Data Viewing

Agilent Genomic Workbench 5.0

User Guide

Agilent Technologies

Notices

Edition

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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 5.0. It is targeted for users who have no DNA Analytics application license(s). If you do have a license and intend to analyze your data, see the corresponding *User Guide*.

1 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.

2 Visualizing 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 visualize the data and content the way you prefer.

3 Data Viewing Reference

This chapter describes the parts of the Genomic Workbench main window that you use to import, organize, manage, export and display array data and other content. It also details the relevant tab commands, shortcut menus, and dialog boxes that can appear.

Contents

1 Importing, Managing, and Exporting Data and Other Content

Use this guide if you have no DNA Analytics application license(s). It does not cover any analysis, or pre- or post-analysis tasks. 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.

To find out how to display log ratio data from imported feature extraction data files, as well as gene and track content, in the Genomic Viewer, see Chapter 2, “Visualizing Data and Other Content”.

To learn about the options for the main window and the dialog boxes for importing, organizing, managing and exporting data, see Chapter 3, “Data Viewing Reference”.

See the *Agilent Genomic Workbench 5.0 Quick Start Guide* for an overview of all the applications you can use with this software, both those that require a license and those that are free capabilities.

Importing Files

You can use the Home tab to import many kinds of files into 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.

Type of file	Comments	See these topics
Microarray data files	• Agilent Feature Extraction (*.txt) data files • GenePix/Axon (*.gpr) data files • Universal Data Files (UDFs) (*.txt files)	"To import Agilent FE or GenePix/Axon data files" on page 13 "To import a UDF file" on page 15
Microarray design files	• Agilent GEML (*.xml) design files • GenePix/Axon (*.gal) design files	"To import Agilent GEML design files" on page 18 "To import GenePix/Axon design files" on page 19
Genome builds	Agilent-supplied genome information for human, mouse and rat genomes	"To import a genome build" on page 19
Tracks	BED format annotation track files	"To import tracks" on page 20
Array attributes	.txt files that you have created yourself or previously exported from Agilent Genomic Workbench	"To import array attributes" on page 22
Experiments	ZIP format file of experiments exported from DNA Analytics	"To import an experiment file" on page 23

NOTE To import Attribute Files, you use the **Sample Manager** tab. See the *Sample Manager Guide*.

To select a new location for data files

By default, the program stores design, data and experiment files in C:\Program Files\Agilent\Genomic Workbench Standard (or Enterprise) Edition 5.0\data. If you like, you can select a different location.

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

The Preferences dialog box appears. See "Preferences – Miscellaneous" on page 163.

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 Preferences dialog box, in Data Location.

4 Click **OK.**

To import Agilent FE or GenePix/Axon data files

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

- Agilent Feature Extraction (FE) *.txt data files
- GenePix/Axon (*.gpr) data files
- Universal Data Files (UDFs) (*.txt files) See "To import a UDF file" on page 15 for instructions on how to import this file type.

If you import Agilent Feature Extraction files, the program requires the representative GEML array design files. If you import GenePix/Axon data files, the program requires the representative GenePix/Axon *.gal design files. See "To import Agilent GEML design files" on page 18 or "To import GenePix/Axon design files" on page 19.

1 In the Home tab, do one of the following:

- To import Agilent FE data files, click **Import > Array Files > FE File...**
- To import GenePix/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 147.

2 To select a file for import, click its name. To select additional files, control-click their names.

3 Do one of the following:

- For Agilent FE files, click **Open.**
- For GenePix/Axon files, click **Import.**

In either case, the Agilent Feature Extraction Importer dialog box appears. See "Agilent Feature Extraction Importer" on page 104.

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, as desired. **c** Press **Enter (Return** on a Mac).
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 ration (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 allows you to work 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:

- 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 provide during import, and the information in the file itself. This design contains all of the arrays represented in the file. The program also creates and populates 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 147. Only *.txt files appear in the dialog box.

2 Select the desired 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 174.

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 as desired. **c** Press **Enter.**

Setting	Comments
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 180.

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 Barcode" that becomes the Chip Barcode attribute for the array(s) in the UDF. To substitute a Virtual Barcode of your own choosing, follow these steps:

   a Under **Barcode Info,** clear **Use System Generated Barcode.**

   b Double-click the number in **Virtual Barcode,** then type the desired new Virtual Barcode.

9 Click **Import**.

   The program validates your column mapping. A dialog box appears. If you need to fix the column map, the dialog box details 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. Control-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 lists 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 179.

11 Click **OK.**

In the Data pane, in the appropriate design type folder within the 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, populated with array data. This experiment bears the name of the imported UDF file, unless you changed it during import.

To import Agilent GEML design files

You must import Agilent GEML (*.xml) microarray design files into Genomic Workbench that match the Agilent Feature Extraction data files. Your imported GEML files contain array-specific information such as probe names, annotations, and chromosomal locations, and are associated with a specific genome build.

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

The Import Design Files dialog box appears. See "Import" on page 147. The dialog box shows only *.xml files.

2 To select a file for import, click its name. To select additional files, control-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 150.

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 its **Remove** button  .

4 Click **Start Import.**

The program imports the file(s). The files appear as new design folders in the Data folder 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. If you do, the program creates a single design folder with two nodes, one for each genome build.

To import GenePix/Axon design files

You can import GenePix/Axon (*.gal) microarray design files into Genomic Workbench. The program requires the GenePix/Axon design files that match all GenePix/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 147. The dialog box shows only *.gal files.

2 To select a file for import, click its name. To select additional files, control-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 175.

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 its **Remove** button  .

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 Data folder of the Data pane, organized by application (CGH, ChIP, or methylation, for example).

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 151.

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 desired file, then click **Open.**
Cyto-band File	This file contains the graphic information on the cyto-bands for Genome and Chromosome Views. **a** Click **Browse...** A dialog box appears. **b** Select the desired file, then click **Open.**

3 Click **OK.**

To import tracks

You can import BED format track files into DNA Analytics. 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 152.

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 57.

To import array attributes

An array attributes file is a tab-delimited *.txt file that contains a list of arrays by barcode, 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 much more easily. See the *Sample Manager User Guide*. This menu item will be eliminated from the next version of the program, and the only way to import array attributes will be through the Sample Manager application.

To import an array attributes file

1 Click **File > Import > ArrayAttributes.**

The Import microarray attributes dialog box appears. See "Import" on page 147.

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

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

Array attributes files must follow these guidelines:

- The first line of the file contains the names of array attributes, separated by tabs.
- The first attribute must be `Chip Barcode`.
- The rest of the lines of the file list the values of each attribute, one line per array. The order of attribute values must follow the order of attributes in the first line of the file.

Here is an example.

Chip Barcode	ArraySet	Hyb'd By
251270010402	E986	Maurice R.
251270010423	E986	Maurice R.
251270019455	E986	Maurice R.

To import an experiment file

In Genomic Workbench, an experiment is a set of links to microarray data and design files, and any associated results. A Genomic Workbench experiment file is a single ZIP file that contains the design and data files associated with one or many experiments. You can import experiment files created in Genomic Workbench on another computer, as well as DNAx 4.0 experiments.

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

The Import Experiments dialog box appears. See "Import" on page 147.

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 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, populated with the appropriate arrays, in the Experiment pane.

NOTE

Genomic Workbench experiment files contain all of the design and array data files associated with 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 38.

Working with Experiments to Organize Imported Data

This section describes how to arrange imported array data and designs into organizational units called *experiments*. Experiments, found in the Experiment pane of the Navigator, contain links to specific array data and design files in the 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 contain saved experiment results.

To view the array designs and data in the program

- To view the directory of data in the program, use the Data pane (Figure 1). Double-click a folder to expand or collapse it, or click the ⊞ and ⊟ buttons.

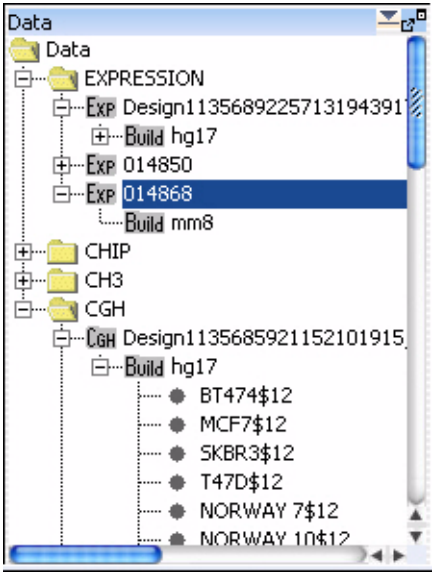


Figure 1 Data pane of the Navigator

In the 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 Data pane to open shortcut menus. For details, see "Data pane – actions and shortcut menus" on page 79.

Many icons can appear in the Data pane. See "Data pane – icons, special text, and buttons" on page 78 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 30.

To create a new experiment

To view or analyze data, you must first create an experiment and associate the desired data files with it.

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

The Create Experiment dialog box appears. See "Create Experiment" on page 119.

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 26.

- To create an experiment and populate it with data now, follow these steps: (You can add or remove data from the experiment later, as well.)

  a Click **Properties.**
  The Experiment Properties dialog box appears. See "Experiment Properties" on page 133.

  b Under **Select Design,** select the design and genome build associated with the desired 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. Control-click the names of additional arrays.

  d 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 133 for details.

  e Click **OK.**
  The program creates the new experiment, and populates it with the selected arrays.

In both cases, a folder with the name of the new experiment appears in the Experiment pane.

To add arrays to an experiment

After you create an experiment, or import one, you can add arrays to it.

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

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

The Experiment Properties dialog box appears. See "Experiment Properties" on page 133.

3 Under **Select Design,** select the design file and genome build associated with the arrays you wish to add.

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

4 In **Array List,** select the arrays you wish to add to the experiment. To select a single array, click its name. To select additional arrays, control-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 133 for details.

6 Click **OK.**

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

You can change the order in which arrays appear in an experiment in tables in Tab View. If you choose to display separate scatter plots in Gene View and Chromosome View for each array, the array order also determines the order in which these plots appear.

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

The Edit Array Order dialog box appears. See "Edit Array Order" on page 132.

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 desired attribute in **Order by.**

4 Click **OK.**

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 given experiment. The name of the array remains unchanged in the Data pane, and in other experiments.

1. Expand the folders in the **Experiment** pane until you can see the array you wish to rename.
2. Right-click the name of the desired array, then click **Rename.**

   An Input dialog box appears.
3. Type the new name for the array, then click **OK.**

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 remain 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 33.

1. In the **Experiment** pane, expand folders until you can see the desired experiment, and the array(s) that you want to remove from it.
2. In the **Arrays** or **Calibration Arrays** folder of the desired experiment, click the name of an array to select if for removal. Control-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 edit the attribute values of a specific array

Array attributes are pieces of array-specific information such as chip barcode or hybridization temperature. You can view a list of attributes for each array that is available in the program.

1 Expand the folders of the **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 - Attribute Tab" on page 154. You can also edit the attributes of a specific array from this dialog box. In addition, if the array is an Agilent array, you can view header and feature information passed through 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 (Data, Gene Lists, Tracks)

This section describes how to create, find, rename, update, combine, and/or remove several types of content stored in Genomic Workbench. To display the data, gene list and track content, see Chapter 2, "Visualizing Data and Other Content".

To view a list of the content stored in the program

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

Data pane – Shows all of the array data files stored in the program, organized by application (CGH, ChIP, or methylation, for example), then by array design, then by applicable genome build. For more information, see "To view the array designs and data in the program" on page 24.

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.

NOTE Content that is available 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 76.

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.

2 By default, the program searches all panes of the Navigator. To restrict 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 retrieved items.

4 To clear the results of a search, click .

To view 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 **Data** pane until you can see the genome build folder(s) within the desired design folder.

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

The Design Properties dialog box appears. See "Design Properties" on page 125.

To update probe annotation in design files

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

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

The Preferences dialog box appears.

2 In the Miscellaneous tab, under **eArray User Details,** type your eArray **Username** and **Password.** See "Preferences – Miscellaneous" on page 163.

3 Click **OK.**

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

5 Right-click the desired design, then click **Update from eArray.** 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 Data pane

This topic describes how to rename an array in the Data pane.

1 Expand the folders of the **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.

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. However, the name of the array is unaffected 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 28.

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 28.

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

3 Do one of the following:

- For array data files, click the name of the first array, then control-click the names of additional arrays within the same design.
- For array design folders, click the name of the first design folder, then control-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 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 desired chromosomal region, skip to step 2.

   a In Genome View, select the desired chromosome.
   The selected chromosome appears in Chromosome View.

   b In Chromosome View, in the plotting area to the right of the chromosome, drag the pointer over the approximate desired chromosomal region.
   The program encloses the region in a blue box, 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 92.

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 121.

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

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

5 Click **OK.**

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

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 that you want to rename.

2 Right-click the desired 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, expand the **Gene List** folder.

2 Click the name of a gene list that you want to delete. Control-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, but only for the CGH application.

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

a In Genome View, select the desired chromosome.
The selected chromosome appears in Chromosome View.

b In Chromosome View, in the plotting area to the right of the chromosome, drag the pointer over the approximate desired chromosomal region.
The program encloses the region in a blue box, 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 92.

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

The Create Track dialog box appears. See "Create Track (CGH only)" on page 123.

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

4 In the dialog box select the desired 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 view the details of a track

The table that you bring up 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 177.

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 that you want to rename.

2 Right-click the desired 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 that you want to delete. Control-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.**

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 that you choose. You first select the arrays and then the attributes that you want exported for your array selection. You can access this capability from the Home tab or 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 – Array" on page 137.

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

2 Under **Select Design,** select the design file and genome build associated with the arrays you wish to add.

The arrays associated with 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, control-click their names.

4 Click > .

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

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

The Export Array Attributes dialog box appears with the Attribute tab displayed. See "Export Array Attributes – Attribute" on page 139.

All of the attributes for the arrays are already located in the Selected Attribute List. If you don't want all the attributes exported, then you must transfer those to the Available List.

6 In the Selected Attributes List, highlight those attributes you do not intend to export.

7 Click  .

8 Click **OK**.

The Export dialog box appears. See "Export" on page 135.

9 Select the folder in which to locate 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 141.

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

3 In **Export Format,** select one of these options:

- **5.0 Format** – Exports the experiment(s) in a format that you can import into Genomic Workbench. This is the most current experiment format, but it is not compatible with previous versions of the program.
- **3.0 Format** – Exports the experiment(s) in a format that you can import into Agilent CGH Analytics 3.0 or later. This is a "legacy" format that you can use to maintain compatibility with earlier versions of the program.

4 Click **OK.**

An Export dialog box appears. See "Export" on page 135.

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

6 Click **Export.**

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

To export filters (CGH only)

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

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

The Export Filters dialog box appears. See "Export Filters (CGH only)" on page 142.

2 Under **Export,** mark the check boxes beside the filter(s) that you want 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 success message appears.

4 Click **OK.**

To export tracks

You can export selected tracks as a BED format track file. You can then import this file into 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 144.

2 Mark the tracks that you want 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 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.

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 Word or PowerPoint.

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

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

The Edit Array Color dialog box appears. See "Edit Array Color" on page 131.

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) associated with the design you want to export.

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

A dialog box appears.

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

2 Visualizing 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 modify the display to visualize the data and content the way you prefer.

To find out how to import, organize, manage and export data and other content, Chapter 1, “Importing, Managing, and Exporting Data and Other Content”.

To learn about the options for the main window and the dialog boxes for visualizing data, see Chapter 3, “Data Viewing Reference”.

See the *Agilent Genomic Workbench 5.0 Quick Start Guide* for an overview of all the applications you can use with this software, both those that require a license and those that are free capabilities.

Activating an Experiment for Visualizing Data

An experiment is a set of links to microarray data and design files, and any associated results.

When you activate an experiment and have no DNA Analytics application license, the program shows the log ratio data of selected arrays in the active experiment, if certain options have been set.

When you activate 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, if certain options have been set.

This section describes how to activate an experiment and select or deselect arrays for further viewing.

To activate an experiment

When you make an experiment active, the program displays log ratio data in a scatter plot, provided it has been turned on.

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 populate it with data. See "To create a new experiment" on page 25.
- Import a saved DNA Analytics 4.0 CGH experiment. See "To import an experiment file" on page 23.

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 details on the available tabs, see "To search Tab View for specific probe information" on page 61.

To select or deselect arrays in the experiment

To include arrays for viewing, you select them from among 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 any more arrays for viewing, only the first one will be displayed when the experiment is activated.

To select the arrays for viewing before experiment activation:

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 activation.

In the Navigator, an array's icon has two appearances after experiment activation:

Array not selected.

Array selected. The specific color matches the color of the column headings for the array in Tab View. 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 46.

To select or deselect arrays in an *active* experiment:

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

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

To include additional arrays, control-click their names. To include a contiguous block of arrays, click the name of the first array in the block, then shift-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 re-analyzes the data set within the experiment and posts the data in Genome, Chromosome, and Gene Views. You can see the data and results for just the selected arrays in the Selected Arrays tab in Tab View.

To customize the appearance of the results in Genome, Chromosome, and Gene Views, see the *Data Viewing Guide*.

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.
- Control-click a column heading to select or deselect an array without affecting the status of other arrays.
- Right-click a column heading to open a shortcut menu with options that allow you to select or deselect that array, or all arrays.

For more details on Tab View, see "Tab View" on page 98.

To change the display color of an array

The color assigned to an array affects the color of its icon when you select the array within an experiment. It also affects 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 whose color you want to edit.
2. Right-click the desired array, then click **Edit Array Color...**

   The Select Color dialog box appears. The dialog box offers three different ways to choose the desired color. "Select Color (Edit Array Color) — Swatches Tab" on page 171.
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 duplicate 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 duplicate 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 details on the dialog box that appears, see "Edit Array Color" on page 131.

Visualizing Array Data

After you activate 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

1 In the Gene View, move your cursor over the down arrow in **Scatter Plot,** and do any of the following:

To do this	Follow these steps
Show or hide all log ratio data points	• To show all data points – Mark the **Log Ratio** check boxes • To hide all data points – Clear the **Log Ratio** check boxes.
Show or hide all raw intensity (CGH) or intensity ratio (ChIP) data points	• To show all data points – Mark all three check boxes for **Raw Intensity** or the one for **Intensity Ratio.** • To hide all data points – Clear all three check boxes for **Raw Intensity** or the one for **Intensity Ratio**.
Show or hide significant or insignificant data points	See "To show significant data points in a scatter plot" on page 48.
Change the size of data points	• In **Point Size,** select a size for the data points.

2 Click X to close the Scatter Plot window.

To show significant data points in a scatter plot

The CGH and CH3 applications can classify log ratio data points as significant, or not, based on a simple cutoff value. The CGH application can do this with raw intensity data points as well.

You select the cutoff value, and the program displays data points whose log ratios are above, below, or within the range of the cutoff value on the scatter plots in Gene and Chromosome Views, in three different colors.

1 In the Gene View, move your cursor over the down arrow in **Scatter Plot**.

2 In **Cutoff,** select the desired cutoff value. The cutoff is an absolute value, and it defines a range. For example, if you select a value of 1.25, the program uses a cutoff range of –1.25 to +1.25 to classify data points.

   If you select **None,** the program classifies all data points as significant.

3 Mark the kinds of points you want to appear in the scatter plot:

    – (Red) Points with log ratios above the selected cutoff range

    – (Green) Points with log ratios below the selected cutoff range

    – (Black) Points with log ratios within the selected cutoff range

4 Select the **Point Size** (in pixels) for the points in the scatter plot.

5 Click X to close the Scatter Plot window.

To change scatter plot appearance

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

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

   The Preferences dialog box appears. See "Preferences – View Tab" on page 167.

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,** in **Scatter Plot,** 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 tool tips for the scatter plot in Gene View	Tool tips 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 separate pages. Chromosomes and genes appear on the printed pages, but tracks do not.

