Agilent
Genomic Workbench 6.5

Data Viewing

User Guide

Agilent Technologies

Notices

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In This Guide...

This guide describes how to import, organize, manage, export and display data and other content (experiments, gene lists, tracks) within Agilent Genomic Workbench 6.5. It is targeted for users who have no DNA Analytics application license(s). If you do have a DNA Analytics license and intend to analyze your data, see the *User Guide* for the type of data you want to analyze.

1 Getting Started

This chapter gives an overview of the capabilities you have in Agilent Genomic Workbench without a license, and describes the parts of the Agilent Genomic Workbench main window that you use to import, organize, manage, export and display array data and other content.

2 Importing, Managing, and Exporting Data and Other Content

This chapter describes how to import, organize, manage, and export data and other content within the user interface of Agilent Genomic Workbench.

3 Displaying Data and Other Content

This chapter shows you how to display log ratio data from imported feature extraction data files, as well as gene list and track content, in the Genomic Viewer. It also gives you instructions on how to modify the display to see the data and content the way you prefer.

4 Data Viewing Reference

This chapter describes the tab commands, shortcut menus, and dialog boxes that can appear.

Contents

1 Getting Started

This guide describes how to use Agilent Genomic Workbench to display data if you do *not* have a CGH, ChIP, or methylation (CH3) DNA Analytics license.

This chapter gives an overview of the window components and how to use Agilent Genomic Workbench to view data. Without a license, you have a number of capabilities, that include the import, management, export, and display of CGH, ChIP, and CH3 data. With a Feature Extraction (FE) license, you can also run an automated feature extraction workflow. For more information, see the *Workflow User Guide*.

To display imported data, you organize the data files into logical units called *experiments*. Experiments are used to define the data you want to display using Agilent Genomic Workbench. After you create them, and add array data, you can then display the data.

For a description of the commands and dialog boxes that appear when you use the program, see Chapter 4, “Data Viewing Reference”.

NOTE

Descriptions in this guide cover only the commands and options that are available for viewing data using Agilent Genomic Workbench *without* a DNA Analytics license. For information on commands and options that are available with a license, or for information on eArrayXD, Sample Manager, Quality, Workflow, or SureSelect Target Enrichment, see the *User Guide* for the module that you want to use.

Transferring Data from the eArray Web Site

When you install Agilent Genomic Workbench, a set of "core data" is transferred to your database. This includes administrative data, control grids, and the names (only) of Catalog and workgroup probe groups, bait groups, microarray designs, and libraries.

Additional data from the eArray Web site are required in order to perform $eArray_{XD}$ functions. This content is downloaded from the eArray Web site using the Data command from the Home tab. For example, to search for expression probes from the Agilent Catalog, you must first transfer the Catalog expression probe data from the eArray Web site to your server. See "To transfer catalog and workgroup data" on page 59. For more information on how to download data from the eArray Web site, see the *$eArray_{XD}$ User Guide*.

In order to import or analyze extracted microarray data using Agilent Genomic Workbench, you must first download the design files that match those microarrays from the eArray Web site, or import them. See "To download a design from eArray" on page 72 and "To import Agilent GEML design files" on page 48. It is not necessary to transfer the entire catalog or workgroup data from eArray to analyze extracted microarrays or run Feature Extraction or analysis workflows.

Using Agilent Genomic Workbench on a Mac

The content of this User Guide applies to both the Windows and Mac versions of Agilent Genomic Workbench. Both of these versions have the same features. However, when you use the Mac version of the program, please note the following:

Windows command	Equivalent Mac command
Right-click	• Command-click (⌘ -click) • On Macs with trackpads, other options are available. On certain machines, you place two fingers on the trackpad while you press the button below the trackpad. See the user guide for your specific machine. • If you have a third-party mouse that has more than one button, you may be able to use one of the buttons as a right mouse button.
Control-click	Control-click (Same as the Windows command)
Shift-click	Shift-click (Same as the Windows command)
(Close button)	(Close button)

Using Main Window Components to Display Data

You can use the data *viewing* capability in Agilent Genomic Workbench without a license. You can view data for many types of arrays, including CGH, ChIP, and Methylation (CH3). You can use the data *analysis* capability in Agilent Genomic Workbench only if you have a license for one or more of the DNA Analytics programs (CGH, ChIP, or Methylation).

What are the main window components?

You use four primary components of the Agilent Genomic Workbench main window to import, manage, export and display extracted data.

- Home tab commands — import, manage and export data
- Navigator — create and fill new experiments with array data

  When you make the experiment active, the data appear in the display, called Genomic Viewer.
- Genomic Viewer — display data and content in four Views: Genomic View, Chromosome View, Gene View, and Tab View
- View tab commands — change appearance of Genomic Viewer display

Figure 1 shows the main window of Agilent Genomic Workbench when the Genomic Viewer tab is selected, and identifies the names of its components.

To learn how to display log ratio data, content, and analyze data to show results, see the *User Guide* for which you have a DNA Analytics program license(s).

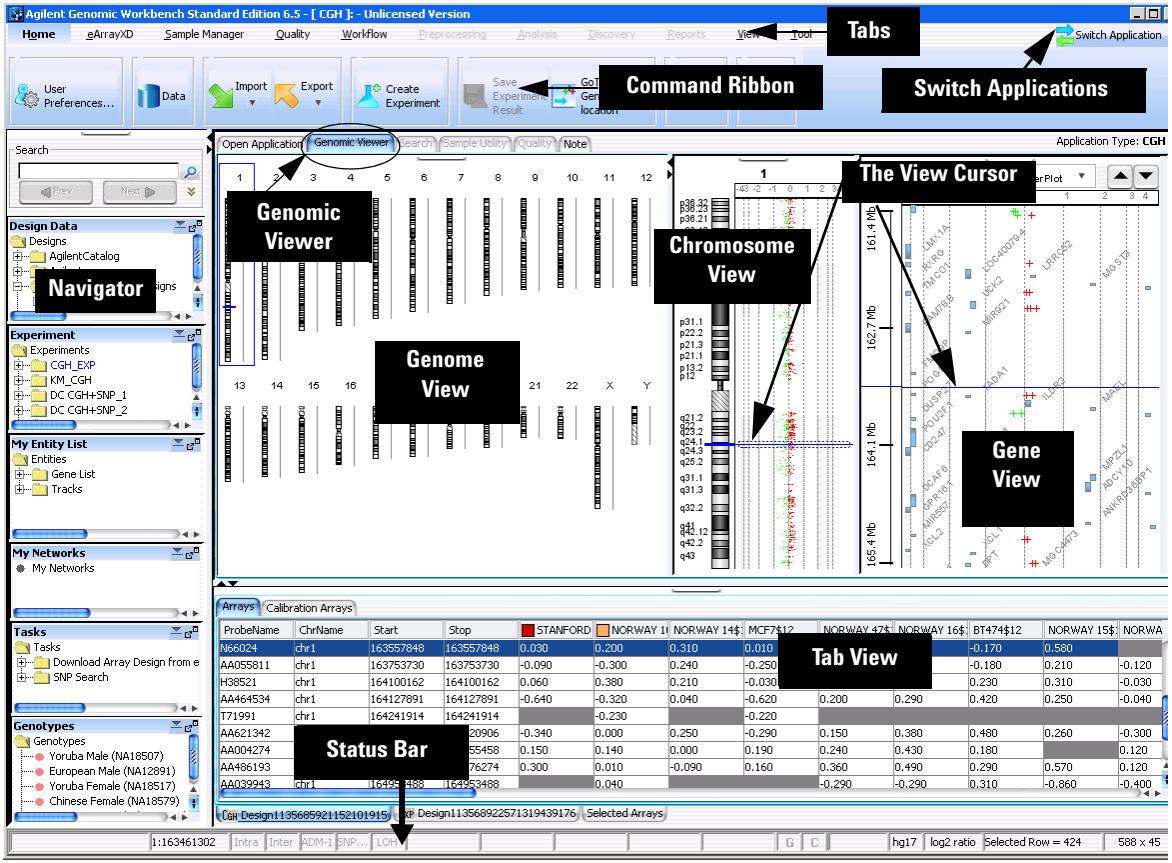


Figure 1 Agilent Genomic Workbench main window with major components – unlicensed CGH version with Feature Extraction license

What can you do with the main components to display data?

See the table below for the parts of the main window you use to display log ratio data, without a license.

Table 1 Components of Agilent Genomic Workbench main window for display of data

To do this	Use this part of the main window
Change program to CGH, ChIP, Methylation (CH3),Expression, microRNA, and SureSelect Target Enrichment	**Switch Application button**: Click the button and click the program you want to open. Do this to display different data types, even if you have no license. The window and options are different for the different program types.
Download design files	**Navigator for Design Files**: Right-click the name of a design file and click **Download**. Icons give the status of a library or microarray design (update required, draft, review, completed, or submitted). See the *eArray$_{XD}$ User Guide* for details,
Import or export data	**Home tab**: Click the **Import** or **Export** button to select the data you want to import or export. See Chapter 2, "Importing, Managing, and Exporting Data and Other Content" for more information.
Select array data to display in the three graphical views or in the Tab View as a table	**Experiment pane of the Navigator**: Create an experiment with the imported data, select the experiment, and then select the data within the experiment to display data. See Chapter 3, "Displaying Data and Other Content" for more information.
Display array data for only a certain portion of a chromosome	**Genome View**: Select a chromosome to display in Chromosome View. You cannot view log ratio data points here. **Chromosome View**: Select a gene region to display in Gene View. You can display log ratio data points here if you select **Scatter Plot** in the View Preferences dialog box. **Gene View**: See the log ratio data next to a selected region of a chromosome, with associated genes and track-based annotation. See Chapter 4, "Data Viewing Reference" for details about these Views.

Table 1 Components of Agilent Genomic Workbench main window for display of data

To do this	Use this part of the main window
Show/Hide or customize the data points for the scatter plots	**Gene View**: Move the mouse pointer over **Scatter Plot** to display the options. Or, right-click and then click **View Preferences**. **Chromosome View**: Right-click and then click **View Preferences**. **View tab**: Click **View Preferences**. See Chapter 3, "Displaying Data and Other Content" for information on how to do this.
Display array data next to tracks or gene lists	**My Entity List pane of Navigator**: Add or select a track or gene list to have it appear in Gene View. See Chapter 3, "Displaying Data and Other Content" for information on how to do this.
Change the appearance of the display	**View Tab**: Click **View Preferences**. From the View Preferences dialog box, you can change the orientation, select what type of data to view, and configure scatter plot options. **Genomic Viewer**: Right-click any View except the Tab View and select **View Preferences**. In the View Preferences dialog box, you can select to show or hide the scatter plots and how to display them. If you have one or more DNA Analytics licenses (CGH, ChIP, or Methylation), you can show or hide the results. See Chapter 3, "Displaying Data and Other Content" for more information.

Switching applications

You can use the Agilent Genomic Workbench to work with a variety of different data types. Because the requirements for the display of data (and calculation of results, if using a license) are different for different data types, you must switch the application for the type of data you want to display.

The Switch Applications menu, located at the upper right corner of the Agilent Genomic Workbench window, is used to change the application. The selected application is marked . The selected application is also displayed in the title bar of the Agilent Genomic Workbench main window.

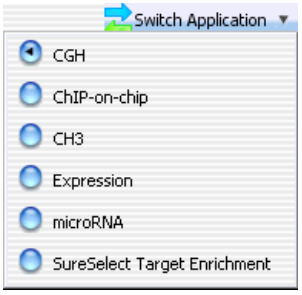


Figure 2 Switch Application menu for the Genomic Workbench

NOTE You cannot display Expression or microRNA data in Agilent Genomic Workbench; you can only design their microarrays.

Using Tabs and Command Ribbons

Tabs

When you click a *tab*, groups of commands or single commands appear that are specific for that tab. The tabs that are displayed change depending on what licenses you have, and what application is selected (such as CGH, ChIP, CH3). Without a license, you only use the Home and View tabs to display data.

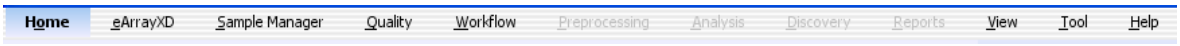


Figure 3 Agilent Genomic Workbench tab menu for CGH without a license

The following table summarizes what you can do from the tabs of Agilent Genomic Workbench, with a DNA Analytics (CGH, ChIP, CH3) application selected, but without any license installed.

Table 2 Capabilities in tabs

Tabs	Capabilities
Home	Set preferences for display of tracks. Set eArray user and data locations. Set licences for analysis applications. Import array files, design files, genome builds, tracks, array attributes, and experiments. Export experiments, tracks, and array attributes. Create an experiment. Find and go to a gene or genomic location.
eArrayXD	Create and search probe groups and microarray designs. See the *eArray$_{XD}$ User Guide* for information.

Table 2 Capabilities in tabs (continued)

Tabs	Capabilities
Sample Manager (Requires Feature Extraction license)	Import attribute files. Export attribute files. Display and edit sample attributes. For more information, see the *Sample Manager User Guide.*
Quality (Requires Feature Extraction license)	Import, query, create, and chart QC Metrics. For details, see the *Quality Tools User Guide.*
Workflow (Requires Feature Extraction license)	Create and run a Feature Extraction workflow. Analysis workflow requires CGH or ChIP license. For more information, see the *Workflow User Guide.*
View	Set up preferences for display of data Copy displayed data to the Clipboard Turn on or off display of Views and Navigator Turn on or off tabular display of signal intensity and annotations Turn on or off display of Cytoband information in Gene View Turn on or off highlight of nonunique probes Turn on or off display of custom data
Tool	Set parameters for plug-ins Display plug-in examples
Help	View program information and User Guides.

Commands

The area where commands appear is called a *command ribbon*. The command ribbon that appears when you click the Home tab is shown below. The commands that appear in the command ribbon change depending on what application module is selected, and which tab in that application module is selected.

Figure 4 Command ribbon for the Home tab

For a complete description of all of the command ribbons and commands you see in Agilent Genomic Workbench, see "Command Ribbons" on page 113.

Using the Navigator to Search for Data

This section gives you instructions on how to search for design files, extracted Feature Extraction data, experiments and other information in the Navigator of Agilent Genomic Workbench. The Navigator contains different panes when you select the eArray$_{XD}$, Sample Manager, or Workflow tabs. See the User Guides for those applications for information on the Navigator contents.

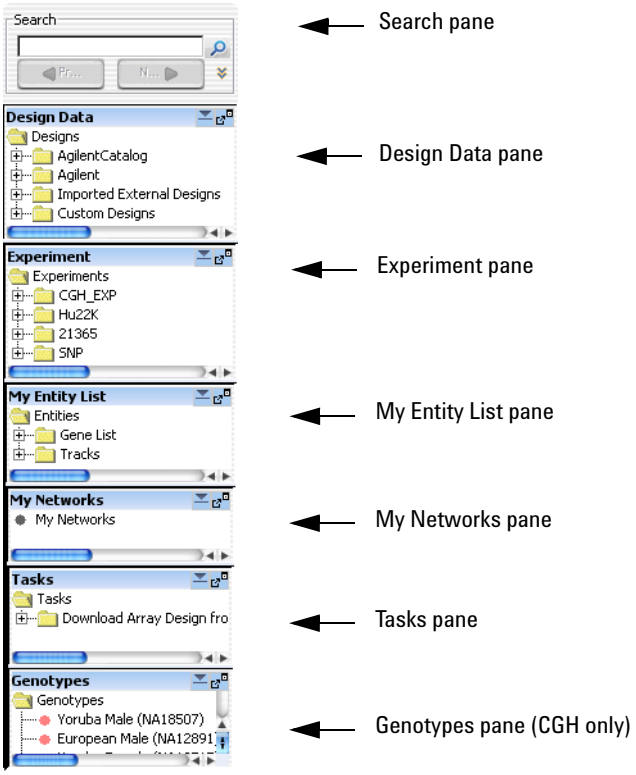


Figure 5 Navigator panes for CGH

The Navigator (Figure 5) shows the array data, experiments, and other content stored in Agilent Genomic Workbench that is available to the logged in user for display. It contains the following panes:

Navigator Pane	Comments
Search	Lets you search within any pane of the Navigator for a specific design or content, or for items that contain a specific string of characters, when using asterisks (*) as wildcards. See "Search pane" on page 123 for more information.
Design Data	Contains microarray data files, organized by design and application type, and then by genome build. Shows all probe groups and microarray designs that are available to you, organized by folders. In general, you can: • Expand or collapse folders to show or hide content • Look at the icon that appears with an item to monitor its status. • Right-click the name of a folder or item to open a shortcut menu that lets you take action on the item. See "Design Data pane – icons, special text, and buttons" on page 129 and "Design Data pane – actions and shortcut menus" on page 131.
Experiment	Contains Agilent Genomic Workbench experiments. Experiments are organizational units that contain links to microarray data and design files. See "Experiments Folder" on page 137, "Experiment pane – icons, special text, and buttons" on page 136, and "Experiment pane – actions and shortcut menus" on page 137.
My Entity List	Contains gene lists and tracks: • **Gene Lists** are collections of genes of interest. You can create them within the program, import and export them, and apply them to Gene View and Chromosome View. • **Tracks** are collections of annotation or other information that map to specific genomic locations. You can import, export, and combine tracks, and display them in Gene View with your array data and analysis results. See "My Entity List pane – icons, buttons, and special text" on page 141 and "My Entity List pane – actions and shortcut menus" on page 141.
My Networks	Contains the biological networks/pathways that you found using Network Search or that you create using a literature search in eArrayXD. For more information, see the *eArray$_{XD}$ Users Guide.*

Navigator Pane	Comments
Tasks	Shows the jobs that you have submitted (such as downloading designs from eArray). Some jobs are completed locally by the $eArray_{XD}$ server program. Others are sent to the eArray Web site for completion. In general, you can: • Look at the icon that appears with a job to monitor its status. • Right-click the name of a pending task to open a shortcut menu that lets you take further action on the job. See "Tasks pane" on page 143.
Genotypes (CGH only)	Shows SNP genotype reference samples in the database. You can import, display details, rename, or delete genotype references from this pane. See "To import a genotype reference file" on page 64.

To search the Navigator

You can search one or all of the panes of the Navigator for items that match a specific search term. Figure 6 shows the search pane of the Navigator, and identifies a couple of its elements.

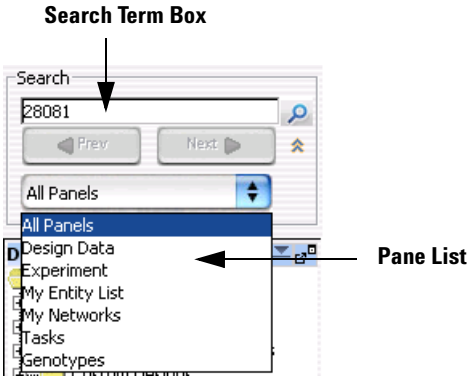


Figure 6 Search pane of the Navigator

1. At the top of the Navigator, in the Pane list, select the pane to be searched. To search in all panes, select **All Panels.** If the pane list is not visible, click ⌄⌄ to show it.
2. In the search term box, type the desired search term. The search term is not case sensitive, but it must contain the complete entry that you want to find. You can use asterisks (*) to represent one or more unspecified characters. For example, type *12345* to find any item that contains "12345".
3. Click 🔍.

   The program searches the selected pane(s) for items that match your search term. If it finds matching items, the program expands the appropriate folders, and displays the names of the matching items in red. The first matching item is highlighted in yellow.
4. Do any of the following:

- To highlight the next matching item, if one is available, click Next.
- To highlight the previous matching item, click Prev.

5 After you complete the search, click  to clear the results of the search, as well as your search term.

Using the Genomic Viewer to Display Data

What is the Genomic Viewer?

Genomic Viewer is the graphics and tabular display section of the Agilent Genomic Workbench main window. In the Genomic Viewer, extracted data and analysis results can be tabulated and displayed next to depictions of the genome, selected chromosome, and selected genes of the species whose array data you are analyzing.

There are four main views in the Genomic Viewer, as shown in Figure 7.

- **Genome View** – A graphical representation of the entire genome for the selected species. Use this view to select the chromosome to show in the other views.
- **Chromosome View** – A graphical representation of the selected chromosome, displayed with cytobands and a plot area. Click or drag the mouse to select a region to display in the Gene View.
- **Gene View** – A more detailed view of the chromosomal region selected in the Chromosome View.
- **Tab View** – Displays design annotation and log ratio data related to the chromosome you select in Chromosome View

For more information on the Genomic Viewer and its views, see Chapter 4, “Data Viewing Reference”.

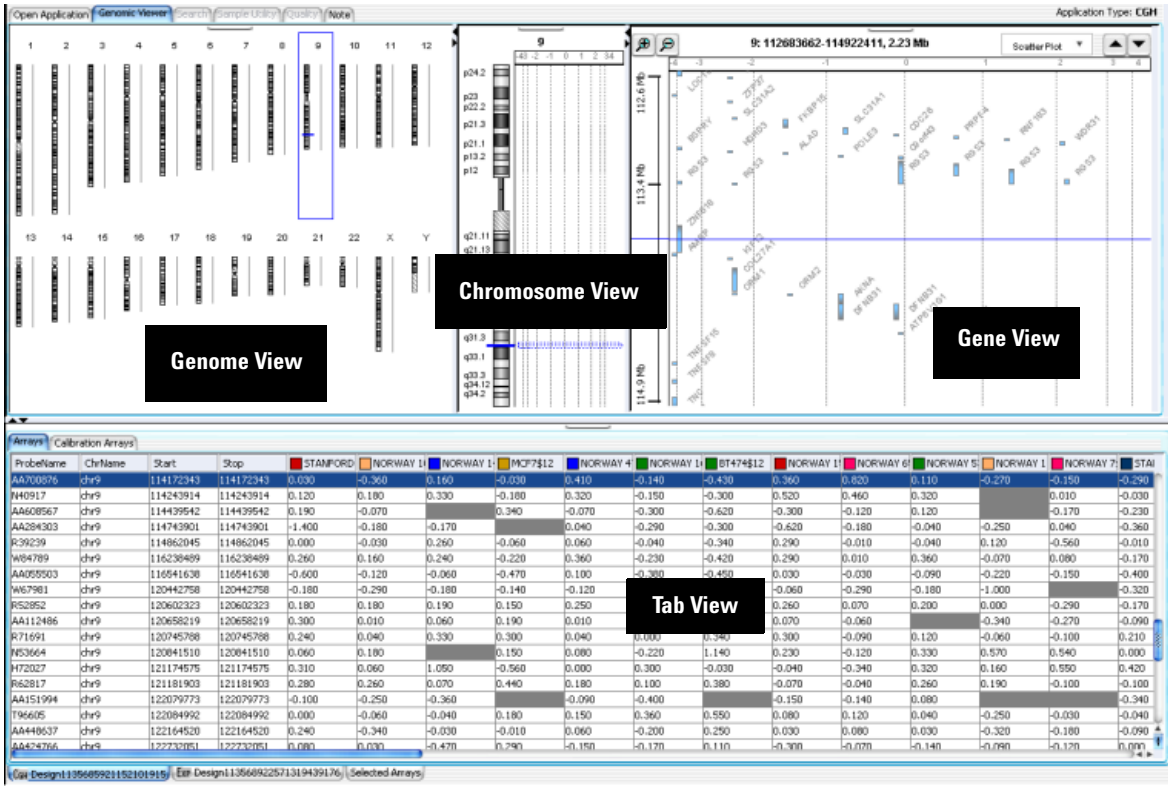


Figure 7 Genomic Viewer in vertical orientation

To change the size of and detach panes from the Agilent Genomic Workbench main window

- To change the size of a pane in the main window, drag one of its inside borders.
- To detach a pane from the main window and open it in a separate window, click its **Detach** button _____ .

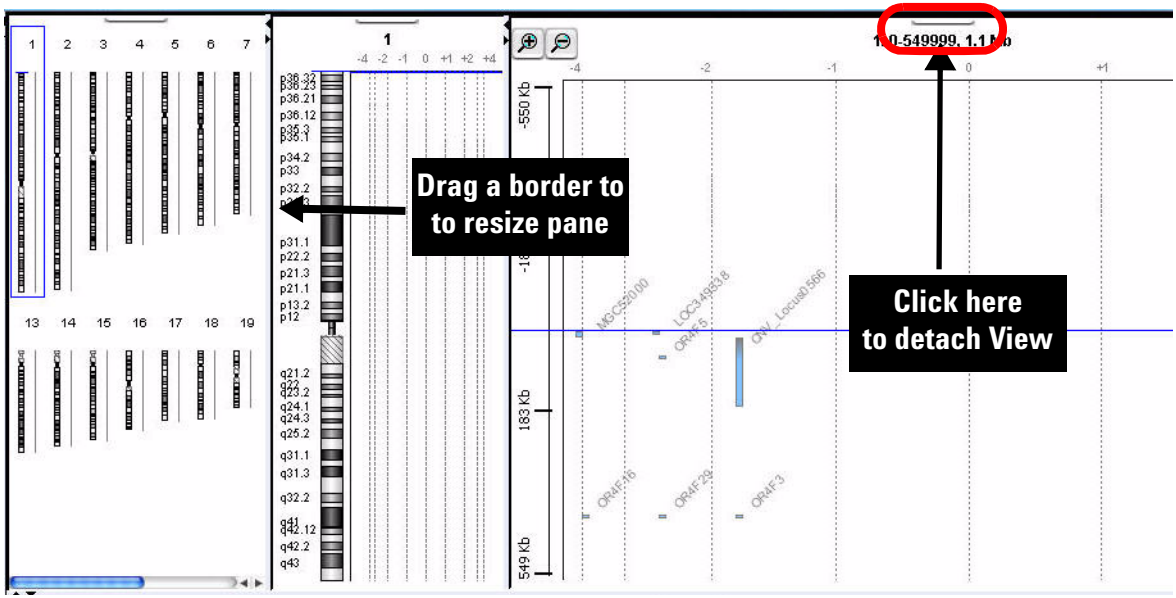


Figure 8 Changing the size of and detaching panes

To maximize and reattach panes to the Agilent Genomic Workbench main window

- To display a view full-screen in a separate window, click its **Maximize** button.
- To reattach a view in a separate window to the main window, click its **Close** button.

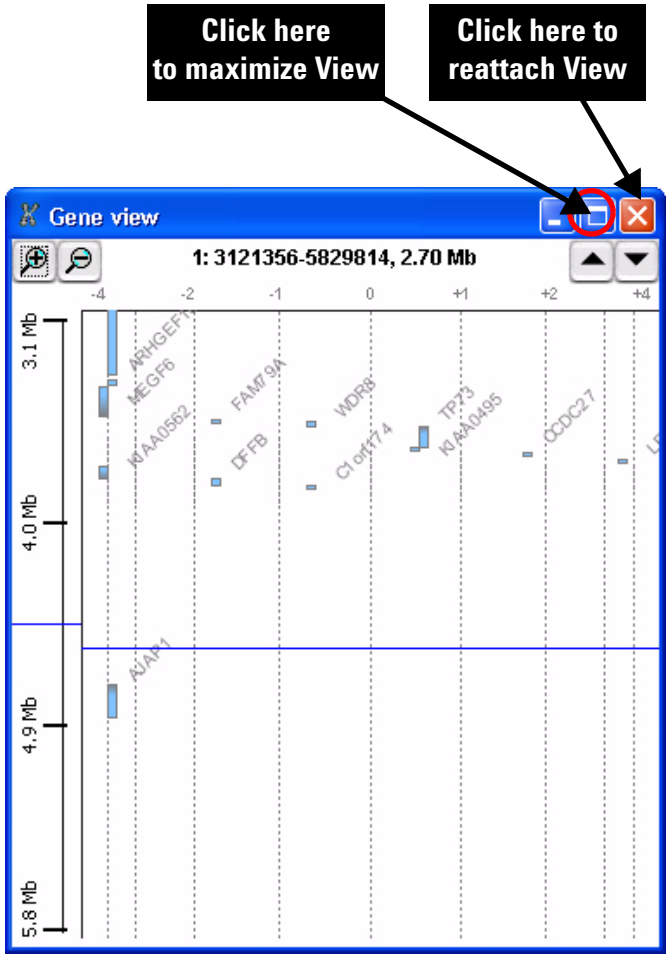


Figure 9 Maximizing and reattaching panes

General Instructions for Displaying Microarray Data

An *experiment* is the folder that holds data from any array set you select for the experiment. The folder also holds analysis results.

You set up experiments to display all data in the Genomic Viewer. To set up an experiment you:

- Import data
- Create a new experiment
- Add the imported data to the experiment
- Select the experiment to display data

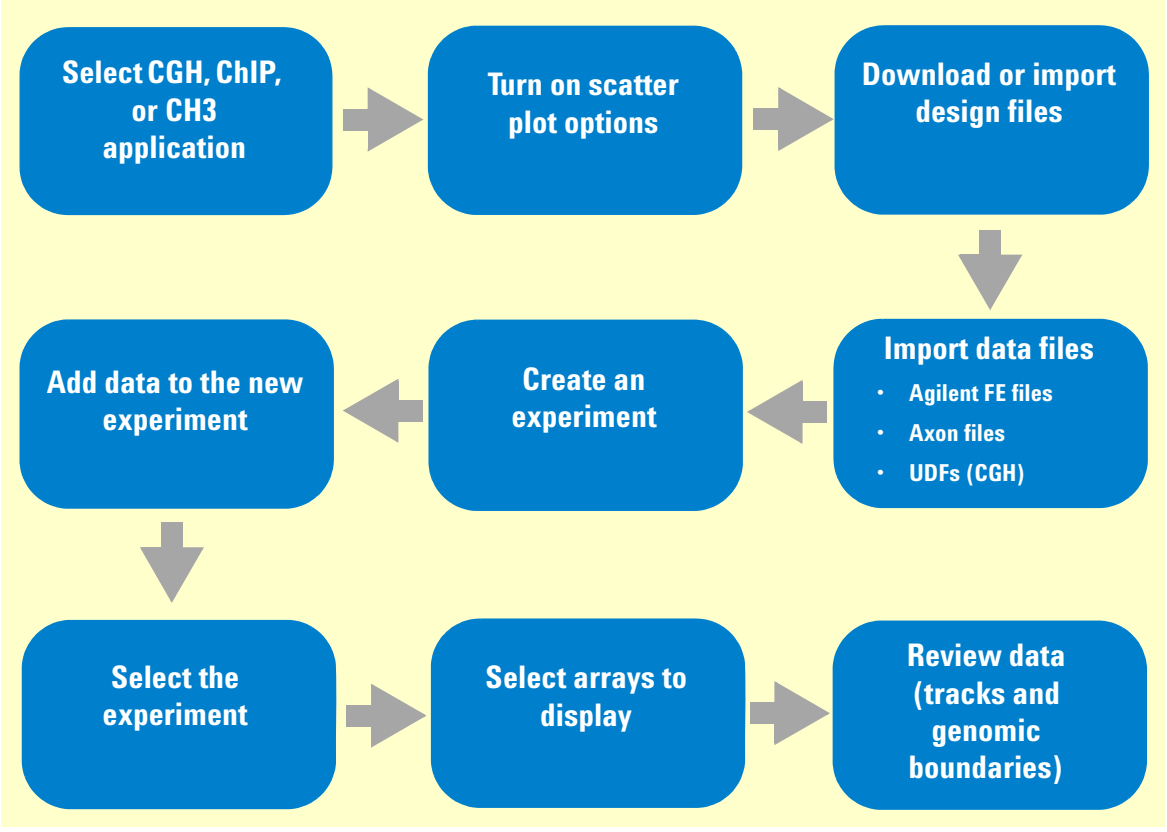


Figure 10 Typical pathway for display of microarray data

Quick-start Instructions for Displaying Microarray Data

The instructions in Table 3 show how to organize imported log ratio Feature Extraction data so you can display your data next to the corresponding cytobands. Without a DNA Analytics license, only log ratio data is displayed, not results.

These instructions assume that:

- All instructions apply whether you have a license or not.
- You use only Agilent data and design files. If you choose to use the demo Agilent design and data files that come with the program, you do not need to import those files.

Table 3 How to display data in Agilent Genomic Workbench

To do this	Follow these instructions	Comments
Select the application	1 If you are in another application, click **Switch Application**. 2 Select the **CGH, ChIP,** or **CH3** application type. You do not need a license to perform the following steps.	• If you are using a licensed version of the application, make sure all the analysis options are turned off. (Clear check boxes in the Analysis command ribbon.)
Turn on scatter plot options	1 By default, the scatter plot for log ratios is turned on for Gene View. To view or change the scatter plot options, in Gene View move the pointer over the arrow next to **Scatter Plot** and mark one or more of the check boxes. See "Gene View" on page 151. 2 To view or change additional options for the scatter plot, or to change the orientation of the panes in the Genomic Viewer, right-click in one of the panes and select **View Preferences**. See "View Preferences" on page 258.	• The check boxes in Scatter Plot set the program to draw data points that represent log ratio or other selected values. • If you do not turn on the scatter plot functions, you will see nothing in the Genomic Viewer. • If you are using the Agilent demo files, continue to *Create an Experiment*.

Table 3 How to display data in Agilent Genomic Workbench (continued)

To do this	Follow these instructions	Comments
Import design files or download them from the eArray Web site.	• To download a design from the eArray Web site, expand the Designs folder of the Navigator, and locate the design. Right-click the design, and select **Download from eArray.com.** **OR** **1** To select Agilent GEML-based microarray design files for import, click **Home > Import > Design Files > GEML File.** **2** In the dialog box that appears, select the file you want to import, then click **Open.** The Import GEML design dialog box appears. **3** If necessary, select the Genome Build for your files. **4** Click **Start Import**. Design Import Summary appears, and the design file with selected genome build appears in the Navigator, in the Imported External Designs folder of the Design Data pane. See "Using the Navigator to Search for Data" on page 25.	• If you want to import an Agilent or Axon array data file, its design file must be in the database. If the design file is not already available in the Navigator, or has a yellow arrow next to it, you must download it from the eArray Web site, or import it. **Note**: Agilent catalog designs must be downloaded from the eArray Web site. • Designs with a green arrow are already downloaded. • When you import a design file, the program shows the genome build(s) that can be used by the design file as nodes under the design file. • The current builds are available in Agilent Genomic Workbench. Should you want to import a design file for a different genome build, you must import the genome build first.
Import data files • **Agilent FE files** • **Axon files** • **UDFs**	**1** To import Agilent FE files, click **Home > Import > Array Files > FE File.** **2** Find and select the desired file, then click **Open.** To select multiple files, hold down the **Ctrl** key and click their names. **3** In the dialog box that appears, in **Dye Flip,** select either **Normal** or **Flipped** for each FE or Universal Data File (UDF). **4** Click **OK.** **5** In the Navigator, check the Design Data folder to make sure that the program imported the correct files.	• In Dye-Flip, select **Normal** if: ◦ The test samples were labeled with cyanine-5 (red). ◦ The control samples were labeled with cyanine-3 (green). ◦ The imported ratio (test/control) will be reported directly. • In Dye-Flip, select **Flipped** if: ◦ The test samples were labeled with cyanine-3 (green). ◦ The control samples were labeled with cyanine-5 (red). ◦ The imported ratio (control/test) will be reported with the ratio inverted (test/control).

Table 3 How to display data in Agilent Genomic Workbench (continued)

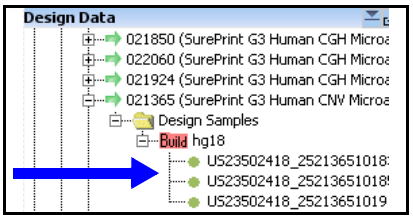
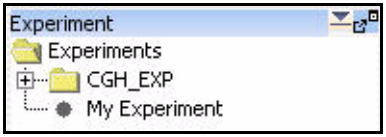
To do this	Follow these instructions	Comments
		• The program automatically puts the imported data under the genome build folder that belongs to the design used with the arrays.
Create an experiment	**1** In the Experiment pane of the Navigator, right-click the **Experiments** folder, then select **New Experiment.** A dialog box appears. **2** Type a name and an optional description for the experiment. **3** Click **OK.** **4** (optional) To add data to the experiment now, click **Properties**. Otherwise continue and add data, as described in the next step.	• The new experiment appears as a node within the Experiment pane of the Navigator. The node becomes a folder once data is added to the experiment. 
Add data to the new experiment	**1** Fully expand the Design Data folder, and click the name of an array you want to add to your new experiment. **2** Drag the selected arrays to the folder of the new experiment.	• To select additional arrays within the same design, hold down the **Ctrl** key and click their names. • You can also right-click the name of the experiment, and select **Show Properties** to add arrays to an experiment.

Table 3 How to display data in Agilent Genomic Workbench (continued)

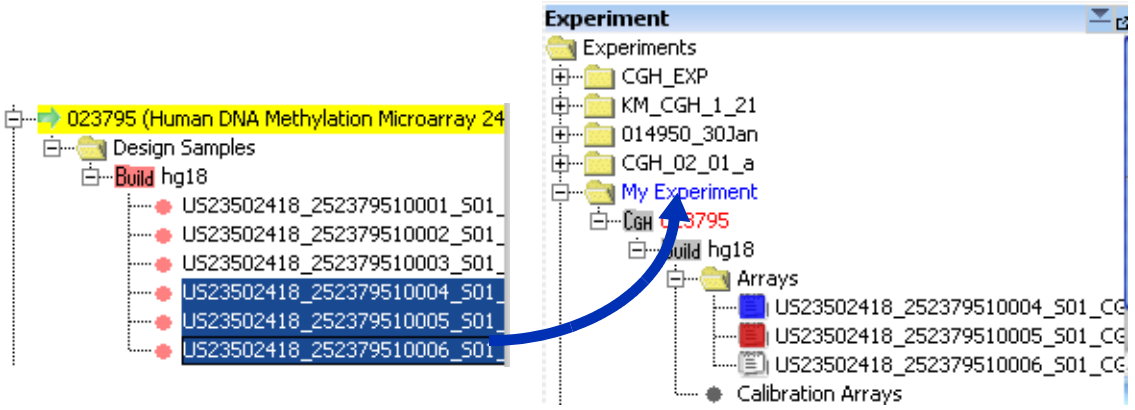
To do this	Follow these instructions	Comments
		
Select the experiment	**1** In the Navigator, double-click the name of the experiment. A dialog box appears. **2** Click **Yes.** • In the Navigator, the name of the experiment turns blue, which indicates that it is the active experiment. • You now see the scatter plot log ratio data in the Chromosome and Gene Views.	• The program automatically selects the first array in the experiment for display. • A data table appears in Tab View. • At this point if the arrays within the experiment use a genome build different from the one represented in the Views, the program changes the chromosomal and gene information used in the Views.

Table 3 How to display data in Agilent Genomic Workbench (continued)

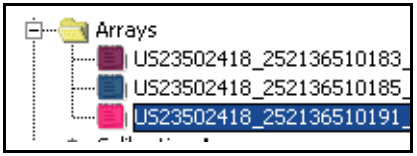
To do this	Follow these instructions	Comments
Select arrays to display	To select an array, right-click the array name, and click **Select.** To clear an array selection, right-click the name of the array in the Navigator, then click **Deselect.**  You can also select or deselect several arrays at a time. Hold down the **Shift** key and click the contiguous arrays whose log ratio data you want to display. Hold down the **Ctrl** key and click the non-contiguous arrays whose log ratio data you want to display.	• In the Navigator, the icons beside the arrays become colored, when enabled for the selected experiment. • In Tab View, colored squares appear in the column heading for the arrays when selected. You can select or deselect only one array at a time in Tab View, or you can select or deselect all arrays at the same time. • The program adds the data from the array to the Chromosome and Gene views.

Table 3 How to display data in Agilent Genomic Workbench (continued)

To do this	Follow these instructions	Comments
Review data	• In Genome View, click a chromosome of interest. • In Chromosome View, drag the pointer over a region of the chromosome graph to display it with more resolution in Gene View. • In Gene View, click the + and – buttons to zoom in and out. • In Gene View, click anywhere within the scatter plot to recenter the view at that location. • To see information for the log ratio data, in Gene View, move the pointer over the arrow next to Scatter Plot to show the options. Under Configure Coloring schemes, mark the check box and select **Log Ratio Values**. • In Gene View, zoom in so that single data points are visible, then place the pointer over a data point. If ToolTip is enabled in View Preferences, a box appears that describes the data point.	• The solid, horizontal blue lines in Chromosome and Gene views are referred to as the *View cursor.* The chromosomal location of the cursor appears in the Status bar, located on the lower left corner of the screen. • If you still cannot see the Scatter Plot data in Chromosome and Gene View or ToolTips in Gene View, do the following: **a** Right-click either View and click **View Preferences**. **b** Under Data Visibility, select **All Views,** then mark the **Scatter Plot** check box. **c** Under Data Visibility, select **Gene View** and then click **Scatter Tool Tip**. • When you right-click an empty area of Gene View, you can also use the shortcut menu to create a gene list or track, or to search the Agilent eArray database for probes from the selected region. See the *User Guide* for your application.

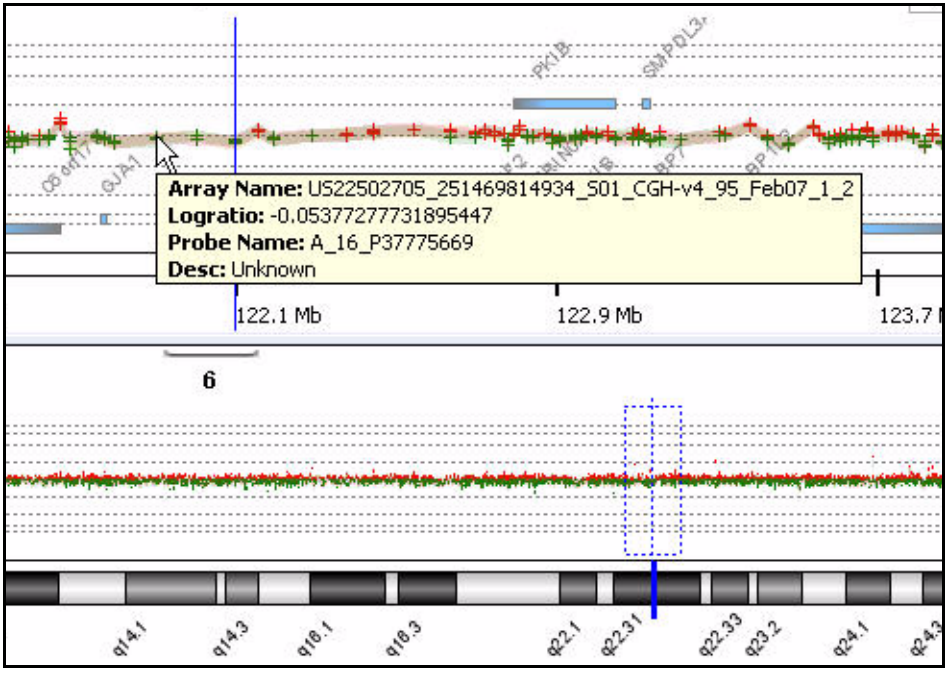


Figure 11 Segment of Chromosome View and Gene View (horizontal orientation) with scatter plot of log ratio data and ToolTip

Getting Help

To get help within Agilent Genomic Workbench

Agilent Genomic Workbench has several help resources. All help guides open in Adobe® Reader®.

