

# GeneMaths XT

## Import Affymetrix data

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# NOTES

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# Import

## 1. Introduction

Since GeneMaths XT is compliant with the AGCC (Affymetrix GeneChip Command Console) specifications we will import an AGCC example data set. While importing the data, GeneMaths XT will automatically download the latest chip annotations from the NetAffx Analysis Center.

## 2. Downloading the data

2.1. Go to the sample data website of Affymetrix: [http://www.affymetrix.com/support/technical/sample\\_data/demo\\_data.affx](http://www.affymetrix.com/support/technical/sample_data/demo_data.affx).

2.2. Scroll down the page and select **Demo Data MPRO AGCC hourly** (Murine U74A from Awad & Collins).

2.3. Save the zipped files on your computer.

2.4. Unzip the files to a folder on your computer.

The folder contains:

- 20 CEL files: probe cell intensity data files.
- 20 CHP files: probe-level summarization files.
- 20 ARR files: files containing sample attribute information, with links to the CEL/CHP files through GUIDs (unique identifiers).

## 3. Import Affymetrix CEL files

First we are going to import the Affymetrix CEL files.

3.1. Start GeneMaths XT by double clicking on the icon



on the desktop or from the task bar with **Start > Programs > Applied Maths > GeneMaths XT**.

3.2. Click **<Next>** in the welcome screen to begin the import of the data. If the welcome screen does not appear, choose **File > Import Wizard** in the *GeneMaths XT Main* window. The *Import Wizard* pops up (see Figure 1-1).

3.3. Select the second option **Import a set of files each containing one array** and hit **<Next>**.

3.4. From the list of available formats select **Affymetrix CEL files**. A short description of the format is shown in the right panel (see Figure 1-2).

3.5. Click **<Next>**.

3.6. In the next window you can specify if you want to add biological information to the array files. For this exercise, choose the first option and press **<Next>** (see Figure 1-3).