1 Click **File > Print.**

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

To locate and view data within the Views

- To navigate 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 view	• In Genome View, click the desired chromosome. All other views switch to the selected chromosome.
View data in a region of the selected chromosome	• In Chromosome View, drag the cursor over the desired region. Gene View expands (or shrinks) to show only the selected region. Tab View scrolls to the new cursor location.
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.
Re-center Gene View or Chromosome view	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.
Center all Views on the location of a specific gene	**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.
Center Chromosome and Gene Views based on data in Tab View	• In Tab View, click any entry in any table, except a column heading. Chromosome and Gene views become centered on the genomic location corresponding to the selected entry.

To do this	Follow these steps
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 169. **b** In **Select Column,** select the desired column. **c** Click **OK.**
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 145. **b** Set the desired search parameters, then click **Find Next.** The program searches the column based on your search parameters, and highlights the row of the first entry that matches. The cursor moves to the location defined in the highlighted row.
View 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 102.

To smooth and plot CGH log ratio data

You use a plug-in to create separate, stacked plots of smoothed log ratio data for each of the selected CGH arrays in the current experiment. It 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 produce the plot immediately after clicking Plugin.

1 Activate an experiment.

2 Select the arrays whose log ratio data you want smoothed and plotted.

3 Select the chromosome whose log ratio data you want plotted.

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

The CGHSmooth Parameters dialog box appears. See "CGHSmooth Parameters" on page 106.

5 Enter 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 108.

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 110. You can also save, print, zoom in or out, or change the auto range of the plot by right-clicking the plot.

To enter parameters from the Plugin Settings command and bring up 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 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 Activate an experiment.

2 Select the arrays whose log ratio data you want plotted.

3 Select the chromosome whose log ratio data you want plotted.

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

5 Enter 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 129.

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 110. You can also save, print, zoom in or out, or change the auto range of the plot by right-clicking the plot.

To produce a MovAvg Example plot (CGH only)

The MovAvgExample plug-in computes 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, located in the Plugins folder of the 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 Activate an experiment.

2 Select the arrays whose log ratio data you want averaged and plotted.

3 Select the chromosome whose log ratio data you want plotted.

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

5 Enter 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 159.

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 110. You can also save, print, zoom in or out, or change the auto range of the plot by right-clicking the plot.

To enter parameters from the Plugin Settings command and bring up 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**.

Visualizing Content (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 restrict 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 34.

To change the appearance of genes in Gene View

You use the 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 **Preferences.**

The Preferences dialog box appears.

2 Click **Tracks**.

"Preferences – Tracks" on page 164.

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

1 Select and show microarray data. See "To activate an experiment" on page 44.

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 **Preferences.**

The Preferences dialog box appears. See "Preferences – Tracks" on page 164.

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.

Change the appearance of tracks

Within the Preferences – Tracks dialog box, you can modify the appearance of tracks in several additional ways. See 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 that falls under 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.**
View the parameters and the list of annotations of a track	• In the list of tracks, next to 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 any 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.

Show track information in reports

1 In the list of tracks, in the **Show in Report** column, mark the check boxes of the desired tracks.

2 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 that falls under that interval in that separate column.

Restrict data to the genomic boundaries of the track

1. In the list of tracks in My Entity List, right-click the track whose boundaries you want to use to restrict the display of the data.

3 Mark **Genomic Boundaries**.

You can remove the boundaries by clearing the check box.

Display tracks in UCSC Browser

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

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

2 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, activate an experiment whose data are based on a design file of a different genome build.

The display automatically changes when you activate an experiment containing 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 19.

To copy Views

You can copy panes of the main window to the clipboard as images, and then paste them into a new document in another program. The images contain only what actually appears on your screen—regions to which you must scroll are not included.

1 Click **View > Copy.**

A menu of Views appears.

2 Click the View you want to copy to the clipboard. To copy all available views as a single image, click **All.**

3 Open a document in another program that accepts images, such as a word processor or graphics program.

4 In the other program, click **Edit > Paste.**

The copied image appears.

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 98.

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 145.

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

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** – Return entries that match upper and lower case characters in the search term. ◦ **Match whole word** – Return 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, **String not found.** appears in black at the bottom of the dialog box.

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

To search Agilent eArray for probe information

You can use the chromosomal region that appears in Gene View, or another chromosomal region as the basis for a probe search on the Agilent eArray Web site. eArray is a powerful microarray design system for CGH, ChIP and gene expression applications. It contains a massive database of validated, annotated probes, and a full complement of tools for custom microarray design.

Before you can search for probes in eArray, you must be a registered eArray user. For more information, go to eArray.chem.agilent.com. You must also provide your eArray user name and password in the Miscellaneous tab of the Preferences dialog box. See "Preferences – Miscellaneous" on page 163.

1 In Gene View, right-click anywhere in the plotting area, then click **Search probes in eArray...**

   The Search probes in eArray dialog box appears. "Search probes in eArray" on page 170.

2 Do one of the following to define the chromosomal region for your search:

   - To set the region to the one that currently appears in Gene View, select **For complete gene view.**
   - To set the region numerically, select **User Defined,** then select a **Chromosome** and type **Start** and **Stop** locations for the desired region.

3 Click **OK.**

   The eArray Web portal opens in your internet browser.

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 you want 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 passes 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, DNA Analytics opens the site in your Web browser and passes 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 124.

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 pass a search string to the site. Use `<target>` as the query string value.

For example, this URL passes 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 you want 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.**

3
Data Viewing Reference

This chapter describes the parts of the Genomic Workbench main window that you use to import, organize, manage, export and display array data and other content. It also details the relevant tab commands, shortcut menus, and dialog boxes that can appear.

For specific instructions on how to use Genomic Workbench to manage data and accomplish related tasks, see Chapter 1, “Importing, Managing, and Exporting Data and Other Content.” To learn how to display data and content, see Chapter 2, “Visualizing Data and Other Content”.

To understand how all the guides work together to help you use Agilent Genomic Workbench, see the *Agilent Genomic Workbench 5.0 Quick Start Guide*.

Genomic Workbench Main Window

The sections that follow describe the main components of the 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 103.

Figure 2 shows the main window of Genomic Workbench, and identifies its main parts.

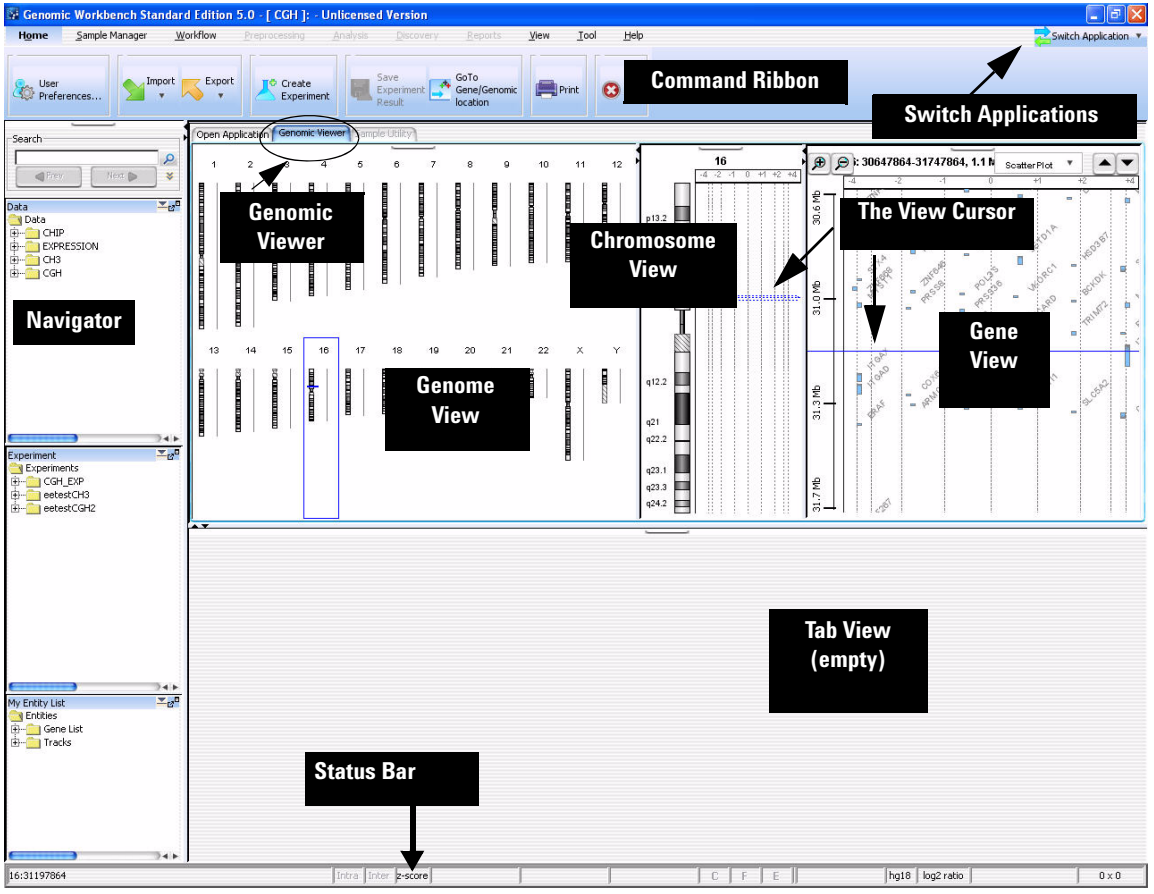


Figure 2 Genomic Workbench Standard Edition main window with Home command ribbon

Switch Application Menu

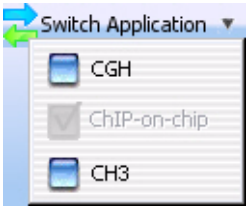


Figure 3 Switch Application menu

The Switch Application menu allows you to switch to the other data display and analysis applications in DNA Analytics. Mark the desired application.

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

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

Command Ribbons

Home command ribbon

Figure 4 Command ribbon in the Home tab of Genomic Workbench

User Preferences... Opens the User Preferences dialog box with four tabs:

Tab	Description
View	Opens a dialog box that lets you change in what form the data will appear in Genomic Viewer. See "Preferences – View Tab" on page 167.
Tracks	Opens a dialog box that lets you manage which tracks to display in Genomic Viewer and how they appear. See "Preferences – Tracks" on page 164.
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 "Preferences – Miscellaneous" on page 163.
License	Opens a dialog box where you can add a DNA Analytics application license, if you choose to purchase one after using the unlicensed version. Preferences – License 161.

Import/Export

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 147 and "To import Agilent FE or GenePix/Axon data files" on page 13. • **Axon File...** – Opens the Import Axon Files dialog box, where you can select Axon (*.gpr) files for import. See "Import" on page 147 and "To import Agilent FE or GenePix/Axon data files" on page 13. • **UDF File...** – Opens the UDF Files dialog box, where you can select a Universal Data File (UDF) to import. See "Import" on page 147 and "To import a UDF file" on page 15.
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 147 and "To import Agilent GEML design files" on page 18. • **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 147 and "To import GenePix/Axon design files" on page 19.
Genome Build...	Opens the Import Genome Build dialog box, where you can import Agilent-provided genome build files. See "Import Genome Build" on page 151 and "To import a genome build" on page 19.
Probe Upload	Allows you to import a file of probe sequences and annotation. For details, see the *eArray XD User Guide*. You see this only if you have installed Genomic Workbench Enterprise Edition.
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 152 and "To import tracks" on page 20.
Experiments	Opens the Import Experiments dialog box, where you can select a ZIP format experiment file for import. See "Import" on page 147 and "To import an experiment file" on page 23.

Export Opens a menu that allows you to 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 141 and "Click Home > Export > Array Attributes..." on page 37.
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 (CGH only)" on page 142 and "To export filters (CGH only)" on page 39.
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 144 and "To export tracks" on page 40.

Create Experiment... Opens the Create Experiment dialog box, where you can create a new, empty experiment and populate it with data. See "Create Experiment" on page 119 and "To create a new experiment" on page 25.

Save Experiment Result (Not available if you have no DNA Analytics application licenses) Saves CGH or ChIP results after analysis. Methylation results cannot be saved because reanalyzing methylation array data takes less time than bringing up saved results.

Go to Gene/Genomic Location Moves the cursor to the location in Chromosome and Gene Views that you specify. See "Go To Gene/Genomic Location" on page 146.

Print Opens the Print window to print the display.

Exit Closes the program.

View Command Ribbon

Figure 5 Command Ribbon of the View tab

Orientation Select one of these options:

- Horizontal – Stacks Genome, Chromosome, and Gene views horizontally. Chromosomes and chromosomal locations appear in left to right orientation.
- Vertical –- Stacks Genome, Chromosome, and Gene views vertically. Chromosomes and chromosomal locations appear in top to bottom orientation.

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 40.

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

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

Scatter Plot See "Scatter Plot" on page 93.

Tool command ribbon

Figure 6 Plugin command ribbon

Plug-ins are ancillary programs that process the selected array data in the active experiment in specific ways.

Plugin

Opens a menu with the options listed below. If you or another user has created custom plug-ins, they also appear in this menu.

CGHSmooth Opens the CGHSmooth Parameters dialog box. See "CGHSmooth Parameters" on page 106. 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 129.

MovAvg Example Opens the MovAvg Example Parameters dialog box. See "MovAvg Example Parameters" on page 157. 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 106.

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 157.

Help command ribbon

The Help command ribbon provides access to the Agilent Genomic Workbench Quick Start Guide and all the other user guides.

Figure 7 Help command ribbon for Genomic Workbench Standard Edition

Table 1 Table of Help for unlicensed version (Click only those ***bolded and Italicized***)

Help Command	Action
Help	Opens the DNA Analytics application user guide for which you have the associated license. CGH Interactive Analysis – Shows how to set up all preprocessing, analysis, discovery and reporting options for analyzing CGH data interactively. Includes details on the algorithms used.
Quick Start	Opens the *Agilent Genomic Workbench 5.0 Quick Start Guide* in Adobe Reader. This guide provides brief instructions on how to install and start the program, and how to use the basic features of the program to create custom microarray designs, and to analyze microarray data.
Data View	Shows you how to import, manage, export and display log ratio data from Agilent and other sources
Workflow	Gives instructions on how to set up a workflow for automated feature extraction and/or analysis. Also shows you how to set up the CGH and ChIP analysis methods to be used in a workflow.
Sample Manager	Shows you how to assign identification and attribute information to image files, imported feature extraction (FE) files or UDF files.
eArray	(***Genomic Workbench Enterprise Edition must be installed***) Gives instructions on how to design your own microarrays on your desktop, not the web site.
About	Opens a message with details about the version number and copyright of the program.

Navigator

This section describes the parts of the Navigator, and the shortcut menus and other functionality available within it.

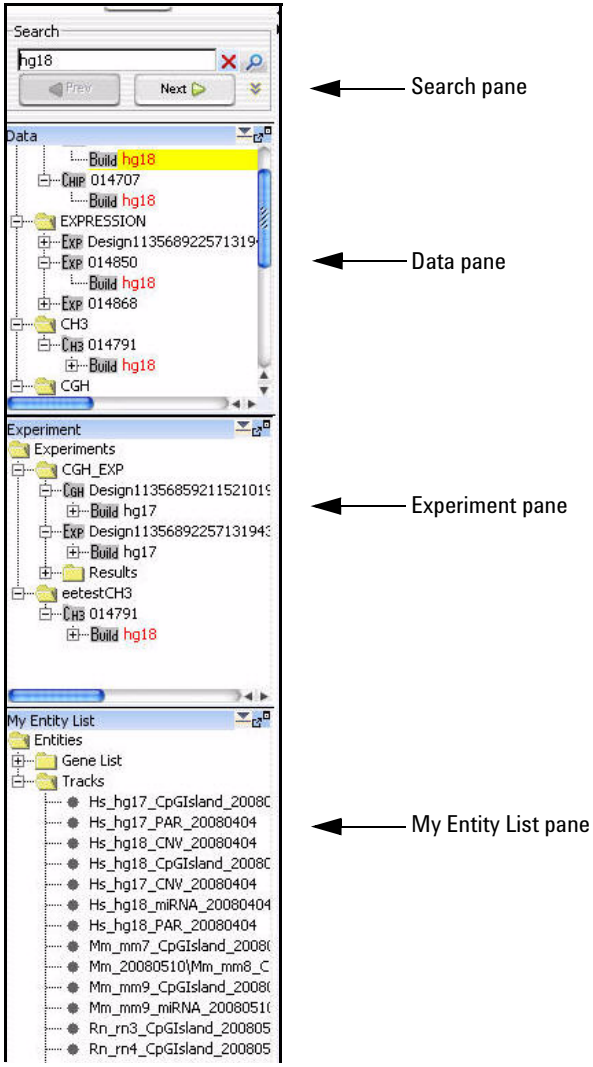


Figure 8 Navigator – note the four panes within the Navigator

The Navigator (Figure 8) catalogs the array data, experiments, and other content stored in Genomic Workbench. It contains four panes:

Pane	Comments
Search	Allows you to find all occurrences of a specific search term in the Data, Experiment, and/or My Entity List panes.
Data	Contains microarray data files, organized by application type and design, and then by genome build.
Experiment	Contains Genomic Workbench experiments. Experiments are organizational units within the program 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 is correlated with specific genomic locations. You can import, export, and combine tracks, and display them in Gene View alongside your array data and analysis results.

Search pane

The Search pane allows you to find all occurrences of a specific search term in the Data, Experiment, and/or My Entity List panes. See "To find specific content items in the Navigator" on page 30. It also contains several buttons that you can use to detach, hide, show or resize the Navigator.

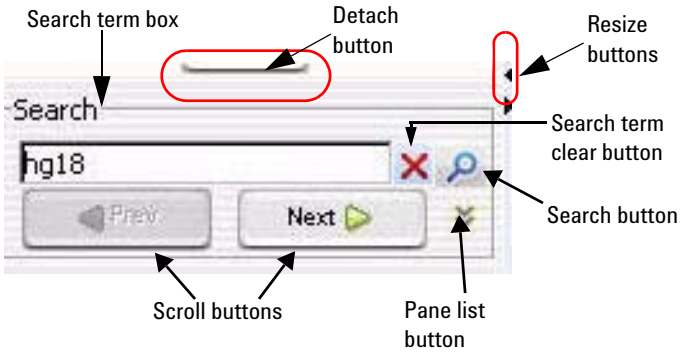


Figure 9 Navigator – Search pane

Detach button Click to detach 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 Provides a box for you to 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.

Pane list Allows you to restrict 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.

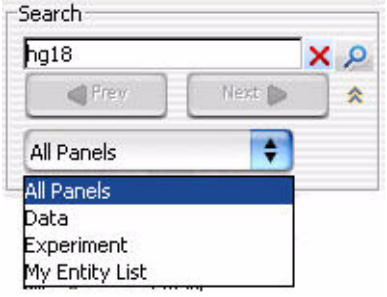


Figure 10 Open Pane List

(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.

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.

Data 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 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
	A single array data file.
	Data created from a multi-pack array.
red text	An item that matches the search term in a search.
	(Dock out button) Detaches the Data pane from the Navigator, and opens it in its own, separate window.
	(Collapse button, available only if the Data pane is not collapsed) Collapses the Data pane, and shows its title bar at the bottom of the Navigator.
	(Expand button, available only if the Data pane is collapsed) Expands the Data pane.

Data pane – actions and shortcut menus

Only the options that are not grayed out are discussed in this section. To activate the grayed-out options, you must have the appropriate license for the DNA Analytics application you are using. These inactivated options are explained in the *User Guide* for your DNA Analytics application.

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

Data Folder

- Right-click the **Data** folder to open a shortcut menu with an Import option. When you select this option, a menu appears with these 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 147 and "To import Agilent GEML design files" on page 18.
Axon Design File...	Opens the Import Axon Files dialog box, where you can select GenePix/Axon design (*.gal) files for import. See "Import" on page 147 and "To import GenePix/Axon design files" on page 19.
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 147 and "To import Agilent FE or GenePix/Axon data files" on page 13.