Help Resource	Description/Instructions
Data Viewing User Guide	This user guide, which you are now reading, supplies comprehensive help on all available Data Viewing tasks. You can access it easily from anywhere within the program. **1** In any tab of Agilent Genomic Workbench, click the **Help** tab. **2** On the Help Ribbon, click **Data Viewing.** The Data Viewing User Guide opens.
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 help guide. The selected guide opens.
Product Overview Guide	An additional guide gives an overview of the capabilities within Agilent Genomic Workbench and describes how to start and find help for all of the programs. In addition, it helps you with system administration and troubleshooting. **1** In any tab of Agilent Genomic Workbench, click the **Open Application** tab. **2** At the upper right corner of the Open Application tab, click **Product Overview**.

To contact Agilent Technical Support

Technical support is available by phone and/or e-mail. A variety of useful information is also available on the Agilent Technical Support Web site.

Resource	To find technical support contact information
Agilent Technical Support Web site	**1** Go to http://chem.agilent.com. **2** Select a country or area. **3** Under Quick Links, select **Technical Support**. **4** Select from the available links to display support information.
Contact Agilent Technical Support by telephone or e-mail (United States and Canada)	Telephone: (800-227-9770) E-mail: informatics_support@agilent.com
Contact Agilent Technical Support by telephone or e-mail (for your country)	**1** Go to http://chem.agilent.com. **2** Select **Contact Us**. **3** Under Worldwide Sales and Support Phone Assistance, click to select a country, and then click **Go**. Complete e-mail and telephone contact information for your country is displayed.

To learn about Agilent products and services

To view information about the Life Sciences and Chemical Analysis products and services that are available from Agilent, go to www.chem.agilent.com.

2 Importing, Managing, and Exporting Data and Other Content

This chapter describes how to import, organize, manage, and export data and other content within the user interface of Agilent Genomic Workbench. The program lets you import many different kinds of files, including array data and design files from Agilent products and other sources, and other content such as annotation tracks.

See Chapter 4, “Data Viewing Reference” for a description of the Agilent Genomic Workbench main window and its contents, and descriptions of the dialog boxes that can appear.

Importing Files

You use the Home tab to import many kinds of files into Agilent Genomic Workbench. The table below summarizes the kinds of files you can import, and the topics in this section that describe how to import them.

The Design Data pane of the Navigator displays all of the content available for the user who is logged in. Some of this content (such as Catalog designs not yet downloaded) must be downloaded from the eArray Web site before it can be used. Some of the content is available for you to use but not change (red, read-only content), and some of the content you imported and can change (green). See "Navigator" on page 125 for more information on the Navigator panes and how to use them.

For information on downloading microarray designs and other content from the eArray Web site, see the *eArray$_{XD}$ User Guide*.

File type	Comments	See these topics
Microarray data files	• Agilent Feature Extraction (*.txt) data files • Axon (*.gpr) data files • Universal Data Files (UDFs) (*.txt files)	"To import Agilent FE or Axon data files" on page 50 "To import a UDF file" on page 51
Microarray design files	• Agilent GEML (*.xml) design files • Axon (*.gal) design files	"To import Agilent GEML design files" on page 48 "To import Axon design files" on page 49
Genome builds	Agilent-supplied genome information for human, mouse and rat genomes	"To import a genome build" on page 54
Tracks	BED format annotation track files	"To import tracks" on page 55
Array attributes	Attribute .txt files that you have created yourself or previously exported from Agilent Genomic Workbench	"To import array attributes" on page 56

File type	Comments	See these topics
Experiments	ZIP file of experiments exported from Agilent Genomic Workbench	"To import an experiment file" on page 57
Custom Genome	ZIP file containing at least one FASTA format sequence file See the *eArray$_{XD}$ User Guide* for requirements and information.	"To import a genome" on page 58
Genotype Reference (CGH only)	Text or .xls file that contains reference genotype and expected number of cuts for each SNP probe in the sample.	"To import a genotype reference file (CGH only)" on page 59.

To select a different location for data files

By default, the program stores microarray and experimental data in C:\Program Files\Agilent\Genomic Workbench Standard Edition <version number>\data. If you want, you can select a different location.

1 In the Home tab, click **User Preferences**.

The User Preferences dialog box appears. See "User Preferences" on page 250.

2 In the **Miscellaneous** tab, under **Data Location,** click **Browse**.

An Open dialog box appears.

3 Select a location, then click **Open.**

The selected location appears in the User Preferences dialog box, in Data Location.

4 Click **OK.**

CAUTION If you change the location for data files, and there is a data folder in that location, the data will be overwritten by the current data.

To import Agilent GEML design files

The Agilent Genomic Workbench database must contain designs that match the Agilent Feature Extraction data files you want to import. Your imported GEML files contain array-specific information such as probe names, annotations, and chromosomal locations, and are associated with a specific genome build.

NOTE Catalog design files must be downloaded from the eArray Web site. You can import multiple genome builds of the same catalog design, but you must download the design from the eArray Web site first.

To import an Agilent GEML file, use the following procedure:

1 In the Home tab, click **Import > Design Files > GEML File.**

The Import Design Files dialog box appears. See "Import" on page 211. The dialog box shows only *.xml files.

2 To select a file for import, click its name. To select additional files, hold down the **Ctrl** key while you click their names.

3 Click **Open.**

The program validates the selected file(s), and the Import GEML Design Files dialog box appears. See "Import GEML design files" on page 215.

- If a design file passes validation, the Status column will show **Valid** in green.
- If a design file is already in the database, the Status column will show **Overwrite** in yellow. You can continue with the import, or cancel.
- If a design file is a catalog design that has not been downloaded from the eArray Web site, the Status will show **Not allowed** in red. You must download that design from eArray first.
- If a design file fails validation, **Corrupt** appears in the Status column beside it, and the program will not import the file. To remove the corrupt array from the list, click **Remove**  .

4 Click **Start Import.**

The program imports the file(s). The files appear as new design folders in the Imported External Designs folder of the Design Data pane of the Navigator, with the genome build as a node within the folder.

You can import two design files with the same name, but associated with different genome builds; for example, Hg17 or Hg18. If you do, the program creates a single design folder with two nodes, one for each genome build.

To import Axon design files

You can import Axon (*.gal) microarray design files into Agilent Genomic Workbench. The program requires the Axon design files that match all Axon array data files you import.

1 In the Home tab, click **Import > Design Files > Axon File**.

The Import Axon Design Files dialog box appears. See "Import" on page 211. The dialog box shows only *.gal files.

2 To select a file for import, click its name. To select additional files, hold down the **Ctrl** key while you click their names.

3 Click **Import.**

The program validates the selected file(s), and the Set genome build and species for Axon design files dialog box appears. See "Set genome build and species for Axon design files" on page 236.

- If a design file passes validation, the Status column will show **Valid** in green.
- If a design file fails validation, **Corrupt** appears in the Status column beside it, and the program will not import the file. To remove the corrupt array from the list, click **Remove**  .

4 For each design file, select the appropriate **Species** and **Genome Build.**

5 Click **Start Import.**

The program imports the file(s). The files appear as new design folders in the Designs folder of the Design Data pane, organized by application (CGH, ChIP, or methylation, for example).

To import Agilent FE or Axon data files

You can import several types of microarray data files into Agilent Genomic Workbench:

- Agilent Feature Extraction (FE) *.txt data files
- Axon (*.gpr) data files
- Universal Data Files (UDFs) (*.txt files) See "To import a UDF file" on page 51 for instructions on how to import this file type.

In order to import Agilent Feature Extraction files, the representative GEML array design files must imported first. In order to import Axon data files, the representative Axon.gal design files must be imported first. See "To import Agilent GEML design files" on page 48 or "To import Axon design files" on page 49.

1 In the Home tab, do one of the following:
   - To import Agilent FE data files, click **Import > Array Files > FE File**.
   - To import Axon data files, click **Import > Array Files > Axon File**.

   A dialog box appears. Only data files of the appropriate type appear. See "Import" on page 211.

2 To select a file for import, click its name. To select additional files, hold down the **Ctrl** key while you click their names.

3 Do one of the following:
   - For Agilent FE files, click **Open.**
   - For Axon files, click **Import.**

   The Agilent Feature Extraction/Axon File Importer dialog box appears. See "Agilent Feature Extraction Importer" on page 163.

4 Set the following, as needed:

Setting	Comments
Name	The names of imported arrays are often cryptic. You can give any array a more meaningful label. **a** Double-click the name of the array. **b** Edit the name. **c** Press **Enter**.

Setting	Comments
Dye Flip	For each array: • Select **Normal** if: ◦ The test samples were labeled with cyanine-5 (red). ◦ The control samples were labeled with cyanine-3 (green). ◦ The imported ratio (test/control) should be reported directly. • Select **Flipped** if: ◦ The test samples were labeled with cyanine-3 (green). ◦ The control samples were labeled with cyanine-5 (red). ◦ The imported ratio (control/test) should be reported with the ratio inverted (test/control). The program does not combine dye-flip pairs.
Overwrite arrays with duplicate names	If you mark this option, the program deletes an existing array data file if it has the same name as one you import.

5 Do one of the following:

- To import the file(s) while you wait, click **OK.**
- To import the file(s) in the background, click **Run in Background.** This lets you continue while the program imports the files.

To import a UDF file

UDF files are plain text files that contain array data in tab-delimited format. Files must contain the following six columns of information, in any order. Each column must contain the following column names, as column headers, or you must "map" the names from the file to these columns in Agilent Genomic Workbench:

- Probe name
- Chromosome name
- Start position
- Stop position
- Description
- Signal intensity data (The file can contain additional columns, each with data from an additional array.)

When you import a UDF file, the program creates a new design based on the information you enter during import, and the information in the file itself. This design contains all of the arrays represented in the file. The program also creates a new experiment that contains the arrays.

1 In the Home tab, click **Import > Array Files > UDF File.**

The UDF Files dialog box appears. See "Import" on page 211. Only *.txt files appear in the dialog box.

2 Select the UDF file, then click **Open.**

The Select data type for experiments dialog box appears. See "Select data type for experiments (UDF files – CGH or CH3)" on page 235.

3 For each array, set the following, as needed:

Setting	Comments
Experiment Name	By default, the program creates an experiment with the same name as the imported file. To change the name: **a** Double-click the name. **b** Edit the name. **c** Press **Enter.**
Data type	• Select the mathematical form of the signal intensity data for the array. The options are **ratio, $\log_2$ ratio, $\log_{10}$ ratio,** and **ln ratio.**
Design type	• Select **cgh, expression,** or **CH3.**

4 Click **Continue.**

The Universal Data Importer – Map column headers dialog box appears. The main table in the dialog box contains the first few rows of data from the file. Column headings derived from the first line of the file appear at the top of the table as a guide, but the program does not interpret these headings. See "Universal Data Importer - Map Column Headers" on page 248.

NOTE

When you "map" a column, you assign the column heading (in an external file) to a column heading in Agilent Genomic Workbench.

5 Below each column heading, select the label that identifies the content of the column. Use each label exactly once, except for LogRatio, which you can use many times. Alternatively, in **Select Mapping,** select a saved column map.

These options are available:

Column Label	This column contains:
ProbeName	Names of probes.
ChrName	Names of chromosomes.
Start	First chromosomal location to which each probe is designed.
Stop	Last chromosomal location to which each probe is designed.
Description	Text annotation related to the probe.
LogRatio	Array data values that correspond to each probe. You can use this label more than once.

6 Under **Species Info,** select the **species** and **Genome Build** appropriate to the data in the file.

7 If you expect to import many similar UDFs in the future, follow these steps to save the column map:

a Under **Mapping Info,** click **Save Mapping As.**
An Input dialog box appears.

b Type a name for the column map, then click **OK.**
The name of the saved map appears in Select Mapping.

In the future, you can select this mapping and apply it to any UDF file that you import.

8 By default, the program creates a "Virtual Array ID" that becomes the ArrayID attribute for the array(s) in the UDF. To create your own virtual Array ID, follow these steps:

a Under **ArrayID Info,** clear **Use System Generated Array ID.**

b Double-click the number in **Virtual Array ID,** then type your own Array ID.

For more information on Array IDs, see the *Sample Manager User Guide*.

9 Click **Import**.

The program validates your column mapping. A dialog box appears. If you need to fix the column map, the dialog box has a list of the missing column label(s). If the column map is complete, a message asks if you want to import additional files with the same mapping.

10 Do one of the following:

- If you want to import additional files with the same column mapping, follow these steps to include these files in the import:
  - **a** Click **Yes.**
    The UDF Files dialog box appears.
  - **b** Click the name of a file to select it for import. Hold down the **Ctrl** key while you click the names of additional files.
  - **c** Click **Open.**
- If you do not want to include additional file(s) in the import, click **No.**

The Program imports all requested files, and the UDF Import Summary dialog box appears. This dialog box shows the imported files, the number of lines of data that were imported for each file, and the number of lines that were skipped, if any. If a file name appears in red, the program may not have imported the file. See "UDF Import Summary (CGH or CH3)" on page 247.

11 Click **OK.**

In the Design Data pane, in the appropriate design type folder within the Design Data folder, a new design folder appears. The design folder contains the imported array data.

A new experiment appears in the Experiments folder in the Experiment pane, that contains the array data. This experiment has the name of the imported UDF file, unless you changed it during import.

To import a genome build

In general, the program uses the genome build specified in the array design file, and protects it from changes. If a genome build is not available in the program, you can import one.

NOTE Use arrays from a single genome build in an experiment.

1 In the Home tab, click **Import > Genome Build**.

The Import Genome Build dialog box appears. See "Import Genome Build" on page 219.

2 Set the following. All are required.

Setting	Instructions
Species	• Type the genome's species of origin, as you would like it to appear within the program.
Build Name	• Type the name of the genome build you want to import, as you would like it to appear within the program.
Refseq File	This file contains information on gene locations for Gene View. **a** Click **Browse**. A dialog box appears. **b** Select the file, then click **Open.**
Cyto-band File	This file contains the graphic information on the cytobands for Genome and Chromosome Views. **a** Click **Browse**. A dialog box appears. **b** Select the file, then click **Open.**

3 Click **OK.**

To import tracks

You can import BED format track files into Agilent Genomic Workbench. Track files contain specific features correlated with chromosomal locations, and apply to a specific genome build of a given species.

1 In the Home tab, click **Import > Track**.

The Import Track dialog box appears. See "Import Track" on page 220.

2 Set the following. All are required.

Setting	Instructions
Species	• Select the species to which the track applies.
Build Name	• Select the specific genome build of the species to which the track applies.
Track Name	• Type a name for the track. This name identifies the track within the program, including the name that appears if you include the track in Gene View.
Track File	**a** Click **Browse**. A dialog box appears. **b** Select the name of the track (*.bed) file that you want to import. **c** Click **Open.** The location of the file appears in Track File.

3 Click **OK.**

The program imports the track. To view the track in Gene View, and to manage tracks, see "To show tracks in Gene View" on page 103.

To import array attributes

An array attributes file is a tab-delimited *.txt file that contains a list of arrays by ArrayID, and values for specific array attributes. Attributes are pieces of array-specific information, such as the hybridization temperature and the name of an array set that contains the array.

Although you can import array attributes with this function, the Sample Manager application lets you import and assign array attributes more easily. See the *Sample Manager User Guide* for more information.

To import an array attributes file

1 From the Home tab, click **Import** and then select **ArrayAttributes**.

The Import Attribute Files dialog box appears. See "Import" on page 211.

2 Select the microarray attributes file, then click **Import.**

The program imports the file. If the ArrayIDs in the file do not match the ArrayIDs of arrays in the program, a dialog box appears. The dialog box has a list of the ArrayIDs in the file that do not match. Click **No** to stop the import process, or click **Yes** to continue anyway.

To import an experiment file

In Agilent Genomic Workbench, an experiment is a set of links to microarray data and design files, and any associated results. An Agilent Genomic Workbench experiment file is a single ZIP file that contains the design and data files for one or more experiments. You can import

- Experiment files created in Agilent Genomic Workbench on another computer
- Agilent Genomic Workbench 5.0 and 6.0 experiment files

1 In the Home tab, click **Import > Experiments.**

The Import Experiments dialog box appears. See "Import" on page 211.

2 Select the ZIP file that contains the experiment(s) you want to import, then click **OK.**

The program imports the experiment file. Designs appear as new folders in the Design Data pane, in the applicable design type folder. Array data appears within the applicable design folder, organized by genome build. In addition, the experiment(s) appear in the Experiment pane, with the appropriate arrays.

NOTE

Agilent Genomic Workbench experiment files contain all of the design and array data files for an experiment, but do not include any analysis parameter settings, array selections, or analysis results. To export the data and design files from one or more experiments, see "To export experiments" on page 82.

To import filters

Filters are used in Agilent Genomic Workbench to include or exclude data from an analysis, based on filter criteria. Filters are created in the interactive CGH and ChIP applications, or in workflow setup.

1 In the Home tab, on the Command Ribbon, click **Import > Filters**.

The Import dialog box appears. See "Import" on page 211 for more information.

2 Select the file that contains the exported filter(s) for import. and then click **Import**.

3 In the filters Import dialog box, mark the **Import** box next to each filter you want to import, and then click **OK.**

To import a probe file

1 In the Home tab, on the Command Ribbon, click **Import > Probe Upload.**

The Probe Upload dialog box appears. See "Probe Upload" on page 228.

2 Complete the dialog box, and click **Preview**. See the *eArray$_{XD}$ User Guide* for more information.

To import a genome

You can import a user-defined genome for use with the Genomic Tiling or Bait Tiling tools. When you do, the genome becomes a permanent part of the database on your Genomic Workbench server, and is available to all of the users in your workgroup. For details on Genomic Tiling and Bait Tiling, and how to use the Import > Custom Genome for Tiling command, see the *eArray$_{XD}$ User Guide*.

To import a genotype reference file (CGH only)

A genotype reference sample is required in order to analyze a CGH+SNP microarray. A genotype reference file contains reference genotypes for one or more genotype reference samples.

NOTE Analysis of CGH+SNP microarrays requires a CGH license.

1 From the Home tab, click **Import > Genotype References**.

The Import Genotype Reference Files dialog box appears.

2 Browse to a location and select the genotype reference file to import.

3 Click **Open**.

The Genotype Reference Importer dialog box appears. See "Genotype Reference Importer (CGH only)" on page 209.

4 Click **OK**.

The imported genotype references appear in the Navigator, in the Genotypes pane.

To transfer catalog and workgroup data

You can transfer probe data and exon boundary data from the eArray Web site to your Agilent Genomic Workbench server. You can also transfer probe data from both the Agilent Catalog and from the folders of your workgroup. Probe data are available by application type (i.e. Expression, ChIP, and so on). Exon boundary data apply to all application types. For more information, see "Catalog and Workgroup Data" on page 165.

1 In the Home tab, click **Data**.

2 For the selected type of data, click **Download.**

A Data Download task is submitted and appears in the Tasks folder of the Navigator.

Working with Experiments to Organize Imported Data

This section describes how to organize imported array data and designs into *experiments*. Experiments, shown in the Experiment pane of the Navigator, contain links to specific array data and design files in the Design Data pane. After you set up an experiment, you can then analyze selected array data within the experiment.

Because experiments only contain *links* to the actual data and design files, any number of experiments can use a given set of files. In the data analysis applications (CGH, ChIP, or methylation, for example), experiments also can contain saved experiment results.

To display the array designs and data in the program

- To display the directory of data in the program, use the Design Data pane (Figure 12). Double-click a folder to expand or collapse it, or click the ⊞ and ⊟ buttons.

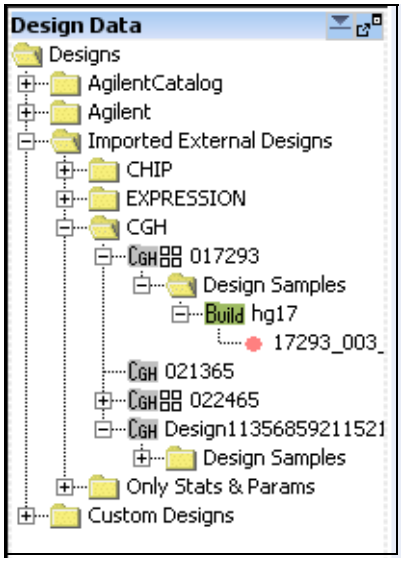


Figure 12 Design Data pane of the Navigator

In the Design Data pane, the program organizes design files by the application (CGH, ChIP, or methylation, for example) to which they apply. It organizes array data files by genome build under the design with which they are associated.

You can right-click many elements of the Design Data pane to open shortcut menus. For more information, see "Design Data pane – actions and shortcut menus" on page 131.

Many icons can appear in the Design Data pane. See "Design Data pane – icons, special text, and buttons" on page 129 for a complete list.

The Search pane can help you find specific data files or other content. See "To find specific content items in the Navigator" on page 71.

For more information on working with and managing microarray design files, see the *eArray*$_{XD}$ *User Guide*.

To create a new experiment

In Agilent Genomic Workbench, *experiments* are organizational units that contain links to data and design files. To view or analyze data, you must first create an experiment and associate the data files with it. Because experiments only contain *links* to the actual data and design files, any number of experiments can use a given set of files. In data analysis applications (CGH, ChIP, or methylation, for example), experiments can also contain saved experiment results.

1 In the Home tab, click **Create Experiment**.

The Create Experiment dialog box appears. See "Create Experiment" on page 178.

2 Type a **Name** and an optional **Description** for the experiment.

3 Do one of the following:

- To create an empty experiment, and add data to it later, click **OK.** The program creates the experiment. To add arrays to the experiment later, see "To add arrays to an experiment" on page 64.
- To create an experiment and add data to it now, follow these steps: (You can add or remove data from the experiment later.)

  a Click **Properties.**
  The Experiment Properties dialog box appears. See "Experiment Properties" on page 195.

  b Under **Select Design,** select the design and genome build for the array data.
  The applicable arrays appear in Array List.

  c In **Array List,** click the name of an array that you want in your experiment. Hold down the **Ctrl** key while you click the names of additional arrays.

  d Click  .
  The program transfers the selected arrays to the Selected Array List.
  The dialog box also has other options for adding arrays. See "Experiment Properties" on page 195 for more information.

  e Click **OK.**
  The program creates the new experiment, and adds data to it from the selected arrays.

- To create an experiment and add data to it using the “drag and drop” method, follow these steps:

  a To create an empty experiment, click **OK.**
  The program creates the experiment.

  b From the Design Data pane, expand a design to see the build and array data.

  c Drag an array from the Design Data pane and drop it onto the experiment folder in the Experiment pane.

In all cases, a folder with the name of the new experiment appears in the Experiment pane of the Navigator. For more information on the Navigator, see “Using the Navigator to Search for Data” on page 25.

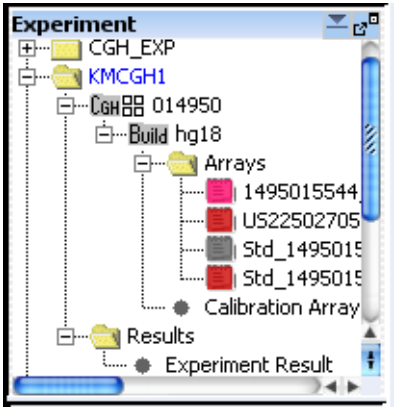


Figure 13 Experiment pane of the Navigator

To add arrays to an experiment

After you create an experiment, or import one, you can add arrays to it. When you add arrays to an experiment, you create links between the experiment and the array data and design files. Because the program does not move the actual files, multiple experiments can share the same arrays.

1 In the **Experiment** pane, double-click the **Experiments** folder to expand it.

2 Right-click the name of the experiment, then click **Show Properties.**

The Experiment Properties dialog box appears. See "Experiment Properties" on page 195.

3 Under **Select Design,** select the design file and genome build for the arrays to add.

The arrays for the selected design file and genome build appear in Array List.

4 In **Array List,** select the arrays to add to the experiment. To select a single array, click its name. To select additional arrays, hold down the **Ctrl** key while you click their names.

5 Click > .

The program transfers the selected arrays to the Selected Array List.

The dialog box also gives you other options for adding arrays. See "Experiment Properties" on page 195 for more information.

6 Click **OK.**

Or, to add array data to an experiment using the "drag and drop" method,

1 From the Design Data pane, expand a design to see the build and array data.

2 Drag an array from the Design Data pane and drop it onto the experiment folder in the Experiment pane.

If needed, the program adds appropriate design and genome build folders to your experiment folder in the Experiment pane. It places the arrays you selected in the appropriate genome build folder.

To change the order of arrays in an experiment

When you select an experiment, a table appears in the Tab View of Genomic Viewer that contains log ratio values and, if selected, signal intensities for arrays in the experiment. See "Tab View" on page 156. You can change the order in which the arrays appear in the table. If you display separate (stacked) scatter plots in Gene View and Chromosome View for each array, the array order also determines the order in which these plots appear. You can use this feature to organize your arrays more logically, or to make it more convenient to display certain arrays. It is especially useful if you have many arrays.

1 In the Experiment pane, right-click the name of the experiment, then click **Edit Array Order**.

  The Edit Array Order dialog box appears. See "Edit Array Order" on page 194.

2 In **Design,** select the design that contains the arrays whose order you want to change.

  The arrays from the selected design appear in Array Name.

3 Do any of the following:

  - To move an array up in the list, click its name, then click  .
  - To move an array down in the list, click its name, then click  .
  - To sort the list based on a specific microarray attribute, select the attribute in **Order by.**

4 Click **OK.**

To change the display names for arrays in an experiment

You can change the name displayed for arrays in an experiment, based on array attributes. When you change the display names for arrays in an experiment, the array names are changed only for the selected experiment. The display names are unchanged in the Design Data pane and in the other experiments.

1 Expand the folders in the Experiment pane until you see the experiment you want to change.

2 Right-click the experiment name, and select **Show Properties**.

3 In the Experiment Properties dialog box, click **Display Name by** and select an attribute to use for display of array names.

4 Click **OK**. The names of the arrays in the experiment are changed to the selected attribute. If the attribute does not exist for an array, the Global Display Name will be displayed.

NOTE To change the name of an array throughout Agilent Genomic Workbench, change its Global Display Name using Sample Manager. For more information, see the *Sample Manager User Guide*.

To rename an array in an experiment

When you rename an array in an experiment, you change the array's name only within the context of the selected experiment. The name of the array is unchanged in the Data pane, and in other experiments.

1 Expand the folders in the **Experiment** pane until you can see the array you want to rename.

2 Right-click the name of the array, then click **Rename.**

An Input dialog box appears.

3 Type the new name for the array, then click **OK.**

The name of the array in the tab view of the selected experiment is renamed. The global display name of the array is not changed.

To remove arrays from an experiment

When you remove arrays from an experiment, you only remove the links between the experiment and the data files. The files are still available in the program for use in other experiments. To completely remove files from the program, see "To remove data or design files from the program" on page 74.

1. In the **Experiment** pane, expand folders until you can see the experiment, and the array(s) that you want to remove from it.
2. In the **Arrays** or **Calibration Arrays** folder of the experiment, click the name of an array to select it for removal. Hold down the **Ctrl** key while you click the names of additional arrays.
3. Right-click one of the selected array names, then click **Delete.**

   A Confirm dialog box appears.
4. Click **Yes.**

   The program removes the links between the experiment and the selected array data files. If the removal of arrays leaves a design folder in the experiment empty, the program removes this folder as well.

To show or hide the attributes of an experiment

Array attributes are pieces of information specific to an array, such as Array ID or hybridization temperature. You can show or hide attributes for the arrays in the experiment with the Experiment Attributes dialog box. See "Experiment Properties" on page 195.

NOTE You cannot hide the required attributes. These include Array ID, Global Display Name, Green Sample, Red Sample (for 2-color arrays), and Polarity.

1. Right-click the experiment whose attributes you want to show or hide, or to change.
2. Click **Edit Attributes**.

   You see the array attributes and their values that were set up in the Sample Manager table. See the *Sample Manager Guide*.

3 Click **Show/Hide Attributes**.

The Show/Hide Columns dialog box appears. See "Show/Hide Columns" on page 238.

4 Mark the check boxes for the attributes you want to show, or clear the check boxes for the attributes you want to hide.

5 Double-click the cell whose array attribute value you want to change.

6 Click **Save Changes**.

7 Click **Close**.

NOTE You cannot create new attributes using this dialog box. To do this, you must use the Sample Manager tab. See the *Sample Manager User Guide*.

To display or edit the attribute values of a specific array

Array attributes are pieces of information specific to an array, such as array type or hybridization temperature. Sample attributes are usually set using the Sample Manager tab. For more information, see the *Sample Manager User Guide*. In the Navigator of the CGH module, you can display or change attributes for each array. You can also select a Genotype Reference to use for a selected CGH+SNP microarray.

NOTE Attributes for arrays that are read-only cannot be edited. For arrays where you are the owner, you can edit the GlobalDisplayName and Green and Red Sample attributes, but you cannot edit the ArrayID or the polarity.

1 Expand the folders of the Design Data pane or the Experiment pane until you can see the array of interest.

2 Right-click the name of the array, then click **Show Properties.**

The Microarray Properties dialog box appears, with a list of array attributes. See "Microarray Properties" on page 221. You can also edit the attributes of an array from this dialog box. In addition, if the array is an Agilent array, you can see header and feature information sent from the Agilent Feature Extraction program.

3 When you are finished, click **Close.**

NOTE You use the Sample Manager tab to organize, create, import, and export array attributes. See the *Sample Manager User Guide*.

Managing Content

This section describes how to create, find, rename, update, combine, and/or remove content such as designs, data, gene lists, and tracks, stored in Agilent Genomic Workbench. To display the data, gene list and track content, see Chapter 3, “Displaying Data and Other Content”.

To display a list of the content stored in the program

The Design Data and My Entity List panes of the Navigator show the content stored in Agilent Genomic Workbench.

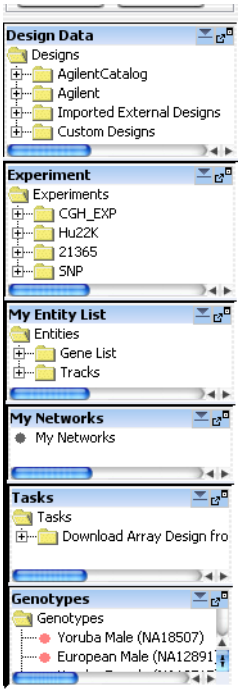


Figure 14 Agilent Genomic Workbench Navigator for CGH

Design Data pane – Shows all of the design and data files stored in the database. For more information, see "To display the array designs and data in the program" on page 60 and "Design Data pane – icons, special text, and buttons" on page 129.

Experiment pane – Shows the experiments that were created or imported to the program. To select an experiment, double-click its name. To display the contents of an experiment, right-click the experiment name and then select **Expand Node**.

My Entity List pane – Shows the gene lists and tracks stored in the program. To view the names of gene lists or tracks available in the program, double-click the names of folders to expand or collapse them, or click the ⊞ or ⊟ buttons.

Genotypes pane (CGH Only) – Shows the genotype reference samples in the database.

NOTE

Content that is used exclusively in the eArray tab, such as the probes and probe groups that you use to create custom microarray designs, is covered in a separate guide. See the *eArray$_{XD}$ User Guide*.

To find specific content items in the Navigator

At the top of the Navigator is a search pane that can help you find specific content items. See "Search pane" on page 123.

Figure 15 Navigator search pane

1 Type a search term in the box at the top of the Navigator. The search term is not case-sensitive, but it must reflect the entire name of the content item that you want to find. You can use asterisks (*) as wildcards to represent a group of unspecified characters. For example,

if you type *1234*, the search will find all items that contain “1234” in the name.

2 By default, the program searches all panes of the Navigator. To limit your search to a specific pane, click . In the list that appears, select the desired pane.

3 Click .

The program searches the selected pane(s). If it finds item(s) that match your search term, it expands folders so that the items are visible, and highlights them in red. You may need to scroll down to see all the search results.

4 To clear the results of a search, click .

To display the properties of a specific design

Design properties include general information about a design, such as its name, application type, and associated species. They also include a list of the names and chromosomal locations of probes.

1 Expand the folders of the Design Data pane until you can see the genome build folder(s) within the design folder.

2 Right-click the genome build folder, then click **Show Properties.**

The Design Properties dialog box appears. See “Design Properties” on page 185.

To download a design from eArray

In order to analyze extracted microarray data in Agilent Genomic Workbench, the design for the microarray must be present in the database. The Design Data pane of the Navigator shows the available design content. See “Design Data pane – icons, special text, and buttons” on page 129.

1 Expand the Agilent Catalog or workgroup folder until you see the design you want to download.

2 Right click the design you want to download, and click **Download from eArray.com.**

An information box appears that lets you know the download task is started.

3 Click **OK.**

The task appears in the Tasks pane of the Navigator. The color of the circle shows the status of the task. See "Tasks pane – icons, buttons, and special text" on page 143.

To update probe annotation in design files

Agilent regularly makes updates to probe annotations on its eArray Web portal. If you have imported Agilent array designs into Agilent Genomic Workbench, and you are a registered eArray user, you can download the updated design files from within Agilent Genomic Workbench. For more information about eArray, go to https://earray.chem.agilent.com and click **Help.**

1 In the Home tab, click **User Preferences.**

The User Preferences dialog box appears.

2 In the Miscellaneous tab, under **eArray User Details,** type your eArray **Username** and **Password.** See "User Preferences" on page 250.

3 Click **OK.**

4 Expand the folders of the Design Data pane until you can see the design that you want to update.

5 Right-click the design, then click **Download from eArray.com.** This option appears only for Agilent designs.

A confirmation dialog box appears.

6 Click **Yes.**

The program downloads an updated design, if one is available.

To rename an array in the Design Data pane

This topic describes how to rename an array in the Design Data pane, which changes the Global Display Name for the array. If you rename an array in this way, and subsequently add the array to an experiment, the array appears in the experiment with the new name. It also changes the

array name in any experiment to which it is already linked. To rename an array only within the context of a specific experiment, see "To rename an array in an experiment" on page 66.

NOTE You can only rename an array that you imported.

1 Expand the folders of the Design Data pane until you can see the array you want to rename.

2 Right-click the name of the array, then click **Rename.**

An Input dialog box appears.

3 Type a new name for the array, then click **OK.**

The program renames the array.

To remove data or design files from the program

You can delete array design and data files from the program when you are finished with them.

1 If an array that you want to delete is associated with an experiment, first delete it from the experiment. See "To remove arrays from an experiment" on page 67.

2 In the Design Data pane, expand folders until you can see the design folder or array that you want to delete.

NOTE You cannot delete data or design files that are read-only.

3 Do one of the following:

- For array data files, click the name of the first array, then hold down the **Ctrl** key while you click the names of additional arrays within the same design.

- For array design folders, click the name of the first design folder, then hold down the **Ctrl** key while you click the names of additional ones. This selects the designs and all array data files within them for deletion.

4 Right-click the name of a selected design folder or array data file, then click **Delete.**

A confirmation dialog box appears.

5 Click **Yes.**

The program deletes the selected files.

CAUTION When you delete files, you permanently remove them from Agilent Genomic Workbench. To restore deleted files, you must import them again.

To create a gene list

When you create a gene list, you create a list of the genes in a contiguous chromosomal region that you define.

1 Follow these steps to define a chromosomal region for your gene list. If you know the exact start and end locations of the chromosomal region, skip to step 2.

a In Genome View, select the chromosome.
The selected chromosome appears in Chromosome View. See "Chromosome View" on page 149,

b In Chromosome View, in the plotting area to the right of the chromosome, drag the pointer over the chromosomal region of interest.
The program draws a blue box around the region, and displays the region in greater detail in Gene View.

c In Gene View, adjust the view so only the genes of interest appear. For a description of the adjustment commands available in Gene View, see "Gene View" on page 151.

2 Right-click anywhere within the log ratio plotting area in Gene View, then click **Create Gene List**.

The Create Gene List dialog box appears. See "Create Gene List" on page 180.

3 In the dialog box set the Name, Description and Color.

4 In the dialog box select the chromosomal region for the new gene list.

5 Click **OK.**

The new gene list appears in the Gene List folder of My Entity List in the Navigator.

To import a gene list

A gene list file is a plain text (*.txt) file that contains one gene name per line. When you import a gene list into Agilent Genomic Workbench, it appears in the Gene List folder in the My Entities List pane. You can use the gene list to highlight specific genes, or to show or hide the appearance of genes and data, in Gene and Chromosome Views. See "To show gene lists in Gene View" on page 102.

1 In the **My Entities List** pane, double click the **Entities** folder to expand it.

2 Right-click the **Gene List** folder, then click **Import Gene List.**

An Import dialog box appears. See "Import" on page 211.

3 Select the desired gene list file. To select additional gene list files, hold down the **Ctrl** key and click their names.

Click **OK.**

To display the genes in a gene list

You can display the genes in a gene list as a table.

1 Expand the folders in the My Entity List pane until you can see the gene list.

2 Right-click the gene list, then click **View In Table.**

The Gene List dialog box appears, with a table that contains the names of the genes in the gene list. You can also use this dialog box to edit the description of the gene list and its display color. See "Gene List" on page 207.

You can also create gene lists. For more information, see "To create a gene list" on page 75.

To add one gene list to another

You can add one gene list (a source gene list) to another (the target gene list). The program appends the source gene list to the end of the target gene list, and leaves the source gene list unchanged.

1 Expand the folders in the My Entity List pane until you can see the gene lists to combine.

2 Right-click the source gene list, then click **Add to Gene List.**

A dialog box appears. For more information, see "Add Gene List <name> to" on page 162.

3 In Select target gene list, select the target gene list.

Click **OK.**

To rename a gene list

The name of a gene list identifies it within the Gene List folder of the My Entity List pane. You can rename gene lists.

1 Expand the folders of the **My Entity List** pane until you can see the gene list to rename.

2 Right-click the gene list, then click **Rename.**

3 Type a new name for the gene list, then click **OK.**

To delete gene list(s)

1. In the **My Entity List** pane of the Navigator, click to expand the **Gene List** folder.
2. Click the name of a gene list to delete. Hold down the **Ctrl** key while you click the names of additional gene lists.
3. Right-click one of the selected gene lists, then click **Delete.**

   A confirmation dialog box appears.
4. Click **Yes.**

To create a track (CGH only)

When you create a track, you create a list of the genes in a contiguous chromosomal region that you define. To create a list of genes or other annotations, such as CNV or miRNA, in multiple regions, create additional tracks, and combine them.

1. Follow these steps to define a chromosomal region for your track. If you know the exact start and end locations of the chromosomal region, skip to step 2.
   a. In Genome View, select the chromosome.
   The selected chromosome appears in Chromosome View.
   b. In Chromosome View, in the plot area to the right of the chromosome, drag the pointer over the approximate chromosomal region of interest.
   The program draws a blue box around the region, and displays the region in greater detail in Gene View.
   c. In Gene View, adjust the view so only the genes of interest appear. For a description of the adjustment commands available in Gene View, see "Gene View" on page 151.
2. Right-click anywhere within the plot area in Gene View, then click **Create Track.**

   The Create Track dialog box appears. See "Closes the dialog box without creating the histogram.Create Track" on page 183.
3. In the dialog box set the Name, Description and Color.
4. In the dialog box select the chromosomal region for the new track.

5 Click **OK.**

The new track appears in the Tracks folder of My Entity List pane in the Navigator.

To display the details of a track

You can display a table that contains the values for a list of track attributes.

1 In **My Entity List** pane, expand the Tracks folder to see the track.

2 Right-click the name of the track, then click **View Details.**

Track data appears in a Track table. See "Track" on page 245.

To rename a track

The name of a track identifies it both within the Tracks folder of the My Entity List pane, and in Gene View when you select **Show In UI** for the track. You can rename tracks.

1 Expand the folders of the My Entity List pane until you can see the track to rename.

2 Right-click the track, then click **Rename.**

3 Type a new name for the track, then click **OK.**

To delete tracks

1 In the My Entity List pane of the Navigator, expand the Tracks folder.

2 Click the name of a track to delete. Hold down the **Ctrl** key while you click the names of additional tracks.

3 Right-click one of the selected tracks, then click **Delete.**

A confirmation dialog box appears.

4 Click **Yes.**

To display genotype reference details (CGH only)

1 In the Genotypes pane of the Navigator, right-click the name of the genotype reference you want to display.

2 Click **Show Properties**.

The Genotype Reference Details dialog box appears. See "Genotype Reference Details (CGH only)" on page 208.

To rename a genotype reference (CGH only)

1 In the Genotypes pane of the Navigator, right-click the name of the genotype reference you want to rename.

The Input dialog box appears.

2 Type the new name for the genotype reference, and then click **OK**.

To delete a genotype reference (CGH only)

1 In the Genotypes pane of the Navigator, right-click the name of the genotype reference you want to delete.

2 Click **Delete**.

A confirmation dialog appears.

3 Click **Yes**.

NOTE When you delete a genotype reference, the green and red sample attributes for any microarray associated with this genotype reference are reset.

Exporting and Saving Content

This section describes how to export several kinds of files from the program.

To export array attributes

You can export selected array attributes for any imported arrays. You first select the arrays and then the attributes for the selected arrays. You can export array attributes from the Home tab or from the short-cut menu for an experiment.

1 Click **Home > Export > Array Attributes**.

OR

In the Experiment pane of the Navigator, right-click an experiment of interest, and click **Export Attributes**.

The Export Array Attributes dialog box appears with the Array tab displayed. See "Export Array Attributes" on page 198.

If you opened this dialog box by right-clicking an experiment, only those arrays selected for the experiment appear in the Selected Array List. You can add or remove attributes from the list.

2 Under **Select Design,** select the design file and genome build for the arrays you want to add.

The arrays for the selected design file and genome build appear in Array List.

3 In **Array List,** select the arrays whose attributes you intend to export. To select a single array, click its name. To select additional arrays, hold down the **Ctrl** key while you click their names.

4 Click  .

The program moves the selected arrays to the Selected Array List.

5 Click **Next** to select attributes for the selected arrays.

The Export Array Attributes dialog box appears with the Attribute tab displayed. See "Export Array Attributes" on page 198.

All of the attributes for the arrays are already located in the Selected Attribute List.

6 Move any attributes you don't want to export to the Available List.

a In the Selected Attributes List, highlight those attributes you do not want to export. To select additional attributes, hold down the **Ctrl** key while you click their names.

b Click  .

7 Click **OK**.

The Export dialog box appears. See "Export" on page 197.

8 Select the folder in which to save the attributes, and click **Export**.

The attributes will be saved to the selected folder as a .txt file.