3.7. In the next window, browse for the CEL files. Select all CEL files and press **<Open>**.

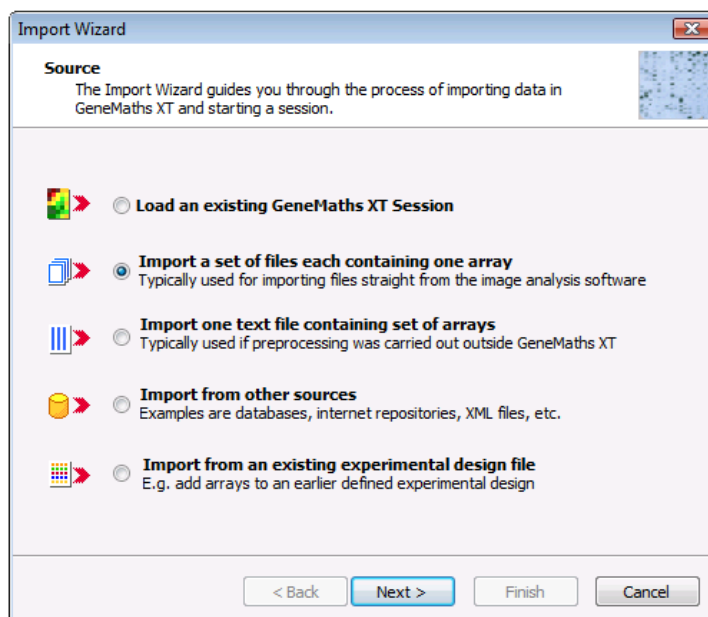


Figure 1-1. *Import wizard: step 1.*

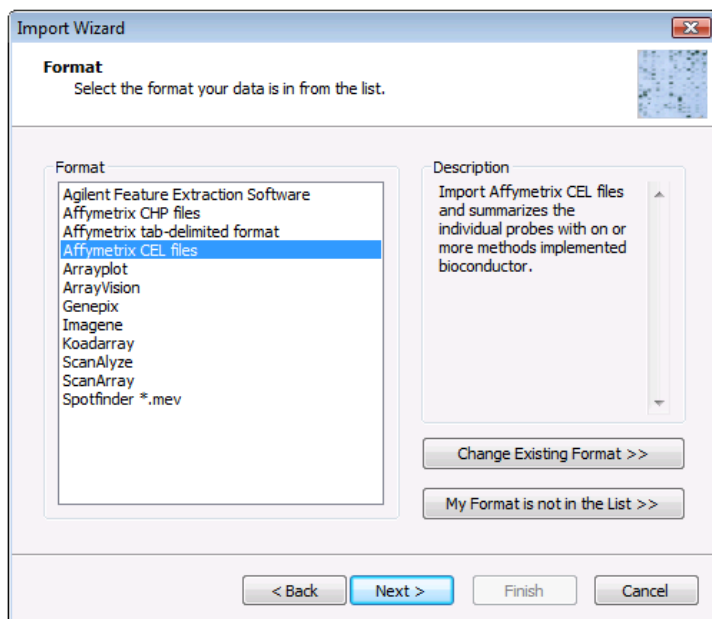


Figure 1-2. Import wizard: step 2.

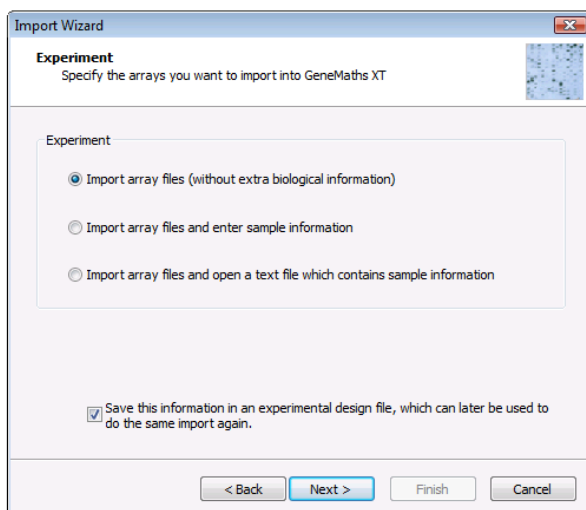


Figure 1-3. Import wizard: step 3.

3.8. Specify the name of the processed file e.g. Murine\_CEL.xps and press **<Save>**.

3.9. If you are importing CEL files for the first time in GeneMaths XT, a dialog box will pop up:

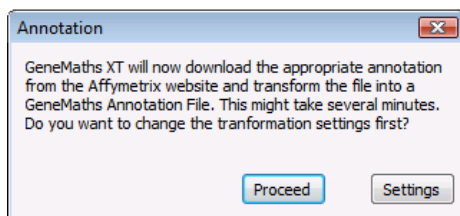


Figure 1-4. Affymetrix annotation.

3.10. If you wish to change the transformation settings, click the **<Settings>** button, else click **<Proceed>**.

NOTE: This can also be done after import of the data (Main window: **Textfields** > **Annotations** > **Affymetrix Settings**).

3.11. In this exercise, we are going to use the default settings. Click **<Proceed>**.

3.12. If this is the first time you are retrieving information from the Affymetrix website, GeneMaths XT will prompt for your Affymetrix username and password. You will only need to enter this once.

3.13. Click **<OK>**.

3.14. The *Calculation* dialog box pops up.

3.15. Once all the appropriate annotation data is fetched from the Affymetrix website, GeneMaths XT will prompt you to choose a probe summarization method (see Figure 1-5).

More information about the different summarization methods can be found on the Affymetrix and/or the R/ BioConductor website. All these procedures are ran as R-routines.

3.16. For this exercise, select *Affymetrix PLIER algorithm* (Probe Logarithmic Error Intensity Estimate) and press **<OK>**.

3.17. The *Calculation* dialog box pops up.

After processing of the data (this may take a couple of minutes), GeneMaths XT will open a session with one layer called 'Plier' (see Figure 1-6), 21 row identifiers (see Figure 1-7) and 3 column identifiers (see Figure 1-8).

