

# How to load Annotations

## 1 From a .txt or .csv file

You can add sample and/or variable annotations to an existing data frame by importing an annotation text file. These files are tab- or comma-delimited text files. The file name extension is .txt if the file is tab-delimited and .csv if the file is comma-delimited.

How to import a sample/variable annotation text file

Select the **File → Import → Sample Annotations** or the **File → Import → Variable Annotations** menu item.

Select the Tab-separated Text (\*.txt) or the Comma-separated Text (\*.csv) file filter.

Select the file and press Open.

Select the annotations you want to import and press OK.

When importing an annotation text file, the samples/variables in the file will be matched with the samples/variables in the data frame using the annotation in the first column of the annotation file and the sample/variable ID annotation defined for the data set. In this way the ordering of the rows in the annotation file and the data frame does not matter.

## 2 Create a sample/variable annotation text file

If you do not already have an annotation file you can create it using for instance a spread sheet program.

Place the data in a spreadsheet, following the layout below. You can use any spreadsheet application. Save the spreadsheet as a tab- or comma-delimited text file. Use the file name extension .txt if the file is tab-delimited and .csv if the file is comma-delimited. We recommend using tab-delimited text files.

The following layout should be used:

Probe Set	Transcript	Gene Symbol	Chromosome	Entrez Gene
1007_s_at	U48705	DDR1	chr6p21.3	780
1053_at	M87338	RFC2	chr7q11.23	5982
117_at	X51757	HSPA6	chr1q23	3310

121_at	X69699	PAX8	chr2q12-q14	7849
1255_g_at	L36861	GUCA1A	chr6p21.1	2978
1294_g_at	L13852	UBA7	chr3p21	7318

The first row contains the name of each annotation. Each of the remaining rows contains the value of each annotation for one sample/variable. The first column should contain an annotation that matches the sample/variable ID in the data set.

### 3 From NetAffx

You can download variable annotations for Affymetrix arrays from the Affymetrix NetAffx server and import them into the data set.

The downloaded annotation files will be stored on your computer, and can be used without having to download them from the server again. When you select to download annotations, you will be notified if updated annotations are available on the Affymetrix server.

When downloading probe set annotations for the Affymetrix whole transcript arrays, Omics Explorer will create simplified annotations (Gene Symbol, Gene Title,...) in addition to the annotations in the downloaded annotation file.

How to download and import annotations from the Affymetrix NetAffx server<sup>1</sup>

Select the **File → Download → Affymetrix Probe Set Annotations** menu item.

Select the array type and press OK .

Select the annotations you want to import and press OK.

### 4 For Agilent arrays

You can download annotations for your data from <https://earray.chem.agilent.com/>. You might need an account for this.

Select the array you are using and select Action | Download after you have marked the file 'Allannotations'.

When you have the file on your computer go to Qlucore Omics Explorer Select the **File → Import → Sample Annotations** or the **File → Import → Variable Annotations**. Select the downloaded file.

---

<sup>1</sup> The first time you use this function, you will also be asked to provide: your *Affymetrix user name* and your *Affymetrix password* and the folder where the downloaded annotation files will be stored. If you do not have an Affymetrix user name and password you can get one by pressing the Register button. This will take you to the registration page on the Affymetrix web site.

## **5 For Illumina arrays**

Illumina provides several instruments for several techniques. The basic principle for importing data into Qlucore Omics Explorer is to use the software provided by Illumina (Bead Studio or Genome Studio) to pre-process and normalize data. When that is done select to export the processed data to a tab separated txt file.

Start Qlucore Omics Explorer and do File and then Open. Select the file with the Illumina data and then select to use the Import Wizard to import the data. In this process you will import both data and annotations.

## **6 R users**

In the FAQ section, on the support pages on [www.qlucore.com](http://www.qlucore.com), a script for data conversion is available. This script converts data in R to a .gedata file. More information is provided in the FAQ.

## Terminology

Samples: We use samples to describe units such as patients, persons, animals, treatments, dates,...

Variables: We use variables to describe quantities that have been measured for each samples, such as Gene Expression Levels, Protein concentrations, answers to a question in a questionnaire,...

Annotation: A description of a sample or a variable. One sample or variable can be described by one or many annotations.

## Decimal point and decimal comma

Both separators are supported in all tab separated .txt files and .csv files.

## Disclaimer

The contents of this document are subject to revision without notice due to continuous progress in methodology, design, and manufacturing.

Qlucore shall have no liability for any error or damages of any kind resulting from the use of this document.

Qlucore Omics Explorer is only intended for research purposes.

## Trademark List

Excel, Windows 2000, Windows XP, Windows Vista and Windows 7 are trademarks of Microsoft.

NetAffx is the trademark of Affymetrix.

Bead Studio and Genome Studio are trademarks of Illumina.