To export experiments

You can export experiments as a ZIP file to transfer them to another computer. Exported experiments contain the associated design and array data files, only. The program does not export information about array selections, or any analysis parameters or results.

1 In the Home command ribbon, click **Export > Experiments**.

The Export Experiments dialog box appears. See "Export Experiments" on page 202.

2 Mark the experiments that you want to export. To export all experiments, click **Select All.**

3 Click **OK.**

An Export dialog box appears. See "Export" on page 197.

4 Select a location and type a name for the exported ZIP file.

5 Click **Export.**

The program exports all selected experiment(s) together as a single ZIP file.

To export filters

You can export selected array, feature, design, metric, and aberration filters that are available in some data analysis applications in Agilent Genomic Workbench. The program exports all selected filters as a single *.xml file that you can import again at a later time.

1 In the **Home** tab, click **Export > Filters**.

The Export Filters dialog box appears. See "Export Filters" on page 203.

2 Under **Export,** mark the check boxes beside the filter(s) to export. To select all filters for export, click **Select All.**

3 Click **OK.**

An Export dialog box appears.

4 Select a location and type a name for the exported file, then click **Export.**

The program exports all selected filters as a single *.xml file.

To export a gene list

You can export a gene list as a text file that contains one gene per line.

1 In the **My Entity List** pane, in the **Gene List** folder, right-click the gene list that you want to export, then click **Save As.**

A Save As dialog box appears.

2 Select a location and type a name for the file.

3 Click **Save.**

A message appears when the operation is complete.

4 Click **OK.**

To export tracks

You can export selected tracks as a BED format track file. You can then import this file into Agilent Genomic Workbench on another computer, or into a genome browser that accepts BED format files.

1 In the **Home** tab, click **Export > Tracks**.

The Export Tracks dialog box appears. See "Export Tracks" on page 204.

2 Mark the tracks to export. To select all tracks for export, click **Select All.**

3 Click **OK.**

An Export dialog box appears.

4 Select a location and type a name for the exported track file, then click **Export.**

The program exports the track(s) as a single BED format track file.

To copy what you see in the main window

You can copy panes of the main window to the Clipboard as images, and then paste them into a new document in another program (such as Microsoft® Word, or PowerPoint). The images contain only what actually appears on your screen; regions to which you must scroll are not included.

1 In the **View** tab, click **Copy.**

2 In the shortcut menu that appears, click the name of the pane that you want to copy. You can copy any view, or the Navigator. To copy all of the panes, click **All.**

The program copies the selected pane(s) to the clipboard.

3 Open a document in a program that accepts images. In that program, click **Edit > Paste,** or the appropriate paste command.

NOTE To adjust how data is displayed in the panes use the View Preferences dialog box. For example, you can turn on or off the cursor. See "View Preferences" on page 258 for more information.

To copy the list of array colors for an experiment

You can copy the list of arrays in an experiment, and the colors assigned to them, to the clipboard as an image. You then paste the image into a document in another program such as Microsoft® Word or PowerPoint.

1 In the **Experiment** pane, expand the **Experiments** folder.

2 Right-click the name of the experiment, then click **Edit Array Color**.

The Edit Array Color dialog box appears. See "Edit Array Color" on page 193.

3 In the dialog box, click **Edit > Copy.**

The program copies the names of the arrays and their colors to the clipboard as an image.

4 Open a program that accepts images. Click **Edit > Paste,** or the appropriate paste command for the specific program.

To save data and design information from an experiment

You can save the data and design information from a single design in an experiment as a tab-delimited text file.

1 In the **Experiment** pane, expand the **Experiments** folder until you see the genome build(s) for the design you want to export.

2 Right-click the name of the genome build, then click **Save As Text File**.

A dialog box appears.

3 Select a location and type a name for the file, then click **Save.**

3 Displaying Data and Other Content

This chapter shows you how to display log ratio data from imported feature extraction data files, as well as gene and track content, in the Genomic Viewer. It also gives you instructions on how to customize the display of data and content to meet your needs.

Selecting an Experiment for Displaying Data

An experiment is a set of links to microarray data and design files, and any associated results. Experiments are displayed in the Experiment pane of the Navigator that appears for applicable tabs. The Experiment pane does not appear if you select the miRNA or Expression modules. See "Using the Navigator to Search for Data" on page 25.

When you select an experiment and have no CGH, ChIP, or CH3 application license, the program shows the log ratio data of selected arrays in the active experiment, if display of the data is enabled in View Preferences. See "View Preferences" on page 258 for more information.

NOTE Without an application license (CGH, ChIP, or CH3) you cannot select an experiment that contains results.

When you select an experiment and Preprocessing and Analysis options have been turned on or set to apply, the program automatically begins the analysis of the selected array data with current settings and displays its results.

This section describes how select an experiment to make it active and select or deselect arrays for further display.

To select an experiment

When you select an experiment, the program displays log ratio data in a scatter plot, if that option is enabled.

1 If necessary, do one of the following to add the desired experiment to the Experiment Pane in the Navigator:
   - Create a new experiment and add data to it. See "To create a new experiment" on page 62.
   - Import a saved experiment file. See "To import an experiment file" on page 57.

2 In the Navigator, double-click the name of the experiment.

   The Experiment Selection dialog box appears.

3 Click **Yes.**

In the Experiment pane of the Navigator, the name of the experiment turns blue. The name also appears in the title bar of the main window. Tables of data and design information appear in Tab View. For more information on the available tabs, see "Tab View" on page 156.

To select or deselect arrays in the experiment

To include arrays for display, you select them from the arrays available, either in an inactive experiment or the active one. When you first create an experiment, the program automatically sets the first array in the experiment for analysis. If you do not select additional arrays for display, only the first one will be shown when the experiment is selected.

To select the arrays for display before experiment selection:

1 Hold down the **Shift** key to highlight contiguous arrays or hold down the **Ctrl** key to highlight noncontiguous arrays.

2 Right-click the highlighted arrays, and click **Select**.

Even though the selected arrays do not change color, they will change color after the experiment is selected.

In the Navigator, the color of an array's icon has the following meaning, after experiment selection:


Array is not selected.


Array is selected. The specific color matches the color of the column headings for the array in Tab View in the lower part of the window. In addition, the program displays aberration results and moving averages related to this array in this color. To configure a custom color for the array, see "To change the display color of an array" on page 90.

To select or deselect arrays in a *selected* experiment:

1 In the Navigator, expand the folders of the selected experiment.

2 Click the name of an array you want to include in the display.

To include additional arrays, hold down the **Ctrl** key while you click their names. To include a contiguous block of arrays, click the name of the first array in the block, then hold down the **Shift** key while you click the name of the last one.

3 Right-click the name of one of the highlighted arrays, then click **Select.**

After you select the arrays, the program reanalyzes the data set within the experiment and displays the data in Genome, Chromosome, and Gene Views. You can see the data for just the selected arrays in the Selected Arrays tab in Tab View.

To customize the appearance of the scatter plot in Genome, Chromosome, and Gene Views, see "To change scatter plot appearance" on page 94.

You can also use the headings of columns in Tab View that contain array data to select and deselect arrays.

- Click a column heading to select that array only.
- Hold down the **Ctrl** key while you click a column heading to select or deselect an array without changing the status of other arrays.
- Right-click a column heading to open a shortcut menu with options that let you select or deselect that array, or all arrays.

For more information on Tab View, see "Tab View" on page 156.

To change the display color of an array

The color assigned to an array sets the color of its icon when you select the array within an experiment. It also changes the colored square in the array's column heading in Tab View.

1 In the Experiment pane of the Navigator, in the **Experiments** folder, expand the folder of an experiment until you can see the array of interest.

2 Right-click the desired array, then click **Edit Array Color.**

The Select Color dialog box appears. The dialog box gives three different ways to select the desired color. "Select Color" on page 231.

3 Select the desired color in one of the following ways:

Dialog box tab	Instructions
Swatches	• Click the desired color swatch.
HSB (Hue/Saturation/Brightness)	Type or adjust the values in H (Hue), S (Saturation), and B (Brightness), or alternately, follow these steps: **a** Select **H**, then drag the slider to select a hue based on the color strip to its right. **b** Click an appropriate location in the large color box to the left of the slider to set the saturation and brightness levels of the color. Both the HSB and equivalent RGB values of the color appear in the dialog box. Note these values—they will be useful if you need to use this color in the future.
RGB (Red/Green/Blue)	Do any of the following. Note the final RGB Values; they will be useful if you need to use this color in the future. • Drag the Red, Green, and Blue sliders. • Type or adjust values in the boxes to the right of the sliders.

Samples of the color in different contexts appear under Preview. The upper half of the right-most color sample shows the original color for comparison.

4 Adjust the color as desired, then click **OK.**

You can also manage all of the colors for all of the arrays in an experiment. Right-click the desired experiment, then click **Edit Array Color.** For more information, see "Edit Array Color" on page 193.

Displaying Array Data

After you select an experiment, you can change how data appear within the Views or change the appearance of the Views that contain the data (or results).

To display the scatter plots

Within the Chromosome and Gene views, there are up to three possible scatter plot display panels that you can turn on and off. These panels are used to let you examine different types of data in more detail.

NOTE At least one scatter plot panel must be selected. The Copy Number Panel is only used for CGH+SNP arrays. Without a CGH license, you cannot display copy number results.

By default, display of log ratio scatter plots is turned On. If you do not see data in the scatter plot(s), do one of the following:

1 From the View tab, click **View Preferences**. See "View Preferences" on page 258 for more information.

2 In the View Preferences dialog box, under Data Visibility, select **All views** and then mark the box next to **Scatter Plot**.

OR

1 Right-click in any of the views, and select **View Preferences**. See "View Preferences" on page 258 for more information.

2 In the View Preferences dialog box, under Data Visibility, select **All views** and then mark the box next to **Scatter Plot**.

To show or hide data in scatter plots

1 In the Gene View, move the mouse pointer over the down arrow in **Scatter Plot** until the Scatter Plot box appears, and do any of the following:

To do this	Follow these steps
Show or hide data points for a selected data type	• To show data points – Mark one or more check boxes under Configure Coloring schemes; then select how you want to color code the data from the Color by list. • To hide all data points – clear the check boxes.

2 Click  to close the Scatter Plot window.

To customize scatter plot ranges and colors

You can customize the display of scatter plot data. For each log ratio or signal intensity scatter plot, you can choose to color code the plotted log ratio or signal intensity values by custom ranges and colors. For channels, you can set custom colors only.

NOTE The View Preferences dialog box contents changes depending on the application type that is selected (CGH, ChIP, CH3).

Add and customize a plot

1 In Gene View, move the mouse pointer over **Scatter Plot** to display the options.

OR

Right-click in any of the views, and select **View Preferences**.

2 Mark the one or all of the check boxes under Configure Coloring schemes.

3 Select a data type from the list.

4 Click **Configure Color and Ranges**.

The Configure Coloring Ranges and Shades dialog box appears where you set ranges and colors for any of the “color by” data types. For more information, see “Configure Coloring Ranges and Shades” on page 176.

5 In the Configure Coloring Ranges and Shades dialog box, click one of the tabs and then select the data type to configure.

6 Type minimum and maximum numbers to define a range for the data type.

7 Click **Color** to open the Select Color dialog box. Use the tabs to select a color for the range. See “Select Color” on page 231 for more information.

8 Click **OK** to close the Select Color dialog box and return to the Configure Coloring Ranges and Shades dialog box.

9 Click **Add Range** to add the custom range to the range list.

10 When you are done, click **OK** to close the dialog box.

Edit or remove a range

1 In the Configure Coloring Ranges and Shades dialog box, click one of the tabs and then select the data type to configure.

2 In the range list, mark the **Edit/Delete** box to select the range. You can mark more than one range.

3 Click **Edit Range** to change the minimum and maximum values, or to change the color for the selected range.

4 Click **Delete Range** to delete the selected range.

5 Click **OK** to close the dialog box.

To change scatter plot appearance

You use the View Preferences dialog box to change the appearance of the scatter plots in Chromosome and Gene views.

1 In the Genomic Viewer, right-click in the Gene View or Chromosome View, and then click **View Preferences**.

Or, click the View tab, and then click **View Preferences**.

The View Preferences dialog box appears. See “View Preferences” on page 258.

2 Do any of the following:

To do this	Follow these steps
Show or hide the scatter plot	**a** In the View tab under **Data Visibility,** in **View,** select **All Views.** **b** Do one of the following: To show the scatter plot, mark **Scatter Plot.** To hide the scatter plot, clear **Scatter Plot.** **c** Click **OK.**
Change the symbol that appears for data points	You can select the symbol separately for each design type. **a** In the View tab, under **Rendering Patterns,** select the desired **Design type.** **b** Under **Styles,** select the desired symbol. **c** Click **Apply.**
Show a separate scatter plot in Gene and Chromosome Views for each selected array	**a** In the View tab, under **View Alignment,** under **Rendering Style,** select **Stacked.** **b** Click **Apply.**
Show one scatter plot that contains data for selected arrays	**a** In the View tab, under **View Alignment,** under **Rendering Style,** select **Overlaid.** **b** Click **Apply.**
Enable ToolTips for the scatter plot in Gene View	ToolTips show information about an individual data point when you place the pointer over it. **a** Click the **View** tab. **b** Under **Data Visibility,** in **View,** select **Gene View.** **c** Mark **Scatter Tool Tip.** **d** Click **Apply.**

3 Click **OK.**

To print the scatter plot

You can print the scatter plot as it appears in Genome, Chromosome, and Gene views. Each view selected in the analysis is printed on a separate page. Chromosomes and genes appear on the printed pages, but tracks do not.

1 In the Home tab, click **Print.**

2 Set print options, as desired, then click **OK.**

To create custom scales for Views

You can customize the scale used for display in the Chromosome View and Gene View. Custom scales are applied to both views.

1 Click the View tab and then click **View Preferences.**

2 In the View Preferences dialog box, under Configure Scales, mark the box next to **Apply** for the plot for which you want to create a custom scale.

In Range, enter a value to use for the range. The range you enter changes the scale for the display of the selected data.

To locate and display data within the Views

To look through the data of the selected arrays, do any of the following. In general, all views are synchronized; if you select a location or region in one view, the other views move there as well.

To do this	Follow these steps
Select a specific chromosome to display	• In Genome View, click the desired chromosome. All other views switch to the selected chromosome.
Display data in a region of the selected chromosome	• In Chromosome View, drag the pointer over the desired region. Gene View expands (or shrinks) to show only the selected region. Tab View scrolls to the new cursor location.

To do this	Follow these steps
Zoom in and out in Gene View	• Click  to zoom in. • Click  to zoom out.
Scroll through the selected chromosome	• Click  to scroll up. • Click  to scroll down. **Note:** These arrows will appear side by side for horizontal orientation.
Return Gene View or Chromosome view to center	• Click anywhere in Chromosome View, or anywhere within the scatter plot in Gene View. The location you click becomes the new cursor location.
Move all Views to a specific genomic location	**a** Click **Home > Go To Gene/Genomic location.** A dialog box appears. **b** Under **Genomic Location,** select a **Chromosome,** and type a **Base Position.** **c** Click **Go.** All views move to the selected location.
Display the location of a specific gene in the center of all Views	**a** Click **Home > Go To Gene/Genomic location.** A dialog box appears. **b** Under **RefSeq by Symbol,** either select the desired gene (if available) or type the name of the gene. **c** Click **Go.** All views move to the location of the selected gene.
Display the data selected in Tab View in the center of Chromosome and Gene Views	• In Tab View, click any entry in any table, except a column heading. Chromosome and Gene views: The genetic location of the selected data appears in the center of Chromosome and Gene Views.
Scroll to a specific column in Tab View	**a** In Tab View, right-click any column heading, then click **Scroll To Column.** The Scroll to Column dialog box appears. See "Scroll to Column" on page 231. **b** In **Select Column,** select the desired column. **c** Click **OK.**

To do this	Follow these steps
Search for a specific column entry in Tab View, and move the cursor there	**a** In Tab View, right-click any entry except a column heading, then click **Find in column.** The Find in column dialog box appears. See "Find in column" on page 205. **b** Set the desired search parameters, then click **Find Next.** The program searches the column using your search parameters, and highlights the row of the first entry that matches. The cursor moves to the location defined in the highlighted row. This search is only for the selected chromosome.
Display the exact chromosomal location of the cursor	At the bottom of the main window, look at the first cell of the Status bar. The location appears as the chromosome followed by the base position. For more information on the status bar, see "Status Bar" on page 161.

To smooth and plot CGH log ratio data

You use a plug-in program to create separate, stacked plots of smoothed log ratio data for each of the selected CGH arrays in the current experiment. The plug-in program can perform one of several varieties of moving-average-like smoothing, and plots the data associated with the currently selected chromosome.

The Plugin Settings command lets you change the parameters when you have selected to display the plot immediately after you click Plugin.

1 Select an experiment.

2 Select the arrays that contain the log ratio data to smooth and plot.

3 Select the chromosome that contains the log ratio data of interest.

4 Click **Tool > Plugin > CGHSmooth**.

The CGHSmooth Parameters dialog box appears. See "CGHSmooth Parameters" on page 167.

5 Type the parameter values for the selected arrays in the active experiment and the selected chromosome.

6 Click **OK**.

The CGHSmooth Plot appears, showing a plot of the log ratio vs. chromosomal position for each of the selected arrays. See "CGHSmooth Plot" on page 169.

7 (optional) To add a title, legend and change the appearance of the plot(s), right-click the plot, and click **Properties**.

See "Chart Properties" on page 171.

8 (optional) To see options to save, print, zoom in or out, or change the auto range of the plot, right-click the plot.

To enter parameters from the Plugin Settings command and display the plot directly from the Plugin command

1 After step 5 above, mark **Don't Show Again**, then click **OK**.

The plot appears.

2 To change the parameter values, exit the plot, and click **Plugin Settings**.

3 Change the values you want to change, and click **OK**.

4 Click **Plugin**.

The plot appears.

5 (optional) To show the CGHSmooth Parameters dialog box again when you click Plugin, click **Plugin Settings**, clear **Don't Show Again**, and click **OK**.

To produce an echo example plot (CGH only)

The Echo Example Plot is the output of the Echo Example plug-in. It displays the log ratio data for the selected chromosome in the active experiment. Data from all of the selected arrays in the experiment appear as a series of stacked plots, one for each array.

1 Select an experiment.

2 Select the arrays that contain the log ratio data to smooth and plot.

3 Select the chromosome that contains the log ratio data of interest.

4 Click **Tool > Plugin > EchoExample**.

5 Type the parameter values for the selected arrays in the active experiment and the selected chromosome.

6 Click **OK**.

The Echo Example Plot appears, showing a plot of the log ratio vs. chromosomal position for each of the selected arrays. See "Echo Example Plot" on page 190.

7 (optional) To add a title, legend and change the appearance of the plot(s), right-click the plot, and click **Properties**.

See "Chart Properties" on page 171. To see options to save, print, zoom in or out, or change the auto range of the plot, right-click the plot.

To produce a moving average example plot (CGH only)

The MovAvgExample plug-in program calculates a 10-point moving average of the data from the selected chromosome in the selected arrays of the active experiment. It displays stacked plots of moving averages for all the arrays, one plot per array.

The plug-in program itself (**MovAvg Example.pl**, in the Plugins folder of the Agilent Genomic Workbench installation folder on your computer) is a short Perl program. It is a good example of how computed columns are processed. You must have Perl installed on your computer to use this plug-in.

1 Select an experiment.

2 Select the arrays that contain the log ratio data to smooth and plot.

3 Select the chromosome that contains the log ratio data of interest.

4 Click **Tool > Plugin > MovAvg Example**.

5 Type the parameter values for the selected arrays in the active experiment and the selected chromosome.

6 Click **OK**.

The MovAvg Example Plot appears, showing a plot of the log ratio vs. chromosomal position for each of the selected arrays. See "MovAvg Example Plot" on page 226.

7 (optional) To add a title, legend and change the appearance of the plot(s), right-click the plot, and click **Properties**.

See "Chart Properties" on page 171. To see options to save, print, zoom in or out, or change the auto range of the plot, right-click the plot.

To enter parameters from the Plugin Settings command and display the plot directly from the Plugin command

1 After step 5 above, mark **Don't Show Again**, then click **OK**.

The plot appears.

2 To change the parameter values, exit the plot, and click **Plugin Settings**.

3 Change the values you want to change, and click **OK**.

4 Click **Plugin**.

The plot appears.

To show the MovAvg Example Parameters dialog box again when you click Plugin, click **Plugin Settings**, clear **Don't Show Again**, and click **OK**.

Displaying Content (Gene Lists/Tracks)

To show gene lists in Gene View

A gene list defines a set of genes of interest.

You cannot show gene lists without a license. With a license you can highlight the genes in the gene list in Gene View, or limit the display of data, genes, and tracks to the regions defined by a gene list.

You also cannot import or export a gene list without a license, but you can create a gene list in the program. See "To create a gene list" on page 75.

To change the appearance of genes in Gene View

You use the User Preferences dialog box to change the appearance of the genes in Chromosome and Gene views.

1 Right-click any part of the Gene View, then click **User Preferences.**

The User Preferences dialog box appears.

2 Click **Tracks**.

See "User Preferences" on page 250.

3 Do any of the following:

To do this	Follow these steps
Show or hide genes in Gene View	**a** Under **Visualization Parameters**: To show genes – Under **Genes,** mark **Show Gene Symbols.** To hide genes – Under **Genes,** clear **Show Gene Symbols.** **b** Click **Apply.**
Change the display font for genes (and track annotations) in Gene View	**a** In the Gene Symbols tab, under **Font,** select a new **Font, Font Style,** and **Font Size.** **b** Click **Apply**

To do this	Follow these steps
Change the display angle for genes (and track annotations) in Gene View	**a** Under **Visualization Parameters,** under **Genes,** in **Orientation (Degrees),** type a new orientation in degrees. 0° is horizontal. **b** Click **Apply.**

4 Click **OK.**

To show tracks in Gene View

Tracks contain information for specific genomic locations. A multitude of tracks from diverse sources is available for many species. You can display tracks next to genes and microarray data in Gene View.

1 Select and show microarray data. See "To select an experiment" on page 88.

2 In the My Entity List pane, open the Tracks folder.

3 Right-click the track you want to display, and click **Show In UI**.

Or, you can do this:

1 In Gene View, right-click anywhere within the scatter plot, then click **User Preferences.**

The User Preferences dialog box appears. See "User Preferences" on page 250.

2 Click **Tracks**.

3 Mark the **Show In UI** check box of each desired track.

4 Click **OK.**

The program displays the selected tracks in Gene View.

To change the appearance of tracks

Within the Tracks tab of the User Preferences dialog box, you can change the appearance of tracks, as described in the table below.

To do this	Follow these steps
Include track information in reports	**a** In the list of tracks, in the **Show in Report** column, mark the check boxes of the desired tracks. **b** Click **Apply.** Doing this adds a column with the hits from the track file. For each aberrant interval, it reports the entries from the track file for that interval in that separate column.
Show or hide annotations in all tracks	• To show annotations in all tracks: under **Tracks,** mark **Show Annotations.** • To hide annotations in all tracks: under **Tracks,** clear **Show Annotations.**
Display all selected tracks as a single track	• Under **Tracks,** mark **Show Overlaid.** The program combines the annotations of all selected tracks into a single track named **Overlaid Track.** • To show tracks individually again, clear **Show Overlaid.**
Display the parameters and the list of annotations of a track	• In the list of tracks, for the desired track, click **Details.**
Change the display font for track annotations (and genes)	**a** Under **Font,** select a new **Font, Font Style,** and **Font Size** for track annotations. **b** Click **Apply.** The program changes the display font of track annotations and genes in Gene View.

To do this	Follow these steps
Change the order in which tracks appear in Gene View.	The order of tracks in the Gene Symbols tab controls the left-to-right order of tracks in Gene View. **a** Click the name of the track you want to move. **b** Do one of the following: • To move the track up in the list of tracks (and farther left in Gene View), click its name, then click **Up.** • To move the track down in the list of tracks (and farther right in Gene View), click its name, then click **Down.** **c** Click **Apply.**
Change the display angle of track annotations (and genes)	• Under **Genes,** in **Orientation,** type a new orientation (in degrees). 0º is horizontal. The program changes the display angle of track annotations and genes in Gene View.

To display tracks in UCSC Browser

1 Right-click Gene View, and click **Show in UCSC**.

The View coordinates in UCSC browser dialog box appears. See "View coordinates in UCSC browser" on page 256.

2 Complete the dialog box with the track parameters, and click **OK**.

The UCSC Browser appears, if you are connected to the Internet.

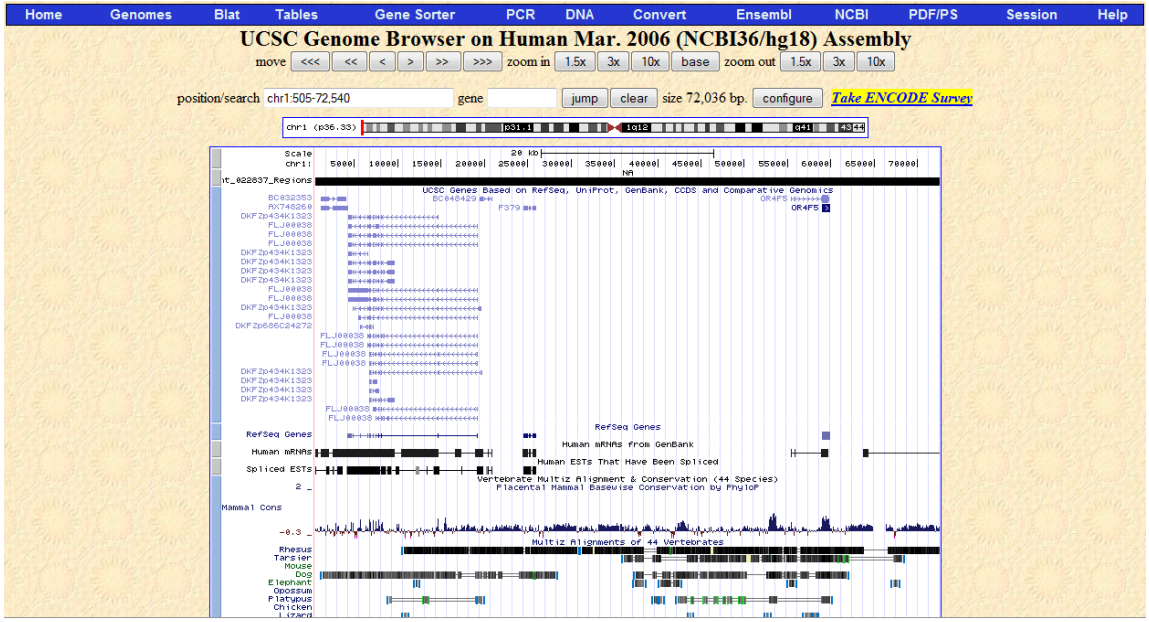


Figure 16 Track displayed in UCSC browser

3 Follow the instructions on the Web site for what you want to do.

To change the graphical display to a different genome build

The default graphical display for Genome, Chromosome and Gene Views represents human genome build 18.

- To change the graphical display to a different genome build, select an experiment whose data are based on a design file of a different genome build.

The display automatically changes when you select an experiment that contains a design file with a different genome build, such as human genome build 17, or a mouse or rat genome build.

If a genome build is not available for the design file you import, you must import the genome build first. See "To import a genome build" on page 54.

Searching for Probe and Gene Information

To search Tab View for specific probe information

You can find a specific entry in a column of a data table in Tab View. For more information on Tab View, see "Tab View" on page 156.

1 In Tab View, right-click anywhere in the column you want to search, then click **Find in column.** See "Find in column" on page 205.

The Find in column dialog box appears. The column to be searched also appears in the title bar of the dialog box.

NOTE The Find in column function works within the selected chromosome.

2 Set the search parameters, as described below.

Parameter	Comments/Instructions
Find in column	• Type the text you want to find (the *search term*). This can be an entire entry, or part of one.

Direction	• Select one of these options:
	  ◦ **Up** – Search the column upwards from the current cursor location (the highlighted row of the table).
	  ◦ **Down** – Search the column downwards from the current cursor location (the highlighted row of the table).
	Tip: Click a row in Tab View to highlight it.

Conditions	• Mark any of these, as desired:
	  ◦ **Match Case** – Find entries that match upper and lower case characters in the search term.
	  ◦ **Match whole word** – Find an entry only if the entire entry matches the search term.

3 Click **Find Next.**

If the program finds a match, it highlights the row that contains the matching entry, and resets the cursor to the corresponding position. You can click **Find Next** as many times as you like, and the program

continues to search for additional matching entries in the column. If it finds no match, the message: **String not found** appears in black in the lower part of the dialog box.

4 When you complete your search, click **Cancel.**

To search eArray for probe information

A High Density (HD) Search from an Agilent HD probe database, retrieves probes that cover specific regions of the genome of a given species. The eArray Web site has separate databases that contain HD probes for CGH, ChIP-on-chip, and methylation microarrays. In a Simple HD Search**,** you set the overall density of retrieved probes. You can find more information about probes in the *eArray$_{XD}$ User Guide***.**

1 Right-click in the data plot area of Gene View, then click **Simple HD Search.** See "Simple HD Probe Search" on page 239**.**

The eArray$_{XD}$ tab opens with the Simple HD Probe Search pane. The Genomic Intervals and Species search criteria reflect the selected region in the Genomic Viewer.

2 To return to the Gene View, click the **Genomic Viewer** tab.

To search for probes in a chromosomal location

Use this to find probes in a chromosomal region that you specify.

1 In Gene View, click on a chromosomal location, or hold down the mouse button and drag a chromosomal region of interest.

2 Right-click in Gene View, and click **Chromosomal Location Search.**

The Probe Search pane opens, with the selected location and species pre-set.

3 Complete the dialog with search parameters, and click **Search**. See the *eArray$_{XD}$ User Guide* for information on how to set the search parameters.

The results of the search appear in the bottom of the pane.

To search the Web for information on probes in Tab View

You can use any entry in a table in Tab View as the basis for a Web search.

1 In Tab View, right-click any data table entry other than a column heading.

2 Click one of the available sites.

If the site of interest does not appear in the shortcut menu, you can create a custom search link. See "To create a custom Web search link" below.

The selected site opens in your Internet browser. The program sends the table entry to the site as a search string.

To create a custom Web search link

If you need to search a different database or site based on data table entries, you can create your own custom search link. When you right-click a table entry in Tab View, a shortcut menu opens, and your custom link appears in it. If you select this link, Agilent Genomic Workbench opens the site in your Web browser and sends the table entry to the site as a search string.

1 Right-click any data table entry in Tab View, except a column heading, then click **Customize Link.**

The Customize Search link dialog box appears. "Customize Search Link" on page 184.

2 Click **New.**

3 In the Input dialog box, in **URL name,** type a name for the link.

This name will appear in the shortcut menu that opens when you right-click a data table entry.

4 Click **OK.**

5 In **URL,** type the complete URL needed to send a search string to the site. Use `<target>` as the query string value.

For example, this URL sends selected table entries to Google.com:
`http://www.google.com/search?hl=eng&q=<target>`

6 Click **Update**, then click **Yes.**

To update or delete a custom Web search link

1 Right-click any data table entry in Tab View other than a column heading, then click **Customize Link.**

The Customize Search link dialog box appears.

2 In **URL Name,** select the custom search link to update or delete.

3 Do one of the following:

To do this	Follow these steps
Update a Web search link	**a** Edit the **URL name** and the **URL** as needed. **b** Click **Update.** A Confirm dialog box appears. **c** Click **Yes.**
Delete a Web search link	• Click **Delete.**

4 Click **Close.**

4
Data Viewing Reference

This chapter describes the command ribbons, Navigator panes, and dialog boxes that can appear when you are using Agilent Genomic Workbench without analysis licenses.

Agilent Genomic Workbench Main Window

The sections that follow describe the main components of the Agilent Genomic Workbench main window – Switch Application Menu, the command ribbons, the Navigator and the Views. You use these to import, organize, manage, export and display data and other content. For descriptions of the dialog boxes for these elements, see "Dialog Boxes" on page 162. Figure 17 shows the main window of Agilent Genomic Workbench, and identifies its main parts.

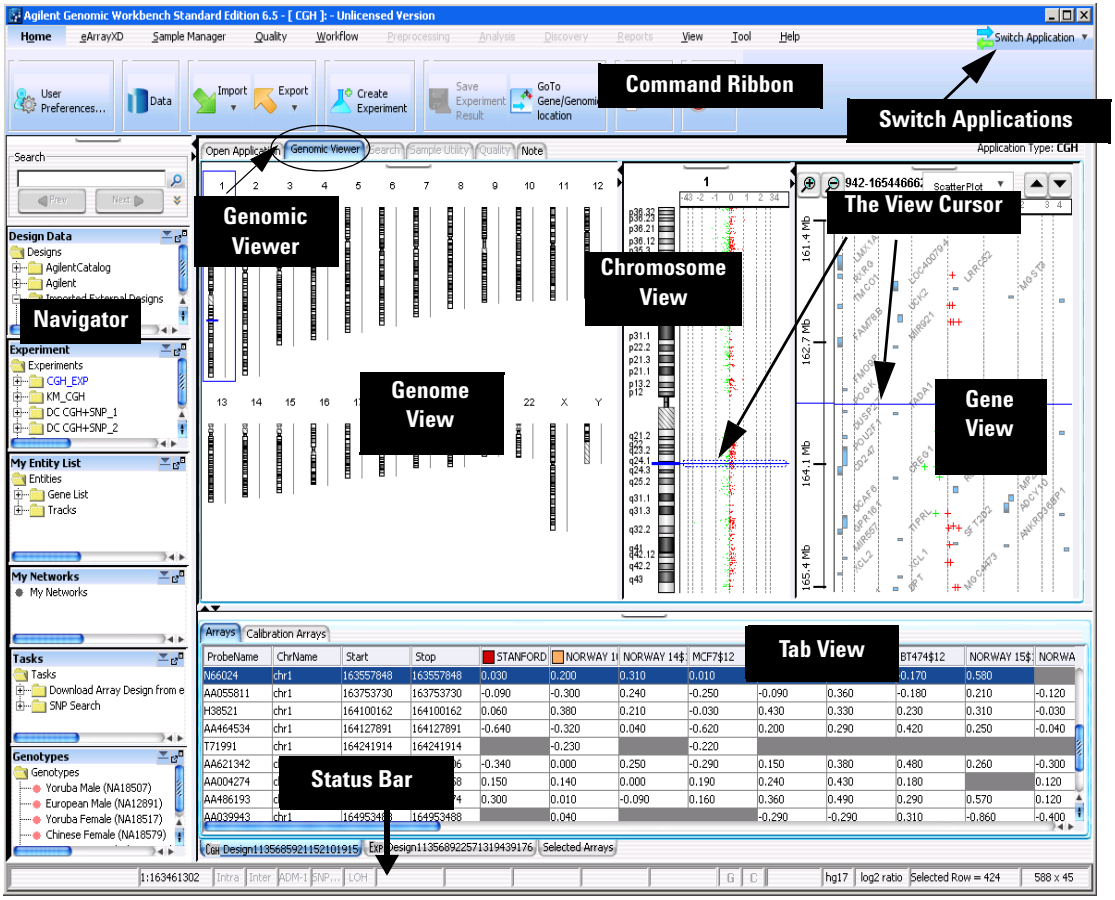


Figure 17 Agilent Genomic Workbench Unlicensed Version main window with Home command ribbon

Command Ribbons

When you click a tab at the top of the Agilent Genomic Workbench main window, groups of commands appear below the tab bar. This group of commands is called a command ribbon, and the commands that appear are available only for the selected tab. The tabs that are displayed change depending on what application is selected (such as CGH, ChIP, CH3). This section describes the ribbon commands used to import, manage, export and display data in Agilent Genomic Workbench. For command ribbons that appear in the eArrayXD, Sample Manager, and Workflow tabs, see the User Guides for those applications.

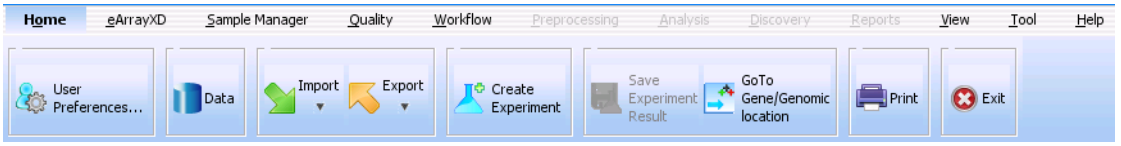


Figure 18 Tab bar and Home command ribbon for unlicensed CGH application

Home command ribbon

Figure 19 Command ribbon in the Home tab of Agilent Genomic Workbench

User Preferences Opens the User Preferences dialog box with the following tabs:

Tab	Description
Tracks	Opens a dialog box that lets you manage which tracks to display in Genomic Viewer and how they appear. See "Tracks tab" on page 251.

Tab	Description
Miscellaneous	Opens a dialog box where you can select a new location for your data files and set up access to the eArray web site. See "Miscellaneous tab" on page 253.
License	Opens a dialog box where you can add a CGH, ChIP, or CH3 application license, if you want to purchase one after using the unlicensed version. See "License tab" on page 255.

Data Opens the Catalog and Workgroup Data window where you can choose to download data from the eArray catalog or from your workgroup. See "Catalog and Workgroup Data" on page 165.

Import Opens a menu of file types that you can import:

Option	Description
Array Files	Opens a menu with these options: • **FE File** – Opens the Import FE Files dialog box, where you can select an Agilent Feature Extraction array data file to import. See "Import" on page 211 and "To import Agilent FE or Axon data files" on page 50. • **Axon File** – Opens the Import Axon Files dialog box, where you can select Axon (*.gpr) files for import. See "Import" on page 211 and "To import Agilent FE or Axon data files" on page 50. • **UDF File** – Opens the UDF Files dialog box, where you can select a Universal Data File (UDF) to import. See "Import" on page 211 and "To import a UDF file" on page 51.
Design Files	Opens a menu with these options: • **GEML File** – Opens the Import Design Files dialog box, where you can select Agilent GEML-based (*.xml) array design files for import. See "Import" on page 211 and "To import Agilent GEML design files" on page 48. • **Axon Design File** – Opens the Import Axon Design Files dialog box, where you can select Axon (*.gal) array design files for import. See "Import" on page 211 and "To import Axon design files" on page 49.
Genome Build	Opens the Import Genome Build dialog box, where you can import Agilent-supplied genome build files. See "Import Genome Build" on page 219 and "To import a genome build" on page 54.

Option	Description
Track	Opens the Import Track dialog box, where you can select a BED format track file for import, and create a display name for the track. See "Import Track" on page 220 and "To import tracks" on page 55.
ArrayAttributes	Opens the Import microarray attributes dialog box, where you select a sample attributes file to import. See "Import" on page 211 and "To import array attributes" on page 56 for more information.
Experiments	Opens the Import Experiments dialog box, where you select an exported experiment .zip file, from which you can select experiments to import. See "Import" on page 211 and "To import an experiment file" on page 57 for more information.
Filters	Opens the Import dialog box, where you select a filter file to import. For more information, see "Import" on page 211 and "To import filters" on page 58.
Probe Upload	Lets you import a file of probe sequences and annotation. For more information, see the *eArray XD User Guide.*
Custom Genome for Tiling	Opens the Import Genome dialog box, where you upload a user defined genome for use with the Genomic Tiling and Bait Tiling tools in eArray XD. For more information, see the *eArray XD User Guide.*
Genotype References (CGH only)	Opens the Import Genotype Reference Files dialog box, where you select a .txt or .xls file that contains one or more genotype references to use for SNP analysis. See "To import a genotype reference file (CGH only)" on page 59.

Export Opens a menu that lets you export several kinds of files.

Option	Description
Experiments	Opens the Export Experiments dialog box, where you can select one or more experiments for export as a single ZIP file. See "Export Experiments" on page 202 and "To export experiments" on page 82.
Filters	Opens the Export Filters dialog box, where you can select one or more filters for export as a single *.xml file. See "Export Filters" on page 203 and "To export filters" on page 83.

Option	Description
Tracks	Opens the Export Tracks dialog box, where you can select one or more tracks to export as a single BED format file. See "Export Tracks" on page 204 and "To export tracks" on page 84.
Array Attributes	Opens the Export Array Attributes dialog box, where you can select arrays and their attributes for export. See "Export Array Attributes" on page 198.

Create Experiment Opens the Create Experiment dialog box, where you can create a new, empty experiment and add data to it. See "Create Experiment" on page 178 and "To create a new experiment" on page 62.

Save Experiment Result (Not available if you do not have a CGH, ChIP, or CH3 application license)

Go to Gene/Genomic Location Moves the cursor to the location in Chromosome and Gene Views that you select. See "Go To Gene/Genomic Location" on page 210.

Print Opens the Print window to print the display.

Exit Closes the program.

View Command Ribbon

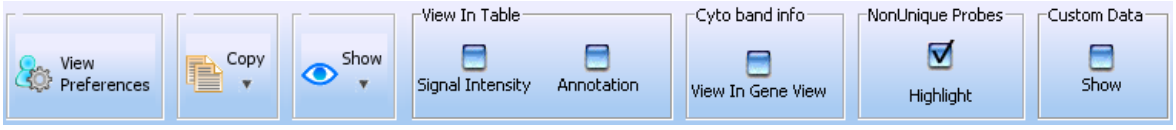


Figure 20 View command ribbon for CGH application

View Preferences Opens the View Preferences dialog box where you can customize the display of data and results in the Genomic Viewer. For more information, see "View Preferences" on page 258.

Copy This command opens a menu with the options listed below. In general, the Copy command copies pane(s) of the main window to the Clipboard as an image. You can then paste the image into a document in another program. See "To copy what you see in the main window" on page 84.

Option	Description
All	Copies all panes of the main window to the Clipboard as an image.
Navigator	Copies only the Navigator to the Clipboard as an image.
Tab View	Copies only the Tab View to the Clipboard as an image.
SampleBySample view	(Available only in data analysis modules, when selected) Copies only the Sample-by-sample View to the Clipboard as an image.
Genome view	Copies only the Genome View to the Clipboard as an image.
Chromosome view	Copies only the Chromosome View to the Clipboard as an image.
Gene view	Copies only the Gene View to the Clipboard as an image.

Show Opens a menu with all available elements of the main window. Mark the check box for the one or ones you want to display.

View In Table

Signal Intensity Mark the check box to see the red and green raw signal intensities of the log ratio data in the Tab View.

Annotation Mark the check box to show annotations in the Tab View.

Cyto band info

View In Gene View Mark the check box to display cytobands in the Gene View.

NonUnique Probes

Highlight Nonunique probes in a microarray design have more than one mapping in the genome that is a perfect match. Because the probes represent the same sequence, the probe log ratio reflects a combination of log ratios from the redundant locations. Mark the check box to display nonunique probes in a different color.