NOTE: For information on the preprocessing and analysis of microarray data please refer to the manual or the other quickguides.

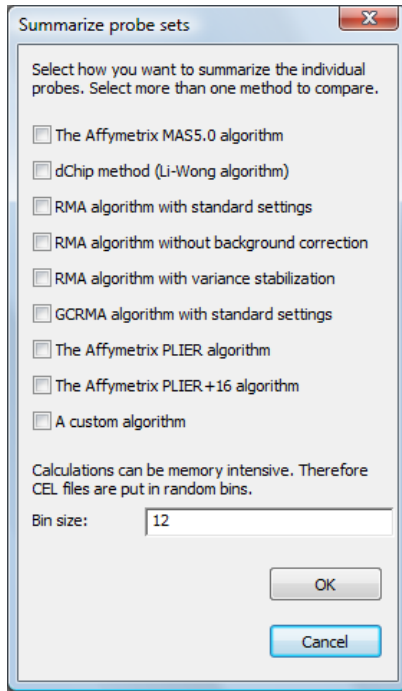


Figure 1-5. Summarizing methods.

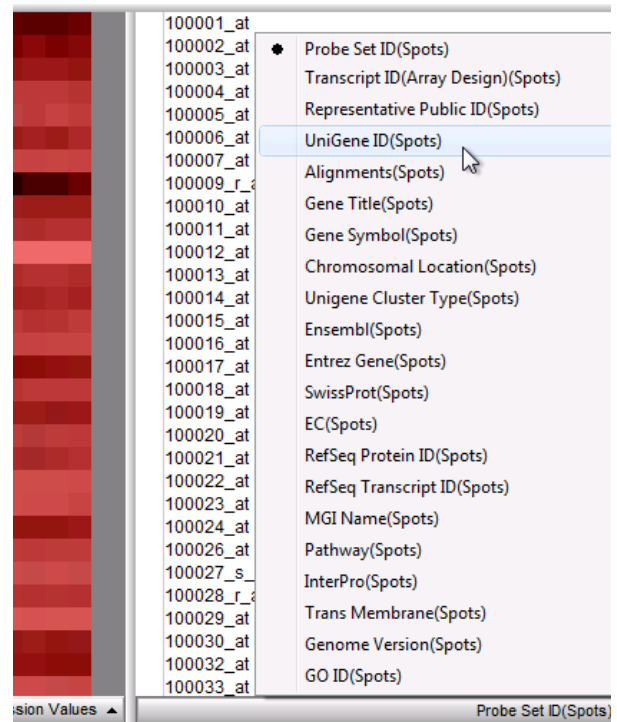


Figure 1-7. Row identifiers.

3.18. In the *Main* window of GeneMaths XT select *File > Save Session as*, give the session a name (e.g. CEL.gms) and press *<Save>*.