Option	Description
Axon File...	Opens the Import Axon Files dialog box, where you can select Axon (*.gpr) files for import. See "Import" on page 147 and "To import Agilent FE or GenePix/Axon data files" on page 13.
UDF File...	Opens the UDF Files dialog box, where you can select a Universal Data File (UDF) to import. See "Import" on page 147 and "To import a UDF file" on page 15.

Design Folder

- Right-click the name of design folder to open a shortcut menu with these options:

Option	Description
Update from eArray	(Available only for Agilent microarrays) Updates the annotations for your array design from the eArray Web site. Agilent regularly updates annotations in eArray as new ones become available. See "To update probe annotation in design files" on page 31.
Delete	Opens a Confirm dialog box. If you click **Yes,** the program permanently deletes the design and all arrays associated with it.

Genome Build Folder

- Right-click the name of a genome build folder to open a shortcut menu with these options:

Option	Description
Show Properties...	Opens the Design Properties dialog box. See "Design Properties" on page 125.
Delete	Opens a Confirm dialog box. If you click **Yes,** the program permanently deletes all of the arrays in this genome build folder.

Specific Arrays

- Right-click the name of an array to open a shortcut menu with these options:

Option	Description
Show Properties	Opens the Microarray Properties dialog box. See"Microarray Properties - Attribute Tab" on page 154 and "To edit the attribute values of a specific array" on page 29.
Rename...	Opens an Input dialog box, where you can type a new name for the array. Click **OK** to rename the array.
Delete	Opens a Confirm dialog box. If you click **Yes,** the program permanently deletes the array.

- Drag an array from the 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. Control-click the additional arrays to select them. You can also select a contiguous block of arrays—click the first array in the block, then shift-click the last one.

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 gene expression array design. This folder contains array data associated with the design, organized by genome build.

Item	Comments
	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.
	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 are derived from this experiment.
red text	An item that matches the search term in a search.
	(Dock out button) Detaches the Experiment pane from the main window, and opens it in its own, 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 activate the grayed-out options, you must have the appropriate license for the DNA Analytics application you are using. These inactivated options are explained in the *User Guide* for your DNA Analytics 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 analysis.

Experiments Folder

- Right-click the **Experiments** folder to open a shortcut menu with these options:

Option	Description
New Experiment	Opens the Create Experiment dialog box, where you can name the new experiment, and open another dialog box that allows you to populate the experiment with microarrays. See "Create Experiment" on page 119.
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 141 and "To export experiments" on page 38.

Specific Experiment Folder

- Right-click the name of an experiment to open a shortcut menu with these options:

Option	Description
Select Experiment	(Appears only if the experiment is not selected.) Opens the Experiment Selection dialog box, which asks if you want to select the experiment. Click **Yes** to select the experiment for view 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 133.
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 141 and "To export experiments" on page 38.
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 – Array" on page 137.
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 details see "Edit Array Color" on page 131.

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 132.
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 open a shortcut menu with these options:

Option	Description
Set for Calibration	(Works only if have license) Designates all arrays associated with this specific genome build and design as calibration arrays.
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 remain in the Data folder.

Individual Arrays

- Within the folder of a specific experiment, in the **Arrays** folder of a design, right-click the name of an individual array to open a shortcut menu with these 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 experiment. Click **OK** to rename the experiment.
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 28. • If you delete an array from an experiment, the program removes the link between the experiment and the array. The actual array data remains in the Data folder.
Show Properties...	Opens the Microarray Properties dialog box, where you can view and edit microarray attributes. For array files from the Agilent Feature Extraction program, you can also view the headers and feature data from the file. See "Microarray Properties - Attribute Tab" on page 154 and "To edit the attribute values of a specific array" on page 29.
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 131 and "To change the display color of an array" on page 46.
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 132 and "To change the order of arrays in an experiment" on page 27.

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 an unapplied gene list that has red chosen 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) Detaches the My Entity List pane from the main window, and opens it in its own, 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 activate the grayed-out options, you must have the appropriate license for the DNA Analytics application you are using. These inactivated options are explained in the *User Guide* for your DNA Analytics 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 open a shortcut menu with these 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.

Track Folder

- Right-click the name of a track to open a shortcut menu with these options:

Option	Comments
Show in UI	Mark this option to display the track in Gene View alongside the data and results of the selected experiment. See "To show tracks in Gene View" on page 57 and "Preferences – Tracks" on page 164.
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 choose to do 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 view the track.
View Details	Opens a table listing 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.

Genomic Viewer

Genome View

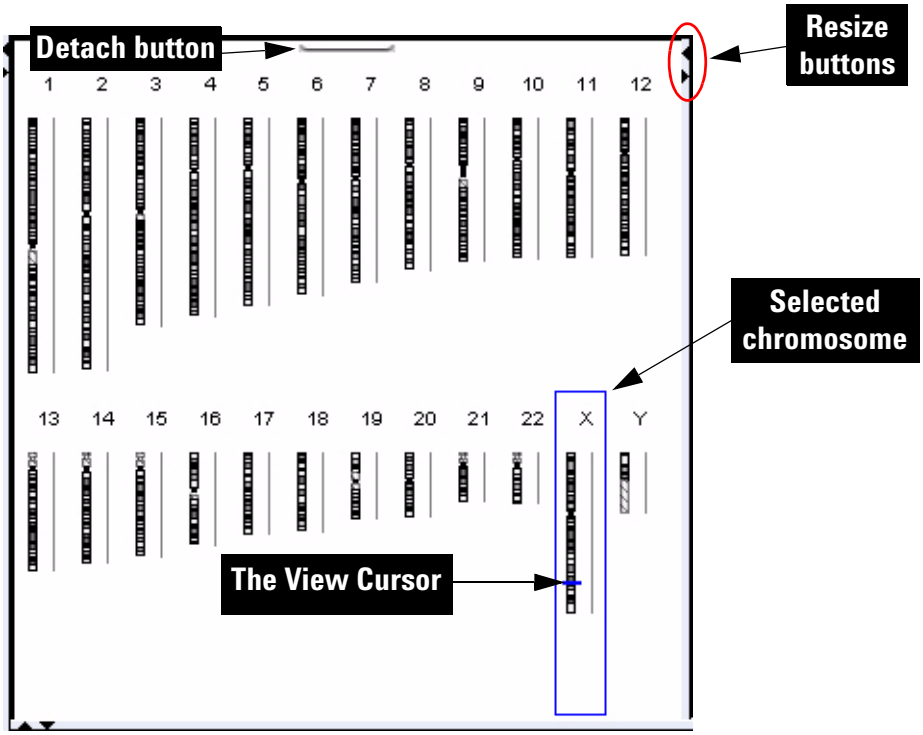


Figure 11 Genome View, with human chromosomes. The X chromosome is selected.

Genome View shows pictures of each of the distinct types of chromosomes in the selected genome. A blue box encloses 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 in which you click the chromosome sets the position of the cursor. See "The View Cursor" on page 97.
- On the selected chromosome, click anywhere to reposition the cursor. See "The View Cursor" on page 97. This also repositions the cursor in Chromosome, Gene, and Tab Views.
- Right-click anywhere within Genome View to open a shortcut menu with a Preferences option. If you click **Preferences,** the Preferences dialog box opens, where you can set user preferences on four separate tabs. See "Preferences – License" on page 161 and the topics that follow.
- Click the **Detach** button (located at the top center of the pane) to remove Genome View from the main window and open in its own separate window. See "Resizing and detaching panes from the Genomic Workbench main window" on page 19 in the *Quick Start Guide*.
- To reattach the view, click its **Close** button  . See "Maximizing and reattaching panes to the Genomic Workbench main window" on page 20 in the *Quick Start Guide*.
- Drag the side or bottom borders of the pane to resize them.
- 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. See "Resizing and detaching panes from the Genomic Workbench main window" on page 19 in the *Quick Start Guide*.

Chromosome View

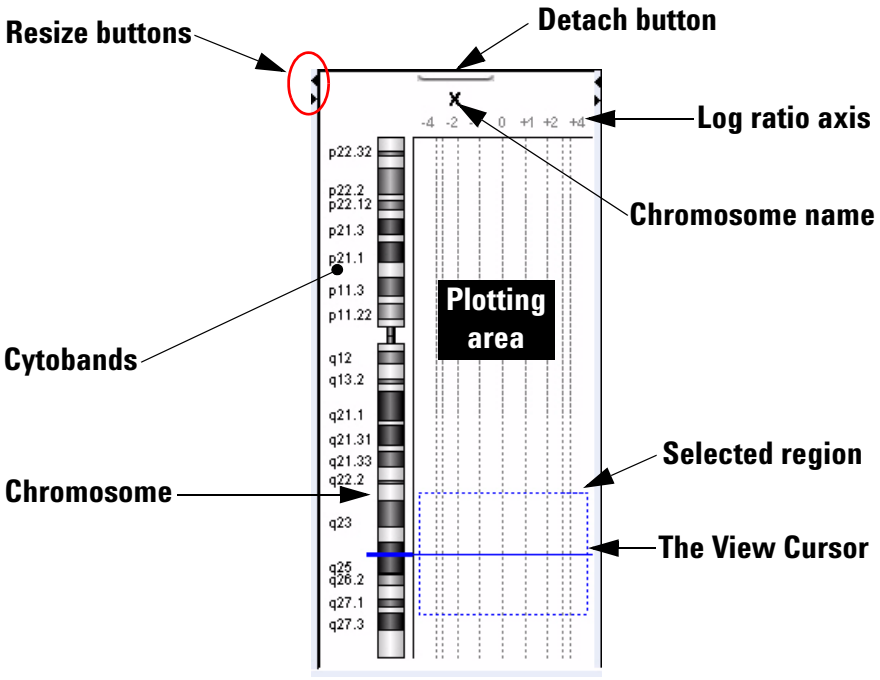


Figure 12 Chromosome View, human X chromosome shown

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

- Cytobands and a plotting area appear alongside 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 reposition the View cursor at that location. See "The View Cursor" on page 97.
- 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 repositions the cursor to the center of the selected region. See "The View Cursor" on page 97.
- Right-click anywhere in the plotting area of Chromosome View to open a shortcut menu with a Preferences option. If you click **Preferences,** the Preferences dialog box opens, where you can set user preferences on four separate tabs. See "Preferences – License" on page 161 and the topics that follow.
- Click the **Detach** button (located at the top center of the pane) to remove Chromosome View from the main window and open in its own separate window. See "Resizing and detaching panes from the Genomic Workbench main window" on page 19 in the *Quick Start Guide*.
- To reattach the view, click its **Close** button  . See "Maximizing and reattaching panes to the Genomic Workbench main window" on page 20 in the *Quick Start Guide*.
- Drag an inside border of Chromosome View to resize the view.
- 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. See "Resizing and detaching panes from the Genomic Workbench main window" on page 19 in the *Quick Start Guide*.

Gene View

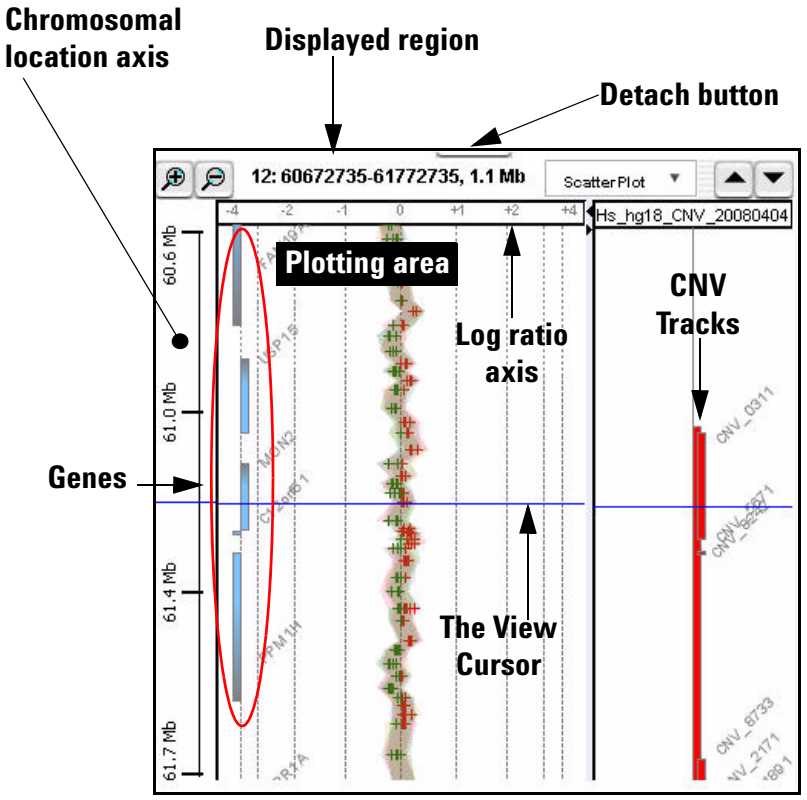


Figure 13 Gene View, with log ratio data from an experiment and CNV tracks.

Gene View shows a more detailed view of the chromosomal region you select in Chromosome View. See "Chromosome View" on page 90.

- Regions occupied by 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 restrict the genes that appear to those in the list. See "To change the appearance of genes in Gene View" on page 56, and "To show gene lists in Gene View" on page 56.

- Log ratio data from selected arrays in the active experiment appear as a scatter plot. Points appear in up to three different colors. See "To show significant data points in a scatter plot" on page 48. You can also customize the scatter plot. See "To change scatter plot appearance" on page 49.
- The location of the cursor matches the location of the cursors in other views. See "The View Cursor" on page 97.
- 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 57.

Scatter Plot

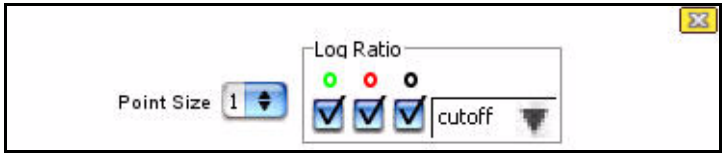


Figure 14 Scatter Plot command group in CH3 Gene View

You access the scatter plot command group through Gene View or the View tab. The commands differ depending on the DNA Analytics application you are working with. All the scatter plot command groups contain the commands for log ratio data in Figure 14. Scatter plots appear in the Chromosome and Gene Views but only if they have been activated in the Preferences dialog box.

Cutoff Select the threshold of CGH or CH3 log ratios to give a visual clue about significance. In the above example, all data points whose log ratios are below the cutoff of +0.125 are significant. If you select **none,** the program classifies all points as significant.

Mark this red check box to display, or clear it to hide, points with log ratios above the Cutoff selected. You select the cutoff for significance in **Cutoff.** These points appear in red.

Mark this green check box to display, or clear it to hide, points that reflect significant decreases. You select the cutoff for significance in **Cutoff.** These points appear in green.

Mark this black check box to display, or clear it to hide, points that reflect insignificant changes. You select the cutoff for significance in **Cutoff.** These point appear in black.

Point size Sets the size (in pixels) of the points in the scatter plots.

In addition to options for log ratio plotting, the CGH command group includes options for raw intensity plotting.

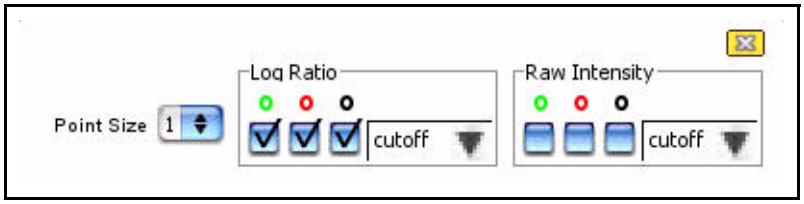


Figure 15 Scatter Plot command group in CGH Gene View

The ChIP command group includes options for intensity ratio plotting.

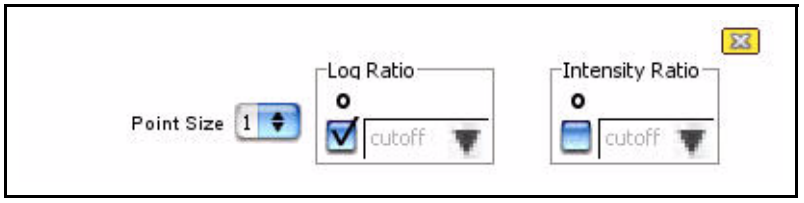


Figure 16 Scatter Plot command group in ChIP Gene View

Gene View buttons

Zooms in to see a smaller region in more detail.

Zooms out to see a larger region in less detail.

(Available when Gene View is in vertical orientation.) Scrolls up through the genes and data to lower-numbered chromosomal coordinates.

(Available when Gene View is in vertical orientation.) Scrolls down through the genes and data to higher-numbered chromosomal coordinates.

(Available when Gene View is in horizontal orientation.) Scrolls left through the genes and data to lower-numbered chromosomal coordinates.

(Available when Gene View is 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. See "Resizing and detaching panes from the Genomic Workbench main window" on page 19 in the *Quick Start Guide*.

(**Detach** button) Removes Gene View from the main window, and opens it in its own separate window. "Resizing and detaching panes from the Genomic Workbench main window" on page 19 in the *Quick Start Guide*.

Gene View shortcut menu and other actions

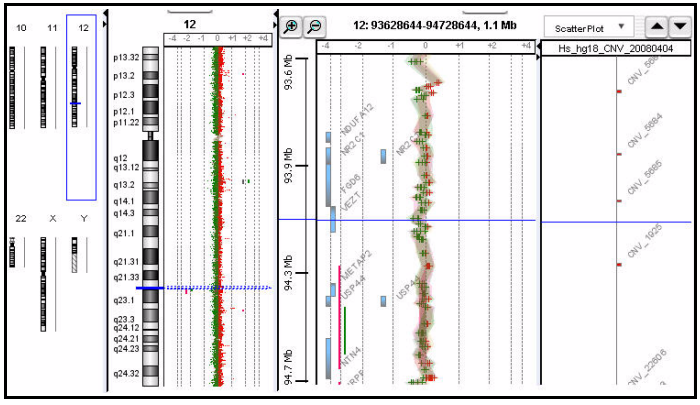
- Click anywhere in the plotting area of Gene View to move the cursor to that location. See "The View Cursor" on page 97.
- Drag an inside border of Gene View to resize the View. See "Resizing and detaching panes from the Genomic Workbench main window" on page 19 in the *Quick Start Guide*.
- Right-click anywhere in the plotting area of Gene View to open a shortcut menu with these 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 121 and "To show gene lists in Gene View" on page 56.
Create Track	Opens the Create Track dialog box, where you specify the chromosome locations for the track. See "To create a track (CGH only)" on page 35 and "Create Track (CGH only)" on page 123.
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 view the track.
Search probes in eArray...	Opens the Search probes in eArray dialog box, where you can start a search of the Agilent eArray web site for probes in the selected (or another) chromosomal region. See "Search probes in eArray" on page 170 and "To search Agilent eArray for probe information" on page 62.
Preferences	Opens the Preferences dialog box, where you can set user preferences on four separate tabs. See "Preferences – License" on page 161 and the related pages that follow.