Custom Data

Show Mark the check box to display custom data in the Genomic Viewer.

Tool command ribbon

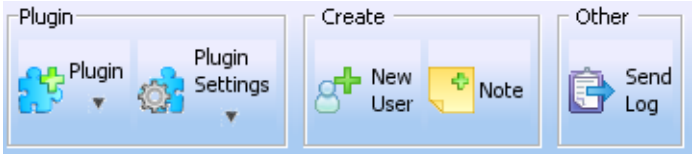


Figure 21 Tool command ribbon

Plugin

Plugins are ancillary programs that operate on the selected array data in the active experiment in specific ways.

Opens a menu with the options described below. Custom plugins also appear in this menu.

CGHSmooth Opens the CGHSmooth Parameters dialog box. See "CGHSmooth Parameters" on page 167. You can set the parameters of the CGHSmooth plug-in, and create separate, stacked plots of smoothed log ratio data for each of the selected arrays in the current experiment. The plug-in plots the data associated with the currently selected chromosome.

When you open this dialog box, you see the default parameters you enter under Plugin Settings.

Echo Example Creates separate, stacked plots of log ratio data for each of the selected arrays in the current experiment. The plug-in plots the data associated with the currently selected chromosome. The plot appears in a new window. Although simple, this plug-in gives you a convenient way to view the log ratio data for selected arrays as separate plots. See "Echo Example Plot" on page 190.

MovAvg Example Opens the MovAvg Example Parameters dialog box. See "MovAvg Example Parameters" on page 224. You can set the parameters of the MovAvg Example plug-in. The plug-in calculates a 10-point moving average of each column of selected microarray data, and produces stacked plots of all of the input data and moving averages. To use this plug-in, you must have Perl installed on your computer.

When you open this dialog box, you see the default parameters you enter under Plugin Settings.

Plugin Settings

Opens another menu with these options:

CGHSmooth Opens the CGHSmooth Parameters dialog box, where you can set the parameters for the plug-in when you have selected to not show the parameters dialog box when you click Plugin. See "CGHSmooth Parameters" on page 167.

MovAvg Example Opens the MovAvg Example Parameters dialog box, where you can set the parameters for the plug-in when you have selected to not show the parameters dialog box when you click Plugin. See "MovAvg Example Parameters" on page 224.

Create

This group contains two options:

New User Opens the eArray Website, where you can add a new eArray user.

Note Opens a dialog box where you can type notes and comments. You can view these notes from the Notes tab in the Agilent Genomic Workbench main window.

Other

Send Log Sends a log file to Agilent customer support. Use this feature if you are working with customer support to troubleshoot a problem.

Help command ribbon

The Help command ribbon lets you display the available Agilent Genomic Workbench help guides, and get information about software version, installation history, and check for software updates. Help guides are opened in Adobe® Reader®.

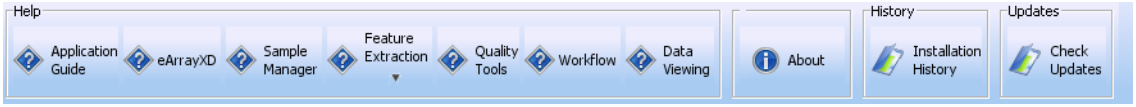


Figure 22 Help command ribbon for Agilent Genomic Workbench CGH application (unlicensed)

Table 4 Table of Help for unlicensed version data viewing

Help Command	Action
Application Guide	Opens the Agilent Genomic Workbench application user guide for the selected application.
eArrayXD	Opens the *eArray$_{XD}$ User Guide*. This guide comprehensive help on all available eArrayXD tools.
Sample Manager	Opens the *Sample Manager User Guide,* that shows how to use the Sample Manager module of Agilent Genomic Workbench to organize microarrays and edit their attributes.
Feature Extraction	Opens a menu that lets you choose from the following Feature Extraction help guides: • **Feature Extraction Quick Start Guide** – An overview of how to use the Feature Extraction software to extract and generate QC reports for Agilent microarrays • **Feature Extraction User Guide** – A comprehensive user guide that explains how to extract and generate QC reports for Agilent microarrays • **Feature Extraction Reference Guide** – Contains tables that list default parameter values and results for Feature Extraction (FE) analyses, and explanations of how FE uses its algorithms to calculate results.
Quality Tools	Opens the *Quality Tools User Guide*, that describes how to query, filter, and evaluate microarray extractions within Agilent Genomic Workbench.

Table 4 Table of Help for unlicensed version data viewing (continued)

Help Command	Action
Workflow	Opens the *Workflow User Guide*, that describes how to use the Workflow module of Agilent Genomic Workbench to extract image files with Agilent Feature Extraction software and/or analyze data using CGH and ChIP analysis software.
Data Viewing	Opens the *Data Viewing User Guide* that describes how to import, organize, manage, export and display data and other content (experiments, gene lists, tracks) within Agilent Genomic Workbench. It is targeted for users who have no DNA Analytics application license(s).
About	Opens a message with information about the version number and copyright of the program.
Installation History	Opens the Installation History dialog box, that shows what versions and updates were installed.
Check Updates	Checks for available updates to the software. If an update is available, you are asked if you want to install it. If no update is available, a message appears to let you know.

An additional guide is available in the Open Application tab of the program. The *Agilent Genomic Workbench Product Overview Guide* gives an overview of the capabilities of Agilent Genomic Workbench. It also describes how to start each of the component programs and find help, and how to enter your license information. In addition, it helps you with system administration and troubleshooting. To open this guide, click the **Open Application** tab, then click **Product Overview**.

Switch Application Menu

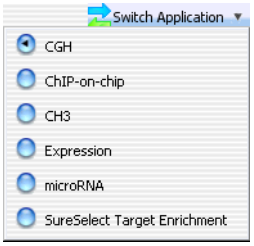


Figure 23 Switch Application menu

The Switch Application menu lets you change to the other data display and analysis application types in Agilent Genomic Workbench. Select the desired application type.

CGH (Separate license required) Import, display, and analyze array-based comparative genomics hybridization (aCGH) data in both an interactive "analyze as you go" mode, and an automated workflow mode.

ChIP (Separate license required) Import, display, and analyze ChIP-on-Chip microarray data in both an interactive "analyze as you go" mode, and an automated workflow mode.

CH3 (Separate license required) Import and display data from microarray-based studies of genomic methylation patterns.

Expression Use eArrayXD for array-based gene expression studies.

microRNA Use eArrayXD for array-based miRNA studies.

SureSelect Target Enrichment Use the Quality Analyzer function for SureSelect Target Enrichment. Import, export, and view data, and use eArrayXD to search, and create Bait Groups. See the *Target Enrichment User Guide* for more information.

Search pane

The Search pane lets you find all occurrences of a specific search term in the Design Data, Experiment, and/or My Entity List panes. See "To find specific content items in the Navigator" on page 71. It also contains several buttons that you can use to move, hide, show or resize the Navigator.

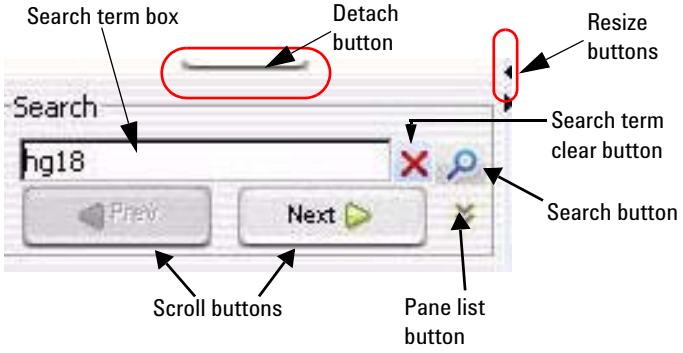


Figure 24 Navigator – Search pane

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.

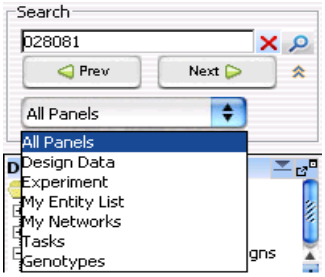


Figure 25 Search Panels list

(Show Pane List button, available only if the Pane list is not visible) Makes the Pane list visible.

(Hide Pane List button, available only if the Pane list is visible) Hides the Pane list.

(Search button) Searches the pane(s) selected in the Pane list for all occurrences of the term you typed in the Search term box. If the program finds a matching item, it expands the folder structure to make the matching item(s) visible, makes the lettering of each item red and highlights the item in yellow. Note: The search term is not case-sensitive, but it must reflect the entire name of the desired items. You can use asterisks (*) as wildcards to represent groups of unspecified characters.

Scroll buttons (Available only after a search) Lets you scroll up and down the lists of highlighted search items after a search.

(Clear button, available only after a search) Clears the search term from the Search term box, and resets the color of any matching item to its original color.

Navigator

The Navigator contains several panes where you can look at program designs, experiments, data, or the status of tasks. Within each pane, you will see icons that tell you the status of the content. In addition, shortcut menus are available to let you perform tasks within the pane. These icons and shortcut menus are described in this section.

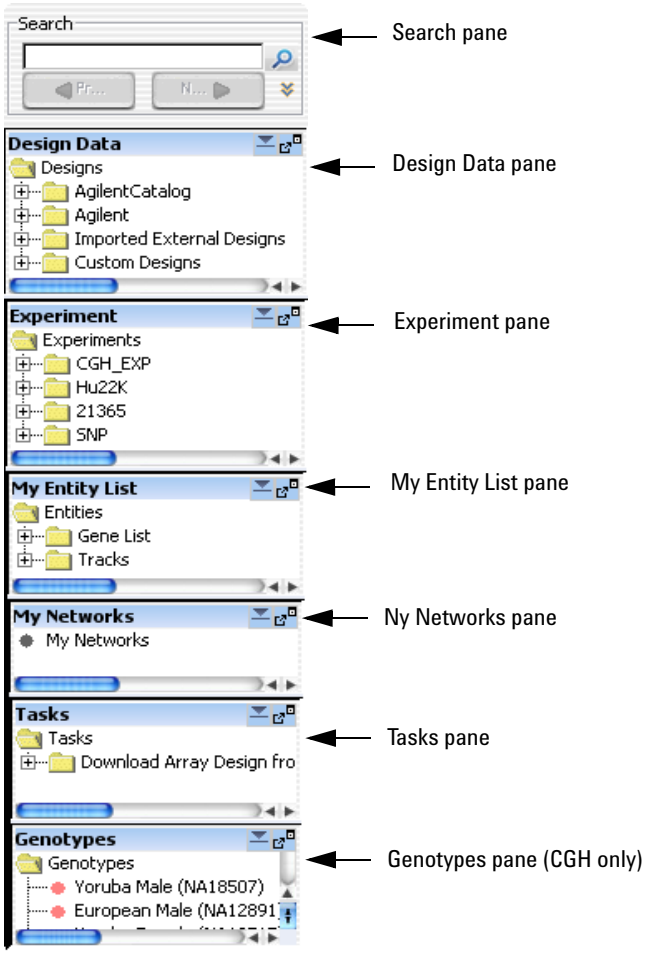


Figure 26 Navigator panes for CGH

Pane	Comments
Search	Lets you search within any pane of the Navigator for a specific item (array or build, for example). You must type the entire array name or term; otherwise, use asterisks (*) as wildcards for unspecified strings. For example, type *1234* to find any item that contains "1234".
Design Data	Contains microarray data files, organized by design and application type, and then by genome build. Shows all probe groups and microarray designs that are available to you, organized by folders. For the SureSelect Target Enrichment application type, the program shows all bait groups and libraries. In general, you can: • Expand or collapse folders to show or hide content. • Look at the icon that appears with an item to monitor its status. • Right-click the name of a folder or item to open a shortcut menu that lets you take action on the item. See "Design Data pane – icons, special text, and buttons" on page 129 and "Design Data pane – actions and shortcut menus" on page 131. For Agilent Catalog content, the names of all available items appear in the Agilent Catalog folder. However, to work with this content, you must specifically request a download of the actual data from the eArray Web site.
Experiment	Contains Agilent Genomic Workbench experiments. Experiments are organizational units that contain links to microarray data and design files. In data analysis modules, experiments also contain saved results.
My Entity List	Contains gene lists and tracks: • **Gene Lists** are collections of genes of interest. You can create them within the program, import and export them, and apply them to Gene View and Chromosome View. • **Tracks** are collections of annotation or other information that map to specific genomic locations. You can import, export, and combine tracks, and display them in Gene View with your array data and analysis results.
My Networks	Contains the biological networks/pathways that you found using Network Search or that you create using a literature search in eArrayXD. For more information, see the *eArray$_{XD}$ Users Guide*

Pane	Comments
Tasks	Shows the jobs that you have submitted. Some jobs are completed locally by the eArray$_{XD}$ server program. Others are sent to the eArray Web site for completion. In general, you can: • Look at the icon that appears with a job to monitor its status. • Right-click the name of a pending task to open a shortcut menu that lets you take further action on the job. See "Tasks pane" on page 143.
Genotypes	Shows the genotype references in the database. From this pane, you can import genotype reference files, and view details, rename, or delete genotype references.

Design Data pane – icons, special text, and buttons

Item	Comments
	An unexpanded folder (domain) that contains subfolders or other items.
	An expanded folder. The items that it contains are visible in the Navigator.
	Expands a folder to show its contents.
	Collapses a folder to hide its contents.
	A folder that can contain microarray design(s) or bait librar(ies).
	A folder that can contain probe group(s) or bait group(s).
	An item that contains Agilent content that you must update from the eArray Web site before you can use it.
	An available microarray design with a status of Draft, or an available probe or bait group with a status of Incomplete.
	An available library or microarray design with a status of Review.
	An available library or microarray design with a status of Completed.
	An available library or microarray design with a status of Submitted.
	An available probe or bait group with a status of Locked.
	A methylation array design. This folder contains array data associated with the design, organized by genome build.
	A CGH array design. This folder contains array data associated with the design, organized by genome build.
	A CGH+SNP array design. This folder contains array data for the design, organized by genome build.
	A gene expression array design. This folder contains array data associated with the design, organized by genome build.
	A ChIP array design. This folder contains array data associated with the design, organized by genome build.
	A genome build folder within a specific design folder. This folder contains arrays associated with the specific genome build and design.

Item	Comments
Build	A folder that contains sample data for a design. The data are read-only to the user who is currently logged in. The data apply to the indicated genome build, and are not used by eArray$_{XD}$.
Build	A folder that contains sample data for a design. The data can be edited the user who is currently logged in. The data apply to the indicated genome build, and are not used by eArray$_{XD}$.
	A single array data file.
	Data from an individual microarray sample. The design from which the data were derived is read-only to the user who is currently logged in. These data are not used by eArray$_{XD}$.
	Data from an individual microarray sample. The design from which the data were derived can be edited by the user who is currently logged in. These data are not used by eArray$_{XD}$.
	Data created from a multi-pack array.
text	An item that matches the search term in a search.
	(Dock out button) Moves the Design Data pane from the Navigator, and opens it in a, separate window.
	(Collapse button, available only if the Design Data pane is not collapsed) Collapses the Design Data pane, and shows its title bar at the bottom of the Navigator.
	(Expand button, available only if the Design Data pane is collapsed) Expands the Design Data pane.

Design Data pane – actions and shortcut menus

The Design Data pane of the Navigator shows available content items that are stored on your server for the selected application type, and any external content that you imported. It also shows the names of items in the Agilent Catalog. For more information on the contents of the Design Data pane, and how to use eArray$_{XD}$, see the *eArray$_{XD}$ Users Guide*.

- Double-click any folder to expand or collapse it.

Design Data Main Folders

The Designs folder in the Design Data pane of the Navigator contains the following main folders:

Folder	Contents
AgilentCatalog	Downloaded content from the Agilent Catalog that is available for the selected application type. See "AgilentCatalog Folder" on page 131.
<Workgroup Name>	This folder, which bears the name of your workgroup, contains downloaded workgroup content that is available for the selected application type. See "<Workgroup Name> Folder" on page 132.
Imported External Designs	Imported design information and array data for downstream processing by the Agilent Genomic Workbench data analysis applications. Designs that you did not import are read-only. "Imported External Designs Folder" on page 134.
Custom Designs	Custom (non catalog) designs created using eArray. Custom designs are hidden if they are not owned by the user who is logged in. "Custom Designs Folder" on page 136

AgilentCatalog Folder

- Right-click the name of a microarray design or probe group to open a shortcut menu with available options. (Note – The availability of the options varies by design status and ownership.) See the *eArray$_{XD}$ User Guide* for information on how to use these options.

<Workgroup Name> Folder

- Double-click the name of a folder to expand or collapse it.
- Right-click on an Array Design or Probe Group and select one of the available actions (described in the *eArray$_{XD}$ User Guide*).

Right-click the name of a domain folder to open a shortcut menu. See the *eArray$_{XD}$ User Guide* for information on how to use these options.**Main Folders**

The Designs folder in the Design Data pane contains the following main folders:

Folder	Contents
AgilentCatalog	Downloaded content from the Agilent Catalog that is available for the selected application type.
<Workgroup Name>	This folder, which bears the name of your workgroup, contains downloaded workgroup content that is available for the selected application type.
Imported External Designs	Imported design information and array data for downstream processing by the Agilent Genomic Workbench data analysis applications. You cannot use eArrayXD to work with any of the items in these folders. Designs that you did not import are read-only. For more information, see the applicable *User Guide* for each data analysis application.
Custom Designs	Custom designs created using eArray.

AgilentCatalog Folder

- Right-click the name of a microarray design or probe group to open a shortcut menu with available options. (Note – The availability of the options varies by design status and ownership.) See the *eArray$_{XD}$ User Guide* for information on how to use these options.

<Workgroup Name> Folder

- Double-click the name of a folder to expand or collapse it.

- Right-click on an Array Design or Probe Group and select one of the available actions (described in the *eArray$_{XD}$ User Guide*).
- Right-click the name of a domain folder to open a shortcut menu. See the *eArray$_{XD}$ User Guide* for information on how to use these options.

Imported External Designs Folder

Imported external designs appear in this folder under folders for the type of design they represent: ChIP, Expression, CGH, or Only Stats and Params (for imported statistics and parameters from Feature Extraction).

- Right-click the **Imported External Designs** folder to open a shortcut menu with an Import option. When you select this option, a menu appears with the following options for file import:

Option	Description
Design File	Opens the Import Design Files dialog box, where you can select an Agilent GEML-based (*,xml) file for import. See "Import" on page 211 and "To import Agilent GEML design files" on page 48. **Note:** You cannot import Catalog designs. They must be downloaded from eArray.
Axon Design File	Opens the Import Axon Files dialog box, where you can select Axon design (*.gal) files for import. See "Import" on page 211 and "To import Axon design files" on page 49.
FE File	Opens the Import FE Files dialog box, where you can select an Agilent Feature Extraction (.txt) data file to import. See "Import" on page 211 and "To import Agilent FE or Axon data files" on page 50.
Axon File	Opens the Import Axon Files dialog box, where you can select Axon (*.gpr) files for import. See "Import" on page 211 and "To import Agilent FE or Axon data files" on page 50.
UDF File	(For CGH and CH3 data only) Opens the UDF Files dialog box, where you can select a Universal Data File (UDF) to import. See "Import" on page 211 and "To import a UDF file" on page 51.

- Only Stats and Params

Double-click the name of an imported design folder, and then double-click the Design Samples folder to display a list of genome builds.

Imported External Designs Folder

Imported external designs appear in this folder under the folders for the type of design they represent: ChIP, Expression, CGH, or Only Stats and Params (for imported statistics and parameters from Feature Extraction).

- Right-click the **Imported External Designs** folder to open a shortcut menu with an Import option. When you select this option, a menu appears with the following options for file import:

Option	Description
Design File	Opens the Import Design Files dialog box, where you can select an Agilent GEML-based (*,xml) file for import. See "Import" on page 211 and "To import Agilent GEML design files" on page 48. **Note:** You cannot import Catalog designs. They must be downloaded from eArray.
Axon Design File	Opens the Import Axon Files dialog box, where you can select Axon design (*.gal) files for import. See "Import" on page 211 and "To import Axon design files" on page 49.
FE File	Opens the Import FE Files dialog box, where you can select an Agilent Feature Extraction (.txt) data file to import. See "Import" on page 211 and "To import Agilent FE or Axon data files" on page 50.
Axon File	Opens the Import Axon Files dialog box, where you can select Axon (*.gpr) files for import. See "Import" on page 211 and "To import Agilent FE or Axon data files" on page 50.
UDF File	Opens the UDF Files dialog box, where you can select a Universal Data File (UDF) to import. See "Import" on page 211 and "To import a UDF file" on page 51.

- Double-click an imported designs folder (ChIP, Expression, CGH, Only Stats and Params) to display the imported designs for that data type.
- Double-click the name of an imported design folder, and then double-click the Design Samples folder to display a list of genome builds.

- Double-click the name of a genome build folder to display imported arrays for that build.

Genome Build Folder

- Right-click the name of a genome build folder to display the following options:

Option	Description
Show Properties	Opens the Design Properties dialog box. See "Design Properties" on page 185.
Delete	Opens a Confirm dialog box. If you click **Yes,** the program permanently deletes all of the arrays in this genome build folder. (Not available for read-only builds.)

Specific Arrays

- Right-click the name of an array to display the following options:

Option	Description
Show Properties	Opens the Microarray Properties dialog box. See"Microarray Properties" on page 221 and "To display or edit the attribute values of a specific array" on page 68.
Rename	Opens an Input dialog box, where you can type a new name for the array. Click **OK** to rename the array. (Not available for read-only builds.)
Delete	Opens a Confirm dialog box. If you click **Yes,** the program permanently deletes the array. (Not available for read-only builds.)

- Drag an array from the Design Data pane to an experiment folder in the Experiment pane to associate it with an experiment. You can drag multiple arrays at once from one genome build in a design. Hold down the **Ctrl** key while you click the additional arrays to select them. You can also select a contiguous block of arrays; click the first array in the block, then hold down the **Shift** key and click the last one.

Custom Designs Folder

This folder displays custom designs available from eArray$_{XD}$.

Experiment pane – icons, special text, and buttons

Item	Comments
	Click to expand a folder and display its contents.
	Click to collapse a folder and hide its contents.
	A folder that contains files or other folders.
	A methylation array design. This folder contains array data associated with the design, organized by genome build.
	A CGH array design. This folder contains array data associated with the design, organized by genome build.
	A CGH+SNP array design. This folder contains array data for the design, organized by genome build.
	A gene expression array design. This folder contains array data associated with the design, organized by genome build.
	A ChIP array design. This folder contains array data associated with the design, organized by genome build.
	A genome build folder within a specific design folder. This folder contains arrays associated with the specific genome build and design.
	A read-only genome build folder within a specific design folder.
	A genome build folder, within a specific design folder, that you can modify.
	An array that is not selected for view
	An array that is selected for view and analysis. The specific color of this icon can vary.
	An empty folder.
	Data created from a multi-pack array.
blue text	The currently active experiment. All data that appear in Chromosome, Gene, and Tab Views come from this experiment.

Item	Comments
red text	An item that matches the search term in a search.
	(Dock out button) Moves the Experiment pane from the main window, and opens it in a separate window.
	(Collapse button, available only if the Experiment pane is not collapsed) Collapses the Experiment pane, and shows its title bar at the bottom of the Navigator.
	(Expand button, available only if the Experiment pane is collapsed) Expands the Experiment pane.

Experiment pane – actions and shortcut menus

Only the options that are not grayed out are discussed in this section. To enable the grayed-out options, you must have the appropriate license for the CGH, ChIP, or CH3 application you are using. These inactive options are explained in the *User Guide* for the application.

- In general, double-click the Experiments folder, and the folders within it, to expand and collapse them. Exception: double-click the name of an unselected experiment to select it for display. Without a license, you cannot select an experiment that contains results.

NOTE The displayed options change depending on the user and status of the designs, builds, and arrays. You may not see all of the options that are described below.

Experiments Folder

- Right-click the **Experiments** folder to display the following options:

Option	Description
New Experiment	Opens the Create Experiment dialog box, where you can name the new experiment, and open another dialog box that lets you add microarray data to the experiment. See "Create Experiment" on page 178.
Export	Opens the Export Experiments dialog box, where you can export one or more experiments as a single ZIP file. See "Export Experiments" on page 202 and "To export experiments" on page 82.

Specific Experiment Folder

- Right-click the name of an experiment to display the following options:

Option	Description
Select Experiment	(Appears only if the experiment is not selected, and if there are no saved results for the experiment.) Opens the Experiment Selection dialog box, which asks if you want to select the experiment. Click **Yes** to select the experiment for display and analysis. Or In the Experiments folder, double-click the name of an experiment that is not selected to open the Experiment Selection dialog box. To select the experiment for analysis, click **Yes.**
Deselect Experiment	(Appears only if the experiment is selected.) Removes the experiment data from display.
Show Properties	Opens the Experiment Properties dialog box. Use this dialog box to see the names of the arrays in the experiment, and also to add or remove arrays from the experiment. See "Experiment Properties" on page 195.
Export	Opens the Export Experiments dialog box, where you can export this and other experiments as a single ZIP file. See "Export Experiments" on page 202 and "To export experiments" on page 82.
Export Attributes	Opens the Export Attributes dialog boxes, one for selecting arrays for which you want attributes exported and one for selecting the attributes you want to export with the selected arrays. See "Export Array Attributes" on page 198.
Edit Array Color	Opens the Edit Array Color dialog box, where you can select a display color for each of the arrays in the experiment. For more information see "Edit Array Color" on page 193.

Option	Description
Edit Array Order	Opens the Array Order dialog box, where you can change the order of the arrays in the Experiment and in Tab View. See "Edit Array Order" on page 194.
Rename	Opens an Input dialog box, where you can type a new name for the experiment. Click **OK** to rename the experiment.
Delete	Opens a Confirm dialog box that asks if you want to delete the Experiment. Click **Yes** to delete it. Note: You can delete any experiment except the selected one.

Design Folder

- Right-click the name of a design to open a shortcut menu with a Delete option. If you select this option, a Confirm dialog box opens. If you click **Yes,** the program removes the links to all of the arrays under the design from the experiment.

Genome Build Folder

- Right-click the name of a genome build within a design to display the following options:

Option	Description
Set for Calibration	Agilent does not recommend using another array to calculate noise for the sample array.
Delete	Opens a Confirm dialog box that asks if you want to disassociate all arrays under the design from the experiment. Click **Yes** to remove the links between the arrays and the experiment. • If you delete a design from an experiment, the program removes the links between the experiment and the design and its arrays. The actual design and array data stay in the Data folder.
Show Properties	Opens the Design Properties dialog box. See "Design Properties" on page 185.

Individual Arrays

- Within the folder of a specific experiment, in the **Arrays** folder of a design, right-click the name of an individual array display the following options:

Option	Description
Select	(Available if the array is not selected) Selects the array for display.
Deselect	(Available if the array is selected) Removes the array data from Genome, Chromosome, and Gene views. Also removes the array from the Selected Arrays tab in Tab View.
Rename	Opens an Input dialog box, where you can type a new name for the array. Click **OK** to accept the new name for the array.
Delete	Opens a Confirm dialog box that asks if you want to disassociate the array from the experiment. Click **Yes** to remove the link between the array and the experiment. See "To remove arrays from an experiment" on page 67. • If you delete an array from an experiment, the program removes the link between the experiment and the array. The actual array data stays in the Data folder.
Show Properties	Opens the Microarray Properties dialog box, where you can display and edit microarray attributes. For array files from the Agilent Feature Extraction program, you can also display the headers and feature data from the file. See "Microarray Properties" on page 221 and "To display or edit the attribute values of a specific array" on page 68.
Edit Array Color	Opens the Edit Array Color dialog box, where you can select a display color for the array. See "Edit Array Color" on page 193 and "To change the display color of an array" on page 90.
Edit Array Order	Opens the Array Order dialog box, where you can change the order of the arrays in the Experiment and in Tab View. See "Edit Array Order" on page 194 and "To change the order of arrays in an experiment" on page 65.

My Entity List pane – icons, buttons, and special text

Item	Comments
	Click to expand a folder and display its contents.
	Click to collapse a folder and hide its contents.
	A folder that contains files or other folders.
	An individual gene list or track.
red regular text	An item that is an exact match with the search term in a search, or a gene list that has not been applied and has red assigned as its custom color.
colored italics	A gene list that has been applied.
red bold italics	A track that is selected for display in Gene View.
black bold italics	A "combined" track that is selected for display in Gene View. A combined track contains information from two or more individual tracks associated by logical criteria.
	(Dock out button) Moves the My Entity List pane from the main window, and opens it in a, separate window.
	(Collapse button, available only if the My Entity List pane is not collapsed) Collapses the My Entity List pane, and shows its title bar at the bottom of the Navigator.
	(Expand button, available only if the My Entity List pane is collapsed) Expands the My Entity List pane.

My Entity List pane – actions and shortcut menus

Only the options that are not grayed out are discussed in this section. To enable the grayed-out options, you must have the appropriate license for the CGH, ChIP or CH3 application you are using. These options are explained in the *User Guide* for the application.

- Double-click the **Gene List** folder to show or hide its gene lists.

Gene List Folder

- In the **Gene List** folder, right-click the name of a gene list to display the following options:

Option	Description
Rename	Opens an Input dialog box, where you can type a new name for the gene list. Click **OK** to accept the new name.
Delete	Opens a confirm dialog box that asks if you are sure you want to delete the gene list. Click **Yes** to confirm.

Tracks Folder

- Right-click the name of a track to display the following options:

Option	Comments
Show in UI	Mark this option to display the track in Gene View next to the data and results of the selected experiment. See "To show tracks in Gene View" on page 103 and "User Preferences" on page 250.
Show in Report	Mark the check box to show the track information in all the reports.
Genomic Boundaries	Click to use the genome track to define only the regions that aberration detection algorithms will run. You can select this for only one track.
Show in UCSC	Opens the UCSC (University of California at Santa Cruz) Genome Browser in your Web browser and uploads the track. You can then see information for the track.
View Details	Opens a table that shows all the chromosome locations defined in the track.
Rename	Opens an Input dialog box, where you can type a new name for the track. Click **OK** to rename the track.
Delete	Opens a Delete Track dialog box that asks if you are sure you want to delete the track. Click **Yes** to delete the track.

My Networks pane

Contains the biological networks/pathways that you found using Network Search or that you create using a literature search in eArray$_{XD}$. For more information, see the *eArray$_{XD}$ Users Guide*.

Tasks pane

Figure 27 Tasks pane of the Navigator

Many tasks that you do in Agilent Genomic Workbench generate jobs that are completed in the background on your Agilent Genomic Workbench server or on the eArray Web site. You use the Tasks pane to keep track of the status of these jobs, and to take action on them when their results become available.

Tasks pane – icons, buttons, and special text

These icons, buttons, and special text items can appear in the Tasks pane of the Navigator:

Item	Details
	Click to expand a folder and display its contents.
	Click to collapse a folder and hide its contents.
	A folder that contains files or other folders.
	A pending task with a status of Submitted. The task has been submitted to the job queue, but no action has been taken on it yet.
	A pending task with a status of Processing. The task has been submitted to the job queue, and the program (or the eArray Web site) is processing the job.
	A pending task with a status of Completed. The results of the job are now available for your use.
	A pending task with a status of Error. An error has occurred, and you must re-submit the job. For probe or bait uploads, an error file is available that lists the errors in your input file.
	(Dock out button) Moves the Tasks pane from the main window, and opens it in a separate window.
	(Collapse button, available only if the Tasks pane is not collapsed) Collapses the Tasks pane, and shows its title bar at the bottom of the Navigator.
	(Expand button, available only if the Tasks pane is collapsed) Expands the Tasks pane.

Tasks pane – Actions and shortcut menus

- Double-click the name of a folder to expand or collapse it.
- Right-click the name of a pending task to open a shortcut menu. The shortcut menu contains commands that are appropriate to the type of job, and its status.

For details on actions in the task menu, see the *eArray$_{XD}$ User Guide*.

Genotypes pane (CGH only)

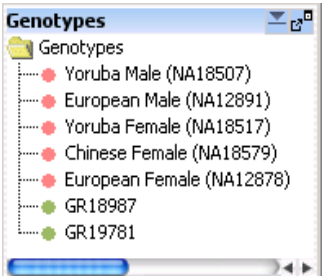


Figure 28 Genotypes pane of the Navigator (CGH only)

In order to perform SNP analysis, there must be genotype references in the database for the CGH+SNP microarrays you want to analyze. The imported genotype references in the database are displayed in this pane. This pane only appears when the CGH module is selected.

NOTE Without a CGH license, you cannot analyze or display results for CGH+SNP data.

Genotypes pane – Actions and shortcut menus (CGH only)

- Right-click on a genotype reference in the list, and select from the following options:

Option	Description
Show Properties	Opens the Genotype Reference Details dialog box, where you can review the information contained in the selected genotype reference. See "Genotype Reference Details (CGH only)" on page 208.

Option	Description
Rename	Opens the Input dialog box, where you can type a new name for the selected genotype reference.
Delete	For genotype references that are not marked as read-only, deletes the selected genotype reference.

Genomic Viewer

This section describes the display areas that appear when you click the Genomic Viewer tab. The orientation of these views (vertical or horizontal) can be changed from View Preferences located in the View tab. See "View Preferences" on page 258 for more information.

Genome View

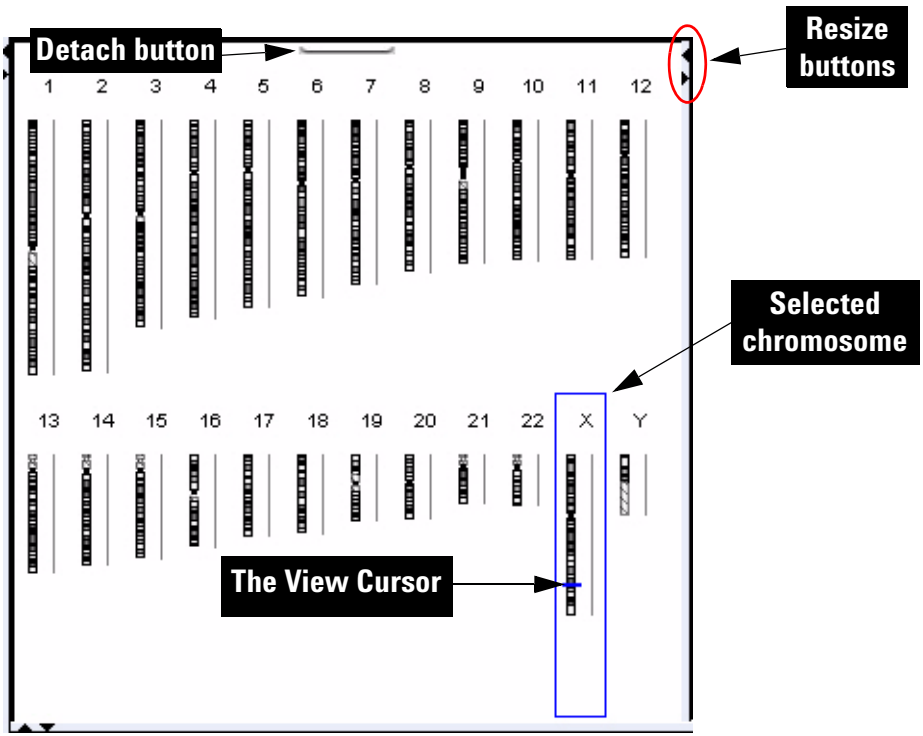


Figure 29 Genome View, vertical orientation, with human chromosomes. The X chromosome is selected.

Genome View shows pictures of each of the distinct types of chromosomes in the selected genome. A blue box is drawn around the currently selected chromosome, and the cursor appears as a blue line across the chromosome.

Genome View actions and shortcut menus

- Click a chromosome to select it. When you select a chromosome, Chromosome, Gene, and Tab Views show only genomic regions, genes, and data associated with it. The specific location where you click the chromosome sets the position of the cursor. See "The View Cursor" on page 155.
- On the selected chromosome, click anywhere to move the cursor. See "The View Cursor" on page 155. This also moves the cursor in Chromosome, Gene, and Tab Views.
- Right-click anywhere within Genome View to display a menu. If you click **View Preferences,** the View Preferences dialog box opens, where you can set preferences for the display. See "View Preferences" on page 258.
- Click the **Detach** button (located at the top center of the pane) to remove Genome View from the main window and open in a separate window. To reattach the view, click its **Close** button  . Drag the side or bottom borders of the pane to resize them.
- Drag the side or bottom borders of the pane to resize it.
- On a border of the pane, click a resize button (for example,  or ) that points away from the pane to move that border all the way to the edge of the main window. To move the border back to its previous location, click the other resize button.

Chromosome View

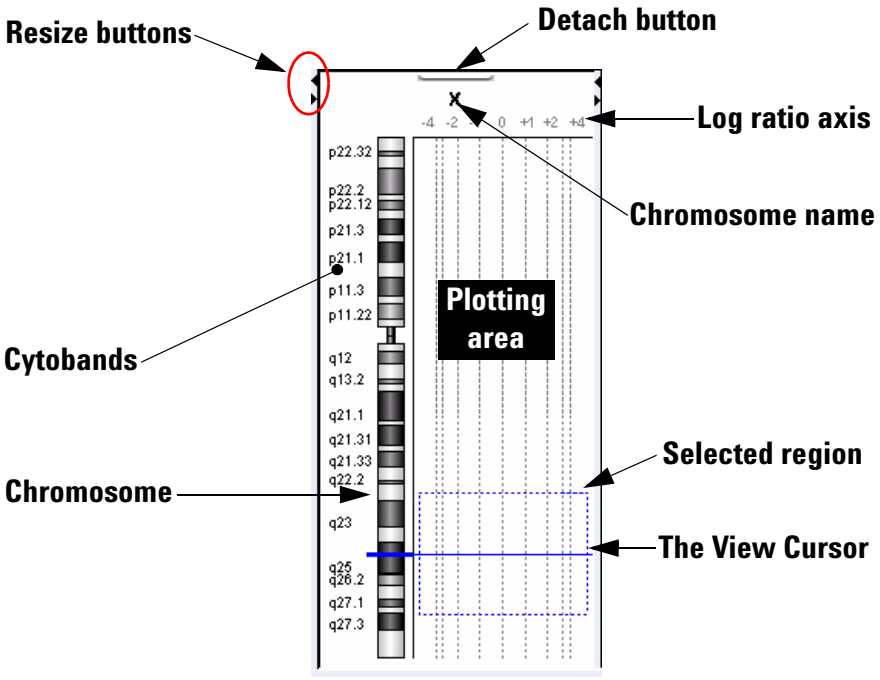


Figure 30 Chromosome View, human X chromosome shown

Chromosome View shows a more detailed diagram of the chromosome you select in Genome View.

- Cytobands and a plotting area appear next to the chromosome.
- When you select arrays for display, their data appear in the plotting area.
- The View cursor appears as a solid blue line across the chromosome and the plotting area.
- The selected region of the chromosome (if any) appears as a dotted blue box in the plotting area.

Chromosome View actions and shortcut menus

- Click a cytoband, any part of the chromosome, or anywhere in the plotting area to move the View cursor to that location. See "The View Cursor" on page 155.
- Drag the pointer over any part of the plotting area to select a chromosomal region for display in Gene View. Drag parallel to the chromosome. This also moves the cursor to the center of the selected region. See "The View Cursor" on page 155.
- Right-click anywhere within Chromosome View to display a menu. If you click **View Preferences,** the View Preferences dialog box opens, where you can set preferences for the display. See "View Preferences" on page 258.
- Click the **Detach** button (located at the top center of the pane) to remove Chromosome View from the main window and open in a separate window. To reattach the view, click its **Close** button  . Drag an inside border of Chromosome View to resize the view.
- Drag the side or bottom borders of the pane to resize it.
- On a border of the pane, click a resize button (for example,  or ) that points away from the pane to move that border all the way to the edge of the main window. To move the border back to its previous location, click the other resize button.

Gene View

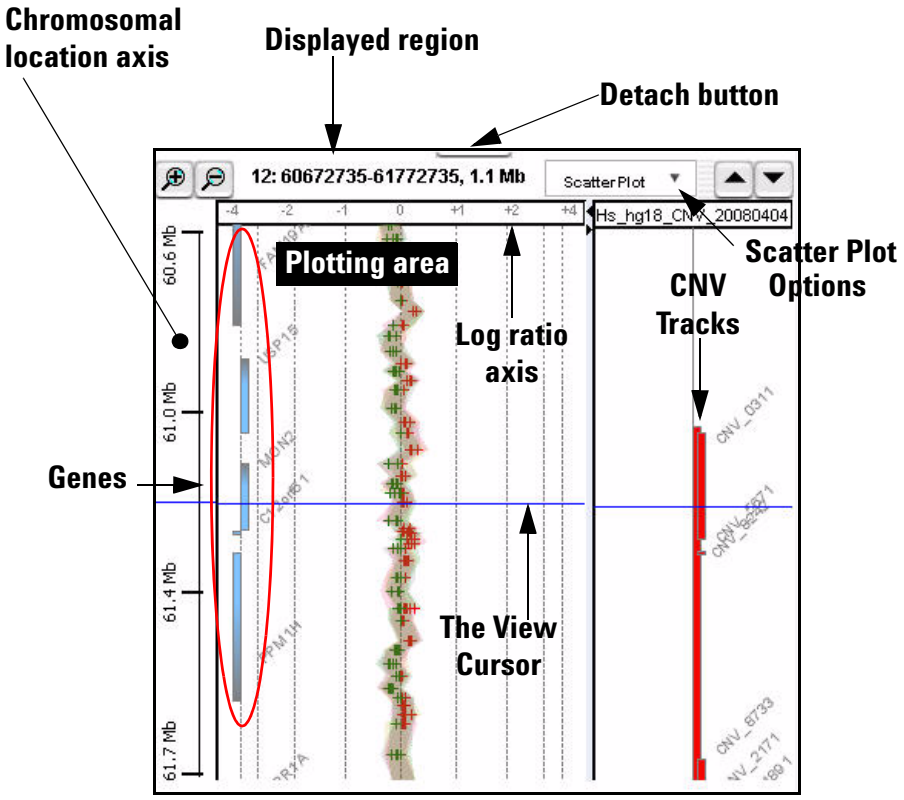


Figure 31 Gene View, with log ratio data from an experiment and CNV tracks.

Gene View shows a more detailed view of the chromosomal region you select in Chromosome View. See "Chromosome View" on page 149.

- Regions that contain genes appear as small blue boxes. Gene names appear nearby. You can customize the appearance of gene names. Also, you can use a gene list to highlight genes of interest, or to display only the genes in the list. See "To change the appearance of genes in Gene View" on page 102, and "To show gene lists in Gene View" on page 102.