3.19. Close the session with *File > Exit*.

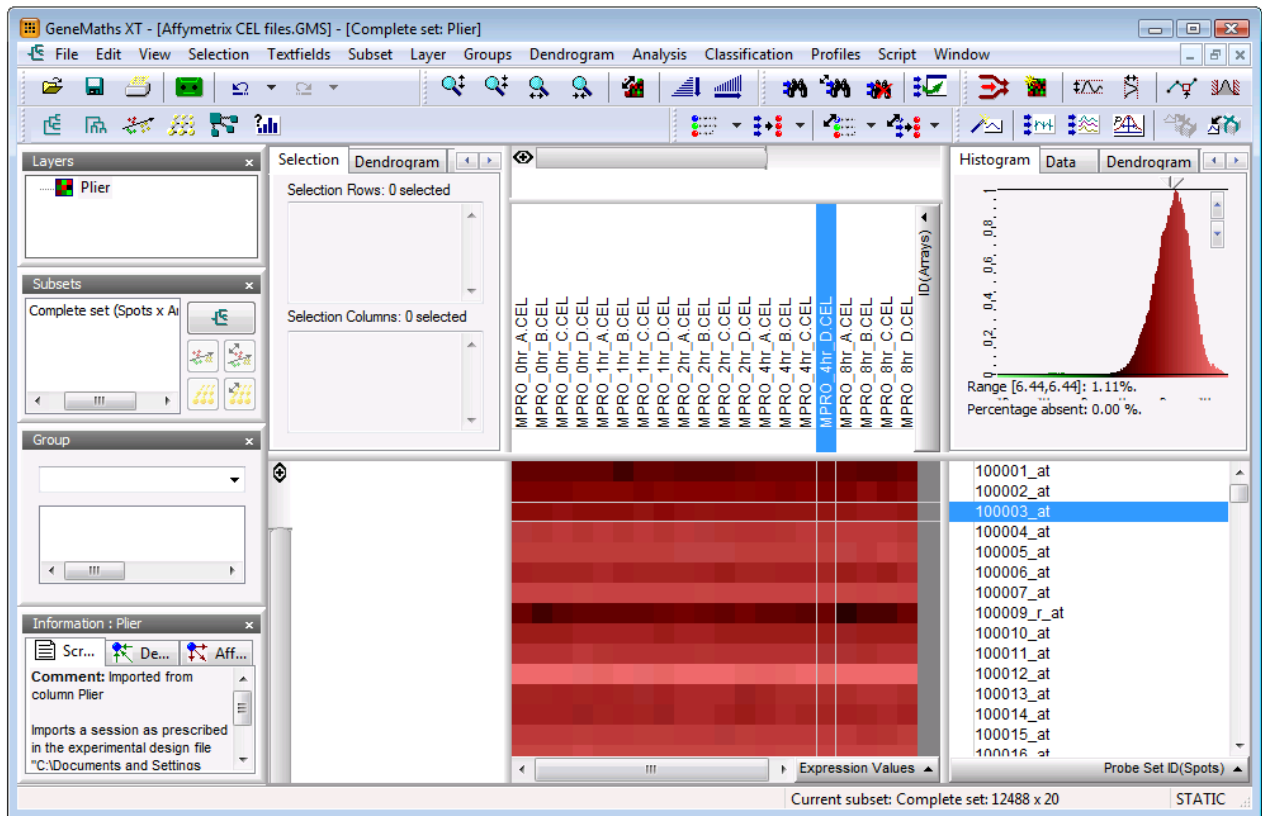


Figure 1-6. The *Main* window of GeneMaths XT after import of the data.

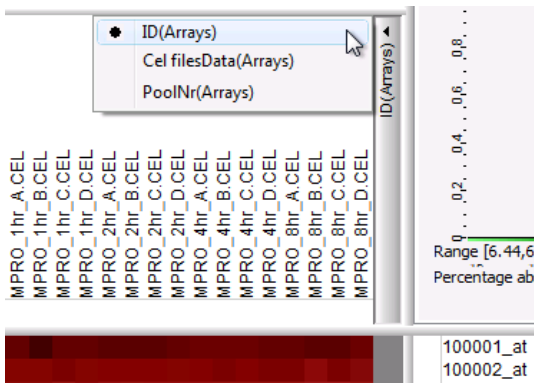


Figure 1-8. Column identifiers.

## 4. Import affymetrix CHP files

In this paragraph we are going to import Affymetrix CHP files.

4.1. Start GeneMaths XT by double clicking on the icon



on the desktop or from the task bar with *Start* >

*Programs* > *Applied Maths* > *GeneMaths XT*.

4.2. Click <Next> in the welcome screen to begin the import of the data. If the welcome screen does not appear, choose *File* > *Import Wizard* in the *GeneMaths XT Main* window. The *Import Wizard* window pops up (see Figure 1-1).

4.3. Select the second option *Import a set of files each containing one array*, and hit <Next>.

4.4. From the list of available formats select *Affymetrix CHP files*. A short description of the format is shown in the right panel (see Figure 1-9).

4.5. In the next window you can specify if you want to add relevant biological information to the array files. For this exercise, choose the first option and press <Next> (see Figure 1-3).