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 affect 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

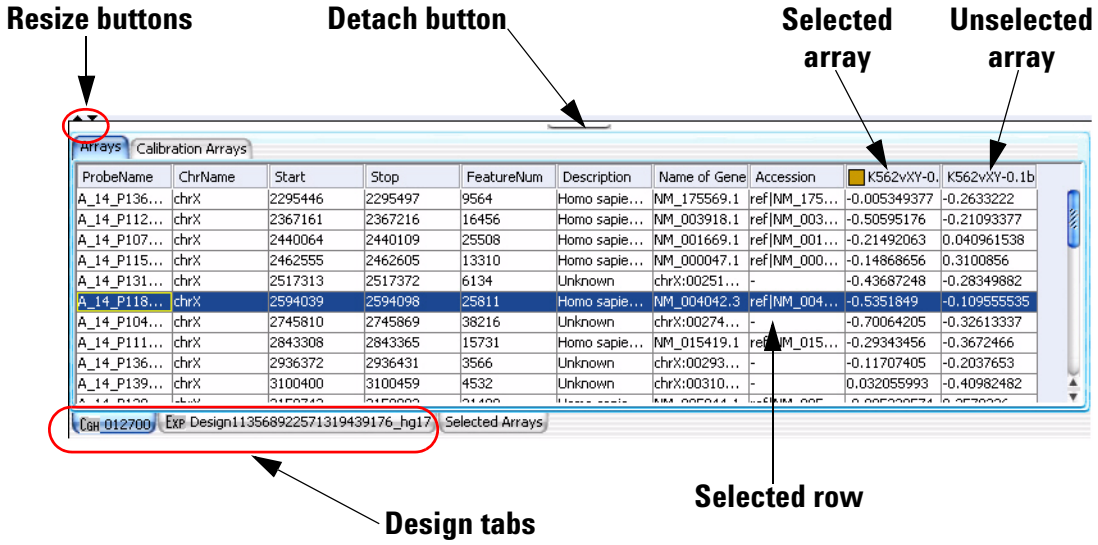


Figure 17 Tab View

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 17 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.
- 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. See "Resizing and detaching panes from the Genomic Workbench main window" on page 19 in the *Quick Start Guide*.

(**Detach** button) Removes Tab View from the main window, and opens it in its own separate window. See "Resizing and detaching panes from the Genomic Workbench main window" on page 19 in the *Quick Start Guide*.

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 shortcut menu with these 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 33.
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.
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 131 and "To change the display color of an array" on page 46.
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 view separate scatter plots for each array, the plots also appear in this order. See "Edit Array Order" on page 132 and "To change the order of arrays in an experiment" on page 27.
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.
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 169.
- 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 open a shortcut menu with these 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 145.
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)	Opens your Web browser, and passes 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 63.
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 passes the column entry you clicked as a search string to the site. See "Customize Search Link" on page 124 and "To update or delete a custom Web search link" on page 64.
(other options)	If other options appear in this shortcut menu, they are custom Web search links. Click them to open your Web browser, and pass the column entry you clicked as a search string to the site.

Status Bar

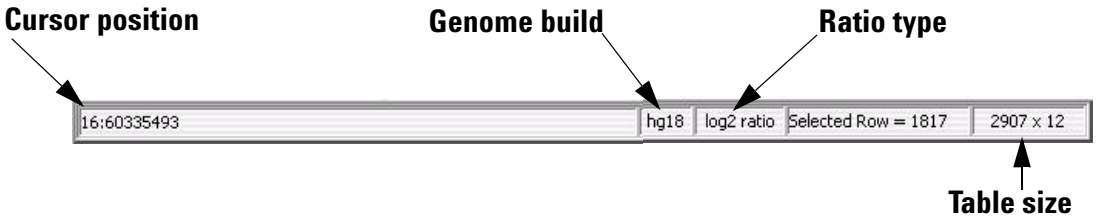


Figure 18 Status bar

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 application license.

Cursor position The chromosomal location of the cursor. See "The View Cursor" on page 97.

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 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 Genomic Workbench. The dialog boxes appear in alphabetical order by name.

Add Gene List <name> to

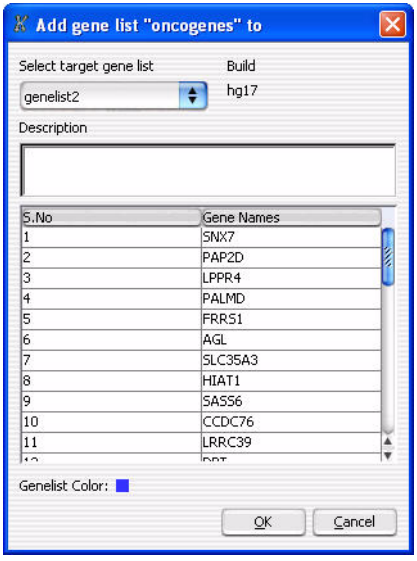


Figure 19 Add Gene List <name> to

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

To open: In the Data 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

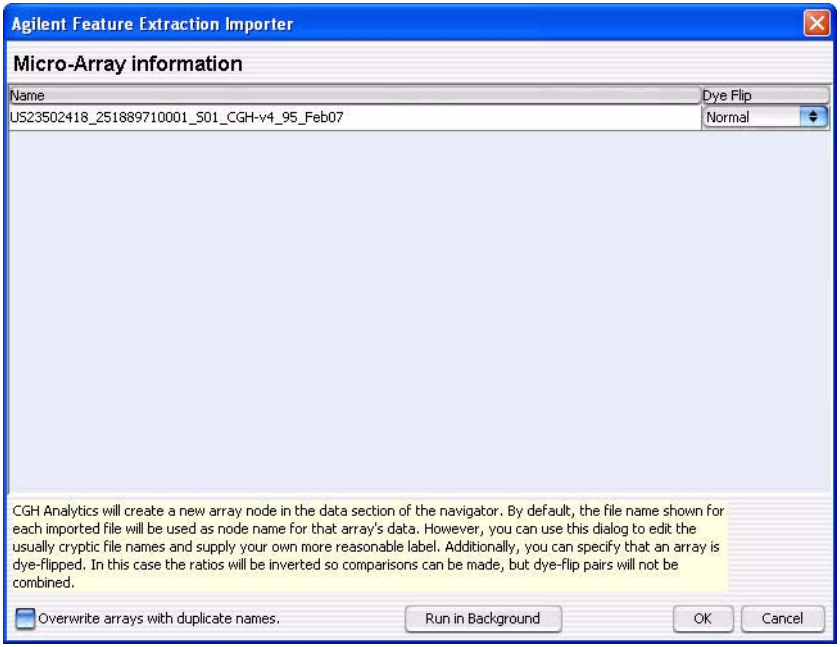


Figure 20 Agilent Feature Extraction Importer

Purpose: Allows you to edit the name of the FE data file you intend to import and to specify if 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 Allows you to edit the names of the FE files. You can change the names of the files to names that you are more likely 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 ration (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 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 allows you to 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.

CGHSmooth Parameters

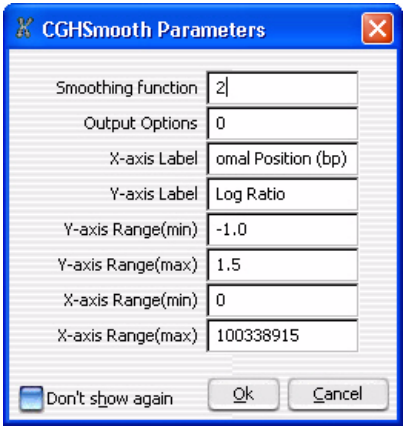


Figure 21 CGHSmooth Parameters dialog box

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 beneath the X-axis of the plot as a label.
Y-axis Label	The text that appears beside 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 further refine the appearance of the plot once the plug-in generates it.

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

CGHSmooth Plot

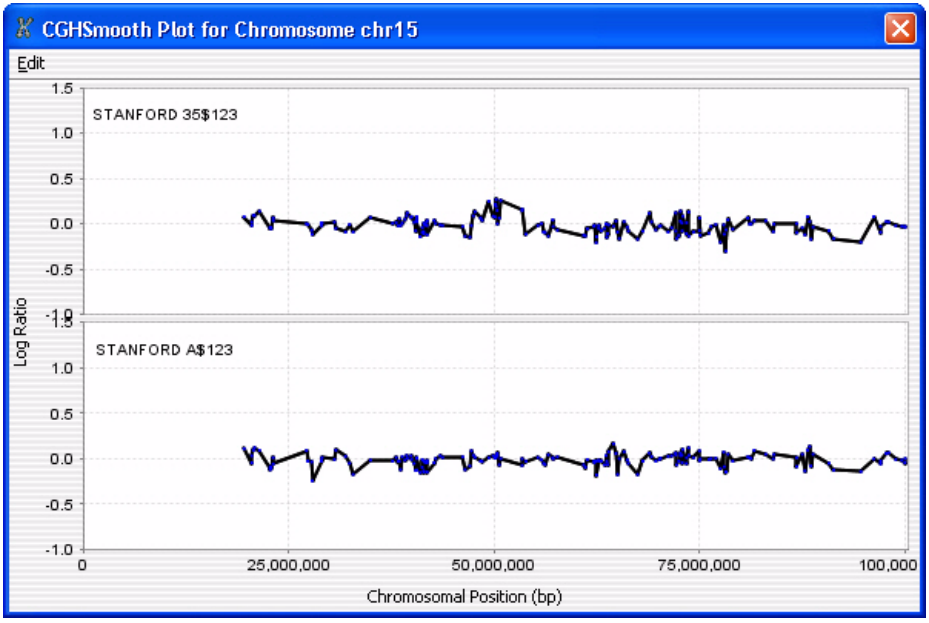


Figure 22 CGHSmooth Plot

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 106.

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, a shortcut menu opens with these 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 110.
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 allows you to 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 zoom in on.
Zoom Out	Opens another menu that allows you to 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 allows you to zoom the plot to encompass 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 encompasses 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 encompass 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 or MovAvg Example plots.

To open: Use the CGHSmooth, Echo Example, or MovAvg Example plug-in to produce a plot. Right-click within the plotting area, then click **Properties** in the shortcut menu. You can also open this dialog box when you right-click within the line plot in the Graphical Differential Aberration Summary dialog box. See "Graphical Differential Aberration Summary" on page 275 in the *CGH Interactive Analysis User Guide*.

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

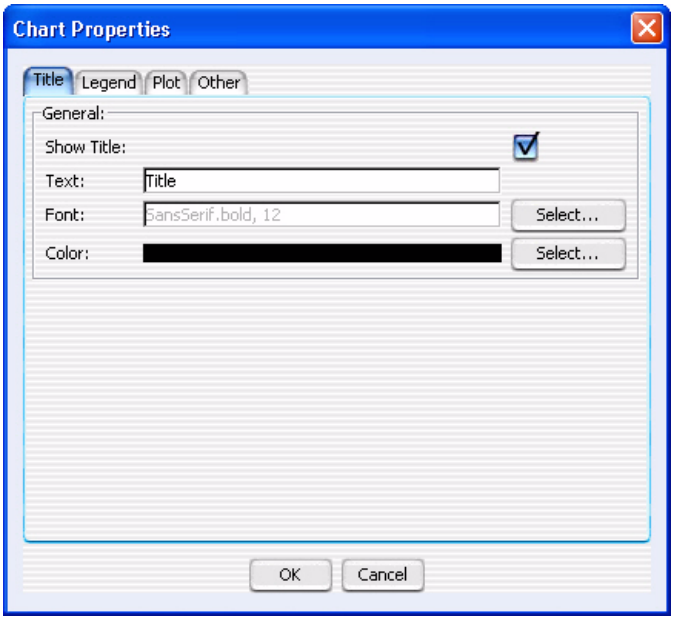


Figure 23 Chart Properties dialog box – Title tab

- **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 (Edit Array Color) – Swatches Tab" on page 171.

Legend tab

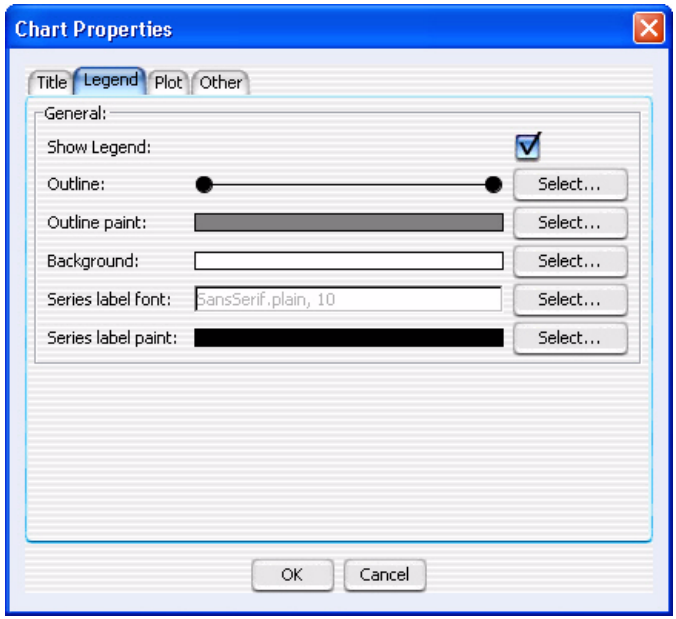


Figure 24 Chart Properties dialog box – Legend tab

- **Show Legend** – Mark this option to display a legend at the bottom of the chart. When you mark this option, the other options in the tab become available.
- **Outline** – The line weight of the box that surrounds the legend. Click **Select** to open the Pen/Stroke Selection dialog box. Select the desired line weight, then click **OK.**
- **Outline paint** – The color of the box that surrounds the legend. 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 (Edit Array Color) – Swatches Tab" on page 171.
- **Background** – The background fill color of the 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 (Edit Array Color) – Swatches Tab" on page 171.

- **Series label font** – The font of the text within the legend. Click **Select** to open the Font Selection dialog box. Select the desired font attributes, then click **OK.**
- **Series label paint** – The color of the text within the legend. Click **Select** to open the Series 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 (Edit Array Color) – Swatches Tab" on page 171.

Plot Tab

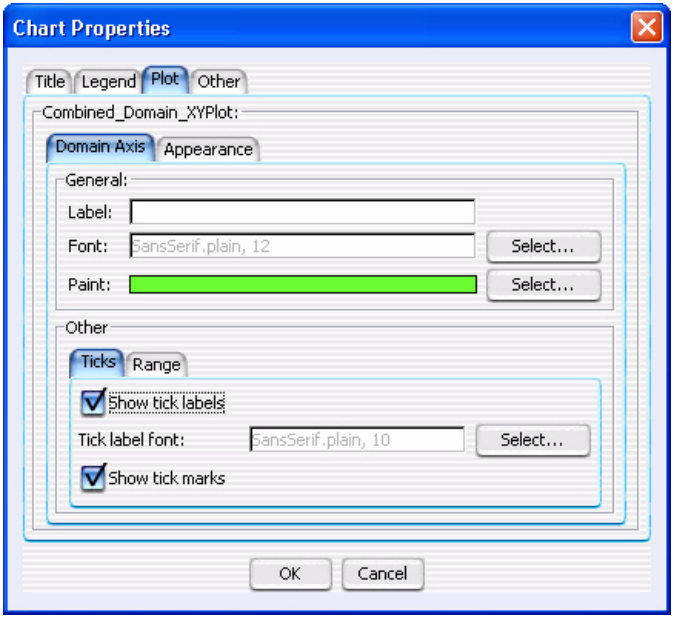


Figure 25 Chart Properties dialog box – Plot tab

- Within the Plot tab, you can set these properties in the Domain Axis tab:

Property	Details
General	
Label	A custom label for the X-axis of the chart. Type the desired label.
Font	The font for the custom label on the 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 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 (Edit Array Color) — Swatches Tab" on page 171.
Other – Ticks tab	
Show tick labels	Mark this option to show, or clear it to hide, the numerical values on the X-axis.
Tick label font	The font for the numerical values on the 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 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	Details
Outline stroke	The thickness of the lines that enclose 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 that enclose 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 (Edit Array Color) — Swatches Tab" on page 171.
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 (Edit Array Color) — Swatches Tab" on page 171.
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

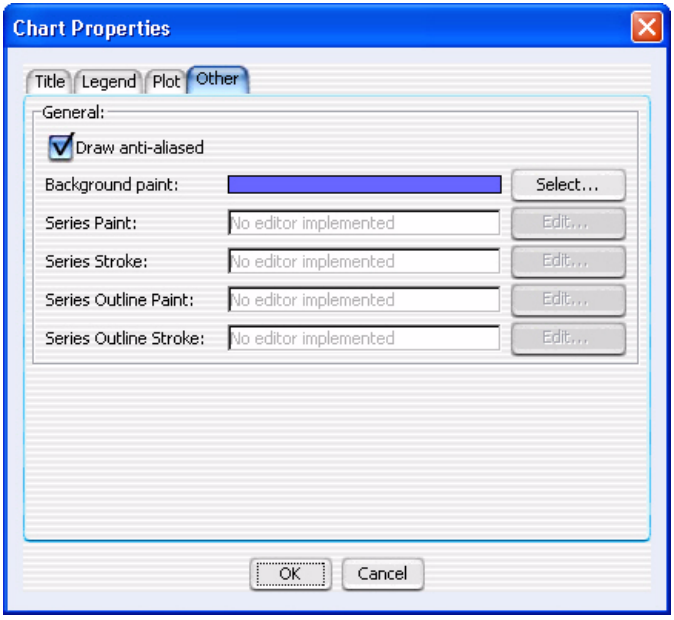


Figure 26 Chart Properties dialog box – Other tab

The Other tab offers these options:

- **Draw anti- aliased** – Mark this option to minimize distortion and visual artifacts in the plot image. This produces 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 (Edit Array Color) – Swatches Tab" on page 171.

The other options are for future expansion, and are not available in the current release of DNA Analytics.

Choose Gene List Color

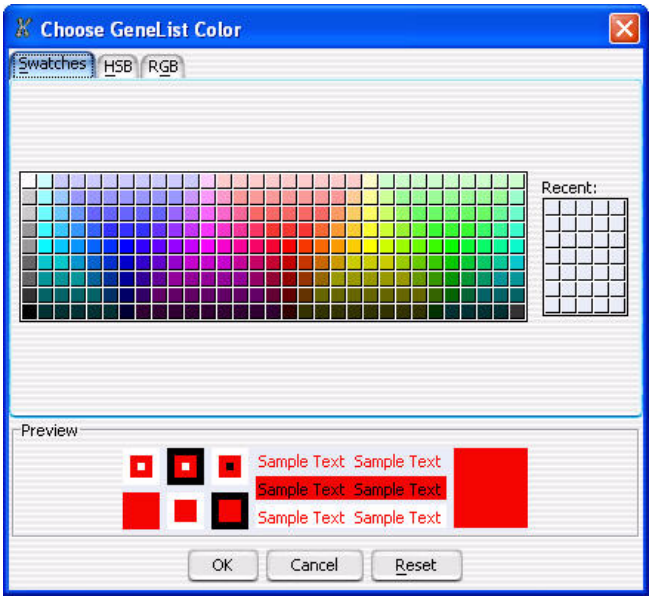


Figure 27 Choose GeneList Color dialog box

Purpose: To distinguish multiple gene list names by color

To open: Right-click Gene View, click **Create Gene List > Change...**, or in Data Navigator, right-click a specific gene list, click **View in Table > Color**.

Swatches Tab Choose color based on color samples (Swatches)

HSB Tab Choose colors based on an HSB schema (Hue, Saturation, and Brightness or Value). See "Select Color (Edit Array Color) – HSB Tab" on page 172.

RGB Tab Choose colors based on an RGB schema (Red-Green-Blue). See "Select Color (Edit Array Color) – RGB Tab" on page 173.

Recent: Choose a recent color selection.

Reset Click to return HSB or RGB values back to default values.

Confirm overwrite

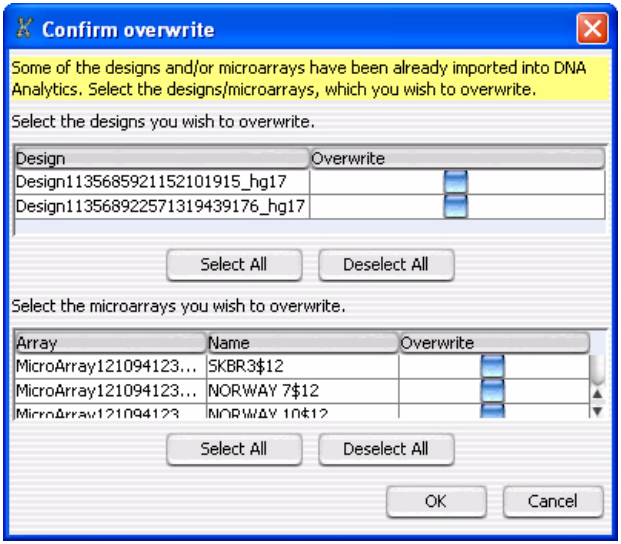


Figure 28 Confirm overwrite dialog box

Purpose: When you import an experiment, it can contain designs and/or arrays that have the same names as those already available in Genomic Workbench. This dialog box allows you to 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 Genomic Workbench. See "To import an experiment file" on page 23.