- Log ratio data from selected arrays in the active experiment appear as a scatter plot. You can also customize the scatter plot. See "To customize scatter plot ranges and colors" on page 93.
- The location of the cursor matches the location of the cursors in other views. See "The View Cursor" on page 155.
- The name of the chromosome, and the coordinates and size of the displayed chromosomal region appear at the top of the pane.
- Imported tracks can also appear in Gene View. See "To show tracks in Gene View" on page 103.

Scatter Plot

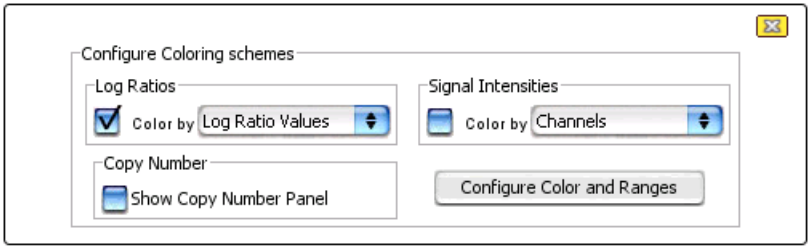


Figure 32 Scatter Plot command group in CGH Gene View

The scatter plot command group is available in Gene View or the View Preferences dialog box. The selections in this box change depending on the DNA Analytics application you are using. Selected scatter plot panels appear in the Chromosome and Gene Views. Use View Preferences to customize the scatter plots and select the data you want to display. See "View Preferences" on page 258.

The drop down lists let you select how the log ratios or signal intensities are colored in the plot. For more information, see "To show or hide data in scatter plots" on page 93 and "To customize scatter plot ranges and colors" on page 93.

Gene View buttons


Zooms in to see a smaller region in more detail.


Zooms out to see a larger region in less detail.


In vertical orientation, scrolls up through the genes and data to lower-numbered chromosomal coordinates.


In vertical orientation, scrolls down through the genes and data to higher-numbered chromosomal coordinates.


In horizontal orientation, scrolls left through the genes and data to lower-numbered chromosomal coordinates.


In horizontal orientation, scrolls right through the genes and data to higher-numbered chromosomal coordinates.


(**Resize** buttons) The button that points away from Gene View expands the view. The other button restores the view to its original size.

(**Detach** button) Removes Gene View from the main window, and opens it in a separate window.

Gene View shortcut menu and other actions

- Click anywhere in the plotting area of Gene View to move the cursor to that location. See "The View Cursor" on page 155.
- Drag an inside border of Gene View to resize the View. Right-click anywhere in the plotting area of Gene View to display the following options:

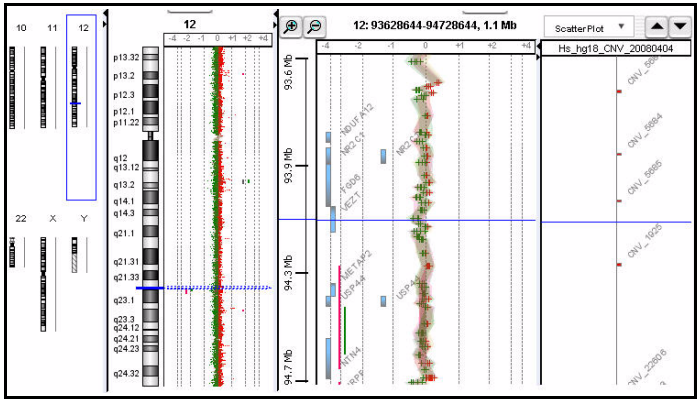
Option	Description
Create Gene List	Opens the Create Gene List dialog box, where you can create a new gene list based on the currently selected (or another) chromosomal region. See "Create Gene List" on page 180 and "To show gene lists in Gene View" on page 102.
Create Track	Opens the Create Track dialog box, where you set the chromosome locations for the track. See "To create a track (CGH only)" on page 78 and "Closes the dialog box without creating the histogram.Create Track" on page 183.

Option	Description
Show Intensity Bar Charts	Opens the Create Signal Bar Chart dialog box, where you select parameters to create a signal intensity chart for the data. See "Create Signal Bar Chart" on page 182.
Show in UCSC	Opens the View Coordinates in UCSC Browser dialog box where you select track information for display in the UCSC (University of California at Santa Cruz) Genome Browser. You can then view the track.
Simple HD Search	Opens Simple HD Probe Search in the Search tab, where you can start a search of the Agilent eArray web site for probes in the selected (or another) chromosomal region. See "Simple HD Probe Search" on page 239 and "To search eArray for probe information" on page 108. See the *eArray$_{XD}$ User Guide* for more information.
Chromosomal Location Search	Opens Probe Search in the Search tab, where you can search for probes based on their chromosomal locations. See the *eArray$_{XD}$ User Guide* for more information.
User Preferences	Opens the User Preferences dialog box, where you can set user preferences on three separate tabs. See "User Preferences" on page 250 and the related pages that follow.
View Preferences	Opens the View Preferences dialog box, where you can set the preferences for viewing data in the Genomic Viewer. See "View Preferences" on page 258.

The View Cursor

The View cursor reflects the center of the current chromosomal location of interest. It appears in several views:

- In Genome View, it appears as a blue bar across the selected chromosome.
- In Chromosome View, it is a blue bar that appears across the chromosome and across the plotting area of the view.
- In Gene View, it is a blue bar that appears across the plotting area and tracks of the view.



The position of the cursor in one View is also the position of the cursor in all Views. The exact chromosomal location of the cursor appears in the first cell of the Status bar. Several actions change the position of the View cursor:

- In Genome View, click anywhere on a chromosome to move the cursor to that location.
- In Chromosome View, click a cytoband name, part of the chromosome, or anywhere in the plotting area to move the cursor to that location.
- In Gene View, click anywhere in the plotting area to move the cursor to that location.

  The cursor used in Gene View is the same cursor used for the tracks.
- In Tab View, click a row of a data table to move the cursor to the chromosomal location associated with that row.

Tab View

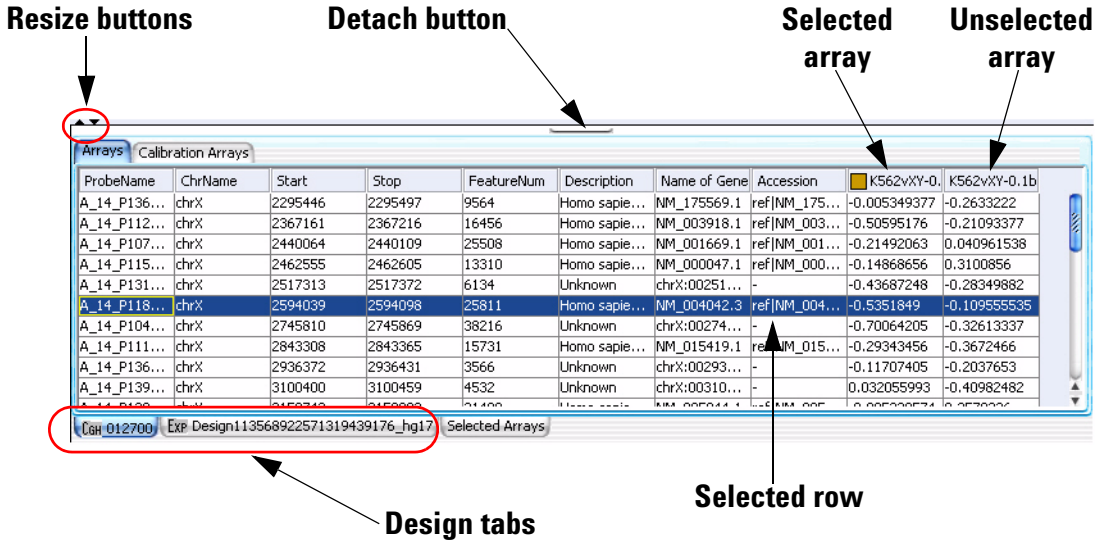


Figure 33 Tab View

Tab View displays design annotation and log ratio data related to the chromosome you select in Chromosome View.

- The exact column content of the tables depends on the specific tab and design, but it always includes chromosomal locations of probes
- The selected row of data appears highlighted in blue. This row represents data that corresponds approximately with the location of the cursor.
- Columns of log ratio data appear below the names of the specific arrays to which they correspond. If an array is selected for display in Chromosome and Gene views, a colored square appears next to its name.

Tab View tabs and buttons

You can see the following tabs and buttons in Tab View. See Figure 33 for a diagram that identifies some of these elements.

Design tabs A separate tab appears for each microarray design included in the active experiment. The name of the design appears on each tab, along with an icon:

- CH3 – A methylation array design
- CGH – An aCGH array design.
- CGH+ – A CGH+SNP array design.
- EXP – A gene expression array design.
- CHIP – A ChIP-on-Chip array design.

When you click a design tab, the data and annotation for the arrays in the design appear in Tab View. The program separates the arrays of the design into the Arrays tab and the Calibration Arrays tab (see below).

Arrays tab (Available when you click a specific design tab.) Contains a table of data and annotation for all arrays in a design that contain biological data.

Selected Arrays tab Contains a table of data and annotation for the selected arrays from all designs in the active experiment.

(**Resize** buttons) The button that points away from Tab View expands the view. The other button restores the view to its original size.

(**Detach** button) Removes Tab View from the main window, and opens it in a separate window.

Tab View actions and shortcut menus

- Click the name of an *array in a column heading* to select the array data for display.
- Right-click the name of an *array in a column heading* to open a display the following options:

Option	Description
Rename Array	Opens an Input dialog box, where you can type a new name for the array. This only changes the name of the array within the active experiment.
Remove Array From Experiment	Opens a confirmation dialog box. Click **Yes** to remove the link between the array and the active experiment. This command does not delete the data file from the program. To do this, see "To remove data or design files from the program" on page 74.
Select Array	(Available if the array is not selected.) Selects the array for display. A colored square appears next to the name of the array.
Deselect Array	(Available if the array is selected.) Removes the array data from scatter plots, and removes the column of the array from the Selected Arrays tab.
Select for Calibration	Selects the array for calibration. Moves the selected array to the Calibration Arrays tab and to the Calibration Arrays folder in the Experiment pane. Calibration arrays in the Experiment pane are marked with a "C". See "To select or remove calibration array(s)" on page 73.
Deselect for Calibration	Removes the selection of the array for calibration.
Edit Array Color	Opens the Select Color dialog box, where you can change the display color of the array. See "Edit Array Color" on page 193 and "To change the display color of an array" on page 90.
Edit Array Order	Opens the Edit Array Order dialog box, where you can change the order in which the names of the arrays in a given design of the active experiment appear in Tab View and in the Data Navigator. In Gene View, when you display separate scatter plots for each array, the plots also appear in this order. See "Edit Array Order" on page 194 and "To change the order of arrays in an experiment" on page 65.
Select All Arrays	Selects all arrays in all designs in the active experiment for display. All arrays appear in the Selected Arrays tab.
Deselect All Arrays	Removes all arrays from display, and from the Selected Arrays tab.

Option	Description
Select All Arrays for Calibration	Selects all arrays in the table as calibration arrays. Moves the selected arrays to the Calibration Arrays tab and to the Calibration Arrays folder in the Experiment pane. Calibration arrays in the Experiment pane are marked with a "C".
Deselect All Arrays from Calibration	Removes all calibration arrays from the Calibration Arrays tab and Calibration Arrays folder in the Experiment pane.
Scroll to Column	Opens the Scroll to Column dialog box, where you can select a column in the current tab. The program then scrolls the data table in the tab so you can see the selected column.

- Right-click a *heading of a column other than an array data column* to open a shortcut menu with a Scroll To Column option. If you click this option, the Scroll to Column dialog box appears, where you can select a column in the current tab. The program then scrolls the data table in the tab so you can see the column. See "Scroll to Column" on page 231.
- Click a *data table entry* to select the row in which it appears. This also moves the cursor to the location of the data point corresponding to the selected row.
- Right-click a *data table entry* to display the following options:

Option	Description
Find in Column	Opens the Find in column dialog box, where you can search for a specific text string within the column you clicked. See "Find in column" on page 205.

Option	Description
Google LocusLink PubMed UCSC HG15(April '03) UCSC HG16(July'03) UCSC HG17(May'04) UCSC HG18(March'06) UCSC mm8(Feb'06) UCSC mm9(July'07) DGV(hg18) GO KEGG(HUMAN)	Opens your Web browser, and sends the column entry you clicked as a search string to the selected site. The UCSC links search the indicated University of California, Santa Cruz database related to the indicated genome build. See "To search the Web for information on probes in Tab View" on page 109.
Customize Link	Opens the Customize Search link dialog box, where you can create or edit a custom Web link that appears in this shortcut menu. When you click a custom link, the program opens your Web browser, and sends the column entry you clicked as a search string to the site. See "Customize Search Link" on page 184 and "To update or delete a custom Web search link" on page 110.
(other options)	If other options appear in this shortcut menu, they are custom Web search links. Click them to open your Web browser, and send the column entry you clicked as a search string to the site.

Status Bar

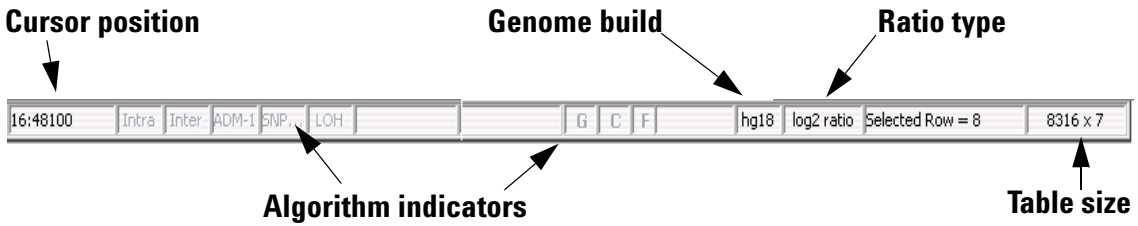


Figure 34 Status bar

The Status Bar displays information related to the currently displayed data. There are other items on the status bar that only become active if you have a DNA Analytics license.

Cursor position The chromosomal location of the cursor. See "The View Cursor" on page 155.

Genome build The genome build associated with the currently displayed data.

Ratio type The mathematical type of the array data. The possible types are:

- **ratio**
- **$\log_2$ ratio**
- **$\log_{10}$ ratio**
- **ln (natural log) ratio**

Selected Row The row in the currently displayed data table that is selected. The location of the cursor is approximately the chromosomal location associated with this row.

Table size The number of rows and columns in the currently displayed tab. The size appears as
<# of rows> x <# of columns>.

Dialog Boxes

This section describes the dialog boxes that can appear when you import, organize, manage, export and display array data and other content in Agilent Genomic Workbench. The dialog boxes appear in alphabetical order by name.

Add Gene List <name> to

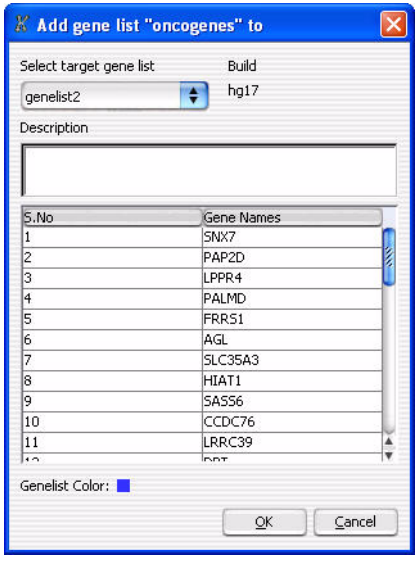


Figure 35 Add Gene List <name> to dialog box

Purpose: Adds genes from one gene list (the source gene list) to another (the target gene list).

To open: In the My Entity List pane, right-click the name of a gene list, then click **Add to Gene List.**

Select target gene list The gene list to which genes will be added. Select one from the list.

Build (Read-only) The genome build associated with the genes in the list. The builds of the two gene lists must match.

Description (Optional) Description of the combined gene list.

List of genes A list of the genes in the target gene list.

Gene List Color (Read-only) The current display color of the target gene list.

OK Adds the genes from the source gene list to the target gene list.

Cancel Closes the dialog box without adding any genes to the target gene list.

Agilent Feature Extraction Importer

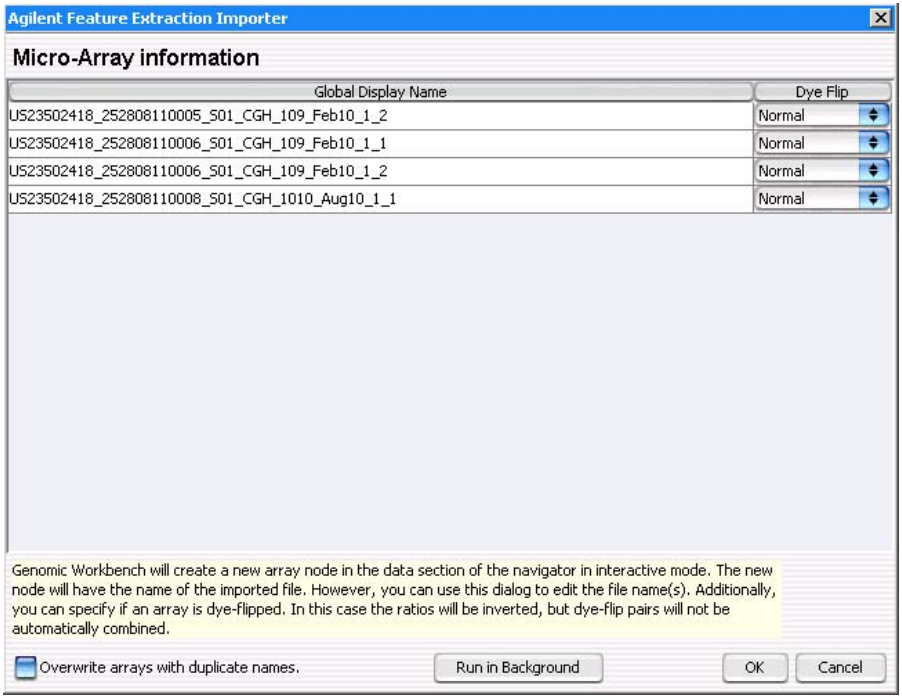


Figure 36 Agilent Feature Extraction Importer dialog box

Purpose: Lets you edit the name of the FE data file you will import and to indicate whether you want to flip the red/green ratio for the data.

To open: In the Home tab, click **Import > Array Files > FE File,** select the desired FE data file(s), then click **Open.**

Name Lets you edit the names of the FE files. You can change the names of the files to names that are easier to recognize or remember.

Dye Flip For each array:

Select **Normal** if:

- The test samples were labeled with cyanine-5 (red).
- The control samples were labeled with cyanine-3 (green).
- The imported ratio (test/control) should be reported as-is.

Select **Flipped** if:

- The test samples were labeled with cyanine-3 (green).
- The control samples were labeled with cyanine-5 (red).
- The imported ratio (control/test) should be reported with the ratio inverted (test/control).

The program does not combine dye-flip pairs.

Overwrite arrays with duplicate names Mark this option to replace existing file(s) in the program with the imported one(s), if they have the same name(s).

Run in Background Imports the files, and lets you use your computer for other purposes while the import occurs. This is especially useful if you have many files to import.

OK Imports the files in the foreground. You cannot use your computer for other purposes while the import occurs.

Cancel Cancels the entire import process without importing anything.

Catalog and Workgroup Data

Figure 37 Catalog and Workgroup Data dialog box

Purpose: Used to download Agilent Catalog and workgroup data sets from the eArray website to the Agilent Genomic Workbench database.

To open: In the Home tab, click **Data**.

After you install the Agilent Genomic Workbench client program, you can transfer probe and bait sequences and annotation, as well as the genomic coordinates of exon boundaries, from the eArray Web site. Although you can transfer these data at any time after you install the client program, you must transfer it before you can do certain tasks in eArray$_{XD}$ that require it For example, to search for expression probes from the Agilent Catalog, you must first transfer the Catalog expression probe data from the eArray Web site to your server. See the *eArray$_{XD}$ User Guide* for more information.

Learn More Opens an information box that describes the type of data that is downloaded for the data type.

Download Submits a data download task that appears in the Tasks pane of the Navigator. To view the status of the download, click **eArrayXD > Job queue > Tasks**.

NOTE If your workgroup contains a large amount of data, the download may take a long time.

CGHSmooth Parameters

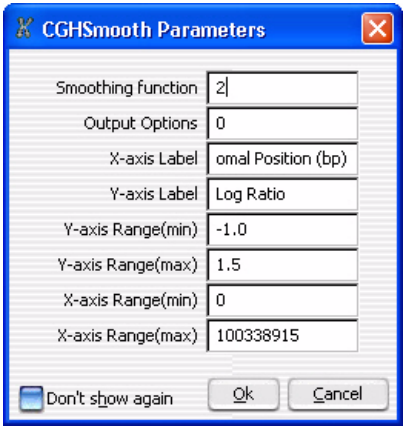


Figure 38 CGHSmooth Parameters dialog box

Purpose: The CGHSmooth Parameters dialog box lets you configure the CGHSmooth plug-in. It can perform one of several varieties of moving-average-like smoothing, and plots the data associated with the currently selected chromosome.

To open: Click **Tool > Plugin > CGHSmooth.**

Parameters Set any of these parameters:

Parameter	Description
Smoothing Function	A number from 0 to 5. The number sets one of the following options as the weighting function used by the moving average algorithm. In general, the options weight measurements closer to the center position more heavily than those more distant from it. 0 – **None.** The plug-in applies no smoothing, and returns the original data. In some cases, the plug-in averages data points with identical positions. This sets, in effect, a window size of 0. 1 – **Rectangular.** The plug-in performs a standard moving average. All points within the rectangle (the window) receive the same weight. 2 – **Gaussian.** Applies a Gaussian weighting function. 3 – **Triangular.** Applies a triangular weighting function. 4 – **Lorentzian.** Applies a Lorentzian weighting function. 5 – **Biexponential.** Applies a biexponential weighting function.
Output Options	A number from 0 to 2. The number sets one of the following options: **0** – Overlays the unsmoothed plot of each array on the smoothed plot. **1** – Displays smoothed and unsmoothed plots for each array. **2** – Displays smoothed, unsmoothed, and error plots for each array.
X-axis Label	The text that appears under the X-axis of the plot as a label.
Y-axis Label	The text that appears next to the Y-axis of the plot as a label.
Y-axis Range (min)	The minimum value on the Y-axis.
Y-axis Range (max)	The maximum value on the Y-axis.
X-axis Range (min)	The minimum value on the X-axis.
X-axis Range (max)	The maximum value on the X-axis.

Don't show again Mark this option to prevent the appearance of this dialog box in the future when you click Tool > Plugins > CGHSmooth. To restore the dialog box so it appears again, click **Tool > Plugin Settings > CGHSmooth,** then clear **Don't show again.**

OK Accepts the parameters and prepares the plot. You can make further changes to the appearance of the plot once the plug-in displays it.

Cancel Ignores any changes you made, and closes the dialog box.

CGHSmooth Plot

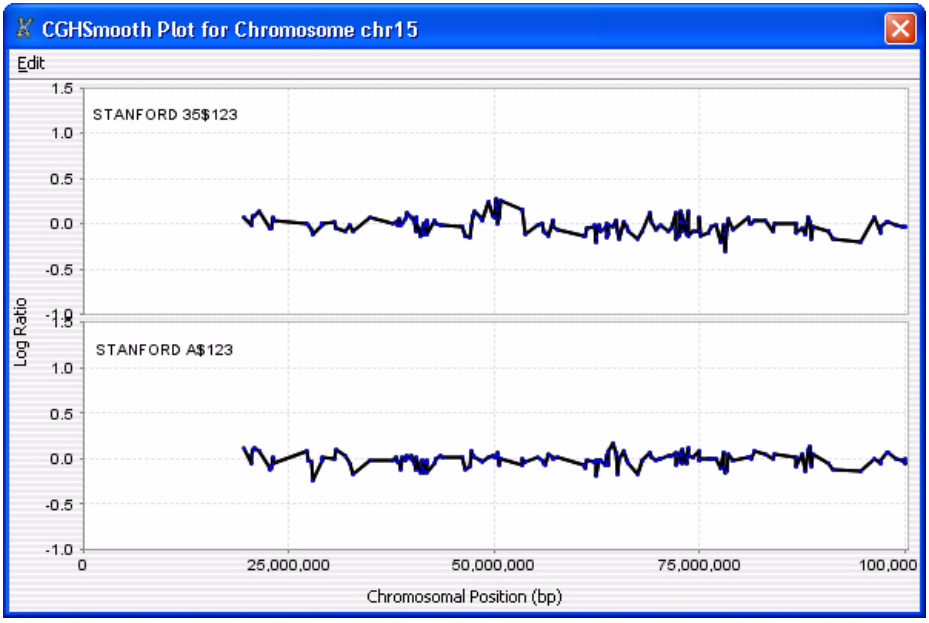


Figure 39 CGHSmooth Plot

Purpose: The CGHSmooth Plot is the output of the CGHSmooth plug-in. It contains separate, stacked plots of smoothed log ratio data for each of the selected arrays in the current experiment.

To open: Click **OK** in the CGHSmooth Parameters dialog box. See "CGHSmooth Parameters" on page 167.

Plot(s) Depending on the selected output option, the main plotting area shows up to three plots for each array in the active experiment. The plots can include unsmoothed and smoothed log ratio plots, and an error plot.

Edit Opens a menu with a Copy Plot(s) to Clipboard option. If you select this option, the program copies the plots to the clipboard as an image. You can then paste the image into a document in another program.

When you right-click anywhere within the plotting area, the following options are displayed:

Option	Description
Properties	Opens the Chart Properties dialog box, where you can change the appearance of many aspects of the plot. See "Chart Properties" on page 171.
Copy	Copies the chart to the Clipboard, where you can paste it into a word processing or other program.
Save as	Opens a Save dialog box, where you can select a location for the *.png image file of the plots.
Print	Opens the Windows Page Setup dialog box, where you can set page size, margins, and orientation, and select a printer. From there, you click **OK** to open the Windows Print dialog box, where you can set print options and print the plot.
Zoom In	Opens another menu that lets you zoom in the plot. You can zoom in several ways: • **Both Axes** – Zooms in the Domain (X) axis for all stacked plots, and zooms in the range Range (Y) axis for the specific plot in which you clicked. • **Domain Axis** – Zooms in the Domain (X) axis for all stacked plots. • **Range Axis** – Zooms in the Range (Y) axis for the specific plot in which you clicked. You can also drag across an area of one of the plots to select an area to expand.
Zoom Out	Opens another menu that lets you zoom out the plot. You can zoom out several ways: • **Both Axes** – Zooms out the Domain (X) axis for all stacked plots, and zooms out the range Range (Y) axis for the specific plot in which you clicked. • **Domain Axis** – Zooms out the Domain (X) axis for all stacked plots. • **Range Axis** – Zooms out the Range (Y) axis for the specific plot in which you clicked.

Option	Description
Auto Range	Opens another menu that lets you zoom the plot to show the full range of the data. You can zoom in several ways: • **Both Axes** – Appropriately zooms both axes of the specific plot to show the full set of data. • **Domain Axis** – Zooms in the Domain (X) axis for all stacked plots so this axis displays the full range of X values of the data. • **Range Axis** – Zooms in the Range (Y) axis for the specific plot in which you clicked to display the full range of Y values of the data.

Chart Properties

Purpose: The Chart Properties dialog box lets you create titles and legends, as well as change the appearance, for the CGHSmooth, Echo Example, and MovAvg Example plots.

To open: Use the CGHSmooth, Echo Example, or MovAvg Example plug-in to draw a plot. Right-click within the plotting area, then click **Properties** in the shortcut menu.

This dialog box has four tabs. At any point, click **OK** to accept the settings in all four tabs, or click **Cancel** to close the dialog box without making any changes to the settings.

Title Tab

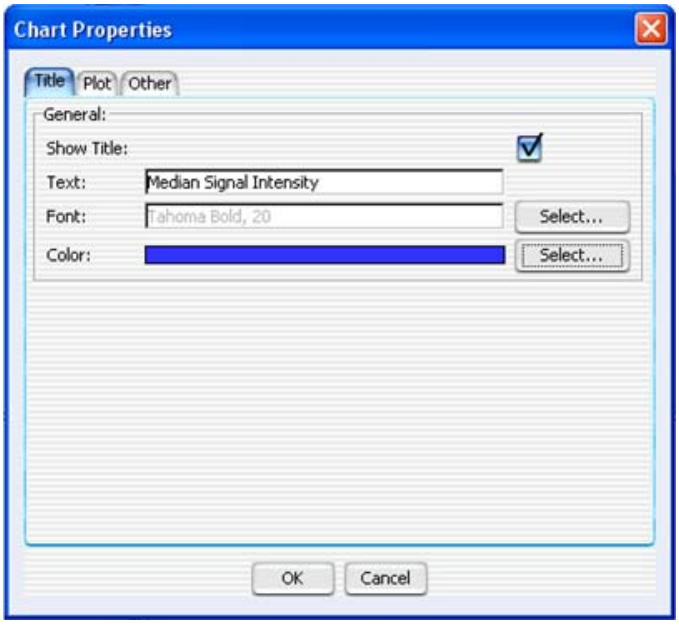


Figure 40 Chart Properties dialog box – Title tab

- **Show Title** – Mark this option to display a title across the top of the chart.
- **Text** – Type a title for the chart.
- **Font** – (Available if you mark **Show Title**) Click **Select** to open the Font Selection dialog box. Select the desired font attributes, then click **OK.**
- **Color** – (Available if you mark **Show Title**) Click **Select** to open the Title Color dialog box. Select or configure a color for the title, then click **OK.** This dialog box is identical to the Select Color dialog box. See "Select Color" on page 231.

Plot Tab

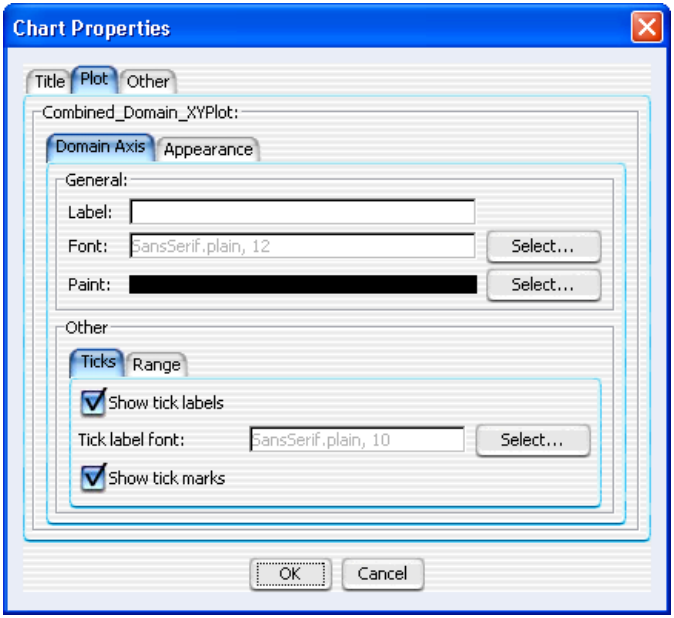


Figure 41 Chart Properties dialog box – Plot tab

- Within the Plot tab, you can set these properties in the Domain Axis tab ("X" axis):

Property	Description
General	
Label	A custom label for the Domain (X) axis of the chart. Type the desired label.
Font	The font for the custom label on the Domain (X) axis. Click **Select** to open the Font Selection dialog box. Select the desired font attributes, then click **OK.**
Paint	The color of the custom label on the Domain (X) axis. Click **Select** to open the Label Color dialog box. Select the desired color, then click **OK.** This dialog box is identical to the Select Color dialog box. See "Select Color" on page 231.

Property	Description
Other – Ticks tab	
Show tick labels	Mark this option to show, or clear it to hide, the numerical values on the domain axis.
Tick label font	The font for the numerical values on the Domain (X) axis. Click **Select** to open the Font Selection dialog box. Select the desired font attributes, then click **OK.**
Show tick marks	Mark this option to show, or clear it to hide, tick marks on the Domain (X) axis.
Other – Range tab	
Auto-adjust range	Mark this option to automatically set the range of values on the X-axis to include all data.
Minimum range value	(Available if you do not mark Auto-adjust range) The lowest value represented on the X-axis.
Maximum range value	(Available if you do not mark Auto-adjust range) The highest value represented on the X-axis. The program automatically converts large numbers to scientific "E" notation – for example, **1.22E8.**

- Within the Plot tab, you can set the following properties in the Appearance tab:

Property	Description
Outline stroke	The thickness of the lines around each plot. Click **Select** to open the Stroke Selection dialog box. Select the desired line thickness, then click **OK**.
Outline paint	The color of the lines around each plot. Click **Select** to open the Outline Color dialog box. Select the desired color, then click **OK.** This dialog box is identical to the Select Color dialog box. See "Select Color" on page 231.
Background paint	The color of the background within each plotting area. Click **Select** to open the Background Color dialog box. Select the desired color, then click **OK.** This dialog box is identical to the Select Color dialog box. See "Select Color" on page 231.
Orientation	Select either Vertical (X-axis on the bottom of the chart) or Horizontal (X-axis on the left side of the chart).

Other tab

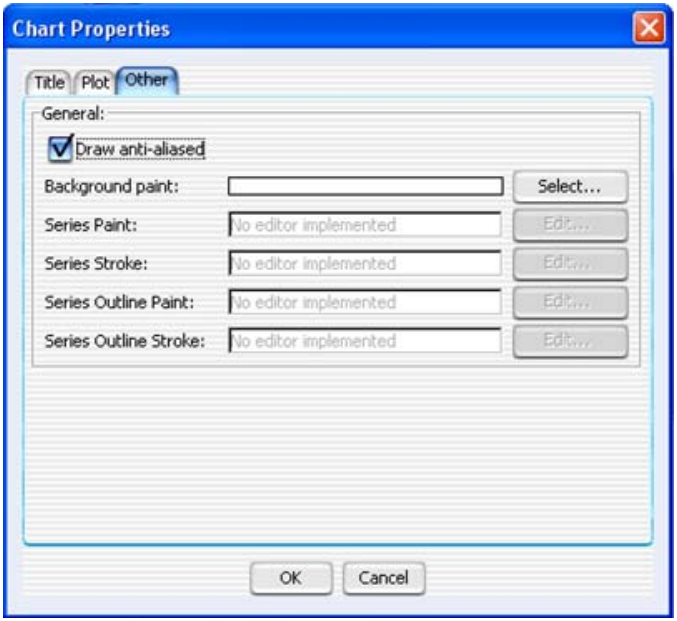


Figure 42 Chart Properties dialog box – Other tab

The Other tab has these options:

- **Draw anti- aliased** – Mark this option to minimize distortion and visual artifacts in the plot image. This will create a smoother image, but it can be less sharp than the original one.
- **Background paint** – The color of the chart outside of the plotting area and legend. Click **Select** to open the Background Color dialog box. Select the desired color, then click **OK.** This dialog box is identical to the Select Color dialog box. See "Select Color" on page 231.

The other options are for future expansion, and are not available in the current release of Agilent Genomic Workbench.

Configure Coloring Ranges and Shades

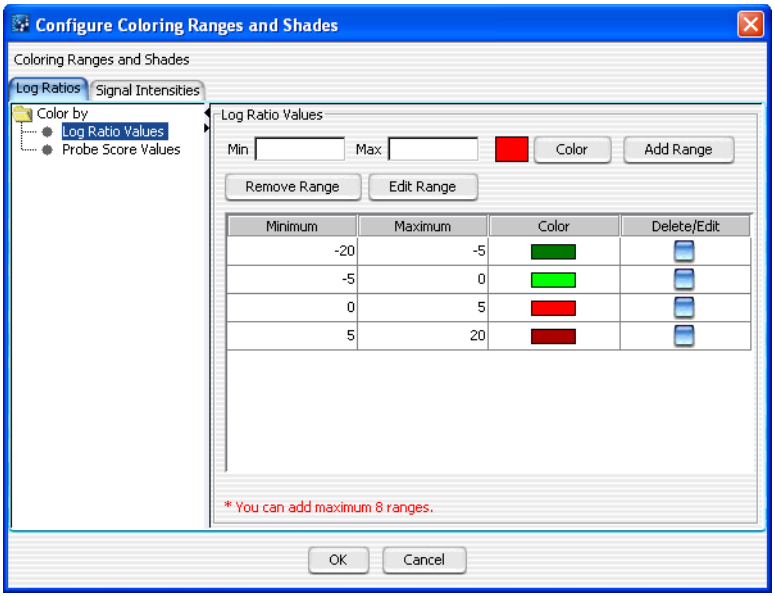


Figure 43 Configure Coloring Ranges and Shades dialog box for CGH

Purpose: This dialog box is used to enter ranges and select colors for scatter plot options. Tabs show scatter plot selections for the selected application type (CGH, ChIP, or CH3).

To open: In Gene View, move the mouse pointer over **Scatter Plot** to display the scatter plot options and then click **Configure Color and Ranges**. Or, click the **View** tab and click **View Preferences**. Then, under Configure Coloring schemes, click **Configure Colors and Ranges.**

For information on the contents of the various tabs, see the *User Guide* for the selected application.

Confirm Overwrite

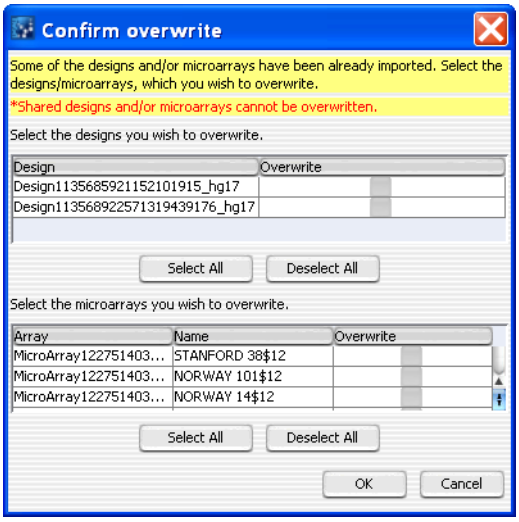


Figure 44 Confirm overwrite dialog box

Purpose: When you import an experiment, it can contain designs and/or arrays that have the same names as those already available in Agilent Genomic Workbench. This dialog box lets you select which designs and/or arrays to overwrite.

To open: This dialog box appears when you import a ZIP format experiment file, and it contains designs and/or arrays that are already available in Agilent Genomic Workbench. See "To import an experiment file" on page 57.

Select the designs to overwrite

Design The names of the designs in the imported file that have the same names as designs that are already available in Agilent Genomic Workbench.

Overwrite Mark the check box for each existing design that you want to overwrite.

Select All Marks all of the check boxes under Overwrite.

Deselect All Clears all of the check boxes under Overwrite.

Select the microarrays to overwrite

Array Identification number or barcode of the array

Name The name of the array in the imported file that has the same name as array that is already available in Agilent Genomic Workbench.

Overwrite Mark the check box for each existing array that you want to overwrite.

Select All Marks all of the check boxes under Overwrite.

Deselect All Clears all of the check boxes under Overwrite.

OK Overwrites the selected files (both designs and arrays) and closes the dialog box.

Cancel Closes the dialog box, and returns you to the Import (experiments) dialog box. See "Import (experiments)" on page 213.

Create Experiment

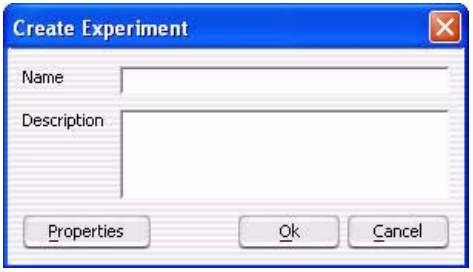


Figure 45 Create Experiment dialog box

Purpose: Creates an organizational unit (an *experiment*) that lets you display and analyze array data in Agilent Genomic Workbench. You add data to the experiment with links to array data files that are available in the program, a process that you can start from this dialog box. See "To create a new experiment" on page 62.

To open: In the Home tab of Agilent Genomic Workbench, click **Create Experiment.**

Name (Required) The name of the new experiment. This name identifies the experiment within the program and in exported reports and files.

Description (Optional) Brief information that will later help to identify the experiment.

Properties Opens the Experiment Properties dialog box, where you can select array data files to add to the new experiment. See "Experiment Properties" on page 195.

OK Closes the dialog box and creates the new experiment.

Cancel Closes the dialog box without creating an experiment.

NOTE Click **Properties** to open the Experiment Properties dialog box to add array data to your new experiment. Otherwise, the program creates an empty experiment. You can also add arrays to the experiment later. See "To add arrays to an experiment" on page 64.

Create Gene List

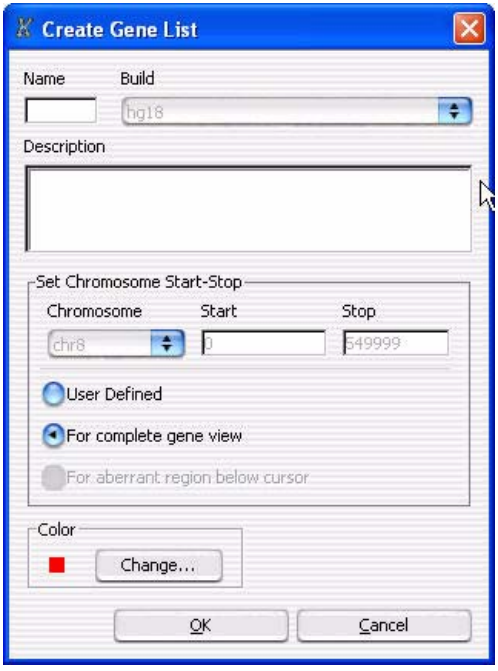


Figure 46 Create Gene List

Purpose: To limit the genes presented in Gene View to a preselected number valuable for interpreting data

To open: Right-click Gene View, and click **Create Gene List**.

Name Type in name of gene list.

Build Select the genome build for the genes to be selected for list.

Description Describe the type or nature of the genes in the list.

Set Chromosome Start-Stop

Select a chromosome and a region in Chromosome View for selecting the genes in the list before you open the Create Gene List dialog box.

User Defined Lets you select a region from which the genes in Gene View will be selected. The chromosome selection list and the Start and Stop positions on the Y axis are enabled when this option is selected. With this option you can override the selections you made before opening Create Gene List.

For complete gene view Select all the genes in Gene View.

For aberrant region below cursor Select those genes that appear in the aberrant region just below where the cursor sits in Gene View. Not operational in Genomic Viewer; depends on analysis.

Chromosome If you select User Defined, you can select a different chromosome than had been selected before opening the Create Gene List dialog box.

Start If you select User Defined, you can type in a Start position for defining the region contained the genes to be in the list.

Stop If you select User Defined, you can type in a Stop position for defining the region contained the genes to be in the list.

Color

Change Click to change the color of the gene list name in Data Navigator. See "Select Color" on page 231.