4.6. In the next window, browse for the CHP files. Select all CHP-files and press <Open>.

4.7. Specify the name of the processed file e.g. *Murine\_CHP.xps* and press <Save>.

4.8. After processing of the data (this may take a couple of minutes) GeneMaths XT will prompt to specify the contents of the columns in the *Define Format* dialog box (see Figure 1-10).

4.9. Select the second column **ProbeSetName**. The column is now highlighted in pink. Specify the kind of data present in this column by changing the settings in the *Column Information* panel: select **Text** in the *Type* box and **SpotID** in the *Text* box (see Figure 1-10).

GeneMaths XT has automatically assigned the correct settings to the last column.

4.10. Press <OK>.

4.11. The *Import mapping* dialog box pops up asking you to create a mapping for your data. This mapping tells GeneMaths XT which quantitations to use in the session.

4.12. Select **ProbeSetName** and hit ">". 'ProbeSet Name' is now placed in the right box (see Figure 1-11).

4.13. Click <Next>.

4.14. In the next step of the import, select **Quantification** in the first column, select **No error** in the second column and hit ">" (see Figure 1-12).

4.15. Click <Next>.

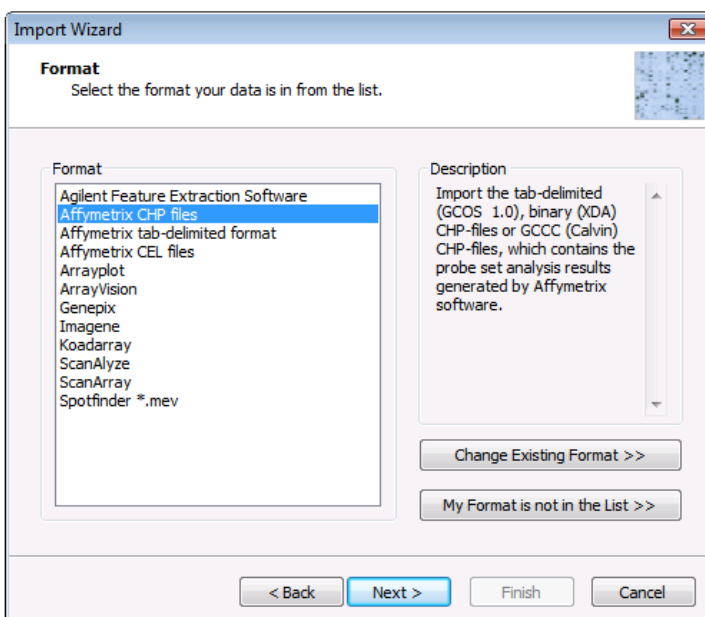


Figure 1-9. Import wizard: step 2.

