Agilent
Genomic Workbench 6.0

Sample Manager

User Guide

Agilent Technologies

Notices

Manual Part Number

G3800-90004

Edition

Revision A, February, 2010

Agilent Technologies, Inc.
5301 Stevens Creek Blvd.
Santa Clara, CA 95051

Trademarks

Microsoft ® is a registered trademark of Microsoft Corporation in the United States and other countries.

Adobe®, Acrobat® and Reader® are either registered trademarks or trademarks of Adobe Systems Incorporated in the United States and/or other countries.

Software Revision

This guide is valid for Agilent Genomic Workbench 6.0 software, until superseded.

Warranty

The material contained in this document is provided "as is," and is subject to being changed, without notice, in future editions. Further, to the maximum extent permitted by applicable law, Agilent disclaims all warranties, either express or implied, with regard to this manual and any information contained herein, including but not limited to the implied warranties of merchantability and fitness for a particular purpose. Agilent shall not be liable for errors or for incidental or consequential damages in connection with the furnishing, use, or performance of this document or of any information contained herein. Should Agilent and the user have a separate written agreement with warranty terms covering the material in this document that conflict with these terms, the warranty terms in the separate agreement shall control.

Technology Licenses

The hardware and/or software described in this document are furnished under a license and may be used or copied only in accordance with the terms of such license.

Restricted Rights Legend

U.S. Government Restricted Rights. Software and technical data rights granted to the federal government include only those rights customarily provided to end user customers. Agilent provides this customary commercial license in Software and technical data pursuant to FAR 12.211 (Technical Data) and 12.212 (Computer Software) and, for the Department of Defense, DFARS 252.227-7015 (Technical Data - Commercial Items) and DFARS 227.7202-3 (Rights in Commercial Computer Software or Computer Software Documentation).

Safety Notices

CAUTION

A **CAUTION** notice denotes a hazard. It calls attention to an operating procedure, practice, or the like that, if not correctly performed or adhered to, could result in damage to the product or loss of important data. Do not proceed beyond a **CAUTION** notice until the indicated conditions are fully understood and met.

WARNING

A WARNING notice denotes a hazard. It calls attention to an operating procedure, practice, or the like that, if not correctly performed or adhered to, could result in personal injury or death. Do not proceed beyond a WARNING notice until the indicated conditions are fully understood and met.

In This Guide...

This guide describes how to use the Sample Manager tab of Agilent Genomic Workbench to organize microarrays and edit their attributes.

1 Getting Started

This chapter describes the Sample Manager main window and dialog boxes.

2 Setting Up Sample Manager

This chapter describes how to organize microarrays and edit their attributes.

3 Sample Manager Reference

This chapter describes the Sample Manager main window and dialog boxes.

Contents

1

Getting Started

Sample Manager is used to organize microarrays and to define and edit their attributes. You do not need a DNA Analytics application license (CGH, ChIP, or CH3) to use Sample Manager.

Sample attributes are used in various ways throughout Agilent Genomic Workbench and are a powerful way to organize your samples. Some uses for sample attributes include:

- Red and Green sample attributes, if added to Sample Manager before you perform an extraction using a Workflow, appear in the Feature Extraction QC Report header.
- Display arrays in an experiment by a selected sample attribute; for example, by Global Display Name, amount of Cy3 used, or a user-entered comment.
- In the Quality tab, create queries for samples with a given attribute.
- In the Quality tab, create QC Charts based on selected attributes.

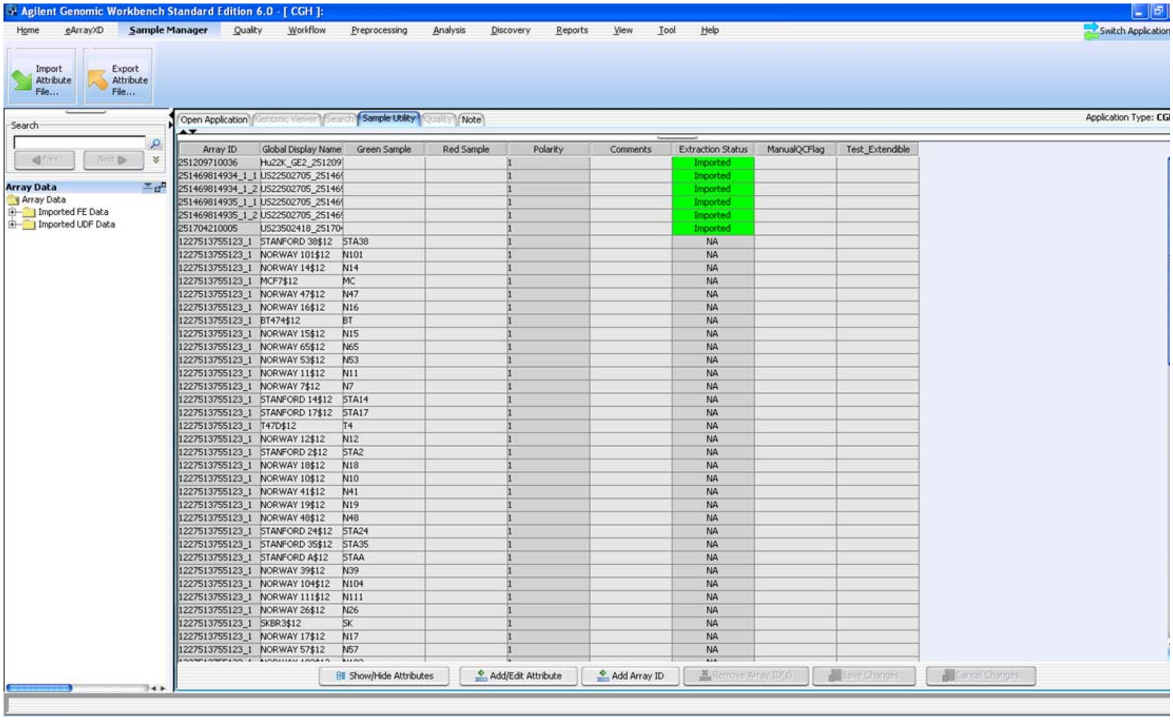
This chapter provides information on how to get started using Sample Manager.

For a description of each part of this module, including all of the dialog boxes that can appear when you click buttons and other elements, see "Main Window Reference" on page 28, and "Dialog Box Reference" on page 35.

Starting Sample Manager

1. Start Agilent Genomic Workbench.
2. On the Agilent Genomic Workbench tab menu, click **Sample Manager**. Or, click **Sample Manager** from the **Open Application** tab.

   The main window for Sample Manager appears. See “Main Window Reference” on page 28 for details.



Array ID	Global Display Name	Green Sample	Red Sample	Polarity	Comments	Extraction Status	ManualQCFlag	Test_Extendible
251209710036	Hu22K_GE2_251209			1		Imported		
251469814934_1_1	US22502705_25146			1		Imported		
251469814934_1_2	US22502705_25146			1		Imported		
251469814935_1_1	US22502705_25146			1		Imported		
251469814935_1_2	US22502705_25146			1		Imported		
251704210005	US23502418_25170			1		Imported		
1227513755123_1	STANFORD 38$12	STA38		1		NA		
1227513755123_1	NORWAY 101$12	N101		1		NA		
1227513755123_1	NORWAY 14$12	N14		1		NA		
1227513755123_1	MCF7$12	MC		1		NA		
1227513755123_1	NORWAY 47$12	N47		1		NA		
1227513755123_1	NORWAY 16$12	N16		1		NA		
1227513755123_1	BT474$12	BT		1		NA		
1227513755123_1	NORWAY 15$12	N15		1		NA		
1227513755123_1	NORWAY 65$12	N65		1		NA		
1227513755123_1	NORWAY 53$12	N53		1		NA		
1227513755123_1	NORWAY 11$12	N11		1		NA		
1227513755123_1	NORWAY 7$12	N7		1		NA		
1227513755123_1	STANFORD 14$12	STA14		1		NA		
1227513755123_1	STANFORD 17$12	STA17		1		NA		
1227513755123_1	T47D$12	T4		1		NA		
1227513755123_1	NORWAY 12$12	N12		1		NA		
1227513755123_1	STANFORD 2$12	STA2		1		NA		
1227513755123_1	NORWAY 18$12	N18		1		NA		
1227513755123_1	NORWAY 10$12	N10		1		NA		
1227513755123_1	NORWAY 41$12	N41		1		NA		
1227513755123_1	NORWAY 19$12	N19		1		NA		
1227513755123_1	NORWAY 48$12	N48		1		NA		
1227513755123_1	STANFORD 24$12	STA24		1		NA		
1227513755123_1	STANFORD 35$12	STA35		1		NA		
1227513755123_1	STANFORD A$12	STAA		1		NA		
1227513755123_1	NORWAY 39$12	N39		1		NA		
1227513755123_1	NORWAY 104$12	N104		1		NA		
1227513755123_1	NORWAY 111$12	N111		1		NA		
1227513755123_1	NORWAY 26$12	N26		1		NA		
1227513755123_1	SKBR3$12	SK		1		NA		
1227513755123_1	NORWAY 17$12	N17		1		NA		
1227513755123_1	NORWAY 57$12	N57		1		NA		

Figure 1 Sample Manager main window

Sample Manager Terminology

The terms in the following table are used in Sample Manager, as well as in other applications in Agilent Genomic Workbench.