Select the designs you wish to overwrite

Design The names of the designs in the imported file that have the same names as designs that are already available in Genomic Workbench.

Overwrite Mark the check box next to 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 you wish 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 Genomic Workbench.

Overwrite Mark the check box next to 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 149.

Create Experiment

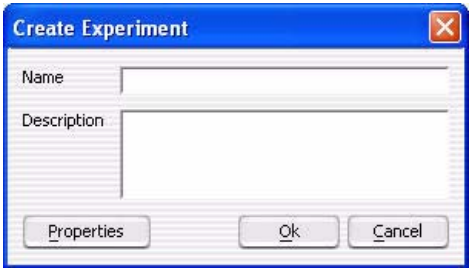


Figure 29 Create Experiment dialog box

Purpose: Creates an organizational unit (an *experiment*) that allows you to view and analyze array data in Genomic Workbench. You populate 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 25.

To open: In the Home tab of 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 populate the new experiment. See "Experiment Properties" on page 133.

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 populate your new experiment with array data. 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 26.

Create Gene List

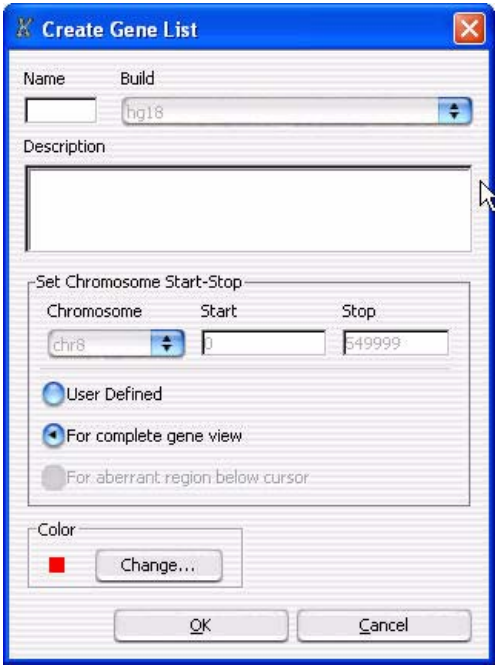


Figure 30 Create Gene List

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 Select to choose 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 activated 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 "Choose Gene List Color" on page 117.

Create Track (CGH only)

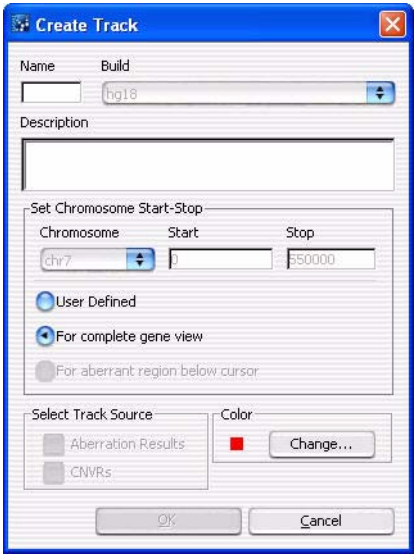


Figure 31 Create Track dialog box

Purpose: The Create Track dialog box allows you to create a track for a chromosomal region based on an assigned chromosomal region. You can display one or more tracks alongside the genes and data in Gene View. See "To show tracks in Gene View" on page 57.

To open: Right-click in the plotting area of Gene View for the CGH 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, lists, and the like.

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** – Allows you to 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 currently appears in Gene View.

OK Creates the track. To view the track in Gene View, use the **Tracks** tab of the User Preferences to enable it. See "Preferences – Tracks" on page 164. To export the track, see "To export tracks" on page 40.

Cancel Closes the dialog box without creating a track.

Customize Search Link

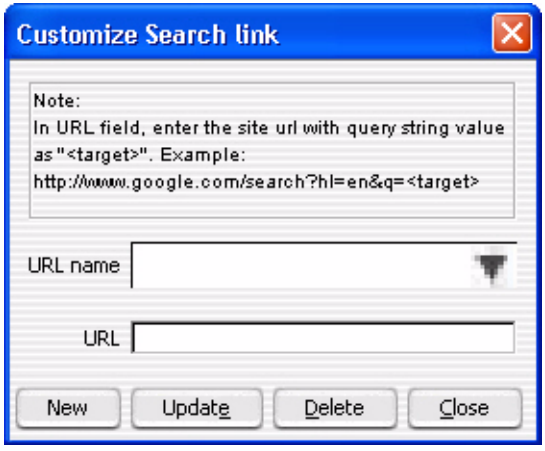


Figure 32 Customize Search Link dialog box

Purpose: This dialog box allows you to create a custom Web search link in the shortcut menu that appears when you right-click a tab entry. The link opens the URL of your choice, and passes the tab entry to it as a search string. See "To create a custom Web search link" on page 63.

To open: Right-click any entry in a tab 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 passes 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: Provides general and detailed information about a given microarray design. See "To view the properties of a specific design" on page 31.

To open: In the **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

Lists general identifying attributes of the array design, and statistics such as the total number of features in the design.

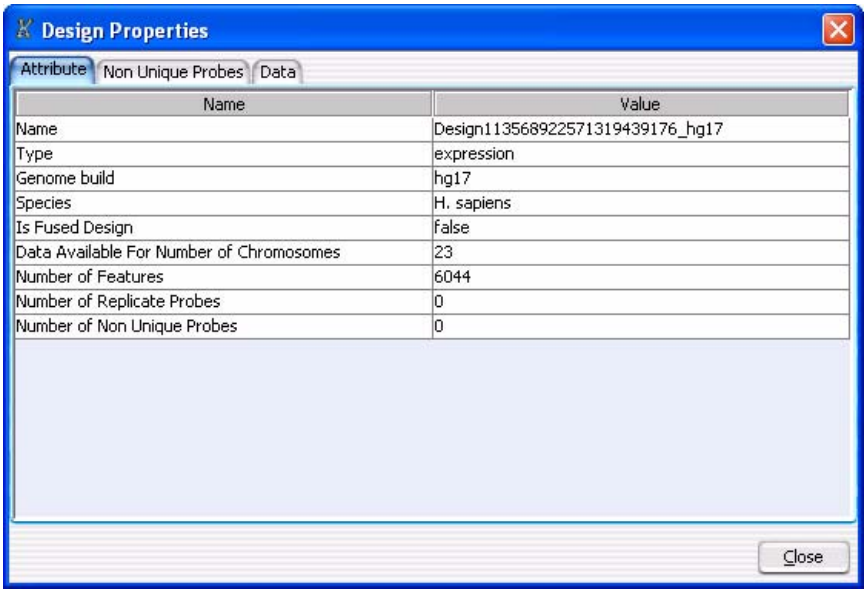


Figure 33 Design Properties dialog box – Attribute tab

Non-Unique Probes tab

Lists the non-unique probes in the design. Non-unique probes bind to more than one location in a target genome.

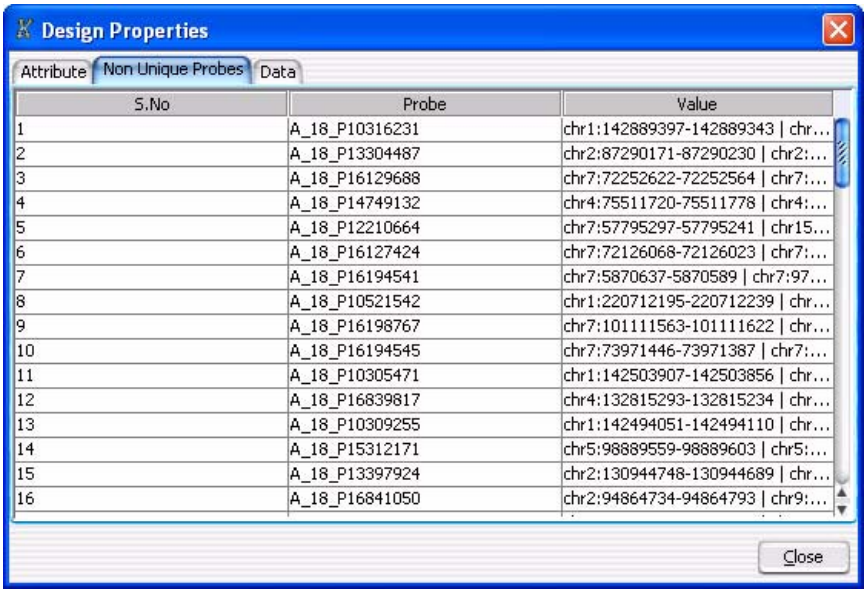


Figure 34 Design Properties dialog box – Non-Unique Probes tab

S. No The sequence order of the probes within the tab.

Probe The name of the each non-unique probe.

Value The chromosomal locations to which each of the probes binds. Because these are non-unique probes, more than one location appear for each probe.

Data tab

Lists the names of the probes in the design and the genomic locations to which they are designed. The tab displays the probes for one chromosome at a time.

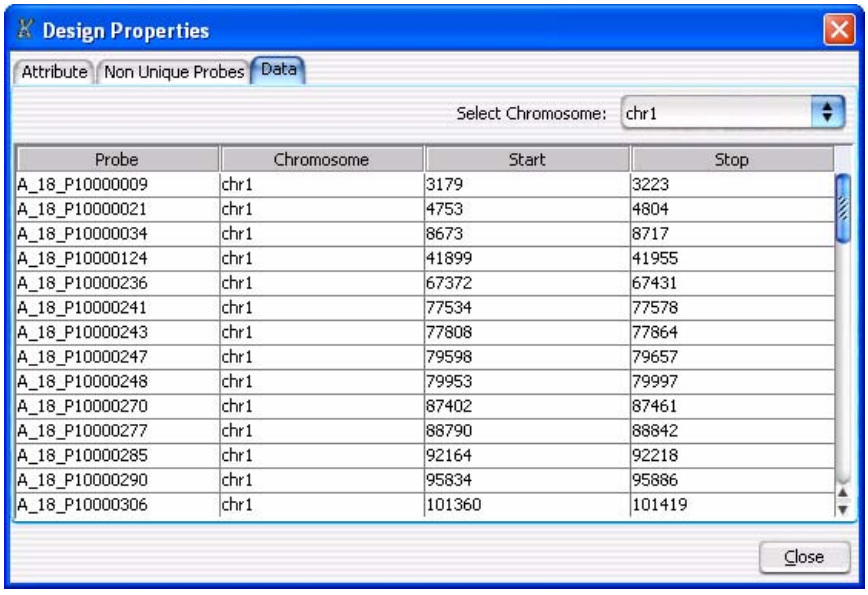


Figure 35 Design Properties dialog box – Data tab

Select Chromosome The chromosome whose probes appear in the list. To view the probes designed to a different chromosome, select one from this list.

Probe The name (Probe ID) of each probe.

Chromosome The name of the chromosome to which the probe is designed.

Start The location on the selected chromosome of the first base pair to which each probe is designed.

Stop The location on the selected chromosome of the last base pair to which each probe is designed.

Echo Example Plot

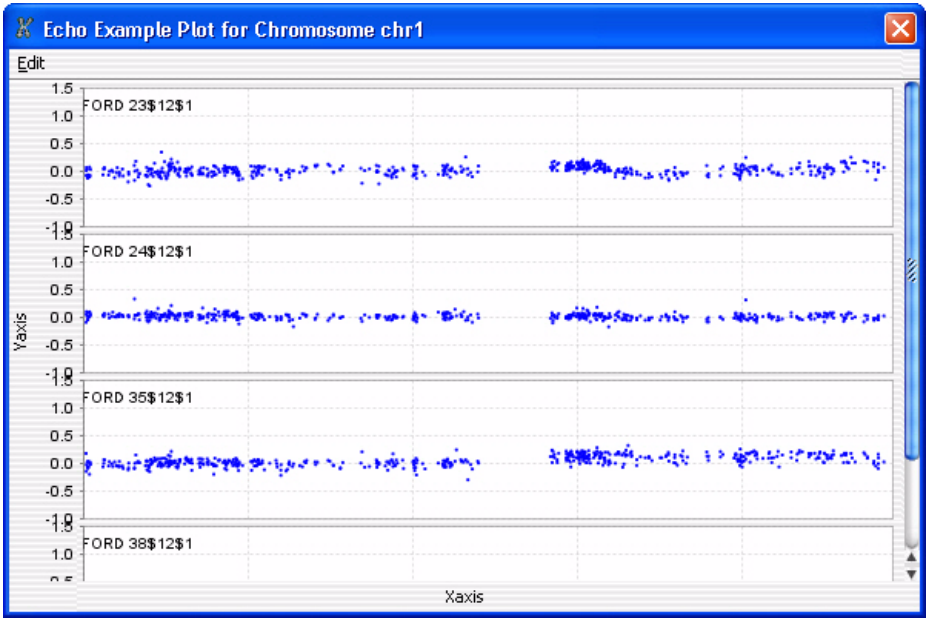


Figure 36 Echo Example Plot

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: Activate 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 open a shortcut menu with these 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 110.
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 allows you to 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 zoom in on.
Zoom Out	Opens another menu that allows you to 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 allows you to zoom the plot to encompass 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 encompasses 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 encompass the full range of Y values of the data.

Edit Array Color

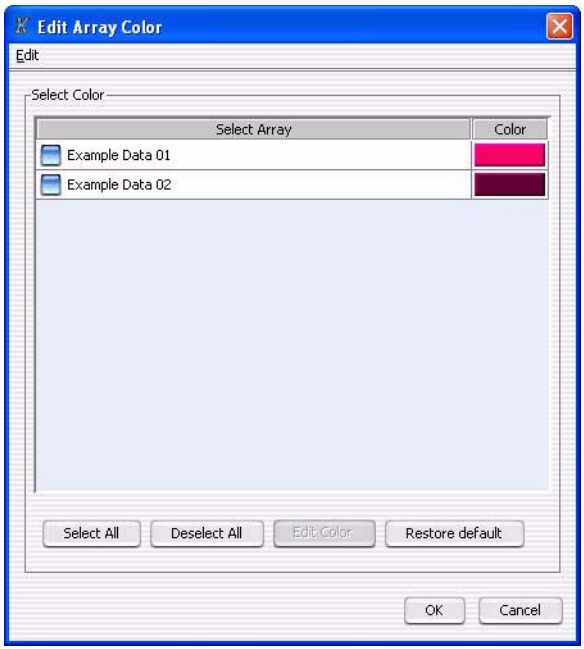


Figure 37 Edit Array Color dialog box

Purpose: Allows you to 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 pick 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 46.

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 pick 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

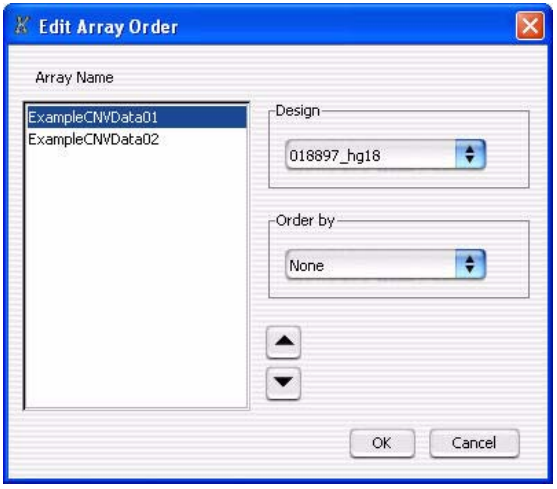


Figure 38 Edit Array Order dialog box

Purpose: Changes the display order of the arrays in an experiment. This can affect 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, listed 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 re-order 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 Reorders the arrays and closes the dialog box.

Cancel Closes the dialog box without reordering any arrays.

Experiment Properties

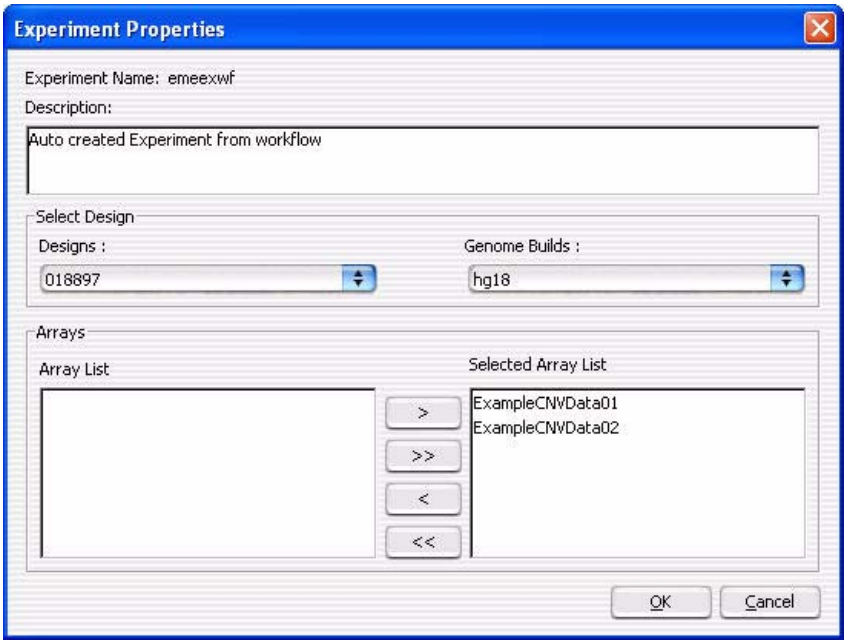


Figure 39 Experiment Properties dialog box

Purpose: Allows you to select array designs and data to link to an experiment. See "To add arrays to an experiment" on page 26.

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 entered when the experiment was created.

Select Design

Designs Lists all of the designs available in the program. Select the design associated with arrays that you want to add to the experiment.

Genome Builds Lists the genome build(s) associated with the design. Select the desired genome build to display the arrays associated with a single genome build.

Arrays

Array List Lists the arrays in the selected design that are available for this experiment.

- To select an array for subsequent transfer to the Selected Array List, click its name.
- To select additional arrays, control-click their names.
- To select a contiguous block of arrays, click the name of the first array, then shift-click the name of the last one.

Selected Array List Lists the arrays that you have selected for this experiment.

Moves the selected arrays in Array List to the Selected Arrays List. You can move arrays from as many designs as you like, as long as they are all associated with the same genome build.

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

OK Populates the experiment with the arrays in the Selected Array List, and closes the dialog box.

Cancel Closes the dialog box without adding any arrays to the experiment.

Export

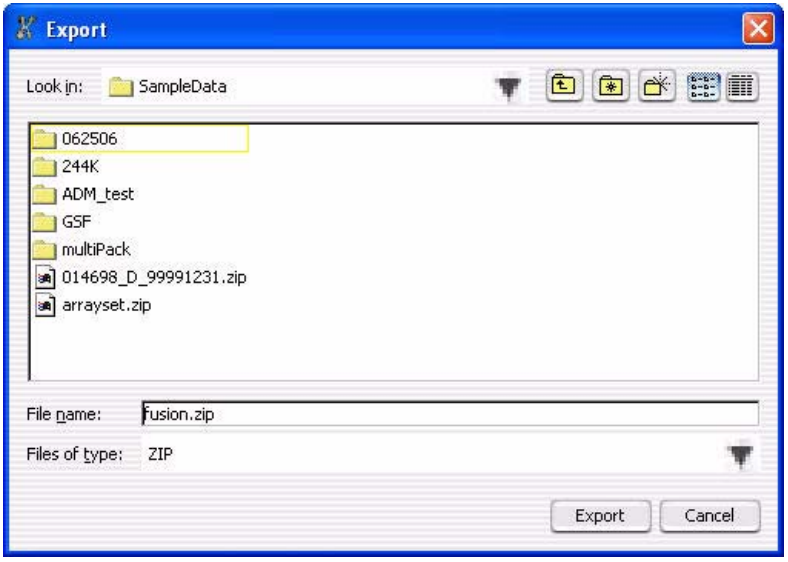


Figure 40 Export dialog box – Several types of file exports use this dialog box. This specific example exports selected experiment(s) as a ZIP format file.