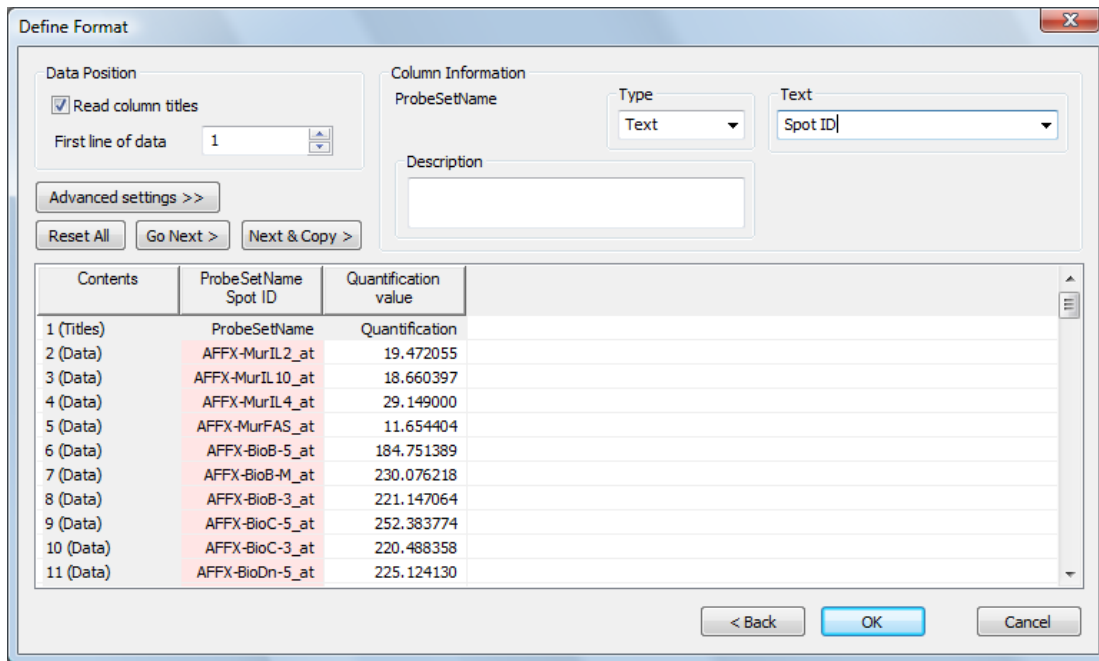


Figure 1-10. Define Format dialog box.

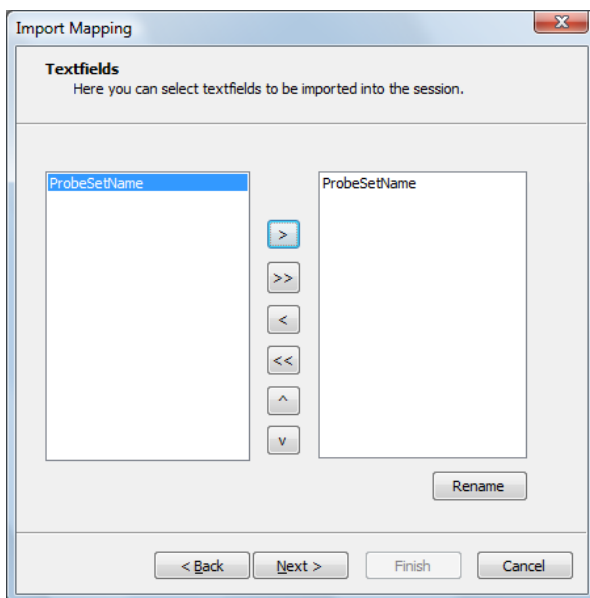


Figure 1-11. Import mapping.

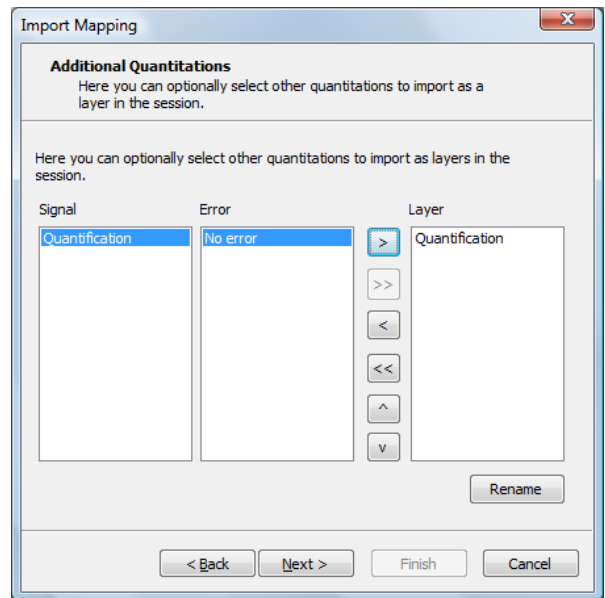


Figure 1-12. Import mapping.

4.16. The Calculation dialog box pops up.

GeneMaths XT will import the data in a new session. The session contains one layer Quantification (see Figure 1-13).