Create Signal Bar Chart

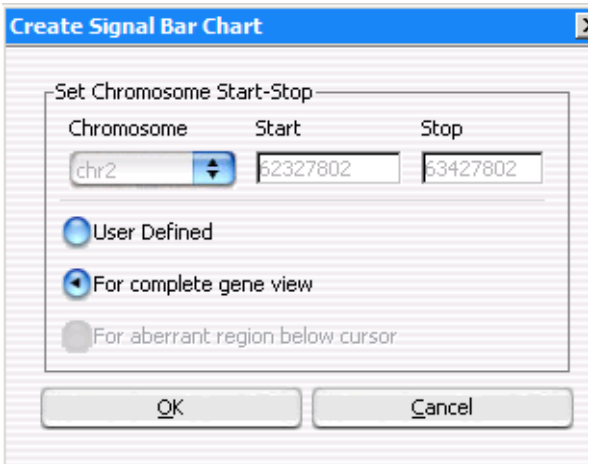


Figure 47 Create Signal Bar Chart dialog box

Purpose: This dialog box lets you set parameters to create a histogram of signal intensities. You can customize the region that you want to display by selections in Set Chromosome Start-Stop.

To open: Right-click in the Gene View and select **Show Intensity Bar Charts**.

Set Chromosome Start-Stop Defines the region of the chromosome for which the bar chart will be defined. Select one of these options:

- **User Defined** – Lets you define an arbitrary region of any chromosome. If you select this option, select the desired chromosome in **Chromosome,** then type the beginning **(Start)** and end **(Stop)** locations of the desired interval.
- **For complete gene view** – The chromosomal region that appears in Gene View.
- **For aberrant region below cursor** – All of the intervals that begin before the cursor position and end after the cursor position. (Not available without a license.)

OK Creates the histogram using the selected region.

Cancel Closes the dialog box without creating the histogram.Create Track

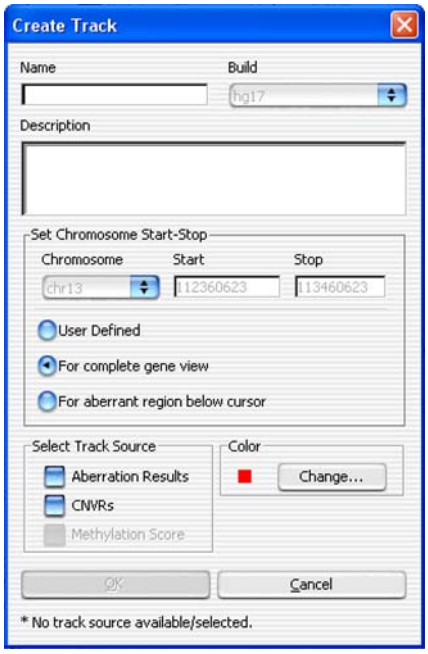


Figure 48 Create Track dialog box

Purpose: The Create Track dialog box lets you create a track for a chromosomal region based on an assigned chromosomal region. You can display one or more tracks next to the genes and data in Gene View. See "To show tracks in Gene View" on page 103.

To open: Right-click in the plotting area of Gene View for the CGH or CH3 application, then click **Create Track** in the shortcut menu.

Name Type a name for the track. This name identifies the track when it appears in views and lists.

Build (Available if you select **User Defined** in **Set Chromosome Start-Stop.**) Select the genome build for the track.

Description Type descriptive text to attach to the track for reference.

Set Chromosome Start-Stop Defines the region of the chromosome for which the track will be defined. Select one of these options:

User Defined – Lets you define an arbitrary region of any chromosome. If you select this option, select the desired chromosome in **Chromosome,** then type the beginning **(Start)** and end **(Stop)** locations for the interval.

- **For complete gene view** – The chromosomal region that currently appears in Gene View.

OK Creates the track. To display the track in Gene View, use the **Tracks** tab of the User Preferences dialog box to enable it. See "User Preferences" on page 250. To export the track, see "To export tracks" on page 84.

Cancel Closes the dialog box without creating a track.

Customize Search Link

Figure 49 Customize Search Link dialog box

Purpose: This dialog box lets you create a custom Web search link in the shortcut menu that appears when you right-click an entry in the Tab View. The link opens the URL of your choice, and sends the selected entry to it as a search string. See "To create a custom Web search link" on page 109.

To open: Right-click any entry in a table in Tab View, other than a column heading, then click **Customize Link.**

URL Name The name of the custom Web search link that appears in the shortcut menu (see above). To edit an existing custom Web search link, select it from the list.

URL The full uniform resource locator (URL) of the desired search page. For the query string value, type `<target>`

For example, this URL sends the selected Tab View entry to google.com:

```
http://www.google.com/search?hl=eng&q=<target>
```

New Opens an Input dialog box, where you can type a name for a new custom Web search link. Click **OK** to accept the name and add it to the URL name list.

Update Saves the settings in the dialog box.

Delete Deletes the currently selected custom Web search link.

Close Closes the dialog box.

Design Properties

Purpose: Gives general and detailed information about a given microarray design. See "To display the properties of a specific design" on page 72.

To open: In the **Design Data** pane of the Navigator, right-click the name of a genome build within a design folder, then click **Show Properties.** Several tabs are available.

Attribute tab

Displays general identifying attributes of the array design, and statistics such as the total number of features in the design, or the date the design was last modified.

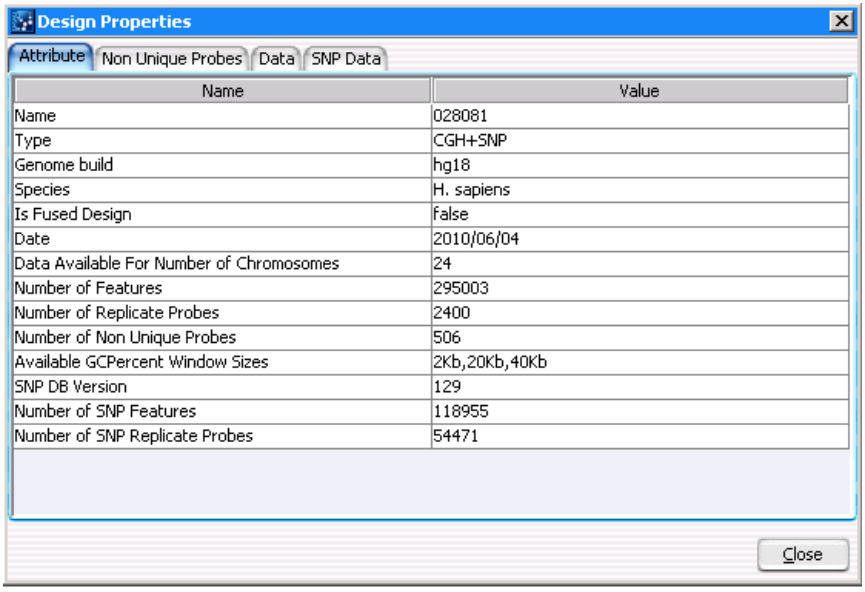


Figure 50 Design Properties dialog box – Attribute tab

Non Unique Probes tab

Shows the nonunique probes in the design. Nonunique probes have more than one mapping in the genome that is a perfect match.

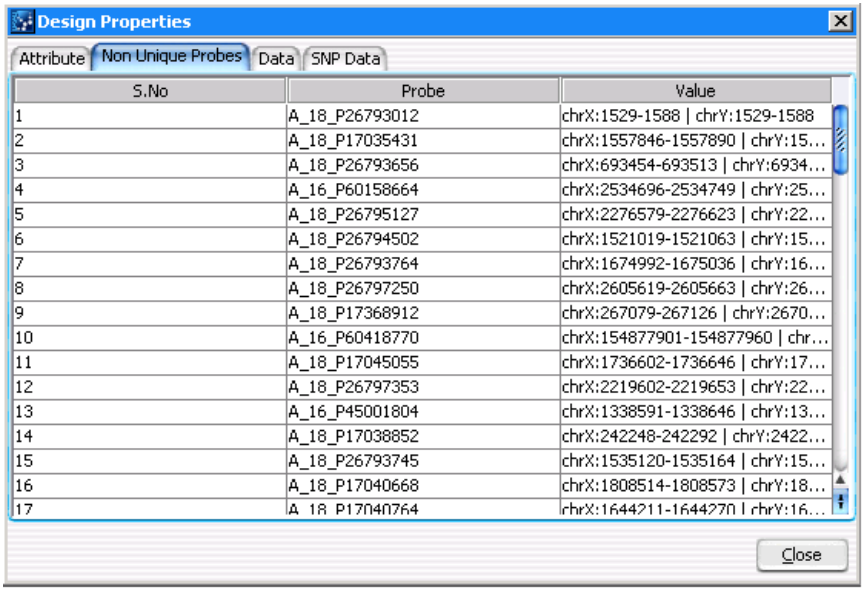


Figure 51 Design Properties dialog box – Non Unique Probes tab

S. No The sequence order of the probes within the table.

Probe The name of each nonunique probe.

Value The chromosomal locations to which each of the probes binds. Because these are nonunique probes, multiple locations appear for each probe.

Data tab

Displays the names of the probes in the design and their target genomic locations. The tab displays the probes for one chromosome at a time.

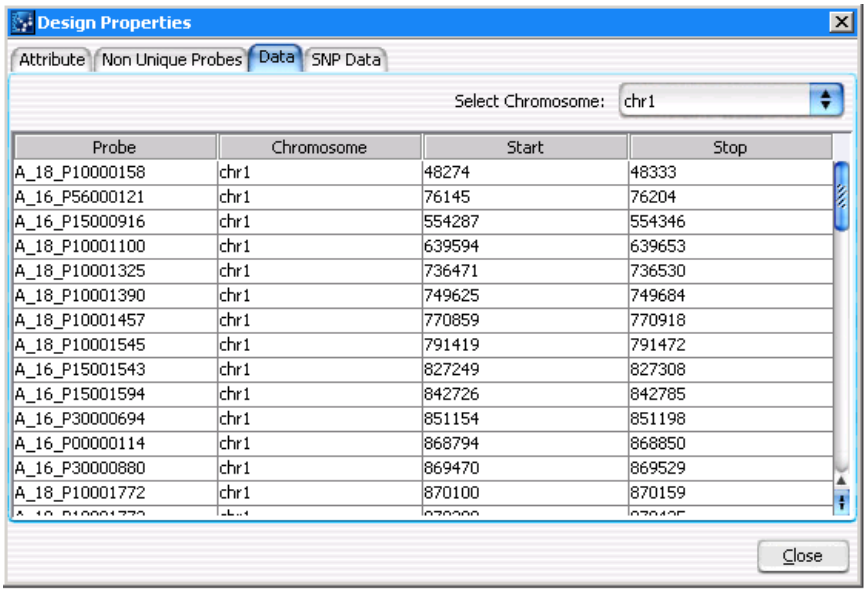


Figure 52 Design Properties dialog box – Data tab

Select Chromosome The chromosome whose probes appear in the list. To view the probes for another chromosome, select one from this list.

Probe The name (Probe ID) of each probe.

Chromosome The name of the probe chromosome.

Start The location on the selected chromosome of the first base pair for the probe.

Stop The location on the selected chromosome of the last base pair for the probe.

SNP Data tab (CGH only)

This tab appears only when you select the CGH module. It shows design information for SNP probes in the design.

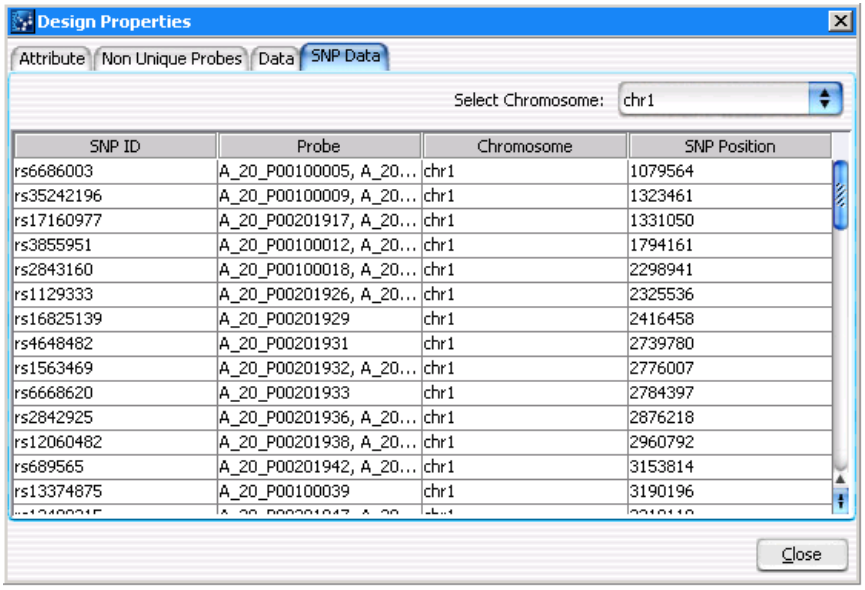


Figure 53 Design Properties dialog box – SNP Data tab

SNP ID The SNP identification.

Probe The name (Probe ID) of the probe. The probe names are separated with a comma.

Chromosome The chromosome on which the probe is located.

SNP Position The position of the SNP on the chromosome.

Echo Example Plot

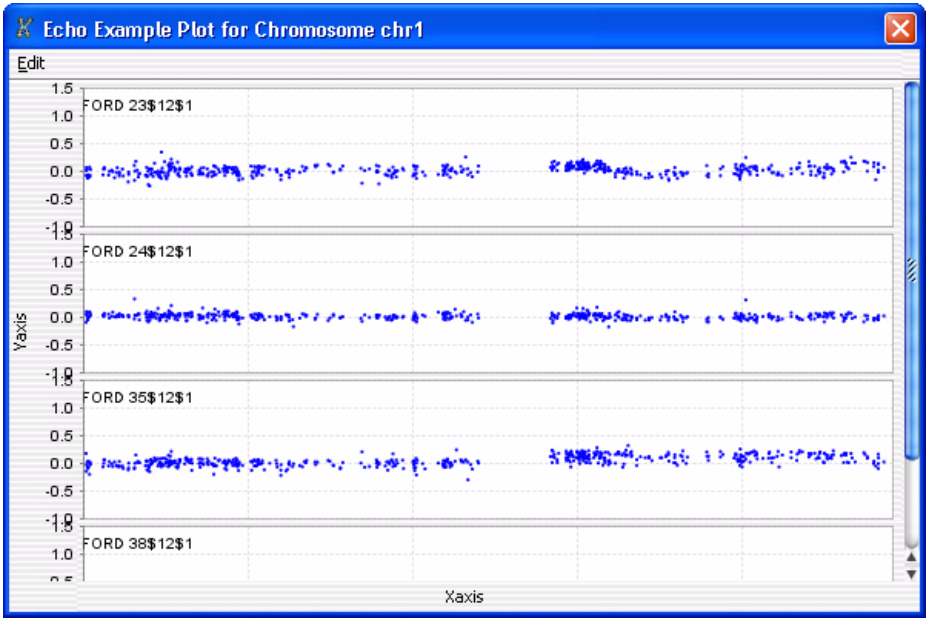


Figure 54 Echo Example Plot

Purpose: The Echo Example Plot is the output of the Echo Example plug-in. It displays the log ratio data for the selected chromosome in the active experiment. Data from all of the selected arrays in the experiment appear as a series of stacked plots, one for each array.

To open: Select the desired experiment, select the desired chromosome in Genome View, then click **Tool > Plugin > Echo Example.**

Edit Opens a menu with a **Copy plots to clipboard** command. This command copies all of the plots to the clipboard as an image. You can then paste the image into a document in another program.

Plots Each plot displays the log ratio data for the selected chromosome from an individual array in the experiment.

You can right-click anywhere within each plot to display the following options:

Option	Description
Properties	Opens the Chart Properties dialog box, where you can change the appearance of many aspects of the plot. See "Chart Properties" on page 171.
Copy	Copies the chart to the Clipboard, where you can paste it into a word processing or other program.
Save as	Opens a Save dialog box, where you can select a location for a saved *.png image file of the plots.
Print	Opens the Windows Page Setup dialog box, where you can set page size, margins, and orientation, and select a printer. From there, you click **OK** to open the Windows Print dialog box, where you can set print options and print the plot.
Zoom In	Opens another menu that lets you zoom in the plot. You can zoom in several ways: • **Both Axes** – Zooms in the Domain (X) axis for all stacked plots, and zooms in the range Range (Y) axis for the specific plot in which you clicked. • **Domain Axis** – Zooms in the Domain (X) axis for all stacked plots. • **Range Axis** – Zooms in the Range (Y) axis for the specific plot in which you clicked. You can also drag across an area of one of the plots to select an area to expand.

Option	Description
Zoom Out	Opens another menu that lets you zoom out the plot. You can zoom out several ways: • **Both Axes** – Zooms out the Domain (X) axis for all stacked plots, and zooms out the range Range (Y) axis for the specific plot in which you clicked. • **Domain Axis** – Zooms out the Domain (X) axis for all stacked plots. • **Range Axis** – Zooms out the Range (Y) axis for the specific plot in which you clicked.
Auto Range	Opens another menu that lets you zoom the plot to display the full range of the data. You can zoom in several ways: • **Both Axes** – Zooms both axes of the specific plot to show the full set of data. • **Domain Axis** – Zooms in the Domain (X) axis for all stacked plots so this axis displays the full range of X values of the data. • **Range Axis** – Zooms in the Range (Y) axis for the specific plot in which you clicked to display the full range of Y values of the data.

Edit Array Color

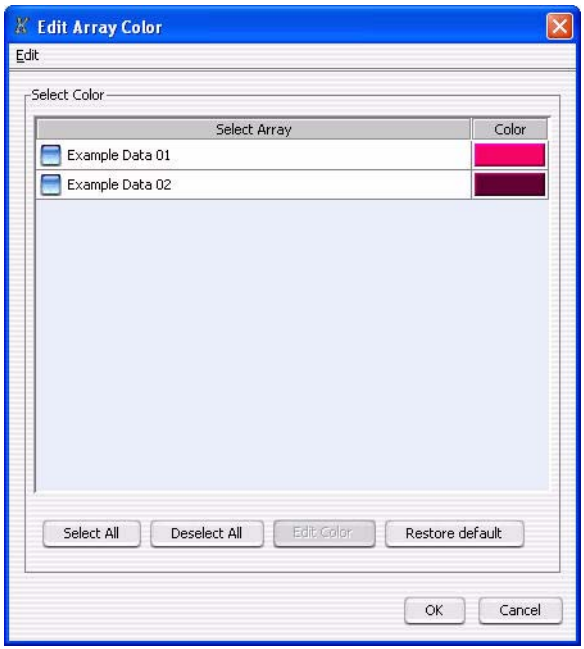


Figure 55 Edit Array Color dialog box

Purpose: Lets you show, change, and/or export the color(s) assigned to the arrays in an experiment.

To open: In the **Experiment** pane, right-click the name of an experiment, then click **Edit Array Color.**

Edit Opens a menu with a Copy command. If you click **Copy,** the program copies the list of arrays and their assigned colors to the Clipboard. You can then paste the list into a document in another program such as Word or PowerPoint.

Select Array Mark the check box for the array(s) whose color you want to change.

Color Opens the Select Color dialog box, where you can select a new color for the selected array(s). If more than one array is selected, all of the selected arrays assume the new color. For more information about selecting array colors, see "To change the display color of an array" on page 90.

Select All Marks all of the check boxes.

Deselect All Clears all of the check boxes.

Edit Color Opens the Select Color dialog box, where you can select a new color for the selected array(s). (Same function as the buttons under Color)

Restore default Restores the system default colors to all arrays.

OK Saves all assigned array colors and closes the dialog box.

Cancel Closes the dialog box without saving any changes.

Edit Array Order

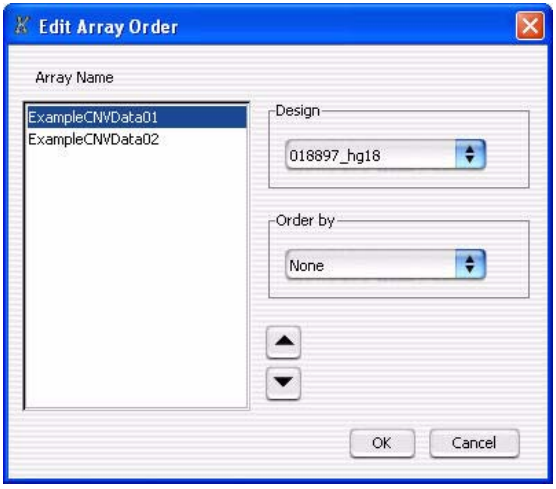


Figure 56 Edit Array Order dialog box

Purpose: Changes the display order of the arrays in an experiment. This can change the order in which array data appear in Gene View and Tab View.

To open: In the Experiment pane, right-click the name of an experiment, then click **Edit Array Order.**

Array Name The arrays in the selected design, shown in the order that they currently appear in the Experiment.

Design Select a design from the list. The arrays from the selected design appear under Array Name.

Order by (Optional) Select an array attribute. The program can set the order of arrays based on their respective values for the selected attribute.

 Moves a selected array up in the list. To select an array, click its name.

 Moves a selected array down in the list. To select an array, click its name.

OK Sets the new order of the arrays and closes the dialog box.

Cancel Closes the dialog box without changing the order of any arrays.

Experiment Properties

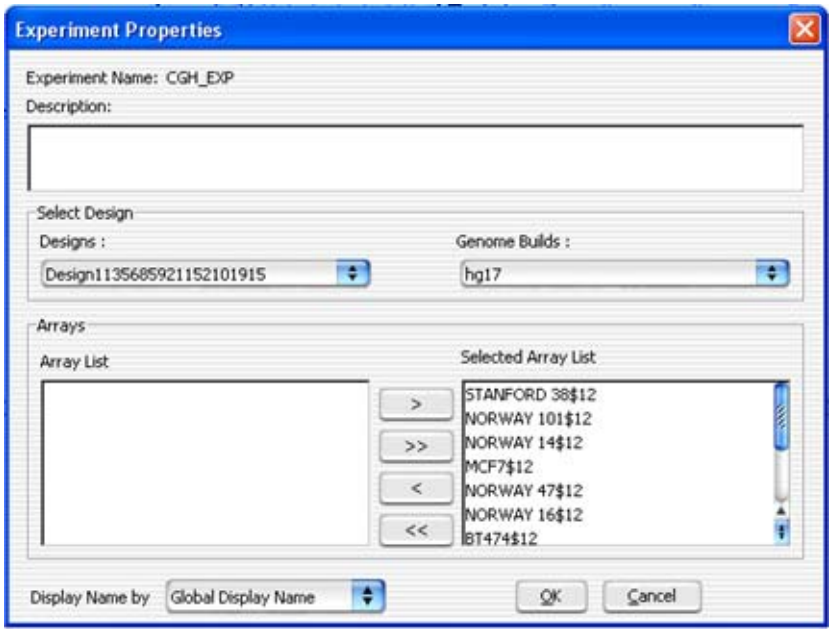


Figure 57 Experiment Properties dialog box

Purpose: Lets you select array designs and data to link to an experiment. See "To add arrays to an experiment" on page 64.

To open: In the Create Experiment dialog box, click **Properties**, or in the **Experiment** pane of the Navigator, right-click the name of an experiment, then click **Show Properties.**

Experiment Name (Read-only) The name of the selected experiment.

Description Description that was typed when the experiment was created.

Select Design

Designs Shows all of the designs available in the program. Select the design associated with arrays that you want to add to the experiment.

Genome Builds Shows the genome build(s) that are associated with the design. Select the desired genome build to display the arrays that are associated with a single genome build.

Arrays

Array List Shows the arrays in the selected design that are available for this experiment.

- To select an array to move to the Selected Array List, click its name.
- To select additional arrays, hold down the **Ctrl** key while you 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 Shows the arrays that you have selected for this experiment.

Moves the selected arrays in Array List to the Selected Array List. You can move arrays from as many designs as you like, if they are all associated with the same genome build.

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 for removal, click its name. If desired, you can re-add an array.

Clears the Selected Array List.

Display name by Click to select an attribute to be used for display of the names of arrays in the experiment. The Global Display name is the name assigned in Sample Manager for the array. See the *Sample Manager User Guide* for more information.

OK Adds the arrays in the Selected Array list to the experiment and closes the dialog box.

Cancel Closes the dialog box without adding any arrays to the experiment.

Export

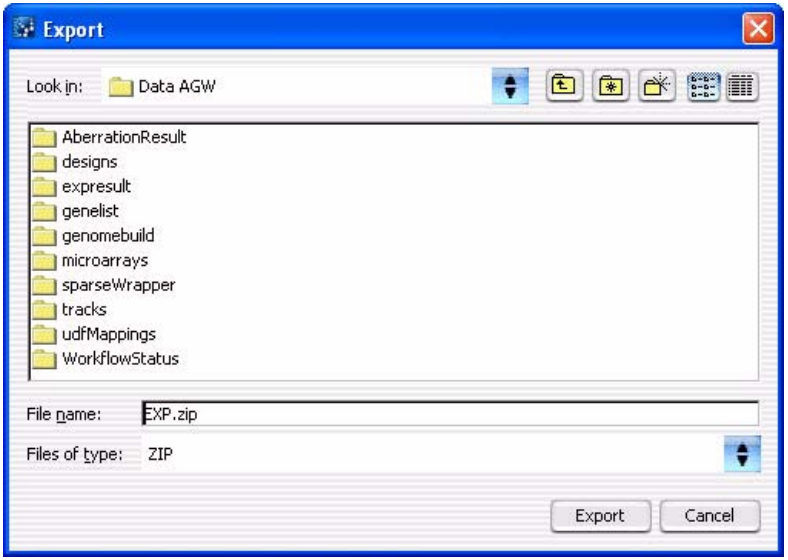


Figure 58 Export dialog box – Several types of file exports use this dialog box. This specific example exports selected experiment(s) as a ZIP format file.

Purpose: Lets you select a location for an exported file.

To open: This dialog box appears after you select specific experiment(s), track(s), filter(s) or array attributes to export. See "To export experiments" on page 82, "To export tracks" on page 84, "To export filters" on page 83 or "To export array attributes" on page 81.

Look in Displays the folder or other location whose contents appear in the main pane of the dialog box. To select another folder or other location, click .


Moves to the next higher folder level.


Opens the Desktop.


Creates a new folder in the selected location in *Look in*.


Displays the names, only, of folders, files, and other locations in the main pane of the dialog box.


Displays both the names and more information about folders, files, and other locations in the main pane of the dialog box.

Main pane Displays the folders, files, and other locations in the selected location in *Look in*. Only files of the selected file type are displayed. To select file, click its name. To open a folder or other location, double-click its name.

File name Displays the name of the file to which the exported content will be saved. To change the name, you can either select a file in the main pane of the dialog box, or type a new name.

Files of type Sets the type of files that are displayed. To show all files, click , then select **All Files.**

Export Saves the selected content to the location given in the dialog box.

Cancel Cancels your selections and closes the dialog box.

Export Array Attributes

Purpose: This dialog box lets you select arrays whose attributes you want to export. It contains two tabs: an Array tab where you select the arrays, and an Attribute tab where you select the attributes of the selected arrays to export. See "To export array attributes" on page 81.

To open: In the Home command ribbon, click **Export > Array Attributes**, or in the **Experiment** pane of the Navigator, right-click the name of an experiment, then click **Export Attributes.**

Array tab

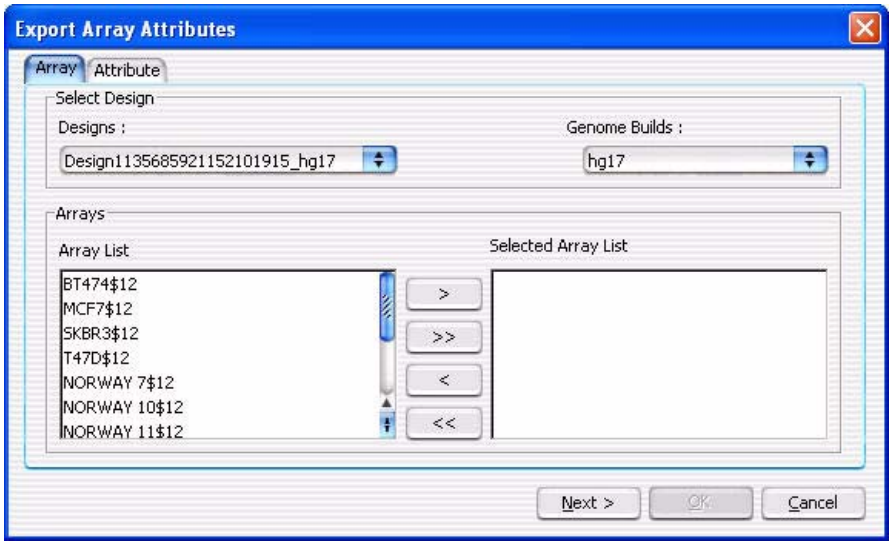


Figure 59 Export Array Attributes – Array tab dialog box

Select Design

Designs Shows all of the designs available in the program. Select the design associated with arrays whose attributes you want to export.

Genome Builds Shows the genome build(s) associated with the design. Select the desired genome build to display the arrays.

Arrays

Array List Shows the arrays in the selected design.

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

Selected Array List Shows the arrays that you have selected for this experiment.

>	Moves the selected arrays in Array List to the Selected Array List. You can move arrays from as many designs as you like, if they are all associated with the same genome build.
>>	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 for removal, click its name. If desired, you can re-add an array.
<<	Clears the Selected Array List.
Next	Moves to Attribute tab for attribute removal.
Cancel	Closes the dialog box without selecting any arrays and their attributes to be exported.

Attribute Tab

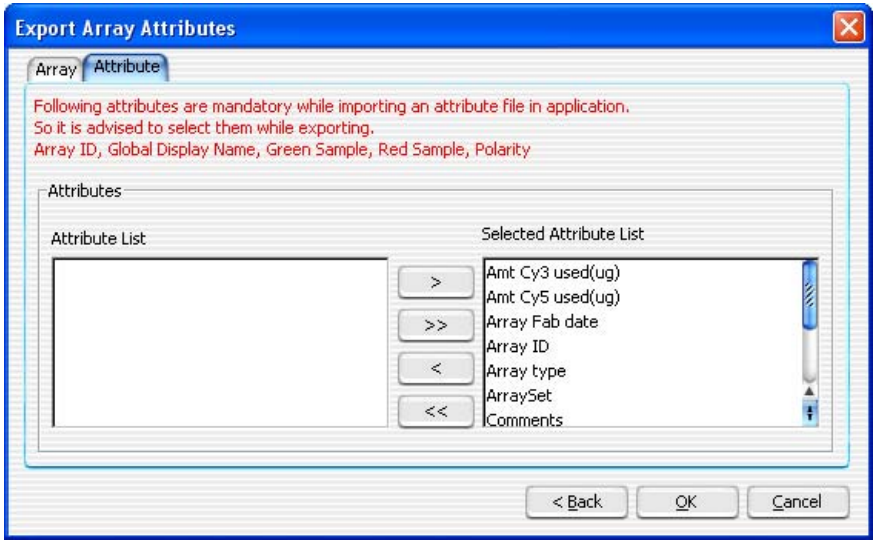


Figure 60 Export Array Attributes – Attribute tab dialog box

Attributes

Selected Attribute List	Shows the attributes for the selected arrays to be exported. • To select an attribute to move to the Attribute List, click its name.

- To select additional attributes, hold down the **Ctrl** key while you click their names.
- To select a contiguous block of attributes, click the name of the first attribute, then hold down the **Shift** key while you click the name of the last one.

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 Shows the attributes that will not be exported for the selected arrays.

Removes an attribute from the Selected Attribute List. To select an attribute for removal, click its name. You can add the attribute to the Selected Attribute List at a later time.

Clears the Selected Attribute List.

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.

Back Moves back to the Array tab for array selection or removal.

OK Opens the Export dialog box. See “Export” on page 197.

Cancel Closes the dialog box without exporting any attributes.

Export Experiments

Figure 61 Export Experiments dialog box

Purpose: Lets you select experiments for export. The program exports all array designs and data associated with the experiments as a single ZIP file. This file does not include any parameter settings, array selections, or results. See "To export experiments" on page 82.

To open: In the Home tab, click **Export > Experiments.**

Select experiments to export Shows all experiments available for export. Mark each experiment you want to export.

Select All Selects all experiments for export.

Deselect All Clears all check boxes under Select experiments to export.

OK Opens an Export dialog box. See "Export" on page 197.

Cancel Cancels the export and closes the dialog box.

Export Filters

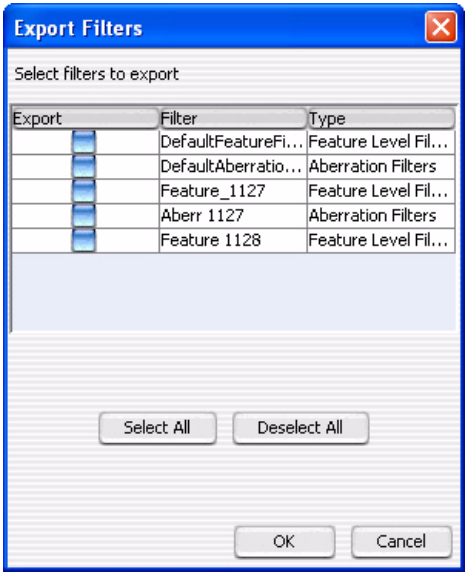


Figure 62 Export Filters dialog box

Purpose: Lets you select feature-level, array-level, design, metric set, and/or aberration filters, to export as a single *.xml file. You can create and use filters only if you have a DNA Analytics application license. See "To export filters" on page 83.

To open: In the **Home** tab, click **Export > Filters.**

Select filters to export Displays all of the filters available in the program. The table has these columns:

- Export – Mark the check box for each filter to export.
- Filter – The name of each filter.
- Type – The type of content to which the program applies each filter.

Select All Selects all available filters for export.

Deselect All Clears all of the check boxes under Select filters to export.

OK Opens the Export dialog box, where you can select a location for the exported *.xml file of filters. See "Export" on page 197.

Cancel Cancels the export and closes the dialog box.

Export Tracks

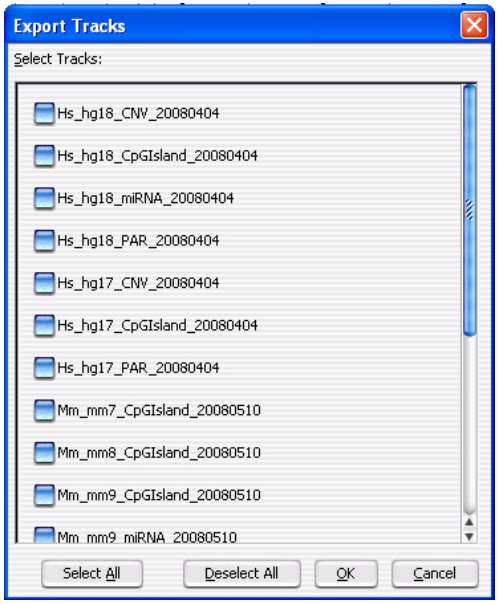


Figure 63 Export Tracks dialog box

Purpose: Lets you select tracks to export as a single BED format file. See "To export tracks" on page 84.

To open: In the **Home** tab, click **Export > Tracks.**

Select tracks Shows all of the tracks available in the program. Mark the check box for each track to export.

For more information about tracks, see "To create a track (CGH only)" on page 78 and "To show tracks in Gene View" on page 103.

Select All Selects all available tracks for export.

Deselect All Clears all of the check boxes under Select Tracks.

OK Opens the Export dialog box, where you can select a location for the exported BED format file. See "Export" on page 197.

Cancel Cancels the export and closes the dialog box.

Find in column

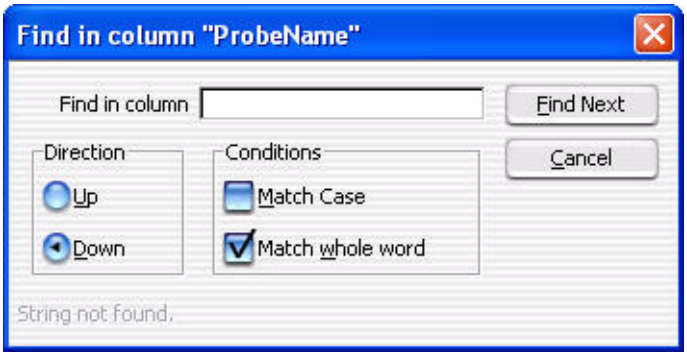


Figure 64 Find in column dialog box

Purpose: This dialog box lets you set search parameters for a specific column entry for the selected chromosome. Based on these parameters, the program can highlight the row of the first entry that matches. The cursor then moves to the location defined in the row.

To open: Right-click any entry in a tab in Tab View other than a column heading, then click **Find in column** in the shortcut menu.

Find in column Type all or part of the entry you want to find.

Direction Select a search direction:

- **Up** – Sets the search to move up in the selected column from the currently highlighted row.
- **Down** – Sets the search to move down in the selected column from the currently highlighted row.

Conditions Mark any of these search options:

- **Match Case** – Mark this option to take case into account. For example, if you mark **Match Case**, and you type `aa351` in Find in column, the search finds the next entry in the column that contains **aa351.** It does *not* find entries that contain **AA351** or **Aa351.**
- **Match whole word** – Mark this option to only find entries in which the complete entry matches what you type in Find in column. For example, if you type `AA351` in Find in column, and mark **Match whole word,** the program finds the next **AA351** entry. It does not find entries such as **AA3512** or **AA351992.**

Find Next Finds the next matching entry in the selected column, and moves the cursor to the location defined in the row that contains the entry. The search is performed only for the chromosome selected in the Genome View.

Cancel Closes the dialog box.

Gene List

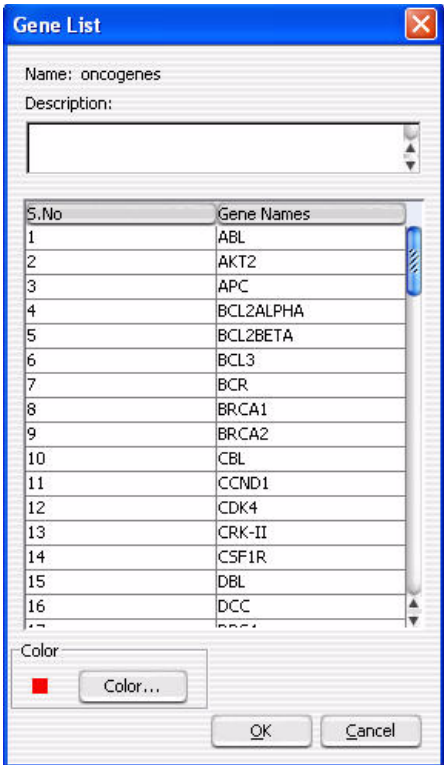


Figure 65 GeneList dialog box

Purpose: Lets you view the names of the genes in a specific gene list and to change the display color of the gene list.

To open: In the My Entity List pane of the Navigator, right-click the name of a gene list, then click **View in Table.**

Name (Read-only) The name of the gene list.

Description (Optional) Brief descriptive comments about the gene list, such as how it was created or the nature of the genes in the list. You can edit the description.

S. No The sort order number. This is the index number of each gene within the gene list.

Gene Names The names of the genes in the gene list.

Color Opens the Choose Gene List Color dialog box, where you can change the display color for the gene list.

OK Saves the gene list with any new description or display color, and closes the dialog box.

Cancel Closes the dialog box without making any changes to the gene list.

Genotype Reference Details (CGH only)

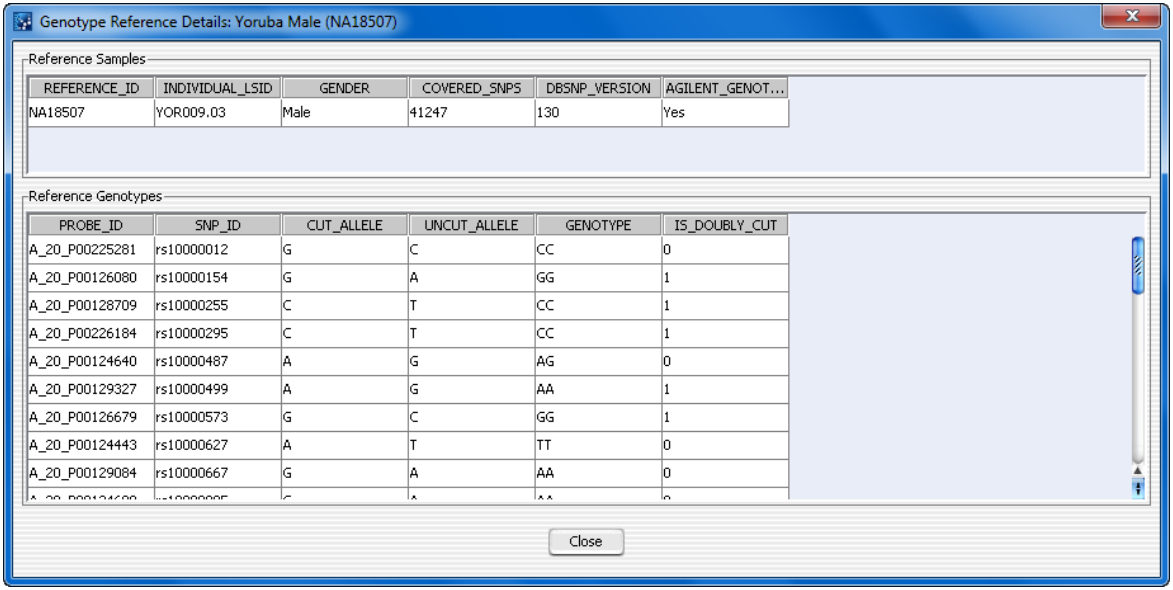


Figure 66 Genotype Reference Details dialog box

Purpose: Shows the details of the genotype reference selected in the Genotype pane of the Navigator. This dialog box is only available only in the CGH module.

To open: In the Genotypes pane of the Navigator, right-click on a genotype reference, and select **Show Properties**.