Term	Definition
Barcode	The barcode identifier for a microarray slide. The barcode identifier is included in the header of the .tif file the Agilent scanner produces when the slide is scanned.
Array ID	The unique identifier for each array on a microarray slide. This cannot be changed by the user.
Global Display Name	By default, the name of the microarray .tif file or the extracted .txt file that was imported. This name is used to identify the microarray throughout Agilent Genomic Workbench, and can be changed by the user.
FE File	A .txt file that contains the Feature Extraction data for the microarray.
Attribute	A piece of information about the specific microarray; for example, hybridization temperature or polarity.
Attribute file	A file that contains attributes for one or more microarrays. Attribute files are created and saved as .xls or .txt files by the user, or they are created within Agilent Genomic Workbench and then exported (saved).

Using Sample Manager to Organize Samples

The purpose of Sample Manager is to help you keep track of samples as you analyze them using Agilent Genomic Workbench. The following steps show how you do this.

Step 1. Create a sample attribute file

An attribute file can be created in the following ways:

- Use a text editor or spreadsheet program to create a list of samples and their attributes that you want to analyze in Agilent Genomic Workbench. Save this file as a tab-delimited text file or Excel 97-2003 .xls worksheet file. See “About attribute files” on page 14 for more information.
- Use Sample Manager to add Array IDs and attributes to the Sample Manager table. You can export this attributes file to edit outside of the Genomic Workbench application, then import it later. See “To export attributes” on page 25.

Step 2. Import the sample attribute file into Agilent Genomic Workbench

When you import a sample attribute file, the samples are added to the Sample Manager table in the Sample Utility tab. See “To import an attribute file” on page 20. This step is not necessary if you created your sample attributes in the Sample Manager table and did not export them.

Step 3. Change or add attributes

From the Sample Manager table, you can add or change attributes for the samples. See “To add, change, or remove attributes” on page 23.

Step 4. Import an extracted Feature Extraction .txt file manually or use a workflow to extract/import and analyze the samples

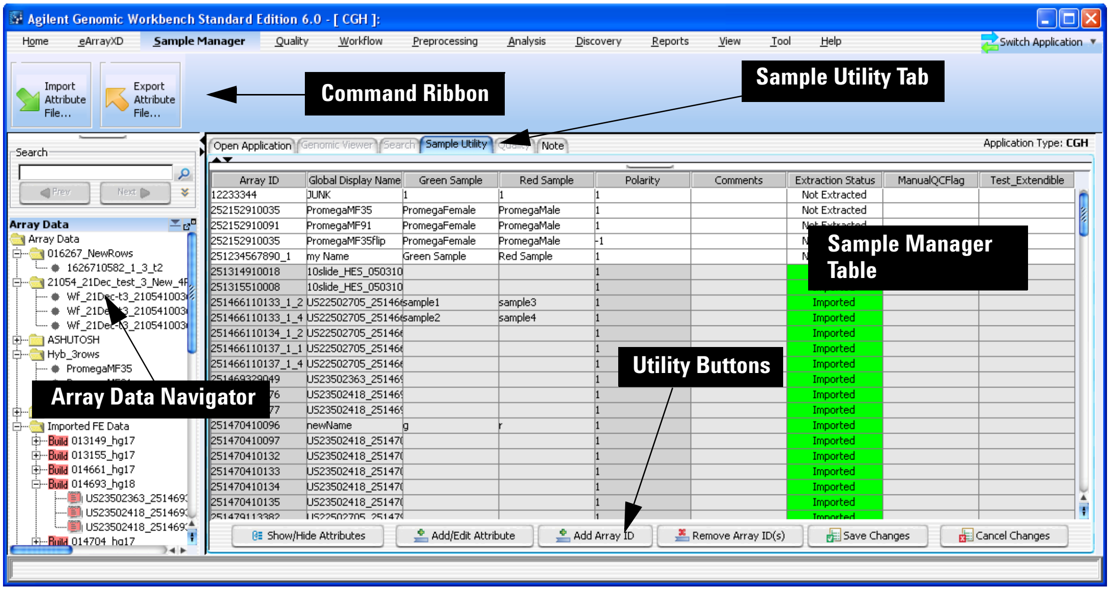
From the Home tab, import an extracted Feature Extraction file to the program. When you import the file, sample attributes in the Sample Manager table are associated with the sample. See the *Data Viewing User Guide* for information on how to import an FE file. After you import a file, if you have a license for one of the analysis applications (CGH, ChIP, or CH3), you can analyze the data interactively.

or

Set up a workflow to extract (FE license required) or import and analyze the samples (CGH or ChIP analysis license required). When you run a workflow, the program matches the samples in the workflow by their Array ID's to the samples in your Sample Manager table. See the *Workflow User Guide* for information on how to set up and run a workflow. After the workflow is complete, the sample row in the Sample Manager table is updated.

About the Sample Manager table

When you import an extracted data file using Agilent Genomic Workbench (either by importing it manually or through a workflow), the Array ID appears as a row in the Sample Utility tab of Sample Manager, and the array data also appears in the Array Data Navigator, under the associated design in the Imported Data folder. These rows will appear gray in the Sample Utility tab.



Array ID	Global Display Name	Green Sample	Red Sample	Polarity	Comments	Extraction Status	ManualQCFlag	Test_Extendible
12233344	JUNK	1	1	1		Not Extracted		
252152910035	PromegaMF35	PromegaFemale	PromegaMale	1		Not Extracted		
252152910091	PromegaMF91	PromegaFemale	PromegaMale	1		Not Extracted		
252152910035	PromegaMF35flip	PromegaFemale	PromegaMale	-1		[illegible]		
251234567890_1	my Name	Green Sample	Red Sample	1		[illegible]		
251314910018	10slide_HES_050310			1		[illegible]		
251315510008	10slide_HES_050310			1		[illegible]		
251466110133_1_2	US22502705_25146	sample1	sample3	1		Imported		
251466110133_1_4	US22502705_25146	sample2	sample4	1		Imported		
251466110134_1_2	US22502705_25146			1		Imported		
251466110137_1_1	US22502705_25146			1		Imported		
251466110137_1_4	US22502705_25146			1		Imported		
251469329049	US23502363_25146			1		Imported		
[illegible]	US23502418_25146			1		Imported		
[illegible]	US23502418_25146			1		Imported		
251470410096	newName	g	r	1		Imported		
251470410097	US23502418_25147			1		Imported		
251470410132	US23502418_25147			1		Imported		
251470410133	US23502418_25147			1		Imported		
251470410134	US23502418_25147			1		Imported		
251470410135	US23502418_25147			1		Imported		
251479113382	US22502705_25147			1		Imported		

Figure 2 Sample Utility tab in Sample Manager

Sample attributes for an Array ID can be added and changed before or after a microarray is added to the database.

NOTE

Read-only attributes and attributes for read-only files cannot be changed.

After you organize your samples and define their attributes, you can use the Workflow feature of Agilent Genomic Workbench to automatically run Feature Extraction (FE license required) and convert the scanned images of your arrays into feature extracted data that you can analyze with other parts of Agilent Genomic Workbench. Note that the capabilities you have depends on the software licenses you have installed. The attributes that are assigned for each Array ID are carried with the Array ID for the rest of the analysis on Agilent Genomic Workbench.

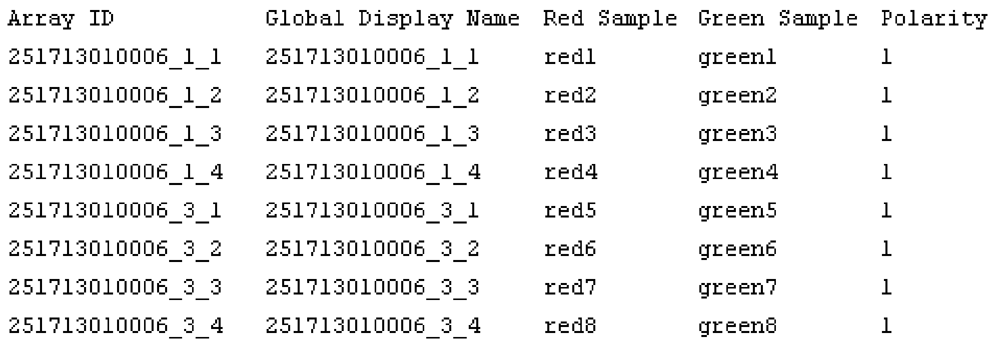
About attribute files

An Attribute File contains identification information (Array ID and Global Display Name) and attributes for one or more microarray samples.