*NOTE: For information on the preprocessing and analysis of microarray data please refer to the manual or the other quickguides.*

4.17. In the Main window of GeneMaths XT select **File > Save Session as**, give the session a name (e.g. CHP.gms) and press **<Save>**.

4.18. Close the session with **File > Exit**.

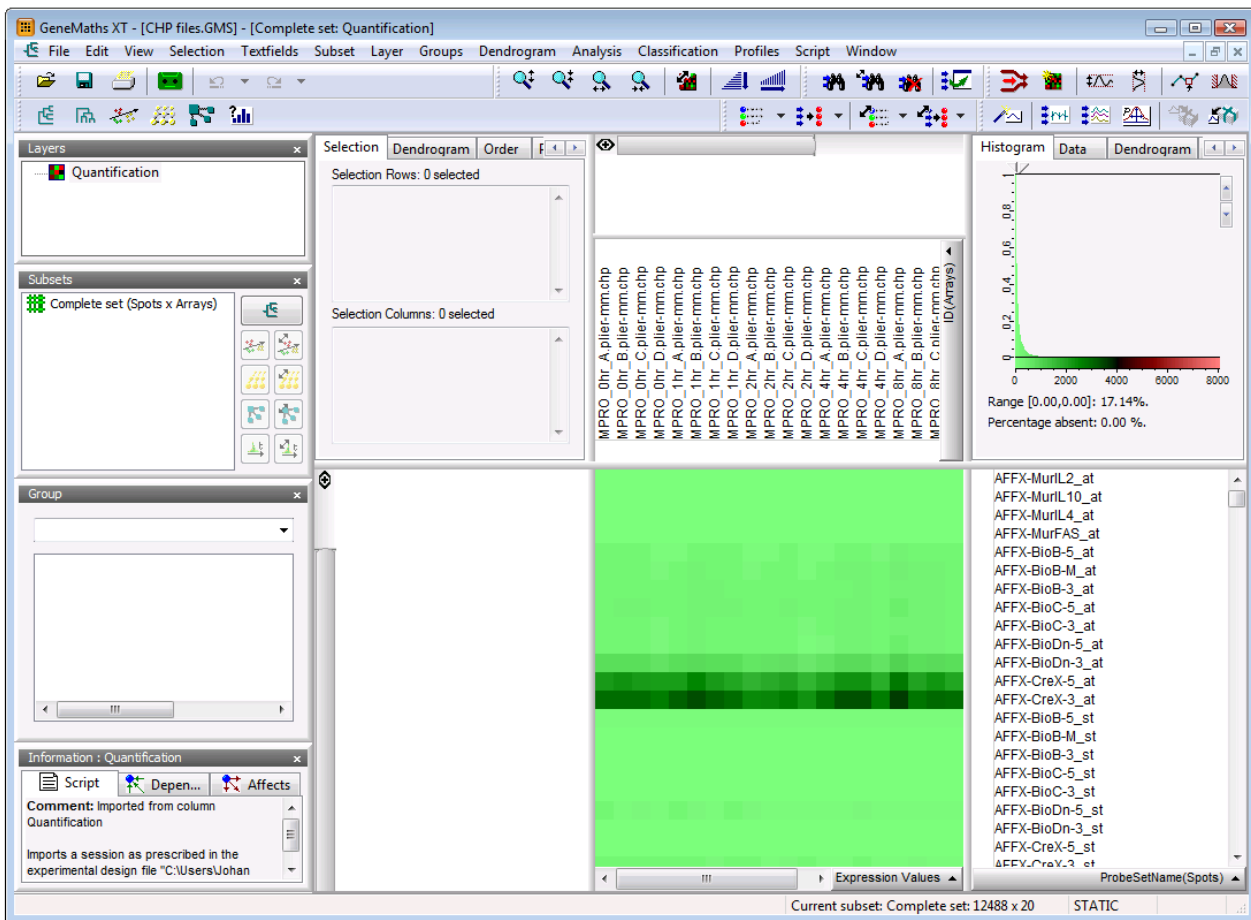


Figure 1-13. The *Main* window of GeneMaths XT after import of the data.