Purpose: Allows you to 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 38, "To export tracks" on page 40, "To export filters (CGH only)" on page 39 or "To export array attributes" on page 37.

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 .

Navigates up one level.

Navigates to 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 details of folders, files, and other locations in the main pain of the dialog box.

Main pane Displays the folders, files, and other locations in the selected location in *Look in*. The program restricts listed files to the type selected in *Files of type*. 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 Restricts the files listed in the main pane to those of the appropriate type for your specific kind of export. To show all files, click ▼, then select **All Files.**

Export Saves the selected content to the location specified in the dialog box.

Cancel Cancels your selections and closes the dialog box.

Export Array Attributes – Array

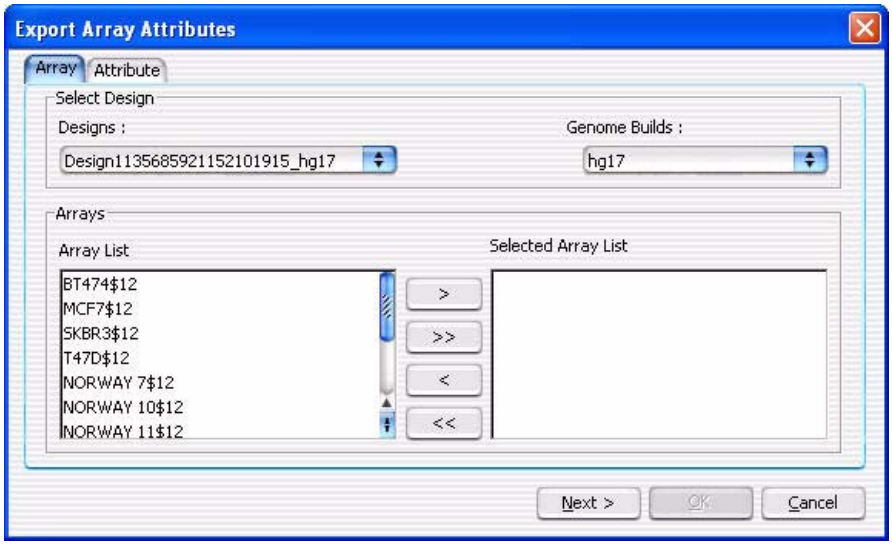


Figure 41 Export Array Attributes – Array tab dialog box

Purpose: Allows you to select array designs whose selected attributes you will then export. See "To export array attributes" on page 37.

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.**

Select Design

Designs Lists all of the designs available in the program. Select the design associated with arrays whose attributes you want to export.

Genome Builds Lists the genome build(s) associated with the design. Select the desired genome build to display the arrays.

Arrays

Array List Lists the arrays in the selected design.

- To select an array for subsequent transfer to the Selected Array List, click its name.
- To select additional arrays, control-click their names.
- To select a contiguous block of arrays, click the name of the first array, then shift-click the name of the last one.

Selected Array List Lists the arrays that you have selected for this experiment.

Moves the selected arrays in Array List to the Selected Arrays List. You can move arrays from as many designs as you like, as long as they are all associated with the same genome build.

Moves all of the arrays in Array List to the Selected Arrays 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. See "Export Array Attributes – Attribute" on page 139.

Cancel Closes the dialog box without selecting any arrays and their attributes to be exported

Export Array Attributes – Attribute

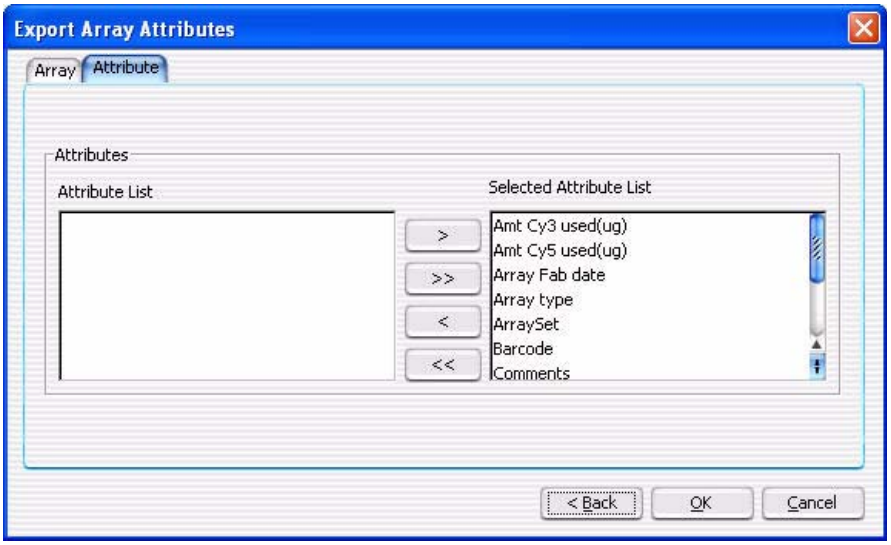


Figure 42 Export Array Attributes – Attribute tab dialog box

Purpose: Allows you to remove selected array attributes from the list you will then export. See "To export array attributes" on page 37.

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.** After selecting the arrays whose attributes you intend to export, click **Next.**

Attributes

Selected Attribute List

Lists the attributes for the selected arrays that will be exported if you click OK.

- To select an attribute for subsequent removal to the Attribute List, click its name.
- To select additional attributes, control-click their names.
- To select a contiguous block of attributes, click the name of the first attribute, then shift-click the name of the last one.

Attribute List Lists 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. If desired, you can re-add an attribute.

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 135.

Cancel Closes the dialog box without exporting any attributes.

Export Experiments

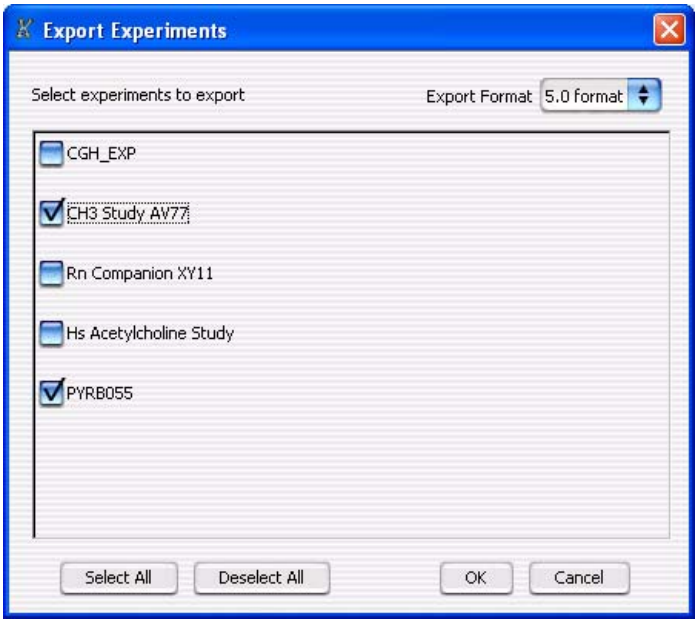


Figure 43 Export Experiments dialog box

Purpose: Allows you to 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 38.

To open: In the Home tab, click **Export > Experiments...**

Export Format The file format for the exported experiment file. Select one of these options:

- **5.0 Format** – Exports the experiment(s) in a format that you can import into Genomic Workbench. This is the most current experiment format, but it is not compatible with previous versions of the program.
- **3.0 Format** – Exports the experiment(s) in a format that you can import into Agilent CGH Analytics 3.0 or later. This is a "legacy" format that you can use to maintain compatibility with earlier versions of the program.

Select experiments to export Lists 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 135.

Cancel Cancels the export and closes the dialog box.

Export Filters (CGH only)

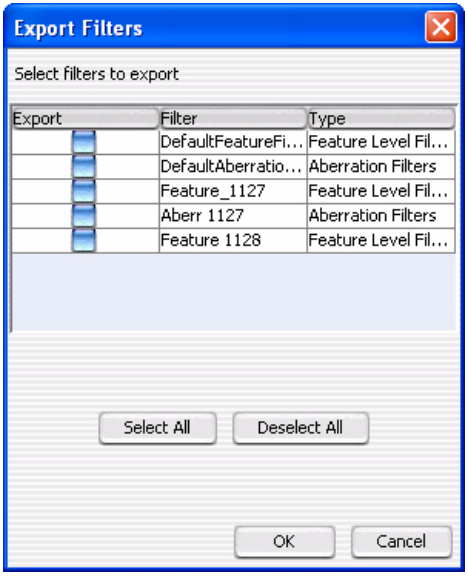


Figure 44 Export Filters dialog box

Purpose: Allows you to select feature-level, array-level, 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 (CGH only)" on page 39.

To open: In the **Home** tab, click **Export > Filters...**

Select filters to export Lists all of the filters available in the program. The table has these columns:

- Export – Mark the check box next to each filter that you want 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 135.

Cancel Cancels the export and closes the dialog box.

Export Tracks

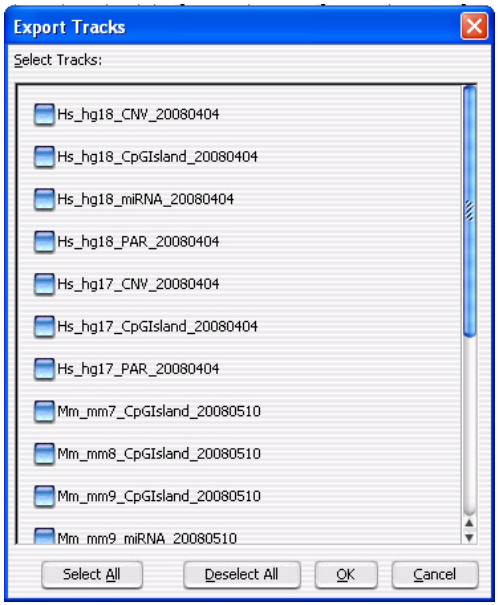


Figure 45 Export Tracks dialog box

Purpose: Allows you to select tracks to export as a single BED format file. See "To export tracks" on page 40.

To open: In the **Home** tab, click **Export > Tracks...**

Select tracks Lists all of the tracks available in the program. Mark the check box next to each track that you want to export.

For more information about tracks, see "To create a track (CGH only)" on page 35 and "To show tracks in Gene View" on page 57.

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 135.

Cancel Cancels the export and closes the dialog box.

Find in column

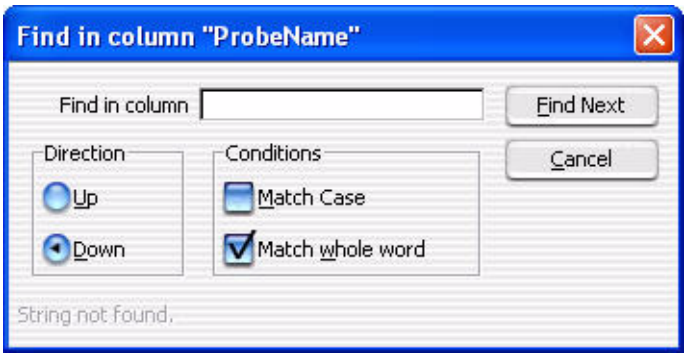


Figure 46 Find in column dialog box

Purpose: This dialog box allows you to set search parameters for a specific column entry. 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 scan the column you clicked in an upward direction from the currently highlighted row.
- **Down** – Sets the search to scan the column you clicked in an downward direction 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.

Cancel Closes the dialog box.

Go To Gene/Genomic Location

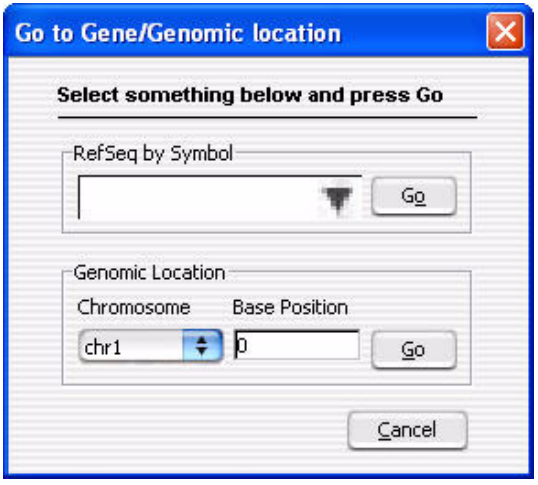


Figure 47 Go To Gene/Genomic location dialog box

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

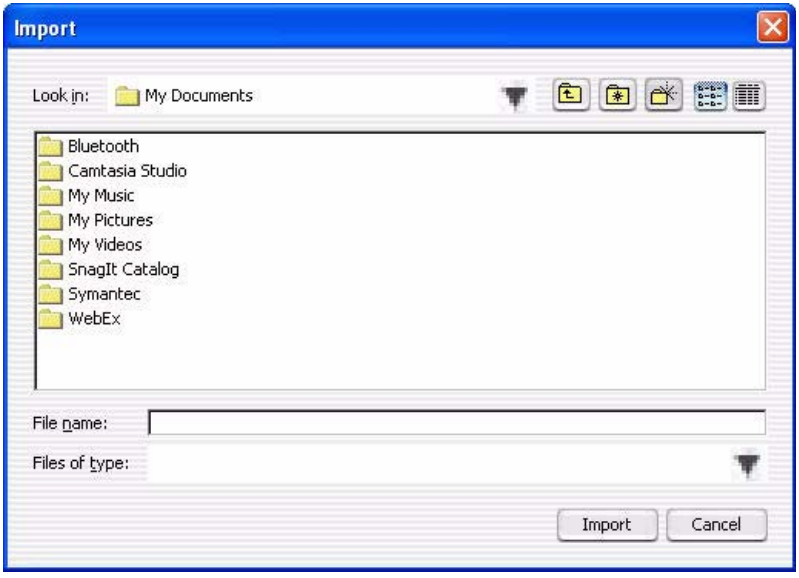


Figure 48 Import dialog box

Purpose: Allows you to select files for import into Genomic Workbench.

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 control-click the names of additional files. To select a contiguous block of files, click the name of the first file in the block, then shift-click the name of the last one.

File name Displays the name of a file you select for import.

Files of type The program restricts the list of files to the specific types expected for the import. To display all files, click ▼,then select **All Files.**

Type of import	File type
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 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) allows you to further define the content for import. See the instructions for each specific type of import in Chapter 1.

Cancel Cancels the import and closes the dialog box.

Import (experiments)

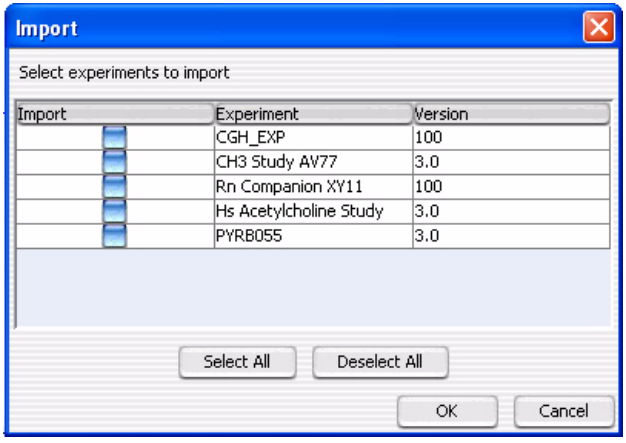


Figure 49 Import dialog box (for experiments)

Purpose: Allows you to select the specific experiments within a ZIP format experiment file to load into the program. See "To import an experiment file" on page 23.

To open: In the **Home** tab, click **Import > Experiments.** In the dialog box that appears, select the desired ZIP format experiment file, then click **Import.**

Select experiments to import

These columns appear:

- **Import** – Mark the check box next to the experiment(s) that you want to import.
- **Experiment** – The names of the experiments available for import in the ZIP format experiment file.
- **Version** – Version of DNA Analytics used to export the original experiment

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 118.

Cancel Cancels the upload and closes the dialog box.

Import GEML design files

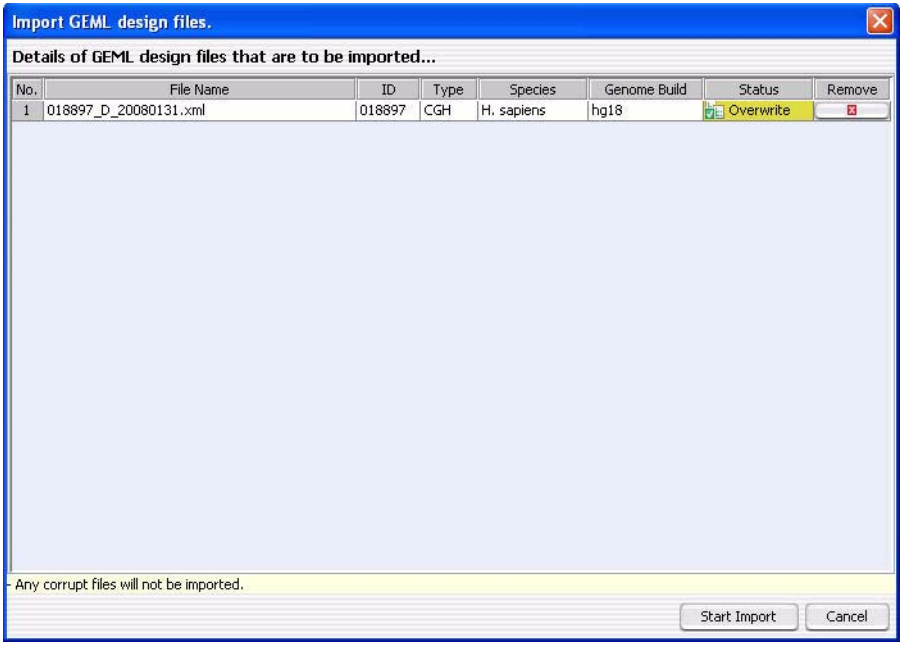


Figure 50 Import GEML design files dialog box

Purpose: To view 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 At present, Genomic Workbench supports these species:

- *H. sapiens*
- *M. musculus*
- *R. norvegicus*

Genome Build The genome build with which this design is associated.

Status

- **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 Build

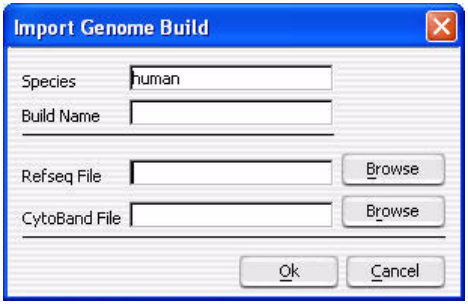


Figure 51 Import Genome Build dialog box

Purpose: To import a new set of genome build files into Genomic Workbench. See "To import a genome build" on page 19.

To open: In the Home tab, click **Import > Genome Build.**

Species The genome's species of origin. The program supports these species:

- *H. sapiens*
- *M. musculus*
- *R. norvegicus*

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

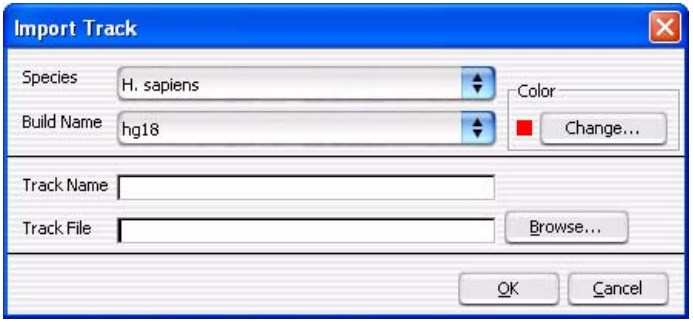


Figure 52 Import Track dialog box

Purpose: Allows you to import a BED format track file. See "To import tracks" on page 20. Track information can appear in Gene View. See "Preferences – Tracks" on page 164.