Array attributes may vary, but array attribute files must follow these guidelines:

- The first line of the file contains the names of array attributes, separated by tabs.
- The rest of the lines of the file contain the values of each attribute, one line per array. The values must be in the same order as the attributes in the first line of the file.
- The file must contain the following mandatory attributes:
  - Array ID
  - Global Display Name
  - Green Sample
  - Red Sample (for 2-color arrays)
  - Polarity (for 2-color arrays)

Here is an example:



Array ID	Global Display Name	Red Sample	Green Sample	Polarity
251713010006_1_1	251713010006_1_1	red1	green1	1
251713010006_1_2	251713010006_1_2	red2	green2	1
251713010006_1_3	251713010006_1_3	red3	green3	1
251713010006_1_4	251713010006_1_4	red4	green4	1
251713010006_3_1	251713010006_3_1	red5	green5	1
251713010006_3_2	251713010006_3_2	red6	green6	1
251713010006_3_3	251713010006_3_3	red7	green7	1
251713010006_3_4	251713010006_3_4	red8	green8	1

Figure 3 Example of an attribute file

Attribute files are often created by the user with a text editor or spreadsheet program, and must be saved as a tab-delimited text file or .xls file. For details on how to open an attribute file, see "To import an attribute file" on page 20.

NOTE If you create an attribute file using Microsoft® Excel, it must be saved as an Excel 97-2003 workbook .xls file or a tab-delimited .txt file only.

About Global Display Names

The Global Display Name for a microarray is, by default, the name of the file. This name is displayed throughout Agilent Genomic Workbench for the microarray; for example, in any experiment that uses the microarray, and in reports. You can change the global display names in Sample Manager to make it easier to identify and organize your microarrays. Each Global Display Name must be unique.

Getting Help

To get help within Agilent Genomic Workbench

Agilent Genomic Workbench has several help resources:

Help Resource	Description/Instructions
Sample Manager User Guide	This user guide, which you are now reading, supplies comprehensive help on all available Sample Manager tasks. You can open it easily from anywhere within the program. **1** In any tab of Agilent Genomic Workbench Standard Edition, click the **Help** tab. **2** In the Command Ribbon, click **Sample Manager.** Sample Manager User Guide opens in Adobe Reader.
Other User Guides	The Help tab in Agilent Genomic Workbench lets you view any of the available user guides that apply to the currently selected application type. **1** Set the desired application type from the Switch Application menu. **2** In the Agilent Genomic Workbench tab bar, click **Help.** The names of the available user guides appear in the command ribbon. **3** Click the desired user guide. The selected user guide opens in Adobe Reader.

2

Setting Up Sample Manager

This chapter gives how-to help for the tasks you do in the Sample Manager tab of Agilent Genomic Workbench. For a description of each part of this tab, including all of the dialog boxes that appear when you click buttons and other elements, see “Main Window Reference” on page 28, and “Dialog Box Reference” on page 35.

To get Array IDs into Sample Manager

The following table summarizes how Array IDs are added to Sample Manager under different conditions. It also includes the results of these actions in Sample Manager and in other locations in Agilent Genomic Workbench.

Starting Condition	Action	Result in Sample Manager	Result in other locations
• No array data in database • No Array ID in Sample Manager	Add Array ID manually in Sample Manager	• White row for each Array ID • Extraction Status *Not Extracted*	
• No array data in database • No Array ID in Sample Manager	Import attributes file containing one or more Array IDs and attributes	• White row for each Array ID, with attributes from the imported file	
• No array data in database • No Array ID in Sample Manager	FE Workflow - extraction only (no analysis)	• Gray row for each Array ID • Extraction Status from extracted FE file	• Extraction results saved in selected data folder on computer • Array appears under appropriate design/build in the Design Data pane of the Navigator • Array ID row is added to Quality table
• No array data in database • No Array ID in Sample Manager	Import extracted FE .txt file from the Home tab	• Gray row for each Array ID • Extraction Status *Imported*	• Array appears under appropriate design/build in the Design Data pane of the Navigator • Array ID row is added to Quality table

Starting Condition	Action	Result in Sample Manager	Result in other locations
• No array data in database • No Array ID in Sample Manager	Workflow FE extraction, followed by CGH or ChIP analysis	• Gray row for each Array ID • Extraction Status from the extracted FE file	• Extraction results saved in selected data folder on computer • Array appears under appropriate design/build in the Design Data pane of the Navigator, and in Experiments pane under the workflow experiment • Array ID row is added to Quality table
• No array data in database • Array ID is in Sample Manager (white row)	Import extracted FE .txt file	• Array ID row turns gray • Extraction status changes to *Imported*	• Array appears under appropriate design/build in the Design Data pane of the Navigator • Array ID row is added to Quality table
• No array data in database • Array ID is in Sample Manager (white row)	FE Workflow - extraction only (no analysis)	• Array ID row turns gray • Extraction Status changes to the status from the extracted FE file	• Extraction results saved in selected data folder on computer • Array appears under appropriate design/build in the Design Data pane of the Navigator • Array ID row is added to Quality table
• No array data in database • Array ID is in Sample Manager (white row)	Workflow FE extraction, followed by CGH or ChIP analysis	• Array ID row turns gray • Extraction Status changes to the status from the extracted FE file	• Extraction results saved in selected data folder on computer • Array appears under appropriate design/build in the Design Data pane and in Experiments pane under workflow experiment • Array ID row is added to the Quality table

Starting Condition	Action	Result in Sample Manager	Result in other locations
• Array ID is in Sample Manager (white or gray row)	Import attribute file with same Array ID but unique Global Display name. Message appears asking if you want to overwrite the Array ID in Sample Manager.	• Click **No** - new white row is added with same Array ID and unique Global Display Name • Click **Yes** - overwrites first white row for that Array ID, otherwise (if no white row) overwrites first gray row with that Array ID	
• Array ID is in Sample Manager (white or gray row)	Import attribute file with same Array ID and same (nonunique) Global Display name. Message appears asking if you want to overwrite the Array ID in Sample Manager.	• Click **No** - that row is skipped and Array ID is not imported • Click **Yes** - row is overwritten with new attributes from the imported file	

To import an attribute file

When you import an attribute file, the information in the file is displayed in rows in the Sample Utility tab. For details on attribute files, see “About attribute files” on page 14.

NOTE Attribute files must be either tab-delimited .txt files or .xls files, and cannot be formulas (only simple text). If you want to import an .xlsx spreadsheet file, first save it as a tab-delimited .txt or .xls file (Excel 97-2003 Workbook format).

1. From the Sample Manager command ribbon, click **Import Attribute File**.
2. Find the attribute file folder, click on the attribute file to select it, and then click **Open**.

   The Import Attribute Files dialog box opens.
3. Browse to a folder location and click to select a file, or type the name of the file to be imported. Click **Open**.

   The Attribute File Importer - Map Column Headers dialog box opens.

4 Complete the information for the attribute file to be imported. See "About attribute files" on page 14 and "Attribute File Importer-Map Column Headers" on page 36 for a description of the available options and commands.

5 Click **Import**.

The data in the file is imported and displayed in the Sample Utility spreadsheet.

NOTE Attribute files must contain the following required attributes for each Array ID; Array ID, Global Display Name (must be unique and not blank), Green Sample, Red Sample, Polarity. Array ID rows that do not contain all required attributes will be skipped and not imported.

NOTE Attribute files contain only Array IDs and the associated sample attributes. They do not contain feature data from the scanned images of microarrays.

To add an Array ID to a data folder

1 In the Sample Utility tab of Sample Manager, click **Add Array ID**.

The Add Array ID to Data Folder dialog box appears. See "Add Array ID to Data Folder" on page 35.

2 Select the folder, or create a new folder, where you want to add an Array ID row.

3 Click **OK**.

4 A row is added to the array list. In the blank fields, type the attributes for the microarray and then click **Save Changes**.

To add an Array ID to a new data folder

1. In the Sample Utility tab of Sample Manager, click **Add Array ID**.

   The Add Array ID to Data Folder dialog box appears. See "Add Array ID to Data Folder" on page 35.
2. Type a name for the new data folder.
3. Click **OK**.
4. A row is added to the array list. In the blank fields, type the attributes for the microarray, and then click **Save Changes**. The new data folder appears in the Array Data folder in the Data Navigator pane.

To remove an Array ID

1. In the Sample Utility tab, click to select an Array ID. To select a series of Array IDs, hold down the **SHIFT** key while you click the first and then the last Array ID to remove.
2. Click **Remove Array ID(s)**.

   The selected Array ID rows are removed from the Sample Utility table.
3. Click **Save Changes** to save the changes.

NOTE You can only remove an Array ID for rows you created. After the data is imported, the Array ID cannot be removed.

To remove a data folder

You can remove an array data folder that contains unextracted Array IDs that have been imported from an attribute file, or that you created in Sample Manager (white rows in the table). To remove a data folder:

1. In the Data Navigator, right-click the data folder you want to delete.
2. Select **Delete**.

   The selected data folder is deleted from the Sample Manager.