Genotype Reference Importer (CGH only)

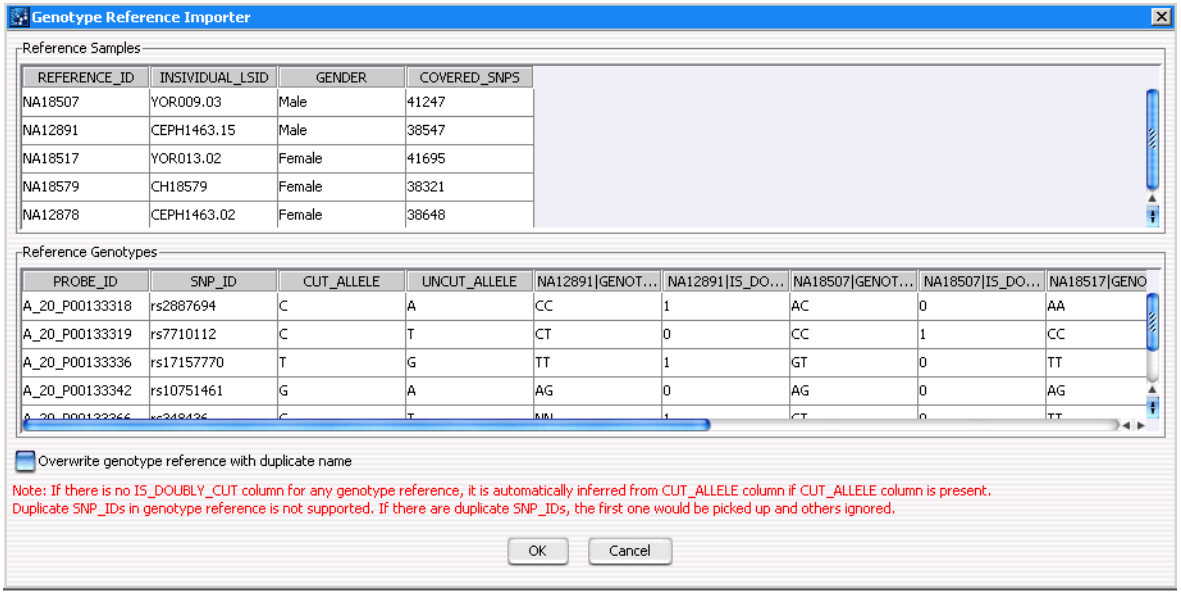


Figure 67 Genotype Reference Importer dialog box

Purpose: Displays the contents of a genotype reference file you want to import, and lets you choose to overwrite existing genotype references in the database when you import the file.

To open: From the Home tab, click **Import > Genotype References**. In the Import Genotype Reference Files dialog box, browse to a location and select the genotype reference file you want to import, then click **OK**.

Reference Samples Displays a table of the samples in the file, including number of SNP probes covered by the sample.

Reference Genotypes Displays a table of the genotypes in the file. Duplicate SNP_IDs are not allowed. If there are duplicate SNP_IDs in the file, only the first SNP_ID is imported.

NOTE If the CUT_ALLELE column is present for a genotype reference, and there is no IS_DOUBLY_CUT column, the IS_DOUBLY_CUT column will be automatically inferred from the CUT_ALLELE column.

Go To Gene/Genomic Location

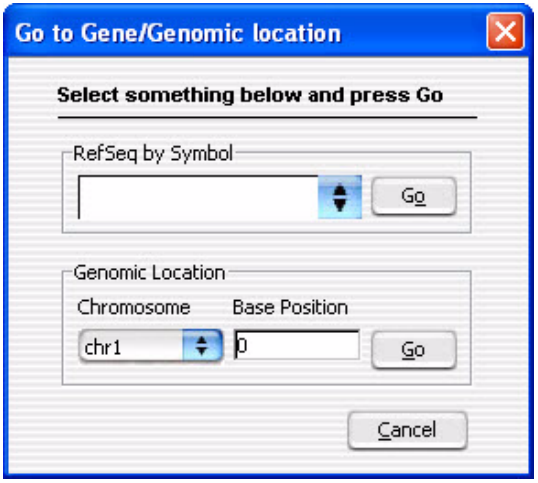


Figure 68 Go To Gene/Genomic location dialog box

Purpose: To find a specific gene location in Gene View by either selecting the RefSeq by Symbol or by selecting the Genomic Location.

To open: Click **Home > Go to Gene/Genomic location**.

RefSeq by Symbol Select the Reference Sequence accession symbol from NCBI, and click **Go.**

Genomic Location

- Chromosome – The chromosome number.

- Base Position – The position on the chromosome.

Click **Go** after selecting the chromosome number and the position of the gene on the chromosome.

Cancel Closes the dialog box.

Import

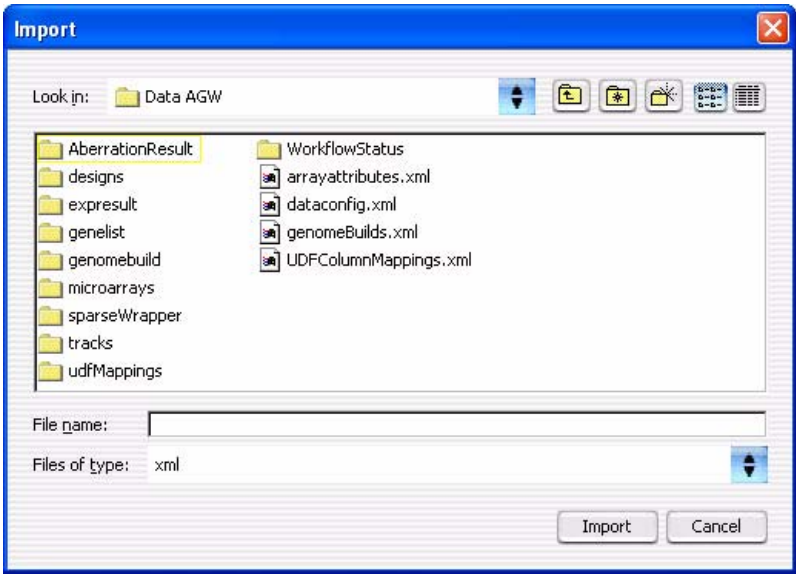


Figure 69 Import dialog box

Purpose: Lets you select files and import them into Agilent Genomic Workbench. The title of this dialog box changes depending on the type of file to import.

To open: In the **Home** tab, click **Import,** then select any kind of import except Genome Build or Track. The type of file to be imported appears in the title of the dialog box. To import a gene list, right-click the **Gene List** folder in the **My Entities List** pane of the Navigator, then click **Import Gene List.**

Use the standard Windows® Explorer commands in the dialog box to select a file for import.

For some imports, you can select multiple files. Click the name of the first file, then hold down the **Ctrl** key while you click the names of additional files. To select a contiguous block of files, click the name of the first file in the block, then hold down the **Shift** key while you click the name of the last one.

File name Displays the name of a file you select for import.

Files of type Lets you select the types of files to display from the types shown in the table below. To display all files, click  ,then select **All Files.**

File type	Extension
FE array File	*.txt
Axon array file	*.gpr
UDF file	*.txt
Design file (GEML)	*.xml
Axon design file	*.gal
Array attributes	*.txt
Experiments	*.zip
Filters	*.xml
Gene list	*.txt

Import or Open Imports the file into the program. In some cases, the name of this button is *Open*, rather than *Import*. Also, when you click **Import,** in many cases one or a series of additional dialog box(es) lets you further define the content for import. See the instructions for each specific type of import in Chapter 2.

Cancel Cancels the import and closes the dialog box.

Import (experiments)

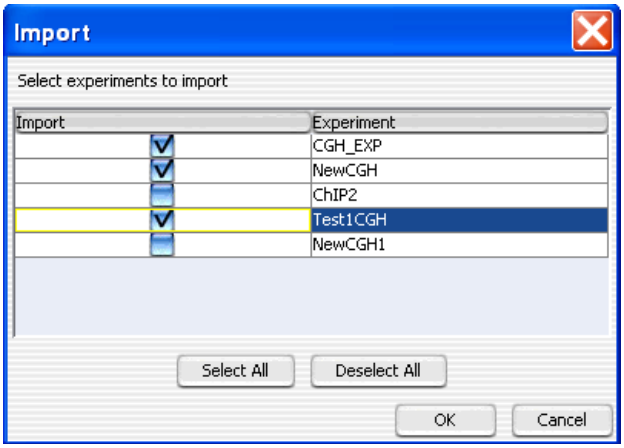


Figure 70 Import dialog box (for experiments)

Purpose: Lets you select the specific experiments within a .zip experiment file to import into the program. See "To import an experiment file" on page 57.

To open: In the **Home** tab, click **Import > Experiments.** In the dialog box that appears, select the desired .zip experiment file, then click **Import.**

Select experiments to import

These columns appear:

- **Import** – Mark the check box for the experiment(s) to import.
- **Experiment** – The names of the experiments available for import in the ZIP format experiment file.
-

Select All Selects all of the experiments in the .zip file for import.

Deselect All Clears all of the check boxes under Import.

OK Imports the selected experiments into the program. If the name of an imported array design or data file matches one that is already available in the program, the Confirm overwrite dialog box appears, where you can select the data and/or design files that you want to overwrite. See "Confirm Overwrite" on page 177.

Cancel Cancels the import and closes the dialog box.

Import (filters)

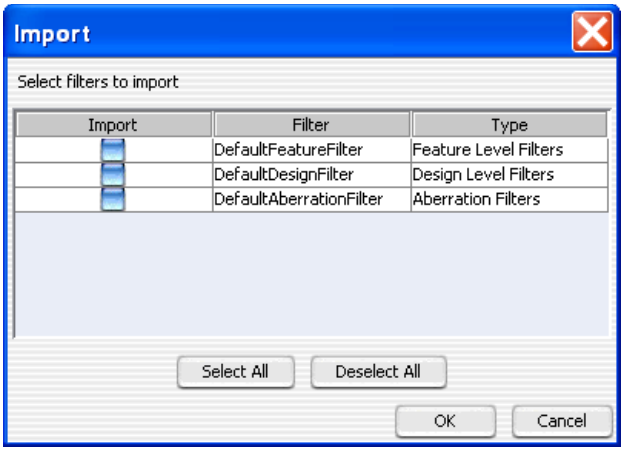


Figure 71 Import (for filters) dialog box

Purpose: Lets you select the specific filters within a .zip exported filter file to import into the program. See "To import filters" on page 58.

To open: In the **Home** tab, click **Import > Filters.** In the dialog box that appears, select the desired ZIP exported filter file, then click **Import.**

Select experiments to import These columns appear:

- **Import** – Mark the check box for the experiment(s) to import.
- **Filter** – The names of the filters available for import in the .zip filter file.
- **Type** – The type of filter

Select All Selects all of the filters in the .zip file for import.

Deselect All Clears all of the check boxes under Import.

OK Imports the selected filters into the program. If the name of a filter matches one that is already available in the program, the Confirm overwrite dialog box appears, where you can select the filters that you want to overwrite. See "Confirm Overwrite" on page 177.

Cancel Cancels the import and closes the dialog box.

Import GEML design files

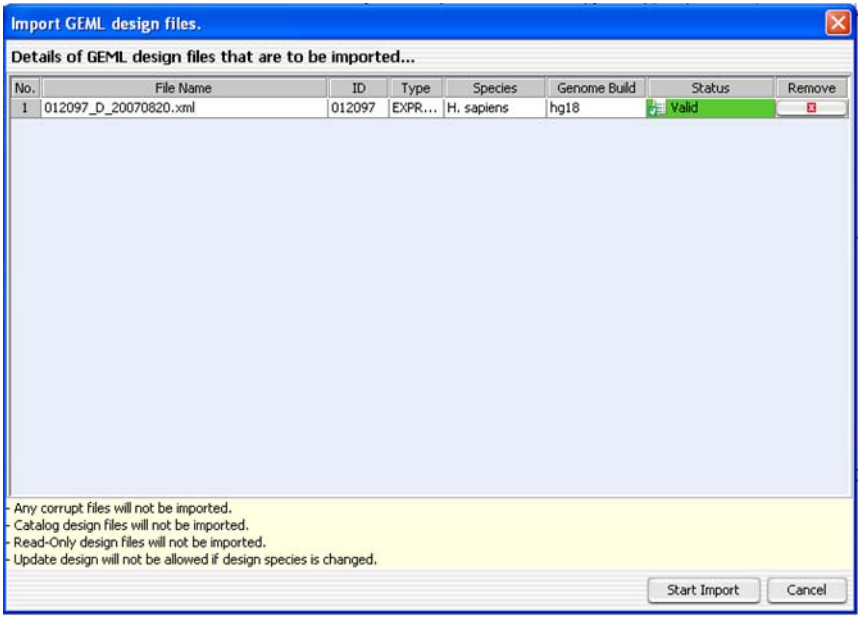


Figure 72 Import GEML design files dialog box

Purpose: To display information in the design file and to remove any files that you don't want to import.

To open: In the Home tab, click **Import > Design Files > GEML File.** Select the desired *.xml design files, then click **Open.**

File Name The name(s) of the design file(s) to be imported.

ID The Agilent ID number for the design file

Type The application type, which can be CGH, ChIP, miRNA, or gene expression.

Species The species for the genome build. This appears automatically when the Genome Build is selected.

Genome Build The genome build for the design. If the genome build is not read automatically, a "?" appears. Click **Genome Build** and select the correct value from the list.

Status

- **Not Set** – Appears if Genome Build and Species information is not shown.
- **Not Allowed** – Appears if a Genome Build is selected that does not match the design, or if the design is a catalog or read-only design.
- **Overwrite** – Appears when the design file has been updated and will overwrite any existing one of the same name.
- **Valid** – Appears when the file is new.
- **Corrupt** – Appears when the file is corrupt.

Remove Click  to remove a specific design file from the list.

Start Import Starts the import of the design files in the list.

Cancel Cancels the upload and closes the dialog box.

Import Genome

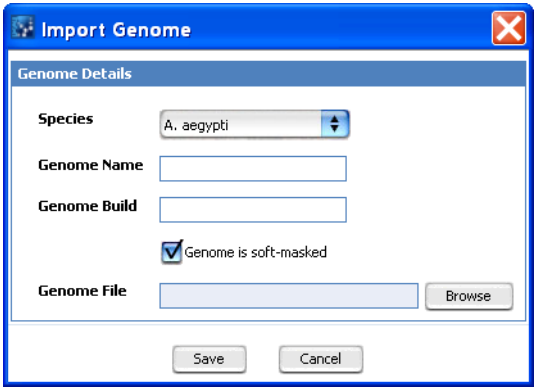


Figure 73 Import Genome dialog box

Purpose: To specify a custom genome to import. For more information, see the *eArray$_{XD}$ User Guide*.

To Open: On the Home Command Ribbon, click **Import** and then select **Custom Genome for Tiling**.

Species Select the species of the user-defined genome to import. The species list contains all of the species currently available in the system. To upload a genome for a species that does not appear in this list, select Na.

To select this genome for tiling, you select Na as the species.

Genome Name Type a name for the genome import job. The program uses this name to identify the job in the Tasks pane of the Navigator.

Genome Build Type the name of the specific build of the genome that is represented in your genome file. Use only letters, numbers, underscores, periods, and dashes.

Genome is soft-masked Mark this check box if repeat sequences in your genome file are represented by lower-case letters. If you do not mark this option, the program changes any lower-case characters in your sequence(s) to capital characters.

Genome File The genome file must be a *.zip archive that contains the FASTA format chromosomal sequence files.

Browse Click this to browse to and locate the genome file to import.

Save The program starts your genome import, and adds the job to the Tasks pane of the Navigator. A dialog box tells you that the job has been submitted.

Cancel Click to close the dialog box without importing any data.

Import Genome Build

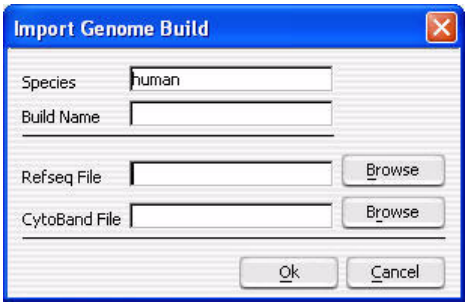


Figure 74 Import Genome Build dialog box

Purpose: To import a new set of genome build files into Agilent Genomic Workbench. See "To import a genome build" on page 54.

To open: In the Home tab, click **Import > Genome Build.**

Species The genome's species of origin.

Build Name The name of the build to be imported.

Refseq File The location of the RefSeq database file. This file contains chromosomal locations of genes. To select a Refseq file, click **Browse.**

CytoBand File The location of the applicable cytoband file. This file contains graphical cytoband information for Gene View and Chromosome View. To select a cytoband file, click **Browse.**

OK Imports the genome build and closes the dialog box.

Cancel Cancels the import and closes the dialog box.

CAUTION Import only Agilent-provided genome build files.

Import Track

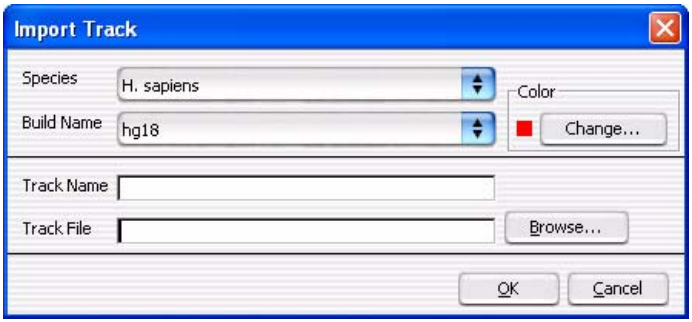


Figure 75 Import Track dialog box

Purpose: Lets you import a BED format track file. See "To import tracks" on page 55. Track information can appear in Gene View. See "User Preferences" on page 250.

To open: In the **Home** tab, click **Import > Track.**

Species Select the species to which the track relates.

Build Name This list contains the available genome builds for the selected species. Select the desired genome build.

Color Shows the currently assigned display color for the track. To change this color, click **Change.** For more information, see "Select Color" on page 231. You select track colors in the same way as gene list colors.

Track Name Type a name to identify the imported track.

Track File Type the location of the BED track file to import, or click **Browse** to select a file.

Browse Opens an Open dialog box, where you can select the BED track file to import.

OK Imports the track into the program.

Cancel Cancels the import and closes the dialog box.

Microarray Properties

Purpose: Displays the properties associated with an array. You can also edit the values of specific attributes. To add attributes to the list, see the *Sample Manager User Guide*.

To open: For any array in the **Data** folder or **Experiments** folder, right-click the array name, then click **Show Properties.** For non-Agilent arrays, only the Attribute tab appears.

Attribute tab

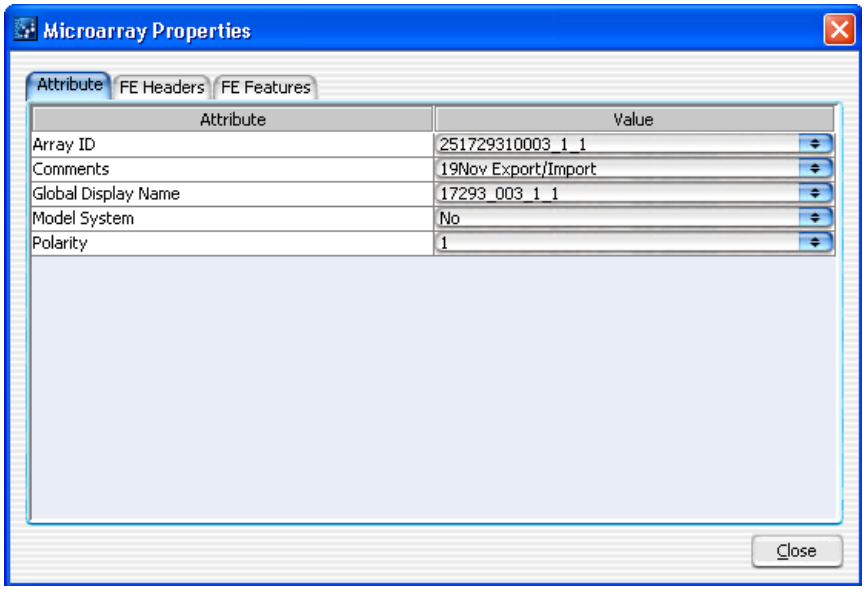


Figure 76 Microarray Properties dialog box with list of Attributes and their values

- **Attribute** – Displays the attributes in the array by name.
- **Value** – Indicates the values, if any, for each array. To edit the value of an attribute, select a new value for it under Value. Alternatively, click , then type or edit the value.

Close Closes the dialog box.

FE Headers tab

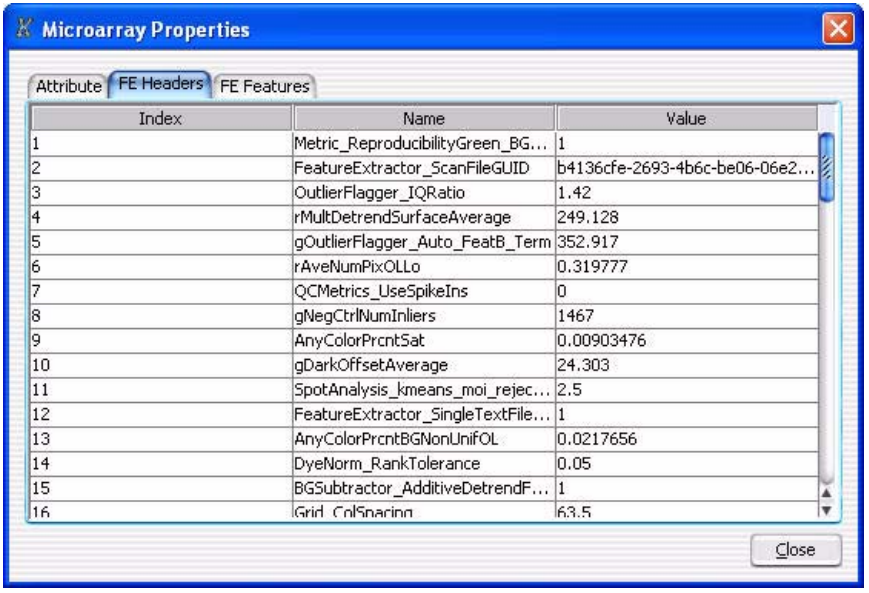


Figure 77 Microarray Properties dialog box with list of FE Headers their values

Index Displays a sequential index to help identify FE properties.

Name Displays feature parameters, statistics, and constants for the whole array.

Value Displays the value for each parameter, statistic, and constant.

Close Closes the dialog box.

FE Features tab

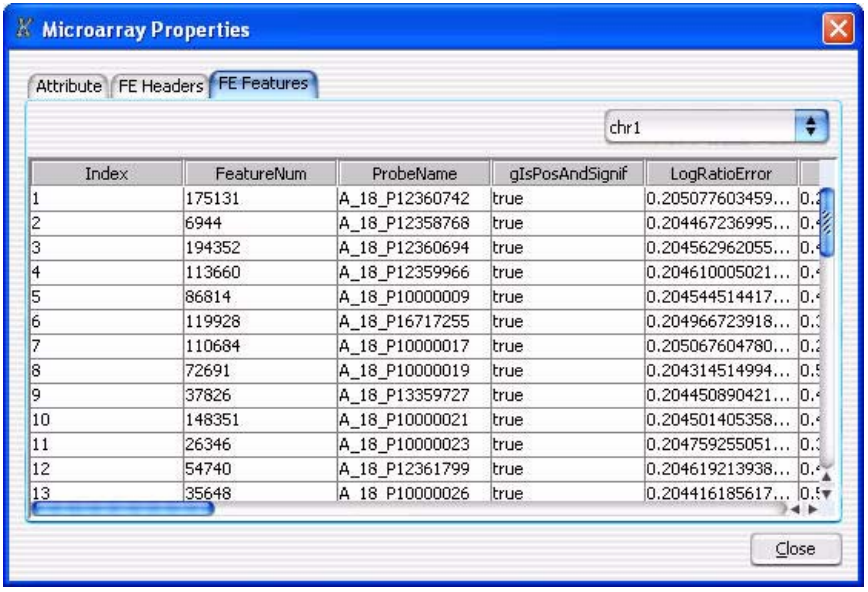


Figure 78 Microarray Properties dialog box with list of FE Features and associated data

Selection List Select the chromosome whose feature information you want to display.

List Box Displays FE features and the associated data. The columns are:

Index	FeatureNum	ProbeName
gIsPosAndSignif	LogRatioError	PValueLogRatio
gProcessedSignal	rProcessedSignal	gMedianSignal
rMedianSignal	gBGSubSignal	rBGSubSignal
gIsSaturated	rIsSaturated	gIsFeatNonUnifOL
rIsFeatNonUnifOL	gIsBGNonUnifOL	rIsBGNonUnifOL
rIsPosAndSignif	gIsWellAboveBG	rIsWellAboveBG

MovAvg Example Parameters

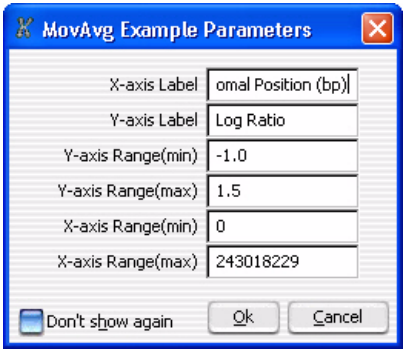


Figure 79 MovAvg Example Parameters dialog box

Purpose: This dialog box lets you set display parameters for the MovAvg Example plug-in. The plug-in calculates a 10-point moving average of the data from the selected chromosome in the selected arrays of the active experiment. It displays stacked plots of moving averages for all the arrays, one plot per array. You must have Perl installed on your computer to use this plug-in.

To open: Click **Tool > Plugin Settings > MovAvg Example.** This dialog box also opens when you click **Tool > Plugin > MovAvg Example,** if **Don't show again** is cleared.

Parameters Set any of these parameters:

Parameter	Description
X-axis Label	The text that appears under the X-axis of the plot as a label.
Y-axis Label	The text that appears next to the Y-axis of the plot as a label.
Y-axis Range (min)	The minimum value on the Y-axis.
Y-axis Range (max)	The maximum value on the Y-axis.
X-axis Range (min)	The minimum value on the X-axis.
X-axis Range (max)	The maximum value on the X-axis.

Don't show again Mark this option to keep this dialog box from being displayed in the future when you click Tool > Plugin > MovAvg Example. To restore the dialog box so it appears again, click **Tool > Plugin Settings > MovAvg Example,** then clear **Don't show again.**

OK Click to accept the parameters and prepare the plot. You can further make additional changes to the appearance of the plot once the plug-in displays it.

Cancel Ignores any changes you made, and closes the dialog box.

How to modify the plugin

The plug-in program (**MovAvg Example.pl**, located in the Plugins folder of the Agilent Genomic Workbench installation folder on your computer) is a short Perl program. It is a good example of how calculated columns are processed.

The plotting is very simple, but the simple plug-in architecture of MovAvg Example.pl lets you write your own computational methods to analyze data from selected arrays in the CGH application.

- Within the code of the plug-in, you can add text strings to column headers to set the format.
- To create a line graph instead of a scatter plot, you append `-plotline` to a column header.
- To prevent the plug-in from plotting a specific column, you append `-noplot` to the column heading. Note that the plug-in removes this extra text from the header before it displays it on the plot. The extra text does not appear in figures, and is only used to set the format of the plot.

MovAvg.pl shows how column-naming can be used. As you read the first line (which contains the header text), you can add text to the existing headers or add text to the headers for your generated columns, as well, to give you a small amount of formatting control.

MovAvg Example Plot

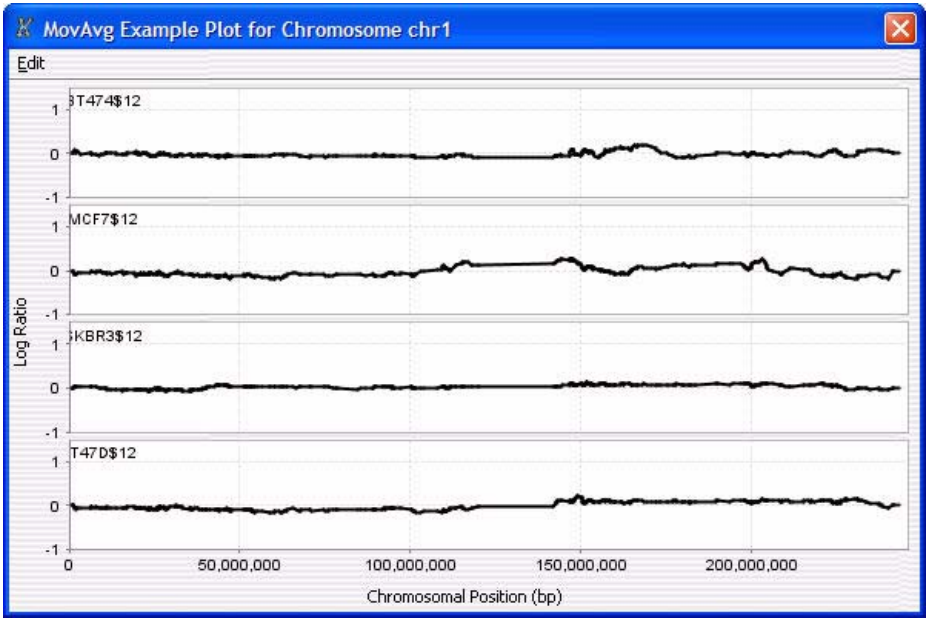


Figure 80 MovAvg Example Plot

Purpose: This plot displays the output of the MovAvg Example plug-in. The plug-in calculates a 10-point moving average of the data from the selected chromosome in the selected arrays of the active experiment.

To open: Click **OK** in the MovAvg Example Parameters dialog box. See "MovAvg Example Parameters" on page 224.

Plot(s) The main plot area shows moving average line plots for the selected chromosome. A separate plot appears for each array.

Edit Opens a menu with a Copy Plot(s) to Clipboard option. If you select this option, the program copies the plots to the clipboard as an image. You can then paste the image into a document in another program.

When you right-click anywhere within the plot area, the following options are displayed:

Option	Description
Properties	Opens the Chart Properties dialog box, where you can change the appearance of many aspects of the plot. See "Chart Properties" on page 171.
Save as	Opens a Save dialog box, where you can select a location for the *.png image file of the plots.
Print	Opens a Page Setup dialog box, where you can set page size, margins, and orientation, and select a printer. From there, you click **OK** to open the Print dialog box, where you can set print options and print the plot.
Zoom In	Opens another menu that lets you zoom in the plot. You can zoom in several ways: • **Both Axes** – Zooms in the Domain (X) axis for all stacked plots, and zooms in the range Range (Y) axis for the specific plot in which you clicked. • **Domain Axis** – Zooms in the Domain (X) axis for all stacked plots. • **Range Axis** – Zooms in the Range (Y) axis for the specific plot in which you clicked. You can also drag across an area of one of the plots to select an area to expand.
Zoom Out	Opens another menu that lets you zoom out the plot. You can zoom out several ways: • **Both Axes** – Zooms out the Domain (X) axis for all stacked plots, and zooms out the range Range (Y) axis for the specific plot in which you clicked. • **Domain Axis** – Zooms out the Domain (X) axis for all stacked plots. • **Range Axis** – Zooms out the Range (Y) axis for the specific plot in which you clicked.
Auto Range	Opens another menu that lets you zoom the plot to display the full range of the data. You can zoom in several ways: • **Both Axes** – Zooms both axes of the specific plot to show the full set of data. • **Domain Axis** – Zooms in the Domain (X) axis for all stacked plots so this axis displays the full range of X values of the data. • **Range Axis** – Zooms in the Range (Y) axis for the specific plot in which you clicked to display the full range of Y values of the data.

Probe Upload

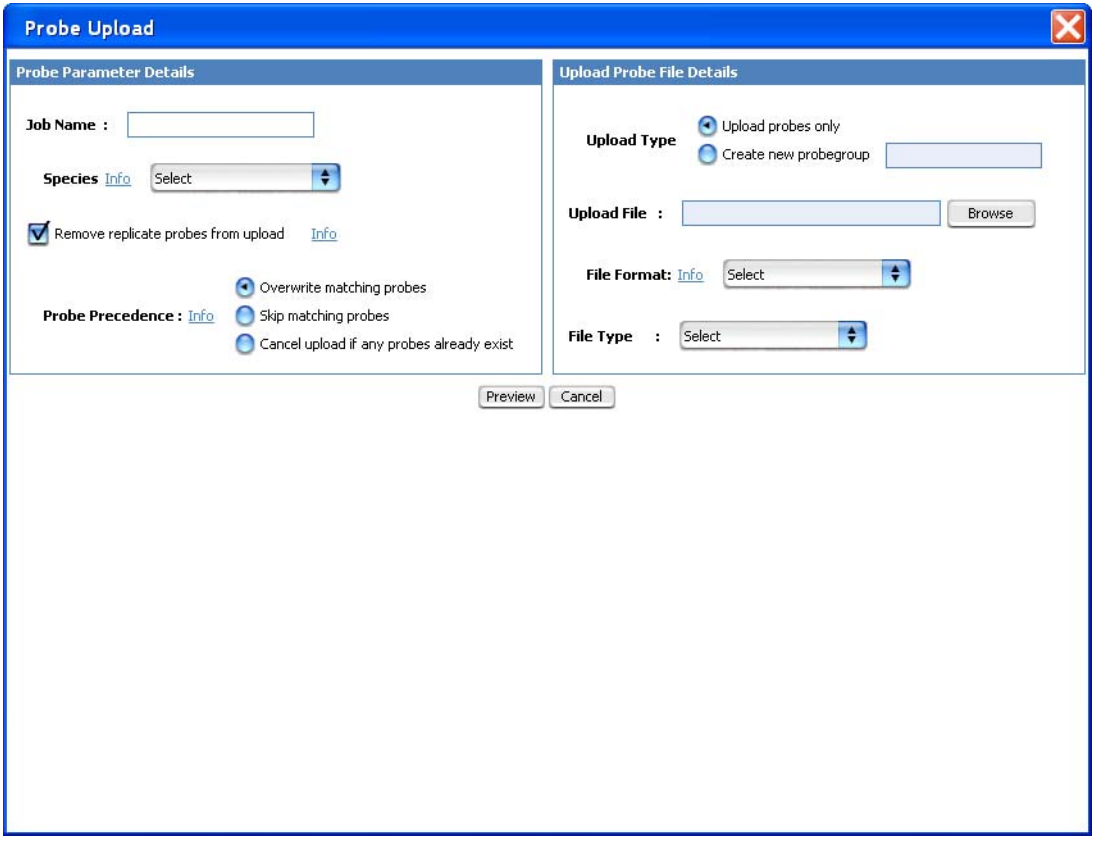


Figure 81 Probe Upload dialog box

Purpose: Lets you set up and start a probe upload. A probe upload transfers probe sequences and annotation to your Agilent Genomic Workbench server. See the *eArrayXD User Guide* for more information.

To open: In the Home tab, on the Command Ribbon, click **Import > Probe Upload**.

Probe Parameter Details

These parameters appear:

Parameter	Description
Job Name	Type a name that will help you to identify this job.
Species	Select the desired species. The program associates all probes in the uploaded file with this species.
Remove replicate probes from upload	Mark this option to upload the first probe in each set of replicate probes in your file, and ignore the others. A replicate probe has the same Probe ID as another probe in the file. If your probe file contains replicate probes, and you do **not** mark **Remove replicate probes from upload**, the program does not upload your file.
Probe Precedence	These options specify what the program does if it finds probes in your uploaded file that have the same Probe ID as probes that already exist in the system. Select one of these options: • **Overwrite matching probes** – The annotation of the matching uploaded probes replaces the annotation of the existing probes. You can use this option to reannotate existing probes. • **Skip matching probes** – The program ignores matching uploaded probes, but does upload other probes. • **Cancel upload if any probes already exist** – The program cancels the entire upload process if it finds a matching uploaded probe.

Upload Probe File Details

Select these options:

Parameter	Description
Probe Group Name	The program creates a probe group that contains the probes in your uploaded file. Type a name for this probe group.
Upload File	The location of the file that contains the probes and annotation to be uploaded. **Browse** – Opens an Open dialog box, where you can select a file of probes and annotation for upload.

Parameter	Description
File Format	The column content of your probe file. Select one of these options: • COMPLETE – The uploaded file contains the columns described in "Complete (for probes)" on page 648. • MINIMAL – The uploaded file contains the columns described in "Minimal (for probes)" on page 656.
File Type	The file type defines how the data items in the file are specified and separated. The program accepts tab-delimited text (*.tdt and *.txt) and Microsoft Excel (*.xls) files. If you use Microsoft Excel 2007 to create the file, save the file as an Excel 97-2003 workbook. This saves the file in the required *.xls format.

CAUTION If you select **Overwrite Matching Probes** in Probe Precedence, the program reannotates matching probes upon upload. The original annotation of these probes cannot be recovered.

Preview Opens the Define Uploaded File Columns pane in the dialog box, which lets you view the first few lines of your uploaded file, and label the content of each column of data within it. See the *eArray$_{XD}$ User Guide* for more information.

Cancel Cancels the probe upload and closes the dialog box.

Scroll to Column

Figure 82 Scroll to Column dialog box

Purpose: This dialog box lets you select a column. The program then scrolls the tab so that you can see the selected column.

To open: Right-click a column heading in Tab View, then click Scroll To Column in the shortcut menu.

Select column Lists the columns available in the currently selected tab. Select the one you want to view.

OK Scrolls the current tab so that you can see the selected column.

Cancel Closes the dialog box.

Select Color

Purpose: To select a color. Three tabs are available for selecting colors:

- Swatches tab - select colors based on samples (swatches)
- HSB tab - select colors based on an HSB schema (Hue, Saturation, and Brightness)
- RGB tab - select colors based on an RGB schema (Red-Green-Blue)

To open: This dialog box opens when a function allows you to change a color. For example, right-click on an array in an experiment, click **Edit Array Color** and click the **Swatches, HSB,** or **RGB** tab.

Swatches tab

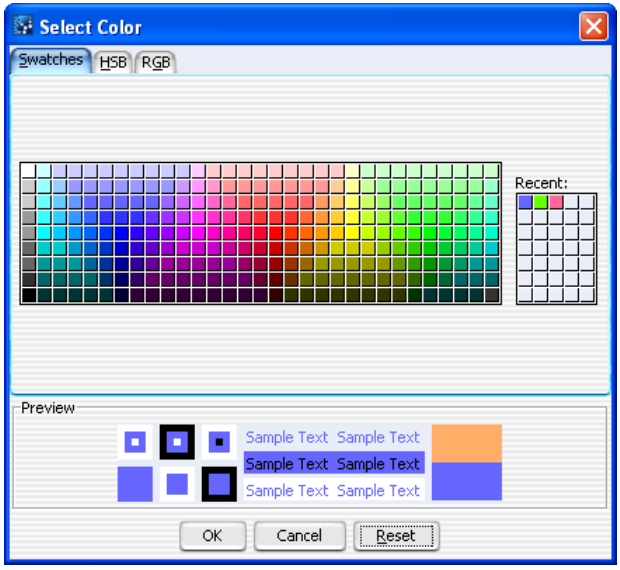


Figure 83 Select Color - Swatches Tab

This tab is used to select a color based on color samples (swatches).

Preview The Preview area shows how the selected color appears. When you change the color, the original color appears at the top of the color box on the right.

Recent: Choose a recent color selection.

OK Click to select the color and close the dialog box.

Cancel Click to close the dialog box without changing the color.

Reset Click to change swatches, HSB, and RGB colors back to the default colors.

HSB Tab

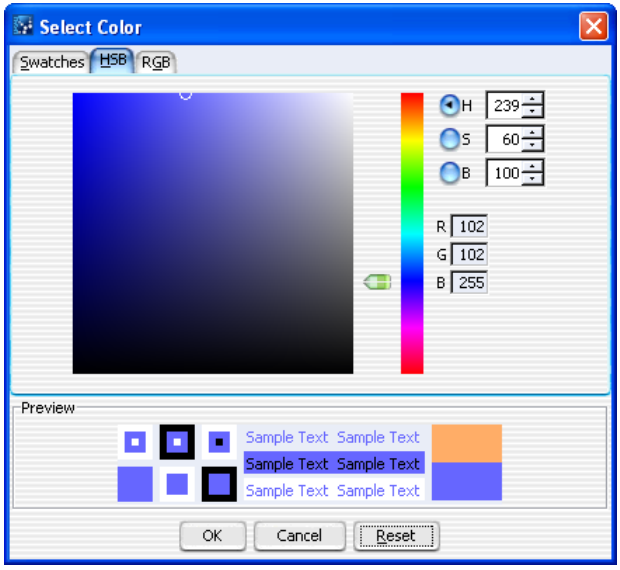


Figure 84 Select Color - HSB Tab

In this tab, you can select a color based on an HSB schema (Hue, Saturation, and Brightness).

Hue Click the **H** button, and move the slider up and down, or go up and down the list of numbers, to select the hue or color of the array.

Saturation Click the **S** button, and move the slider up and down, or go up and down the list of numbers, to select the saturation level for the color.

Brightness Click the **B** button and move the slider up and down, or go up and down the list of numbers, to select the brightness level for the color.

RGB Numbers Reflect the amount of red, green and blue in the resulting color.

Preview The Preview area shows how the selected color appears. When you change the color, the original color appears at the top of the color box on the right.

OK Click to select the color and close the dialog box.

Cancel Click to close the dialog box without changing the color.

Reset Click to change the swatches, HSB, and RGB colors back to default values.

RGB Tab

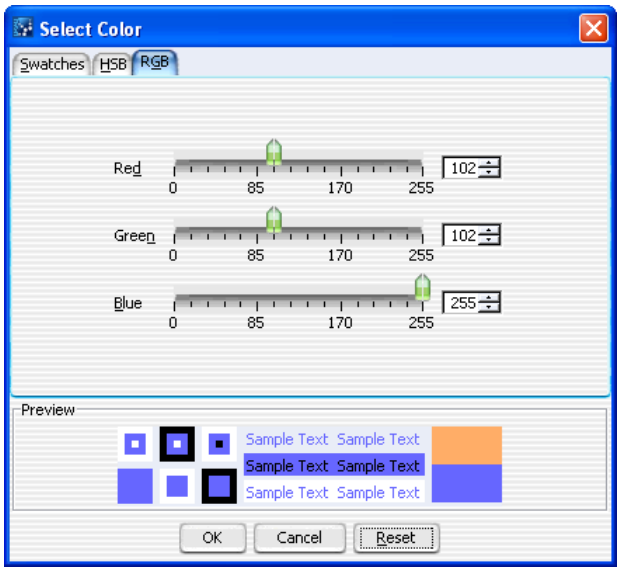


Figure 85 Select Color - RGB Tab

This tab is used to select a color based on an RGB (Red, Green Blue) schema.

Red Move the slider to change the amount of red in the color. Or, click the up or down arrow to select a number.

Green Move the slider to change the amount of green in the color. Or, click the up or down arrow to select a number.

Blue Move the slider to change the amount of blue in the color. Or, click the up or down arrow to select a number.

Preview The Preview area shows how the selected color appears. When you change the color, the original color appears at the top of the color box on the right.

OK Click to select the color and close the dialog box.

Cancel Click to close the dialog box without changing the color.

Reset Click to return the swatches, HSB, and RGB colors back to default values.