To open: In the **Home** tab, click **Import > Track...**

Species Select the species to which the track relates. The program supports these species:

- *H. sapiens*
- *M. musculus*
- *R. norvegicus*

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 details, see "Choose Gene List Color" on page 117. You select track colors in exactly 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 that you want to import, or click **Browse...** to select a file.

Browse... Opens an Open dialog box, where you can select the BED track file that you want to import.

OK Imports the track into the program.

Cancel Cancels the import and closes the dialog box.

Microarray Properties - Attribute Tab

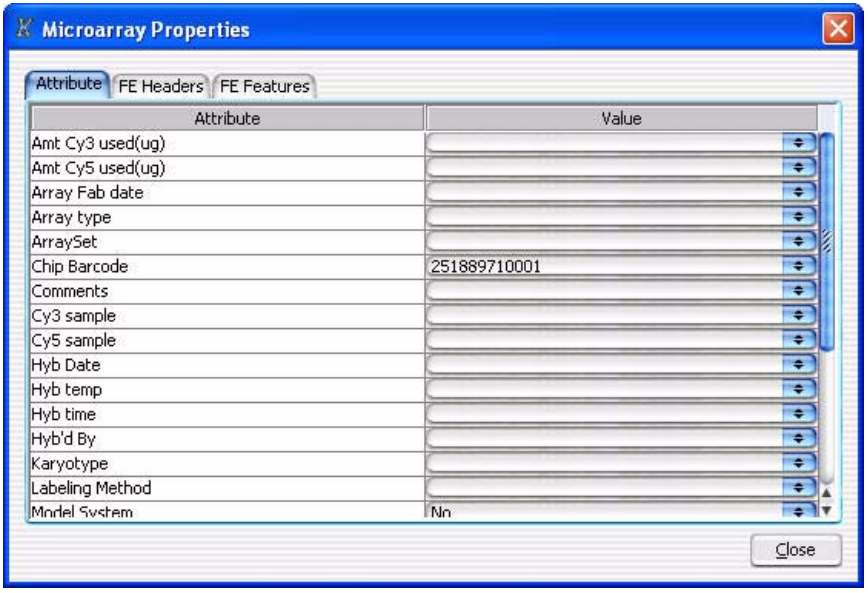


Figure 53 Microarray Properties dialog box listing Attributes and their values

Purpose: Lists the values of attributes associated with an array. You can also edit the values of specific attributes. To create a new attribute, 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

- **Attribute** — Lists 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.

For information about the options in the other tabs in this dialog box, see "Microarray Properties - FE Headers" on page 156, and "Microarray Properties - FE Features Tab" on page 155.

Microarray Properties - FE Features Tab

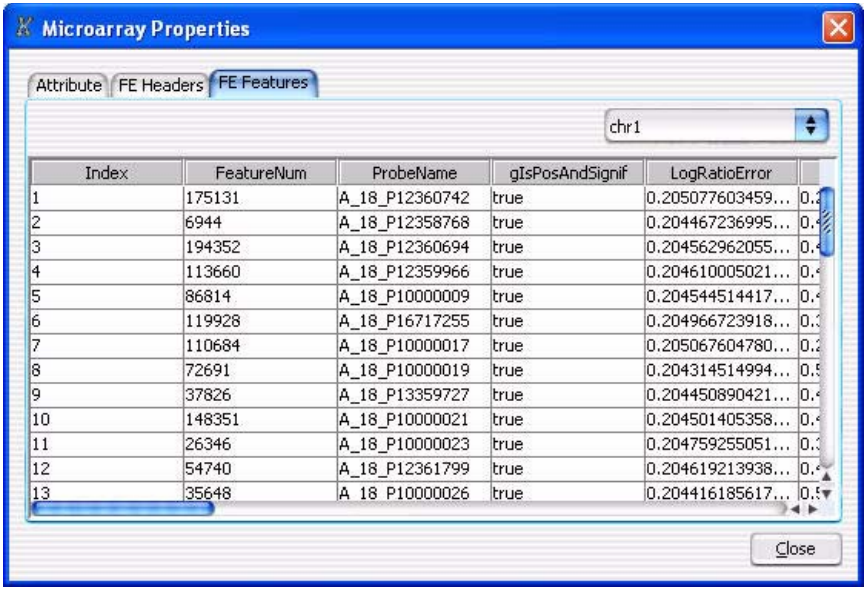


Figure 54 Microarray Properties dialog box listing FE Features and associated data

Purpose: Allows you to view feature information for arrays extracted with Agilent Feature Extraction software.

To open: Right-click an array name, then click **Show Properties.**

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

Microarray Properties - FE Headers

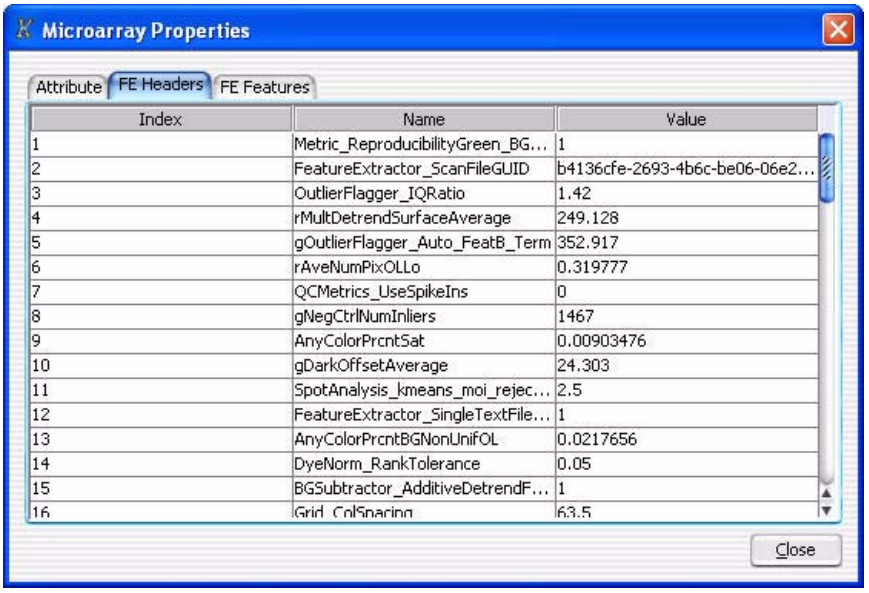


Figure 55 Microarray Properties dialog box listing FE Headers their values

Purpose: Allows you to view feature parameters, statistics and constants for an array extracted with Agilent Feature Extraction software.

To open: For Agilent arrays in the Data folder or Experiments folder, right-click the name of the array, then click **Show Properties.**

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.

MovAvg Example Parameters

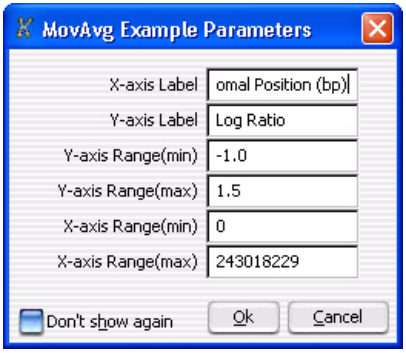


Figure 56 MovAvg Example Parameters dialog box

Purpose: This dialog box allows you to set display parameters for the MovAvg Example plug-in. The plug-in computes 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 beneath the X-axis of the plot as a label.
Y-axis Label	The text that appears beside 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 > 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 refine the appearance of the plot once the plug-in generates it.

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

The plug-in program itself (MovAvg Example.pl, located in the Plugins folder of the DNA Analytics installation folder on your computer) is a short Perl program. It is a good example of how computed columns are processed.

The plotting is very simple, but the simple plug-in architecture of MovAvg Example.pl allows you to 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 control 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 control 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

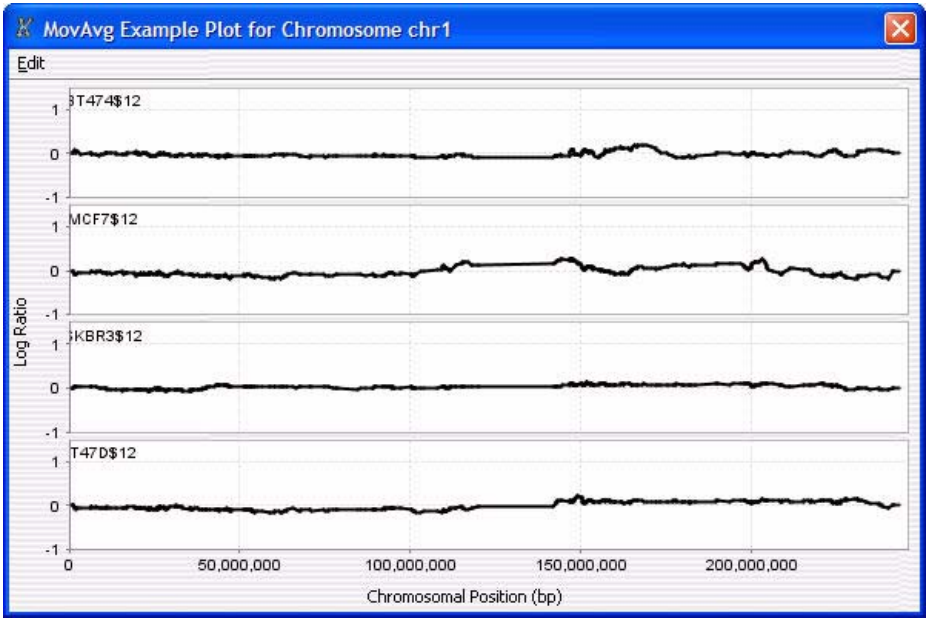


Figure 57 MovAvg Example Plot

Purpose: This plot displays the output of the MovAvg Example plug-in. The plug-in computes 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 157.

Plot(s) The main plotting 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 plotting area, a shortcut menu opens with these 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 110.
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 allows you to 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 zoom in on.
Zoom Out	Opens another menu that allows you to 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 allows you to zoom the plot to encompass 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 encompasses 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 encompass the full range of Y values of the data.

Preferences – License

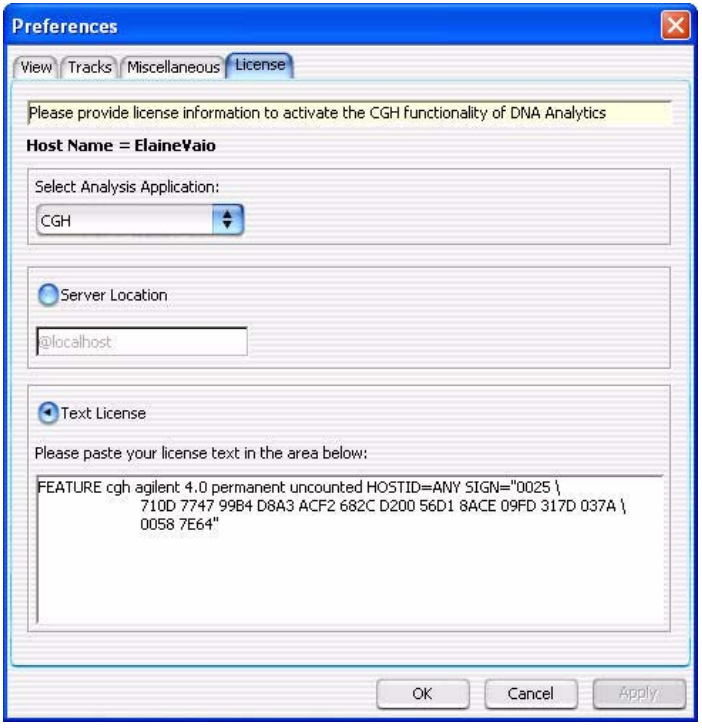


Figure 58 Preferences dialog box displaying License tab options

Purpose: To view and update the license for each application you have installed with the DNA Analytics software, if necessary.

To open: Right-click anywhere in the graphical interface, either in Genome View, Chromosome View or Gene View, click **Preferences** and click the **License** tab.

Host Name Displays the host name, automatically.

Select Analysis Application Select the DNA Analytics application for which you have a license.

Server Location Server location should be selected if you have a concurrent user license. If appropriate, click to enable and type in the name of your license server. The default is @localhost. Replace localhost with the name of the computer used as the license server. **Text License** is disabled (grayed) if **Server Location** is enabled.

Text License Text licenses are used if you have a workstation license. If you do have a workstation license, paste your license in the text box. If you have entered a license previously, it is displayed in the text box. **Server Location** is disabled (grayed) when **Text License** is enabled.

Apply Apply your changes to the parameters.

OK/Cancel Accept your changes and exit, or cancel all changes and return to the previously selected parameters.

Preferences – Miscellaneous

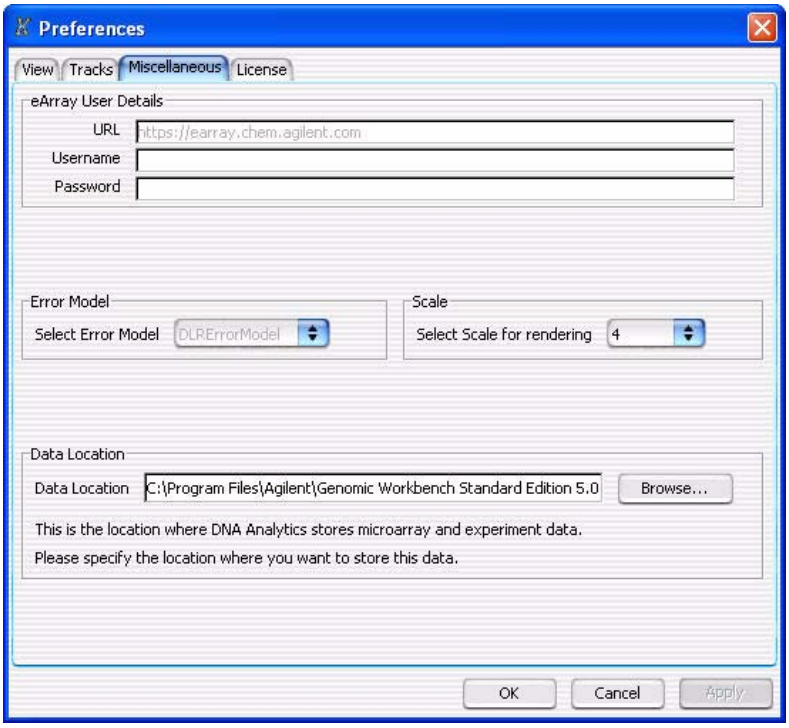


Figure 59 Preferences dialog box – Miscellaneous tab

Purpose: This dialog box allows you to set up eArray access and to change the location for data.

To open: In the **Home** tab, click **User Preferences...,** then click the **Miscellaneous** tab.

The following options are relevant to data/content set-up in Genomic Workbench. For information about the other tabs in this dialog box, see "Preferences – View Tab" on page 167, "Preferences – Tracks" on page 164 and "Preferences – License" on page 161.

eArray User Details

Sets login details for the Agilent eArray Web site.

- **URL** – At present, https://earray.chem.agilent.com and grayed out

- **Username** – The name registered on the eArray site.
- **Password** – The password registered on the eArray site.

Scale Select the scale for rendering the appearance of data in the display.

Data Location The folder where the program stores array data and design files. To select a location, click **Browse...**

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.

Preferences – Tracks

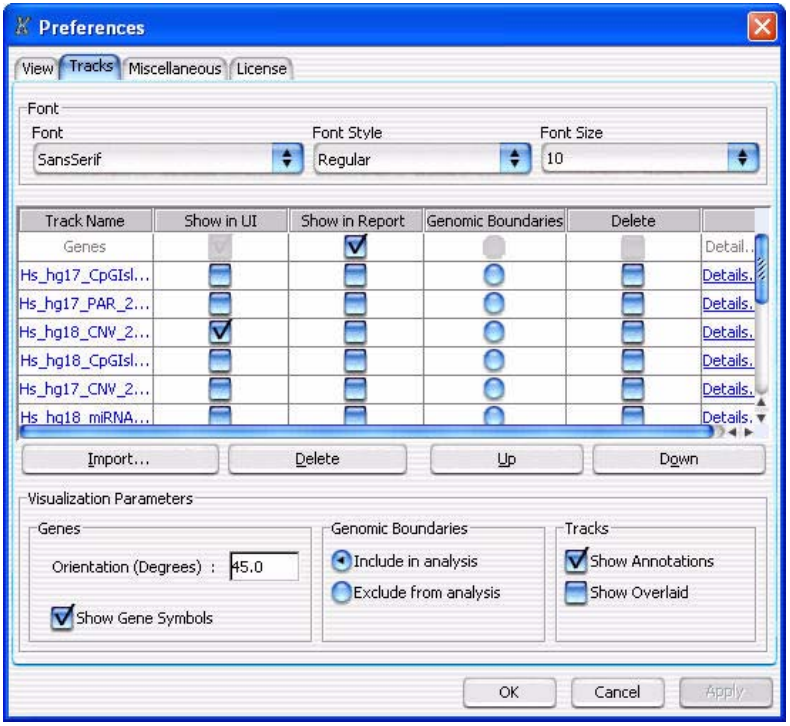


Figure 60 Preferences dialog box displaying Tracks Tab options

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 and that align with genomic coordinates in Gene View.

To open: Right-click anywhere in the graphical interface, either in Genome View, Chromosome View or Gene View, click **Preferences** and 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 view the track next to Gene View.

Show in Report Mark the check box to view 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 Click to delete the track from the list.

Details Click to view all the chromosome locations defined in the track.

Import Click to import new tracks.

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 Gene View.

- Orientation – Type in a number in degrees 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 them in Gene View, and clear the check box to hide them.

Genomic Boundaries These options allow you to 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 view the information in separate tracks.

Preferences – View Tab

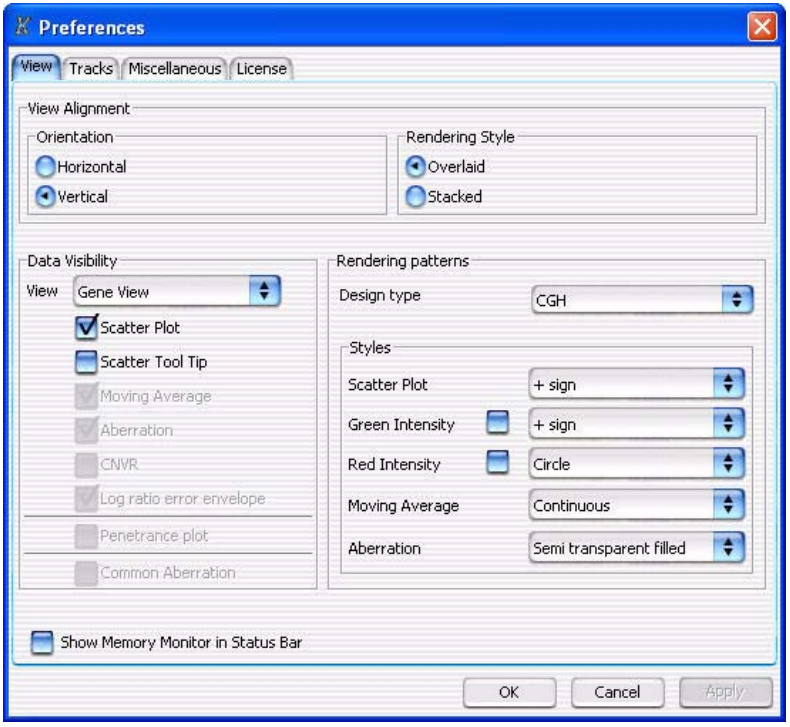


Figure 61 Preferences dialog box displaying View tab options for Data Viewing

Purpose: To set up how the Views are aligned and settings displayed for the scatter plot in Genome Viewer

To open: Right-click anywhere in the graphical interface, either in Genome View, Chromosome View or Gene View, click **Preferences** and click the **View** tab.