NOTE You can only remove a new data folder that you created. After data is imported, the data folder cannot be removed.

NOTE Array data from imported FE or UDF files cannot be deleted from Sample Manager. They must be deleted from one of the interactive tabs. See the *Data Viewing User Guide* for more information.

To add, change, or remove attributes

Sample attributes are pieces of microarray-specific information, such as hybridization temperature or sample name. Agilent Genomic Workbench maintains a standard set of attributes that you can define for individual microarrays. You can add new attributes to this set and delete existing ones. You can also edit existing attributes.

For information about how to define attributes for a specific microarray, see "To edit the attribute values of a specific microarray" on page 24.

To add a microarray attribute

1. Click **Add/Edit Attribute.**

   The Attributes dialog box appears. See "Attributes" on page 39.

2. At the bottom of the dialog box, click **New** (*not* New Value).

   The Input dialog box appears.

3. Type a name for the attribute of up to 50 characters in length, and then click **OK.**

   The new name appears in the Attributes dialog box.

4. Edit the details of the new attribute. See "Attributes" on page 39 for a description of the available options and commands.
5. Click **Update.**
6. Click **Close.**

   The new attribute is now available for any sample in the program.

To change an existing attribute

1 Click **Add/Edit Attribute.**

The Attributes dialog box appears.

2 Click the **Name** arrow and select the attribute you want to change.

3 Edit the details of the attribute. For details about editing options, see "Attributes" on page 39.

4 Click **Update.**

5 Click **Close.**

To delete a attribute

1 Click **Add/Edit Attribute.**

The Attributes dialog box appears.

2 Click the **Name** arrow and select the attribute you want to delete.

3 Click **Delete** (*Not* Delete Value).

CAUTION Deleting an attribute permanently removes the attribute and its associated values from Agilent Genomic Workbench. To restore the attribute, you must create it again.

4 You are asked to confirm that you want to delete the attribute. Click **Yes** to permanently delete the attribute.

5 Click **Close.**

To edit the attribute values of a specific microarray

You can define or change the values of attributes assigned to a specific microarray.

1 In the Sample Utility tab, click a microarray to select it.

2 Double-click the sample attribute you want to change for this microarray.

The selected attribute field becomes active.

3 Type the new attribute value or click the arrow to select the new value from a list.

4 When finished, click **Save Changes**.

NOTE

Save Changes updates only the Agilent Genomic Workbench database. It does not update an external attribute file on a hard disk. In order to save the changes in the attribute file, you must first export the attribute file. See “To export attributes” on page 25**.** To change the preset values of attributes that are seen in drop-down lists, use the Add/Edit Attribute function.This applies to attributes that have defined extendible list or predefined list values. See “Attributes” on page 39.

You can also edit the attribute values for microarrays from the Experiment pane of the Navigator in the interactive analysis tabs of Agilent Genomic Workbench. For details, see the *User Guide* for the analysis application (CGH, ChIP, or CH3).

To export attributes

After you organize microarrays and define their attributes, you optionally use export to save one or more of them in an attribute file. (See “To edit the attribute values of a specific microarray” on page 24.) This lets you edit the attributes using a text editor or spreadsheet program. To recreate or restore the attributes at a later time, import this attribute file.

1. Click **Export Attribute File.**

   The Export Attribute Files dialog box appears. See “Export Attribute Files” on page 43.

2. In the Array tab, select the attribute file containing the microarrays to export**.**
3. In the Array list select the sample arrays to export. Click one or more of the arrow buttons to move them to the Selected Array List.
4. Click **Next**.

   The Attribute tab is displayed.

5. Select the Attributes to export and then click **OK**.

   The Export dialog box opens. See “Attributes” on page 39

6. In the Export dialog box, find the folder to save the exported attribute file, type a name for the file, and then click **Export** to save it.

To show or hide attributes

To customize the attributes columns that are displayed in the Sample Utility tab:

1 In the Sample Utility tab of Sample Manager, click **Show/Hide Attributes**.

  The Show/Hide Columns dialog box appears. Columns that show by default are grayed-out. See “Show/Hide Columns” on page 48 for details.

2 Mark the check box next to each attribute you want to display in the Sample Utility tab. Click again to deselect a box.

3 When all desired attributes are selected, click **Save** to update the Sample Utility table.

4 Click **Close** to close the Show/Hide Columns dialog box.

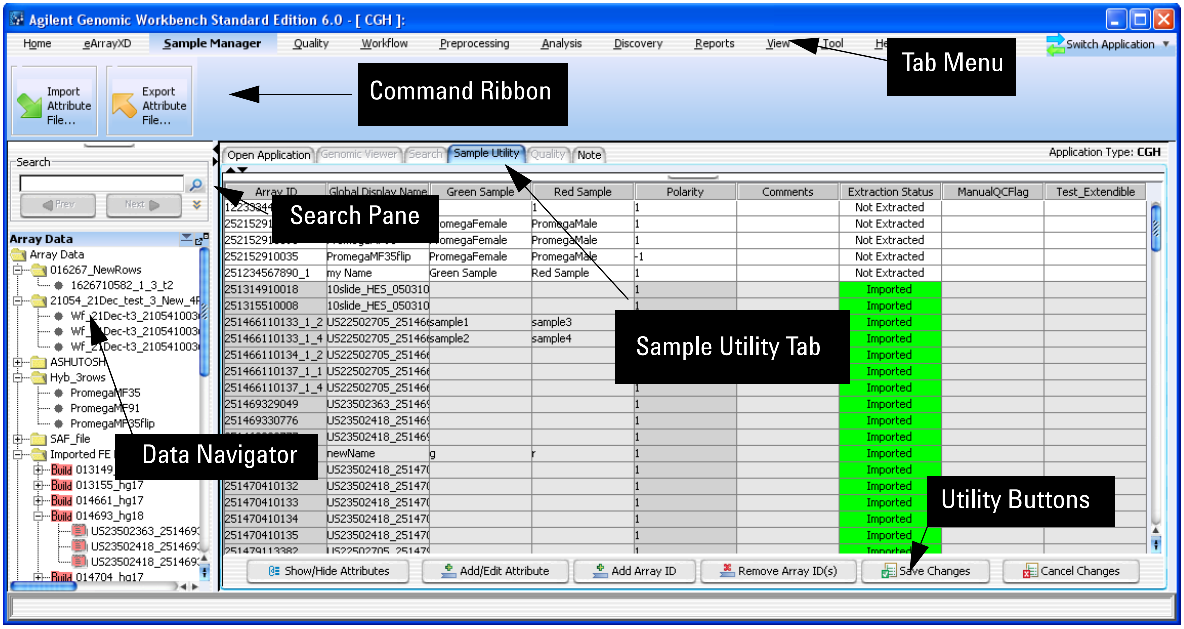
3

Sample Manager Reference

This chapter describes the Agilent Genomic Workbench Sample Manager main window and dialog boxes.

Main Window Reference

This section contains descriptions of each element of the Sample Manager tab. The main window opens when you click the Sample Manager tab in Agilent Genomic Workbench. The window contains elements identified and described in Figure 4 and Table 1.



Array ID	Global Display Name	Green Sample	Red Sample	Polarity	Comments	Extraction Status	ManualQCFlag	Test_Extendible
[illegible]	[illegible]		1	1		Not Extracted		
[illegible]	[illegible]	[illegible]	PromegaMale	1		Not Extracted		
[illegible]	[illegible]	[illegible]	PromegaMale	1		Not Extracted		
252152910035	PromegaMF35flip	PromegaFemale	PromegaMale	-1		Not Extracted		
251234567890_1	my Name	Green Sample	Red Sample	1		Not Extracted		
251314910018	10slide_HES_050310			1		Imported		
251315510008	10slide_HES_050310			1		Imported		
251466110133_1_2	US22502705_25146	sample1	sample3	[illegible]	[illegible]	Imported		
251466110133_1_4	US22502705_25146	sample2	sample4	[illegible]	[illegible]	Imported		
251466110134_1_2	US22502705_25146			[illegible]	[illegible]	Imported		
251466110137_1_1	US22502705_25146			[illegible]	[illegible]	Imported		
251466110137_1_4	US22502705_25146			1		Imported		
251469329049	US23502363_25146			1		Imported		
251469330776	US23502418_25146			1		Imported		
[illegible]	US23502418_25146			1		Imported		
[illegible]	newName	g	r	1		Imported		
[illegible]	US23502418_25147			1		Imported		
251470410132	US23502418_25147			1		Imported	[illegible]	[illegible]
251470410133	US23502418_25147			1		Imported	[illegible]	[illegible]
251470410134	US23502418_25147			1		Imported	[illegible]	[illegible]
251470410135	US23502418_25147			1		Imported		
251479113382	US22502705_25147			1		Imported		

Figure 4 Sample Manager – Main Window

Table 1 Sample Manager – Main Window Elements

Part	Purpose
Tab menu	Click tabs to display a different functional area of Agilent Genomic Workbench.
Command Ribbon	Contains the commands used to perform Sample Manager functions, such as import and export Attribute Files.
Data Navigator	Displays list of microarrays, organized into folders that represent imported files or user-added attribute records.
Search Pane	Lets you find an array ID or any part of a Global Display name in the list.
Sample Utility tab	Contains a list of sample microarrays, organized by Array ID. You can select which attributes to display, but at a minimum Array ID, Green Sample, Red Sample, Polarity, and Extraction Status are displayed. To display only the microarrays for an Array Data node, double-click the name of the data node in the Array Data Navigator.
Utility Buttons	Buttons that let you edit and add to the sample microarray list, and for saving or canceling changes.