Select data type for experiments (UDF files – CGH or CH3)

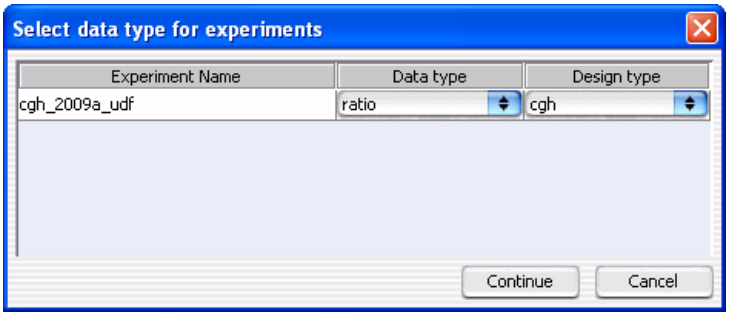


Figure 86 Select data type for experiments dialog box

Purpose: Lets you specify the mathematical form of the data in an imported UDF file, and its associated application type. See "To import a UDF file" on page 51.

To open: In the **Home** tab, click **Import > Array Files > UDF File.** In the dialog box that appears, select the desired UDF file, then click **Open.**

Experiment Name By default, the experiment name is the name of the imported UDF file. To change the name, double-click it, then edit it as desired.

Data Type Select the mathematical form of the array data in the UDF file. The options are:

- **ratio**
- **$\log_2$ ratio**
- **$\log_{10}$ ratio**
- **ln ratio** (base e)

Design type Select the application type (CGH or CH3, for example) associated with the array data in the UDF file.

Continue Accepts your selections, and goes to the next step in the UDF import process.

Cancel Cancels the UDF import.

Set genome build and species for Axon design files

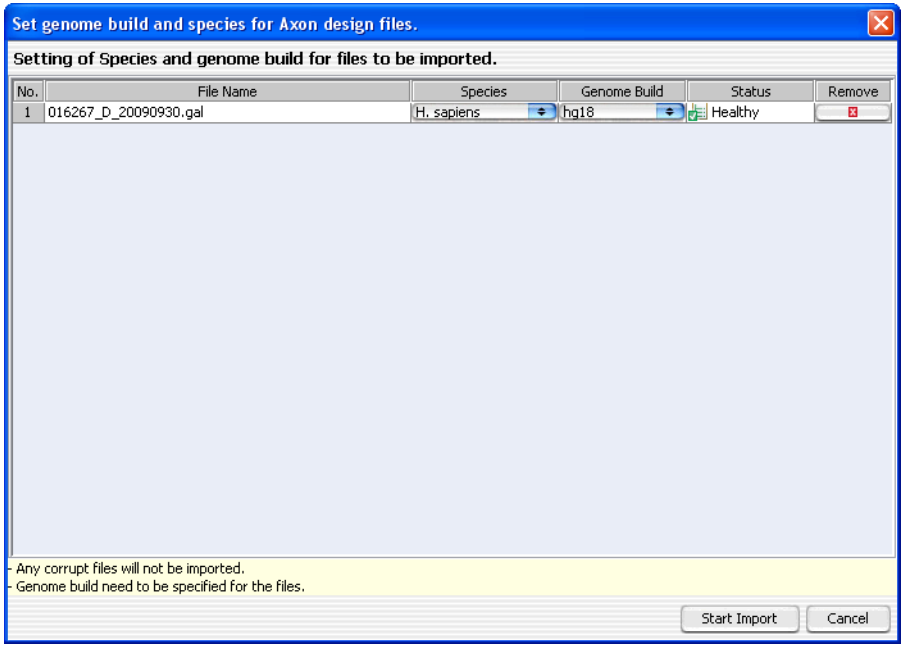


Figure 87 Set genome build and species for Axon design files dialog box

Purpose: Lets you set the species and genome builds associated with imported Axon design file(s), and to remove specific designs files from the import, if necessary. See "To import Axon design files" on page 49.

To open: In the **Home** tab, click **Import > Design Files > Axon File.** In the dialog box that appears, select at least one Axon design file, then click **Import.**

No. An index number within the dialog box for each Axon file.

File Name The names of each Axon design file selected for import.

Species The species associated with each design file. If a species is incorrect, select the correct one from the appropriate list.

Genome Build The genome build associated with each of the design files. If a genome build is incorrect, select the correct one from the appropriate list.

Status The status of the file is one of the following:

- **Valid** – The file is a new file that can be imported.
- **Overwrite** – The file is a valid design file, but when you import it, it will replace an existing design that has the same name.
- **Corrupt** – The file failed validation. When you start the import process, the program ignores the file.

Remove Click  to remove a specific design file from the list. This can be useful if you select a design file in error, or if you do not want to overwrite an existing one.

Start Import Imports the file(s) and closes the dialog box.

Cancel Cancels the import and closes the dialog box.

Show/Hide Columns

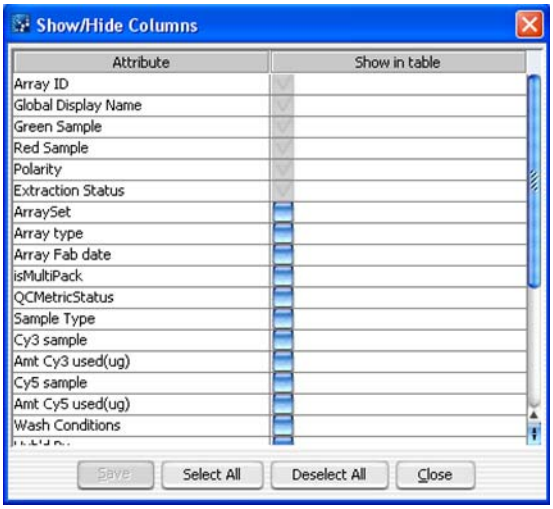


Figure 88 Show/Hide Columns dialog box

Purpose: Used to select the attributes to be displayed in the Experiment Attributes dialog box and the Sample Utility tab. The Sample Utility tab is available when you go to Sample Manager. See the *Sample Manager User Guide* for information about Sample Manager.

To open: This dialog box appears when you click **Show/Hide Attributes** at the bottom of the Experiment Attributes dialog box.

All available attributes are shown in the Attributes column. Attributes with a check-mark next to them will be displayed in the Experiment Attributes and Sample Utilities tab for each sample. To select an attribute for display, mark the **Show in Table** box next to it. To deselect an attribute, clear the **Show in Table** box again.

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

Select All Selects all the attributes in the list.

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

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

Simple HD Probe Search

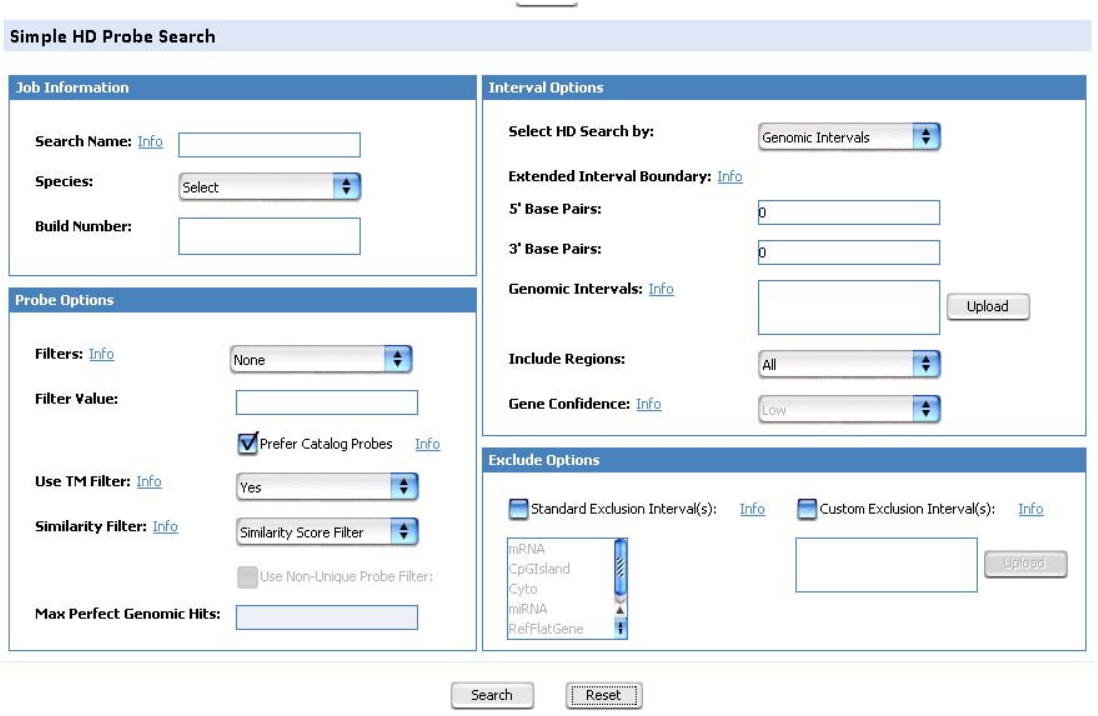


Figure 89 Simple HD Probe Search pane in the Search tab

Purpose: Lets you set up and submit a Simple HD Probe Search job to the eArray Web site. Two main options are available for this type of search:

- **Simple Genomic Intervals HD Searc**h – (Available for CGH, ChIP-on-chip, and methylation applications) Retrieves probes from the Agilent HD probe database on the eArray Web site based on genomic coordinates that you enter.

- **Simple Gene Annotations HD Search** – (Available for the CGH application type) Retrieves probes from the Agilent HD probe database on the eArray Web site based on gene annotations that you enter, such as gene symbols or GenBank accession numbers.

NOTE For more information on search functions for the eArray Web site, see the *eArray$_{XD}$ User Guide*.

To open: Right-click in the Gene View, and select **Simple HD Search.**

Search Parameters

The table below describes the search parameters that can appear. You **must** set the **Search Name,** the **Species,** the **Select HD Search by** setting, and one or more **Genomic Intervals** or **Gene Annotations.** All other parameters are optional, or can be left as is.

Parameter	Instructions/Details
Job Information	
Search Name	Type a name that will help you to identify this search job and its results.
Species	Select the desired species. The species that appear in the list reflect the species available in the HD probe database for your application type.
Build Number	(Read-only) The name of the applicable genome build for the selected species. The HD probe database only contains probes designed to the most current genome build for each species.

Parameter	Instructions/Details
Probe Options	
Filters	Select one of the options below. If relevant, type a value for the filter in **FIlter Value.** Filters restrict the list of returned probes, based on specific criteria. • **None** – The search does not apply any of the filters in the list. • **Average Spacing** – In **Filter Value,** type the desired number of base pairs. This defines the average number of base pairs between the centers of the retrieved probes in each genomic interval. • **Probes Per Interval** – In **Filter Value,** type the desired number of probes. This defines the maximum number of probes that HD Search retrieves for each genomic interval. • **Total Probes** – In **Filter Value,** type the desired number of probes. This defines the total number of probes HD Search collectively retrieves for all specified genomic intervals.
Filter Value	(Available if you select a filter) Type the desired value for your selected filter.
Prefer Catalog Probes	(Available for HD-CGH probe searches, if you select a filter) To give preference to Agilent catalog probes in the probe selection process, mark this check box. If two probes are close to each other for a given probe interval, HD search selects the Agilent catalog probe.
Use TM Filter	Removes probes with T_ms that produce unsatisfactory results on the Agilent platform. The search always applies this filter.
Similarity Filter	The options below can appear. The availability of specific options depends on species and application type. • **No Filter** – The program does not apply a similarity filter. If you select this option, the Use Non-Unique Probe Filter check box becomes available (see below). Non-unique probes map to more than one location in the target genome. • **Perfect Match Filter** – Removes a probe from the search results if it has more than one perfect match in the genome of the selected species. • **Similarity Score Filter** – Removes a probe from the search results if it is designed to a given genomic region, but it also has significant similarity to other parts of the target genome. Probes such as this can cause cross-hybridization problems.

Parameter	Instructions/Details
Use Non-Unique Probe Filter	(Available if you select no similarity filter) Mark this check box to remove a probe if it maps to multiple locations in the target genome. You can set the stringency of this filter. See below, "Max Perfect Genomic Hits".
Max Perfect Genomic Hits	(Available if you select no similarity filter, and mark **Use Non-Unique Probe Filter**) Sets the maximum number of locations to which a probe can map in the target genome, and still pass the non-unique probes filter. Type the desired number of locations. **Example:** Probe A maps to two locations in the target genome, and Probe B maps to three locations. You select **No Filter** in Similarity Filter, mark **Use Non-Unique Probe Filter,** and type `2` in Max Perfect Genomic Hits. The filter removes Probe B, but does not remove Probe A.
Interval Options	
Select HD Search by	**Genomic Intervals** – Sets up the search to retrieve probes based on genomic intervals that you enter. **Gene Annotations** – Sets up the search to retrieve probes based on gene annotations that you enter, such as gene symbols or GenBank accession numbers.
Extend Interval Boundary	Type the number of 5' base pairs and 3' base pairs by which to move out the start and end points of all of your genomic intervals. This can help retrieve additional probes that lie outside the initially defined regions of your genomic intervals. **Example:** You type `500` in 5' base pairs and `300` in 3' base pairs. eArray extends an original interval of 9000–10000 to 8500–10300.
Genomic Intervals	(Available if you select **Genomic Intervals** in Select HD Search By) Type either a chromosomal location or a cytoband in the box. Separate multiple intervals with pipe "|" characters. All of the intervals must be of the same type. For information about how to enter genomic intervals, see the *eArray$_{XD}$ User Guide*. **Upload** – Opens a File Upload dialog box, where you can upload a file of chromosomal locations or cytobands.

Parameter	Instructions/Details
Gene Annotations	(Available if you select **Gene Annotations** in Select HD Search By) Type a gene annotation such as a GenBank accession number (for example, NM_016660 or AY884282) or a gene symbol (for example, H3N2 or CTSB) in the box. Use pipe "|" characters to separate multiple annotations. eArray resolves annotations to genomic intervals before it starts your search. **Upload** – Opens a File Upload dialog box, where you can upload a *.txt file of gene annotations. In the file, list one accession or gene symbol per line. In a given search, the annotations must all be of the same type.
Include Regions	(Available only for HD-CGH searches) Select one of the options below. You can use this parameter to limit your HD-CGH probe search to only exonic, or only intragenic regions of the genome. • **All** – Retrieves probes in all of the specified genomic region, both within and outside of gene boundaries. • **Exonic** – Retrieves probes in exonic sequences within genes in the specified genomic region. When you select this option, the Gene Confidence list becomes available. Select the appropriate Gene Confidence. See below. • **Intragenic** – Retrieves probes found within gene boundaries, whether or not they are found in exonic sequences. When you select this option, the Gene Confidence list becomes available. Select the appropriate Gene Confidence.
Gene Confidence	(Available if you select **Exonic** or **Intragenic** in Include Regions. See above, "Include Regions.") Select the desired gene confidence level. This level reflects the relative confidence in the source defining the gene boundaries. For example, High confidence genes have known proteins defined for them. If you set Gene Confidence to **Low,** the search returns all High and Medium confidence genes as well as ESTs and predicted genes.

Parameter	Instructions/Details
Exclude Options	
Standard Exclusion Interval(s)	eArray lets you select from among many sets of standard exclusion intervals, based on annotation tracks. To ignore genomic regions defined in one or more of these sets, mark this option, then select the desired set(s) from the list that appears. Control-click the names of additional sets to select them.
Custom Exclusion Interval(s)	To ignore the genomic intervals defined in a file of genomic intervals, mark this option. **Upload** – Opens a File Upload dialog box, where you can upload a file of the desired genomic intervals. You can set both standard and custom exclusion intervals in the same search.

Search Submits the search job to the eArray Web site.

Reset Clears all parameters, or restores them to their default values.

Track

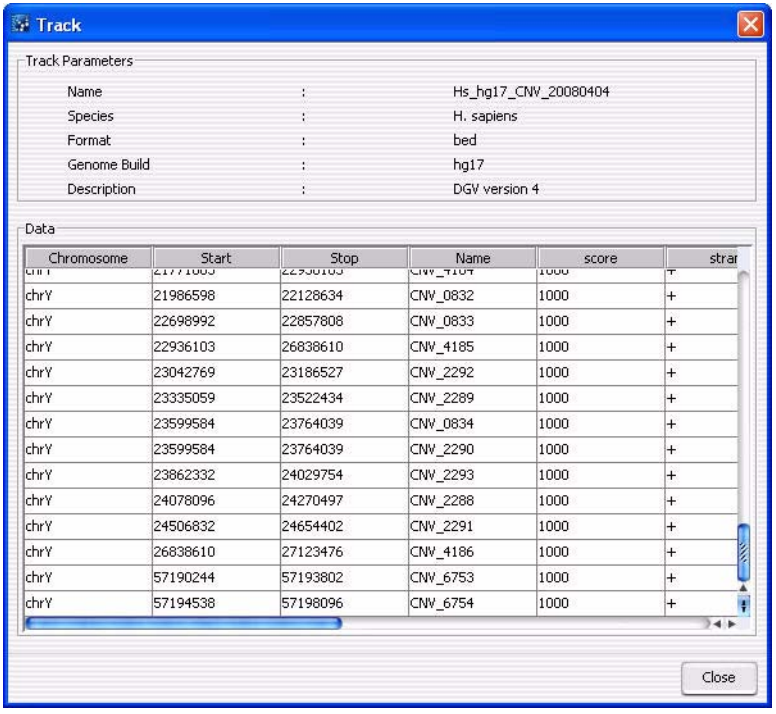


Figure 90 Track details

Purpose: This dialog box lets you view the chromosome locations in the track.

To open: Click the **Details** link for the desired track in the **Tracks** tab of the Preferences dialog box. See "User Preferences" on page 250.

Track Parameters These parameters appear:

Parameter	Description
Name	The name of the track.
Species	The species to which the track applies.

Parameter	Description
Format	The format of the track data. Agilent Genomic Workbench supports the BED format.
Genome Build	The specific genome build of the species to which the track applies.
Description	Descriptive text saved with the track.

Data Tracks must contain entries for at least these four columns in the table:

Column	Description
Chromosome	The name of the chromosome
Start	The first base pair of the particular feature in the chromosome.
Stop	The last base pair of the particular feature in the chromosome.
Name	The name of the feature. This name appears next to the defined region for the feature.

The other columns are additional BED track file columns that can appear for some tracks. Agilent Genomic Workbench does not display these.

Close Closes the Track dialog box.

UDF Import Summary (CGH or CH3)

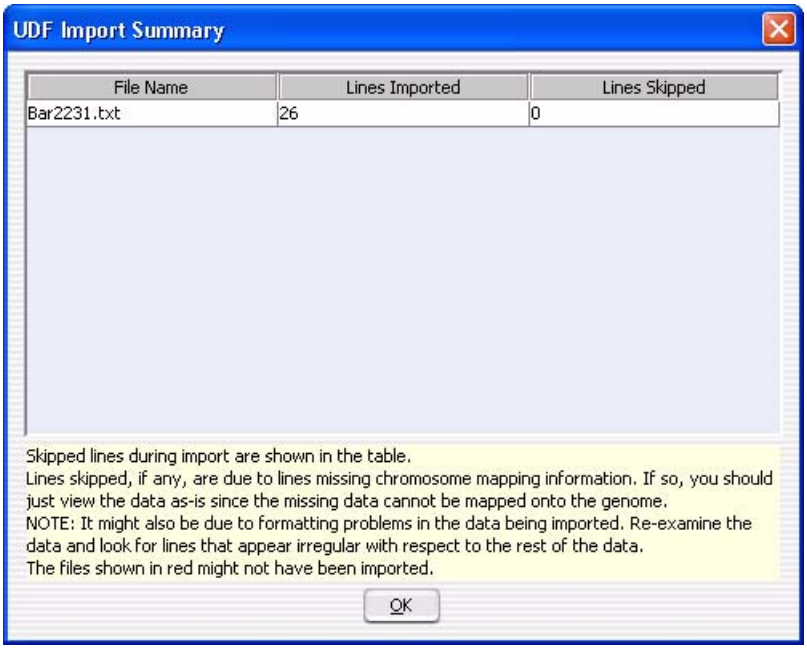


Figure 91 UDF Import Summary dialog box

Purpose: Reports how many lines of data were successfully imported from a UDF file, and how many lines were skipped. Skipped lines can be caused by missing chromosome mapping information, or improper formatting of the UDF file.

To open: Import a UDF file (see "To import a UDF file" on page 51). This dialog box appears after you map the columns of the UDF file.

Table Displays the file name of the imported UDF file, the number of lines that were successfully imported, and the number of lines, if any, that were skipped during import. If many lines were skipped, review the data for improper formatting or missing chromosome mapping information.

OK Closes the dialog box.

Universal Data Importer - Map Column Headers

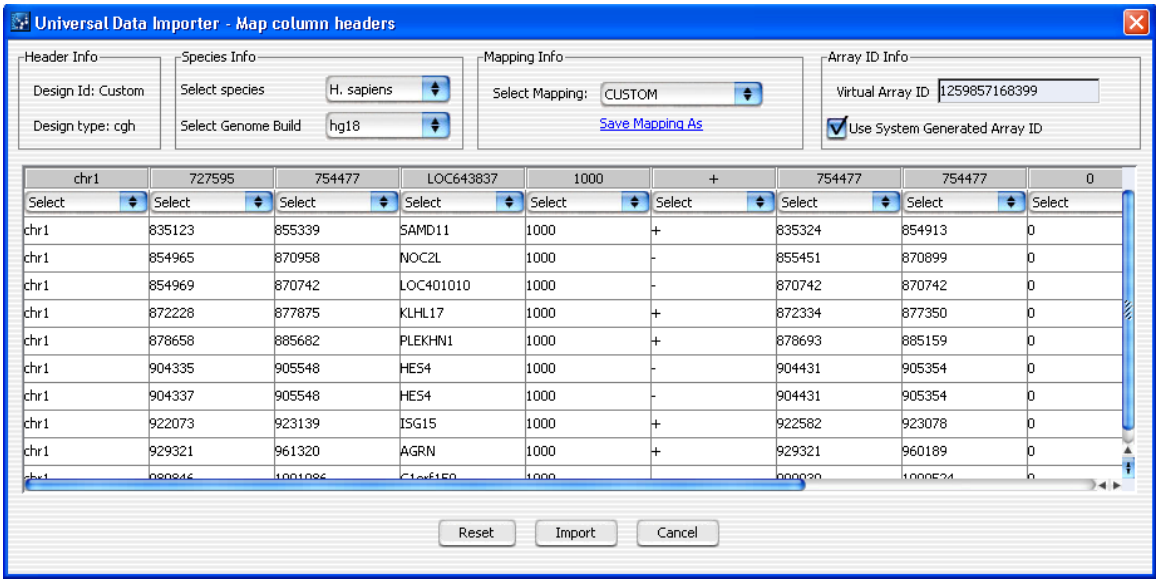


Figure 92 Universal Data Importer - Map Column Headers dialog box

Purpose: Lets you set up a universal data file (UDF) for import. You define several properties associated with the UDF, and identify the contents of each column of data in the file. You can also save column mappings for re-use.

To open: As you go through the UDF import process (see "To import a UDF file" on page 51), in the Select data type for experiments dialog box, click **Continue.** See "Select data type for experiments (UDF files – CGH or CH3)" on page 235.

Species Info

Select Species Select the species associated with the array data in the UDF. The program supports these species:

Select Genome Build Sets the species-specific build to use.

Mapping Info

Select Mapping Applies an existing column map to the current UDF. A column map identifies the contents of each column of data. To create a new column map for the current UDF, select **CUSTOM.**

Save Mapping As Saves the column map under a new name. Opens an Input dialog box, where you can type a name for the new map.

ArrayID Info

Virtual Array ID A number that uniquely identifies the data in the UDF. Typically, an Agilent microarray slide has a physical Array ID that enables Agilent Genomic Workbench to track the data from the slide as it goes through the steps of an analysis workflow. A "virtual" Array ID is, by default, a system-generated ID that serves the same purpose for data from UDFs. You can also create your own virtual Array ID.

Use System Generated Barcode By default, the virtual Array ID assigned to the array data in a UDF is a number that is created by the program. To create your own Array ID, clear **Use System Generated Array ID,** then type a new number in **Virtual Array ID.**

Table

This table lets you identify the contents of the columns of data in the UDF. The first row of the table gives the column heading information from the UDF. The second row contains lists of labels that you apply to each column, and the rest of the table displays lines of data from the UDF. If the UDF contains data from Agilent CGH arrays, the column headings will exactly match the labels in the lists.

In the list below each column heading, select the applicable label. You must use each of the labels exactly once, except LogRatio, which you can use more than once. These labels are available:

Column Label	This column contains:
ProbeName	Names of probes.
ChrName	Names of chromosomes.

Column Label	This column contains:
Start	First chromosomal location for each probe.
Stop	Last chromosomal location for each probe.
Description	Text annotation for the probe.
LogRatio	Array data values that correspond to each probe. You can use this label more than once.

NOTE If you select a saved column mapping, then change or reset the column labels in the table, the program changes or resets the saved column map as well.

Reset Clears all the column labels in the second row of the table. If you have selected a saved column mapping, this command also clears the labels in the saved map.

Import Imports the UDF file with the specified parameters, and opens the UDF Import Summary dialog box (see "UDF Import Summary (CGH or CH3)" on page 247).

Cancel Cancels the import and closes the dialog box.

User Preferences

Purpose: This dialog box is used to set up preferences for display of tracks, data storage locations, and licenses.

To open: From the Home tab, click **User Preferences**. Or, right-click in the Gene View, Chromosome View, or Genome View, and click **User Preferences**.

Tracks tab

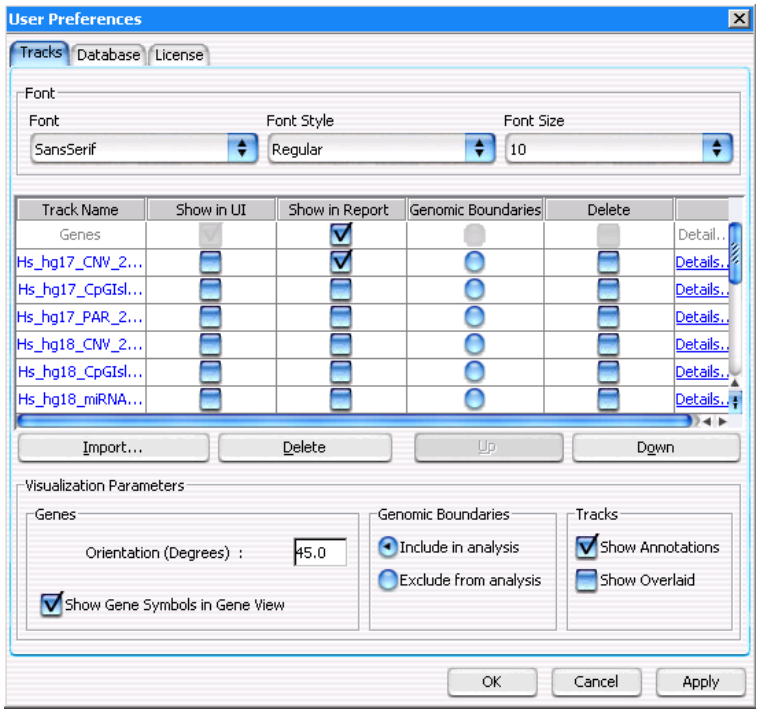


Figure 93 User Preferences dialog box - Tracks tab

Purpose: To import and set up the appearance of tracks next to the Gene View. Tracks are additional graphic displays of genomic information loaded from an external file. They align with genomic coordinates in Gene View.

To open: In the User Preferences dialog box, click the **Tracks** tab.

Font Options

Select the font type, style and size for the gene annotations that appear in the selected tracks.

Tracks List

Track Name Name of the track already loaded or imported

Show in UI Mark the check box to display the track next to Gene View.

Show in Report Mark the check box to display the track information in all the reports.

Genomic Boundaries Click to use the track to define only the regions that aberration detection algorithms will run. You can choose to do this for only one track.

Delete Mark the check box to delete the track from the list. Then, click **Delete** to delete the track from the list.

Details Click to display all the chromosome locations defined in the track.

Import Click to import new tracks.

Delete Click to delete the tracks selected in the Delete column.

Up Click to move a track up the list.

Down Click to move a track down the list.

Visualization Parameters

Genes These options affect the appearance of the Track and Gene View.

- Orientation – Type a number to set the angle at which the Gene Symbols will appear in Gene View and the Track Annotations appear in the tracks.
- Show Gene Symbols – Mark to show gene symbols in Gene View, and clear the check box to hide them.

Genomic Boundaries These options let you include or exclude the Genomic Boundaries from the analysis.

Tracks These options affect the appearance of the Track Views.

- Show Annotations – Mark to show the names of the gene regions for the tracks, and clear to hide them.
- Show Overlaid – Mark to overlay all the tracks that appear next to Gene View, and clear the check box to display the information in separate tracks.

Miscellaneous tab

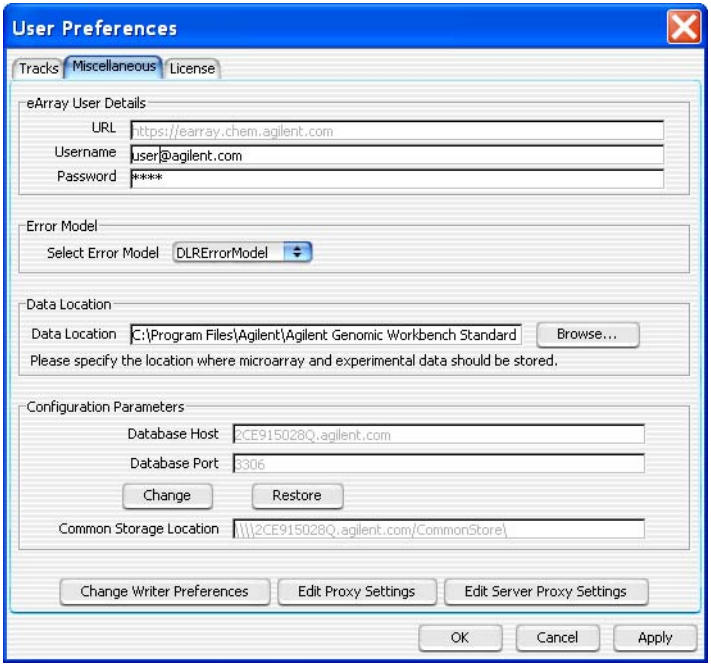


Figure 94 User Preferences dialog box – Miscellaneous tab

Purpose: For data/content set-up, this dialog box allows you to set up eArray access and to change the location for data.

To open: In the User Preferences dialog box, click the **Miscellaneous** tab.

eArray User Details Sets login details for the Agilent eArray Web site.

- **URL** – At present, https://earray.chem.agilent.com
- **Username** – The name registered on the eArray site.
- **Password** – The password registered on the eArray site.

Error Model The DLRErrorModel (Derivative Log Ratio) is the only selection. This measures noise in the data for CGH analyses.

Data Location The folder where the program stores array data and design files. To select a location, click **Browse.**

Configuration Parameters Lets you set or change location for the database server. Do not change these unless directed to do so by your network or database administrator.

- **Database host** – The fully qualified name for the computer that contains the Agilent Genomic Workbench database.
- **Database port** – The port number on which MySQL Server listens for its clients.
- **Common Storage Location** – (for display only) The location of the common file storage area used to store and access files created during various operations of Agilent Genomic Workbench. The location is set during installation of Agilent Genomic Workbench server and cannot be changed here.

Change Click to enable configuration parameters.

Restore Click to restore configuration parameters to the original settings.

Change Writer Preferences Opens the File Writer Preferences dialog box, where you select file types that eArray creates for new microarray designs (in addition to the defaults). See the *eArray$_{XD}$ User Guide* for more information.

Edit Proxy Settings Opens the Edit Proxy Settings dialog box, where you select to use a proxy and type the proxy settings to use.

Edit Server Proxy Settings Opens the Edit Server Proxy Settings dialog box, where you select to use a proxy server and type the proxy server settings to use.

Apply Applies any changes to the preferences.

OK Accepts any changes and closes the dialog box.

Cancel Cancels all changes and closes the dialog box.

License tab

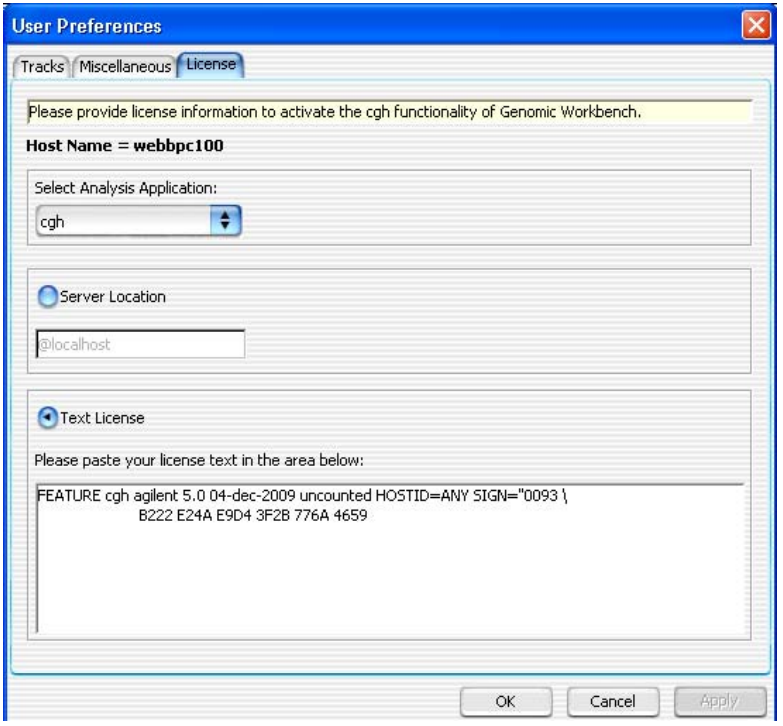


Figure 95 User Preferences dialog box – License tab

Purpose: The License tab allows you to display and update your DNA Analytics application license(s). The license enables the analysis application, and allows you to use it to analyze array data.

To open: In the User Preferences dialog box, click the **License** tab.

Host Name Displays the host computer name automatically.

Select Analysis Application Select the Agilent Genomic Workbench application for which you have a license.

Server Location Select this option if you have a concurrent user license. To edit this name, select **Server Location,** then type the name of the computer used as your license server. If you select this option, the Text License option is unavailable.

Text License Select this option if you have an application license (CGH, ChIP, CH3). To change the license, delete the old license text, and paste the new license text in the box.

OK Accepts any changes you have made, and closes the dialog box.

Cancel Closes the dialog box without changing any license information.

Apply Accepts any changes you have made, but does not close the dialog box.

View coordinates in UCSC browser

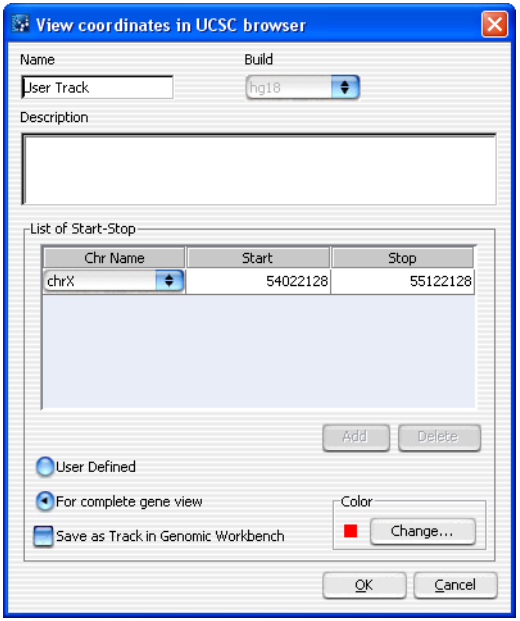


Figure 96 View coordinates in UCSC browser

Purpose: Defines a track to upload to the UCSC Web site so that you can see the information in the UCSC Genome Browser.

To open: Right-click in the Gene View, and select **Show in UCSC**.

Name Type a name for the track. This name identifies the track when it appears in lists and displays.

Build (Available if you select **User Defined** in **Set Chromosome Start-Stop.**) Select the genome build with which to associate the track.

Description Type descriptive text to attach to the track for reference.

Set Chromosome Start-Stop This parameter defines the region of the chromosome for which the track will be defined. Select one of these options:

- **User Defined** – Lets you define an arbitrary region of any chromosome. If you select this option, select the desired chromosome in **Chromosome,** then type the beginning **(Start)** and end **(Stop)** locations of the desired interval.
- **For complete gene view** – The chromosomal region that appears in Gene View.

Save as Track in Genomic Workbench Mark the check box to save this track in the Tracks folder in the My Entity List pane of the Navigator.

Change Click to open the Choose Track Color dialog box to select the color to use for display of the track in the Tracks folder. See "Select Color" on page 231.

OK Creates the track and opens the UCSC Web site, where you can display the track and associated information. For information on using the UCSC Web site, see the help and information provided there.

Cancel Closes the dialog box without creating a track.

View Preferences

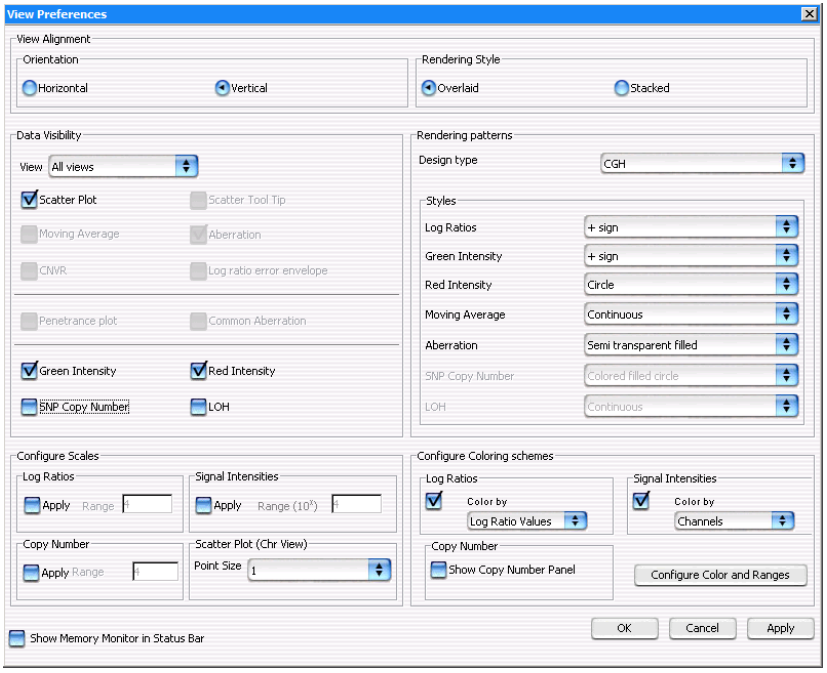


Figure 97 View Preferences dialog box for CGH

Purpose: This dialog box allows you to configure how data and results appear in Genome, Chromosome, and Gene views.

To open: In the **View** tab, click **View Preferences.**

NOTE

The View Preferences dialog box contents changes depending on what application is selected. For information on View Preferences for ChIP and CH3 applications, see the User Guide for the applicable module. Not all options are available when you do not have a license.

View Alignment Selects the orientation and rendering style (described below).

Option	Description
Orientation	
Horizontal	Stacks Genome, Chromosome, and Gene views horizontally in the main program window. Genomic locations appear across the bottom of each view.
Vertical	Displays Genome, Chromosome, and Gene views from left to right as side-by-side panes in the main program window.
Rendering Style	
Overlaid	In Chromosome View and in Gene View, displays data and results as a single, combined pane for all arrays. (Default)
Stacked	In Chromosome View and in Gene View, displays a separate pane for each array.

Data Visibility For each view, or all views, selects the kind(s) of data and results to display.

In **View,** select the view you want to configure. To set availability of display items for all views, select **All views.** Some display items are only available for certain views. When you select a display item, it enables the item for display – for some items, you must take additional steps to display them. For example, you may need to configure a specific algorithm in the toolbar.

Mark any of the following options, as available:

Display item	Description/Comments
Scatter Plot	The plot(s) of individual log ratio data points.
Scatter Tool Tip	The ToolTips that appear when you place the pointer over specific data points on the scatter plot(s) in Gene View. The tool tip shows the array of origin and the numerical log ratio value for the data point.
Moving Average	The result of the Moving Average algorithm. See the *CGH Interactive Analysis User Guide* for more information.
Aberration	The result of the selected aberration detection algorithm. See the *CGH Interactive Analysis User Guide* for more information.

Display item	Description/Comments
CNVR	Detected copy number variant regions. See the *CGH Interactive Analysis User Guide* for more information.
Log Ratio Error Envelope	The log ratio error envelope is a visual representation of the log ratio error calculated by Feature Extraction.
Penetrance plot	The probe penetrance plot for the active experiment. If you select this option, all other display items are unavailable. In addition, because the probe penetrance plot takes into account all arrays, this option overrides the *stacked* rendering style.
Common Aberration	The results of a common aberration analysis. To display this, you must first perform a common aberration analysis. See the *CGH Interactive Analysis User Guide* for more information.
Green Intensity	Mark the check box to display green raw signal intensity.
Red Intensity	Mark the check box to display red raw signal intensity.

Rendering Patterns

These options control the specific appearance of data and results in Genome, Chromosome, and Gene views. You configure these options separately for each type of application design.

- **Design Type** – Select the application design type for which you want to define rendering patterns.
- **Styles** – Select the display style for each of these elements:

Display element	Details
Scatter Plot	Select the symbol used for log ratio data points in the scatter plots in Chromosome and Gene views.

Display element	Details
Moving Average	Select the line style for the moving average display. Lines appear in the display color defined for each array. See the *CGH Interactive Analysis User Guide* for more information. • **Continuous** – A solid line. • **Dashed** – A dashed line. • **Dotted** – A dotted line. • **Do not show area** – No line.
Aberration	Select the rendering style for detected aberrations. • **Semi transparent filled** – Solid, colored regions (in the display colors defined for each array, if applicable). • **Hatched** – Cross-hatched colored lines (in the display colors defined for each array, if applicable). • **Do not show area** – Aberrations do not appear.

Scatter Plot (Chr View) Point Size Select a point size to use for display of scatter plot data points in the Chromosome View.

NOTE Rendering scatter plots for more than 10 high density arrays in the Chromosome View may take significant time. Selecting filled circles as the rendering style for CGH scatter plots can also decrease performance. For faster performance, change the rendering style for CGH data from the filled circle to the plus (+) or cross hair sign.

Configure Scales For Log Ratios or Signal Intensities plots, mark **Apply** to enable the custom scale. In Range, type the value to use as the range for the scatter plot.

Configure Coloring schemes Use these options to change the display of the scatter plot in the Gene View. These options are the same as those displayed in the Scatter Plot ToolTip in the Gene View.

Show Memory Monitor in Status Bar Displays a memory usage monitor in the eighth cell of the status bar. For information about the Status Bar, see "Status Bar" on page 161.

OK Applies the changes you made to all preferences and closes the dialog box.

Cancel Closes the dialog box without applying changes.

Apply Applies changes without closing the dialog box.

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In this book

This guide describes how to import, organize, manage, export and display data and other content within Agilent Genomic Workbench if you don't have any DNA Analytics application license(s).

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