The View tab options control the general characteristics of how data are displayed on your monitor, but in Data Viewing all the data analysis options are grayed out.

View Alignment

Orientation Selects the orientation of three views in the main window:

- Horizontal – Reorients three views to a horizontal aspect in the order of Gene, Chromosome, and Genome views, top to bottom. The Navigator and Tab View orientation remains unchanged.
- Vertical – Displays all views in a vertical aspect, left to right: Navigator, Genome, Chromosome, and Gene views. This is the default display. See "Genomic Workbench Main Window" on page 66.

Rendering Style Selects the way Chromosome and Gene data are rendered on your screen.

- Overlaid – Displays data from multiple arrays superimposed one on top of another (default).
- Stacked – Displays data from each array in a separate plot.

Data Visibility

View Choose what features you want to display for the Genome, Chromosome, and Gene views, either individually or together. Select one or more check boxes:

- Scatter Plot
- Scatter Tool Tip (Gene View only)

Rendering patterns

Design type Specify the type of design to which you are applying these patterns: **CGH, Expression, or Other.**

Styles Set up the parameters for displaying your data.

- Scatter Plot -- Specify how to display individual data points as: **Color filled circles (ellipses), + signs, x signs, circles, rectangles** and **filled rectangles** for all the points or for red and/or green intensities**.**

NOTE Rendering scatter plots for more then 10 high density arrays in the Chromosome View may take significant time. Selecting ellipses as the rendering style for CGH scatter plots can also decrease performance. Please change the rendering style for CGH data from ellipse to the plus (+) or cross hair sign.

Apply Apply your changes to the parameters.

Scroll to Column

Figure 62 Scroll to Column dialog box

Purpose: This dialog box allows you to 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.

Search probes in eArray

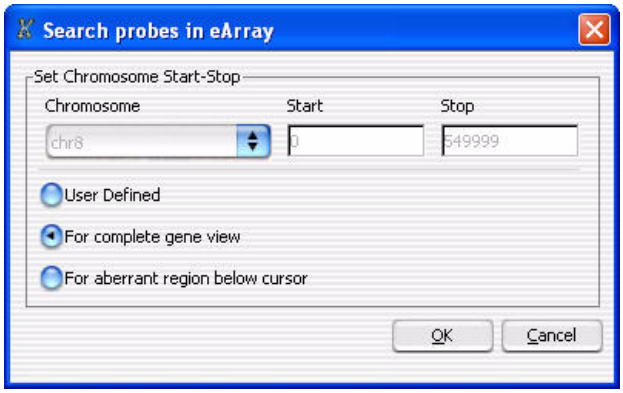


Figure 63 Search probes in eArray

Purpose: To select the probes you want to update in eArray

To open: Right-click Gene View, and click **Search probes in eArray**.

Select a chromosome and a region in Chromosome View for selecting the probes related to the genes in this region.

User Defined Select to choose the region from which the probes to be searched in eArray will be selected. The chromosome selection list and the Start and Stop positions on the Y axis are activated when this option is selected.

For complete gene view All the probes related to the genes in Gene View will be searched.

For aberrant region below cursor Selects those probes for the genes that appear just below where the cursor sits in Gene View. Not operational without a license.

Chromosome If you select User Defined, you can select a different chromosome than had been selected before opening this dialog box.

Start/Stop If you select User Defined, you can type in Start and Stop positions for defining the region contained the genes to be in the list.

Select Color (Edit Array Color) — Swatches Tab

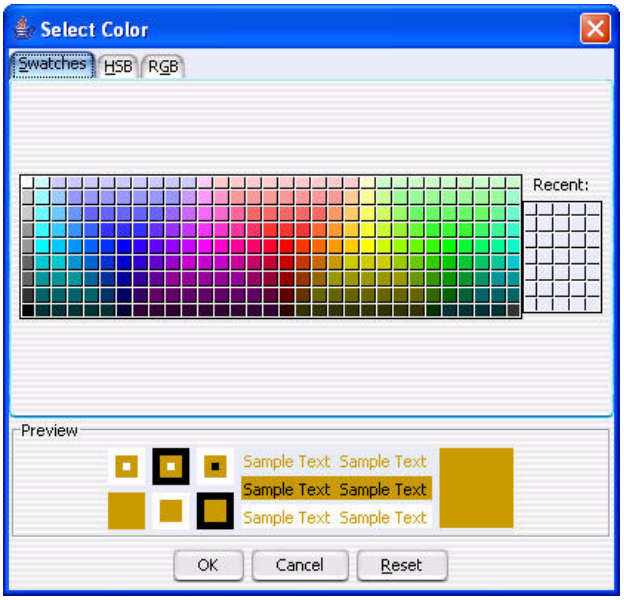


Figure 64 Select Color — Swatches Tab

Purpose: To select a color for each array based on color samples (swatches)

To open: Right-click on an array in an experiment, click **Edit Array Color** and click **Swatches** tab.

HSB Tab Choose colors based on an HSB schema (Hue, Saturation, and Brightness or Value). See

RGB Tab Choose colors based on an RGB schema (Red-Green-Blue).

Recent: Choose a recent color selection.

Reset Click to return HSB or RGB values back to default values.

Select Color (Edit Array Color) — HSB Tab

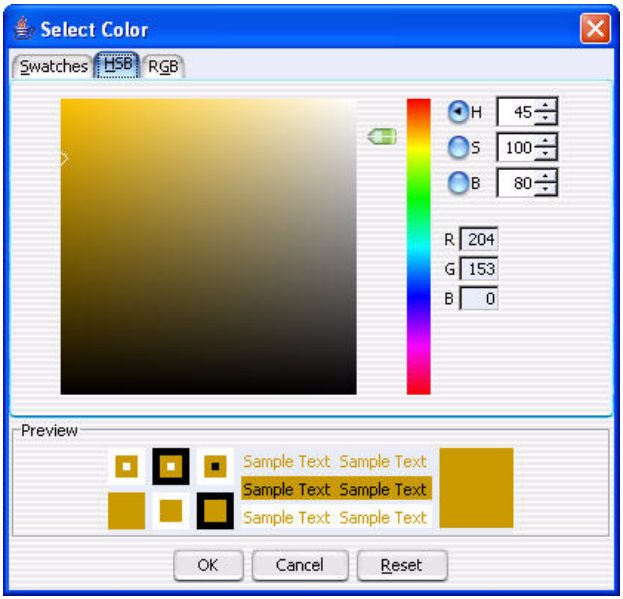


Figure 65 Select Color — HSB Tab

Purpose: To select a color for each array based on an HSB schema (Hue, Saturation, and Brightness)

To open: Right-click on an array in an experiment, click **Edit Array Color** and click **HSB** tab.

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.

Reset Click to return HSB values back to default values.

Select Color (Edit Array Color) — RGB Tab

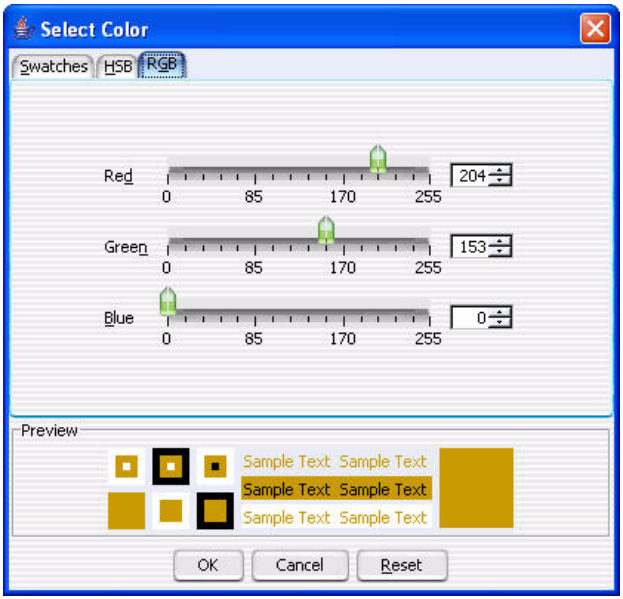


Figure 66 Select Color — RGB Tab

Purpose: To select a color for each array based on an RGB schema (Red- Green- Blue)

To open: Right- click on an array in an experiment, click **Edit Array Color** and click **RGB** tab.

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.

Reset Click to return RGB values back to default values.

Select data type for experiments (UDF files – CGH or CH3)

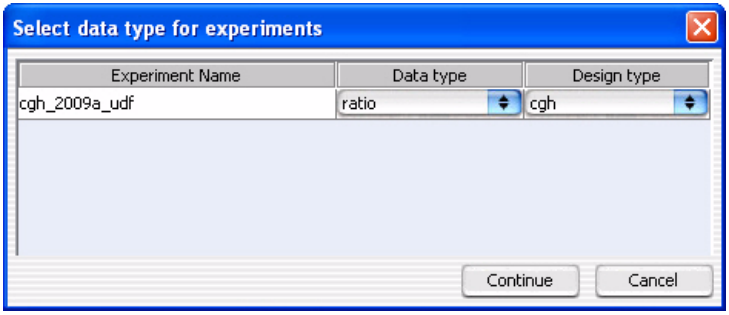


Figure 67 Select data type for experiments dialog box

Purpose: Allows you to 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 15.

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, ChIP, or expression, 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

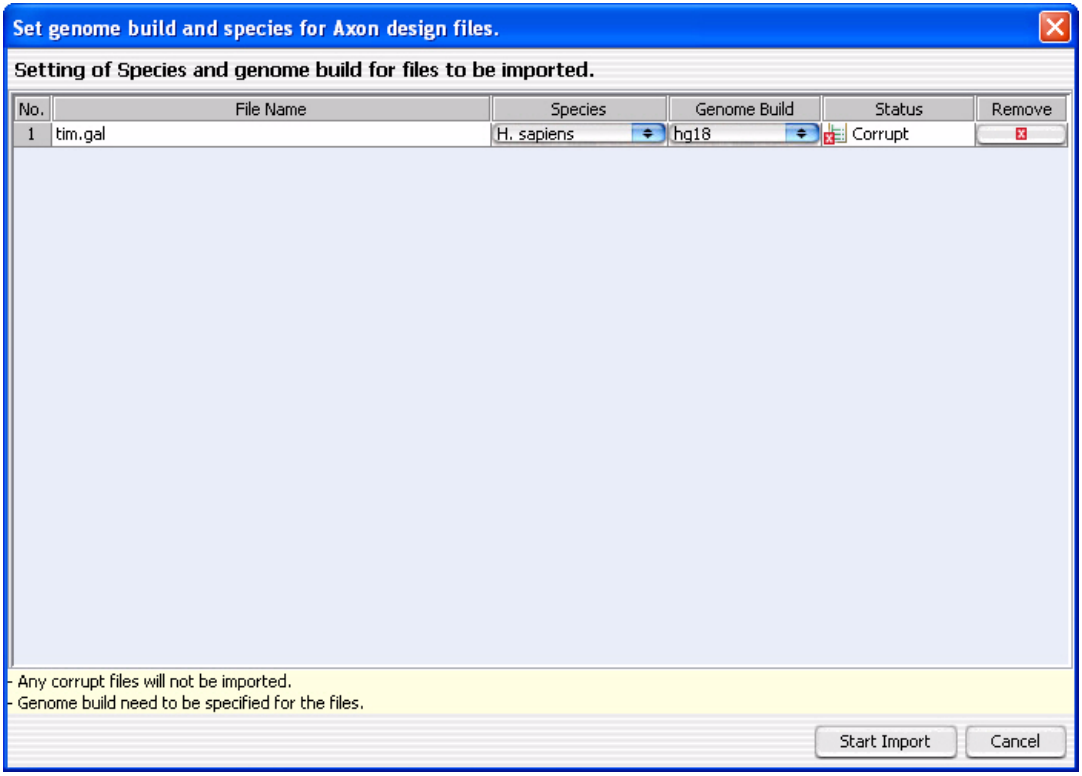


Figure 68 Set genome build and species for Axon design files dialog box

Purpose: Allows you to 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 GenePix/Axon design files" on page 19.

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.

Track

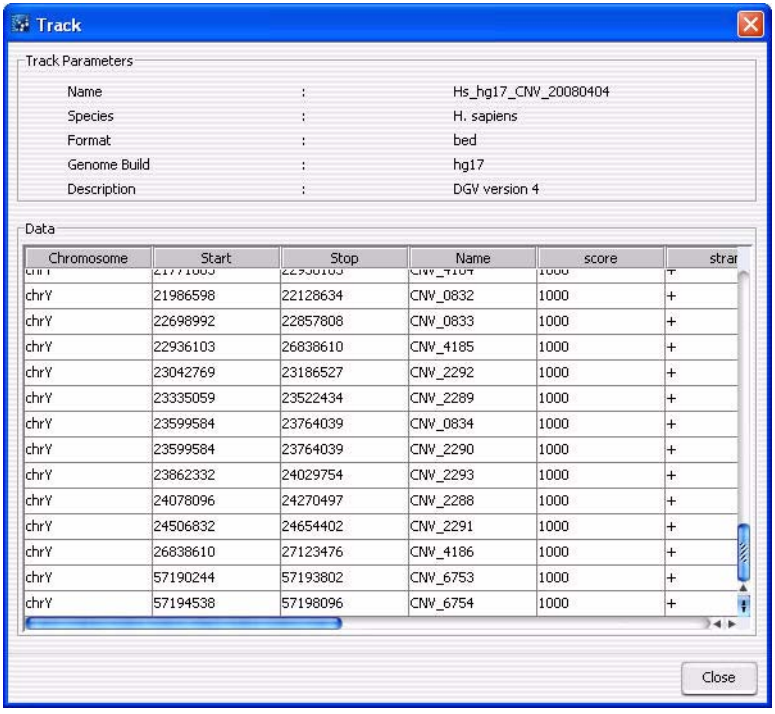


Figure 69 Track details

Purpose: This dialog box allows you to view the chromosome locations in the track.

To open: Click the **Details** link next to the desired track in the **Tracks** tab of the Preferences dialog box. See "Preferences – Tracks" on page 164.

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. DNA Analytics 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 alongside the defined region for the feature.

The other columns are additional BED track file columns that can appear for some tracks. DNA Analytics does not render these.

Close Closes the Track dialog box.

UDF Import Summary (CGH or CH3)

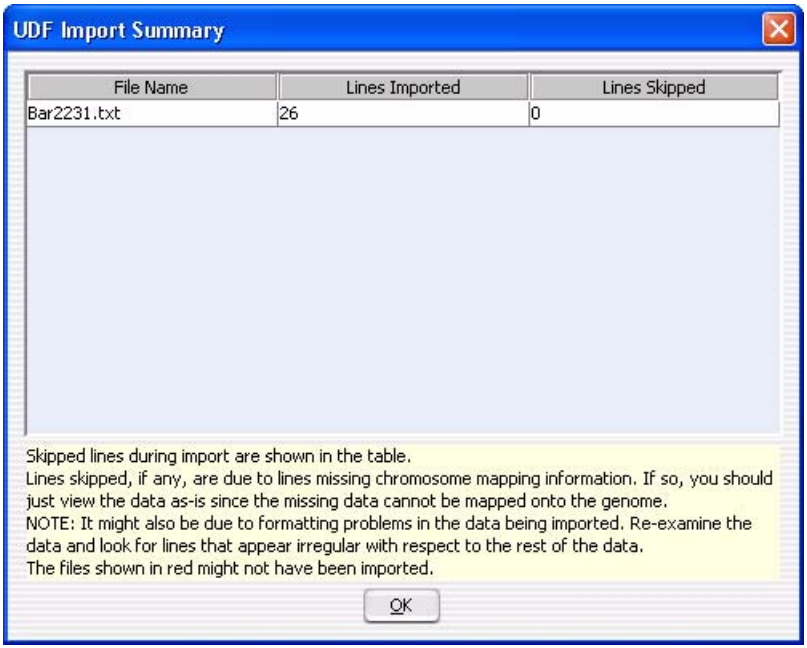


Figure 70 UDF Import Summary dialog box

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 15). 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, re-examine the data for improper formatting or missing chromosome mapping information.

OK Closes the dialog box.

Universal Data Importer - Map Column Headers

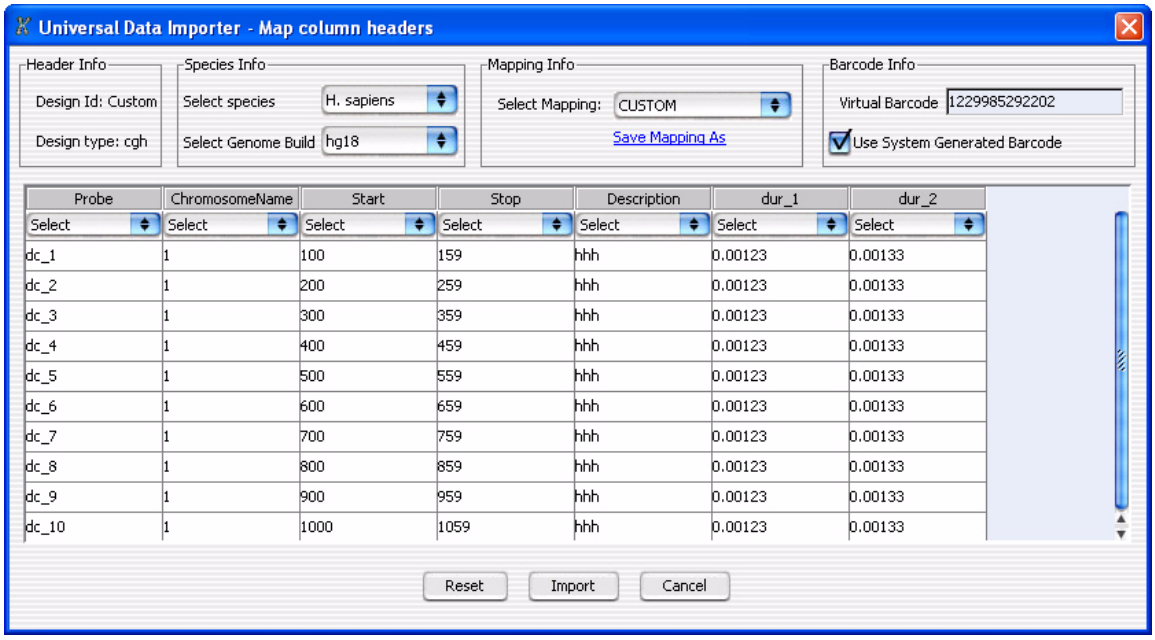


Figure 71 Universal Data Importer - Map Column Headers dialog box

Purpose: Allows you to set up a universal data file (UDF) for import. You specify 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 15), in the Select data type for experiments dialog box, click **Continue.** See "Select data type for experiments (UDF files – CGH or CH3)" on page 174.

Species Info

Select Species Select the species associated with the array data in the UDF. The program supports these species:

- *M. musculus*

- *H. sapiens*
- *R. norvegicus*

Select Genome Build Sets the species-specific build to use.

Mapping Info

Select Mapping Applies a previously saved 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.

Barcode Info

Virtual Barcode A number that uniquely identifies the data in the UDF. Typically, an Agilent microarray slide has a physical barcode that enables Genomic Workbench to track the data from the slide as it goes through the steps of an analysis workflow. A "virtual" barcode is, by default, a system-generated ID that serves the same purpose for data from UDFs. You can also specify a virtual barcode of your own choosing.

Use System Generated Barcode By default, the virtual barcode assigned to the array data in a UDF is a number that is generated internally by the program. To specify a virtual barcode of your own choosing, clear **Use System Generated Barcode,** then type a new number in **Virtual Barcode.**

Table

This table allows you to identify the contents of the columns of data in the UDF. The first row of the table lists 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.
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.

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 179).

Cancel Cancels the import and closes the dialog box.

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In This Book

This guide describes how to import, manage, export and display data and other content within Agilent Genomic Workbench.

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