Sample Manager Command Ribbon

Figure 5 Sample Manager Command Ribbon

The Sample Manager Command Ribbon contains the commands used for importing and exporting attribute files.

Table 2 Sample Manager Ribbon

Select	Purpose
Import Attribute File	To import contents of an Attribute File.
Export Attribute File	To export the selected Sample Utility data to an Attribute File.

Search pane

The Search pane lets you find all occurrences of an entire name or specific search string in the Array Data Navigator. It also contains several buttons that you can use to move, hide, show or resize the Navigator.

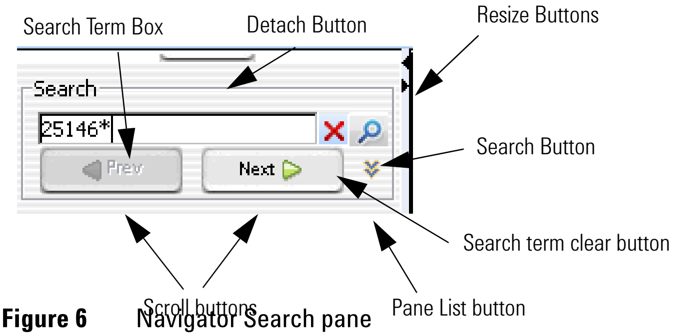


Figure 6 Navigator Search pane

Detach button	Click to move the Navigator from the main window of the program and open it in a new, separate window.
Resize buttons	Click to hide, show, or expand the Navigator.
Search term box	The place where you type your desired search term. Search terms are not case-sensitive, but they must reflect the entire name of an array or other content item that you want to find. You can use asterisks (*) as wildcards to represent groups of unspecified characters. For example, a search term *25887* searches for any content that contains the string "25887".
Pane list	Lets you limit a search to a specific pane. Select the name of the desired pane from the list. To select all panes, select **All Panels.** By default, the program searches all panes.

Data Navigator

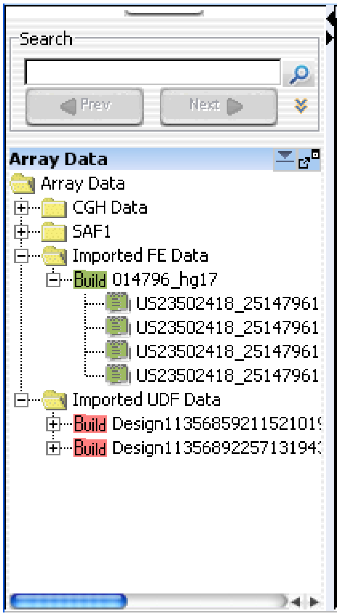


Figure 7 Sample Manager Array Data Navigator

The Array Data Navigator for Sample Manager contains an Array Data folder, which contains one or more data folders. Each of these folders contains a list of microarrays for which attributes exist in Sample Manager.

You can use the Array Data Navigator to:

- display the microarrays for each imported attribute file
- delete a single unimported microarray
- delete a user-created folder of unimported microarrays
- search for Array IDs or Global Display Names

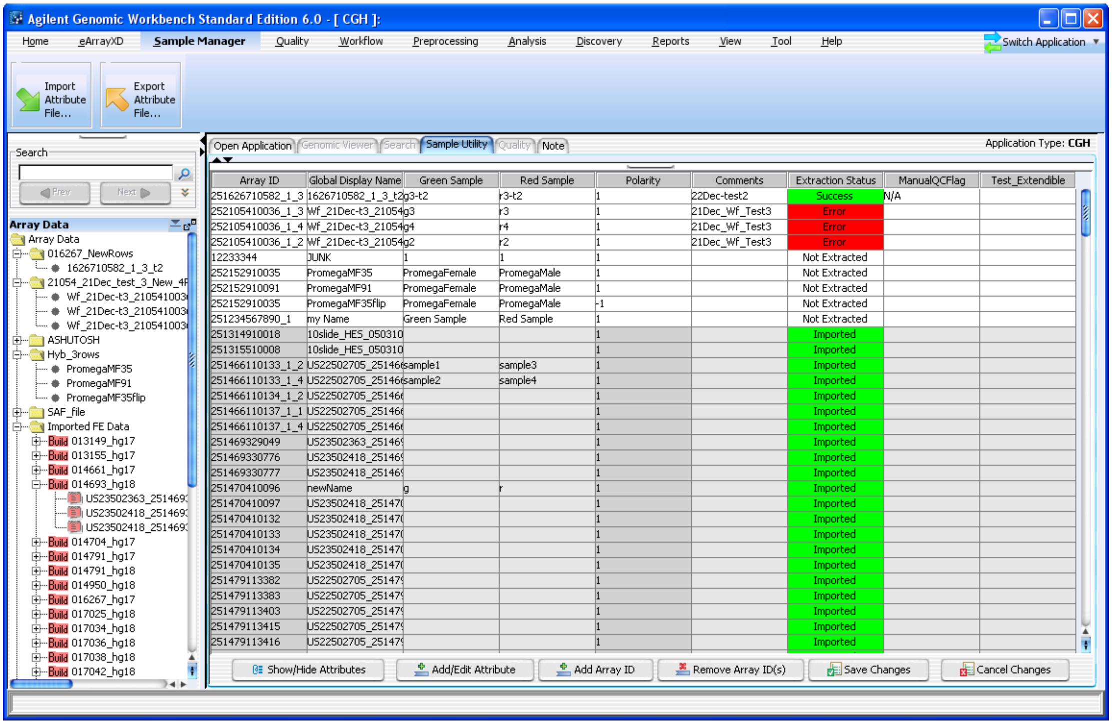
Table 3 Array Data Navigator icons, special text, and buttons

Icon	Comments
⊞	Click to expand a folder and display its contents.
⊟	Click to collapse a folder and hide its contents.
📁	A folder that contains data. In the case of Array Data, each folder, or "Data folder" contains a list of the microarrays in that imported or user-created attribute file. Arrays that were imported using one of the interactive tabs will appear "grayed out" in the Sample Utility list. These rows cannot be deleted from Sample Manager; they must be deleted from the Home tab.
🟩	A microarray that you imported.
🟥	A read-only microarray that was imported by another user.
Build	A design that you imported.
Build	A read-only design that was imported by another user.
—	The **Detach** button, located at the top of the Data Navigator pane, removes the Data Navigator pane from the main window, and opens it in a separate window.
↗	Click to detach only the Array Data panel. Click again to re-attach the panel to the Data Navigator.
🔍	Click to find an Array ID or Global Display Name entered in the Search box.

The Array Data Navigator has the following shortcuts and actions.

- Single-click a data folder to expand or collapse it.
- Double-click the name of a folder to display a list of the Array IDs and their attributes in the Sample Utility tab.

Sample Utility Tab



Array ID	Global Display Name	Green Sample	Red Sample	Polarity	Comments	Extraction Status	ManualQCFlag	Test_Extendible
251626710582_1_3	1626710582_1_3_t2	g3-t2	r3-t2	1	22Dec-test2	Success	N/A	
252105410036_1_3	Wf_21Dec-t3_21054	g3	r3	1	21Dec_Wf_Test3	Error		
252105410036_1_4	Wf_21Dec-t3_21054	g4	r4	1	21Dec_Wf_Test3	Error		
252105410036_1_2	Wf_21Dec-t3_21054	g2	r2	1	21Dec_Wf_Test3	Error		
12233344	JUNK	1	1	1		Not Extracted		
252152910035	PromegaMF35	PromegaFemale	PromegaMale	1		Not Extracted		
252152910091	PromegaMF91	PromegaFemale	PromegaMale	1		Not Extracted		
252152910035	PromegaMF35flip	PromegaFemale	PromegaMale	-1		Not Extracted		
251234567890_1	my Name	Green Sample	Red Sample	1		Not Extracted		
251314910018	10slide_HES_050310			1		Imported		
251315510008	10slide_HES_050310			1		Imported		
251466110133_1_2	US22502705_25146	sample1	sample3	1		Imported		
251466110133_1_4	US22502705_25146	sample2	sample4	1		Imported		
251466110134_1_2	US22502705_25146			1		Imported		
251466110137_1_1	US22502705_25146			1		Imported		
251466110137_1_4	US22502705_25146			1		Imported		
251469329049	US23502363_25146			1		Imported		
251469330776	US23502418_25146			1		Imported		
251469330777	US23502418_25146			1		Imported		
251470410096	newName	g	r	1		Imported		
251470410097	US23502418_25147			1		Imported		
251470410132	US23502418_25147			1		Imported		
251470410133	US23502418_25147			1		Imported		
251470410134	US23502418_25147			1		Imported		
251470410135	US23502418_25147			1		Imported		
251479113382	US22502705_25147			1		Imported		
251479113383	US22502705_25147			1		Imported		
251479113403	US22502705_25147			1		Imported		
251479113415	US22502705_25147			1		Imported		
251479113416	US22502705_25147			1		Imported		

Figure 8 Sample Manager – Sample Utility tab

The Sample Utility tab displays the list of microarrays that are selected in the Data Navigator. See "Data Navigator" on page 31. Each microarray is displayed along with its sample attributes and extraction status. Buttons at the bottom of the tab let you display or edit sample attributes and do other tasks in the list, as described in the table below. See "Dialog Box Reference" beginning on page 35 for more information on these buttons and their use.

