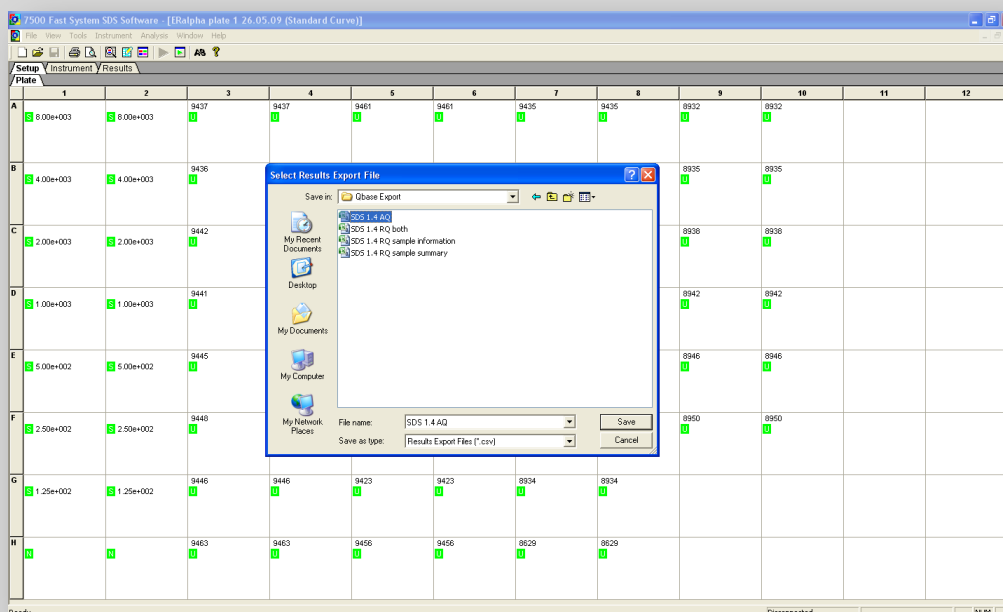
Import files should contain a list of Quantification Cycle (Cq) values. Depending on the instrument software that generates the data, Cq values may have alternative names such as Ct, Cp, or TOP. Cq is the official abbreviation in the Real-time PCR Data Markup Language (more info on <http://www.rdml.org>). The qbase^{PLUS} calculation engine starts with 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 - .xlsx). OpenOffice.org Calc (.ods) and proprietary or binary instrument files are not (yet) supported.

Generating 7300, 7500 and 7500 FAST data export files

1. Open your data file in the SDS software and analyze it according to your needs.
2. Click *File – Export* and export Results Table as comma separated file (*.csv) file (Figure 1).

Figure 1 – Generating export files



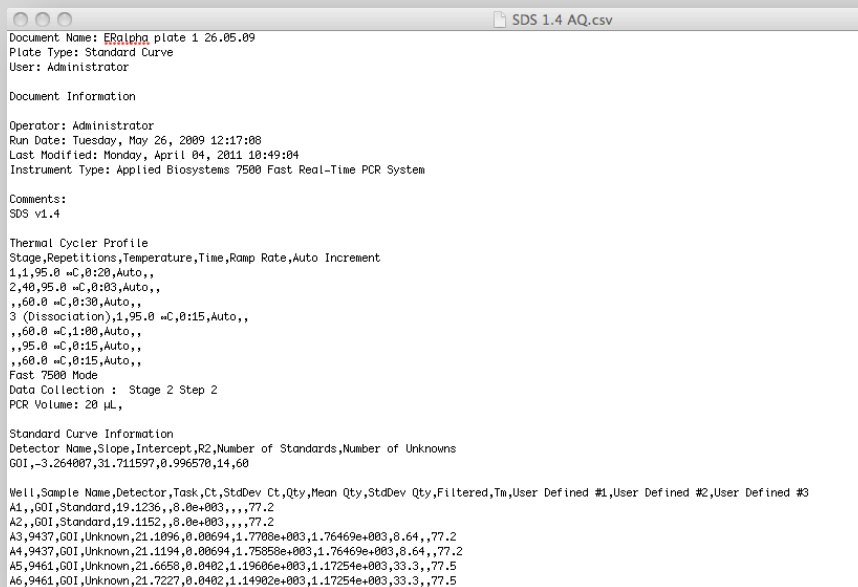
7300, 7500 and 7500 FAST data table format

The 7300, 7500 and 7500 FAST 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
- Sample Name
- Detector Name (= target name)
- Task (= sample type)
- Ct
- StdDev Ct
- Qty (not always present)
- Etc.

Figure 2 – Data table format: absolute quantification – a single run



```
Document Name: Eppalpha plate 1 26.05.09
Plate Type: Standard Curve
User: Administrator

Document Information

Operator: Administrator
Run Date: Tuesday, May 26, 2009 12:17:08
Last Modified: Monday, April 04, 2011 10:49:04
Instrument Type: Applied Biosystems 7500 Fast Real-Time PCR System

Comments:
SDS v1.4

Thermal Cycler Profile
Stage,Repetitions,Temperature,Time,Ramp Rate,Auto Increment
1,1,95.0 °C,0:20,Auto,,
2,40,95.0 °C,0:03,Auto,,
,60.0 °C,0:30,Auto,,
3 (Dissociation),1,95.0 °C,0:15,Auto,,
,60.0 °C,1:00,Auto,,
,95.0 °C,0:15,Auto,,
,60.0 °C,0:15,Auto,,
Fast 7500 Mode
Data Collection : Stage 2 Step 2
PCR Volume: 20 µL

Standard Curve Information
Detector Name,Slope,Intercept,R2,Number of Standards,Number of Unknowns
G01,-3.264007,31.711597,0.996570,14,60

Well,Sample Name,Detector,Task,Ct,StdDev Ct,Qty,Mean Qty,StdDev Qty,Filtered,Tm,User Defined #1,User Defined #2,User Defined #3
A1,,G01,Standard,19.1236,,8.0e+003,,,,,77.2
A2,,G01,Standard,19.1152,,8.0e+003,,,,,77.2
A3,9437,G01,Unknown,21.1096,0.00694,1.7708e+003,1.76469e+003,8.64,,77.2
A4,9437,G01,Unknown,21.1194,0.00694,1.75858e+003,1.76469e+003,8.64,,77.2
A5,9461,G01,Unknown,21.6658,0.0402,1.19606e+003,1.17254e+003,33.3,,77.5
A6,9461,G01,Unknown,21.7227,0.0402,1.14902e+003,1.17254e+003,33.3,,77.5
```

Import 7300, 7500 and 7500 FAST files into qbase^{PLUS}

Detailed information on the import functionality within qbase^{PLUS} can be found in the dedicated manual chapter 'data import' (<http://www.biogazelle.com/support/qBasePlus/manual>).

As of qbase^{PLUS} version 2.1, the software attempts to automatically determine the separator. In previous versions, make sure to select the correct as a separator.

Figure 3 – Run import window