The columns (attributes) in the Sample Utility table will change, but the following required attributes are always displayed, in addition to extraction status:

Table 4 Default attribute columns in the Sample Utility tab

Attribute	Description
Array ID	The unique identifier for each array on a microarray slide. This cannot be changed by the user.
Global Display Name	By default, the name of the microarray .tif file or the extracted .txt file that was imported. This name is used to identify the microarray throughout Agilent Genomic Workbench, and can be changed by the user.
Green Sample	Names of Cy3- labeled samples; can be changed by the user
Red Sample	Names of Cy5- labeled samples; can be changed by the user
Polarity	Sample polarity (1 or -1); can be changed by the user before import of the extraction, not after import
Extraction status	For arrays extracted using Feature Extraction, shows the results status from the FE results file. See the *Feature Extraction Reference Guide* for more information. For new rows added by the user and not yet imported (white rows), displays *Not Extracted.* For arrays that are imported, not extracted within Agilent Genomic Workbench, displays *Imported*.

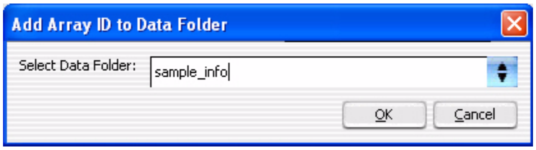
Table 5 Sample Utility Tab Buttons

Button	Function
Show/Hide Attributes	Opens Show/Hide Columns dialog box where you can select which attributes to display. See "Show/Hide Columns" on page 48.
Add/Edit Attribute	Opens Attributes dialog box where you can add a new attribute or edit an existing attribute. "Attributes" on page 39.
Add Array ID	Lets you add a single Array ID to a folder. See "Add Array ID to Data Folder" on page 35.
Remove Array ID	Removes selected Array ID from the list. See "To remove an Array ID" on page 22
Save Changes	Saves changes made to the array list.
Cancel Changes	Cancels changes made to the array list.

Dialog Box Reference

This section describes the dialog boxes that appear in the Sample Manager tab. They are listed in alphabetical order by title.

Add Array ID to Data Folder



sample_info

Figure 9 Add Array ID to Data Folder dialog box

Purpose: Adds an Array ID row to the list in the Sample Utility tab. Also used to add a new Array folder to the Array Data.

To open: This dialog box appears when you click **Add Array ID** at the bottom of the Sample Utility tab.

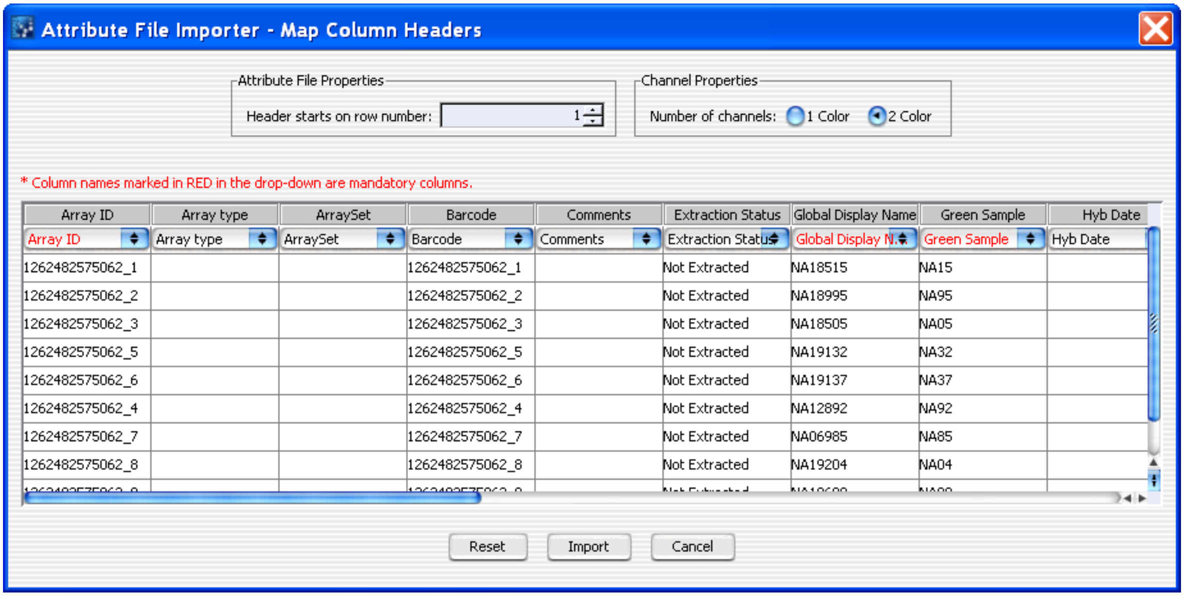
Select Node Click the arrow and select one of the current data folders, or type the name of a new data folder.

OK Click **OK** to add a blank array row to the selected data folder, or to create the new data folder and add an Array ID row to it.

Cancel Click **Cancel** to cancel the operation without adding an array ID.

NOTE When you use the Add Array ID function to add an Array ID, you must enter the required attributes for the new array and then save the changes in order for it to appear in the Array Data list. If you don’t add all of the required attributes, when you save the row, an error message appears and the row is not saved. See Table 6 for a list of required attributes.

Attribute File Importer-Map Column Headers



Attribute File Properties

Header starts on row number: 1

Channel Properties

Number of channels: ○ 1 Color ● 2 Color

* Column names marked in RED in the drop-down are mandatory columns.

Array ID	Array type	ArraySet	Barcode	Comments	Extraction Status	Global Display Name	Green Sample	Hyb Date
Array ID	Array type	ArraySet	Barcode	Comments	Extraction Status	Global Display N...	Green Sample	Hyb Date
1262482575062_1			1262482575062_1		Not Extracted	NA18515	NA15	
1262482575062_2			1262482575062_2		Not Extracted	NA18995	NA95	
1262482575062_3			1262482575062_3		Not Extracted	NA18505	NA05	
1262482575062_5			1262482575062_5		Not Extracted	NA19132	NA32	
1262482575062_6			1262482575062_6		Not Extracted	NA19137	NA37	
1262482575062_4			1262482575062_4		Not Extracted	NA12892	NA92	
1262482575062_7			1262482575062_7		Not Extracted	NA06985	NA85	
1262482575062_8			1262482575062_8		Not Extracted	NA19204	NA04	

Figure 10 Attribute File Importer - Map Column Headers dialog box

Purpose: Use this dialog box to assign column headers from an attribute file created with a spreadsheet program to the headers expected by the Sample Manager program (if necessary). This dialog box is also used to import the attribute file.

To open: This dialog box opens when you click **Open** in the Import Attribute Files dialog box.

To map a column header

1 Click the arrow and select the attribute header to be assigned from the list of currently-defined attributes.
2 When all columns are assigned, click **Import** to import the file.

Header starts on row number Select the number of the row that contains the header in the imported file.

Channel Properties Click the arrow to change the number of channels for the file. For a 1-color experiment, select **1**. For a 2-color experiment, select **2**.

Reset Resets the column headers to the defaults when the file was opened.

Import Imports the file. A list of exceptions and conditions that may occur when you import a file are shown in Table 7 on page 38.

Cancel Cancels the file import operation and closes the dialog box.

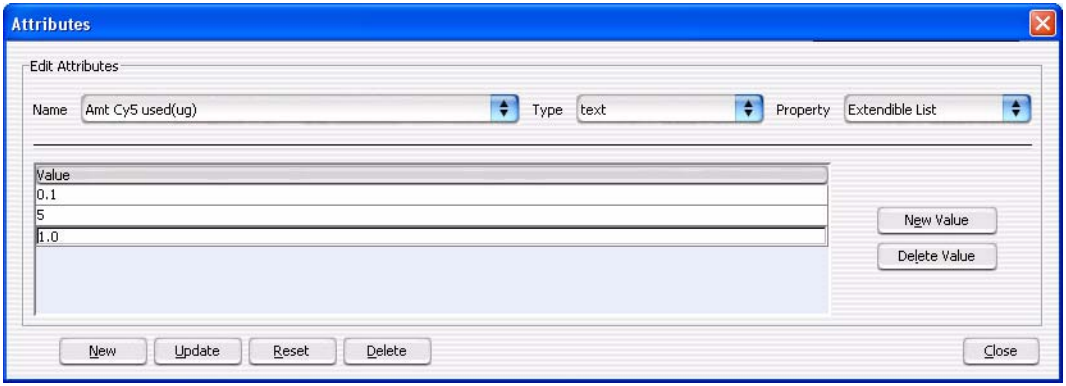
Table 6 Required Columns in an Attribute File

Column	**Requirements**
For one-channel arrays	
Array ID	Unique for each sample
Global Display Name	By default, this is the file name. Must be unique for each microarray and cannot be blank.
Green Sample	Green sample ID.
For two-channel arrays	
Array ID	Unique for each sample
Global Display Name	By default, this is the file name. Must be unique for each microarray and cannot be blank.
Green Sample	Green Sample ID.
Red Sample	Red Sample ID.
Polarity	Value of 1 or -1 only. Blank value is set to “1”. Values other than 1, -1 or blank will cause the row to be ignored and not imported. If a polarity is assigned as -1, then for later analysis using Agilent Genomic Workbench, it is processed as a dye-flip array. Dye-flip arrays are described in the *Data Viewing Guide*.

Table 7 Exceptions and Conditions for Importing Attribute Files

Condition	Outcome
The attribute file being imported has more than 1 entry for the same Array ID.	Error message appears. User is asked whether the last entry should overwrite the previous entry.
The attribute file to be imported has rows with missing required column values.	The row is skipped and an error message appears that shows which required columns are missing.
The attribute file to be imported has rows with values that do not match the data type for the particular column.	Those rows are skipped and a warning message appears.
The attribute file to be imported has rows with Array IDs already present in the table.	Error message appears “Some Array ID’s are already present - Do you want to over-write these rows?” Click **Yes** to overwrite the existing rows with the duplicate rows from the attribute file. Click **No** to cancel the import.
The attribute file to be imported has rows with ArrayID already present in the table as FE data (gray row).	Polarity and isMultiPack value will not be overwritten.

Attributes



Name: Amt Cy5 used(ug)
Type: text
Property: Extendible List

Value
0.1
5
1.0

Figure 11 Attributes dialog box

Purpose: You use this dialog box to create, change, or delete available sample attributes. Attributes are pieces of sample-specific information, such as hybridization temperature or sample name.

To open: From the Sample Utility view, click **Add/Edit Attribute**.

NOTE

When you add or change an attribute from this dialog box, that attribute/value is then available for you to associate with a microarray. To assign values to attributes for individual samples, see "To edit the attribute values of a specific microarray" on page 24.

Name The name of the attribute whose details appear in the dialog box. Click the arrow to select the desired attribute from the list.

Two lists appear to the right of the attribute name. These lists define the type of value the program will use for the attribute. You select one value from each list.

The Type list has these options:

Option	The attribute is:
int	an integer
double	a double-precision floating point number (a high-precision number that can include decimals)

Option	The attribute is:
boolean	true or false
text	a string of plain text

NOTE If you select an option (other than “text”), and type a value that does not match the selected type, you will get the following error: “Invalid Value for column”.

The Property list has these options:

Option	Description
Extendible List	This lets you define a choice of values that are displayed when the attribute is selected. It also displays a text box where you can type a custom value.
Single valued	The program displays a single text box to edit this attribute for a sample.
Dynamic valued	The program does not allow you to edit the value of this attribute for a sample. Instead, it defines the value of the attribute, based on information in the array data file.
Pre-defined list	This lets you define a choice of values that are displayed when the attribute is selected.

Value For extendible and predefined lists, the program displays these values as choices when you edit the selected attribute for a sample. Double-click a value to change it. Click **Update** to accept the edited value. Click **Reset** to return the values to their previous state.

New Value For extendible and predefined lists, adds another value to the Value list. Click **New Value** to make it available for editing. Click **Update** to accept the edited value.

Delete Value For extendible and predefined lists, deletes a value from the Value list. Click the value you want to delete, then click **Delete Value**.

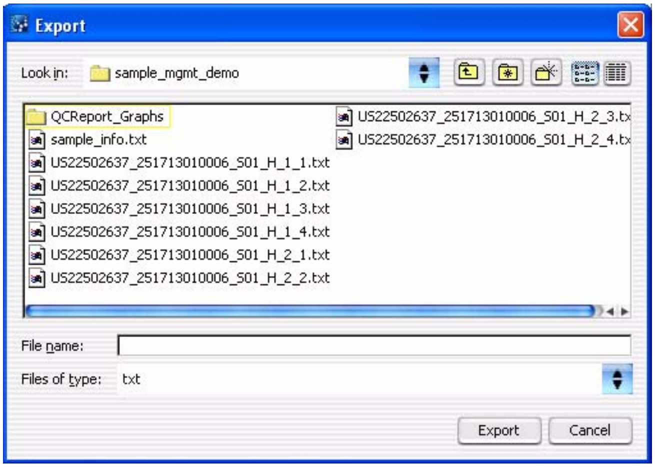
New Use this command to create a new attribute. It opens an Input dialog box, where you type a name for the new attribute. See “Input Attribute Name” on page 47.

Update	(Enabled only if there are unsaved changes to the attribute.) Saves the changes you made to the attribute without closing the Attributes dialog box.
Reset	(Enabled only if there are unsaved changes to the attribute.) Restores the attribute it to its state before you made any changes.
Delete	Deletes the attribute from the program.

CAUTION If you delete an attribute, the program also deletes all values assigned to it for all samples. To restore the attribute, you must create the attribute again, and reassign the desired value to each array.

Close	Closes the Attributes dialog box. If you made changes to the attribute, but did not save them, a dialog box asks if you want to save the changes to the attribute. Click **Yes** to save the changes, or click **No** to close the dialog box without saving the changes, or click **Cancel** to go back to the Attributes dialog box without saving the changes.

Export



Look in: sample_mgmt_demo

QCReport_Graphs
sample_info.txt
US22502637_251713010006_S01_H_1_1.txt
US22502637_251713010006_S01_H_1_2.txt
US22502637_251713010006_S01_H_1_3.txt
US22502637_251713010006_S01_H_1_4.txt
US22502637_251713010006_S01_H_2_1.txt
US22502637_251713010006_S01_H_2_2.txt
US22502637_251713010006_S01_H_2_3.tx
US22502637_251713010006_S01_H_2_4.tx

File name:

Files of type: txt

Figure 12 Export dialog box

Purpose: Lets you select a file name and location for exporting data to an attribute file.

To open: From the Attributes tab of the Export Array Attributes dialog box, click **Export**.

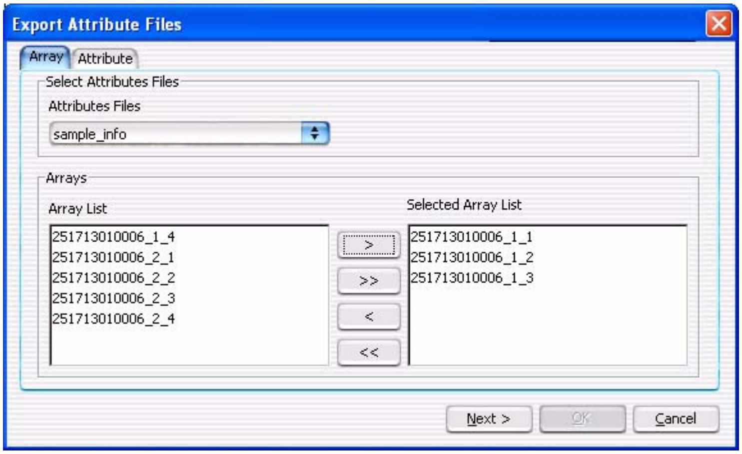
Look in	Use the arrow to select the folder location for the attribute file. If necessary, use the adjacent buttons to move up one folder, look in the desktop, or create a new folder. You can also change the file view to include a list or details.
File name	Type the name to use for the attribute file.
Files of type	Click the arrow to change the file types displayed.
Export	Saves the selected microarray attributes in the selected file. A message appears to let you know that the file was exported successfully.
Cancel	Closes the Export Attribute Files dialog box without exporting an Attribute File.

Export Attribute Files

Purpose: This dialog box contains two tabs used to define what Array IDs and attributes are exported to the exported attribute file.

To open: On the Sample Manager command ribbon, click **Export Attribute File**.

Array tab



Attributes Files: sample_info

Array List:
251713010006_1_4
251713010006_2_1
251713010006_2_2
251713010006_2_3
251713010006_2_4

Selected Array List:
251713010006_1_1
251713010006_1_2
251713010006_1_3

Figure 13 Export Attribute Files dialog box - Array tab

Purpose: This tab lets you select the arrays to export. Once you have selected the arrays you want to export, click **Next**. This opens the Export Attribute Files - Attribute tab.

To open: From the Sample Manager command ribbon, click **Export Attribute File** and then click the **Array** tab.

Attribute Files Select an attribute file from the list. The sample arrays from this attribute file are displayed in the Arrays list. After you select arrays for export from this file, you can select another attribute file and then select more arrays. In this way, you create a custom attribute file that contains some or all of the arrays from different attribute files.

Array list Displays a list of available arrays for export. Move desired arrays for export to the Selected Array List using one of the following methods.

- To select an array to move to the Selected Array List, click its name.
- To select additional arrays, hold down the **Ctrl** key and click their names.
- To select a contiguous block of arrays, click the name of the first array, then hold down the **Shift** key and click the name of the last one.

Selected Array List Displays the arrays that are currently selected for export.

> Moves the selected arrays in Array List to the Selected Array List.

>> Moves all of the arrays in Array List to the Selected Array List.

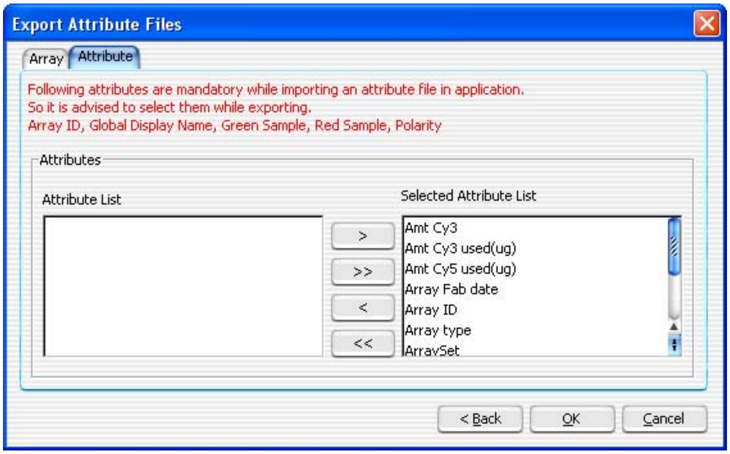
< Removes an array from the Selected Array List. To select an array to be removed, click its name. If desired, you can add the array again.

<< Clears the Selected Array List.

Next Displays the Attribute tab that allows you to select attributes.

Cancel Closes the dialog box without selecting any array attributes to be exported.

Attribute Tab



Following attributes are mandatory while importing an attribute file in application.
So it is advised to select them while exporting.
Array ID, Global Display Name, Green Sample, Red Sample, Polarity

Amt Cy3
Amt Cy3 used(ug)
Amt Cy5 used(ug)
Array Fab date
Array ID
Array type
ArraySet

Figure 14 Export Attribute Files dialog box - Attribute tab

Purpose: This tab lets you select the attributes to include in the sample attribute file. When you have finished selecting the attributes for export, click **OK** and the Export dialog box will appear where you type the file name. See “Export” on page 42.

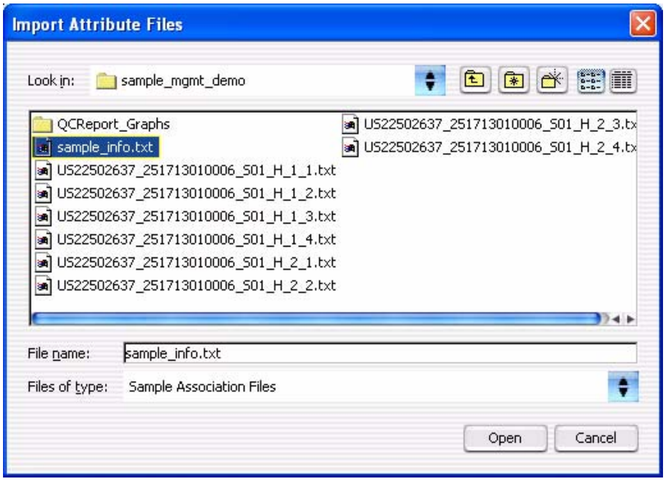
To open: In the Array tab of the Export Attribute Files dialog box, click **Next>** after you add one or more arrays to the Selected Array List.

NOTE Because certain attributes are required for importing an attributes file, it is important that you select these attributes when you export an attributes file. Required attributes are: Array ID, Global Display Name, Green Sample, Red Sample, and Polarity.

Attribute list	Displays a list of available attributes for export. Move desired attributes for export to the Selected Attribute List, using one of the following methods. • To select an attribute for subsequent transfer to the Selected Attribute List, click its name. • To select additional attributes, hold down the **Ctrl** key and click their names. • To select a contiguous block of attributes, click the name of the first attribute, then hold down the **Shift** key and click the name of the last one.
Selected Attribute List	Displays the attributes currently selected for export.
>	Moves the selected attributes in the Attribute List to the Selected Attribute List.
>>	Moves all of the attributes in the Attribute List to the Selected Attribute List.
<	Removes an attribute from the Selected Attribute List. To select an attribute for removal, click its name. If desired, you can add the attribute again.
<<	Clears the Selected Attribute List.
Back	Moves to Array tab for selection of arrays.
Cancel	Closes the dialog box without selecting any array attributes to be exported.

OK Opens the **Export** dialog box, where you find a location, type a file name, and export the data. See “Export” on page 42**.** You must select one or more arrays and one or more attributes before you can export an attribute file.

Import Attribute Files



Look in: sample_mgmt_demo

File name: sample_info.txt

Files of type: Sample Association Files

Figure 15 Import Attribute Files dialog box

Purpose: You use this dialog box to import an attribute file into the program.

To open: From the Sample Manager command ribbon, click **Import Attribute File**.

Look in Use the arrow to select the folder where the attribute file is located. If necessary, use the adjacent buttons to move up one folder or look on the desktop. You can also change the file view to show files as a list or include file details.

File name Type the attribute file name or click to select it from the list of files.

Files of type Click the arrow to change the file types displayed.

Open Once you have selected a file name and location, click **Open** to open the Attribute File Importer dialog box. See "Attribute File Importer-Map Column Headers" on page 36.

Cancel Closes the dialog box without importing any files.

Input Attribute Name

Enter name for new attribute.

Figure 16 Input dialog box

Purpose: To type the name of a new attribute.

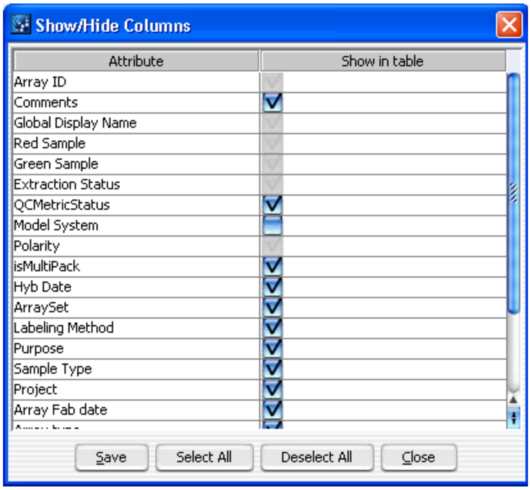
To Open: At the bottom of the Sample Utility tab, click **Add/Edit Attribute**; then click **New**. Or, from the Attributes dialog box, click **New**.

Enter name for new attribute Type the name for the attribute to add.

OK Click **OK** to accept the new attribute name. The new attribute is added to the list of attributes in the Attributes dialog box.

Cancel Click this to close the dialog box without creating the new attribute.

Show/Hide Columns



Attribute	Show in table
Array ID	✓
Comments	☑
Global Display Name	✓
Red Sample	✓
Green Sample	✓
Extraction Status	✓
QCMetricStatus	☑
Model System	☐
Polarity	✓
isMultiPack	☑
Hyb Date	☑
ArraySet	☑
Labeling Method	☑
Purpose	☑
Sample Type	☑
Project	☑
Array Fab date	☑

Figure 17 Show/Hide Columns dialog box

Purpose: Lets you select the attributes that are displayed in the Sample Utility tab.

To open: At the bottom of the Sample Utility tab, click **Show/Hide Attributes**.

Attribute All available attributes are shown in the Attributes column. Attributes with a check mark next to them are displayed in the Sample Utility tab for each sample.

Show in Table To select an attribute for display, select the **Show in Table** check box next to it. To deselect an attribute, click the **Show in Table** box again. Required attributes are always displayed; these check boxes are not available.

Save Saves the current list of selected attributes and updates the Sample Utility table based on the selections.

Select All Selects all the attributes in the list.

Deselect All Removes all check marks from attributes in the list.

NOTE Mandatory attributes are always shown in the table; their check boxes appear “grayed out”.

Close Closes the dialog box. If changes have been made, the program asks if you want to save your changes before closing.

www.agilent.com

In this book

This guide describes how to use the Sample Manager tab of Agilent Genomic Workbench to organize microarrays and edit their attributes.

Revision A, February, 2010

G3800-90004

Agilent Technologies